Online Supplementary Material S1. The benchmark dataset used in this study contains 7329 sequences classified into 1070 superfamilies (SFs), which were extracted from the astral database and the identity of two sequences was lower than 95%.

>d1dlwa_ a.1.1.1 (A:) Truncated hemoglobin {Ciliate (Paramecium caudatum)}
SLFEQLGGQAAVQAVTAQFYANIQADATVATFFNGIDMPNQTNKTAAFLCAALGGPNAWTGRNLK
EVHANMGVSNAQFTTVIGHLRSALTGAGVAAALVEQTVAVAETVRGDVVTV
>d1dlya_ a.1.1.1 (A:) Truncated hemoglobin {Green alga (Chlamydomonas eugametos)}
SLFAKLGGREAVEAAVDKFYNKIVADPTVSTYFSNTDMKVQRSKQFAFLAYALGGASEWKGKDMR
TAHKDLVPHLSDVHFQAVARHLSDTLTELGVPPEDITDAMAVVASTRTEVLNMPQQ
>d1idra_ a.1.1.1 (A:) Truncated hemoglobin {Mycobacterium tuberculosis}
GLLSRLRKREPISIYDKIGGHEAIEVVVEDFYVRVLADDQLSAFFSGTNMSRLKGKQVEFFAAAL
GGPEPYTGAPMKQVHQGRGITMHHFSLVAGHLADALTAAGVPSETITEILGVIAPLAVDVTS
>d1scta_ a.1.1.2 (A:) Hemoglobin I {Ark clam (Scapharca inaequivalvis)}
VDAAVAKVCGSEAIKANLRRSWGVLSADIEATGLMLMSNLFTLRPDTKTYFTRLGDVQKGKANSK
LRGHAITLTYALNNFVDSLDDPSRLKCVVEKFAVNHINRKISGDAFGAIVEPMKETLKARMGNYY
SDDVAGAWAALVGVVQAAL
>d1sctb_ a.1.1.2 (B:) Hemoglobin I {Ark clam (Scapharca inaequivalvis)}
KVAELANAVVSNADQKDLLRMSWGVLSVDMEGTGLMLMANLFKTSPSAKGKFARLGDVSAGKDNS
KLRGHSITLMYALQNFVDALDDVERLKCVVEKFAVNHINRQISADEFGEIVGPLRQTLKARMGNY
FDEDTVAAWASLVAVVQASL
>d3sdha_ a.1.1.2 (A:) Hemoglobin I {Ark clam (Scapharca inaequivalvis)}
SVYDAAAQLTADVKKDLRDSWKVIGSDKKGNGVALMTTLFADNQETIGYFKRLGNVSQGMANDKL
RGHSITLMYALQNFIDQLDNPDDLVCVVEKFAVNHITRKISAAEFGKINGPIKKVLASKNFGDKY
ANAWAKLVAVVQAAL
>d1b0b__ a.1.1.2 (-) Hemoglobin I {Clam (Lucina pectinata)}
SLSAAQKDNVKSSWAKASAAWGTAGPEFFMALFDAHDDVFAKFSGLFSGAAKGTVKNTPEMAAQA
QSFKGLVSNWVDNLDNAGALEGQCKTFAANHKARGISAGQLEAAFKVLAGFMKSYGGDEGAWTAV
AGALMGMIRPDM
>d1h97a_ a.1.1.2 (A:) Trematode hemoglobin/myoglobin {Paramphistomum epiclitum}
TLTKHEQDILLKELGPHVDTPAHIVETGLGAYHALFTAHPQYISHFSRLEGHTIENVMQSEGIKH
YARTLTEAIVHMLKEISNDAEVKKIAAQYGKDHTSRKVTKDEFMSGEPIFTKYFQNLVKDAEGKA
AVEKFLKHVFPMMAAEI
>d1vrea_ a.1.1.2 (A:) Glycera globin {Marine bloodworm (Glycera dibranchiata)}
GLSAAQRQVVASTWKDIAGSDNGAGVGKECFTKFLSAHHDMAAVFGFSGASDPGVADLGAKVLAQ
IGVAVSHLGDEGKMVAEMKAVGVRHKGYGNKHIKAEYFEPLGASLLSAMEHRIGGKMNAAAKDAW

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AAAYADISGALISGLQS
>d2hbg__ a.1.1.2 (-) Glycera globin {Marine bloodworm (Glycera
dibranchiata)}
GLSAAQRQVIAATWKDIAGADNGAGVGKKCLIKFLSAHPQMAAVFGFSGASDPGVAALGAKVLAQ
IGVAVSHLGDEGKMVAQMKAVGVRHKGYGNKHIKAQYFEPLGASLLSAMEHRIGGKMNAAAKDAW
AAAYADISGALISGLQS
>d1a6m__ a.1.1.2 (-) Myoglobin {Sperm whale (Physeter catodon)}
VLSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDLKKHG
VTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPGDFGADAQGA
MNKALELFRKDIAAKYKELGY
>d1mba__ a.1.1.2 (-) Myoglobin {Sea hare (Aplysia limacina)}
SLSAAEADLAGKSWAPVFANKNANGLDFLVALFEKFPDSANFFADFKGKSVADIKASPKLRDVSS
RIFTRLNEFVNNAANAGKMSAMLSQFAKEHVGFGVGSAQFENVRSMFPGFVASVAAPPAGADAAW
TKLFGLIIDALKAAGA
>d1mbs__ a.1.1.2 (-) Myoglobin {Common seal (Phoca vitulina)}
GLSDGEWHLVLNVWGKVETDLAGHGQEVLIRLFKSHPETLEKFDKFKHLKSEDDMRRSEDLRKHG
NTVLTALGGILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSKHPAEFGADAQAA
MKKALELFRNDIAAKYKELGFHG
>d1mwca_ a.1.1.2 (A:) Myoglobin {Pig (Sus scrofa)}
GLSDGEWQLVLNVWGKVEADVAGHGQEVLIRLFKGHPETLEKFDKFKHLKSEDEMKASEDLKKHG
NTVLTALGGILKKKGHHEAELTPLAQSHATKHKIPVKYLEFISEAIIQVLQSKHPGDFGADAQGA
MSKALELFRNDMAAKYKELGFQG
>d1dwta_ a.1.1.2 (A:) Myoglobin {Horse (Equus caballus)}
GLSDGEWQQVLNVWGKVEADIAGHGQEVLIRLFTGHPETLEKFDKFKHLKTEAEMKASEDLKKHG
TVVLTALGGILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISDAIIHVLHSKHPGDFGADAQGA
MTKALELFRNDIAAKYKELGFQ
>d2mm1__ a.1.1.2 (-) Myoglobin {Human (Homo sapiens)}
GLSDGEWQLVLNVWGKVEADIPGHGQEVLIRLFKGHPETLEKFDRFKHLKSEDEMKASEDLKKHG
ATVLTALGGILKKKGHHEAEIKPLAQSHATKHKIPVKYLEFISEAIIQVLQSKHPGDFGADAQGA
MNKALELFRKDMASNYKELGFQG
>d1emy__ a.1.1.2 (-) Myoglobin {Asian elephant (Elephas maximus)}
GLSDGEWELVLKTWGKVEADIPGHGETVFVRLFTGHPETLEKFDKFKHLKTEGEMKASEDLKKQG
VTVLTALGGILKKKGHHEAEIQPLAQSHATKHKIPIKYLEFISDAIIHVLQSKHPAEFGADAQGA
MKKALELFRNDIAAKYKELGFQG
>d1lht__ a.1.1.2 (-) Myoglobin {Loggerhead sea turtle (Caretta
caretta)}
GLSDDEWNHVLGIWAKVEPDLSAHGQEVIIRLFQLHPETQERFAKFKNLTTIDALKSSEEVKKHG
TTVLTALGRILKQKNNHEQELKPLAESHATKHKIPVKYLEFICEIIVKVIAEKHPSDFGADSQAA
MKKALELFRNDMASKYKEFGFQG
>d1myt__ a.1.1.2 (-) Myoglobin {Yellowfin tuna (Thunnus albacares)}
ADFDAVLKCWGPVEADYTTMGGLVLTRLFKEHPETQKLFPKFAGIAQADIAGNAAISAHGATVLK
KLGELLKAKGSHAAILKPLANSHATKHKIPINNFKLISEVLVKVMHEKAGLDAGGQTALRNVMGI
IIADLEANYKELGFSG
>d1eco__ a.1.1.2 (-) Erythrocruorin {Midge (Chironomus thummi thummi),
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fraction III}
LSADQISTVQASFDKVKGDPVGILYAVFKADPSIMAKFTQFAGKDLESIKGTAPFETHANRIVGF
FSKIIGELPNIEADVNTFVASHKPRGVTHDQLNNFRAGFVSYMKAHTDFAGAEAAWGATLDTFFG
MIFSKM
>d2gdm__ a.1.1.2 (-) Leghemoglobin {Yellow lupin (Lupinus luteus)}
GALTESQAALVKSSWEEFNANIPKHTHRFFILVLEIAPAAKDLFSFLKGTSEVPQNNPELQAHAG
KVFKLVYEAAIQLEVTGVVVTDATLKNLGSVHVSKGVADAHFPVVKEAILKTIKEVVGAKWSEEL
NSAWTIAYDELAIVIKKEMDDAA
>d1fsla_ a.1.1.2 (A:) Leghemoglobin {Soybean (Glycine max), isoform
A}
VAFTEKQDALVSSSFEAFKANIPQYSVVFYTSILEKAPAAKDLFSFLANGVDPTNPKLTGHAEKL
FALVRDSAGQLKASGTVVADAALGSVHAQKAVTDPQFVVVKEALLKTIKAAVGDKWSDELSRAWE
VAYDELAAAIKKA
>d1d8ua_ a.1.1.2 (A:) Non-symbiotic plant hemoglobin {Rice (Oryza
sativa)}
ALVEDNNAVAVSFSEEQEALVLKSWAILKKDSANIALRFFLKIFEVAPSASQMFSFLRNSDVPLE
KNPKLKTHAMSVFVMTCEAAAQLRKAGKVTVRDTTLKRLGATHLKYGVGDAHFEVVKFALLDTIK
EEVPADMWSPAMKSAWSEAYDHLVAAIKQEMKPAE
>d1i3da_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Human (Homo sapiens)}
GHFTEEDKATITSLWGKVNVEDAGGETLGRLLVVYPWTQRFFDSFGNLSSASAIMGNPKVKAHGK
KVLTSLGDAIKHLDDLKGTFAQLSELHCDKLHVDPENFKLLGNVLVTVLAIHFGKEFTPEVQASW
QKMVTAVASALSSRYH
>d1irda_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Human (Homo sapiens)}
VLSPADKTNVKAAWGKVGAHAGEYGAEALERMFLSFPTTKTYFPHFDLSHGSAQVKGHGKKVADA
LTNAVAHVDDMPNALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLA
SVSTVLTSKYR
>d1jeba_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Human (Homo sapiens),
zeta isoform}
SLTKTERTIIVSMWAKISTQADTIGTETLERLFLSHPQTKTYFPHFDLHPGSAQLRAHGSKVVAA
VGDAVKSIDDIGGALSKLSELHAYILRVDPVNFKLLSHCLLVTLAARFPADFTAEAHAAWDKFLS
VVSSVLTEKYR
>d1ibea_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Horse (Equus
caballus)}
VLSAADKTNVKAAWSKVGGHAGEFGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGKKVGDA
LTLAVGHLDDLPGALSDLSNLHAHKLRVDPVNFKLLSHCLLSTLAVHLPNDFTPAVHASLDKFLS
SVSTVLTSKYR
>d1hdsa_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Deer (Odocoileus
virginianus)}
VLSAANKSNVKAAWGKVGGNAPAYGAQALQRMFLSFPTTKTYFPHFDLSHGSAQQKAHGQKVANA
LTKAQGHLNDLPGTLSNLSNLHAHKLRVNPVNFKLLSHSLLVTLASHLPTNFTPAVHANLNKFLA
NDSTVLTSKYR
>d1g08a_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Cow (Bos taurus)}
VLSAADKGNVKAAWGKVGGHAAEYGAEALERMFLSFPTTKTYFPHFDLSHGSAQVKGHGAKVAAA
LTKAVEHLDDLPGALSELSDLHAHKLRVDPVNFKLLSHSLLVTLASHLPSDFTPAVHASLDKFLA
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NVSTVLTSKYR
>d1qpwa_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Pig (Sus scrofa)}
VLSAADKANVKAAWGKVGGQAGAHGAEALERMFLGFPTTKTYFPHFNLSHGSDQVKAHGQKVADA
LTKAVGHLDDLPGALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHHPDDFNPSVHASLDKFLA
NVSTVLTSKYR
>d1fhja_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Maned wolf (Chrysocyon
brachyurus)}
VLSPADKTNIKSTWDKIGGHAGDYGGEALDRTFQSFPTTKTYFPHFDLSPGSAQVKAHGKKVADA
LTTAVAHLDDLPGALSALSDLHAYKLRVDPVNFKLLSHCLLVTLACHHPTEFTPAVHASLDKFFT
AVSTVLTSKYR
>d1hbra_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Chicken (Gallus
gallus)}
MLTAEDKKLIQQAWEKAASHQEEFGAEALTRMFTTYPQTKTYFPHFDLSPGSDQVRGHGKKVLGA
LGNAVKNVDNLSQAMAELSNLHAYNLRVDPVNFKLLSQCIQVVLAVHMGKDYTPEVHAAFDKFLS
AVSAVLAEKYR
>d1a4fa_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Bar-headed goose
(Anser indicus)}
VLSAADKTNVKGVFSKISGHAEEYGAETLERMFTAYPQTKTYFPHFDLQHGSAQIKAHGKKVVAA
LVEAVNHIDDIAGALSKLSDLHAQKLRVDPVNFKFLGHCFLVVVAIHHPSALTAEVHASLDKFLC
AVGTVLTAKYR
>d1outa_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Trout (Oncorhynchus
mykiss)}
SLTAKDKSVVKAFWGKISGKADVVGAEALGRMLTAYPQTKTYFSHWADLSPGSGPVKKHGGIIMG
AIGKAVGLMDDLVGGMSALSDLHAFKLRVDPGNFKILSHNILVTLAIHFPSDFTPEVHIAVDKFL
AAVSAALADKYR
>d1cg5a_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Cartilaginous fish
akaei (Dasyatis akajei)}
VLSSQNKKAIEELGNLIKANAEAWGADALARLFELHPQTKTYFSKFSGFEACNEQVKKHGKRVMN
ALADATHHLDNLHLHLEDLARKHGENLLVDPHNFHLFADCIVVTLAVNLQAFTPVTHCAVDKFLE
LVAYELSSCYR
>d1t1na_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Fish (Trematomus
newnesi)}
SLSDKDKAAVRALWSKIGKSSDAIGNDALSRMIVVYPQTKIYFSHWPDVTPGSPNIKAHGKKVMG
GIALAVSKIDDLKTGLMELSEQHAYKLRVDPSNFKILNHCILVVISTMFPKEFTPEAHVSLDKFL
SGVALALAERYR
>d1spga_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Teleost fish
(Leiostomus xanthurus)}
SLSATDKARVKALWDKIEGKSAELGAEALGRMLVSFPQTKIYFSEWGQDLGPQTPQVRNHGAVIM
AAVGKAVKSIDNLVGGLSQLSELHAFKLRVDPANFKILAHNIILVISMYFPGDFTPEVHLSVDKF
LACLALALSEKYR
>d1gcva_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Houndshark (Mustelus
griseus)}
AFTACEKQTIGKIAQVLAKSPEAYGAECLARLFVTHPGSKSYFEYKDYSAAGAKVQVHGGKVIRA
VVKAAEHVDDLHSHLETLALTHGKKLLVDPQNFPMLSECIIVTLATHLTEFSPDTHCAVDKLLSA
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ICQELSSRYR
>d1irdb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Human (Homo sapiens)}
VHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPKVKAHGK
KVLGAFSDGLAHLDNLKGTFATLSELHCDKLHVDPENFRLLGNVLVCVLAHHFGKEFTPPVQAAY
QKVVAGVANALAHKYH
>d1a9we_ a.1.1.2 (E:) Hemoglobin, beta-chain {Human (Homo sapiens), embryonic gower II}
VHFTAEEKAAVTSLWSKMNVEEAGGEALGRLLVVYPWTQRFFDSFGNLSSPSAILGNPKVKAHGK
KVLTSFGDAIKNMDNLKPAFAKLSELHCDKLHVDPENFKLLGNVMVIILATHFGKEFTPEVQAAW
QKLVSAVAIALAHKY
>d1ibeb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Horse (Equus caballus)}
VQLSGEEKAAVLALWDKVNEEEVGGEALGRLLVVYPWTQRFFDSFGDLSNPGAVMGNPKVKAHGK
KVLHSFGEGVHHLDNLKGTFAALSELHCDKLHVDPENFRLLGNVLVVVLARHFGKDFTPELQASY
QKVVAGVANALAHKYH
>d1hdsb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Deer (Odocoileus virginianus)}
MLTAEEKAAVTGFWGKVDVDVVGAQALGRLLVVYPWTQRFFQHFGNLSSAGAVMNNPKVKAHGKR
VLDAFTQGLKHLDDLKGAFAQLSGLHCNKLHVNPQNFRLLGNVLALVVARNFGGQFTPNVQALFQ
KVVAGVANALAHKYH
>d1g08b_ a.1.1.2 (B:) Hemoglobin, beta-chain {Cow (Bos taurus)}
MLTAEEKAAVTAFWGKVKVDEVGGEALGRLLVVYPWTQRFFESFGDLSTADAVMNNPKVKAHGKK
VLDSFSNGMKHLDDLKGTFAALSELHCDKLHVDPENFKLLGNVLVVVLARNFGKEFTPVLQADFQ
KVVAGVANALAHRYH
>d1qpwb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Pig (Sus scrofa)}
VHLSAEEKEAVLGLWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSNADAVMGNPKVKAHGK
KVLQSFSDGLKHLDNLKGTFAKLSELHCDQLHVDPENFRLLGNVIVVVLARRLGHDFNPDVQAAF
QKVVAGVANALAHKYH
>d1fhjb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Maned wolf (Chrysocyon brachyurus)}
VHLTAEEKSLVSGLWGKVNVDEVGGEALGRLLIVYPWTQRFFDSFGDLSTPDAVMSNAKVKAHGK
KVLNSFSDGLKNLDNLKGTFAKLSELHCDKLHVDPENFKLLGNVLVCVLAHHFGKEFTPQVQAAY
QKVVAGVANALAHKYH
>d1jebb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Mouse (Mus musculus)}
VHLTDAEKAAVSGLWGKVNADEVGGEALGRLLVVYPWTQRYFDSFGDLSSASAIMGNAKVKAHGK
KVITAFNDGLNHLDSLKGTFASLSELHCDKLHVDPENFRLLGNMIVIVLGHHLGKDFTPAAQAAF
QKVVAGVAAALAH
>d1hbrb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Chicken (Gallus gallus)}
VHWTAEEKQLITGLWGKVNVAECGAEALARLLIVYPWTQRFFASFGNLSSPTAILGNPMVRAHGK
KVLTSFGDAVKNLDNIKNTFSQLSELHCDKLHVDPENFRLLGDILIIVLAAHFSKDFTPECQAAW
QKLVRVVAHALARK
>d1a4fb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Bar-headed goose (Anser indicus)}
VHWSAEEKQLITGLWGKVNVADCGAEALARLLIVYPWTQRFFSSFGNLSSPTAILGNPMVRAHGK
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KVLTSFGDAVKNLDNIKNTFAQLSELHCDKLHVDPENFRLLGDILIIVLAAHFAKEFTPDCQAAW
QKLVRVVAHALARKYH
>d1outb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Trout (Oncorhynchus mykiss)}
VEWTDAEKSTISAVWGKVNIDEIGPLALARVLIVYPWTQRYFGSFGNVSTPAAIMGNPKVAAHGK
VVCGALDKAVKNMGNILATYKSLSETHANKLFVDPDNFRVLADVLTIVIAAKFGASFTPEIQATW
QKFMKVVVAAMGSRYF
>d1pbxb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Antarctic fish (Pagothenia bernacchii)}
VEWTDKERSIISDIFSHMDYDDIGPKALSRCLIVYPWTQRHFSGFGNLYNAEAIIGNANVAAHGI
KVLHGLDRGVKNMDNIAATYADLSTLHSEKLHVDPDNFKLLSDCITIVLAAKMGHAFTAETQGAF
QKFLAVVVSALGKQYH
>d1cg5b_ a.1.1.2 (B:) Hemoglobin, beta-chain {Cartilaginous fish akaei (Dasyatis akajei)}
VKLSEDQEHYIKGVWKDVDHKQITAKALERVFVVYPWTTRLFSKLQGLFSANDIGVQQHADKVQR
ALGEAIDDLKKVEINFQNLSGKHQEIGVDTQNFKLLGQTFMVELALHYKKTFRPKEHAAAYKFFR
LVAEALSSNYH
>d1t1nb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Fish (Trematomus newnesi)}
VEWTDKERSIISDIFSHMDYDDIGPKALSRCLVVYPWTQRYFSGFGNLYNAEGIMSNANVAAHGI
KVLHGLDRGMKNMDNIADAYTDLSTLHSEKLHVDPDNFKLLSDCITIVLAAKMGHAFTAETQGAF
QKFLAAVVSALGKQYH
>d1spgb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Teleost fish (Leiostomus xanthurus)}
VDWTDAERAAIKALWGKIDVGEIGPQALSRLLIVYPWTQRHFKGFGNISTNAAILGNAKVAEHGK
TVMGGLDRAVQNMDNIKNVYKQLSIKHSEKIHVDPDNFRLLGEIITMCVGAKFGPSAFTPEIHEA
WQKFLAVVVSALGRQYH
>d1gcvb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Houndshark (Mustelus griseus)}
VHWTQEERDEISKTFQGTDMKTVVTQALDRMFKVYPWTNRYFQKRTDFRSSIHAGIVVGALQDAV
KHMDDVKTLFKDLSKKHADDLHVDPGSFHLLTDCIIVELAYLRKDCFTPHIQGIWDKFFEVVIDA
ISKQYH
>d1ch4a_ a.1.1.2 (A:) Chimeric hemoglobin beta-alpha {Synthetic, based on Homo sapiens sequence}
VHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPKVKAHGK
KVLGAFSDGLAHLDNLKGTFATLSELHCDKLRVDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASL
DKVLASVSTVLTSKYR
>d1it2a_ a.1.1.2 (A:) Hagfish hemoglobin {Inshore hagfish (Eptatretus burgeri)}
PIIDQGPLPTLTDGDKKAINKIWPKIYKEYEQYSLNILLRFLKCFPQAQASFPKFSTKKSNLEQD
PEVKHQAVVIFNKVNEIINSMDNQEEIIKSLKDLSQKHKTVFKVDSIWFKELSSIFVSTIDGGAE
FEKLFSIICILLRSAY
>d2lhb__ a.1.1.2 (-) Lamprey globin {Sea lamprey (Petromyzon marinus)}
PIVDTGSVAPLSAAEKTKIRSAWAPVYSTYETSGVDILVKFFTSTPAAQEFFPKFKGLTTADELK
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KSADVRWHAERIINAVDDAVASMDDTEKMSMKLRNLSGKHAKSFQVDPEYFKVLAAVIADTVAAG
DAGFEKLMSMICILLRSAY
>d1ash__ a.1.1.2 (-) Ascaris hemoglobin, domain 1 {Pig roundworm (Ascaris suum)}
ANKTRELCMKSLEHAKVDTSNEARQDGIDLYKHMFENYPPLRKYFKSREEYTAEDVQNDPFFAKQ
GQKILLACHVLCATYDDRETFNAYTRELLDRHARDHVHMPPEVWTDFWKLFEEYLGKKTTLDEPT
KQAWHEIGREFAKEINK
>d1itha_ a.1.1.2 (A:) Hemoglobin {Innkeeper worm (Urechis caupo)}
GLTAAQIKAIQDHWFLNIKGCLQAAADSIFFKYLTAYPGDLAFFHKFSSVPLYGLRSNPAYKAQT
LTVINYLDKVVDALGGNAGALMKAKVPSHDAMGITPKHFGQLLKLVGGVFQEEFSADPTTVAAWG
DAAGVLVAAMK
>d1hlb__ a.1.1.2 (-) Hemoglobin, different isoforms {Sea cucumber (Caudina (Molpadia) arenicola)}
GGTLAIQAQGDLTLAQKKIVRKTWHQLMRNKTSFVTDVFIRIFAYDPSAQNKFPQMAGMSASQLR
SSRQMQAHAIRVSSIMSEYVEELDSDILPELLATLARTHDLNKVGADHYNLFAKVLMEALQAELG
SDFNEKTRDAWAKAFSVVQAVLLVKHG
>d1hlm__ a.1.1.2 (-) Hemoglobin, different isoforms {Sea cucumber (Caudina (Molpadia) arenicola)}
GATQSFQSVGDLTPAEKDLIRSTWDQLMTHRTGFVADVFIRIFHNDPTAQRKFPQMAGLSPAELR
TSRQMHAHAIRVSALMTTYIDEMDTEVLPELLATLTRTHDKNHVGKKNYDLFGKVLMEAIKAELG
VGFTKQVHDAWAKTFAIVQGVLITKHAS
>d1vhba_ a.1.1.2 (A:) Bacterial dimeric hemoglobin {Vitreoscilla stercoraria}
LDQQTINIIKATVPVLKEHGVTITTTFYKNLFAKHPEVRPLFDMGRQESLEQPKALAMTVLAAAQ
NIENLPAILPAVKKIAVKHCQAGVAAAHYPIVGQELLGAIKEVLGDAATDDILDAWGKAYGVIAD
VFIQVEADLYAQAV
>d1cqxa1 a.1.1.2 (A:1-150) Flavohemoglobin, N-terminal domain {Alcaligenes eutrophus}
MLTQKTKDIVKATAPVLAEHGYDIIKCFYQRMFEAHPELKNVFNMAHQEQGQQQQALARAVYAYA
ENIEDPNSLMAVLKNIANKHASLGVKPEQYPIVGEHLLAAIKEVLGNAATDDIISAWAQAYGNLA
DVLMGMESELYERSAEQPGG
>d1ew6a_ a.1.1.2 (A:) Dehaloperoxidase {Marine worm (Amphitrite ornata)}
GFKQDIATIRGDLRTYAQDIFLAFLNKYPDERRYFKNYVGKSDQELKSMAKFGDHTEKVFNLMME
VADRATDCVPLASDANTLVQMKQHSSLTTGNFEKLFVALVEYMRASGQSFDSQSWDRFGKNLVSA
LSSAGMK
>d1phna_ a.1.1.3 (A:) Phycocyanin {Red alga (Cyanidium caldarium)}
MKTPITEAIAAADNQGRFLSNTELQAVNGRYQRAAASLEAARSLTSNAERLINGAAQAVYSKFPY
TSQMPGPQYASSAVGKAKCARDIGYYLRMVTYCLVVGGTGPMDEYLIAGLEEINRTFDLSPSWYV
EALNYIKANHGLSGQAANEANTYIDYAINALS
>d1phnb_ a.1.1.3 (B:) Phycocyanin {Red alga (Cyanidium caldarium)}
MLDAFAKVVAQADARGEFLSNTQLDALSKMVSEGNKRLDVVNRITSNASAIVTNAARALFSEQPQ
LIQPGGNAYTNRRMAACLRDMEIILRYVSYAIIAGDSSILDDRCLNGLRETYQALGVPGASVAVG
IEKMKDSAIAIANDPSGITTGDCSALMAEVGTYFDRAATAVQ
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>d1f99a_ a.1.1.3 (A:) Phycocyanin {Red alga (Polysiphonia urceolata)}
MKTPLTEAIAAADSQGRFLSNTELQVVNGRYNRATSSLEAAKALTANADRLISGAANAVYSKFPY
TTQMPGPNYSSTAIGKAKCARDIGYYLRMVTYCLVVGGTGPMDDYLVAGLEEINRTFELSPSWYI
EALKYIKNNHGLSGDVANEANTYIDYAINTLS
>d1f99b_ a.1.1.3 (B:) Phycocyanin {Red alga (Polysiphonia urceolata)}
MLDAFAKVVAQADARGEFLSNTQIDALLAIVSEGNKRLDVVNKITNNASAIVTNAARALFAEQPQ
LISPGGNAYTSRRMAACLRDMEIVLRYVSYAMIAGDASVLDDRCLNGLRETYQALGTPGASVAVA
IQKMKDAALALVNDTTGTPAGDCASLVAEIATYFDRAAAAVA
>d1cpca_ a.1.1.3 (A:) Phycocyanin {Cyanobacterium (Fremyella diplosiphon)}
MKTPLTEAVAAADSQGRFLSSTEIQTAFGRFRQASASLAAAKALTEKASSLASGAANAVYSKFPY
TTSQNGPNFASTQTGKDKCVRDIGYYLRMVTYCLVVGGTGPLDDYLIGGIAEINRTFDLSPSWYV
EALKYIKANHGLSGDPAVEANSYIDYAINALS
>d1cpcb_ a.1.1.3 (B:) Phycocyanin {Cyanobacterium (Fremyella diplosiphon)}
MLDAFAKVVSQADARGEYLSGSQIDALSALVADGNKRMDVVNRITGNSSTIVANAARSLFAEQPQ
LIAPGGNAYTSRRMAACLRDMEIILRYVTYAIFAGDASVLDDRCLNGLKETYLALGTPGSSVAVG
VQKMKDAALAIAGDTNGITRGDCASLMAEVASYFDKAASAVA
>d1i7ya_ a.1.1.3 (A:) Phycocyanin {Synechococcus vulcanus}
MKTPITEAIAAADTQGRFLSNTELQAVDGRFKRAVASMEAARALTNNAQSLIDGAAQAVYQKFPY
TTTMQGSQYASTPEGKAKCARDIGYYLRMITYCLVAGGTGPMDEYLIAGLSEINSTFDLSPSWYI
EALKYIKANHGLTGQAAVEANAYIDYAINALS
>d1i7yb_ a.1.1.3 (B:) Phycocyanin {Synechococcus vulcanus}
MLDAFAKVVAQADARGEFLTNAQFDALSNLVKEGNKRLDAVNRITSNASTIVANAARALFAEQPQ
LIQPGGNAYTNRRMAACLRDMEIILRYVTYAILAGDSSVLDDRCLNGLRETYQALGTPGSSVAVA
IQKMKDAAIAIANDPNGITPGDCSALMSEIAGYFDRAAAAVA
>d1gh0a_ a.1.1.3 (A:) Phycocyanin {Spirulina platensis}
MKTPLTEAVSVADSQGRFLSSTEIQVAFGRFRQAKAGLEAAKALTSKADSLISGAAQAVYNKFPY
TTQMQGPNYAADQRGKDKCARDIGYYLRMVTYCLIAGGTGPMDEYLIAGIDEINRTFELSPSWYI
EALKYIKANHGLSGDAAVEANSYLDYAINALS
>d1gh0b_ a.1.1.3 (B:) Phycocyanin {Spirulina platensis}
MFDAFTKVVSQADTRGEMLSTAQIDALSQMVAESNKRLDVVNRITSNASTIVSNAARSLFAEQPQ
LIAPGGNAYTSRRMAACLRDMEIILRYVTYAVFAGDASVLEDRCLNGLRETYLALGTPGSSVAVG
VGKMKEAALAIVNDPAGITPGDCSALASEIAGYFDRAAAAVS
>d1alla_ a.1.1.3 (A:) Allophycocyanin {Spirulina platensis}
SIVTKSIVNADAEARYLSPGELDRIKSFVTSGERRVRIAETMTGARERIIKQAGDQLFGKRPDVV
SPGGNAYGADMTATCLRDLDYYLRLITYGIVAGDVTPIEEIGVVGVREMYKSLGTPIEAIAEGVR
AMKSVATSLLSGADAAEAGSYFDYLIGAMS
>d1allb_ a.1.1.3 (B:) Allophycocyanin {Spirulina platensis}
MQDAITSVINSSDVQGKYLDASAIQKLKAYFATGELRVRAATTISANAANIVKEAVAKSLLYSDV
TRPGGNMYTTRRYAACIRDLDYYLRYATYAMLAGDPSILDERVLNGLKETYNSLGVPIGATVQAI
QAMKEVTAGLVGGGAGKEMGIYFDYICSGLS
>d1b33a_ a.1.1.3 (A:) Allophycocyanin {Cyanobacterium (Mastigocladus laminosus)}
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SIVTKSIVNADAEARYLSPGELDRIKSFVSSGEKRLRIAQILTDNRERIVKQAGDQLFQKRPDVV
SPGGNAYGQEMTATCLRDLDYYLRLITYGIVAGDVTPIEEIGIVGVREMYKSLGTPIDAVAAGVS
AMKNVASSILSAEDAAEAGAYFDYVAGALA
>d1b33b_ a.1.1.3 (B:) Allophycocyanin {Cyanobacterium (Mastigocladus
laminosus)}
MQDAITAVINSSDVQGKYLDTAALEKLKSYFSTGELRVRAATTIAANAAAIVKEAVAKSLLYSDI
TRPGGNMYTTRRYAACIRDLDYYLRYATYAMLAGDPSILDERVLNGLKETYNSLGVPISATVQAI
QAMKEVTASLVGPDAGKEMGVYFDYICSGLS
>d1liaa_ a.1.1.3 (A:) Phycoerythrin {Red alga (Polysiphonia
urceolata)}
MKSVITTTISAADAAGRYPSTSDLQSVQGNIQRAAARLEAAEKLGSNHEAVVKEAGDACFSKYGY
NKNPGEAGENQEKINKCYRDIDHYMRLINYTLVVGGTGPLDEWGIAGAREVYRTLNLPSAAYIAA
FVFTRDRLCIPRDMSAQAGVEFCTALDYLINSLS
>d1liab_ a.1.1.3 (B:) Phycoerythrin {Red alga (Polysiphonia
urceolata)}
MLDAFSRVVVNSDSKAAYVSGSDLQALKTFINDGNKRLDAVNYIVSNSSCIVSDAISGMICENPG
LITPGGNCYTNRRMAACLRDGEIILRYVSYALLAGDASVLEDRCLNGLKETYIALGVPTNSTVRA
VSIMKAAAVCFISNTASQRKVEVIEGDCSALASEVASYCDRVVAAVS
>d1b8da_ a.1.1.3 (A:) Phycoerythrin {Red alga (Griffithsia monilis)}
MKSVITTTISAADAAGRFPSSSDLESIQGNIQRAAARLEAAQKLSGNHEAVVKEAGDACFAKYSY
LKNAGEAGDSPEKINKCYRDIDHYMRLINYSLVVGGTGPVDEWGIAGSREVYRALNLPGSAYIAA
FTFTRDRLCVPRDMSSQAGVEFTSALDYVINSLC
>d1b8db_ a.1.1.3 (B:) Phycoerythrin {Red alga (Griffithsia monilis)}
MLDAFSRVVVTSDAKAAYVGGSDLQSLKSFINDGNKRLDAVNYIVSNASCIVSDAVSGMICENPG
LIAPGGNCYTNRRMAACLRDGEIILRYVSYALLAGDSSVLDDRCLNGLKETYIALGVPTASSSRA
VSIMKATATAFITNTASGRKVEVAAGDCQALQAEAASYFDKVGSSID
>d1eyxa_ a.1.1.3 (A:) Phycoerythrin {Red algae (Gracilaria
chilensis)}
MKSVITTVISAADSAGRFPSSSDLESVQGNIQRASARLEAAEKLASNHEAVVKEAGDACFGKYGY
LKNPGEAGENQEKINKCYRDIDHYMRLVNYSLVIGGTGPLDEWGIAGAREVYRTLNLPTSAYIAA
FAFTRDRLCGPRDMSAQAGVEYSTALDYIINSLS
>d1eyxb_ a.1.1.3 (B:) Phycoerythrin {Red algae (Gracilaria
chilensis)}
MLDAFSRVISNADAKAAYVGGSDLQALRTFISDGNKRLDAVNYIVSNSSCIVSDAISGMICENPG
LITPGGNCYTNRRMAACLRDGEIILRYISYALLAGDSSVLEDRCLNGLKETYIALGVPTNSTVRA
VSIMKAAVGAFISNTASQRKGEVIEGDCSALAAEIASYCDRISAAVS
>d1qgwc_ a.1.1.3 (C:) Phycoerythrin {Cryptophite (Rhodomonas sp.),
cs24}
DAFSRVVTNADSKAAYVGGADLQALKKFISEGNKRLDSVNSIVSNASCIVSDAVSGMICENPSLI
SPSGNCYTNRRMAACLRDGEIILRYVSYALLSGDASVLEDRCLNGLKETYSSLGVPANSNARAVS
IMKACAVAFVNNTASQKKLSTPQGDCSGLASEVGGYFDKVTAAIS
>d1fumb1 a.1.2.1 (B:106-243) Fumarate reductase iron-sulfur protein,
C-terminal domain {Escherichia coli}
MTHFIESLEAIKPYIIGNSRTADQGTNIQTPAQMAKYHQFSGCINCGLCYAACPQFGLNPEFIGP
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AAITLAHRYNEDSRDHGKKERMAQLNSQNGVWSCTFVGYCSEVCPKHVDPAAAIQQGKVESSKDF
LIATLKPR
>d1qlab1 a.1.2.1 (B:107-239) Fumarate reductase iron-sulfur protein,
C-terminal domain {Wolinella succinogenes}
TGNWFNGMSQRVESWIHAQKEHDISKLEERIEPEVAQEVFELDRCIECGCCIAACGTKIMREDFV
GAAGLNRVVRFMIDPHDERTDEDYYELIGDDDGVFGCMTLLACHDVCPKNLPLQSKIAYLRRKMV
SVN
>d1h7wa1 a.1.2.2 (A:2-183) Dihydropyrimidine dehydrogenase,
N-terminal domain {Pig (Sus scrofa)}
APVLSKDVADIESILALNPRTQSHAALHSTLAKKLDKKHWKRNPDKNCFHCEKLENNFDDIKHTT
LGERGALREAMRCLKCADAPCQKSCPTHLDIKSFITSISNKNYYGAAKMIFSDNPLGLTCGMVCP
TSDLCVGGCNLYATEEGSINIGGLQQFASEVFKAMNIPQIRNPCLPSQEKMP
>d1grj_1 a.2.1.1 (2-79) GreA transcript cleavage protein, N-terminal
domain {Escherichia coli}
QAIPMTLRGAEKLREELDFLKSVRRPEIIAAIAEAREHGDLKENAEYHAAREQQGFCEGRIKDIE
AKLSNAQVIDVTK
>d1jj2u_ a.2.2.1 (U:) Ribosomal protein L29 (L29p) {Archaeon
Haloarcula marismortui}
TVLHVQEIRDMTPAEREAELDDLKTELLNARAVQAAGGAPENPGRIKELRKAIARIKTIQGEEGD
>d1fpoa1 a.2.3.1 (A:1-76) HSC20 (HSCB), N-terminal (J) domain
{Escherichia coli}
MDYFTLFGLPARYQLDTQALSLRFQDLQRQYHPDKFASGSQAEQLAAVQQSATINQAWQTLRHPL
MRAEYLLSLHG
>d1hdj__ a.2.3.1 (-) HSP40 {Human (Homo sapiens)}
MGKDYYQTLGLARGASDEEIKRAYRRQALRYHPDKNKEPGAEEKFKEIAEAYDVLSDPRKREIFD
RYGEEGLKGSGC
>d1xbl__ a.2.3.1 (-) DnaJ chaperone, N-terminal (J) domain
{Escherichia coli}
AKQDYYEILGVSKTAEEREIRKAYKRLAMKYHPDRNQGDKEAEAKFKEIKEAYEVLTDSQKRAAY
DQYGHAAFEQ
>d1fafa_ a.2.3.1 (A:) Large T antigen, the N-terminal J domain {Murine
polyomavirus}
MDRVLSRADKERLLELLKLPRQLWGDFGRMQQAYKQQSLLLHPDKGGSHALMQELNSLWGTFKTE
VYNLRMNLGGTGFQ
>d1gh6a_ a.2.3.1 (A:) Large T antigen, the N-terminal J domain {Simian
virus 40, Sv40}
SHMREESLQLMDLLGLERSAWGNIPLMRKAYLKKCKEFHPDKGGDEEKMKKMNTLYKKMEDGVKY
AHQPDFGGFWDATEIPTYGTDEWEQWWNAFNEENLFCSEEMPSSDDEAT
>d1du2a_ a.2.4.1 (A:) Theta subunit of DNA polymerase III {Escherichia
coli}
MLKNLAKLDQTEMDKVNVDLAAAGVAFKERYNMPVIAEAVEREQPEHLRSWFRERLIAHRLASVN
LSRLPYEPKLK
>d1fxkc_ a.2.5.1 (C:) Prefoldin alpha subunit {Archaeon
Methanobacterium thermoautotrophicum}
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AALAEIVAQLNIYQSQVELIQQQMEAVRATISELEILEKTLSDIQGKDGSETLVPVGAGSFIKAE
LKDTSEVIMSVGAGVAIKKNFEDAMESIKSQKNELESTLQKMGENLRAITDIMMKLSPQAEELLA
AVA
>d1fxka_ a.2.5.1 (A:) Prefoldin beta subunit {Archaeon
Methanobacterium thermoautotrophicum}
QNVQHQLAQFQQLQQQAQAISVQKQTVEMQINETQKALEELSRAADDAEVYKSSGNILIRVAKDE
LTEELQEKLETLQLREKTIERQEERVMKKLQEMQVNIQEAMK
>d1cxzb_ a.2.6.1 (B:) Effector domain of the protein kinase pkn/prk1
{Human (Homo sapiens)}
WSLLEQLGLAGADLAAPGVQQQLELERERLRREIRKELKLKEGAENLRRATTDLGRSLGPVELLL
RGSSRRLDLLHQQLQELHAHV
>d1seta1 a.2.7.1 (A:1-110) Seryl-tRNA synthetase (SerRS) {Thermus
thermophilus, strain hb27}
MVDLKRLRQEPEVFHRAIREKGVALDLEALLALDREVQELKKRLQEVQTERNQVAKRVPKAPPEE
KEALIARGKALGEEAKRLEEALREKEARLEALLLQVPLPPWPGAP
>d1eiya1 a.2.7.2 (A:6-84) Phenylalanyl-tRNA synthetase (PheRS)
{Thermus thermophilus}
LAAIQNARDLEELKALKARYLGKKGLLTQEMKGLSALPLEERRKRGQELNAIKAALEAALEAREK
ALEEAALKEALERE
>d1a36a1 a.2.8.1 (A:641-712) Eukaryotic DNA topoisomerase I,
dispensable insert domain {Human (Homo sapiens)}
EKSMMNLQTKIDAKKEQLADARRDLKSAKADAKVMKDAKTKKVVESKKKAVQRLEEQLMKLEVQA
TDREENK
>d1e52a_ a.2.9.1 (A:) C-terminal, UvrC-binding domain of UvrB
{Escherichia coli}
LEPDNVPMDMSPKALQQKIHELEGLMMQHAQNLEFEEAAQIRDQLHQLRELFIAAS
>d1qoja_ a.2.9.1 (A:) C-terminal, UvrC-binding domain of UvrB
{Escherichia coli}
SPKALQQKIHELEGLMMQHAQNLEFEEAAQIRDQLHQLRELFIAAS
>d1aqt_1 a.2.10.1 (87-136) Epsilon subunit of F1F0-ATP synthase
C-terminal domain {Escherichia coli}
QDLDEARAMEAKRKAEEHISSSHGDVDYAQASAELAKAIAQLRVIELTKK
>d1e79h1 a.2.10.1 (H:101-145) Epsilon subunit of F1F0-ATP synthase
C-terminal domain {Cow (Bos taurus)}
DMLDLGAAKANLEKAQSELLGAADEATRAEIQIRIEANEALVKAL
>d1idsa1 a.2.11.1 (A:2-85) Fe superoxide dismutase (FeSOD)
{Mycobacterium tuberculosis}
AEYTLPDLDWDYGALEPHISGQINELHHSKHHATYVKGANDAVAKLEEARAKEDHSAILLNEKNL
AFNLAGHVNHTIWWKNLSP
>d1dt0a1 a.2.11.1 (A:1-83) Fe superoxide dismutase (FeSOD)
{Pseudomonas ovalis}
AFELPPLPYAHDALQPHISKETLEFHHDKHHNTYVVNLNNLVPGTEFEGKTLEEIVKTSSGGIFN
NAAQVWNHTFYWNCLSPN
>d3sdpa1 a.2.11.1 (A:5-83) Fe superoxide dismutase (FeSOD)
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{Pseudomonas ovalis}
PPLPYAHDALQPHISKETLEYHHDKHHNTYVVNLNNLVPGTPEFEGKTLEEIVKSSSGGIFNNAA
QVWNHTFYWNCLSP
>d1isaa1 a.2.11.1 (A:1-82) Fe superoxide dismutase (FeSOD)
{Escherichia coli}
SFELPALPYAKDALAPHISAETIEYHYGKHHQTYVTNLNNLIKGTAFEGKSLEEIIRSSEGGVFN
NAAQVWNHTFYWNCLAP
>d1coja1 a.2.11.1 (A:2-90) Fe superoxide dismutase (FeSOD) {Aquifex
pyrophilus}
VHKLEPKDHLKPQNLEGISNEQIEPHFEAHYKGYVAKYNEIQEKLADQNFADRSKANQNYSEYRE
LKVEETFNYMGVVLHELYFGMLTP
>d1sssa1 a.2.11.1 (A:4-92) Fe superoxide dismutase (FeSOD) {Archaeon
Sulfolobus solfataricus}
IQFKKYELPPLPYKIDALEPYISKDIIDVHYNGHHKGYVNGANSLLERLEKVVKGDLQTGQYDIQ
GIIRGLTFNINGHKLHALYWENMA
>d1b06a1 a.2.11.1 (A:3-92) Fe superoxide dismutase (FeSOD) {Archaeon
Sulfolobus acidocaldarius}
VIQLKRYEFPQLPYKVDALEPYISKDIIDVHYNGHHKGYVNGANSLLDRLEKLIKGDLPQGQYDL
QGILRGLTFNINGHKLHAIYWNNMA
>d1ap6a1 a.2.11.1 (A:1-83) Mn superoxide dismutase (MnSOD) {Human
(Homo sapiens)}
KHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAFVNNLNVTEEKYQEALAKGDVTAQIALQPALK
FNGGGHINHSIFWTNLSP
>d1kkca1 a.2.11.1 (A:14-97) Mn superoxide dismutase (MnSOD)
{Aspergillus fumigatus}
QQYTLPPLPYPYDALQPYISQQIMELHHKKHHQTYVNGLNAALEAQKKAAEATDVPKLVSVQQAI
KFNGGGHINHSLFWKNLAP
>d1i0ha1 a.2.11.1 (A:1-90) Mn superoxide dismutase (MnSOD)
{Escherichia coli}
SYTLPSLPYAYDALEPHFDKQTMEIHHTKHHQTYVNNANAALESLPEFANLPVEELITKLDQLPA
DKKTVLRNNAGGHANHSLFWKGLKK
>d1mnga1 a.2.11.1 (A:1-92) Mn superoxide dismutase (MnSOD) {Thermus
thermophilus}
PYPFKLPDLGYPYEALEPHIDAKTMEIHHQKHHGAYVTNLNAALEKYPYLHGVEVEVLLRHLAAL
PQDIQTAVRNNGGGHLNHSLFWRLLTP
>d1bsma1 a.2.11.1 (A:1-86) Cambialistic superoxide dismutase
{Propionibacterium shermanii}
AVYTLPELPYDYSALEPYISGEIMELHHDKHHKAYVDGANTALDKLAEARDKADFGAINKLEKDL
AFNLAGHVNHSVFWKNMAPKG
>d1qnna1 a.2.11.1 (A:1-84) Cambialistic superoxide dismutase
{Porphyromonas gingivalis}
MTHELISLPYAVDALAPVISKETVEFHHGKHLKTYVDNLNKLIIGTEFENADLNTIVQKSEGGIF
NNAGQTLNHNLYFTQFRPG
>d1dava_ a.139.1.1 (A:) Cellulosome endoglucanase SS {Clostridium
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thermocellum}
MSTKLYGDVNDDGKVNSTDAVALKRYVLRSGISINTDNADLNEDGRVNSTDLGILKRYILKEIDT
LPYKNG
>d1h9ea_ a.140.1.1 (A:) Thymopoietin, LAP2 {Human (Homo sapiens)}
PEFLEDPSVLTKDKLKSELVANNVTLPAGEQRKDVYVQLYLQHLTARNRPPLPAGT
>d1h9fa_ a.140.1.1 (A:) Thymopoietin, LAP2 {Human (Homo sapiens)}
RQEDKDDLDVTELTNEDLLDQLVKYGVNPGPIVGTTRKLYEKKLLKLREQGTESRSS
>d1jeia_ a.140.1.1 (A:) Inner nuclear membrane protein emerin {Human
(Homo sapiens)}
DNYADLSDTELTTLLRRYNIPHGPVVGSTRRLYEKKIFEYETQRRRLSPPSSS
>d1jeqa1 a.140.2.1 (A:559-609) DNA binding C-terminal domain of ku70
{Human (Homo sapiens)}
YSEEELKTHISKGTLGKFTVPMLKEACRAYGLKSGLKKQELLEALTKHFQD
>d1kcfa1 a.140.2.1 (A:3-38) Mitochondrial resolvase ydc2 N-terminal
domain {Fission yeast (Schizosaccharomyces pombe)}
TVKLSFLQHICKLTGLSRSGRKDELLRRIVDSPIYP
>d1a62_1 a.140.3.1 (1-47) Rho termination factor, N-terminal domain
{Escherichia coli}
MNLTELKNTPVSELITLGENMGLENLARMRKQDIIFAILKQHAKSGE
>d1e7la1 a.140.4.1 (A:104-157) Recombination endonuclease VII,
C-terminal and dimerization domains {Bacteriophage T4}
IHPNFVGDKSKEFSRLGKEEMMAEMLQRGFEYNESDTKTQLIASFKKQLRKSLK
>d1c75a_ a.3.1.1 (A:) Cytochrome c6 (synonym: cytochrome c553)
{Bacillus pasteurii}
VDAEAVVQQKCISCHGGDLTGASAPAIDKAGANYSEEEILDIILNGQGGMPGGIAKGAEAEAVAA
WLAEKK
>d1ctj__ a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553)
{Monoraphidium braunii}
EADLALGKAVFDGNCAACHAGGGNNVIPDHTLQKAAIEQFLDGGFNIEAIVYQIENGKGAMPAWD
GRLDEDEIAGVAAYVYDQAAGNKW
>d1c53__ a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553)
{Desulfovibrio vulgaris, different strains}
ADGAALYKSCVGCHGADGSKQAMGVGHAVKGQKADELFKKLKGYADGSYGGEKKAVMTNLVKRYS
DEEMKAMADYMSKL
>d2dvh__ a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553)
{Desulfovibrio desulfuricans}
ADGAALYKSCIGCHGADGSKAAMGSAKPVKGQGAEELYKKMKGYADGSYGGERKAMMTNAVKKAS
DEELKALADYMSKL
>d1cyi__ a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553)
{Chlamydomonas reinhardtii}
ADLALGAQVFNGNCAACHMGGRNSVMPEKTLDKAALEQYLDGGFKVESIIYQVENGKGAMPAWAD
RLSEEEIQAVAEYVFKQATDAAWK
>d1c6s__ a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553)
{Cyanobacterium (Synechococcus elongatus)}
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ADLANGAKVFSGNCAACHMGGGNVVMANKTLKKEALEQFGMYSEDAIIYQVQHGKNAMPAFAGRL
TDEQIQDVAAYVLDQAAKGWAG
>d1f1fa_ a.3.1.1 (A:) Cytochrome c6 (synonym: cytochrome c553)
{Arthrospira maxima}
DVAAGASVFSANCAACHMGGRNVIVANKTLSKSDLAKYLKGFDDDAVAAVAYQVTNGKNAMPGFN
GRLSPLQIEDVAAYVVDQAEKGW
>d1c6ra_ a.3.1.1 (A:) Cytochrome c6 (synonym: cytochrome c553) {Green
alga (Scenedesmus obliquus)}
ADLALGKQTFEANCAACHAGGNNSVIPDHTLRKAAMEQFLQGGFNLEAITYQVENGKGAMPAWSG
TLDDDEIAAVAAYVYDQASGDKW
>d1gdva_ a.3.1.1 (A:) Cytochrome c6 (synonym: cytochrome c553) {Red
alga (Porphyra yezoensis)}
ADLDNGEKVFSANCAACHAGGNNAIMPDKTLKKDVLEANSMNTIDAITYQVQNGKNAMPAFGGRL
VDEDIEDAANYVLSQSEKGW
>d1c52__ a.3.1.1 (-) Cytochrome c552 {Thermus thermophilus}
QADGAKIYAQCAGCHQQNGQGIPGAFPPLAGHVAEILAKEGGREYLILVLLYGLQGQIEVKGMKY
NGVMSSFAQLKDEEIAAVLNHIATAWGDAKKVKGFKPFTAEEVKKLRAKKLTPQQVLAERKKLGL
K
>d1cnoa_ a.3.1.1 (A:) Cytochrome c552 {Pseudomonas nautica}
AGDIEAGKAKAAVCAACHGQNGISQVPIYPNLAGQKEQYLVAALKAYKAGQRQGGQAPVMQGQAT
ALSDADIANLAAYYASNPAAA
>d1ql3a_ a.3.1.1 (A:) Cytochrome c552 {Paracoccus denitrificans}
ADPAAGEKVFGKCKACHKLDGNDGVGPHLNGVVGRTVAGVDGFNYSDPMKAHGGDWTPEALQEFL
TNPKAVVKGTKMAFAGLPKIEDRANLIAYLEGQQ
>d1ayg__ a.3.1.1 (-) Cytochrome c552 {Hydrogenobacter thermophilus}
NEQLAKQKGCMACHDLKAKKVGPAYADVAKKYAGRKDAVDYLAGKIKKGGSGVWGSVPMPPQNVT
DAEAKQLAQWILSIK
>d1a56__ a.3.1.1 (-) Cytochrome c552 {Nitrosomonas europaea}
DADLAKKNNCIACHQVETKVVGPALKDIAAKYADKDDAATYLAGKIKGGSSGVWGQIPMPPNVNV
SDADAKALADWILTLK
>d1e29a_ a.3.1.1 (A:) Photosystem II associated cytochrome c549
{Synechocystis sp., pcc 6803}
VELTESTRTIPLDEAGGTTTLTARQFTNGQKIFVDTCTQCHLQGKTKTNNNVSLGLADLAGAEPR
RDNVLALVEFLKNPKSYDGEDDYSELHPNISRPDIYPEMRNYTEDDIFDVAGYTLIAPKLDERWG
GTIYF
>d1f1ca_ a.3.1.1 (A:) Photosystem II associated cytochrome c549
{Arthrospira maxima}
LTEELRTFPINAQGDTAVLSLKEIKKGQQVFNAACAQCHALGVTRTNPDVNLSPEALALATPPRD
NIAALVDYIKNPTTYDGFVEISELHPSLKSSDIFPKMRNISEDDLYNVAGYILLQPKVRGEQWG
>d1ycc__ a.3.1.1 (-) Mitochondrial cytochrome c {Baker's yeast
(Saccharomyces cerevisiae)}
TEFKAGSAKKGATLFKTRCLQCHTVEKGGPHKVGPNLHGIFGRHSGQAEGYSYTDANIKKNVLWD
ENNMSEYLTNPKKYIPGTKMAFGGLKKEKDRNDLITYLKKACE
>d1yeb__ a.3.1.1 (-) Mitochondrial cytochrome c {Baker's yeast
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(Saccharomyces cerevisiae)}
TEFKAGSAKKGATLFKTRCQQCHTIEEGGPNKVGPNLHGIFGRHSGQVKGYSYTDANINKNVKWD
EDSMSEYLTNPKKYIPGTKMAFGGLKKEKDRNDLITYLKKACE
>d1ytc__ a.3.1.1 (-) Mitochondrial cytochrome c {Baker's yeast
(Saccharomyces cerevisiae)}
AKESTGFKPGSAKKGATLFKTRCQQCHTIEEGGPNKVGPNLHGIFGRHSGQVKGYSYTDAIINKN
VKWDEDSMSEYLTNPKKYIPGTKMAFAGLKKEKDRNDLITYMTKAAK
>d1wejf_ a.3.1.1 (F:) Mitochondrial cytochrome c {Horse (Equus
caballus)}
GDVEKGKKIFVQKCAQCHTVEKGGKHKTGPNLHGLFGRKTGQAPGFTYTDANKNKGITWKEETLM
EYLENPKKYIPGTKMIFAGIKKKTEREDLIAYLKKATNE
>d1ccr__ a.3.1.1 (-) Mitochondrial cytochrome c {Rice embryos (Oryza
sativa)}
ASFSEAPPGNPKAGEKIFKTKCAQCHTVDKGAGHKQGPNLNGLFGRQSGTTPGYSYSTADKNMAV
IWEENTLYDYLLNPKKYIPGTKMVFPGLKKPQERADLISYLKEATS
>d5cytr_ a.3.1.1 (R:) Mitochondrial cytochrome c {Tuna (Thunnus
alalunga and Thunnus thynnus)}
GDVAKGKKTFVQKCAQCHTVENGGKHKVGPNLWGLFGRKTGQAEGYSYTDANKSKGIVWNNDTLM
EYLENPKKYIPGTKMIFAGIKKKGERQDLVAYLKSATS
>d1qn2a_ a.3.1.1 (A:) Cytochrome ch {Methylobacterium extorquens}
EGDAAAGEKAFAPCKACHNFEKNGVGPTLKGVVGAKAGEGADGYAFSDALKKSGLTWDQADLKQW
LADPKKKVPGTKMVFPGISDPKKVDDIIAYLKTK
>d3c2c__ a.3.1.1 (-) Cytochrome c2 {Rhodospirillum rubrum}
EGDAAAGEKVSKKCLACHTFDQGGANKVGPNLFGVFENTAAHKDNYAYSESYTEMKAKGLTWTEA
NLAAYVKNPKAFVLEKSGDPKAKSKMTFKLTKDDEIENVIAYLKTLK
>d1c2ra_ a.3.1.1 (A:) Cytochrome c2 {Rhodobacter capsulatus}
GDAAKGEKEFNKCKTCHSIIAPDGTEIVKGAKTGPNLYGVVGRTAGTYPEFKYKDSIVALGASGF
AWTEEDIATYVKDPGAFLKEKLDDKKAKTGMAFKLAKGGEDVAAYLASVVK
>d1cxc__ a.3.1.1 (-) Cytochrome c2 {Rhodobacter sphaeroides}
QEGDPEAGAKAFNQCQTCHVIVDDSGTTIAGRNAKTGPNLYGVVGRTAGTQADFKGYGEGMKEAG
AKGLAWDEEHFVQYVQDPTKFLKEYTGDAKAKGKMTFKLKKEADAHNIWAYLQQVAVRP
>d1co6a_ a.3.1.1 (A:) Cytochrome c2 {Rhodopseudomonas viridis}
QDAASGEQVFKQCLVCHSIGPGAKNKVGPVLNGLFGRHSGTIEGFAYSDANKNSGITWTEEVFRE
YIRDPKAKIPGTKMIFAGVKDEQKVSDLIAYIKQFNADGSKK
>d1i8oa_ a.3.1.1 (A:) Cytochrome c2 {Rhodopseudomonas palustris}
EDAKAGEAVFKQCMTCHRADKNMVGPALAGVVGRKAGTAAGFTYSPLNHNSGEAGLVWTADNIVP
YLADPNAFLKKFLTEKGKADQAVGVTKMTFKLANEQQRKDVVAYLATLK
>d1hroa_ a.3.1.1 (A:) Cytochrome c2 {Rhodopila globiformis}
SAPPGDPVEGKHLFHTICITCHTDIKGANKVGPSLYGVVGRHSGIEPGYNYSEANIKSGIVWTPD
VLFKYIEHPQKIVPGTKMGYPGQPDPQKRADIIAYLETLK
>d155c__ a.3.1.1 (-) Cytochrome c2 {Paracoccus denitrificans}
NEGDAAKGEKEFNKCKACHMIQAPDGTDIKGGKTGPNLYGVVGRKIASEEGFKYGEGILEVAEKN
PDLTWTEANLIEYVTDPKPLVKKMTDDKGAKTKMTFKMGKNQADVVAFLAQDDPDAXXXXXXXXX
XXXX
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>d1cot__ a.3.1.1 (-) Cytochrome c2 {Paracoccus denitrificans}
DGDAAKGEKEFNKCKACHMIQAPDGTDIIKGGKTGPNLYGVVGRKIASEEGFKYGEGILEVAEKN
PDLTWTEADLIEYVTDPKPWLVKMTDDKGAKTKMTFKMGKNQADVVAFLAQNSPDA
>d1jdla_ a.3.1.1 (A:) Cytochrome c2 {Rhodospirillum centenum}
GDPAKGEAVFKKCMACHRVGPDAKNLVGPALTGVIDRQAGTAPGFNYSAINHAAGEAGLHWTPEN
IIAYLPDPNAFLRKFLADAGHAEQAKGSTKMVFKLPDEQERKDVVAYLKQFSP
>d1cc5__ a.3.1.1 (-) Cytochrome c5 {Azotobacter vinelandii}
GGGARSGDDVVAKYCNACHGTGLLNAPKVGDSAAWKTRADAKGGLDGLLAQSLSGLNAMPPKGTC
ADCSDDELKAAIGKMSGL
>d1kx2a_ a.3.1.1 (A:) Mono-heme c-type cytochrome ScyA {Shewanella
putrefaciens}
ADLQDAEAIYNKACTVCHSMGVAGAPKSHNTADWEPRLAKGVDNLVKSVKTGLNAMPPGGMCTDC
TDEDYKAAIEFMSKAK
>d1cch__ a.3.1.1 (-) Cytochrome c551 {Pseudomonas stutzeri}
QDGEALFKSKPCAACHSVDTKMVGPALKEVAAKNAGVEGAADTLALHIKNGSQGVWGPIPMPPNP
VTEEEAKILAEWVLSLK
>d1cor__ a.3.1.1 (-) Cytochrome c551 {Pseudomonas stutzeri}
EDGEALFKSKPCAACHSIDAKLVGPAFKEVAAKYAGQDGAADLLAGHIKNGSQGVWGPIPMPPNP
VTEEEAKILAEWILSQK
>d1dvva_ a.3.1.1 (A:) Cytochrome c551 {Pseudomonas aeruginosa}
EDPEVLAKNKGCMACHAIDTKMVGPAYKDVAAKYAGQAGAEAYLAQRIKNGSQGVWGPIPMPPNA
VSDDEAQTLAKWILSQK
>d451c__ a.3.1.1 (-) Cytochrome c551 {Pseudomonas aeruginosa}
EDPEVLFKNKGCVACHAIDTKMVGPAYKDVAAKFAGQAGAEAELAQRIKNGSQGVWGPIPMPPNA
VSDDEAQTLAKWVLSQK
>d2mtac_ a.3.1.1 (C:) Cytochrome c551 {Paracoccus denitrificans}
APQFFNIIDGSPLNFDDAMEEGRDTEAVKHFLETGENVYNEDPEILPEAEELYAGMCSGCHGHYA
EGKIGPGLNDAYWTYPGNETDVGLFSTLYGGATGQMGPMWGSLTLDEMLRTMAWVRHLYTGDPKD
ASWLTDEQKAGFTPFQP
>d1gks__ a.3.1.1 (-) Cytochrome c551 {Ectothiorhodospira halophila}
DGESIYINGTAPTCSSCHDRGVAGAPELNAPEDWADRPSSVDELVESTLAGKGAMPAYDGRADRE
DLVKAIEYMLSTL
>d05c1__ a.3.1.1 (-) Cytochrome c555 {Chlorobium thiosulfatophilum}
YDAAAGKATYDASCAMCHKTGMMGAPKVGDKAAWAPHIAKGMNVMVANSIKGYKGTKGMMPAKGG
NPKLTDAQVGNAVAYMVGQSK
>d1dw0a_ a.3.1.1 (A:) SHP, an oxygen binding cytochrome c {Rhodobacter
sphaeroides}
GDTSPAQLIAGYEAAAGAPADAERGRALFLSTQTGGKPDTPSCTTCHGADVTRAGQTRTGKEIAP
LAPSATPDRFTDSARVEKWLGRNCNSVIGRDCTPGEKADLLAWLAAQ
>d1e8ea_ a.3.1.1 (A:) Cytochrome c'' {Methylophilus methylotrophus,
strain w3a1}
DVTNAEKLVYKYTNIAHSANPMYEAPSITDGKIFFNRKFKTPSGKEAACASCHTNNPANVGKNIV
TGKEIPPLAPRVNTKRFTDIDKVEDEFTKHCNDILGADCSPSEKANFIAYLLTETKPTK
>d1diqc_ a.3.1.1 (C:) p-Cresol methylhydroxylase, cytochrome c
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subunit {Pseudomonas putida}
SQWGSGKNLYDKVCGHCHKPEVGVGPVLEGRGLPEAYIKDIVRNGFRAMPAFPASYVDDESLTQV
AEYLSSLPA
>d1dy7b1 a.3.1.2 (B:32-135) N-terminal (heme c) domain of cytochrome
cd1-nitrite reductase {Paracoccus pantotrophus}
LAQQDVAAPGAPEGVSALSDAQYNEANKIYFERCAGCHGVLRKGATGKALTPDLTRDLGFDYLQS
FITYGSPAGMPNWGTSGELSAEQVDLMANYLLLDPAAPP
>d1h9xa1 a.3.1.2 (A:42-133) N-terminal (heme c) domain of cytochrome
cd1-nitrite reductase {Paracoccus pantotrophus}
APEGVSALSDAQYNEANKIYFERCAGCHGVLRKGATGKALTPDLTRDLGFDYLQSFITYGSPAGM
PNWGTSGELSAEQVDLMANYLLLDPAA
>d1hj3a1 a.3.1.2 (A:17-133) N-terminal (heme c) domain of cytochrome
cd1-nitrite reductase {Paracoccus pantotrophus}
HKTRTDNRYEPSLDNLAQQDVAAPGAPEGVSALSDAQYNEANKIYFERCAGCHGVLRKGATGKAL
TPDLTRDLGFDYLQSFITYGSPAGMPNWGTSGELSAEQVDLMANYLLLDPAA
>d1hzua1 a.3.1.2 (A:23-117) N-terminal (heme c) domain of cytochrome
cd1-nitrite reductase {Pseudomonas aeruginosa}
VRTNGAPDMSESEFNEAKQIYFQRCAGCHGVLRKGATGKPLTPDITQQRGQQYLEALITYGTPLG
MPNWGSSGELSKEQITLMAKYIQHTPPQPP
>d1nira1 a.3.1.2 (A:6-117) N-terminal (heme c) domain of cytochrome
cd1-nitrite reductase {Pseudomonas aeruginosa}
AAEQYQGAASAVDPAHVVRTNGAPDMSESEFNEAKQIYFQRCAGCHGVLRKGATGKPLTPDITQQ
RGQQYLEALITYGTPLGMPNWGSSGELSKEQITLMAKYIQHTPPQPP
>d1e2rb1 a.3.1.2 (B:25-135) N-terminal (heme c) domain of cytochrome
cd1-nitrite reductase {Paracoccus denitrificans}
YEPSLDNLAQQDVAAPGAPEGVTALSDAQYNEANKIYFERCAGCHGVLRKGATGKALTPDLTRDL
GFDYLQSFITYASPAGMPNWGTSGELSAEQVDLMANYLLLDPAAPP
>d1qksa1 a.3.1.2 (A:9-135) N-terminal (heme c) domain of cytochrome
cd1-nitrite reductase {Paracoccus denitrificans}
DPAAALEDHKTRTDNRYEPSLDNLAQQDVAAPGAPEGVTALSDAQYNEANKIYFERCAGCHGVLR
KGATGKALTPDLTRDLGFDYLQSFITYASPAGMPNWGTSGELSAEQVDLMANYLLLDPAAPP
>d1kb0a1 a.3.1.6 (A:579-675) Quinoprotein alcohol dehydrogenase,
C-terminal domain {Comamonas testosteroni}
TGQLLQGVKYDPAKVEAGTMLYVANCVFCHGVPGVDRGGNIPNLGYMDASYIENLPNFVFKGPAM
VRGMPDFTGKLSGDDVESLKAFIQGTADAIRP
>d1qcrd2 a.3.1.3 (D:167-195) Cytochrome bc1 domain {Cow (Bos taurus)}
EVLEFDDGTPATMSQVAKDVCTFLRWAAE
>d1bccd2 a.3.1.3 (D:1-195) Cytochrome bc1 domain {Chicken (Gallus
gallus)}
SDLELHPPSYPWSHRGPLSSLDHTSIRRGFQVYKQVCSSCHSMDYVAYRHLVGVCYTEDEAKALA
EEVEVQDGPNEDGEMFMRPGKLSDYFPKPYPNPEAARAANNGALPPDLSYIVRARHGGEDYVFSL
LTGYCEPPTGVSVREGLYFNPYFPGQAIGMAPPIYNDVLEFDDGTPATMSQVAKDVCTFLRWAAE
>d1ezvd1 a.3.1.3 (D:62-260) Cytochrome bc1 domain {Baker's yeast
(Saccharomyces cerevisiae)}
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MTAAEHGLHAPAYAWSHNGPFETFDHASIRRGYQVYREVCAACHSLDRVAWRTLVGVSHTNEEVR
NMAEEFEYDDEPDEQGNPKKRPGKLSDYIPGPYPNEQAARAANQGALPPDLSLIVKARHGGCDYI
FSLLTGYPDEPPAGVALPPGSNYNPYFPGGSIAMARVLFDDMVEYEDGTPATTSQMAKDVTTFLN
WCAE
>d1etpa1 a.3.1.4 (A:1-92) Cytochrome c4 {Pseudomonas stutzeri}
AGDAEAGQGKVAVCGACHGVDGNSPAPNFPKLAGQGERYLLKQLQDIKAGSTPGAPEGVGRKVLE
MTGMLDPLSDQDLEDIAAYFSSQKGSV
>d1etpa2 a.3.1.4 (A:93-190) Cytochrome c4 {Pseudomonas stutzeri}
GYADPALAKQGEKLFRGGKLDQGMPACTGCHAPNGVGNDLAGFPKLGGQHAAYTAKQLTDFREGN
RTNDGDTMIMRGVAAKLSNKDIEALSSYIQGLH
>d1fcdc1 a.3.1.4 (C:1-80) Flavocytochrome c sulfide dehydrogenase, FCSD, cytochrome subunit {Purple phototrophic bacterium (Chromatium vinosum)}
EPTAEMLTNNCAGCHGTHGNSVGPASPSIAQMDPMVFVEVMEGFKSGEIASTIMGRIAKGYSTAD
FEKMAGYFKQQTYQP
>d1fcdc2 a.3.1.4 (C:81-174) Flavocytochrome c sulfide dehydrogenase, FCSD, cytochrome subunit {Purple phototrophic bacterium (Chromatium vinosum)}
AKQSFDTALADTGAKLHDKYCEKCHVEGGKPLADEEDYHILAGQWTPYLQYAMSDFREERRPMEK
KMASKLRELLKAEGDAGLDALFAFYASQQ
>d1eb7a1 a.3.1.5 (A:1-164) Di-haem cytochrome c peroxidase {Pseudomonas aeruginosa}
DALHDQASALFKPIPEQVTELRGQPISEQQRELGKKLFFDPRLSRSHVLSCNTCHNVGTGGADNV
PTSVGHGWQKGPRNSPTVFNAVFNAAQFWDGRAKDLGEQAKGPIQNSVEMHSTPQLVEQTLGSIP
EYVDAFRKAFPKAGKPVSFDNMALAIEAYEATLV
>d1eb7a2 a.3.1.5 (A:165-323) Di-haem cytochrome c peroxidase {Pseudomonas aeruginosa}
TPDSPFDLYLKGDDKALDAQQKKGLKAFMDSGCSACHNGINLGGQAYFPFGLVKKPDASVLPSGD
KGRFAVTKTQSDEYVFRAAPLRNVALTAPYFHSGQVWELKDAVAIMGNAQLGKQLAPDDVENIVA
FLHSLSGKQPRVEYPLLPASTETTPRPAE
>d1iqca1 a.3.1.5 (A:1-150) Di-haem cytochrome c peroxidase {Nitrosomonas europaea}
ANEPIQPIKAVTPENADMAELGKMLFFDPRLSKSGFISCNSCHNLSMGGTDNITTSIGHKWQQGP
INAPTVLNSSMNLAQFWDGRAKDLKEQAAGPIANPKEMASTHEIAEKVVASMPQYRERFKKVFGS
DEVTIDRITTAIAQFEETLV
>d1iqca2 a.3.1.5 (A:151-308) Di-haem cytochrome c peroxidase {Nitrosomonas europaea}
TPGSKFDKWLEGDKNALNQDELEGYNLFKGSGCVQCHNGPAVGGSSYQKMGVFKPYETKNPAAGR
MDVTGNEADRNVFKVPTLRNIELTYPYFHDGGAATLEQAVETMGRIQLNREFNKDEVSKIVAFLK
TLTGDQPDFKLPILPPSNNDTPRSQPYE
>d1jjua1 a.3.1.7 (A:1-85) Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2 {Paracoccus denitrificans}
VTGEEVLQNACAACHVQHEDGRWERIDAARKTPEGWDMTVTRMMRNHGVALEPEERAAIVRHLSD
TRGLSLAETEERRYILEREP

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>d1jjua2 a.3.1.7 (A:86-165) Quinohemoprotein amine dehydrogenase A
chain, domains 1 and 2 {Paracoccus denitrificans}
VAWDEGPDTSMTQTCGRCHSYARVALQRRTPEDWKHLVNFHLGQFPTLEYQALARDRDWWGIAQA
EIIPFLARTYPLGEA
>d1jmxa1 a.3.1.7 (A:2-85) Quinohemoprotein amine dehydrogenase A
chain, domains 1 and 2 {Pseudomonas putida}
EQGPSLLQNKCMGCHIPEGNDTYSRISHQRKTPEGWLMSIARMQVMHGLQISDDDRRTLVKYLAD
KQGLAPSETDGVRYAMERR
>d1jmxa2 a.3.1.7 (A:86-162) Quinohemoprotein amine dehydrogenase A
chain, domains 1 and 2 {Pseudomonas putida}
LNTVEQFDTQLSETCGRCHSGARVALQRRPAKEWEHLVNFHLGQWPSLEYQAQARDRDWLPIALQ
QVVPDLAKRYPL
>d1enh__ a.4.1.1 (-) Engrailed Homeodomain {Drosophila melanogaster}
RPRTAFSSEQLARLKREFNENRYLTERRRQQLSSELGLNEAQIKIWFQNKRAKI
>d2hdda_ a.4.1.1 (A:) Engrailed Homeodomain {Drosophila melanogaster}
RTAFSSEQLARLKREFNENRYLTERRRQQLSSELGLNEAQIKIWFKNKRAKIKKS
>d1akha_ a.4.1.1 (A:) Mating type protein A1 Homeodomain {Baker's yeast
(Saccharomyces cerevisiae)}
ISPQARAFLEEVFRRKQSLNSKEKEEVAKKCGITPLQVRVWFINKRMRS
>d1f43a_ a.4.1.1 (A:) Mating type protein A1 Homeodomain {Baker's yeast
(Saccharomyces cerevisiae)}
KKEKSPKGKSSISPQARAFLEQVFRRKQSLNSKEKEEVAKKCGITPLQVRVWFINKRMRSK
>d1akhb_ a.4.1.1 (B:) mat alpha2 Homeodomain {Baker's yeast
(Saccharomyces cerevisiae)}
TKPYRGHRFTKENVRILESWFAKNIENPYLDTKGLENLMKNTSLSRIQIKNWVSNRRRKEKTITI
APELADLLSGEPL
>d1aplc_ a.4.1.1 (C:) mat alpha2 Homeodomain {Baker's yeast
(Saccharomyces cerevisiae)}
YRGHRFTKENVRILESWFAKNIENPYLDTKGLENLMKNTSLSRIQIKNWVSNRRRKEKT
>d1mnmc_ a.4.1.1 (C:) mat alpha2 Homeodomain {Baker's yeast
(Saccharomyces cerevisiae)}
GLVFNVVTQDMINKSTKPYRGHRFTKENVRILESWFAKNIENPYLDTKGLENLMKNTSLSRIQIK
NWVSNRRRKEKT
>d1lfb__ a.4.1.1 (-) Transcription factor LFB1 {Rat (Rattus rattus)}
RFKWGPASQQILFQAYERQKNPSKEERETLVEECNRAECIQRGVSPSQAQGLGSNLVTEVRVYNW
FANRRKEEAFRHK
>d2lfb__ a.4.1.1 (-) Transcription factor LFB1 {Rat (Rattus rattus)}
MARIDPTKKGRRNRFKWGPASQQILFQAYERQKNPSKEERETLVEECNRAECIQRGVSPSQAQGL
GSNLVTEVRVYNWFANRRKEEAFRHKLAMDTYKLN
>d1e3oc1 a.4.1.1 (C:104-160) Oct-1 POU Homeodomain {Human (Homo
sapiens)}
KRTSIETNIRVALEKSFMENQKPTSEDITLIAEQLNMEKEVIRVWFSNRRQKEKRIN
>d1hf0a1 a.4.1.1 (A:102-159) Oct-1 POU Homeodomain {Human (Homo
sapiens)}
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RKKRTSIETNIRVALEKSFLENQKPTSEEITMIADQLNMEKEVIRVWFSNRRQKEKRI
>d1au7a1 a.4.1.1 (A:103-160) Pit-1 POU homeodomain {Rat (Rattus norvegicus)}
KRRTTISIAAKDALERHFGEHSKPSSQEIMRMAEELNLEKEVVRVWFCNRRQREKRVK
>d1ftt__ a.4.1.1 (-) Thyroid transcription factor 1 homeodomain {Rat (Rattus norvegicus)}
MRRKRRVLFSQAQVYELERRFKQQKYLSAPEREHLASMIHLTPTQVKIWFQNHRYKMKRQAKDKAAQQ
>d1hdp__ a.4.1.1 (-) Oct-2 POU Homeodomain {Human (Homo sapiens)}
RRKKRTSIETNVRFALEKSFLANQKPTSEEILLIAEQLHMEKEVIRVWFCNRRQKEKRINPCS
>d1ocp__ a.4.1.1 (-) Oct-3 POU Homeodomain {Mouse (Mus musculus)}
METLVQARKRKRTSIENRVRWSLETMFLKCPKPSLQQITHIANQLGLEKDVVRVWFCNRRQKGKRSS
>d1b72a_ a.4.1.1 (A:) Homeobox protein hox-b1 {Human (Homo sapiens)}
ARTFDWMKVKRNPPKTAKVSEPGLGSPSGLRTNFTTRQLTELEKEFHFNKYLSRARRVEIAATLELNETQVKIWFQNRRMKQKKRERE
>d1b72b_ a.4.1.1 (B:) pbx1 {Human (Homo sapiens)}
RKRRNFNKQATEILNEYFYSHLSNPYPSEEAKEELAKKCGITVSQVSNWFGNKRIRYKKNIGKFQEEANIYAA
>d1du6a_ a.4.1.1 (A:) pbx1 {Mouse (Mus musculus)}
SSGHIEGRHMNKQATEILNEYFYSHLSNPYPSEEAKEELAKKCGITVSQVSNWFGNKRIRYKKN
>d1bw5__ a.4.1.1 (-) Insulin gene enhancer protein isl-1 {Rat (Rattus norvegicus)}
MKTTRVRTVLNEKQLHTLRTCYAANPRPDALMKEQLVEMTGLSPRVIRVWFQNKRCKDKKRSIMMK
>d1ig7a_ a.4.1.1 (A:) Msx-1 homeodomain {Mouse (Mus musculus)}
RKPRTPFTTAQLLALERKFRQKQYLSIAERAEFSSSLSLTETQVKIWFQNRRAKAKRL
>d1ahdp_ a.4.1.1 (P:) Antennapedia Homeodomain {Drosophila melanogaster}
MRKRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALSLTERQIKIWFQNRRMKWKKENKTKGEPG
>d1san__ a.4.1.1 (-) Antennapedia Homeodomain {Drosophila melanogaster}
MTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALSLTERQIKIWFQNRRMKWKKENKTKGEPG
>d9anta_ a.4.1.1 (A:) Antennapedia Homeodomain {Drosophila melanogaster}
RQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALSLTERQIKIWFQNRRMKWKKEN
>d1b8ia_ a.4.1.1 (A:) Ultrabithorax (ubx) homeodomain {Drosophila melanogaster}
FYPWMAIAGTNGLRRRGRQTYTRYQTLELEKEFHTNHYLTRRRRIEMAHALSLTERQIKIWFQNRRMKLKKEI
>d1b8ib_ a.4.1.1 (B:) Extradenticle (exd) homeodomain {Drosophila melanogaster}
RRNFSKQASEILNEYFYSHLSNPYPSEEAKEELARKCGITVSQVSNWFGNKRIRYKKN
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>d1jgga_ a.4.1.1 (A:) Even-skipped homeodomain {Fruit fly (Drosophila
melanogaster)}
RYRTAFTRDQLGRLEKEFYKENYVSRPRRCELAAQLNLPESTIKVWFQNRRMKDKRQ
>d1ftz__ a.4.1.1 (-) Fushi Tarazu protein {Fruit fly (Drosophila
melanogaster)}
MDSKRTRQTYTRYQTLELEKEFHFNRYITRRRRIDIANALSLSERQIKIWFQNRRMKSKKDRTLD
SSPEH
>d1nk3p_ a.4.1.1 (P:) VND/NK-2 protein {Fruit fly (Drosophila
melanogaster)}
KKRKRRVLFTKAQTYELERRFRQQRYLSAPEREHLASLIRLTPTQVKIWFQNHRYKTKRAQNE
>d1vnd__ a.4.1.1 (-) VND/NK-2 protein {Fruit fly (Drosophila
melanogaster)}
ASDGLPNKKRKRRVLFTKAQTYELERRFRQQRYLSAPEREHLASLIRLTPTQVKIWFQNHRYKTK
RAQNEKGYEGHP
>d1fjla_ a.4.1.1 (A:) Paired protein {Fruit fly (Drosophila
melanogaster)}
KQRRSRTTFSASQLDELERAFERTQYPDIYTREELAQRTNLTEARIQVWFQNRRARLRKQHTSVS
>d1fjlb_ a.4.1.1 (B:) Paired protein {Fruit fly (Drosophila
melanogaster)}
QRRSRTTFSASQLDELERAFERTQYPDIYTREELAQRTNLTEARIQVWFQNRRARLRK
>d1hcra_ a.4.1.2 (A:) HIN recombinase (DNA-binding domain)
{Synthetic}
GRPRAINKHEQEQISRLLEKGHPRQQLAIIFGIGVSTLYRYFPASSIKKRMN
>d1ijwc_ a.4.1.2 (C:) HIN recombinase (DNA-binding domain)
{Synthetic}
GRPRAINKHEQEQISRLLEKGHPRQQLAIIFGIGVSTLYRYFPASSI
>d1gdta1 a.4.1.2 (A:141-183) gamma,delta resolvase (C-terminal domain)
{Escherichia coli}
GRKRKIDRDAVLNMWQQGLGASHISKTMNIARSTVYKVINESN
>d1tc3c_ a.4.1.2 (C:) Transposase tc3a1-65 {Caenorhabditis elegans}
PRGSALSDTERAQLDVMKLLNVSLHEMSRKISRSRHCIRVYLKDPVSYGTS
>d2ezl__ a.4.1.2 (-) Ibeta subdomain of the mu end DNA-binding domain
of phage mu transposase {Bacteriophage mu}
MIARPTLEAHDYDREALWSKWDNASDSQRRLAEKWLPAVQAADEMLNQGISTKTAFATVAGHYQV
SASTLRDKYYQVQKFAKPDWAAALVDGRGASRRN
>d2ezh__ a.4.1.2 (-) Transposase {Bacteriophage mu}
SEFDEDAWQFLIADYLRPEKPAFRKCYERLELAAREHGWSIPSRATAFRRIQQLDEAMVVACREG
>d2ezi__ a.4.1.2 (-) Transposase {Bacteriophage mu}
MNVHKSEFDEDAWQFLIADYLRPEKPAFRKCYERLELAAREHGWSIPSRATAFRRIQQLDEAMVV
ACREGEHALM
>d1h88c1 a.4.1.3 (C:39-88) c-Myb, DNA-binding domain {Mouse (Mus
musculus)}
GKTRWTREEDEKLKKLVEQNGTDDWKVIANYLPNRTDVQCQHRWQKVLNP
>d1h88c2 a.4.1.3 (C:89-143) c-Myb, DNA-binding domain {Mouse (Mus
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musculus)}
ELIKGPWTKEEDQRVIKLVQKYGPKRWSVIAKHLKGRIGKQCRERWHNHLNPEVK
>d1idz__ a.4.1.3 (-) c-Myb, DNA-binding domain {Mouse (Mus musculus)}
MEVKKTSWTEEEDRILYQAHKRLGNRWAEIAKLLPGRTDNAIKNHWNSTMRRKV
>d1a5j_1 a.4.1.3 (1-55) b-Myb DNA binding domain {Chicken (Gallus
gallus)}
GIPDLVKGPWTKEEDQKVIELVKKYGTKQWTLIAKHLKGRLGKQCRERWHNHLNP
>d1a5j_2 a.4.1.3 (56-110) b-Myb DNA binding domain {Chicken (Gallus
gallus)}
EVKKSSWTEEEDRIIFEAHKVLGNRWAEIAKLLPGRTDNAVKNHWNSTIKRKVDT
>d1h8ac1 a.4.1.3 (C:87-143) v-Myb {Avian myeloblastosis virus}
NPELNKGPWTKEEDQRVIEHVQKYGPKRWSDIAKHLKGRIGKQCRERWHNHLNPEVK
>d1h8ac2 a.4.1.3 (C:144-191) v-Myb {Avian myeloblastosis virus}
KTSWTEEEDRIIYQAHKRLGNRWAEIAKLLPGRTDNAVKNHWNSTMRR
>d1fexa_ a.4.1.3 (A:) Rap1 {Human (Homo sapiens)}
GRIAFTDADDVAILTYVKENARSPSSVTGNALWKAMEKSSLTQHSWQSLKDRYLKHLRG
>d1ba5__ a.4.1.4 (-) DNA-binding domain of human telomeric protein,
htrf1 {Human (Homo sapiens)}
RKRQAWLWEEDKNLRSGVRKYGEGNWSKILLHYKFNNRTSVMLKDRWRTMKKL
>d1k78a1 a.4.1.5 (A:19-81) Pax-5 {Human (Homo sapiens)}
GVNQLGGVFVNGRPLPDVVRQRIVELAHQGVRPCDISRQLRVSHGCVSKILGRYYETGSIKPG
>d1k78a2 a.4.1.5 (A:82-142) Pax-5 {Human (Homo sapiens)}
VIGGSKPKVATPKVVEKIAEYKRQNPTMFAWEIRDRLLAERVCDNDTVPSVSSINRIIRTK
>d6paxa1 a.4.1.5 (A:1-68) Pax-6 {Human (Homo sapiens)}
SHSGVNQLGGVFVNGRPLPDSTRQRIVELAHSGARPCDISRILQVSNGCVSKILGRYYATGSIRP
RAI
>d6paxa2 a.4.1.5 (A:69-133) Pax-6 {Human (Homo sapiens)}
GGSKPRVATPEVVSKIAQYKQECPSIFAWEIRDRLLSEGVCTNDNIPSVSSINRVLRNLASEKQQ
>d1pdnc_ a.4.1.5 (C:) Paired protein (prd) {Fruit fly (Drosophila
melanogaster)}
QGRVNQLGGVFINGRPLPNNIRLKIVEMAADGIRPCVISRQLRVSHGCVSKILNRYQETGSIRPG
VIGGSKPRIATPEIENRIEEYKRSSPGMFSWEIREKLIREGVCDRSTAPSVSAISRLV
>d1igna1 a.4.1.6 (A:360-445) DNA-binding domain of rap1 {Baker's yeast
(Saccharomyces cerevisiae)}
KASFTDEEDEFILDVVRKNPTRRTTHTLYDEISHYVPNHTGNSIRHRFRVYLSKRLEYVYEVDKF
GKLVRDDDGNLIKTKVLPPSI
>d1igna2 a.4.1.6 (A:446-594) DNA-binding domain of rap1 {Baker's yeast
(Saccharomyces cerevisiae)}
KRKFSADEDYTLAIAVKKQFYRDLFQIDPDTGRSLITDEDTPTAIARRNMTMDPNHVPGSEPNFA
AYRTQSRRGPIAREFFKHFAEEHAAHTENAWRDRFRKFLLAYGIDDYISYYEAEKAQNREPEPMK
NLTNRPKRPGVPTPGNYNS
>d1bw6a_ a.4.1.7 (A:) DNA-binding domain of centromere binding protein
B (CENP-B) {Human (Homo sapiens)}
MGPKRRQLTFREKSRIIQEVEENPDLRKGEIARRFNIPPSTLSTILKNKRAILASE
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>d1hlva1 a.4.1.7 (A:1-66) DNA-binding domain of centromere binding
protein B (CENP-B) {Human (Homo sapiens)}
MGPKRRQLTFREKSRIIQEVEENPDLRKGEIARRFNIPPSTLSTILKNKRAILASERKYGVASTC
R
>d1hlva2 a.4.1.7 (A:67-131) DNA-binding domain of centromere binding
protein B (CENP-B) {Human (Homo sapiens)}
KTNKLSPYDKLEGLLIAWFQQIRAAGLPVKGIILKEKALRIAEELGMDDFTASNGWLDRFRRRRS
>d1g2ha_ a.4.1.10 (A:) Transcriptional regulator TyrR, C-terminal
domain {Haemophilus influenzae}
SAVISLDEFENKTLDEIIGFYEAQVLKLFYAEYPSTRKLAQRLGVSHTAIANKLKQYGIGK
>d1bl0a1 a.4.1.8 (A:9-62) MarA {Escherichia coli}
DAITIHSILDWIEDNLESPLSLEKVSERSGYSKWHLQRMFKKETGHSLGQYIRS
>d1bl0a2 a.4.1.8 (A:63-124) MarA {Escherichia coli}
RKMTEIAQKLKESNEPILYLAERYGFESQQTLTRTFKNYFDVPPHKYRMTNMQGESRFLHPL
>d1d5ya1 a.4.1.8 (A:3-56) Rob transcription factor, N-terminal domain
{Escherichia coli}
QAGIIRDLLIWLEGHLDQPLSLDNVAAKAGYSKWHLQRMFKDVTGHAIGAYIRA
>d1d5ya2 a.4.1.8 (A:57-121) Rob transcription factor, N-terminal
domain {Escherichia coli}
RRLSKSAVALRLTARPILDIALQYRFDSQQTFTRAFKKQFAQTPALYRRSPEWSAFGIRPPLRLG
>d1a6i_1 a.4.1.9 (2-67) Tetracyclin repressor (Tet-repressor, TetR)
{Escherichia coli}
SRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAVEILARHHDY
S
>d2tct_1 a.4.1.9 (2-67) Tetracyclin repressor (Tet-repressor, TetR)
{Escherichia coli}
ARLNRESVIDAALELLNETGIDGLTTRKLAQKLGIEQPTLYWHVKNKRALLDALAVEILARHHDY
S
>d1jt6a1 a.4.1.9 (A:2-72) Multidrug binding protein QacR
{Staphylococcus aureus}
NLKDKILGVAKELFIKNGYNATTTGEIVKLSESSKGNLYYHFKTKENLFLEILNIEESKWQEQWK
KEQIKA
>d1sfe_1 a.4.2.1 (93-176) Ada DNA repair protein {Escherichia coli}
GTAFQQQVWQALRTIPCGETVSYQQLANAIGKPKAVRAVASACAANKLAIVIPCHRVVRGDGSLS
GYRWGVSRKAQLLRREAEN
>d1qnta1 a.4.2.1 (A:92-176) O6-alkylguanine-DNA alkyltransferase
{Human (Homo sapiens)}
ESFTRQVLWKLLKVVKFGEVISYQQLAALAGNPKAARAVGGAMRGNPVPILIPCHRVVCSSGAVG
NYSGGLAVKEWLLAHEGHRL
>d1mgta1 a.4.2.1 (A:89-169) O6-alkylguanine-DNA alkyltransferase
{Archaeon Pyrococcus kodakaraensis}
VTPFEKKVYEWLTKNVKRGSVITYGDLAKALNTSPRAVGGAMKRNPYPIVVPCHRVVAHDGIGYY
SSGIEEKKFLLEIEGV
>d1c20a_ a.4.3.1 (A:) DNA-binding domain from the dead ringer protein
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{Fruit fly (Drosophila melanogaster)}
GWSFEEQFKQVRQLYEINDDPKRKEFLDDLFSFMQKRGTPINRLPIMAKSVLDLYELYNLVIARG
GLVDVINKKLWQEIIKGLHLPSSITSAAFTLRTQYMKYLYPYECEKKNLSTPAELQAAIDGNR
>d1ig6a_ a.4.3.2 (A:) MRF-2 DNA-binding domain {Human (Homo sapiens)}
RADEQAFLVALYKYMKERKTPIERIPYLGFKQINLWTMFQAAQKLGGYETITARRQWKHIYDELG
GNPGSTSAATCTRRHYERLILPYERFIKGEEDKPLPPIKPRK
>d1bia_1 a.4.5.1 (1-63) Biotin repressor, N-terminal domain
{Escherichia coli}
MKDNTVPLKLIALLANGEFHSGEQLGETLGMSRAAINKHIQTLRDWGVDVFTVPGKGYSLPEP
>d1jhfa1 a.4.5.2 (A:2-72) LexA repressor, N-terminal DNA-binding
domain {Escherichia coli}
KALTARQQEVFDLIRDHISQTGMPPTRAEIAQRLGFRSPNAAEEHLKALARKGVIEIVSGASRGI
RLLQEE
>d1aoy__ a.4.5.3 (-) Arginine repressor (ArgR), N-terminal
DNA-binding domain {Escherichia coli}
MRSSAKQEELVKAFKALLKEEKFSSQGEIVAALQEQGFDNINQSKVSRMLTKFGAVRTRNAKMEM
VYCLPAELGVPTT
>d1b4aa1 a.4.5.3 (A:4-78) Arginine repressor (ArgR), N-terminal
DNA-binding domain {Bacillus stearothermophilus}
GQRHIKIREIIMSNDIETQDELVDRLREAGFNVTQATVSRDIKEMQLVKVPMANGRYKYSLPSDQ
RFNPLQKLKR
>d1f9na1 a.4.5.3 (A:3-78) Arginine repressor (ArgR), N-terminal
DNA-binding domain {Bacillus subtilis}
KGQRHIKIREIITSNEIETQDELVDMLKQDGYKVTQATVSRDIKELHLVKVPTNNGSYKYSLPAD
QRFNPLSKLKR
>d1hw5a1 a.4.5.4 (A:138-208) Catabolite gene activator protein (CAP),
C-terminal domain {Escherichia coli}
DVTGRIAQTLLNLAKQPDAMTHPDGMQIKITRQEIGQIVGCSRETVGRILKMLEDQNLISAHGKT
IVVYGT
>d1ft9a1 a.4.5.4 (A:134-213) CO-sensing protein CooA, C-terminal
domain {Rhodospirillum rubrum}
DIKQRIAGFFIDHANTTGRQTQGGVIVSVDFTVEEIANLIGSSRQTTSTALNSLIKEGYISRQGR
GHYTIPNLVRLKAAA
>d1i1ga1 a.4.5.32 (A:2-61) LprA {Archaeon Pyrococcus furiosus}
IDERDKIILEILEKDARTPFTEIAKKLGISETAVRKRVKALEEKGIIEGYTIKINPKKLG
>d1smta_ a.4.5.5 (A:) SmtB repressor {Cyanobacteria (Synechococcus),
pcc7942}
ELQAIAPEVAQSLAEFFAVLADPNRLRLLSLLARSELCVGDLAQAIGVSESAVSHQLRSLRNLRL
VSYRKQGRHVYYQLQDHHIVALYQNALDHLQEC
>d1jgsa_ a.4.5.28 (A:) Multiple antibiotic resistance repressor, MarR
{Escherichia coli}
LFNEIIPLGRLIHMVNQKKDRLLNEYLSPLDITAAQFKVLCSIRCAACITPVELKKVLSVDLGAL
TRMLDRLVCKGWVERLPNPNDKRGVLVKLTTGGAAICEQCHQLVGQDLHQELTKNLTADEVATLE
YLLKKVLP
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>d1hsja1 a.4.5.28 (A:373-487) staphylococcal accessory regulator A homolog, SarR {Staphylococcus aureus}
MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYL
TKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYIKN
>d1fzpb_ a.4.5.28 (B:) Pleiotropic regulator of virulence genes, SarA {Staphylococcus aureus}
AITKINDCFELLSMVTYADKLKSLIKKEFSISFEEFAVLTYISENKEKEYYLKDIINHLNYKQPQ
VVKAVKILSQEDYFDKKRNEHDERTVLILVNAQQRKKIESLLSRVNKRIT
>d1hw1a1 a.4.5.6 (A:5-78) Fatty acid responsive transcription factor FadR, N-terminal domain {Escherichia coli}
AQSPAGFAEEYIIESIWNNRFPPGTILPAERELSELIGVTRTTLREVLQRLARDGWLTIQHGKPT
KVNNFWETS
>d1bm9a_ a.4.5.7 (A:) Replication terminator protein (RTP) {Bacillus subtilis}
EEKRSSTGFLVKQRAFLKLYMITMTEQERLYGLKLLEVLRSEFKEIGFKPNHTEVYRSLHELLDD
GILKQIKVKKEGAKLQEVVLYQFKDYEAAKLYKKQLKVELDRCKKLIEKALSDNF
>d1b9ma1 a.4.5.8 (A:-1-126) N-terminal domain of molybdate-dependent transcriptional regulator ModE {Escherichia coli}
HMQAEILLTLKLQQKLFADPRRISLLKHIALSGSISQGAKDAGISYKSAWDAINEMNQLSEHILV
ERATGGKGGGGAVLTRYGQRLIQLYDLLAQIQQKAFDVLSDDDALPLNSLLAAISRFSLQTS
>d1bjaa_ a.4.5.9 (A:) Transcription factor MotA, activation domain {Bacteriophage T4}
SKVTYIIKASNDVLNEKTATILITIAKKDFITAAEVREVHPDLGNAVVNSNIGVLIKKGLVEKSG
DGLIITGEAQDIISNAATLYAQENAPELLK
>d1repc1 a.4.5.10 (C:15-143) RepE54 {Escherichia coli, mini-F plasmid}
SPRIVQSNDLTEAAYSLSRDQKRMLYLFVDQIRKSDGTLQEHDGICEIHVAKYAEIFGLTSAEAS
KDIRQALKSFAGKEVVFYRPEEDAGDEKGYESFPWFIKPAHSPSRGLYSVHINPYLIPFFIGLQ
>d1repc2 a.4.5.10 (C:144-246) RepE54 {Escherichia coli, mini-F plasmid}
NRFTQFRLSETKEITNPYAMRLYESLCQYRKPDGSGIVSLKIDWIIERYQLPQSYQRMPDFRRRF
LQVCVNEINSRTPMRLSYIEKKKGRQTTHIVFSFRDIT
>d1hqca1 a.4.5.11 (A:243-318) Holliday junction helicase RuvB {Thermus thermophilus}
LGLEKRDREILEVLILRFGGGPVGLATLATALSEDPGTLEEVHEPYLIRQGLLKRTPRGRVPTEL
AYRHLGYPPPV
>d1in4a1 a.4.5.11 (A:255-329) Holliday junction helicase RuvB {Thermotoga maritima}
EGLDEFDRKILKTIIEIYRGGPVGLNALAASLGVEADTLSEVYEPYLLQAGFLARTPRGRIVTEK
AYKHLKYEVP
>d1fnna1 a.4.5.11 (A:277-388) CDC6, C-terminal domain {Archaeon Pyrobaculum aerophilum}
ISEEVLIGLPLHEKLFLLAIVRSLKISHTPYITFGDAEESYKIVCEEYGERPRVHSQLWSYLNDL
REKGIVETRQNKRGEGVRGRTTLISIGTEPLDTLEAVITKLIKEELR
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>d1foka3 a.4.5.12 (A:287-386) Restriction endonuclease FokI, N-terminal (recognition) domain {Flavobacterium okeanokoites}
VPKRVYWEMLATNLTDKEYVRTRRALILEILIKAGSLKIEQIQDNLKKLGFDEVIETIENDIKGL
INTGIFIEIKGRFYQLKDHILQFVIPNRGVTKQLV
>d2foka1 a.4.5.12 (A:5-143) Restriction endonuclease FokI, N-terminal (recognition) domain {Flavobacterium okeanokoites}
IRTFGWVQNPGKFENLKRVVQVFDRNSKVHNEVKNIKIPTLVKESKIQKELVAIMNQHDLIYTYK
ELVGTGTSIRSEAPCDAIIQATIADQGNKKGYIDNWSSDGFLRWAHALGFIEYINKSDSFVITDV
GLAYSKSAD
>d2foka2 a.4.5.12 (A:144-286) Restriction endonuclease FokI, N-terminal (recognition) domain {Flavobacterium okeanokoites}
GSAIEKEILIEAISSYPPAIRILTLLEDGQHLTKFDLGKNLGFSGESGFTSLPEGILLDTLANAM
PKDKGEIRNNWEGSSDKYARMIGGWLDKLGLVKQGKKEFIIPTLGKPDNKEFISHAFKITGEGLK
VLRRAKGSTKFTR
>d2foka3 a.4.5.12 (A:287-386) Restriction endonuclease FokI, N-terminal (recognition) domain {Flavobacterium okeanokoites}
VPKRVYWEMLATNLTDKEYVRTRRALILEILIKAGSLKIEQIQDNLKKLGFDEVIETIENDIKGL
INTGIFIEIKGRFYQLKDHILQFVIPNRLGKPDLV
>d1f1za1 a.4.5.27 (A:169-267) TnsA endonuclease, C-terminal domain {Escherichia coli}
NPVVKENIEWLYSVKTEEVSAELLAQLSPLAHILQEKGDENIINVCKQVDIAYDLELGKTLSEIR
ALTANGFIKFNIYKSFRANKCADLCISQVVNMEE
>d1fp1d1 a.4.5.29 (D:19-128) Chalcone O-methyltransferase {Alfalfa (Medicago sativa)}
QTEDSACLSAMVLTTNLVYPAVLNAAIDLNLFEIIAKATPPGAFMSPSEIASKLPASTQHSDLPN
RLDRMLRLLASYSVLTSTTRTIEDGGAERVYGLSMVGKYLVPDES
>d1fp2a1 a.4.5.29 (A:8-108) Isoflavone O-methyltransferase {Alfalfa (Medicago sativa)}
RKPSEIFKAQALLYKHIYAFIDSMSLKWAVEMNIPNIIQNHGKPISLSNLVSILQVPSSKIGNVR
RLMRYLAHNGFFEIITKEEESYALTVASELLVRGSD
>d1hsta_ a.4.5.13 (A:) Histone H5, globular domain {Chicken (Gallus gallus)}
SHPTYSEMIAAAIRAEKSRGGSSRQSIQKYIKSHYKVGHNADLQIKLSIRRLLAAGVLKQTKGVG
ASGSFRLAK
>d1ghc__ a.4.5.13 (-) Histone H1, globular domain {Chicken (Gallus gallus)}
MAGPSVTELITKAVSASKERKGLSLAALKKALAAGGYDVEKNNSRIKLGLKSLVSKGTLVQTKGT
GASGSFRLSK
>d1e17a_ a.4.5.14 (A:) Afx (Foxo4) {Human (Homo sapiens)}
SRRNAWGNQSYAELISQAIESAPEKRLTLAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSL
HSKFIKVHNEATGKSSWWMLNPEGG
>d1d5va_ a.4.5.14 (A:) Adipocyte-transcription factor FREAC-11 (s12, fkh-14) {Human (Homo sapiens)}
MLVKPPYSYIALITMAIQNAPEKKITLNGIYQFIMDRFPFYRENKQGWQNSIRHNLSLNECFVKV

PRDDKKPGKGSYWTLDPDSYNMFENGSFL
>d2hdca_ a.4.5.14 (A:) Genesis {Rat (Rattus norvegicus)}
VKPPYSYIALITMAILQSPQKKLTLSGICEFISNRFPYYREKFPAWQNSIRHNLSLNDCFVKIPR
EPGNPGKGNYWTLDPQSEDMFDNGSFLRRRKR
>d1kq8a_ a.4.5.14 (A:) HFH-1 (HNF-3 forkhead homolog-1) {Rat (Rattus norvegicus)}
YIALITMAIRDSAGGRLTLAEINEYLMGKFPFFRGSYTGWRNSVRHNLSLNDCFVKVLRDPSRPW
GKDNYWMLNP
>d2bby__ a.4.5.15 (-) DNA-binding domain from rap30 {Human (Homo sapiens)}
RARADKQHVLDMLFSAFEKHQYYNLKDLVDITKQPVVYLKEILKEIGVQNVKGIHKNTWELKPEY
RHYQ
>d1i27a_ a.4.5.30 (A:) C-terminal domain of the rap74 subunit of TFIIF {Human (Homo sapiens)}
GPLGSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTKKTGLSSEQTVNVLAQILKRLNPERKMIND
KMHFSLKE
>d1dpua_ a.4.5.16 (A:) C-terminal domain of RPA32 {Human (Homo sapiens)}
ANGLTVAQNQVLNLIKACPRPEGLNFQDLKNQLKHMSVSSIKQAVDFLSNEGHIYSTVDDDHFKS
TDAE
>d1fsha_ a.4.5.31 (A:) Segment polarity protein Dishevelled-1 {Mouse (Mus musculus)}
EAPLTVKSDMSAIVRVMQLPDSGLEIRDRMWLKITIANAVIGADVVDWLYTHVEGFKERREARKY
ASSMLKHGFLRHTVNKITFSEQCYYVFGD
>d1cf7a_ a.4.5.17 (A:) Cell cycle transcription factor e2f-dp {Human (Homo sapiens)}
SRHEKSLGLLTTKFVSLLQEAKDGVLDLKLAADTLAVRQKRRIYDITNVLEGIGLIEKKSKNSIQ
WK
>d1cf7b_ a.4.5.17 (B:) Cell cycle transcription factor e2f-dp {Human (Homo sapiens)}
GKGLRHFSMKVCEKVQRKGTTSYNEVADELVSEFTNSNNHLAADSAYDQKNIRRRVYDALNVLMA
MNIISKEKKEIKWIGLP
>d1d8ja_ a.4.5.18 (A:) The central core domain of TFIIE beta {Human (Homo sapiens)}
ALSGSSGYKFGVLAKIVNYMKTRHQRGDTHPLTLDEILDETQHLDIGLKQKQWLMTEALVNNPKI
EVIDGKYAFKPKYNVR
>d1qbja_ a.4.5.19 (A:) Z-alpha domain of dsRNA-specific adenosine deaminase, ADAR1 {Human (Homo sapiens)}
SIYQDQEQRILKFLEELGEGKATTAHDLSGKLGTPKKEINRVLYSLAKKGKLQKEAGTPPLWKIA
>d1qgpa_ a.4.5.19 (A:) Z-alpha domain of dsRNA-specific adenosine deaminase, ADAR1 {Human (Homo sapiens)}
LSSHFQELSIYQDQEQRILKFLEELGEGKATTAHDLSGKLGTPKKEINRVLYSLAKKGKLQKEAG
TPPLWKIAVSD
>d1j75a_ a.4.5.19 (A:) Dlm-1 {Mouse (Mus musculus)}

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NLEQKILQVLSDDGGPVKIGQLVKKCQVPKKTLNQVLYRLKKEDRVSSPEPATWSIG
>d1dp7p_ a.4.5.20 (P:) MHC class II transcription factor RFX1 {Human
(Homo sapiens)}
TVQWLLDNYETAEGVSLPRSTLYNHYLLHSQEQKLEPVNAASFGKLIRSVFMGLRTRRLGTRGNS
KYHYYGLRIKA
>d1flia_ a.4.5.21 (A:) Fli-1 {Human (Homo sapiens)}
PGSGQIQLWQFLLELLSDSANASCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALR
YYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHP
>d1k78b_ a.4.5.21 (B:) ETS-1 transcription factor, residues 331-440
{Mouse (Mus musculus)}
IQLWQFLLELLTDKSCQSFISWTGDGWEFKLSDPDEVARRWGKRKNKPKMNYEKLSRGLRYYYDK
NIIHKTAGKRYVYRFVCDLQSLLGYTPEELHAMLDVK
>d2stta_ a.4.5.21 (A:) ETS-1 transcription factor, residues 331-440
{Human (Homo sapiens)}
VIPAAALAGYTGSGPIQLWQFLLELLTDKSCQSFISWTGDGWEFKLSDPDEVARRWGKRKNKPKM
NYEKLSRGLRYYYDKNIIHKTAGKRYVYRFV
>d1puee_ a.4.5.21 (E:) Transcription factor PU.1, residues 171-259
{Mouse (Mus musculus)}
KIRLYQFLLDLLRSGDMKDSIWWVDKDKGTFQFSSKHKEALAHRWGIQKGNRKKMTYEKMARALR
NYGKTGEVKKVKKKLTYQFSGEV
>d1awca_ a.4.5.21 (A:) GA binding protein (GABP) alpha {Mouse (Mus
musculus)}
IQLWQFLLELLTDKDARDCISWVGDEGEFKLNQPELVAQKWGQRKNKPTMNYEKLSRALRYYYDG
DMICKVQGKRFVYKFVCDLKTLIGYSAAELNRLVIECEQKKLARM
>d1bc8c_ a.4.5.21 (C:) Serum responce factor accessory protein 1a,
SAP-1 {Human (Homo sapiens)}
MDSAITLWQFLLQLLQKPQNKHMICWTSNDGQFKLLQAEEVARLWGIRKNKPNMNYDKLSRALRY
YYVKNIIKKVNGQKFVYKFVSYPEILNM
>d1hbxg_ a.4.5.21 (G:) Serum responce factor accessory protein 1a,
SAP-1 {Human (Homo sapiens)}
DSAITLWQFLLQLLQKPQNKHMICWTSNDGQFKLLQAEEVARLWGIRKNKPNMNYDKLSRALRYY
YVKNIIKKVNGQKFVYKFVSYPEILNMDPMTVGRIEGDCESLNFSEVSSSSKDVENGGKDKPPQP
GAKTSSRNDYIHSGLYSSFTLNSLN
>d1duxc_ a.4.5.21 (C:) Elk-1 {Human (Homo sapiens)}
VTLWQFLLQLLREQGNGHIISWTSRDGGEFKLVDAEEVARLWGLRKNKTNMNYDKLSRALRYYYD
KNIIRKVSGQKFVYKFVSYPE
>d1hks__ a.4.5.22 (-) Heat-shock transcription factor {Drosophila
melanogaster}
GSGVPAFLAKLWRLVDDADTNRLICWTKDGQSFVIQNQAQFAKELLPLNYKHNNMASFIRQLNMY
GFHKITSIDNGGLRFDRDEIEFSHPFFKRNSPFLLDQIKRK
>d1fbqa_ a.4.5.22 (A:) Heat-shock transcription factor {Milk yeast
(Kluyveromyces lactis)}
PAFVNKLWSMVNDKSNEKFIHWSTSGESIVVPNRERFVQEVLKKYFKHSNFASFVRQLNMYGWHK
VQDVKSGSMLSNNDSRWEFENERH
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>d2hts__ a.4.5.22 (-) Heat-shock transcription factor {Milk yeast (Kluyveromyces lactis)}
ARPAFVNKLWSMVNDKSNEKFIHWSTSGESIVVPNRERFVQEVLPKYFKHSNFASFVRQLNMYGW
HKVQDVKSGSNDSRWEFENERHA
>d1if1a_ a.4.5.23 (A:) Interferon regulatory factor 1 (IRF-1) {Mouse (Mus musculus)}
RMRPWLEMQINSNQIPGLIWINKEEMIFQIPWKHAAKHGWDINKDACLFRSWAIHTGRYKAGEKE
PDPKTWKANFRCAMNSLPDIEEVKDQSRNKGSSAVRVYRM
>d2irfg_ a.4.5.23 (G:) Interferon regulatory factor-2, IRF-2 {Mouse (Mus musculus)}
RMRMRPWLEEQINSNTIPGLKWLNKEKKIFQIPWMHAARHGWDVEKDAPLFRNWAIHTGKHQPGI
DKPDPKTWKANFRCAMNSLPDIEEVKDRSIKKGNNAFRVYRMLP
>d1g3sa1 a.4.5.24 (A:4-64) Diphtheria toxin repressor (DtxR) {Corynebacterium diphtheriae}
LVDTTEMYLRTIYELEEEGVTPLRARIAERLEQSGPTVSQTVARMERDGLVVVASDRSLQM
>d1fx7a1 a.4.5.24 (A:1-64) Iron-dependent regulator IdeR {Mycobacterium tuberculosis}
MNELVDTTEMYLRTIYDLEEEGVTPLRARIAERLDQSGPTVSQTVSRMERDGLLRVAGDRHLEL
>d1xgsa1 a.4.5.25 (A:195-271) Methionine aminopeptidase, insert domain {Archaeon Pyrococcus furiosus}
GQVIEVPPTLIYMYVRDVPVRVAQARFLLAKIKREYGTLPFAYRWLQNDMPEGQLKLALKTLEKA
GAIYGYPVLKEI
>d1b6a_1 a.4.5.25 (375-448) Methionine aminopeptidase, insert domain {Human (Homo sapiens)}
HDDMECSHYMKNFDVGHVPIRLPRTKHLLNVINENFGTLAFCRRWLDRLGESKYLMALKNLCDLG
IVDPYPPLC
>d1g4da_ a.4.5.26 (A:) mu transposase, DNA-binding domain {Bacteriophage mu}
KSIWCSPQEIMAADGMPGSVAGVHYRANVQGWTKRKKEGVKGGKAVEYDVMSMPTKEREQVIAHL
GLST
>d1tns__ a.4.5.26 (-) mu transposase, DNA-binding domain {Bacteriophage mu}
MELWVSPKELANLPGLPKTSAGVIYVAKKQGWQNRTRAGVKGGKAIEYNANSLPVEAKAALLLRQ
GEIETSLGYFE
>d1opc__ a.4.6.1 (-) OmpR {Escherichia coli}
VIAFGKFKLNLGTREMFREDEPMPLTSGEFAVLKALVSHPREPLSRDKLMNLARGREYSAMERSI
DVQISRLRRMVEEDPAHPRYIQTVWGLGYVFVPD
>d1kgsa1 a.4.6.1 (A:124-225) PhoB {Thermotoga maritima}
SKSTKLVCGDLILDTATKKAYRGSKEIDLTKKEYQILEYLVMNKNRVVTKEELQEHLWSFDDEVF
SDVLRSHIKNLRKKVDKGFKKKIIHTVRGIGYVARDE
>d1qqia_ a.4.6.1 (A:) PhoB {Escherichia coli}
MAVEEVIEMQGLSLDPTSHRVMAGEEPLEMGPTEFKLLHFFMTHPERVYSREQLLNHVWGTNVYV
EDRTVDVHIRRLRKALEPGGHDRMVQTVRGTGYRFSTRF
>d1fsea_ a.4.6.2 (A:) Germination protein GerE {Bacillus subtilis}

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SKPLLTKREREVFELLVQDKTTKEIASELFISEKTVRNHISNAMQKLGVKGRSQAVVELLRMGEL
EL
>d1a04a1 a.4.6.2 (A:150-216) Nitrate/nitrite response regulator (NarL)
{Escherichia coli}
ERDVNQLTPRERDILKLIAQGLPNKMIARRLDITESTVKVHVKHMLKKMKLKSRVEAAVWVHQER
IF
>d1fc3a_ a.4.6.3 (A:) SpoOA {Bacillus stearothermophilus}
NKPKNLDASITSIIHEIGVPAHIKGYLYLREAIAMVYHDIELLGSITKVLYPDIAKKYNTTASRV
ERAIRHAIEVAWSRGNLESISSLFGYTVSVSKAKPTNSEFIAMVADKLRLEHKA
>d1fox__ a.4.7.1 (-) Ribosomal protein L11, C-terminal domain
{Bacillus stearothermophilus}
MTFITKTPPAAVLLKKAAGIESGSGEPNRNKVATIKRDKVREIAELKMPDLNAASIEAAMRMIEG
TARSMGIVVED
>d1qa6a_ a.4.7.1 (A:) Ribosomal protein L11, C-terminal domain
{Bacillus stearothermophilus}
KTPPAAVLLKKAAGIESGSGEPNRNKVATIKRDKVREIAELKMPDLNAASIEAAMRMIEGTARSM
GI
>d1mmsa1 a.4.7.1 (A:71-140) Ribosomal protein L11, C-terminal domain
{Thermotoga maritima}
KTPPASFLLKKAAGIEKGSSEPKRKIVGKVTRKQIEEIAKTKMPDLNANSLEAAMKIIEGTAKSM
GIEVV
>d1fjgr_ a.4.8.1 (R:) Ribosomal protein S18 {Thermus thermophilus}
PSRKAKVKATLGEFDLRDYRNVEVLKRFLSETGKILPRRRTGLSGKEQRILAKTIKRARILGLLP
FTEKLVRK
>d1g1xc_ a.4.8.1 (C:) Ribosomal protein S18 {Thermus thermophilus}
DLRDYRNVEVLKRFLSETGKILPRRRTGLSGKEQRILAKTIKRARILGLLPFT
>d1i94r_ a.4.8.1 (R:) Ribosomal protein S18 {Thermus thermophilus}
KPKKEAQRRPSRKAKVKATLGEFDLRDYRNVEVLKRFLSETGKILPRRRTGLSGKEQRILAKTIK
RARILGLLPFTEKLVRK
>d1e3ha1 a.4.9.1 (A:263-345) Polynucleotide phosphorylase/guanosine
pentaphosphate synthase (PNPase/GPSI), domain 3 {Streptomyces
antibioticus}
YQDDVLEALSAAVRPELSAALTIAGKQDREAELDRVKALAAEKLLPEFEGREKEISAAYRALTKS
LVRERVIAEKKRIDGRGV
>d1k6ya1 a.4.10.1 (A:1-46) N-terminal Zn binding domain of HIV
integrase {Human immunodeficiency virus type 1}
FLDGIDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDKCQLK
>d1wjba_ a.4.10.1 (A:) N-terminal Zn binding domain of HIV integrase
{Human immunodeficiency virus type 1}
FLDGIDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDKCQLKGEAMHGQVD
>d1e0ea_ a.4.10.1 (A:) N-terminal Zn binding domain of HIV integrase
{Human immunodeficiency virus type 2}
FLEKIEPAQEEHEKYHSNVKELSHKFGIPNLVARQIVNSCAQCQQK
>d1ef4a_ a.4.11.1 (A:) RNA polymerase subunit RPB10 {Archaeon
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Methanobacterium thermoautotrophicum}
MIPVRCLSCGKPVSAYFNEYQRRVADGEDPKDVLDDLGLKRYCCRRMLISHVETW
>d1i50j_ a.4.11.1 (J:) RNA polymerase subunit RPB10 {Baker's yeast
(Saccharomyces cerevisiae)}
MIVPVRCFSCGKVVGDKWESYLNLLQEDELDEGTALSRLGLKRYCCRRMILTHVDLIEKFLRYNP
>d1cuk_1 a.5.1.1 (156-203) DNA helicase RuvA subunit, C-terminal
domain {Escherichia coli}
TDDAEQEAVARLVALGYKPQEASRMVSKIARPDASSETLIREALRAAL
>d1bvsa1 a.5.1.1 (A:148-203) DNA helicase RuvA subunit, C-terminal
domain {Mycobacterium leprae}
NAVRGSVVEALVGLGFAAKQAEEATDQVLDGELGKDGAVATSSALRAALSLLGKTR
>d1f4ia_ a.5.2.1 (A:) C-terminal UBA domain of the hhr23a DNA repair
protein {Human (Homo sapiens)}
QEKEAIERLKALGFEESLVIQAYFACEKNENLAANFLLSQNFDDE
>d1efub3 a.5.2.2 (B:1-54) Elongation factor Ts (EF-Ts), N-terminal
domain {Escherichia coli}
AEITASLVKELRERTGAGMMDCKKALTEANGDIELAIENMRKSGAIKAAKKAGN
>d1aipc1 a.5.2.2 (C:2-53) Elongation factor Ts (EF-Ts), N-terminal
domain {Thermus thermophilus}
SQMELIKKLREATGAGMMDVKRALEDAGWDEEKAVQLLRERGAMKAAKKADR
>d1go5a_ a.5.2.3 (A:) FG-binding, C-terminal domain of TAP {Human (Homo
sapiens)}
PAPTPSSSPVPTLSPEQQEMLQAFSTQSGMNLEWSQKCLQDNNWDYTRSAQAFTHLKAKGEIPEV
AFMK
>d1aua_1 a.5.3.1 (4-96) N-terminal domain of phosphatidylinositol
transfer protein sec14p {Baker's yeast (Saccharomyces cerevisiae)}
QQEKEFLESYPQNCPPDALPGTPGNLDSAQEKALAELRKLLEDAGFIERLDDSTLLRFLRARKFD
VQLAKEMFENCEKWRKDYGTDTILQDFH
>d1enwa_ a.5.4.1 (A:) Elongation factor TFIIS domain 2 {Baker's yeast
(Saccharomyces cerevisiae)}
GSHMPRNSKNDGVDTAIYHHKLRDQVLKALYDVLAKESEHPPQSILHTAKAIESEMNKVNNCDTN
EAAYKARYRIIYSNVISKNNPDLKHKIANGDITPEFLATCDAKDLAPAP
>d1fjgm_ a.5.5.1 (M:) Ribosomal protein S13 {Thermus thermophilus}
ARIAGVEIPRNKRVDVALTYIYGIGKARAKEALEKTGINPATRVKDLTEAEVVRLREYVENTWKL
EGELRAEVAANIKRLMDIGCYRGLRHRRGLPVRGQRTRTNARTRKGPRKTVAGKKKAPRK
>d1i94m_ a.5.5.1 (M:) Ribosomal protein S13 {Thermus thermophilus}
ARIAGVEIPRNKRVDVALTYIYGIGKARAKEALEKTGINPATRVKDLTEAEVVRLREYVENTWKL
EGELRAEVAANIKRLMDIGCYRGLRHRR
>d1eija_ a.5.6.1 (A:) Hypothetical protein MTH1615 {Archaeon
Methanobacterium thermoautotrophicum}
MRQQLEMQKKQIMMQILTPEARSRLANLRLTRPDFVEQIELQLIQLAQMGRVRSKITDEQLKELL
KRVAGKK
>d1jjcb1 a.6.1.1 (B:1-38,B:152-190) Domains B1 and B5 of PheRS-beta,
PheT {Thermus thermophilus (Thermus aquaticus)}
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MRVPFSWLKAYVPELESPEVLEERLAGLGFETDRIERVXEEVVLDLEVTPNRPDALGLLGLARDL
HALGYALVEPEAA
>d1jjcb2 a.6.1.1 (B:400-474) Domains B1 and B5 of PheRS-beta, PheT
{Thermus thermophilus (Thermus aquaticus)}
PPEAIPFRPEYANRLLGTSYPEAEQIAILKRLGCRVEGEGPTYRVTPPSHRLDLRLEEDLVEEVA
RIQGYETIPL
>d1d4ua1 a.6.1.2 (A:37-111) DNA repair factor XPA DNA- and RPA-binding
domain, C-terminal subdomain {Human (Homo sapiens)}
DKHKLITKTEAKQEYLLKDCDLEKREPPLKFIVKKNPHHSQWGDMKLYLKLQIVKRSLEVWGSQE
ALEEAKEVRQ
>d1exja1 a.6.1.3 (A:3-120) Transcription activator BmrR {Bacillus
subtilis}
ESYYSIGEVSKLANVSIKALRYYDKIDLFKPAYVDPDTSYRYYTDSQLIHLDLIKSLKYIGTPLE
EMKKAQDLEMEELFAFYTEQERQIREKLDFLSALEQTISLVKKRMKRQMEYPA
>d1jbga_ a.6.1.3 (A:) Multidrug transporter activator MtaN {Bacillus
subtilis}
KYQVKQVAEISGVSIRTLHHYDNIELLNPSALTDAGYRLYSDADLERLQQILFFKEIGFRLDEIK
EMLDHPNFDRKAALQSQKEILMKKKQRMDEMIQTIDRTLLS
>d2spca_ a.7.1.1 (A:) Spectrin {Fruit fly (Drosophila sp.)}
QNLDLQLYMRDCELAESWMSAREAFLNADDDANAGGNVEALIKKHEDFDKAINGHEQKIAALQTV
ADQLIAQNHYASNLVDEKRKQVLERWRHLKEGLIEKRSRLGD
>d1aj3__ a.7.1.1 (-) Spectrin {Chicken (Gallus gallus)}
HQFFRDMDDEESWIKEKKLLVSSEDYGRDLTGVQNLRKKHKRLEAELAAHEPAIQGVLDTGKKLS
DDNTIGKEEIQQRLAQFVDHWKELKQLAAARGQ
>d1cuna1 a.7.1.1 (A:7-115) Spectrin {Chicken (Gallus gallus)}
MVHQFFRDMDDEESWIKEKKLLVSSEDYGRDLTGVQNLRKKHKRLEAELAAHEPAIQSVLDTGKK
LSDDNTIGKEEIQQRLAQFVDHWKELKQLAAARGQRLEESLEYQ
>d1cuna2 a.7.1.1 (A:116-219) Spectrin {Chicken (Gallus gallus)}
QFVANVEEEEAWINEKMTLVASEDYGDTLAAIQGLLKKHEAFETDFTVHKDRVNDVCANGEDLIK
KNNHHVENITAKMKGLKGKVSDLEKAAAQRKAKLDENSA
>d1hcia1 a.7.1.1 (A:272-396) alpha-actinin {Human (Homo sapiens)}
SSAVNQENERLMEEYERLASELLEWIRRTIPWLENRTPEKTMQAMQKKLEDFRDYRRKHKPPKVQ
EKCQLEINFNTLQTKLRISNRPAFMPSEGKMVSDIAGAWQRLEQAEKGYEEWLLNEIRRL
>d1hcia4 a.7.1.1 (A:633-746) alpha-actinin {Human (Homo sapiens)}
HANERLRRQFAAQANAIGPWIQNKMEEIARSSIQITGALEDQMNQLKQYEHNIINYKNNIDKLEG
DHQLIQEALVFDNKHTNYTMEHIRVGWELLLTTIARTINEVETQILTRD
>d1quua1 a.7.1.1 (A:1-124) alpha-actinin {Human (Homo sapiens)}
GSSNEIRRLERLEHLAEKFRQKASTHETWAYGKEQILLQKDYESASLTEVRALLRKHEAFESDLA
AHQDRVEQIAAIAQELNELDYHDAVNVNDRCQKICDQWDRLGTLTQKRREALERMEKLL
>d1quua2 a.7.1.1 (A:125-248) alpha-actinin {Human (Homo sapiens)}
ETIDQLHLEFAKRAAPFNNWMEGAMEDLQDMFIVHSIEEIQSLITAHEQFKATLPEADGERQSIM
AIQNEVEKVIQSYNIRISSSNPYSTVTMDELRTKWDKVKQLVPIRDQSLQEELARQHAN
>d1e2aa_ a.7.2.1 (A:) Enzyme IIa from lactose specific PTS, IIa-lac
{Lactococcus lactis}
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MNREEMTLLGFEIVAYAGDARSKLLEALKAAENGDFAKADSLVVEAGSCIAEAHSSQTGMLAREA
SGEELPYSVTMMHGQDHLMTTILLKDVIHHLIELYKR
>d1chua1 a.7.3.1 (A:423-533) L-aspartate oxidase {Escherichia coli}
DESRVENPDERVVIQHNWHELRLFMWDYVGIVRTTKRLERALRRITMLQQEIDEYYAHFRVSNNL
LELRNLVQVAELIVRCAMMRKESRGLHFTLDYPELLTHSGPSILSP
>d1fuma1 a.7.3.1 (A:443-575) Fumarate reductase flavoprotein subunit
{Escherichia coli}
DGGENWAKIRDEMGLAMEEGCGIYRTPELMQKTIDKLAELQERFKRVRITDTSSVFNTDLLYTIE
LGHGLNVAECMAHSAMARKESRGAHQRLDEGCTERDDVNFLKHTLAFRDADGTTRLEYSDVKITT
LPP
>d1qlaa1 a.7.3.1 (A:458-655) Fumarate reductase flavoprotein subunit
{Wolinella succinogenes}
KGTEDVFKIKNRMKDVMDDNVGIFRDGPHLEKSVKELEELYKKSKNVGIKNKRLHANPELEEAYR
VPMMLKVALCVAKGALDRTESRGAHNREDYPKRDDINWLNRTLASWPNPEQTLPTLEYEALDVNE
MEIAPRYRGYGAKGNYIENPLSVKRQEEIDKIQSELEAAGKDRHAIQEALMPYELPAKYKARNER
LGD
>d1jnra1 a.7.3.1 (A:503-643) Adenylylsulfate reductase A subunit
{Archaeon Archaeoglobus fulgidus}
TADDVNPEYILPWQGLVRLQKIMDEYAAGIATIYKTNEKMLQRALELLAFLKEDLEKLAARDLHE
LMRAWELVHRVWTAEAHVRHMLFRKETRWPGYYYRTDYPELNDEEWKCFVCSKYDAEKDEWTFEK
VPYVQVIEWSF
>d1fewa_ a.7.4.1 (A:) Smac/diablo {Human (Homo sapiens)}
SLSSEALMRRAVSLVTDSTSTFLSQTTYALIEAITEYTKAVYTLTSLYRQYTSLLGKMNSEEEDE
VWQVIIGARAEMTSKHQEYLKLETTWMTAVGLSEMAAEAAYQTGADQASITARNHIQLVKLQVEE
VHQLSRKAETKLAEAQIEELKQKTQEEGEERAESEQEAYLRED
>d1g73a_ a.7.4.1 (A:) Smac/diablo {Human (Homo sapiens)}
AVPIAQKSEPHSLSSEALMRRAVSLVTDSTSTDLSQTTYALIEAITEYTKAVYTLTSLYRQYTSL
LGKMNSEEEDEVWQVIIGARAEMTSKHQEYLKLETTWMTAVGLSEMAAEAAYQTGADQASITARN
HIQLVKLQVEEVHQLSRKAETKLAEAQ
>d1hx1b_ a.7.7.1 (B:) BAG-family molecular chaperon regulator-1, BAG1
{Human (Homo sapiens)}
GNSPQEEVELKKLKHLEKSVEKIADQLEELNKELTGIQQGFLPKDLQAEALCKLDRRVKATIEQF
MKILEEIDTLILPENFKDSRLKRKGLVKKVQAFLAECDTVEQNICQE
>d1i6za_ a.7.7.1 (A:) BAG-family molecular chaperon regulator-1, BAG1
{Mouse (Mus musculus)}
GSPEFMLIGEKSNPEEEVELKKLKDLEVSAEKIANHLQELNKELSGIQQGFLAKELQAEALCKLD
RKVKATIEQFMKILEEIDTMVLPEQFKDSRLKRKNLVKKVQVFLAECDTVEQYICQETERLQSTN
LALAE
>d1qsda_ a.7.5.1 (A:) beta-Tubulin binding post-chaperonin cofactor
Rbl2p {Baker's yeast (Saccharomyces cerevisiae)}
TQLDIKVKALKRLTKEEGYYQQELKDQEAHVAKLKEDKSVDPYDLKKQEEVLDDTKRLLPTLYEK
IREFKEDLEQFLKTYQGTEDVSDARSAITSAQELLDS
>d1fjgt_ a.7.6.1 (T:) Ribosomal protein S20 {Thermus thermophilus}
RNLSALKRHRQSLKRRLRNKAKKSAIKTLSKKAVQLAQEGKAEEALKIMRKAESLIDKAAKGSTL
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HKNAAARRKSRLMRKVRQLLEAAGAPLIGGGLSA
>d1bdc__ a.8.1.1 (-) Immunoglobulin-binding protein A modules
{Staphylococcus aureus}
TADNKFNKEQQNAFYEILHLPNLNEEQRNGFIQSLKDDPSQSANLLAEAKKLNDAQAPKA
>d1deeg_ a.8.1.1 (G:) Immunoglobulin-binding protein A modules
{Staphylococcus aureus}
DQQSAFYEILNMPNLNEAQRNGFIQSLKDDPSQSTNVLGEAKKLNESQAPK
>d1edj__ a.8.1.1 (-) Immunoglobulin-binding protein A modules
{Staphylococcus aureus}
AQHDEAQQNAFYQVLNMPNLNADQRNGFIQSLKDDPSQSANVLGEAQKLNDSQAPK
>d1fc2c_ a.8.1.1 (C:) Immunoglobulin-binding protein A modules
{Staphylococcus aureus}
FNKEQQNAFYEILHLPNLNEEQRNGFIQSLKDDPSQSANLLAEA
>d2spza_ a.8.1.1 (A:) Immunoglobulin-binding protein A modules
{Staphylococcus aureus}
VDNKFNKEQQNAFYEILHLPNLNEEQRNAFIQSLKDDPSQSANLLAEAKKLNDAQAPK
>d1gab__ a.8.1.2 (-) PAB {Peptostreptococcus magnus}
TIDQWLLKNAKEDAIAELKKAGITSDFYFNAINKAKTVEEVNALKNEILKAHA
>d1gjta_ a.8.1.2 (A:) IgG binding protein G {Streptococcus sp., group
G}
MKAIFVLNAQHDEAVDANSLAEAKVLANRELDKYGVSDYYKNLINNAKTVEGVKALIDEILAALP
>d1ebdc_ a.9.1.1 (C:) E3-binding domain of dihydrolipoamide
acetyltransferase {Bacillus stearothermophilus}
IAMPSVRKYAREKGVDIRLVQGTGKNGRVLKEDIDAFLAGG
>d1bal__ a.9.1.1 (-) E3-binding domain of dihydrolipoamide
succinyltransferase {Escherichia coli}
YASLEEQNNDALSPAIRRLLAEHNLDASAIKGTGVGGRLTREDVEKHLAKA
>d1bbl__ a.9.1.1 (-) E3-binding domain of dihydrolipoamide
succinyltransferase {Escherichia coli}
LSPAIRRLLAEHNLDASAIKGTGVGGRLTREDVEKHL
>d2erl__ a.10.1.1 (-) ER-1 {Euplotes raikovi}
DACEQAAIQCVESACESLCTEGEDRTGCYMYIYSNCPPYV
>d1erd__ a.10.1.1 (-) ER-2 {Euplotes raikovi}
DPMTCEQAMASCEHTMCGYCQGPLYMTCIGITTDPECGLP
>d1erp__ a.10.1.1 (-) ER-10 {Euplotes raikovi}
DLCEQSALQCNEQGCHNFCSPEDKPGCLGMVWNPELCP
>d1ery__ a.10.1.1 (-) ER-11 {Euplotes raikovi}
DECANAAAQCSITLCNLYCGPLIEICELTVMQNCEPPFS
>d1hd6a_ a.10.1.1 (A:) ER-22 {Euplotes raikovi}
DICDIAIAQCSLTLCQDCENTPICELAVKGSCPPPWS
>d1aca__ a.11.1.1 (-) Acyl-CoA binding protein {Cow (Bos taurus)}
SQAEFDKAAEEVKHLKTKPADEEMLFIYSHYKQATVGDINTERPGMLDFKGKAKWDAWNELKGTS
KEDAMKAYIDKVEELKKKYGI
>d1hbka_ a.11.1.1 (A:) Acyl-CoA binding protein {Plasmodium
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falciparum}
HMAQQVFEEECVSFINGLPRTINNLPNELKLDLYKYYKQSTIGNCNIKEPSAHKYIDRKKYEEAW
KSVENLNREDAQKKRYVDIVSEIFPYWQD
>d1ef1a1 a.11.2.1 (A:88-198) Moesin {Human (Homo sapiens)}
DVSEELIQDITQRLFFLQVKEGILNDDIYCPPETAVLLASYAVQSKYGDFNKEVHKSGYLAGDKL
LPQRVLEQHKLNKDQWEERIQVWHEEHRGMLREDAVLEYLKIAQDL
>d1gc7a1 a.11.2.1 (A:88-198) Radixin {Mouse (Mus musculus)}
DVSEELIQEITQRLFFLQVKEAILNDEIYCPPETAVLLASYAVQAKYGDYNKEIHKPGYLANDRL
LPQRVLEQHKLTKEQWEERIQNWHEEHRGMLREDSMMEYLKIAQDL
>d1gg3a1 a.11.2.1 (A:82-187) Erythroid membrane protein 4.1R {Human (Homo sapiens)}
PDPAQLTEDITRYYLCLQLRQDIVAGRLPCSFATLALLGSYTIQSELGDYDPELHGVDYVSDFKL
APNQTKELEEKVMELHKSYRSMTPAQADLEFLENAKKLSMY
>d1h4ra1 a.11.2.1 (A:104-214) Merlin {Human (Homo sapiens)}
NAEEELVQEITQHLFFLQVKKQILDEKIYCPPEASVLLASYAVQAKYGDYDPSVHKRGFLAQEEL
LPKRVINLYQMTPEMWEERITAWYAEHRGRARDEAEMEYLKIAQDL
>d1kdxa_ a.12.1.1 (A:) Kix domain of CBP (creb binding protein) {Mouse (Mus musculus)}
GVRKGWHEHVTQDLRSHLVHKLVQAIFPTPDPAALKDRRMENLVAYAKKVEGDMYESANSRDEYY
HLLAEKIYKIQKELEE
>d1lre__ a.13.1.1 (-) alpha-2-Macroglobulin receptor associated protein (RAP) domain 1 {Human (Homo sapiens)}
GEEFRMEKLNQLWEKAQRLHLPPVRLAELHADLKIQERDELAWKKLKLDGLDEDGEKEARLIRNL
NVILAKYGLDGKKDAR
>d1qqva_ a.14.1.1 (A:) Thermostable subdomain from chicken villin headpiece {Chicken (Gallus gallus)}
PTKLETFPLDVLVNTAAEDLPRGVDPSRKENHLSDEDFKAVFGMTRSAFANLPLWKQQNLKKEKG
LF
>d1vii__ a.14.1.1 (-) Thermostable subdomain from chicken villin headpiece {Chicken (Gallus gallus)}
MLSDEDFKAVFGMTRSAFANLPLWKQQNLKKEKGLF
>d1tbaa_ a.15.1.1 (A:) TAF(II)230 TBP-binding fragment {Fruit fly (Drosophila melanogaster)}
EGSIGNGLDLTGILFGNIDSEGRLLQDDDGEGRGGTGFDAELRENIGSLSKLGLDSMLLEVIDLK
EA
>d1ail__ a.16.1.1 (-) N-terminal, RNA-binding domain of nonstructural protein NS1 {Influenza A virus}
MDSNTVSSFQVDCFLWHVRKQVVDQELGDAPFLDRLRRDQKSLRGRGSTLGLNIEAATHVGKQIV
EKILK
>d1a32__ a.16.1.2 (-) Ribosomal protein S15 {Bacillus stearothermophilus}
LTQERKREIIEQFKVHENDTGSPEVQIAILTEQINNLNEHLRVHKKDHHSRRGLLKMVGKRRRLL
AYLRNKDVARYREIVEKLGL
>d1dk1a_ a.16.1.2 (A:) Ribosomal protein S15 {Thermus thermophilus}
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PITKEEKQKVMQEFARFPGDTGSTEVQVALLTLRINRLSEHLKVHKKDHHSHRGLLMMVGQRRRL
LRYLQREDPERYRMLIEKLGI
>d1g1xb_ a.16.1.2 (B:) Ribosomal protein S15 {Thermus thermophilus}
PITKEEKQKVIQEFARFPGDTGSTEVQVALLTLRINRLSEHLKVHKKDHHSHRGLLMMVGQRRRL
LRYLQREDPERYREIVEKLGLRG
>d1d2da_ a.16.1.3 (A:) Multifunctional Glu-Pro-tRNA synthase (EPRS)
second repeated element {Chinese hamster (Cricetulus griseus)}
MVYDKIAAQGEVVRKLKAEKAPKAKVTEAVECLLSLKAEYKEKTGKEYVPGLEHHH
>d1fyja_ a.16.1.3 (A:) Multifunctional Glu-Pro-tRNA synthase (EPRS)
second repeated element {Human (Homo sapiens)}
DSLVLYNRVAVQGDVVRELKAKKAPKEDVDAAVKQLLSLKAEYKEKTGQEYKPGNPP
>d2hp8__ a.17.1.1 (-) p8-MTCP1 {Human (Homo sapiens)}
MPQKDPCQKQACEIQKCLQANSYMESKCQAVIQELRKCCAQYPKGRSVVCSGFEKEEEENLTRKS
ASK
>d1ijxa_ a.141.1.1 (A:) Secreted Frizzled-related protein 3
(SFRP-3;fzb) {Mouse (Mus musculus)}
AACEPVRIPLCKSLPWEMTKMPNHLHHSTQANAILAMEQFEGLLGTHCSPDLLFFLCAMYAPICT
IDFQHEPIKPCKSVCERARQGCEPILIKYRHSWPESLACDELPVYDRGVCISPEAIVTAD
>d1ijya_ a.141.1.1 (A:) Frizzled 8 (FZ8) {Mouse (Mus musculus)}
ELACQEITVPLCKGIGYEYTYMPNQFNHDTQDEAGLEVHQFWPLVEIQCSPDLKFFLCSMYTPIC
LEDYKKPLPPCRSVCERAKAGCAPLMRQYGFAWPDRMRCDRLPEQGNPDTLCMDYER
>d2end__ a.18.1.1 (-) T4 endonuclease V {Bacteriophage T4 (Escherichia
coli)}
TRINLTLVSELADQHLMAEYRELPRVFGAVRKHVANGKRVRDFKISPTFILGAGHVTFFYDKLEF
LRKRQIELIAECLKRGFNIKDTTVQDISDIPQEFRGDYIPHEASIAISQARLDEKIAQRPTWYKY
YGKAIYA
>d2lisa_ a.19.1.1 (A:) Lysin {Red abalone (Haliotis rufescens)}
HYVEPKFLNKAFEVALKVQIIAGFDRGLVKWLRVHGRTLSTVQKKALYFVNRRYMQTHWANYMLW
INKKIDALGRTPVVGDYTRLGAEIGRRIDMAYFYDFLKDKNMIPKYLPYMEEINRMRPADVPVKY
M
>d3lyna_ a.19.1.1 (A:) Lysin {Green abalone (Haliotis fulgens)}
INKAYEVTMKIQIISGFDRQLTAWLRVHGRRLTNNQKKTLFFVNRRYMQTHWQNYMLWVKRKIKA
LGRPAAVGDYTRLGAEIGRRVDMVFFYNFLSGRKMIPPYSAYMAKLNALRPADVPVK
>d1gaka_ a.19.1.1 (A:) SP18 {Abalone (Haliotis fulgens)}
FDDVVVSRQEQSYVQRGMVNFLDEEMHKLVKRFRDMRWNLGPGFVFLLKKVNRERMMRYCMDYAR
YSKKILQLKHLPVNKKTLTKMGRFVGYRNYGVIRELYADVFRDVQGFRGPKMTAAMRKYSSKDPG
TFPCKNE
>d1lbu_1 a.20.1.1 (1-83) Zn2+ DD-carboxypeptidase, N-terminal domain
{Streptomyces albus G}
DGCYTWSGTLSEGSSGEAVRQLQIRVAGYPGTGAQLAIDGQFGPATKAAVQRFQSAYGLAADGIA
GPATFNKIYQLQDDDCTP
>d1ck7a6 a.20.1.2 (A:31-107) Gelatinase A {Human (Homo sapiens)}
PSPIIKFPGDVAPKTDKELAVQYLNTFYGCPKESCNLFVLKDTLKKMQKFFGLPQTGDLDQNTIE
TMRKPRCGNPDV
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>d1slm_1 a.20.1.2 (16-80) Stromelysin-1 (MMP-3) {Human (Homo sapiens), fibroblast}
LVQKYLENYYDLKKDVKQFVRRKDSGPVVKKIREMQKFLGLEVTGKLDSDTLEVMRKPRCGVPDV
>d1aab__ a.21.1.1 (-) HMG1, domains A and B {Rat (Rattus norvegicus)}
GKGDPKKPRGKMSSYAFFVQTSREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKA
DKARYEREMKTYIPPKGE
>d1ckta_ a.21.1.1 (A:) HMG1, domains A and B {Rat (Rattus norvegicus)}
KPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYE
REMKTY
>d1hme__ a.21.1.1 (-) HMG1, domains A and B {Rat (Rattus norvegicus)}
FKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKE
KYEKDIAAYRAK
>d1hsm__ a.21.1.1 (-) HMG1, domains A and B {Hamster (Cricetulus griseus)}
NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEK
DIAAYRAKGKPDAA
>d1qrva_ a.21.1.1 (A:) HMG-D {Drosophila melanogaster}
SDKPKRPLSAYMLWLNSARESIKRENPGIKVTEVAKRGGELWRAMKDKSEWEAKAAKAKDDYDRA
VKEFEANG
>d1cg7a_ a.21.1.1 (A:) NHP6a {Baker's yeast (Saccharomyces cerevisiae)}
MVTPREPKKRTTRKKKDPNAPKRALSAYMFFANENRDIVRSENPDITFGQVGKKLGEKWKALTPE
EKQPYEAKAQADKKRYESEKELYNATLA
>d1hrza_ a.21.1.1 (A:) SRY {Human (Homo sapiens)}
DRVKRPMNAFIVWSRDQRRKMALENPRMRNSEISKQLGYQWKMLTEAEKWPFFQEAQKLQAMHRE
KYPNYKYR
>d1j46a_ a.21.1.1 (A:) SRY {Human (Homo sapiens)}
MQDRVKRPMNAFIVWSRDQRRKMALENPRMRNSEISKQLGYQWKMLTEAEKWPFFQEAQKLQAMH
REKYPNYKYRPRRKAKMLPK
>d1i11a_ a.21.1.1 (A:) Sox-5 {Mouse (Mus musculus)}
PHIKRPMNAFMVWAKDERRKILQAFPDMHNSNISKILGSRWKAMTNLEKQPYYEEQARLSKQHLE
KYPDY
>d2lefa_ a.21.1.1 (A:) Lymphoid enhancer-binding factor, LEF1 {Mouse (Mus musculus)}
MHIKKPLNAFMLYMKEMRANVVAESTLKESAAINQILGRRWHALSREEQAKYYELARKERQLHMQ
LYPGWSARDNYGKKKKRKREK
>d1k99a_ a.21.1.1 (A:) Upstream binding factor, the first HMG box {Human (Homo sapiens)}
MKKLKKHPDFPKKPLTPYFRFFMEKRAKYAKLHPEMSNLDLTKILSKKYKELPEKKKMKYIQDFQ
REKQEFERNLARFREDHPDLIQNAKK
>d1eqza_ a.22.1.1 (A:) Histone H2A {Chicken (Gallus gallus), erythrocytes}
SGRGKQGGKARAKAKSRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAAVLEYLTAEILEL
AGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTIAQGGVLPNIQAVLLPKKTDSHKA

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>d1hioa_ a.22.1.1 (A:) Histone H2A {Chicken (Gallus gallus),
erythrocytes}
KSRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAAVLEYLTAEILELAGNAARDNKKTRII
PRHLQLAIRNDEELNKLLGKVTIAQGGVLP
>d1hq3a_ a.22.1.1 (A:) Histone H2A {Chicken (Gallus gallus),
erythrocytes}
KAKSRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAAVLEYLTAEILELAGNAARDNKKTR
IIPRHLQLAIRNDEELNKLLGKVTIAQGGVLPNIQAVLLPK
>d1aoic_ a.22.1.1 (C:) Histone H2A {African clawed frog (Xenopus
laevis)}
GKQGGKTRAKAKTRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAAVLEYLTAEILELAGN
AARDNKKTRIIPRHLQLAVRNDEELNKLLGRVTIAQGGVLPNIQSVLLPK
>d1f66c_ a.22.1.1 (C:) Histone H2A {Human (Homo sapiens), variant
H2A.Z}
AVSRSQRAGLQFPVGRIHRHLKSRTTSHGRVGATAAVYSAAILEYLTAEVLELAGNASKDLKVKR
ITPRHLQLAIRGDEELDSLIKATIAGGGVIPHIHKSLI
>d1id3c_ a.22.1.1 (C:) Histone H2A {Baker's yeast (Saccharomyces
cerevisiae), H2A.1}
QSRSAKAGLTFPVGRVHRLLRRGNYAQRIGSGAPVYLTAVLEYLAAEILELAGNAARDNKKTRII
PRHLQLAIRNDDELNKLLGNVTIAQGGVLPNIHQNLLPKKSAKAT
>d1eqzb_ a.22.1.1 (B:) Histone H2B {Chicken (Gallus gallus),
erythrocytes}
VTKTQKKGDKKRKKSRKESYSIYVYKVLKQVHPDTGISSKAMGIMNSFVNDIFERIAGEASRLAH
YNKRSTITSREIQTAVRLLLPGELAKHAVSEGTKAVTKYTSSK
>d1hiob_ a.22.1.1 (B:) Histone H2B {Chicken (Gallus gallus),
erythrocytes}
SYSIYVYKVLKQVHPDTGISSKAMGSMNSFVNDIFERIAGLASRLAHYNKRSTITSREIQTAVRL
LLPGELAKHAVSEGTKAVTKHTSSK
>d1hq3b_ a.22.1.1 (B:) Histone H2B {Chicken (Gallus gallus),
erythrocytes}
RKESYSIYVYKVLKQVHPDTGISSKAMGIMNSFVNDIFERIAGEASRLAHYNKRSTITSREIQTA
VRLLLPGELAKHAVSEGTKAVTKYTSS
>d1aoid_ a.22.1.1 (D:) Histone H2B {African clawed frog (Xenopus
laevis)}
KKRRKTRKESYAIYVYKVLKQVHPDTGISSKAMSIMNSFVNDVFERIAGEASRLAHYNKRSTITS
REIQTAVRLLLPGELAKHAVSEGTKAVTKYTSAK
>d1id3d_ a.22.1.1 (D:) Histone H2B {Baker's yeast (Saccharomyces
cerevisiae), H2B.2}
RKETYSSYIYKVLKQTHPDTGISQKSMSILNSFVNDIFERIATEASKLAAYNKKSTISAREIQTA
VRLILPGELAKHAVSEGTRAVTKYSSST
>d1eqzc_ a.22.1.1 (C:) Histone H3 {Chicken (Gallus gallus),
erythrocytes}
APATGGVKKPHRYRPGTVALREIRRYQKSTELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQ
EASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA
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>d1eqzg_ a.22.1.1 (G:) Histone H3 {Chicken (Gallus gallus),
erythrocytes}
PRKQLATKAARKSAPATGGVKKPHRYRPGTVALREIRRYQKSTELLIRKLPFQRLVREIAQDFKT
DLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA
>d1hq3c_ a.22.1.1 (C:) Histone H3 {Chicken (Gallus gallus),
erythrocytes}
YRPGTVALREIRRYQKSTELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFE
DTNLCAIHAKRVTIMPKDIQLARRIRGERA
>d1id3a_ a.22.1.1 (A:) Histone H3 {Baker's yeast (Saccharomyces
cerevisiae)}
PHRYKPGTVALREIRRFQKSTELLIRKLPFQRLVREIAQDFKTDLRFQSSAIGALQESVEAYLVS
LFEDTNLAAIHAKRVTIQKKEIKLARRLRGER
>d1eqzh_ a.22.1.1 (H:) Histone H4 {Chicken (Gallus gallus),
erythrocytes}
KGLGKGGAKRHRKVLRDNIQGITKPAIRRLARRGGVKRISGLIYEETRGVLKVFLENVIRDAVTY
TEHAKRKTVTAMDVVYALKRQGRTLYGFGG
>d1hq3d_ a.22.1.1 (D:) Histone H4 {Chicken (Gallus gallus),
erythrocytes}
KVLRDNIQGITKPAIRRLARRGGVKRISGLIYEETRGVLKVFLENVIRDAVTYTEHAKRKTVTAM
DVVYALKRQGRTLYGFGG
>d1id3b_ a.22.1.1 (B:) Histone H4 {Baker's yeast (Saccharomyces
cerevisiae)}
DNIQGITKPAIRRLARRGGVKRISGLIYEEVRAVLKSFLESVIRDSVTYTEHAKRKTVTSLDVVY
ALKRQGRTLYGFGG
>d1b67a_ a.22.1.2 (A:) Archaeal histone {Archaeon Methanothermus
fervidus, histone A}
GELPIAPIGRIIKNAGAERVSDDARIALAKVLEEMGEEIASEAVKLAKHAGRKTIKAEDIELARK
MFK
>d1a7w__ a.22.1.2 (-) Archaeal histone {Archaeon Methanothermus
fervidus, histone B}
MELPIAPIGRIIKDAGAERVSDDARITLAKILEEMGRDIASEAIKLARHAGRKTIKAEDIELAVR
RFK
>d1f1ea_ a.22.1.2 (A:) Archaeal histone {Archaeon Methanopyrus
kandleri}
ELPKAAIERIFRQGIGERRLSQDAKDTIYDFVPTMAEYVANAAKSVLDASGKKTLMEEHLKALAD
VLMVEGVEDYDGELFGRATVRRILKRAGIERASSDAVDLYNKLICRATEELGEKAAEYADEDGRK
TVQGEDVEKAITYSMPKGGEL
>d1tafa_ a.22.1.3 (A:) TAF(II)42 {Fruit fly (Drosophila
melanogaster)}
PKDAQVIMSILKELNVQEYEPRVVNQLLEFTFRYVTSILDDAKVYANHARKKTIDLDDVRLATEV
TLD
>d1tafb_ a.22.1.3 (B:) TAF(II)62 {Fruit fly (Drosophila
melanogaster)}
MLYGSSISAESMKVIAESIGVGSLSDDAAKELAEDVSIKLKRIVQDAAKFMNHAKRQKLSVRDID
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MSLKV
>d1bh9a_ a.22.1.3 (A:) TAF(II)18 {Human (Homo sapiens)}
LFSKELRCMMYGFGDDQNPYTESVDILEDLVIEFITEMTHKAMSI
>d1bh9b_ a.22.1.3 (B:) TAF(II)28 {Human (Homo sapiens)}
FSEEQLNRYEMYRRSAFPKAAIKRLIQSITGTSVSQNVVIAMSGISKVFVGEVVEEALDVCEKWG
EMPPLQPKHMREAVRRLKSKGQIP
>d1jfia_ a.22.1.3 (A:) Negative cofactor 2, NC2, alpha chain {Human
(Homo sapiens)}
ARFPPARIKKIMQTDEEIGKVAAAVPVIISRALELFLESLLKKACQVTQSRNAKTMTTSHLKQCI
E
>d1jfib_ a.22.1.3 (B:) Negative cofactor 2, NC2, beta chain {Human
(Homo sapiens)}
DDLTIPRAAINKMIKETLPNVRVANDARELVVNCCTEFIHLISSEANEICNKSEKKTISPEHVIQ
ALESLGFGSYISEVKEVLQECKTVALKRRKASSRLENLGIPEEELLRQQQELFAKARQQQAELAQ
QEWLQ
>d1fpoa2 a.23.1.1 (A:77-171) HSC20 (HSCB), C-terminal oligomerisation
domain {Escherichia coli}
FDLASEQHTVRDTAFLMEQLELREELDEIEQAKDEARLESFIKRVKKMFDTRHQLMVEQLDNETW
DAAADTCRKLRFLDKLRSSAEQLEEKLLDF
>d1eexg_ a.23.2.1 (G:) Diol dehydratase, gamma subunit {Klebsiella
oxytoca}
SARVSDYPLANKHPEWVKTATNKTLDDFTLENVLSNKVTAQDMRITPETLRLQASIAKDAGRDRL
AMNFERAAELTAVPDDRILEIYNALRPYRSTKEELLAIADDLESRYQAKICAAFVREAATLYVER
KKLKGDD
>d1mtyg_ a.23.3.1 (G:) Methane monooxygenase hydrolase, gamma subunit
{Methylococcus capsulatus}
LGIHSNDTRDAWVNKIAHVNTLEKAAEMLKQFRMDHTTPFRNSYELDNDYLWIEAKLEEKVAVLK
ARAFNEVDFRHKTAFGEDAKSVLDGTVAKMNAAKDKWEAEKIHIGFRQAYKPPIMPVNYFLDGER
QLGTRLMELRNLNYYDTPLEELRKQRGVRVVH
>d1mhyg_ a.23.3.1 (G:) Methane monooxygenase hydrolase, gamma subunit
{Methylosinus trichosporium}
AKREPIHDNSIRTEWEAKIAKLTSVDQATKFIQDFRLAYTSPFRKSYDIDVDYQYIERKIEEKLS
VLKTEKLPVADLITKATTGEDAAAVEATWIAKIKAAKSKYEAEAIHIEFRQLYKPPVLPVNVFLR
TDAALGTVLMEIRNTDYYGTPLEGLRKERGVKVLHLQ
>d1om2a_ a.23.4.1 (A:) Mitochondrial import receptor subunit Tom20
{Rat (Rattus norvegicus)}
RAGLSKLPDLKDAEAVQKFFLEEIQLGEELLAQGDYEKGVDHLTNAIAVCGQPQQLLQVLQQTLP
PPVFQMLLTKLPTISQRIVSAQSLGEDDVE
>d1jw2a_ a.23.5.1 (A:) Hemolysin expression modulating protein HHA
{Escherichia coli}
MSEKPLTKTDYLMRLRRCQTIDTLERVIEKNKYELSDNELAVFYSAADHRLAELTMNKLYDKIPS
SVWKFIR
>d1nfn__ a.24.1.1 (-) Apolipoprotein E3 {Human (Homo sapiens)}
GQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELRALMDETMKELKAYKSELEEQLTPVAE
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ETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRKRLLRDA
DDLQKRLAVYQA
>d2asr__ a.24.2.1 (-) Aspartate receptor, ligand-binding domain
{Escherichia coli}
KSFVVSNQLREQQGELTSTWDLMLQTRINLSRSAVRMMMDSSNQQSNAKVELLDSARKTLAQAAT
HYKKFKSMAPLPEMVATSRNIDEKYKNYYTALTELIDYLDYGNTGAYFAQPTQGMQNAMGERFAQ
YALSSEKLYRDI
>d1vlta_ a.24.2.1 (A:) Aspartate receptor, ligand-binding domain
{Salmonella typhimurium}
GFVISNELRQQQSELTSTWDLMLQTRINLSRSAARMMMDASNQQSSAKTDLLQNAKTTLAQAAAH
YANFKNMTPLPAMAEASANVDEKYQRYQAALAELIQFLDNGNMDAYFAQPTQGMQNALGEALGNY
ARVSENLYRQTF
>d2liga_ a.24.2.1 (A:) Aspartate receptor, ligand-binding domain
{Salmonella typhimurium}
MGGLLFSSLQHCQQGFVISNELRQQQSELTSTWDLMLQTRINLSRSAARMMMDASNQQSSAKTDL
LQNAKTTLAQAAAHYANFKNMTPLPAMAEASANVDEKYQRYQAALAELIQFLDNGNMDAYFAQPT
QGMQNALGEALGNYARVSENLYRQTFD
>d256ba_ a.24.3.1 (A:) Cytochrome b562 {Escherichia coli}
ADLEDNMETLNDNLKVIEKADNAAQVKDALTKMRAAALDAQKATPPKLEDKSPDSPEMKDFRHGF
DILVGQIDDALKLANEGKVKEAQAAAEQLKTTRNAYHQKYR
>d2ccya_ a.24.3.2 (A:) Cytochrome c' {Rhodospirillum molischianum}
QSKPEDLLKLRQGLMQTLKSQWVPIAGFAAGKADLPADAAQRAENMAMVAKLAPIGWAKGTEALP
NGETKPEAFGSKSAEFLEGWKALATESTKLAAAAKAGPDALKAQAAATGKVCKACHEEFKQD
>d1bbha_ a.24.3.2 (A:) Cytochrome c' {Chromatium vinosum}
AGLSPEEQIETRQAGYEFMGWNMGKIKANLEGEYNAAQVEAAANVIAAIANSGMGALYGPGTDKN
VGDVKTRVKPEFFQNMEDVGKIAREFVGAANTLAEVAATGEAEAVKTAFGDVGAACKSCHEKYRA
K
>d1e85a_ a.24.3.2 (A:) Cytochrome c' {Alcaligenes sp.}
EFAKPEDAVKYRQSALTLMASHFGRMTPVVKGQAPYDAAQIKANVEVLKTLSALPWAAFGPGTEG
GDARPEIWSDAASFKQKQQAFQDNIVKLSAAADAGDLDKLRAAFGDVGASCKACHDAYRK
>d1jafa_ a.24.3.2 (A:) Cytochrome c' {Rhodocyclus gelatinosus}
QFQKPGDAIEYRQSAFTLIANHFGRVAAMAQGKAPFDAKVAAENIALVSTLSKLPLTAFGPGTDK
GHGTEAKPAVWSDAAGFKAAADKFAAAVDKLDAAGKTGDFAQIKAAVGETGGACKGCHDKFKE
>d1cpq__ a.24.3.2 (-) Cytochrome c' {Rhodobacter capsulatus}
ADTKEVLEAREAYFKSLGGSMKAMTGVAKAFDAEAAKVEAAKLEKILATDVAPLFPAGTSSTDLP
GQTEAKAAIWANMDDFGAKGKAMHEAGGAVIAAANAGDGAAFGAALQKLGGTCKACHDDYREED
>d1a7va_ a.24.3.2 (A:) Cytochrome c' {Rhodopseudomonas palustris}
QTDVIAQRKAILKQMGEATKPIAAMLKGEAKFDQAVVQKSLAAIADDSKKLPALFPADSKTGGDT
AALPKIWEDKAKFDDLFAKLAAAATAAQGTIKDEASLKANIGGVLGNCKSCHDDFRAKKS
>d2hmza_ a.24.4.1 (A:) Hemerythrin {Sipunculid worm (Themiste
dyscrita)}
GFPIPDPYCWDISFRTFYTIVDDEHKTLFNGILLLSQADNADHLNELRRCTGKHFLNEQQLMQAS
QYAGYAEHKKAHDDFIHKLDTWDGDVTYAKNWLVNHIKTIDFKYRGKI
>d1hrb__ a.24.4.1 (-) Hemerythrin {Phascolopsis gouldii}
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GFPIPDPYVWDPSFRTFYSIIDDEHKTLFNGIFHLAIDDNADNLGELRRCTGKHFLNQEVLMEAS
QYQFYDEHKKEHDGFINALDNWKGDVKWAKAWLVNHIKTIDFKYKGKI
>d1i4ya_ a.24.4.1 (A:) Hemerythrin {Phascolopsis gouldii}
GFPIPDPYVWDPSFRTFYSIIDDEHKTLFNGIFHLAIDDNADNLGELRRCTGKHFLNEQVLMQAS
QYQFYDEHKKEHETFIHALDNWKGDVKWAKSWLVNHIKTIDFKYKGKI
>d2mhr__ a.24.4.1 (-) Myohemerythin {Sipunculan worm (Themiste
zostericola)}
GWEIPEPYVWDESFRVFYEQLDEEHKKIFKGIFDCIRDNSAPNLATLVKVTTNHFTHEEAMMDAA
KYSEVVPHKKMHKDFLEKIGGLSAPVDAKNVDYCKEWLVNHIKGTDFKYKGKL
>d1ei7a_ a.24.5.1 (A:) Tobacco mosaic virus coat protein {Tobacco
mosaic virus, vulgare strain}
SYSITTPSQFVFLSSAWADPIELINLCTNALGNQFQTQQARTVVQRQFSEVWKPSPQVTVRFPDS
DFKVYRYNAVLDPLVTALLGAFDTRNRIIEVENQANPTTAETLDATRRVDDATVAIRSAINNLIV
ELIRGTGSYNRSSFESSSGLVWTSGPAT
>d1vtmp_ a.24.5.1 (P:) Tobacco mosaic virus coat protein {Tobacco
mosaic virus, vulgare strain}
PYTINSPSQFVYLSSAYADPVELINLCTNALGNQFQTQQARTTVQQQFADAWKPSPVMTVRFPAS
DFYVYRYNSTLDPLITALLNSFDTRNRIIEVNNQPAPNTTEIVNATQRVDDATVAIRASINNLAN
ELVRGTGMFNQAGFETASGLVWTTTPAT
>d1cgme_ a.24.5.1 (E:) Cucumber green mottle mosaic virus {Cucumber
green mottle mosaic virus, strain watermelon}
AYNPITPSKLIAFSASYVPVRTLLNFLVASQGTAFQTQAGRDSFRESLSALPSSVVDINSRFPDA
GFYAFLNGPVLRPIFVSLLSSTDTRNRVIEVVDPSNPTTAESLNAVKRTDDASTAARAEIDNLIE
SISKGFDVYDRASFEAAFSVVWSEATTSKA
>d1rmva_ a.24.5.1 (A:) Ribgrass mosaic virus {Ribgrass mosaic virus}
SYNITNSNQYQYFAAVWAEPTPMLNQCVSALSQSYQTQAGRDTVRQQFANLLSTIVAPNQRFPDT
GFRVYVNSAVIKPLYEALMKSFDTRNRIIETEEESRPSASEVANATQRVDDATVAIRSQIQLLLN
ELSNGHGYMNRAEFEAILPWTTAPAT
>d3fapb_ a.24.7.1 (B:) FKBP12-rapamycin-binding domain of
FKBP-rapamycin-associated protein (FRAP) {Human (Homo sapiens)}
VAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGRDLMEAQE
WCRKYMKSGNVKDLTQAWDLYYHVFRRIS
>g1avo.1 a.24.8.1 (A:,B:) Proteasome activator reg(alpha) {Human
(Homo sapiens)}
LRVQPEAQAKVDVFREDLCTKTENLLGSYFPKKISELDAFLKEPALNEANLSNLKAPLDIXAVNC
NEKIVVLLQRLKPEIKDVIEQLNLVTTWLQLQIPRIEDGNNFGVAVQEKVFELMTSLHTKLEGFH
TQISKYFSERGDAVTKAAKQPHVGDYRQLVHELDEAEYRDIRLMVMEIRNAYAVLYDIILKNFEK
LKKPRG
>d1dova_ a.24.9.1 (A:) alpha-catenin {Mouse (Mus musculus)}
ESQFLKEELVVAVEDVRKQGDLMKSAAGEFADDPCSSVKRGNMVRAARALLSAVTRLLILADMAD
VYKLLVQLKVVEDGILKLRNAGNEQDLGIQYKALKPEVDKLNIMAAKRQQELKDVGNRDQMAAAR
GILQKNVPILYTASQACLQHPDVAAYKANRDLIYKQLQQAVTGISNAAQAT
>d1dowa_ a.24.9.1 (A:) alpha-catenin {Mouse (Mus musculus)}
KAHVLAASVEQATENFLEKGDKIAKESQFLKEELVVAVEDVRKQGDLMKSAAGEFADDPCSSVKR
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GNMVRAARALLSAVTRLLILADMADVYKLLVQLKVVEDGILKLRNAGNEQDLGIQYKALKPEVDK
LNIMAAKRQQELKDVGNRDQMAAARGILQKNVPILYTASQACLQHPDVAAYKANRDLIYKQLQQA
VTGISNAAQA
>d1h6ga1 a.24.9.1 (A:377-507) alpha-catenin {Human (Homo sapiens)}
DLRRQLRKAVMDHVSDSFLETNVPLLVLIEAAKNGNEKEVKEYAQVFREHANKLIEVANLACSIS
NNEEGVKLVRMSASQLEALCPQVINAALALAAKPQSKLAQENMDLFKEQWEKQVRVLTDAVDDIT
S
>d1h6ga2 a.24.9.1 (A:508-631) alpha-catenin {Human (Homo sapiens)}
IDDFLAVSENHILEDVNKCVIALQEKDVDGLDRTAGAIRGRAARVIHVVTSEMDNYEPGVYTEKV
LEATKLLSNTVMPRFTEQVEAAVEALSSDPAQPMDENEFIDASRLVYDGIRDIRKAVLM
>d1h6gb1 a.24.9.1 (B:392-507) alpha-catenin {Human (Homo sapiens)}
DSFLETNVPLLVLIEAAKNGNEKEVKEYAQVFREHANKLIEVANLACSISNNEEGVKLVRMSASQ
LEALCPQVINAALALAAKPQSKLAQENMDLFKEQWEKQVRVLTDAVDDITS
>d1qkra_ a.24.9.1 (A:) Vinculin {Chicken (Gallus gallus)}
KDEEFPEQKAGEAINQPMMMAARQLHDEARKWSSKGNDIIAAAKRMALLMAEMSRLVRGGSGNKR
ALIQCAKDIAKASDEVTRLAKEVAKQCTDKRIRTNLLQVCERIPTISTQLKILSTVKATMLGRTN
ISDEESEQATEMLVHNAQNLMQSVKETVREAEAASIKIRTDAGFTLRWVRK
>d1k04a_ a.24.14.1 (A:) FAT domain of focal adhesion kinase {Human
(Homo sapiens)}
EISPPPTANLDRSNDKVYENVTGLVKAVIEMSSKIQPAPPEEYVPMVKEVGLALRTLLATVDETI
PLLPASTHREIEMAQKLLNSDLGELINKMKLAQQYVMTSLQQEYKKQMLTAAHALAVDAKNLLDV
IDQARLKMLGQT
>d1k40a_ a.24.14.1 (A:) FAT domain of focal adhesion kinase {Mouse
(Mus musculus)}
NDKVYENVTGLVKAVIEMSSKIQPAPPEEYVPMVKEVGLALRTLLATVDETIPALPASTHREIEM
AQKLLNSDLGELISKMKLAQQYVMTSLQQEYKKQMLTAAHALAVDAKNLLDVIDQARLKML
>d2a0b__ a.24.10.1 (-) Aerobic respiration control sensor protein,
ArcB {Escherichia coli}
SKSEALLDIPMLEQYLELVGPKLITDGLAVFEKMMPGYVSVLESNLTAQDKKGIVEEGHKIKGAA
GSVGLRHLQQLGQQIQSPDLPAWEDNVGEWIEEMKEEWRHDVEVLKAWVAKAT
>d1c02a_ a.24.10.2 (A:) Phosphorelay protein ypd1 {Baker's yeast
(Saccharomyces cerevisiae)}
STIPSEIINWTILNEIISMDDDDSDFSKGLIIQFIDQAQTTFAQMQRQLDGEKNLTELDNLGHFL
KGSSAALGLQRIAWVCERIQNLGRKMQHFFPNKTELVNTLSDKSIINGINIDEDDEEIKIQVDDK
DENSIYLILIAKALNQSRLEFKLARIELSKYYNTNL
>d1i5na_ a.24.10.3 (A:) Chemotaxis protein CheA P1 domain {Salmonella
typhimurium}
DISDFYQTFFDEADELLADMEQHLLDLVPESPDAEQLNAIFRAAHSIKGGAGTFGFTILQETTHL
MENLLDEARRGEMQLNTDIINLFLETKDIMQEQLDAYKNSEEPDAASFEYICNALRQLALEAK
>d1he1a_ a.24.11.1 (A:) ExoS toxin {Pseudomonas aeruginosa}
ASSAVVFKQMVLQQALPMTLKGLDKASELATLTPEGLAREHSRLASGDGALRSLSTALAGIRAGS
QVEESRIQAGRLLERSIGGIALQQWGTTGGAASQLVLDASPELRREITDQLHQVMSEVALLRQAV
ESEVS
>d1g4us1 a.24.11.1 (S:167-296) SptP tyrosine phosphatase {Salmonella
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typhimurium}
SKQPLLDIALKGLKRTLPQLEQMDGNSLRENFQEMASGNGPLRSLMTNLQNLNKIPEAKQLNDYV
TTLTNIQVGVARFSQWGTCGGEVERWVDKASTHELTQAVKKIHVIAKELKNVTAELEKIEAGAPM
>d1hy5a_ a.24.11.1 (A:) YopE {Yersinia pestis}
TSFSDSIKQLAAETLPKYMQQLNSLDAEMLQKNHDQFATGSGPLRGSITQCQGLMQFCGGELQAE
ASAILNTPVCGIPFSQWGTIGGAASAYVASGVDLTQAANEIKGLAQQMQKLLSLM
>d1f1ma_ a.24.12.1 (A:) Outer surface protein C (OspC) {Lyme disease
spirochete (Borrelia burgdorferi), different strains?}
PNLTEISKKITESNAVVLAVKEVETLLTSIDELAKAIGKKIKSDVSLDNEADHNGSLMSGAYLIS
TLITKKISAIKDSGELKAEIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKG
ADELEKLFESVKNLSKAAKEMLTNSVKELTSP
>d1g5za_ a.24.12.1 (A:) Outer surface protein C (OspC) {Lyme disease
spirochete (Borrelia burgdorferi), different strains?}
PNLTEISKKITESNAVVLAVKEVETLLASIDELATKAIGKKIGNNGLEANQSKNTSLLSGAYAIS
DLIAEKLNVLKNEELKEKIDTAKQCSTEFTNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGA
AELEKLFKAVENLSKAAQDTLKNAVKELTSPIVA
>d1ggqa_ a.24.12.1 (A:) Outer surface protein C (OspC) {Lyme disease
spirochete (Borrelia burgdorferi), different strains?}
GPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIGKKIHQNNGLDTENNHNGSLLAGAYA
ISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLKEKHTDLGKEGVTDADAKEAILKTNGTKTK
GAEELGKLFESVEVLSKAAKEMLANSVKELTS
>d1jpna1 a.24.13.1 (A:1-88) Signal sequence recognition protein Ffh
{Thermus aquaticus}
MFQQLSARLQEAIGRLRGRGRITEEDLKATLREIRRALMDADVNLEVARDFVERVREEALGKQVL
ESLTPAEVILATVYEALKEALGG
>d1j8mf1 a.24.13.1 (F:3-86) Signal sequence recognition protein Ffh
{Archaeon Acidianus ambivalens}
LLDNLRDTVRKFLTGSSSYDKAVEDFIKELQKSLISADVNVKLVFSLTNKIKERLKNEKPPTYIE
RREWFIKIVYDELSNLFGG
>d1fts_1 a.24.13.1 (201-284) Signal recognition particle receptor,
FtsY {Escherichia coli}
RSLLKTKENLGSGFISLFRGKKIDDDLFEELEEQLLIADVGVETTRKIITNLTEGASRKQLRDAE
ALYGLLKEEMGEILAKVDE
>d1jr8a_ a.24.15.1 (A:) Thiol oxidase Erv2p {Baker's yeast
(Saccharomyces cerevisiae)}
DDKVKKEVGRASWKYFHTLLARFPDEPTPEEREKLHTFIGLYAELYPCGECSYHFVKLIEKYPVQ
TSSRTAAAMWGCHIHNKVNEYLKKDIYDCATILEDYDCGC
>d1h99a1 a.142.1.1 (A:54-168) Transcriptional antiterminator LicT
{Bacillus subtilis}
GAMEKFKTLLYDIPIECMEVSEEIISYAKLQLGKKLNDSIYVSLTDHINFAIQRNQKGLDIKNAL
LWETKRLYKDEFAIGKEALVMVKNKTGVSLPEDEAGFIALHIVNAELNEE
>d1h99a2 a.142.1.1 (A:169-275) Transcriptional antiterminator LicT
{Bacillus subtilis}
MPNIINITKVMEEILSIVKYHFKIEFNEESLHYYRFVTDLKFFAQRLFNGTHMESEDDFLLDTVK
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EKYHRAYECTKKIQTYIEREYEHKLTSDELLYLTIDIERVVK
>d1dvba1 a.25.1.1 (A:1-147) Rubrerythrin, N-terminal domain {Desulfovibrio vulgaris}
MKSLKGSRTEKNILTAFAGESQARNRYNYFGGQAKKDGFVQISDIFAETADQEREHAKRLFKFLE
GGDLEIVAAFPAGIIADTHANLIASAAGEHHEYTEMYPSFARIAREEGYEEIARVFASIAVAEEF
HEKRFLDFARNIKEGRV
>d1bcfa_ a.25.1.1 (A:) Bacterioferritin (cytochrome b1) {Escherichia coli}
MKGDTKVINYLNKLLGNELVAINQYFLHARMFKNWGLKRLNDVEYHESIDEMKHADRYIERILFL
EGLPNLQDLGKLNIGEDVEEMLRSDLALELDGAKNLREAIGYADSVHDYVSRDMMIEILRDEEGH
IDWLETELDLIQKMGLQNYLQAQIREEG
>d1jgca_ a.25.1.1 (A:) Bacterioferritin (cytochrome b1) {Rhodobacter capsulatus}
MKGDAKVIEFLNAALRSELTAISQYWVHFRLQEDWGLAKMAKKSREESIEEMGHADKIIARILFL
EGHPNLQKLDPLRIGEGPRETLECDLAGEHDALKLYREARDYCAEVGDIVSKNIFESLITDEEGH
VDFLETQISLYDRLGPQGFALLNAAPMDAA
>d1euma_ a.25.1.1 (A:) Non-hem ferritin {Escherichia coli, ecFtnA}
LKPEMIEKLNEQMNLELYSSLLYQQMSAWCSYHTFEGAAAFLRRHAQEEMTHMQRLFDYLTDTGN
LPRINTVESPFAEYSSLDELFQETYKHEQLITQKINELAHAAMTNQDYPTFNFLQWYVSEQHEEE
KLFKSIIDKLSLAGKSGEGLYFIDKELSTLD
>d1krqa_ a.25.1.1 (A:) Non-hem ferritin {Campylobacter jejuni}
MLSKEVVKLLNEQINKEMYAANLYLSMSSWCYENSLDGAGAFLFAHASEESDHAKKLITYLNETD
SHVELQEVKQPEQNFKSLLDVFEKTYEHEQFITKSINTLVEHMLTHKDYSTFNFLQWYVSEQHEE
EALFRGIVDKIKLIGEHGNGLYLADQYIKNIALSR
>d1dpsa_ a.25.1.1 (A:) Dodecameric ferritin homolog DPS {Escherichia coli}
SKATNLLYTRNDVSDSEKKATVELLNRQVIQFIDLSLITKQAHWNMRGANFIAVHEMLDGFRTAL
IDHLDTMAERAVQLGGVALGTTQVINSKTPLKSYPLDIHNVQDHLKELADRYAIVANDVRKAIGE
AKDDDTADILTAASRDLDKFLWFIECNIE
>d1qgha_ a.25.1.1 (A:) Dodecameric ferritin homolog DPS {Listeria innocua}
VDTKEFLNHQVANLNVFTVKIHQIHWYMRGHNFFTLHEKMDDLYSEFGEQMDEVAERLLAIGGSP
FSTLKEFLENASVEEAPYTKPKTMDQLMEDLVGTLELLRDEYKQGIELTDKEGDDVTNDMLIAFK
ASIDKHIWMFKAFLGKAPLE
>d2fha__ a.25.1.1 (-) (Apo)ferritin {Human (Homo sapiens), H chain}
TSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYYFDRDDVALKNFAKYFLHQSHEEREHAEKL
MKLQNQRGGRIFLQDIQKPDCDDWESGLNAMECALHLEKNVNQSLLELHKLATDKNDPHLCDFIE
THYLNEQVKAIKELGDHVTNLRKMGAPESGLAEYLFDKHTLG
>d1aew__ a.25.1.1 (-) (Apo)ferritin {Horse (Equus caballus), L chain}
SQIRQNYSTEVEAAVNRLVNLYLRASYTYLSLGFYFDRDDVALEGVCHFFRELAEEKREGAERLL
KMQNQRGGRALFQDLQKPSQDEWGTTPDAMKAAIVLEKSLNQALLDLHALGSAQADPHLCDFLES
HFLDEEVKLIKKMGDHLTNIQRLVGSQAGLGEYLFERLTL
>d1h96a_ a.25.1.1 (A:) (Apo)ferritin {Mouse (Mus musculus)}
TSQIRQNYSTEVEAAVNRLVNLHLRASYTYLSLGFFFDRDDVALEGVGHFFRELAEEKREGAERL
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LEFQNDRGGRALFQDVQKPSQDEWGKTQEAMEAALAMEKNLNQALLDLHALGSARADPHLCDFLE
SHYLDKEVKLIKKMGNHLTNLRRVAGPQPAQTGAPQGSLGEYLFERLTLK
>d1bg7__ a.25.1.1 (-) (Apo)ferritin {Bullfrog (Rana catesbeiana)}
DSQVRQNFHRDCEAAINRMVNMELYASYTYLSMAFYFDRDDIALHNVAKFFKEQSHEEREHAEKL
MKDQNKRGGRIVLQDVQKPERDEWGNTLEAMQAALQLEKTVNQALLDLHKVGSDKVDPHLCDFLE
TEYPEEQVKSIKQLGDYITNLKRLGLPQNGMGEYLFDKHTMGE
>d1mfra_ a.25.1.1 (A:) (Apo)ferritin {Bullfrog (Rana catesbeiana)}
VSQVRQNYHSDCEAAVNRMLNLELYASYTYSSMYAFFDRDDVALHNVAEFFKEHSHEEREHAEKF
MKYQNKRGGRVVLQDIKKPERDEWGNTLEAMQAALQLEKTVNQALLDLHKLATDKVDPHLCDFLE
SEYLEEQVKDIKRIGDFITNLKRLGLPENGMGEYLFDKHSV
>d1rcd__ a.25.1.1 (-) (Apo)ferritin {Bullfrog (Rana catesbeiana)}
SQVRQNFHQDCEAGLNRTVNLKFHSSYVYLSMASYFNRDDVALSNFAKFFRERSEEEKEHAEKLI
EYQNQRGGRVFLQSVEKPERDDWANGLEALQTALKLQKSVNQALLDLHAVAADKSDPHMTDFLES
PYLSESVETIKKLGDHITSLKKLWSSHPGMAEYLFNKHTLG
>d1mtyb_ a.25.1.2 (B:) Methane monooxygenase hydrolase, beta and alpha
subunits {Methylococcus capsulatus}
ERRRGLTDPEMAAVILKALPEAPLDGNNKMGYFVTPRWKRLTEYEALTVYAQPNADWIAGGLDWG
DWTQKFHGGRPSWGNETTELRTVDWFKHRDPLRRWHAPYVKDKAEEWRYTDRFLQGYSADGQIRA
MNPTWRDEFINRYWGAFLFNEYGLFNAHSQGAREALSDVTRVSLAFWGFDKIDIAQMIQLERGFL
AKIVPGFDESTAVPKAEWTNGEVYKSARLAVEGLWQEVFDWNESAFSVHAVYDALFGQFVRREFF
QRLAPRFGDNLTPFFINQAQTYFQIAKQGVQDLYYNCLGDDPEFSDYNRTVMRNWTGKWLEPTIA
ALRDFMGLFAKLPAGTTDKEEITASLYRVVDDWIEDYASRIDFKADRDQIVKAVLAGLK
>d1mtyd_ a.25.1.2 (D:) Methane monooxygenase hydrolase, beta and alpha
subunits {Methylococcus capsulatus}
AANRAPTSVNAQEVHRWLQSFNWDFKNNRTKYATKYKMANETKEQFKLIAKEYARMEAVKDERQF
GSLQVALTRLNAGVRVHPKWNETMKVVSNFLEVGEYNAIAATGMLWDSAQAAEQKNGYLAQVLDE
IRHTHQCAYVNYYFAKNGQDPAGHNDARRTRTIGPLWKGMKRVFSDGFISGDAVECSLNLQLVGE
ACFTNPLIVAVTEWAAANGDEITPTVFLSIETDELRHMANGYQTVVSIANDPASAKYLNTDLNNA
FWTQQKYFTPVLGMLFEYGSKFKVEPWVKTWDRWVYEDWGGIWIGRLGKYGVESPRSLKDAKQDA
YWAHHDLYLLAYALWPTGFFRLALPDQEEMEWFEANYPGWYDHYGKIYEEWRARGCEDPSSGFIP
LMWFIENNHPIYIDRVSQVPFCPSLAKGASTLRVHEYNGEMHTFSDQWGERMWLAEPERYECQNI
FEQYEGRELSEVIAELHGLRSDGKTLIAQPHVRGDKLWTLDDIKRLNCVFKNPVKAF
>d1mhyb_ a.25.1.2 (B:) Methane monooxygenase hydrolase, beta and alpha
subunits {Methylosinus trichosporium}
KRGLTDPERAAIIAAAVPDHALDTQRKYHYFIQPRWKPLSEYEQLSCYAQPNPDWIAGGLDWGDW
TQKFHGGRPSWGNESTELRTTDWYRHRDPARRWHHPYVKDKSEEARYTQRFLAAYSSEGSIRTID
PYWRDEILNKYFGALLYSEYGLFNAHSSVGRDCLSDTIRQTAVFAALDKVDNAQMIQMERLFIAK
LVPGFDASTDVPKKIWTTDPIYSGARATVQEIWQGVQDWNEILWAGHAVYDATFGQFARREFFQR
LATVYGDTLTPFFTAQSQTYFQTTRGAIDDLFVYCLANDSEFGAHNRTFLNAWTEHYLASSVAAL
KDFVGLYAKVEKVAGATDSAGVSEALQRVFGDWKIDYADKIGFRVDVDQKVDAVLAGY
>d1mhyd_ a.25.1.2 (D:) Methane monooxygenase hydrolase, beta and alpha
subunits {Methylosinus trichosporium}
NRAPVGVEPQEVHKWLQSFNWDFKENRTKYPTKYHMANETKEQFKVIAKEYARMEAAKDERQFGT
LLDGLTRLGAGNKVHPRWGETMKVISNFLEVGEYNAIAASAMLWDSATAAEQKNGYLAQVLDEIR
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HTHQCAFINHYYSKHYHDPAGHNDARRTRAIGPLWKGMKRVFADGFISGDAVECSVNLQLVGEAC
FTNPLIVAVTEWASANGDEITPTVFLSVETDELRHMANGYQTVVSIANDPASAKFLNTDLNNAFW
TQQKYFTPVLGYLFEYGSKFKVEPWVKTWNRWVSEDWGGIWIGRLGKYGVESPRSLRDAKRDAYW
AHHDLALAAYAMWPLGFARLALPDEEDQAWFEANYPGWADHYGKIFNEWKKLGYEDPKSGFIPYQ
WLLANGHDVYIDRVSQVPFIPSLAKGTGSLRVHEFNGKKHSLTDDWGERQWLIEPERYECHNVFE
QYEGRELSEVIAEGHGVRSDGKTLIAQPHTRGDNLWTLEDIKRAGCVFPDPLAKF
>d1jqca_ a.25.1.2 (A:) Ribonucleotide reductase R2 {Escherichia coli}
AYTTFSQTKNDQLKEPMFFGQPVNVARYDQQKYDIFEKLIEKQLSFFWRPEEVDVSRDRIDYQAL
PEHEKHIFISNLKYQTLLDSIQGRSPNVALLPLISIPELETWVETWAFSETIHSRSYTHIIRNIV
NDPSVVFDDIVTNEQIQKRAEGISSYYDELIEMTSYWHLLGEGTHTVNGKTVTVSLRELKKKLYL
CLMSVNALEAIRFYVSFACSFAFAERELMEGNAKIIRLIARDEALHLTGTQHMLNLLRSGADDPE
MAEIAEECKQECYDLFVQAAQQEKDWADYLFRDGSMIGLNKDILCQYVEYITNIRMQAVGLDLPF
QTRSNPIPWINTWLV
>d1r2fa_ a.25.1.2 (A:) Ribonucleotide reductase R2 {Salmonella typhimurium}
ISAINWNKIQDDKDLEVWNRLTSNFWLPEKVPLSNDIPAWQTLSAAEQQLTIRVFTGLTLLDTIQ
NIAGAPSLMADAITPHEEAVLSNISFMEAVHARSYSSIFSTLCQTKEVDAAYAWSEENPPLQRKA
QIILAHYVSDEPLKKKIASVFLESFLFYSGFWLPMYFSSRGKLTNTADLIRLIIRDEAVHGYYIG
YKYQIALQKLSAIEREELKLFALDLLMELYDNEIRYTEALYAETGWVNDVKAFLCYNANKALMNL
GYEALFPPEMADVNPAILAALSP
>d1kgna_ a.25.1.2 (A:) Ribonucleotide reductase R2 {Corynebacterium ammoniagenes}
SNEYDEYIANHTDPVKAINWNVIPDEKDLEVWDRLTGNFWLPEKIPVSNDIQSWNKMTPQEQLAT
MRVFTGLTLLDTIQGTVGAISLLPDAETMHEEAVYTNIAFMESVHAKSYSNIFMTLASTPQINEA
FRWSEENENLQRKAKIIMSYYNGDDPLKKKVASTLLESFLFYSGFYLPMYLSSRAKLTNTADIIR
LIIRDESVHGYYIGYKYQQGVKKLSEAEQEEYKAYTFDLMYDLYENEIEYTEDIYDDLGWTEDVK
RFLRYNANKALNNLGYEGLFPTDETKVSPAILSSLS
>d1xsm__ a.25.1.2 (-) Ribonucleotide reductase R2 {Mouse (Mus musculus)}
NPSVEDEPLLRENPRRFVVFPIEYHDIWQMYKKAEASFWTAEEVDLSKDIQHWEALKPDERHFIS
HVLAFFAASDGIVNENLVERFSQEVQVTEARCFYGFQIAMENIHSEMYSLLIDTYIKDPKEREYL
FNAIETMPCVKKKADWALRWIGDKEATYGERVVAFAAVEGIFFSGSFASIFWLKKRGLMPGLTFS
NELISRDEGLHCDFACLMFKHLVHKPAEQRVREIITNAVRIEQEFLTEALPVKLIGMNCTLMKQY
IEFVADRLMLELGFNKIFRVENPFDFME
>d1jk0a_ a.25.1.2 (A:) Ribonucleotide reductase R2 {Baker's yeast (Saccharomyces cerevisiae)}
LNKELETLREENRVKSDMLKEKLSKDAENHKAYLKSHQVHRHKLKEMEKEEPLLNEDKERTVLFP
IKYHEIWQAYKRAEASFWTAEEIDLSKDIHDWNNRMNENERFFISRVLAFFAASDGIVNENLVEN
FSTEVQIPEAKSFYGFQIMIENIHSETYSLLIDTYIKDPKESEFLFNAIHTIPEIGEKAEWALRW
IQDADALFGERLVAFASIEGVFFSGSFASIFWLKKRGMMPGLTFSNELICRDEGLHTDFACLLFA
HLKNKPDPAIVEKIVTEAVEIEQRYFLDALPVALLGMNADLMNQYVEFVADRLLVAFGNKKYYKV
ENPFDFMEN
>d1jk0b_ a.25.1.2 (B:) Ribonucleotide reductase R2 {Baker's yeast (Saccharomyces cerevisiae)}

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FQKERHDMKEAEKDEILLMENSRRFVMFPIKYHEIWAAYKKVEASFWTAEEIELAKDTEDFQKLT
DDQKTYIGNLLALSISSDNLVNKYLIENFSAQLQNPEGKSFYGFQIMMENIYSEVYSMMVDAFFK
DPKNIPLFKEIANLPEVKHKAAFIERWISNDDSLYAERLVAFAAKEGIFQAGNYASMFWLTDKKI
MPGLAMANRNICRDRGAYTDFSCLLFAHLRTKPNPKIIEKIITEAVEIEKEYYSNSLPVEKFGMD
LKSIHTYIEFVADGLLQGFGNEKYY
>d1afra_  a.25.1.2  (A:)  delta  9-stearoyl-acyl  carrier  protein
desaturase {Castor bean (Ricinus communis)}
MPPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEKCWQPQDFLPDPASDGFDEQVREL
RERAKEIPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASPTSWAIWTRAWTAEENRHGD
LLNKYLYLSGRVDMRQIEKTIQYLIGSGMDPRTENSPYLGFIYTSFQERATFISHGNTARQAKEH
GDIKLAQICGTIAADEKRHETAYTKIVEKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNL
FDHFSAVAQRLGVYTAKDYADILEFLVGRWKVDKLTGLSAEGQKAQDYVCRLPPRIRRLEERAQG
RAKEAPTMPFSWIFDRQVKL
>d1rhga_ a.26.1.1 (A:) Granulocyte-colony stimulating factor (G-CSF)
{Human (Homo sapiens)}
LPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAPLSSCPSQALQLAG
CLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQMEELGMAPALQPTQGAMP
AFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLA
>d1bgc__ a.26.1.1 (-) Granulocyte-colony stimulating factor (G-CSF)
{Cow (Bos taurus)}
SLPQSFLLKCLEQVRKIQADGAELQERLCAAHKLCHPEELMLLRHSLGIPQAPLSSCSSQSLQLR
GCLNQLHGGLFLYQGLLQALAGISPELAPTLDTLQLDVTDFATNIWLQMEDLGAAPAVQPTQGAM
PTFTSAFQRRAGGVLVASQLHRFLELAYRGLRYLA
>d1bgea_ a.26.1.1 (A:) Granulocyte-colony stimulating factor (G-CSF)
{Dog (Canis familiaris)}
PLPQSFLLKCLEQMRKVQADGTALQETLCATHQLCHPEELVLLGHALGIPQPPLSSCSSQALQLM
GCLRQLHSGLFLYQGLLQALAGISPELAPTLDTLQLDTTDFAINIWQQMEDLGMAPAVPPTQGTM
PAFTSAFQRRAGGVLVASNLQSFLELAYRALRHFAK
>d1alu__ a.26.1.1 (-) Interleukin-6 {Human (Homo sapiens)}
LTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFQSGFNEETC
LVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLL
TKLQAQNQWLQDMTTHLILRSFKEFLQSSLRALRQM
>d1i1rb_ a.26.1.1 (B:) Interleukin-6 {Human herpesvirus 8, Kaposi's
sarcoma herpes-virus}
EFEKDLLIQRLNWMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAINDTDHCGLIGFNETSC
LKKLADGFFEFEVLFKFLTTEFGKSVINVDVMELLTKTLGWDIQEELNKLTKTHYSPPKFDRGLL
GRLQGLKYWVRHFASFYVLSAMEKFAGQAVRVLDSIP
>d1a7m__ a.26.1.1 (-) Leukemia inhibitory factor (LIF) {Mouse (Mus
musculus)}
SPLPITPVNATCAIRHPCHGNLMNQIKNQLAQLNGSANALFISYYTAQGEPFPNNLDKLCGPNVT
DFPPFHANGTEKAKLVELYRMVAYLSASLTNITRDQKVLNPSAVSLHSKLNATIDVMRGLLSNVL
CRLCNKYRVGHVDVPPVPDHSDKEVFQKKKLGCQLLGTYKQVISVVVQAF
>d1lki__ a.26.1.1 (-) Leukemia inhibitory factor (LIF) {Mouse (Mus
musculus)}
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NATCAIRHPCHGNLMNQIKNQLAQLNGSANALFISYYTAQGEPFPNNVEKLCAPNMTDFPSFHGN
GTEKTKLVELYRMVAYLSASLTNITRDQKVLNPTAVSLQVKLNATIDVMRGLLSNVLCRLCNKYR
VGHVDVPPVPDHSDKEAFQRKKLGCQLLGTYKQVISVVVQAF
>d1emra_ a.26.1.1 (A:) Leukemia inhibitory factor (LIF) {Human (Homo sapiens)}
LMNQIRSQLAQLNGSANALFILYYTAQGEPFPNNLEKLCGPNVTDFPPFHANGTEKAKLVELYRI
VVYLGTSLGNITRDQKILNPSALSLHSKLNATADILRGLLSNVLCRLCSKYHVGHVDVTYGPDTS
GKDVFQKKKLGCQLLGKYKQVISVLAQAF
>d1a22a_ a.26.1.1 (A:) Growth hormone, somatotropin {Human (Homo sapiens)}
FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLCFSESIPTPSNRE
ETQQKSNLELLRISLLLIQSWLEPVQFLRSVFANSLVYGASDSNVYDLLKDLEERIQTLMGRLEG
QIFKQTYSKFDTDALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF
>d1axia_ a.26.1.1 (A:) Growth hormone, somatotropin {Human (Homo sapiens)}
TIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLCFSESIPTPSNREET
QQKSNLELLRISLLLIQSWLEPVQFLRSVFANSLVYGASDSNVYDLLKDLEERIQTLMGRLTDGS
PRTGQIFKQTYSKFDTNSHNDDALLKNYGLLYCFRRDMTYVATYLRIVQCRSVEGSCGF
>d1hgu__ a.26.1.1 (-) Growth hormone, somatotropin {Human (Homo sapiens)}
PTIPLSRLFQNAMLRAHRLHQLAFDTYEEFEEAYIPKEQKYSFLQAPQASLCFSESIPTPSNREQ
AQQKSNLQLLRISLLLIQSWLEPVGFLRSVFANSLVYGASDSDVYDLLKDLEEGIQTLMGRLEDG
SPRTGQAFKQTYAKFDANSHNDDALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCG
>d1huw__ a.26.1.1 (-) Growth hormone, somatotropin {Human (Homo sapiens)}
FPTIPLSRLADNAWLRADRLNQLAFDTYQEFEEAYIPKEQIHSFWWNPQTSLCPSESIPTPSNKE
ETQQKSNLELLRISLLLIQSWLEPVQFLRSVFANSLVYGASDSNVYDLLKDLEEGIQTLMGRLEA
LLKNYGLLYCFNKDMSKVSTYLRTVQCRSVEGSCGF
>d1f6fa_ a.26.1.1 (A:) Placental lactogen {Sheep (Ovis aries)}
AQHPPYCRNQPGKCQIPLQSLFDRATTVANYNSKLAGEMVNRFDEQYGQGINSESKVINCHTSSI
TTPNSKAEAINTEDKILFKLVISLLHSWDEPLHHAVTELANSKGTSPALLTKAQEIKEKAKVLVD
GVEVIQKRIHPGEKNEPYPVWSEQSSLTSQDENVRRVAFYRLFHCLHRDSSKIYTYLRILKCRLT
SC
>d1cnt1_ a.26.1.1 (1:) Ciliary neurotrophic factor (CNTF) {Human (Homo sapiens)}
PHRRDLCSRSIWLARKIRSDLTALTESYVKHQGLNKNINLDSADGMPVASTDQWSELTEAERLQE
NLQAYRTFHVLLARLLEDQQVHFTPTEGDFHQAIHTLLLQVAAFAYQIEELMILLEYKIPRNEAD
GMPINVGDGGLFEKKLWGLKVLQELSQWTVRSIHDLRFISSHQTGIP
>d1ax8__ a.26.1.1 (-) Leptin (obesity protein) {Human (Homo sapiens)}
IQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVYQQILTS
MPSRNVIQISNDLENLRDLLHVLAFSKSCHLPEASGLETLDSLGGVLEASGYSTEVVALSRLQGS
LQDMLWQLDLSPGC
>d1evsa_ a.26.1.1 (A:) Oncostatin M {Human (Homo sapiens)}
GSCSKEYRVLLGQLQKQTDLMQDTSRLLDPYIRIQGLDVPKLREHCRERPGAFPSEETLRGLGRR
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GFLQTLNATLGCVLHRLADLEQRLPKAQDLERSGLNIEDLEKLQMARPNILGLRNNIYCMAQLLD
NSDTAEPTKAGRGASQPPTPTPASDAFQRKLEGCRFLHGYHRFMHSVGRVFSKW
>d1f45b_ a.26.1.1 (B:) Heterodimeric interleukin-12 alpha chain
{Human (Homo sapiens)}
QNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFIT
NGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALN
FNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS
>d1eera_ a.26.1.2 (A:) Erythropoietin {Human (Homo sapiens)}
APPRLICDSRVLERYLLEAKEAEKITTGCAEHCSLNEKITVPDTKVNFYAWKRMEVGQQAVEVWQ
GLALLSEAVLRGQALLVKSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAISNSDAASAAPL
RTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR
>d2gmfa_ a.26.1.2 (A:) Granulocyte-macrophage colony-stimulating
factor (GM-CSF) {Human (Homo sapiens)}
RSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLELYKQGLRG
SLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFDCWEP
>d1hzia_ a.26.1.2 (A:) Interleukin-4 (IL-4) {Human (Homo sapiens)}
HKCDITLQAIIKTLNSLTEQKTLCTELTVTDIFAASKNTTEKETFCRAATVLRQFYSHHEKDTRC
LGATAQQFHRHKQLIRFLKRLDRNLWGLAGLNSCPVKEANQSTLENFLERLKTIMREKYSKCSS
>d1hula_ a.26.1.2 (A:) Interleukin-5 {Human (Homo sapiens)}
IPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGGTVERLF
KNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQEFLGVMNTEWI
>d1hmca_ a.26.1.2 (A:) Macrophage colony-stimulating factor (M-CSF)
{Human (Homo sapiens)}
SEYCSHMIGSGHLQSLQRLIDSQMETSCQITFEFVDQEQLKDPVCYLKKAFLLVQDIMEDTMRFR
DNTPNAIAIVQLQELSLRLKSCFTKDYEEHDKACVRTFYETPLQLLEKVKNVFNETKNLLDKDWN
IFSKNCNNSFAECSSQGH
>d1etea_ a.26.1.2 (A:) Flt3 ligand {Human (Homo sapiens)}
TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDDELCGGLWRLVLAQRWMERLKTVAG
SKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLEL
QCQP
>d1scfa_ a.26.1.2 (A:) Stem cell factor, SCF {Human (Homo sapiens)}
NVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSI
IDKLVNIVDDLVECVKENSSKDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVV
S
>d1scfc_ a.26.1.2 (C:) Stem cell factor, SCF {Human (Homo sapiens)}
NVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSI
IDKLVNIVDDLVECVKENSSKDLKKSFKSPEPRLFTPEEFFRIFNRSIDAF
>d3inkc_ a.26.1.2 (C:) Interleukin-2 (IL-2) {Human (Homo sapiens)}
STKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVL
NLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT
>d1jli__ a.26.1.2 (-) Interleukin-3 (IL-3) {Human (Homo sapiens)}
ANCSIMIDEIIHHLKRPPNPLLDPNNLNSEDMDILMERNLRTPNLLAFVRAVKHLENASAIESIL
KNLLPCLPLATAAPTRHPIHIKDGDWNEFRRKLTFYLKTLENAQAQQ
>d1ga3a_ a.26.1.2 (A:) Interleukin-13 (IL-13) {Human (Homo sapiens)}
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GGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEKTQR
MLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLLHLKKLFREGRFN
>d2ilk__ a.26.1.3 (-) Interleukin-10 (cytokine synthesis inhibitory
factor, CSIF) {Human (Homo sapiens)}
TQSENSCTHFPGNLPNMLRDLRDAFSRVKTFFQMKDQLDNLLLKESLLEDFKGYLGCQALSEMIQ
FYLEEVMPQAENQDPDIKAHVNSLGENLKTLRLRLRRCHRFLPCENKSKAVEQVKNAFNKLQEKG
IYKAMSEFDIFINYIEAYMTMKIRN
>d1vlk__ a.26.1.3 (-) Interleukin-10 (cytokine synthesis inhibitory
factor, CSIF) {Epstein-Barr virus}
CDNFPQMLRDLRDAFSRVKTFFQTKDEVDNLLLKESLLEDFKGYLGCQALSEMIQFYLEEVMPQA
ENQDPEAKDHVNSLGENLKTLRLRLRRCHRFLPCENKSKAVEQIKNAFNKLQEKGIYKAMSEFDI
FINYIEAYMTIK
>d1au1a_ a.26.1.3 (A:) Interferon-beta {Human (Homo sapiens)}
MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIYEMLQN
IFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSLHLKRYYGRIL
HYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
>d1rmi__ a.26.1.3 (-) Interferon-beta {Mouse (Mus musculus)}
INYKQLQLQERTNIRKCQELLEQLNGKINLTYRADFKIPMEMTEKMQKSYTAFAIQEMLQNVFLV
FRNNFSSTGWNETIVVRLLDELHQQTVFLKTVLEEKQEERLTWEMSSTALHLKSYYWRVQRYLKL
MKYNSYAWMVVRAEIFRNFLIIRRLTRNFQ
>d1rh2a_ a.26.1.3 (A:) Interferon-alpha 2b {Human (Homo sapiens)}
THSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTK
DSSAAWDETLLDKFYTELYQQLNDLEACVIQGVGVTETPLMNEDSILAVRKYFQRITLYLKEKKY
SPCAWEVVRAEIMRSFSLSTNLQE
>d1b5l__ a.26.1.3 (-) Interferon-tau {Sheep (Ovis aries)}
CYLSRKLMLDARENLKLLDRMNRLSPHSCLQDRKDFGLPQEMVEGDQLQKDQAFPVLYEMLQQSF
NLFYTEHSSAAWDTTLLEQLCTGLQQQLDHLDTCRGQVMGEEDSELGNMDPIVTVKKYFQGIYDY
LQEKGYSDCAWEIVRVEMMRALTVSTTLQKRLTK
>d1d9ca_ a.26.1.3 (A:) Interferon-gamma {Cow (Bos taurus)}
QGQFFREIENLKEYFNASSPDVAKGGPLFSEILKNWKDESDKKIIQSQIVSFYFKLFENLKDNQV
IQRSMDIIKQDMFQKFLNGSSEKLEDFKKLIQIPVDDLQIQRKAINELIKVMNDLS
>d1fyha1 a.26.1.3 (A:0-124) Interferon-gamma {Human (Homo sapiens)}
MQDPYVKEAENLKKYFNAGHSDVADNGTLFLGILKNWKEESDRKIMQSQIVSFYFKLFKNFKDDQ
SIQKSVETIKEDMNVKFFNSNKKKRDDFEKLTNYSVTDLNVQRKAIDELIQVMAELGANV
>d1fyha2 a.26.1.3 (A:201-324) Interferon-gamma {Human (Homo sapiens)}
SGEFVKEAENLKKYFNAGHSDVADNGTLFLGILKNWKEESDRKIMQSQIVSFYFKLFKNFKDDQS
IQKSVETIKEDMNVKFFNSNKKKRDDFEKLTNYSVTDLNVQRKAIHELIQVMAELSPAA
>d2rig__ a.26.1.3 (-) Interferon-gamma {Rabbit (Oryctolagus
cuniculus)}
QDTLTRETEHLKAYLKANTSDVANGGPLFLNILRNWKEESDNKIIQSQIVSFYFKLFDNLKDHEV
IKKSMESIKEDIFVKFFNSNLTKMDDFQNLTRISVDDRLVQRKAVSELSNVLNF
>d1a8h_1 a.27.1.1 (349-500) Methionyl-tRNA synthetase (MetRS)
{Thermus thermophilus}
LADDLGNLVQRTRAMLFRFAEGRIPEPVAGEELAEGTGLAGRLRPLVRELKFHVALEEAMAYVKA
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LNRYINEKKPWELFKKEPEEARAVLYRVVEGLRIASILLTPAMPDKMAELRRALGLKEEVRLEEA
ERWGLAEPRPIPEEAPVLFPKK
>d1f4la1 a.27.1.1 (A:389-548) Methionyl-tRNA synthetase (MetRS)
{Escherichia coli}
VVNLASRNAGFINKRFDGVLASELADPQLYKTFTDAAEVIGEAWESREFGKAVREIMALADLANR
YVDEQAPWVVAKQEGRDADLQAICSMGINLFRVLMTYLKPVLPKLTERAEAFLNTELTWDGIQQP
LLGHKVNPFKALYNRIDMRQVEALVEASKE
>d1ile_1 a.27.1.1 (642-821) Isoleucyl-tRNA synthetase (IleRS)
{Thermus thermophilus}
YFLTLWNVYSFFVTYANLDRPDLKNPPPPEKRPEMDRWLLARMQDLIQRVTEALEAYDPTTSARA
LRDFVVEDLSQWYVRRNRRRFWKNEDALDREAAYATLYEALVLVATLAAPFTPFLAEVLWQNLVR
SVRLEAKESVHLADWPEADPALADEALVAQMRAVLKVVDLARAARAKSGV
>d1ffya1 a.27.1.1 (A:645-917) Isoleucyl-tRNA synthetase (IleRS)
{Staphylococcus aureus}
YRKIRNTLRFMLGNINDFNPDTDSIPESELLEVDRYLLNRLREFTASTINNYENFDYLNIYQEVQ
NFINVELSNFYLDYGKDILYIEQRDSHIRRSMQTVLYQILVDMTKLLAPILVHTAEEVWSHTPHV
KEESVHLADMPKVVEVDQALLDKWRTFMNLRDDVNRALETARNEKVIGKSLEAKVTIASNDKFNA
SEFLTSFDALHQLFIVSQVKVVDKLDDQATAYEHGDIVIEHADGEKCERCWNYSEDLGAVDELTH
LCPRCQQVVKSLV
>d1qu3a1 a.27.1.1 (A:645-881) Isoleucyl-tRNA synthetase (IleRS)
{Staphylococcus aureus}
YRKIRNTLRFMLGNINDFNPDTDSIPESELLEVDRYLLNRLREFTASTINNYENFDYLNIYQEVQ
NFINVELSNFYLDYGKDILYIEQRDSHIRRSMQTVLYQILVDMTKLLAPILVHTAEEVWSHTPHV
KEESVHLADMPKVVEVDQALLDKWRTFMNLRDDVNRALETARNEKVIGKSLEAKVTIASNDKFNA
SEFLTSFDALHQLFIVSQVKVVDKLDDQATAYEHGDIVIEHA
>d1gaxa1 a.27.1.1 (A:579-862) Valyl-tRNA synthetase (ValRS) {Thermus
thermophilus}
ANKLYNAARFVLLSREGFQAKEDTPTLADRFMRSRLSRGVEEITALYEALDLAQAAREVYELVWS
EFCDWYLEAAKPALKAGNAHTLRTLEEVLAVLLKLLHPMMPFLTSELYQALTGKEELALEAWPEP
GGRDEEAERAFEALKQAVTAVRALKAEAGLPPAQEVRVYLEGETAPVEENLEVFRFLSRADLLPE
RPAKALVKAMPRVTARMPLEGLLDVEEWRRRQEKRLKELLALAERSQRKLASPGFREKAPKEVVE
AEEARLKENLEQAERIREALSQIG
>d1f7ua1 a.27.1.1 (A:484-607) Arginyl-tRNA synthetase (ArgRS)
{Baker's yeast (Saccharomyces cerevisiae)}
DTGPYLQYAHSRLRSVERNASGITQEKWINADFSLLKEPAAKLLIRLLGQYPDVLRNAIKTHEPT
TVVTYLFKLTHQVSSCYDVLWVAGQTEELATARLALYGAARQVLYNGMRLLGLTPVERM
>d1iq0a1 a.27.1.1 (A:467-592) Arginyl-tRNA synthetase (ArgRS)
{Thermus thermophilus}
GDTGPYVQYAHARAHSILRKAGEWGAPDLSQATPYERALALDLLDFEEAVLEAAEERTPHVLAQY
LLDLAASWNAYYNARENGQPATPVLTAPEGLRELRLSLVQSLQRTLATGLDLLGIPAPEVM
>d1acp__ a.28.1.1 (-) Acyl carrier protein {Escherichia coli}
STIEERVKKIIGEQLGVKQEEVTNNASFVEDLGADSLDTVELVMALEEEFDTEIPDEEAEKITTV
QAAIDYINGHQA
>d1f80d_ a.28.1.1 (D:) Acyl carrier protein {Bacillis subtilis}
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SADTLERVTKIIVDRLGVDEADVKLEASFKEDLGADXLDVVELVMELEDEFDMEISDEDAEKIAT
VGDAVNYIQ
>d1af8__ a.28.1.1 (-) Actinorhodin polyketide synthase acyl carrier
protein, ACT ACP {Streptomyces coelicolor, A3(2)}
MATLLTTDDLRRALVECAGETDGTDLSGDFLDLRFEDIGYDSLALMETAARLESRYGVSIPDDVA
GRVDTPRELLDLINGALAEAA
>d1dnya_ a.28.1.2 (A:) Peptidyl carrier protein (PCP), thioester
domain {Bacillus brevis}
YVAPTNAVESKLAEIWERVLGVSGIGILDNFFQIGGHSLKAMAVAAQVHREYQVELPLKVLFAQP
TIKALAQYVAT
>d1dv5a_ a.28.1.3 (A:) apo-D-alanyl carrier protein {Lactobacillus
casei}
ADEAIKNGVLDILADLTGSDDVKKNLDLNLFETGLLDSMGTVQLLLELQSQFGVDAPVSEFDRKE
WDTPNKIIAKVEQAQ
>d1unka_ a.28.2.1 (A:) ImmE7 protein (Im7) {Escherichia coli}
MELKNSISDYTEAEFVQLLKEIEKENVAATDDVLDVLLEHFVKITEHPDGTDLIYYPSDNRDDSP
EGIVKEIKEWRAANGKPGFKQG
>d1imy__ a.28.2.1 (-) ImmE8 (Im8) {Escherichia coli}
MELKNSISDYTETEFKKIIEDIINCEGDEKKQDDNLEHFISVTEHPSGSDLIYYPEGNNDGSPEA
VIKEIKEWRAANGKSGFKQG
>d1emva_ a.28.2.1 (A:) ImmE9 protein (Im9) {Escherichia coli}
LKHSISDYTEAEFLQLVTTICNADTSSEEELVKLVTHFEEMTEHPSGSDLIYYPKEGDDDSPSGI
VNTVKQWRAANGKSGFKQ
>d2eiaa1 a.28.3.1 (A:148-222) EIAV capsid protein p26 {Equine
infectious anemia virus}
PKAQNIRQGAKEPYPEFVDRLLSQIKSEGHPQEISKFLTDTLTIQNANEECRNAMRHLRPEDTLE
EKMYACRDIG
>d1qrjb1 a.28.3.1 (B:131-214) HTLV-I capsid protein {Human T-cell
leukemia virus type 1}
PSWASILQGLEEPYHAFVERLNIALDNGLPEGTPKDPILRSLAYSNANKECQKLLQARGHTNSPL
GDMLRACQTWTPKDKTKVL
>d1a8o__ a.28.3.1 (-) HIV capsid protein, dimerisation domain {Human
immunodeficiency virus type 1}
MDIRQGPKEPFRDYVDRFYKTLRAEQASQEVKNWMTETLLVQNANPDCKTILKALGPGATLEEMM
TACQG
>d1d1da1 a.28.3.1 (A:151-230) RSV capsid protein {Rous sarcoma virus}
GPWADITQGPSESFVDFANRLIKAVEGSDLPPSARAPVIIDCFRQKSQPDIQQLIRAAPSTLTTP
GEIIKYVLDRQKIAP
>d1eoqa_ a.28.3.1 (A:) RSV capsid protein {Rous sarcoma virus}
MDIMQGPSESFVDFANRLIKAVEGSDLPPSARAPVIIDCFRQKSQPDIQQLIRTAPSTLTTPGEI
IKYVLDRQKTAP
>d1e6ia_ a.29.2.1 (A:) GCN5 {Baker's yeast (Saccharomyces
cerevisiae)}
RGPHDAAIQNILTELQNHAAAWPFLQPVNKEEVPDYYDFIKEPMDLSTMEIKLESNKYQKMEDFI
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YDARLVFNNCRMYNGENTSYYKYANRLEKFFNNKVKEIPEYSHLID
>d1f68a_ a.29.2.1 (A:) GCN5 {Human (Homo sapiens)}
GDQLYTTLKNLLAQIKSHPSAWPFMEPVKKSEAPDYYEVIRFPIDLKTMTERLRSRYYVTRKLFV
ADLQRVIANCREYNPPDSEYCRCASALEKFFYFKLKEG
>d1b91a_ a.29.2.1 (A:) P300/CAF histone acetyltransferase bromodomain {Human (Homo sapiens)}
GSHMSKEPRDPDQLYSTLKSILQQVKSHQSAWPFMEPVKRTEAPGYYEVIRSPMDLKTMSERLKN
RYYVSKKLFMADLQRVFTNCKEYNAPESEYYKCANILEKFFFSKIKEAGLIDK
>d1eqfa1 a.29.2.1 (A:1359-1497) TAFII250 double bromodomain module {Human (Homo sapiens)}
GTTVHCDYLNRPHKSIHRRRTDPMVTLSSILESIINDMRDLPNTYPFHTPVNAKVVKDYYKIITR
PMDLQTLRENVRKRLYPSREEFREHLELIVKNSATYNGPKHSLTQISQSMLDLCDEKLKEKEDKL
ARLEKAINP
>d1eqfa2 a.29.2.1 (A:1498-1625) TAFII250 double bromodomain module {Human (Homo sapiens)}
LLDDDDQVAFSFILDNIVTQKMMAVPDSWPFHHPVNKKFVPDYYKVIVNPMDLETIRKNISKHKY
QSRESFLDDVNLILANSVKYNGPESQYTKTAQEIVNVCYQTLTEYDEHLTQLEKDICTAKEAA
>d1gm5a1 a.29.4.1 (A:7-105) RecG, N-terminal domain {Thermotoga maritima}
FTSSLFLWGEALPTLLEEFLNEVEKMLKNQVNTRRIHQLLKELDDPLLENKDLEEKLQAFLDYVK
EIPNLPEARKRYRIQKSLEMIEKLRSWFLIDYLE
>d1gkza1 a.29.5.1 (A:38-185) Branched-chain alpha-ketoacid dehydrogenase kinase (BCK) {Rat (Rattus norvegicus)}
VRLTPTMMLYSGRSQDGSHLLKSGRYLQQELPVRIAHRIKGFRSLPFIIGCNPTILHVHELYIRA
FQKLTDFPPIKDQADEAQYCQLVRQLLDDHKDVVTLLAEGLRESRKHIEDEKLVRYFLDKTLTSR
LGIRMLATHHLALHEDKP
>d1jm6a1 a.29.5.1 (A:1003-1169) Pyruvate dehydrogenase kinase {Rat (Rattus norvegicus), isozyme 2}
ASLAGAPKYIEHFSKFSPSPLSMKQFLDFGSSNACEKTSFTFLRQELPVRLANIMKEINLLPDRV
LSTPSVQLVQSWYVQSLLDIMEFLDKDPEDHRTLSQFTDALVTIRNRHNDVVPTMAQGVLEYKDT
YGDDPVSNQNIQYFLDRFYLSRISIRMLINQHTLIFD
>d1buca1 a.29.3.1 (A:233-383) Butyryl-CoA dehydrogenase {Megasphaera elsdenii}
GKGFKIAMMTLDGGRIGVAAQALGIAEAALADAVEYSKQRVQFGKPLCKFQSISFKLADMKMQIE
AARNLVYKAACKKQEGKPFTVDAAIAKRVASDVAMRVTTEAVQIFGGYGYSEEYPVARHMRDAKI
TQIYEGTNEVQLMVTGGALLR
>d1jqia1 a.29.3.1 (A:235-387) Butyryl-CoA dehydrogenase {Rat (Rattus norvegicus)}
MGFKIAMQTLDMGRIGIASQALGIAQASLDCAVKYAENRHAFGAPLTKLQNIQFKLADMALALES
ARLLTWRAAMLKDNKKPFTKESAMAKLAASEAATAISHQAIQILGGMGYVTEMPAERYYRDARIT
EIYEGTSEIQRLVIAGHLLRSYR
>d3mdda1 a.29.3.1 (A:242-395) Medium chain acyl-CoA dehydrogenase {Pig (Sus scrofa)}
GAGFKIAMGTFDKTRPPVAAGAVGLAQRALDEATKYALERKTFGKLLAEHQGISFLLADMAMKVE
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LARLSYQRAAWEIDSGRRNTYYASIAKAYAADIANQLATDAVQVFGGNGFNTEYPVEKLMRDAKI
YQIYEGTAQIQRIIIAREHIGRYK
>d1egda1 a.29.3.1 (A:242-396) Medium chain acyl-CoA dehydrogenase
{Human (Homo sapiens)}
GAGFKVAMGAFDKERPVVAAGAVGLAQRALDEATKYALERKTFGKLLVEHQAISFMLAEMAMKVE
LARMSYQRAAWEVDSGRRNTYYASIAKAFAGDIANQLATDAVQILGGNGFNTEYPVEKLMRDAKI
YQIYGGTSQIQRLIVAREHIDKYKN
>d1ivha1 a.29.3.1 (A:242-392) Isovaleryl-CoA dehydrogenase {Human
(Homo sapiens)}
KGVYVLMSGLDLERLVLAGGPLGLMQAVLDHTIPYLHVREAFGQKIGHFQLMQGKMADMYTRLMA
CRQYVYNVAKACDEGHCTAKDCAGVILYSAECATQVALDGIQCFGGNGYINDFPMGRFLRDAKLY
EIGAGTSEVRRLVIGRAFNAD
>d1b6q__ a.30.1.1 (-) ROP protein {Escherichia coli}
MTKQEKTALNMARFIRSQTLTLLEKLNELDPDEQADICESLHDHADELYRSCLARF
>d1f4na_ a.30.1.1 (A:) ROP protein {Escherichia coli}
GTKQEKTILNMARFIRSQALTILEKANELDADEIADIAESIHDHADEIYRSALARFGDDG
>d1f4nb_ a.30.1.1 (B:) ROP protein {Escherichia coli}
EKTILNMARFIRSQALTILEKANELDADEIADIAESIHDHADEIYRSALAR
>d1gtoa_ a.30.1.1 (A:) ROP protein {Escherichia coli}
GTKQEKTALNMARFIRSQTLTLLEKLNELGADEQADICESLHDHADELYRSCLARFGDDGEN
>d1nkd__ a.30.1.1 (-) ROP protein {Escherichia coli}
MTKQEKTALNMARFIRSQTLTLLEKLNELADAADEQADICESLHDHADELYRSCLARFG
>d1joya_ a.30.2.1 (A:) EnvZ histidine kinase {Escherichia coli}
MAAGVKQLADDRTLLMAGVSHDLRTPLTRIRLATEMMSEQDGYLAESINKDIEECNAIIEQFIDY
LR
>d1b3qa1 a.30.2.1 (A:293-354) Histidine kinase CheA {Thermotoga
maritima}
SQTVRVDIEKLDNLMDLMGELVIARSRILETLKKYNIKELDESLSHLSRITLDLQNVVMKIR
>d1r2aa_ a.31.1.1 (A:) Dimerization-anchoring domain of
cAMP-dependent type II PK regulatory subunit {Mouse (Mus musculus)}
HMGHIQIPPGLTELLQGYTVEVLRQQPPDLVDFAVEYFTRLREARR
>d1ytfb1 a.32.1.1 (B:) Transcription factor IIA (TFIIA), N-terminal
domain {Baker's yeast (Saccharomyces cerevisiae)}
SNAEASRVYEIIVESVVNEVREDFENAGIDEQTLQDLKNIWQKKLT
>d1ytfd1 a.32.1.1 (D:5-54) Transcription factor IIA (TFIIA),
N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
GYYELYRRSTIGNSLVDALDTLISDGRIEASLAMRVLETFDKVVAETLKD
>d1ecia_ a.33.1.1 (A:) Ectatomin, A & B chains {Ant (Ectatomma
tuberculatum), venom}
GVIPKKIWETVCPTVEPWAKKCSGDIATYIKRECGKL
>d1ecib_ a.33.1.1 (B:) Ectatomin, A & B chains {Ant (Ectatomma
tuberculatum), venom}
WSTIVKLTICPTLKSMAKKCEGSIATMIKKKCDK
>d1b0na1 a.34.1.1 (A:74-108) SinR repressor (dimerisation
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domain)-SinI anti-repressor complex {Bacillus subtilis}
LDSEWEKLVRDAMTSGVSKKQFREFLDYQKWRKSQ
>d1b0nb1 a.34.1.1 (B:) SinR repressor (dimerisation domain)-SinI
anti-repressor complex {Bacillus subtilis}
FELDQEWVELMVEAKEANISPEEIRKYLLLN
>d1f93f_ a.34.1.1 (F:) Dimerization cofactor of HNF-1 alpha {Mouse
(Mus musculus)}
LSQLQTELLAALLESGLSKEALIQALG
>d1g2ya_ a.34.1.1 (A:) Dimerization cofactor of HNF-1 alpha {Mouse
(Mus musculus)}
MVSKLSQLQTEMLAALLESGLSKEALIQALG
>d1g2za_ a.34.1.1 (A:) Dimerization cofactor of HNF-1 alpha {Mouse
(Mus musculus)}
MVSKLSQLQTELMAALLESGLSKEALIQALGE
>d1g39a_ a.34.1.1 (A:) Dimerization cofactor of HNF-1 alpha {Mouse
(Mus musculus)}
MVSKLSQLQTELLAALLESGLSKEALIQ
>d1jb6b_ a.34.1.1 (B:) Dimerization cofactor of HNF-1 alpha {Mouse
(Mus musculus)}
SKLSQLQTELMAALLESGLSKEALIQAL
>d1e3oc2 a.35.1.1 (C:1-75) Oct-1 {Human (Homo sapiens)}
EEPSDLEELEQFAKTFKQRRIKLGFTQGDVGLAMGKLYGNDFSQTTISRFEALNLSFKNMSKLKP
LLEKWLNDAE
>d1au7a2 a.35.1.1 (A:5-76) Pit-1 {Rat (Rattus norvegicus)}
GMRALEQFANEFKVRRIKLGYTQTNVGEALAAVHGSEFSQTTICRFENLQLSFKNACKLKAILSK
WLEEAEQ
>d1llib_ a.35.1.2 (B:) lambda C1 repressor, DNA-binding domain
{Bacteriophage lambda (Escherichia coli)}
STKKKPLTQEQLEDARRLKAIYEKKKNELGLSQESLADKLGMGQSGIGALFNGINALNAYNAALL
AKILKVSVEEFSPSIAREIYEMYEAVS
>d1lmb3_ a.35.1.2 (3:) lambda C1 repressor, DNA-binding domain
{Bacteriophage lambda (Escherichia coli)}
PLTQEQLEDARRLKAIYEKKKNELGLSQESVADKMGMGQSGVGALFNGINALNAYNAALLAKILK
VSVEEFSPSIAREIYEMYEAVS
>d1r69__ a.35.1.2 (-) 434 C1 repressor, DNA-binding domain
{Bacteriophage 434 (Escherichia coli)}
SISSRVKSKRIQLGLNQAELAQKVGTTQQSIEQLENGKTKRPRFLPELASALGVSVDWLLNGT
>d2cro__ a.35.1.2 (-) cro 434 {Bacteriophage 434}
MQTLSERLKKRRIALKMTQTELATKAGVKQQSIQLIEAGVTKRPRFLFEIAMALNCDPVWLQYGT
>d1adr__ a.35.1.2 (-) P22 C2 repressor, DNA-binding domain {Salmonella
bacteriophage P22}
MNTQLMGERIRARRKKLKIRQAALGKMVGVSNVAISQWERSETEPNGENLLALSKALQCSPDYLL
KGDLSQTNVAY
>d1copd_ a.35.1.2 (D:) cro lambda repressor {Bacteriophage lambda
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(Escherichia coli)}
MEQRITLKDYAMRFGQTKTAKDLGVYQSAINKAIHAGRKIFLTINADGSVYAEEVKPFPSNKKTT
A
>d1d1la_ a.35.1.2 (A:) cro lambda repressor {Bacteriophage lambda
(Escherichia coli)}
MEQRITLKDYAMRFGQTKTAKDLGVYQSAINKAIHAGRKIFLTINADGSVYAEEVKPWPSN
>d3orca_ a.35.1.2 (A:) cro lambda repressor {Bacteriophage lambda
(Escherichia coli)}
EQRITLKDYAMRFGQTKTAKDLGVYQSAINKAIHAGRKIFLTINADGSVYAEEVKDGEVKPFPSN
>d1ner__ a.35.1.2 (-) Ner {Bacteriophage mu}
CSNEKARDWHRADVIAGLKKRKLSLSALSRQFGYAPTTLANALERHWPKGEQIIANALETKPEVI
WPSRYQAGE
>d1b0na2 a.35.1.3 (A:1-68) SinR repressor, DNA-binding domain
{Bacillus subtilis}
MIGQRIKQYRKEKGYSLSELAEKAGVAKSYLSSIERNLQTNPSIQFLEKVSAVLDVSVHTLLDEK
HET
>d1dw9a1 a.35.1.4 (A:1-86) Cyanase N-terminal domain {Escherichia
coli}
MIQSQINRNIRLDLADAILLSKAKKDLSFAEIADGTGLAEAFVTAALLGQQALPADAARLVGAKL
DLDEDSILLLQMIPLRGCIDD
>d1pru__ a.35.1.5 (-) Purine repressor (PurR), N-terminal domain
{Escherichia coli}
MATIKDVAKRANVSTTTVSHVINKTRFVAEETRNAVWAAIKELHYSPSAVARSLKV
>d1vpwa1 a.35.1.5 (A:3-58) Purine repressor (PurR), N-terminal domain
{Escherichia coli}
TIKDVAKRANVSTTTVSHVINKTRFVAEETRNAVWAAIKELHYSPSAVARSMKVNH
>d1efaa1 a.35.1.5 (A:2-60) Lac repressor (LacR), N-terminal domain
{Escherichia coli}
KPVTLYDVAEYAGVSYQTVSRVVNQASHVSAKTREKVEAAMAELNYIPNRVAQQLAGKQ
>d1lcca_ a.35.1.5 (A:) Lac repressor (LacR), N-terminal domain
{Escherichia coli}
MKPVTLYDVAEYAGVSYQTVSRVVNQASHVSAKTREKVEAAMAELNYIPNR
>d1uxc__ a.35.1.5 (-) Fructose repressor (FruR), N-terminal domain
{Escherichia coli}
MKLDEIARLAGVSRTTASYVINGKAKQYRVSDKTVEKVMAVVREHNYHPN
>d1uxd__ a.35.1.5 (-) Fructose repressor (FruR), N-terminal domain
{Escherichia coli}
MKLDEIARLAGVSRTTASYVINGKAKQYRVSDKTVEKVMAVVREHNYHPNAVAAGLRLQ
>d1dula_ a.36.1.1 (A:) Signal sequence binding protein Ffh
{Escherichia coli}
FDLNDFLEQKVLVRMEAIINSMTMKERAKPEIIKGSRKRRIAAGSGMQVQDVNRLLKQFDDMQRM
MKKM
>d1hq1a_ a.36.1.1 (A:) Signal sequence binding protein Ffh
{Escherichia coli}
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GFDLNDFLEQLRQMKNMGGMASLMGKLPGMGQIPDNVKSQMDDKVLVRMEAIINSMTMKERAKPE
IIKGSRKRRIAAGSGMQVQDVNRLLKQFDDMQRMMKKMK
>d2ffha2 a.36.1.1 (A:319-418) Signal sequence binding protein Ffh
{Thermus aquaticus}
ELSLEDFLKQMQNLKRLGPFSEILGLLPGVPQGLKVDEKAIKRLEAIVLSMTPEERKDPRILNGS
RRKRIAKGSGTSVQEVNRFIKAFEEMKALMKSLEK
>d1qb2a_ a.36.1.1 (A:) SRP54M {Human (Homo sapiens)}
QFTLRDMYEQFQNIMKMGPFSQILGMIPGFGTDFMSKGNEQESMARLKKLMTIMDSMNDQELDST
DGAKVFSKQPGRIQRVARGSGVSTRDVQELLTQYTKFAQMVK
>d1sknp_ a.37.1.1 (P:) Binding domain of Skn-1 {Caenorhabditis
elegans}
GRQSKDEQLASDNELPVSAFQISEMSLSELQQVLKNESLSEYQRQLIRKIRRRGKNKVAARTCRQ
RRTDRHDKM
>d1hloa_ a.38.1.1 (A:) Max protein {Human (Homo sapiens)}
NDDIEVESDADKRAHHNALERKRRDHIKDSFHSLRDSVPSLQGEKASRAQILDKATEYIQYMRRK
NHTHQQDIDDLKRQN
>d1an2a_ a.38.1.1 (A:) Max protein {Mouse (Mus musculus)}
ADKRAHHNALERKRRDHIKDSFHSLRDSVPSLQGEKASRAQILDKATEYIQYMRRKNHTHQQDID
DLKRQNALLEQQVRALEKARS
>d1mdya_ a.38.1.1 (A:) Myod B/HLH domain {Mouse (Mus musculus)}
MELKRKTTNADRRKAATMRERRRLSKVNEAFETLKRSTSSNPNQRLPKVEILRNAIRYIEGLQAL
LRD
>d1an4a_ a.38.1.1 (A:) Usf B/HLH domain {Human (Homo sapiens)}
MDEKRRAQHNEVERRRRDKINNWIVQLSKIIPDSSMESTKSGQSKGGILSKASDYIQELRQSNHR
>d1a0aa_ a.38.1.1 (A:) Pho4 B/HLH domain {Baker's yeast (Saccharomyces
cerevisiae)}
MKRESHKHAEQARRNRLAVALHELASLIPAEWKQQNVSAAPSKATTVEAACRYIRHLQQNGST
>d1am9a_ a.38.1.1 (A:) SREBP-1a {Human (Homo sapiens)}
QSRGEKRTAHNAIEKRYRSSINDKIIELKDLVVGTEAKLNKSAVLRKAIDYIRFLQHSNQKLKQE
NLSLRTAVHKSKSLK
>d1bod__ a.39.1.1 (-) Calbindin D9K {Cow (Bos taurus)}
MKSPEELKGIFEKYDKEGDGQLSKEELKLLLQTEFPSLLKGMSTLDELFEELDKNGDGEVSFEEF
QVLVKKISQ
>d1ig5a_ a.39.1.1 (A:) Calbindin D9K {Cow (Bos taurus)}
KSPEELKGIFEKYAAKEGDPNQLSKEELKLLLQTEFPSLLKGPSTLDELFEELDKNGDGEVSFEE
FQVLVKKISQ
>d1cb1__ a.39.1.1 (-) Calbindin D9K {Pig (Sus scrofa)}
SAQKSPAELKSIFEKYAAKEGDPNQLSKEELKQLIQAEFPSLLKGPRTLDDLFQELDKNGDGEVS
FEEFQVLVKKISQ
>d1a03a_ a.39.1.2 (A:) Calcyclin (S100) {Rabbit (Oryctolagus
cuniculus)}
MASPLDQAIGLLIGIFHKYSGKEGDKHTLSKKELKELIQKELTIGSKLQDAEIVKLMDDLDRNKD
QEVNFQEYITFLGALAMIYNEALKG
>d1k2ha_ a.39.1.2 (A:) Calcyclin (S100) {Rat (Rattus norvegicus),
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s100a1}
GSELETAMETLINVFHAHSGKEGDKYKLSKKELKDLLQTELSSFLDVQKDADAVDKIMKELDENG
DGEVDFQEFVVLVAALTVACNNFFWENS
>d1qlka_ a.39.1.2 (A:) Calcyclin (S100) {Rat (Rattus norvegicus),
s100b}
MSELEKAMVALIDVFHQYSGREGDKHKLKKSELKELINNELSHFLEEIKEQEVVDKVMETLDEDG
DGECDFQEFMAFVSMVTTACHEFFEHE
>d1mho__ a.39.1.2 (-) Calcyclin (S100) {Cow (Bos taurus), s100b}
SELEKAVVALIDVFHQYSGREGDKHKLKKSELKELINNELSHFLEEIKEQEVVDKVMETLDSDGD
GECDFQEFMAFVAMITTACHEFF
>d1a4pa_ a.39.1.2 (A:) Calcyclin (S100) {Human (Homo sapiens), P11
s100a10, calpactin}
PSQMEHAMETMMFTFHKFAGDKGYLTKEDLRVLMEKEFPGFLENQKDPLAVDKIMKDLDQCRDGK
VGFQSFFSLIAGLTIACNDYFVVHMKQ
>d1psra_ a.39.1.2 (A:) Calcyclin (S100) {Human (Homo sapiens),
psoriasin s100a7}
SNTQAERSIIGMIDMFHKYTRRDDKIDKPSLLTMMKENFPNFLSACDKKGTNYLADVFEKKDKNE
DKKIDFSEFLSLLGDIATDYHKQSHGAAPCSGGSQ
>d1qlsa_ a.39.1.2 (A:) Calcyclin (S100) {Pig (Sus scrofa), calgizzarin
s100c (s100a11)}
PTETERCIESLIAIFQKHAGRDGNNTKISKTEFLIFMNTELAAFTQNQKDPGVLDRMMKKLDLDS
DGQLDFQEFLNLIGGLAIACHDSFIKSTQK
>d1mr8a_ a.39.1.2 (A:) Calcyclin (S100) {Human (Homo sapiens),
calgranulin s100a8, MRP8}
MLTELEKALNSIIDVYHKYSLIKGNFHAVYRDDLKKLLETECPQYIRKKGADVWFKELDINTDGA
VNFQEFLILVIKMGVAAHKKSHEES
>d1e8aa_ a.39.1.2 (A:) Calcyclin (S100) {Human (Homo sapiens),
calgranulin C, s100a12}
TKLEEHLEGIVNIFHQYSVRKGHFDTLSKGELKQLLTKELANTIKNIKDKAVIDEIFQGLDANQD
EQVDFQEFISLVAIALKAAHYH
>d1irja_ a.39.1.2 (A:) Calcyclin (S100) {Human (Homo sapiens), s100a9
(mrp14)}
TCKMSQLERNIETIINTFHQYSVKLGHPDTLNQGEFKELVRKDLQNFLKKENKNEKVIEHIMEDL
DTNADKQLSFEEFIMLMARL
>d1sra__ a.39.1.3 (-) C-terminal (EC) domain of
BM-40/SPARC/osteonectin {Human (Homo sapiens)}
PPCLDSELTEFPLRMRDWLKNVLVTLYERDEDNNLLTEKQKLRVKKIHENEKRLEAGDHPVELLA
RDFEKNYNMYIFPVHWQFGQLDQHPIDGYLSHTELAPLRAPLIPMEHCTTRFFETCDLDNDKYIA
LDEWAGCFGIKQKDIDKDLVI
>d1rro__ a.39.1.4 (-) Oncomodulin {Rat (Rattus norvegicus)}
SITDILSAEDIAAALQECQDPDTFEPQKFFQTSGLSKMSASQVKDIFRFIDNDQSGYLDGDELKY
FLQKFQSDARELTESETKSLMDAADNDGDGKIGADEFQEMVHS
>d1cdp__ a.39.1.4 (-) Parvalbumin {Carp (Cyprinus carpio)}
AFAGVLNDADIAAALEACKAADSFNHKAFFAKVGLTSKSADDVKKAFAIIDQDKSGFIEEDELKL
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FLQNFKADARALTDGETKTFLKAGDSDGDGKIGVDEFTALVKA
>d1pvaa_ a.39.1.4 (A:) Parvalbumin {Pike (Esox lucius)}
AAKDLLKADDIKKALDAVKAEGSFNHKKFFALVGLKAMSANDVKKVFKAIDADASGFIEEEELKF
VLKSFAADGRDLTDAETKAFLKAADKDGDGKIGIDEFETLVHEA
>d2pvba_ a.39.1.4 (A:) Parvalbumin {Pike (Esox lucius)}
SFAGLKDADVAAALAACSAADSFKHKEFFAKVGLASKSLDDVKKAFYVIDQDKSGFIEEDELKLF
LQNFSPSARALTDAETKAFLADGDKDGDGMIGVDEFAAMIKA
>d5pal__ a.39.1.4 (-) Parvalbumin {Leopard shark (Triakis
semifasciata)}
PMTKVLKADDINKAISAFKDPGTFDYKRFFHLVGLKGKTDAQVKEVFEILDKDQSGFIEEEELKG
VLKGFSAHGRDLNDTETKALLAAGDSDHDGKIGADEFAKMVAQA
>d1a75a_ a.39.1.4 (A:) Parvalbumin {Whiting (Merlangius merlangus)}
AGILADADCAAAVKACEAADSFSYKAFFAKCGLSGKSADDIKKAFVFIDQDKSGFIEEDELKLFL
QVFKAGARALTDAETKAFLKAGDSDGDGAIGVEEWVALVKA
>d1bu3__ a.39.1.4 (-) Parvalbumin {Silver hake (Merluccius
bilinearis)}
AFSGILADADVAAALKACEAADSFNYKAFFAKVGLTAKSADDIKKAFFVIDQDKSGFIEEDELKL
FLQVFSAGARALTDAETKAFLKAGDSDGDGAIGVDEWAALVKA
>d1g33a_ a.39.1.4 (A:) Parvalbumin {Rat (Rattus rattus)}
MKSADDVKKVFHILDKDKSGFIEEDELGSILKGFSSDARDLSAKETKTLMAAGDKDGDGKIGVEE
FSTLVAES
>d1rtp1_ a.39.1.4 (1:) Parvalbumin {Rat (Rattus rattus)}
SMTDLLSAEDIKKAIGAFTAADSFDHKKFFQMVGLKKKSADDVKKVFHILDKDKSGFIEEDELGS
ILKGFSSDARDLSAKETKTLMAAGDKDGDGKIGVEEFSTLVAES
>d1avsa_ a.39.1.5 (A:) Troponin C {Chicken (Gallus gallus)}
QAEARAFLSEEMIAEFKAAFDMFDADGGGDISTKELGTVMRMLGQNPTKEELDAIIEEVDEDGSG
TIDFEEFLVMMVRQMK
>d1ctda_ a.39.1.5 (A:) Troponin C {Chicken (Gallus gallus)}
KSEEELANAFRIFDKNADGYIDIEELGEILRATG
>d1dtla_ a.39.1.5 (A:) Troponin C {Chicken (Gallus gallus)}
YKAAVEQLTEEQKNEFKAAFDIFVLGAEDGSISTKELGKVMRMLGQNPTPEELQEMIDEVDEDGS
GTVDFDEFLVMMVRSMKDDSKGKSEEELSDLFRMFDKNADGYIDLEELKIMLQATGETITEDDIE
ELMKDGDKNNDGRIDYDEFLEFMKGV
>d1jc2a_ a.39.1.5 (A:) Troponin C {Chicken (Gallus gallus)}
EDAKGKSEEELANCFRIFDKNADGFIDIEELGEILRATGEHVIEEDIEDLMKDSDKNNDGRIDFD
EFLKMMEGVQ
>d1ncx__ a.39.1.5 (-) Troponin C {Chicken (Gallus gallus)}
ASMTDQQAEARAFLSEEMIAEFKAAFDMFDADGGGDISTKELGTVMRMLGQNPTKEELDAIIEEV
DEDGSGTIDFEEFLVMMVRQMKEDAKGKSEEELANCFRIFDKNADGFIDIEELGEILRATGEHVT
EEDIEDLMKDSDKNNDGRIDFDEFLKMMEGVQ
>d1smg__ a.39.1.5 (-) Troponin C {Chicken (Gallus gallus)}
ASMTDQQAEARAFLSEEMIAEFKAAFDMFDADGGGDISTKALGTVMRMLGQNPTKEELDAIIEEV
DEDGSGTIDFEEFLVMMVRQMKEDA
>g1pon.1 a.39.1.5 (A:,B:) Troponin C {Chicken (Gallus gallus)}
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KSEEELANAFRIFDKNADGYIDIEELGEILRATGXVTEEDIEDLMKDSDKNNDGRIDFDEFLKMM
EGVQ
>d1tn4__ a.39.1.5 (-) Troponin C {Rabbit (Oryctolagus cuniculus)}
TDQQAEARSYLSEEMIAEFKAAFDMFDADGGGDISVKELGTVMRMLGQTPTKEELDAIIEEVDED
GSGTIDFEEFLVMMVRQMKEDAKGKSEEELAELFRIFDRNADGYIDAEELAEIFRASGEHVTDEE
IESLMKDGDKNNDGRIDFDEFLKMMEG
>d1fi5a_ a.39.1.5 (A:) Troponin C {Chicken (Gallus gallus), cardiac
isoform}
MVRCMKDDSKGKTEEELSDLFRMFDKNADGYIDLEELKIMLQATGETITEDDIEELMKDGDKNND
GRIDYDEFLEFMKGVE
>d1ap4__ a.39.1.5 (-) Troponin C {Human (Homo sapiens), cardiac
isoform}
MDDIYKAAVEQLTEEQKNEFKAAFDIFVLGAEDGCISTKELGKVMRMLGQNPTPEELQEMIDEVD
EDGSGTVDFDEFLVMMVRCMKDDS
>d1ih0a_ a.39.1.5 (A:) Troponin C {Human (Homo sapiens), cardiac
isoform}
GKSEEELSDLFRMFDKNADGYIDLEELKIMLQATGETITEDDIEELMKDGDKNNDGRIDYDEFLE
FMKGVE
>d2scpa_ a.39.1.5 (A:) Sarcoplasmic calcium-binding protein {Sandworm
(Nereis diversicolor)}
SDLWVQKMKTYFNRIDFDKDGAITRMDFESMAERFAKESEMKAEHAKVLMDSLTGVWDNFLTAVA
GGKGIDETTFINSMKEMVKNPEAKSVVEGPLPLFFRAVDTNEDNNISRDEYGIFFGMLGLDKTMA
PASFDAIDTNNDGLLSLEEFVIAGSDFFMNDGDSTNKVFWGPLV
>d2sas__ a.39.1.5 (-) Sarcoplasmic calcium-binding protein {Amphioxus
(Branchiostoma lanceolatum)}
GLNDFQKQKIKFTFDFFLDMNHDGSIQDNDFEDMMTRYKEVNKGSLSDADYKSMQASLEDEWRDL
KGRADINKDDVVSWEEYLAMWEKTIATCKSVADLPAWCQNRIPFLFKGMDVSGDGIVDLEEFQNY
CKNFQLQCADVPAVYNVITDGGKVTFDLNRYKELYYRLLTSPAADAGNTLMGQKP
>d1c7va_ a.39.1.5 (A:) Calcium vector protein {Amphioxus
(Branchiostoma lanceolatum)}
EEEILRAFKVFDANGDGVIDFDEFKFIMQKVGEEPLTDAEVEEAMKEADEDGNGVIDIPEFMDLI
KKS
>d1j7qa_ a.39.1.5 (A:) Calcium vector protein {Amphioxus
(Branchiostoma lanceolatum)}
AAPKARALGPEEKDECMKIFDIFDRNAENIAPVSDTMDMLTKLGQTYTKRETEAIMKEARGPKGD
KKNIGPEEWLTLCSKWVRQDD
>d1j7ra_ a.39.1.5 (A:) Calcium vector protein {Amphioxus
(Branchiostoma lanceolatum)}
LGPEEKDECMKIFDIFDRNAENIAPVSDTMDMLTKLGQTYTKRETEAIMKEARGPKGDKKNIGPE
EWLTLCSKWVRQ
>d1ej3a_ a.39.1.5 (A:) Calcium-regulated photoprotein {Jellyfish
(Aequorea aequorea), aequorin}
LTSDFDNPRWIGRHKHMFNFLDVNHNGKISLDEMVYKASDIVINNLGATPEQAKRHKDAVEAFFG
GAGMKYGVETDWPAYIEGWKKLATDELEKYAKNEPTLIRIWGDALFDIVDKDQNGAITLDEWKAY
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TKAAGIIQSSEDCEETFRVCDIDESGQLDVDEMTRQHLGFWYTMDPACEKLYGGAVP
>d1el4a_ a.39.1.5 (A:) Calcium-regulated photoprotein {Hydrozoa
(Obelia longissima), obelin}
SSKYAVKLKTDFDNPRWIKRHKHMFDFLDINGNGKITLDEIVSKASDDICAKLEATPEQTKRHQV
CVEAFFRGCGMEYGKEIAFPQFLDGWKQLATSELKKWARNEPTLIREWGDAVFDIFDKDGSGTIT
LDEWKAYGKISGISPSQEDCEATFRHCDLDNSGDLDVDEMTRQHLGFWYTLDPEADGLYGNGVP
>d1jf0a_ a.39.1.5 (A:) Calcium-regulated photoprotein {Hydrozoa
(Obelia geniculata), obelin}
KYAVKLQTDFDNPKWIKRHKFMFDYLDINGNGQITLDEIVSKASDDICKNLGATPAQTQRHQDCV
EAFFRGCGLEYGKETKFPEFLEGWKNLANADLAKWARNEPTLIREWGDAVFDIFDKDGSGTITLD
EWKAYGRISGISPSEEDCEKTFQHCDLDNSGELDVDEMTRQHLGFWYTLDPEADGLYGNGVP
>d1jfja_ a.39.1.5 (A:) EHCABP {Entamoeba (Entamoeba histolytica)}
MAEALFKEIDVNGDGAVSYEEVKAFVSKKRAIKNEQLLQLIFKSIDADGNGEIDQNEFAKFYGSI
QGQDLSDDKIGLKVLYKLMDVDGDGKLTKEEVTSFFKKHGIEKVAEQVMKADANGDGYITLEEFL
EFSL
>d1cmg__ a.39.1.5 (-) Calmodulin {Cow (Bos taurus)}
MKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEE
FVQMMTAK
>d1fw4a_ a.39.1.5 (A:) Calmodulin {Cow (Bos taurus)}
SEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEFVQMM
>d1g4yr_ a.39.1.5 (R:) Calmodulin {Rat (Rattus rattus)}
ADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDF
PEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADI
DGDGQVNYEEFVQMMTA
>d1f70a_ a.39.1.5 (A:) Calmodulin {African frog (Xenopus laevis)}
ADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDF
PEFLTMMARKM
>d1exra_ a.39.1.5 (A:) Calmodulin {Ciliate (Paramecium tetraurelia)}
EQLTEEQIAEFKEAFALFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDFP
EFLSLMARKMKEQDSEEELIEAFKVFDRDGNGLISAAELRHVMTNLGEKLTDDEVDEMIREADID
GDGHINYEEFVRMMVS
>d1ggwa_ a.39.1.5 (A:) Cdc4p {Fission yeast (Schizosaccharomyces
pombe)}
STDDSPYKQAFSLFDRHGTGRIPKTSIGDLLRACGQNPTLAEITEIESTLPAEVDMEQFLQVLNR
PNGFDMPGDPEEFVKGFQVFDKDATGMIGVGELRYVLTSLGEKLSNEEMDELLKGVPVKDGMVNY
HDFVQMILAN
>d1wdcb_ a.39.1.5 (B:) Myosin Essential Chain {Bay scallop
(Aequipecten irradians)}
LPQKQIQEMKEAFSMIDVDRDGFVSKEDIKAISEQLGRAPDDKELTAMLKEAPGPLNFTMFLSIF
SDKLSGTDSEETIRNAFAMFDEQETKKLNIEYIKDLLENMGDNFNKDEMRMTFKEAPVEGGKFDY
VKFTAMIKGSGE
>d1br1b_ a.39.1.5 (B:) Myosin Essential Chain {Chicken (Gallus
gallus)}
FSEEQTAEFKEAFQLFDRTGDGKILYSQCGDVMRALGQNPTNAEVMKVLGNPKSDEMNLKTLKFE
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QFLPMMQTIAKNKDQGCFEDYVEGLRVFDKEGNGTVMGAEIRHVLVTLGEKMTEEEVEQLVAGHE
DSNGCINYEELVRMVLSG
>d2mysb_ a.39.1.5 (B:) Myosin Essential Chain {Chicken (Gallus gallus)}
FDETEIEDFKEAFTVIDQNADGIIDKDDLRETFAAMGRLNVKNEELDAMIKEASGPINFTVFLTM
FGEKLKGADPEDVIMGAFKVLDPDGKGSIKKSFLEELLTTGGGRFTPEEIKNMWAAFPPDVAGNV
DYKNICYVITHGEDA
>d1wdcc_ a.39.1.5 (C:) Myosin Regulatory Chain {Bay scallop (Aequipecten irradians)}
LSQDEIDDLKDVFELFDFWDGRDGAVDAFKLGDVCRCLGINPRNEDVFAVGGTHKMGEKSLPFEE
FLPAYEGLMDCEQGTFADYMEAFKTFDREGQGFISGAELRHVLTALGERLSDEDVDEIIKLTDLQ
EDLEGNVKYEDFVKKVMAGPYP
>d2mysc_ a.39.1.5 (C:) Myosin Regulatory Chain {Chicken (Gallus gallus)}
AAADDFKEAFLLFDRTGDAKITASQVGDIARALGQNPTNAEINKILGNPSKEEMNAAAITFEEFL
PMLQAAANNKDQGTFEDFVEGLRVFDKEGNGTVMGAELRHVLATLGEKMTEEEVEELMKGQEDSN
GCINYEAFVKHIMSV
>d1auib_ a.39.1.5 (B:) Calcineurin regulatory subunit (B-chain) {Human (Homo sapiens)}
SYPLEMCSHFDADEIKRLGKRFKKLDLDNSGSLSVEEFMSLPELQQNPLVQRVIDIFDTDGNGEV
DFKEFIEGVSQFSVKGDKEQKLRFAFRIYDMDKDGYISNGELFQVLKMMVGNNLKDTQLQQIVDK
TIINADKDGDGRISFEEFCAVVGGLDIHKKMVVDV
>d1rec__ a.39.1.5 (-) Recoverin {Cow (Bos taurus)}
LSKEILEELQLNTKFTEEELSSWYQSFLKECPSGRITRQEFQTIYSKFFPEADPKAYAQHVFRSF
DANSDGTLDFKEYVIALHMTSAGKTNQKLEWAFSLYDVDGNGTISKNEVLEIVTAIFKMISPEDT
KHLPEDENTPEKRAEKIWGFFGKKDDDKLTEKEFIEGTLANKEILRLIQFEPQKVKEKLK
>d1g8ia_ a.39.1.5 (A:) Frequenin (neuronal calcium sensor 1) {Human (Homo sapiens)}
SNSKLKPEVVEELTRKTYFTEKEVQQWYKGFIKDCPSGQLDAAGFQKIYKQFFPFGDPTKFATFV
FNVFDENKDGRIEFSEFIQALSVTSRGTLDEKLRWAFKLYDLDNDGYITRNEMLDIVDAIYQMVG
NTVELPEEENTPEKRVDRIFAMMDKNADGKLTLQEFQEGSKADPSIVQALSLYDGLV
>d1fpwa_ a.39.1.5 (A:) Frequenin (neuronal calcium sensor 1) {Baker's yeast (Saccharomyces cerevisiae)}
MGAKTSKLSKDDLTCLKQSTYFDRREIQQWHKGFLRDCPSGQLAREDFVKIYKQFFPFGSPEDFA
NHLFTVFDKDNNGFIHFEEFITVLSTTSRGTLEEKLSWAFELYDLNHDGYITFDEMLTIVASVYK
MMGSMVTLNEDEATPEMRVKKIFKLMDKNEDGYITLDEFREGSKVDPSIIGALNLYDGLI
>d1jbaa_ a.39.1.5 (A:) Guanylate cyclase activating protein 2, GCAP-2 {Cow (Bos taurus)}
GQQFSWEEAEENGAVGAADAAQLQEWYKKFLEECPSGTLFMHEFKRFFKVPDNEEATQYVEAMFR
AFDTNGDNTIDFLEYVAALNLVLRGTLEHKLKWTFKIYDKDRNGCIDRQELLDIVESIYKLKKAC
SVEVEAEQQGKLLTPEEVVDRIFLLVDENGDGQLSLNEFVEGARRDKWVMKMLQMDLNP
>d1bjfa_ a.39.1.5 (A:) Neurocalcin {Cow (Bos taurus)}
NSKLRPEVMQDLLESTDFTEHEIQEWYKGFLRDCPSGHLSMEEFKKIYGNFFPYGDASKFAEHVF
RTFDANGDGTIDFREFIIALSVTSRGKLEQKLKWAFSMYDLDGNGYISKAEMLEIVQAIYKMVSS
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VMKMPEDESTPEKRTEKIFRQMDTNRDGKLSLEEFIRGAKSDPSIVRLLQC
>d1dgua_ a.39.1.5 (A:) Calcium- and integrin-binding protein, CIB
{Human (Homo sapiens)}
SKELLAEYQDLTFLTKQEILLAHRRFCELLPQEQRSVESSLRAQVPFEQILSLPELKANPFKERI
CRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFDFDDDGTLNREDLSRLVNCLTGE
GEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISRSPDFASSFKIVL
>d1qjta_ a.39.1.6 (A:) Eps15 {Mouse (Mus musculus)}
LSLTQLSSGNPVYEKYYRQVEAGNTGRVLALDAAAFLKKSGLPDLILGKIWDLADTDGKGVLSKQ
EFFVALRLVACAQNGLEVSLSSLSLAVPPPRFHD
>d1c07a_ a.39.1.6 (A:) Eps15 {Human (Homo sapiens)}
TWVVSPAEKAKYDEIFLKTDKDMDGFVSGLEVREIFLKTGLPSTLLAHIWSLCDTKDCGKLSKDQ
FALAFHLISQKLIKGIDPPHVLTPEMIPPS
>d1f8ha_ a.39.1.6 (A:) Eps15 {Human (Homo sapiens)}
PWAVKPEDKAKYDAIFDSLSPVNGFLSGDKVKPVLLNSKLPVDILGRVWELSDIDHDGMLDRDEF
AVAMFLVYCALEKEPVPMSLPPALVPPSKR
>d1iq3a_ a.39.1.6 (A:) Pob1 {Human (Homo sapiens)}
GSLQDNSSYPDEPWRITEEQREYYVNQFRSLQPDPSSFISGSVAKNFFTKSKLSIPELSYIWELS
DADCDGALTLPEFCAAFHLIVARKNGYPLPEGLPPTLQPEFIVTD
>d1fi6a_ a.39.1.6 (A:) Reps1 {Mouse (Mus musculus)}
WKITDEQRQYYVNQFKTIQPDLNGFIPGSAAKEFFTKSKLPILELSHIWELSDFDKDGALTLDEF
CAAFHLVVARKNGYDLPEKLPESLMPK
>d1hqva_ a.39.1.8 (A:) Apoptosis-linked protein alg-2 {Mouse (Mus
musculus)}
PGPGGGPGPAAGAALPDQSFLWNVFQRVDKDRSGVISDNELQQALSNGTWTPFNPVTVRSIISMF
DRENKAGVNFSEFTGVWKYITDWQNVFRTYDRDNSGMIDKNELKQALSGFGYRLSDQFHDILIRK
FDRQGRGQIAFDDFIQGCIVLQRLTDIFRRYDTDQDGWIQVSYEQYLSMVF
>d1juoa_ a.39.1.8 (A:) Sorcin {Human (Homo sapiens)}
FPGQTQDPLYGYFAAVAGQDGQIDADELQRCLTQSGIAGGYKPFNLETCRLMVSMLDRDMSGTMG
FNEFKELWAVLNGWRQHFISFDTDRSGTVDPQELQKALTTMGFRLSPQAVNSIAKRYSTNGKITF
DDYIACCVKLRALTDSFRRRDTAQQGVVNFPYDDFIQCVMSV
>d1djxb1 a.39.1.7 (B:158-298) Phosphoinositide-specific
phospholipase C, isozyme D1 (PLC-D!) {Rat (Rattus norvegicus)}
NKMNFKELKDFLKELNIQVDDGYARKIFRECDHSQTDSLEDEEIETFYKMLTQRAEIDRAFEEAA
GSAETLSVERLVTFLQHQQREEEAGPALALSLIERYEPSETAKAQRQMTKDGFLMYLLSADGNAF
SLAHRRVYQDM
>d1qasa1 a.39.1.7 (A:205-298) Phosphoinositide-specific
phospholipase C, isozyme D1 (PLC-D!) {Rat (Rattus norvegicus)}
YKMLTQRAEIDRAFEEAAGSAETLSVERLVTFLQHQQREEEAGPALALSLIERYEPSETAKAQRQ
MTKDGFLMYLLSADGNAFSLAHRRVYQDM
>d1k94a_ a.39.1.7 (A:) Grancalcin {Human (Homo sapiens)}
SVYTYFSAVAGQDGEVDAEELQRCLTQSGINGTYSPFSLETCRIMIAMLDRDHTGKMGFNAFKEL
WAALNAWKENFMTVDQDGSGTVEHHELRQAIGLMGYRLSPQTLTTIVKRYSKNGRIFFDDYVACC
VKLRALTDFFRKRDHLQQGSANFIYDDFLQGTMAI
>d1kfus_ a.39.1.7 (S:) Calpain small (regulatory) subunit (domain VI)
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{Human (Homo sapiens)}
THYSNIEANESEEVRQFRRLFAQLAGDDMEVSATELMNILNKVVTRHPDLKTDGFGIDTCRSMVA
VMDSDTTGKLGFEEFKYLWNNIKRWQAIYKQFDTDRSGTICSSELPGAFEAAGFHLNEHLYNMII
RRYSDESGNMDFDNFISCLVRLDAMFRAFKSLDKDGTGQIQVNIQEWLQLTMYS
>d1dvia_ a.39.1.7 (A:) Calpain small (regulatory) subunit (domain VI)
{Rat (Rattus norvegicus)}
EEERQFRKLFVQLAGDDMEVSATELMNILNKVVTRHPDLKTDGFGIDTSRSMVAVMDSDTTGKLG
FEEFKYLWNNIKKWQGIYKRFDTDRSGTIGSNELPGAFEAAGFHLNQHIYSMIIRRYSDETGNMD
FDNFISCLVRLDAMFRAFRSLDKNGTGQIQVNIQEWLQLTMYS
>d1alva_ a.39.1.7 (A:) Calpain small (regulatory) subunit (domain VI)
{Pig (Sus scrofa)}
EEVRQFRRLFAQLAGDDMEVSATELMNILNKVVTRHPDLKTDGFGIDTCRSMVAVMDSDTTGKLG
FEEFKYLWNNIKKWQAIYKQFDVDRSGTIGSSELPGAFEAAGFHLNEHLYSMIIRRYSDEGGNMD
FDNFISCLVRLDAMFRAFKSLDKDGTGQIQVNIQEWLQLTMYS
>d1kful1 a.39.1.7 (L:515-700) Calpain large subunit, C-terminal
domain (domain IV) {Human (Homo sapiens)}
EIEANLEEFDISEDDIDDGVRRLFAQLAGEDAEISAFELQTILRRVLAKRQDIKSDGFSIETCKI
MVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMRKALEEAGFKMPCQLHQ
VIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIELDLISWLCFSVL
>d1df0a1 a.39.1.7 (A:515-700) Calpain large subunit, C-terminal
domain (domain IV) {Rat (Rattus norvegicus)}
EIEANIEEIEANEEDIGDGFRRLFAQLAGEDAEISAFELQTILRRVLAKREDIKSDGFSIETCKI
MVDMLDEDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMRKALEEAGFKLPCQLHQ
VIVARFADDELIIDFDNFVRCLVRLEILFKIFKQLDPENTGTIQLDLISWLSFSVL
>d1eg3a1 a.39.1.7 (A:85-209) Dystrophin {Human (Homo sapiens)}
HPKMTELYQSLADLNNVRFSAYRTAMKLRRLQKALCLDLLSLSAACDALDQHNLKQNDQPMDILQ
IINCLTTIYDRLEQEHNNLVNVPLCVDMCLNWLLNVYDTGRTGRIRVLSFKTGIISLCKA
>d1eg3a2 a.39.1.7 (A:210-306) Dystrophin {Human (Homo sapiens)}
HLEDKYRYLFKQVASSTGFCDQRRLGLLLHDSIQIPRQLGEVASFGGSNIEPSVRSCFQFANNKP
EIEAALFLDWMRLEPQSMVWLPVLHRVAAAET
>d2cbla1 a.39.1.7 (A:178-263) Cbl {Human (Homo sapiens)}
TFRITKADAAEFWRKAFGEKTIVPWKSFRQALHEVHPISSGLEAMALKSTIDLTCNDYISVFEFD
IFTRLFQPWSSLLRNWNSLAV
>d1h8ba_ a.39.1.7 (A:) alpha-Actinin {Human (Homo sapiens)}
MADTDTAEQVIASFRILASDKPYILAEELRRELPPDQAQYCIKRMPAYSGPGSVPGALDYAAFSS
ALYGESDL
>d1c3za_ a.39.2.1 (A:) Thp12-carrier protein {Yellow mealworm
(Tenebrio molitor)}
ETPREKLKQHSDACKAESGVSEESLNKVRNREEVDDPKLKEHAFCILKRAGFIDASGEFQLDHIK
TKFKENSEHPEKVDDLVAKCAVKKDTPQHSSADFFKCVHDNRS
>d1dqea_ a.39.2.1 (A:) Pheromone binding protein {Silkworm (Bombyx
mori)}
SQEVMKNLSLNFGKALDECKKEMTLTDAINEDFYNFWKEGYEIKNRETGCAIMCLSTKLNMLDPE
GNLHHGNAMEFAKKHGADETMAQQLIDIVHGCEKSTPANDDKCIWTLGVATCFKAEIHKLNWAPS
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MDVAVGE
>d1iioa_ a.39.4.1 (A:) Hypothetical protein MTH865 {Archaeon
Methanobacterium thermoautotrophicum}
GSHMKMGVKEDIRGQIIGALAGADFPINSPEELMAALPNGPDTTCKSGDVELKASDAGQVLTADD
FPFKSAEEVADTIVNKAGL
>d1cpo_1 a.39.3.1 (0-119) Cloroperoxidase {Fungus (Caldariomyces
fumago)}
EEPGSGIGYPYDNNTLPYVAPGPTDSRAPCPALNALANHGYIPHDGRAISRETLQNAFLNHMGIA
NSVIELALTNAFVVCEYVTGSDCGDSLVNLTLLAEPHAFEHDHSFSRKDYKQGVA
>d1cpo_2 a.39.3.1 (120-298) Cloroperoxidase {Fungus (Caldariomyces
fumago)}
NSNDFIDNRNFDAETFQTSLDVVAGKTHFDYADMNEIRLQRESLSNELDFPGWFTESKPIQNVES
GFIFALVSDFNLPDNDENPLVRIDWWKYWFTNESFPYHLGWHPPSPAREIEFVTSASSAVLAASV
TSTPSSLPSGAIGPGAEAVPLSFASTMTPFLLATNAPYYAQDPTLGPND
>d1h67a_ a.40.1.1 (A:) Calponin {Chicken (Gallus gallus)}
MPQTERQLRVWIEGATGRRIGDNFMDGLKDGVILCELINKLQPGSVQKVNDPVQNWHKLENIGNF
LRAIKHYGVKPHDIFEANDLFENTNHTQVQSTLIALASQAKTK
>d1bkra_ a.40.1.1 (A:) beta-spectrin {Human (Homo sapiens)}
KSAKDALLLWCQMKTAGYPNVNIHNFTTSWRDGMAFNALIHKHRPDLIDFDKLKKSNAHYNLQNA
FNLAEQHLGLTKLLDPEDISVDHPDEKSIITYVVTYYHYFSKM
>d1aoa_1 a.40.1.1 (121-251) N-terminal actin-crosslinking domain from
fimbrin {Human (Homo sapiens)}
YSEEEKYAFVNWINKALENDPDCRHVIPMNPNTDDLFKAVGDGIVLCKMINLSVPDTIDERAINK
KKLTPFIIQENLNLALNSASAIGCHVVNIGAEDLRAGKPHLVLGLLWQIIKIGLFADIELSRNEA
L
>d1aoa_2 a.40.1.1 (260-375) N-terminal actin-crosslinking domain from
fimbrin {Human (Homo sapiens)}
TLEELMKLSPEELLLRWANFHLENSGWQKINNFSADIKDSKAYFHLLNQIAPKGQKEGEPRIDIN
MSGFNETDDLKRAESMLQQADKLGCRQFVTPADVVSGNPKLNLAFVANLFN
>d1bhda_ a.40.1.1 (A:) Utrophin {Human (Homo sapiens)}
LQQTNSEKILLSWVRQTTRPYSQVNVLNFTTSWTDGLAFNAVLHRHKPDLFSWDKVVKMSPIERL
EHAFSKAQTYLGIEKLLDPEDVAVRLPDKKSIIMYLTSLFEVL
>d1qaga1 a.40.1.1 (A:31-151) Utrophin {Human (Homo sapiens)}
DVQKKTFTKWINARFSKSGKPPINDMFTDLKDGRKLLDLLEGLTGTSLPKERGSTRVHALNNVNR
VLQVLHQNNVELVNIGGTDIVDGNHKLTLGLLWSIILHWQVKDVMKDVMSDLQQTN
>d1dxxa1 a.40.1.1 (A:9-119) Dystrophin {Human (Homo sapiens)}
DSYEREDVQKKTFTKWVNAQFSKFGKQHIENLFSDLQDGRRLLDLLEGLTGQKLPKEKGSTRVHA
LNNVNKALRVLQNNNVDLVNIGSTDIVDGNHKLTLGLIWNIILHWQ
>d1dxxa2 a.40.1.1 (A:120-246) Dystrophin {Human (Homo sapiens)}
VKNVMKNIMAGLQQTNSEKILLSWVRQSTRNYPQVNVINFTTSWSDGLALNALIHSHRPDLFDWN
SVVSQQSATQRLEHAFNIARYQLGIEKLLDPEDVDTTYPDKKSILMYITSLFQVLPQQVSIE
>d1a26_1 a.41.1.1 (662-796) Domain of poly(ADP-ribose) polymerase
{Chicken (Gallus gallus)}
KSKLAKPIQDLIKMIFDVESMKKAMVEFEIDLQKMPLGKLSKRQIQSAYSILNEVQQAVSDGGSE
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SQILDLSNRFYTLIPHDFGMKKPPLLSNLEYIQAKVQMLDNLLDIEVAYSLLRGGNEDGDKDPIDINYEK
>d1ycqa_ a.42.1.1 (A:) MDM2 {African clawed frog (Xenopus laevis)}
EKLVQPTPLLLSLLKSAGAQKETFTMKEVIYHLGQYIMAKQLYDEKQQHIVHCSNDPLGELFGVQEFSVKEPRRLYAMISRNLVSANV
>d1ycra_ a.42.1.1 (A:) MDM2 {Human (Homo sapiens)}
ETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVYCSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVV
>d1b28a_ a.43.1.1 (A:) Arc repressor {Salmonella bacteriophage P22}
MKGMSKMPQFNLRWPREVLDLVRKVAEENGMSVNSYIYQLVMESFKKEGRIGA
>d1baza_ a.43.1.1 (A:) Arc repressor {Salmonella bacteriophage P22}
SKMPQVNLRWPREVLDLVRKVAEENGRSVNSEIYQRVMESFKKEGRIGA
>d1bazb_ a.43.1.1 (B:) Arc repressor {Salmonella bacteriophage P22}
KMPQVNLRWPREVLDLVRKVAEENGRSVNSEIYQRVMESFK
>d1bdta_ a.43.1.1 (A:) Arc repressor {Salmonella bacteriophage P22}
MKGMSKMPQFNLRWPREVLDLVRKVAEENGRSVNSEIYQRVMESFKKEGRIG
>d1myka_ a.43.1.1 (A:) Arc repressor {Salmonella bacteriophage P22}
KMLQFNLRWPREVLDLVRKVAEENGRSVNSEIYQRVMESFKKEGRIG
>d1myla_ a.43.1.1 (A:) Arc repressor {Salmonella bacteriophage P22}
KMPQFNLRWPREVLDLVRKVAEENGMSVNSYIYQLVMESFKKEGR
>d1mylb_ a.43.1.1 (B:) Arc repressor {Salmonella bacteriophage P22}
MPQFNLRWPREVLDLVRKVAEENGMSVNSYIYQLVMESFK
>d1mnta_ a.43.1.1 (A:) Mnt repressor {Salmonella bacteriophage P22}
ARDDPHFNFRMPMEVREKLKFRAEANGRSMNSELLQIVQDALSKPSPVTGYRNDAERLADEQSELV
>d2cpga_ a.43.1.2 (A:) Transcriptional repressor CopG {Streptococcus agalactiae}
MKKRLTITLSESVLENLEKMAREMGLSKSAMISVALENYKKGQ
>d1irqa_ a.43.1.2 (A:) Omega transcriptional repressor {Streptococcus pyogenes}
IMGDKTVRVRADLHHIIKIETAKNGGNVKEVMDQALEEYIRKYLPDKL
>d1cmba_ a.43.1.2 (A:) Met repressor, MetR {Escherichia coli}
AEWSGEYISPYAEHGKKSEQVKKITVSIPLKVLKILTDERTRRQVNNLRHATNSELLCEAFLHAFTGQPLPDDADLRKERSDEIPEAAKEIMREMGINPETWEY
>d1fvka1 a.44.1.1 (A:65-128) Disulphide-bond formation facilitator (DSBA), insertion domain {Escherichia coli}
GGDLGKDLTQAWAVAMALGVEDKVTVPLFEGVQKTQTIRSASDIRDVFINAGIKGEEYDAAWNS
>d1bed_1 a.44.1.1 (63-126) Disulphide-bond formation facilitator (DSBA), insertion domain {Vibrio cholerae}
GNMGQAMSKAYATMIALEVEDKMVPVMFNRIHTLRKPPKDEQELRQIFLDEGIDAAKFDAAYNG
>d1aqwa1 a.45.1.1 (A:77-209) Glutathione S-transferase {Human (Homo sapiens), class pi}
GLYGKDQQEAALVDMVNDGVEDLRCKYISLIYTNYEAGKDDYVKALPGQLKPFETLLSQNQGGKTFIVGDQISFADYNLLDLLLIHEVLAPGCLDAFPLLSAYVGRLSARPKLKAFLASPEYVNLPINGN

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GKQ
>d2gsra1 a.45.1.1 (A:77-207) Glutathione S-transferase {Pig (Sus
scrofa), class pi}
YGKDQKEAALVDMVNDGVEDLRCKYATLIYTNYEAGKEKYVKELPEHLKPFETLLSQNQGGQAFV
VGSQISFADYNLLDLLRIHQVLNPSCLDAFPLLSAYVARLSARPKIKAFLASPEHVNRPINGNGK
Q
>d1glqa1 a.45.1.1 (A:79-209) Glutathione S-transferase {Mouse (Mus
musculus), class pi}
YGKNQREAAQMDMVNDGVEDLRGKYVTLIYTNYENGKNDYVKALPGHLKPFETLLSQNQGGKAFI
VGDQISFADYNLLDLLLIHQVLAPGCLDNFPLLSAYVARLSARPKIKAFLSSPEHVNRPINGNGK
Q
>d1gtua1 a.45.1.1 (A:85-217) Glutathione S-transferase {Human (Homo
sapiens), class mu}
LCGETEEEKIRVDILENQTMDNHMQLGMICYNPEFEKLKPKYLEELPEKLKLYSEFLGKRPWFAG
NKITFVDFLVYDVLDLHRIFEPKCLDAFPNLKDFISRFEGLEKISAYMKSSRFLPRPVFSKMAVW
GNK
>d1hna_1 a.45.1.1 (85-217) Glutathione S-transferase {Human (Homo
sapiens), class mu}
LCGESEKEQIREDILENQFMDSRMQLAKLCYDPDFEKLKPEYLQALPEMLKLYSQFLGKQPWFLG
DKITFVDFIAYDVLERNQVFEPSCLDAFPNLKDFISRFEGLEKISAYMKSSRFLPRPVFTKMAVF
GNK
>d3gtub1 a.45.1.1 (B:85-224) Glutathione S-transferase {Human (Homo
sapiens), class mu}
RKHNMCGETEEEKIRVDIIENQVMDFRTQLIRLCYSSDHEKLKPQYLEELPGQLKQFSMFLGKFS
WFAGEKLTFVDFLTYDILDQNRIFDPKCLDEFPNLKAFMCRFEALEKIAAYLQSDQFCKMPINNK
MAQWGNKPVC
>d4gtua1 a.45.1.1 (A:85-217) Glutathione S-transferase {Human (Homo
sapiens), class mu}
LCGETEEEKIRVDILENQAMDVSNQLARVCYSPDFEKLKPEYLEELPTMMQHFSQFLGKRPWFVG
DKITFVDFLAYDVLDLHRIFEPNCLDAFPNLKDFISRFEGLEKISAYMKSSRFLPKPLYTRVAVW
GNK
>d2gsta1 a.45.1.1 (A:85-217) Glutathione S-transferase {Rat (Rattus
norvegicus), class mu}
LCGETEEERIRADIVENQVMDNRMQLIMLCYNPDFEKQKPEFLKTIPEKMKLYSEFLGKRPWFAG
DKVTYVDFLAYDILDQYHIFEPKCLDAFPNLKDFLARFEGLKKISAYMKSSRYLSTPIFSKLAQW
SNK
>d1gsua1 a.45.1.1 (A:85-217) Glutathione S-transferase {Chicken
(Gallus gallus), class mu}
MCGETEVEKQRVDVLENHLMDLRMAFARLCYSPDFEKLKPAYLEQLPGKLRQLSRFLGSRSWFVG
DKLTFVDFLAYDVLDQQRMFVPDCPELQGNLSQFLQRFEALEKISAYMRSGRFMKAPIFWYTALW
NNK
>d1gsea1 a.45.1.1 (A:81-222) Glutathione S-transferase {Human (Homo
sapiens), class alpha (a1-1)}
LYGKDIKERALIDMYIEGIADLGEMILLLPVCPPEEKDAKLALIKEKIKNRYFPAFEKVLKSHGQ
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DYLVGNKLSRADIHLVELLYYVEELDSSLISSFPLLKALKTRISNLPTVKKFLQPGSPRKPPMDE
KSLEEARKIFRF
>d1gula1 a.45.1.1 (A:81-220) Glutathione S-transferase {Human (Homo
sapiens), class alpha (a1-1)}
LFGKNLKERTLIDMYVEGTLDLLELLIMHPFLKPDDQQKEVVNMAQKAIIRYFPVFEKILRGHGQ
SFLVGNQLSLADVILLQTILALEEKIPNILSAFPFLQEYTVKLSNIPTIKRFLEPGSKKKPPPDE
IYVRTVYNIF
>d1ev4a1 a.45.1.1 (A:80-222) Glutathione S-transferase {Rat (Rattus
norvegicus), class alpha (a1-1)}
DLYGKDMKERALIDMYSEGILDLTEMIMQLVICPPDQKEAKTALAKDRTKNRYLPAFEKVLKSHG
QDYLVGNKLTRVDIHLLELLLYVEEFDASLLTSFPLLKAFKSRISSLPNVKKFLQPGSQRKLPMD
AKQIEEARKIYKF
>d1ev4c1 a.45.1.1 (C:80-208) Glutathione S-transferase {Rat (Rattus
norvegicus), class alpha (a1-1)}
DLYGKDMKERALIDMYSEGILDLTEMIMQLVICPPDQKEAKTALAKDRTKNRYLPAFEKVLKSHG
QDYLVGNKLTRVDIHLLELLLYVEEFDASLLTSFPLLKAFKSRISSLPNVKKFLQPGSQRKLPM
>d1f3aa1 a.45.1.1 (A:80-221) Glutathione S-transferase {Mouse (Mus
musculus), class alpha (a1-1)}
LYGKDMKERALIDMYSEGILDLTEMIGQLVLCPPDQREAKTALAKDRTKNRYLPAFEKVLKSHGQ
DYLVGNRLTRVDIHLLEVLLYVEEFDASLLTPFPLLKAFKSRISSLPNVKKFLQPGSQRKPPMDA
KQIQEARKAFKI
>d1b48a1 a.45.1.1 (A:80-222) Glutathione S-transferase {Mouse (Mus
musculus), class alpha (a1-4)}
NLYGKDLKERVRIDMYADGTQDLMMMIAVAPFKTPKEKEESYDLILSRAKTRYFPVFEKILKDHG
EAFLVGNQLSWADIQLLEAILMVEELSAPVLSDFPLLQAFKTRISNIPTIKKFLQPGSQRKPPPD
GPYVEVVRIVLKF
>d1ljra1 a.45.1.1 (A:80-244) Glutathione S-transferase {Human (Homo
sapiens), class theta}
TPDHWYPSDLQARARVHEYLGWHADCIRGTFGIPLWVQVLGPLIGVQVPEEKVERNRTAMDQALQ
WLEDKFLGDRPFLAGQQVTLADLMALEELMQPVALGYELFEGRPRLAAWRGRVEAFLGAELCQEA
HSIILSILEQAAKKTLPTPSPEAYQAMLLRIARIP
>d1pd211 a.45.1.1 (1:76-199) Glutathione S-transferase {Rat (Rattus
norvegicus), class sigma}
DLAGKTELEQCQVDAVVDTLDDFMSLFPWAEENQDLKERTFNDLLTRQAPHLLKDLDTYLGDKEW
FIGNYVTWADFYWDICSTTLLVLKPDLLGIYPRLVSLRNKVQAIPAISAWILKRPQTKL
>d2gsq_1 a.45.1.1 (76-202) Glutathione S-transferase {Squid
(Ommastrephes sloani pacificus), class sigma}
LDGKTSLEKYRVDEITETLQDIFNDVVKIKFAPEAAKEAVQQNYEKSCKRLAPFLEGLLVSNGGG
DGFFVGNSMTLADLHCYVALEVPLKHTPELLKDCPKIVALRKRVAECPKIAAYLKKRPVRDF
>d1eema1 a.45.1.1 (A:103-241) Glutathione S-transferase {Human (Homo
sapiens), class omega}
LPDDPYEKACQKMILELFSKVPSLVGSFIRSQNKEDYAGLKEEFRKEFTKLEEVLTNKKTTFFGG
NSISMIDYLIWPWFERLEAMKLNECVDHTPKLKLWMAAMKEDPTVSALLTSEKDWQGFLELYLQN
SPEACDYGL
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>d1fw1a1 a.45.1.1 (A:88-212) Glutathione S-transferase {Human (Homo sapiens), class zeta}
LLPQDPKKRASVRMISDLIAGGIQPLQNLSVLKQVGEEMQLTWAQNAITCGFNALEQILQSTAGI
YCVGDEVTMADLCLVPQVANAERFKVDLTPYPTISSINKRLLVLEAFQVSHPCRQPDTPT
>d1bg5_1 a.45.1.1 (81-254) Glutathione S-transferase {Schistosoma japonicum}
MLGGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNG
DHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAWPLQGWQATF
GGGDHPPKSDLVPRGSSYYQEAKSSKIMESFKNMVPQQALVNSS
>d1duga1 a.45.1.1 (A:81-220) Glutathione S-transferase {Schistosoma japonicum}
LGGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGD
HVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAWPLQGWQATFG
GGDHPPKSDP
>d1gne_1 a.45.1.1 (80-232) Glutathione S-transferase {Schistosoma japonicum}
MLGGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNG
DHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAWPLQGWQATF
GGGDHPPKSDLVPRGSMELDKWA
>d1fhe_1 a.45.1.1 (81-214) Glutathione S-transferase {Fasciola hepatica}
LGTTPEERARISMIEGAAMDLRIGFGRVCYNPKFEEVKEEYVKELPKTLKMWSDFLGDRHYLTGS
SVSHVDFMLYETLDSIRYLAPHCLDEFPKLKEFKSRIEALPKIKAYMESKRFIKWPLNGWAASFG
AGDA
>d2fhea1 a.45.1.1 (A:81-216) Glutathione S-transferase {Fasciola hepatica}
IGTTSEERARVSMIEGAAVDLRQGISRISYQPKFEQLKEGYLKDLPTTMKMWSDFLGKNPYLRGT
SVSHVDFMVYEALDAIRYLEPHCLDHFPNLQQFMSRIEALPSIKAYMESNRFIKWPLNGWHAQFG
GGDAPP
>d1gnwa1 a.45.1.1 (A:86-211) Glutathione S-transferase {Mouse-ear cress (Arabidopsis thaliana)}
LQTDSKNISQYAIMAIGMQVEDHQFDPVASKLAFEQIFKSIYGLTTDEAVVAEEEAKLAKVLDVY
EARLKEFKYLAGETFTLTDLHHIPAIQYLLGTPTKKLFTERPRVNEWVAEITKRPASEKVQ
>d1axda1 a.45.1.1 (A:81-210) Glutathione S-transferase {Maize (Zea mays), type I}
ELLREGNLEEAAMVDVWIEVEANQYTAALNPILFQVLISPMLGGTTDQKVVDENLEKLKKVLEVY
EARLTKCKYLAGDFLSLADLNHVSVTLCLFATPYASVLDAYPHVKAWWSGLMERPSVQKVAALM
>d1aw9_1 a.45.1.1 (83-217) Glutathione S-transferase {Maize (Zea mays), type III}
GTDLLPATASAAKLEVWLEVESHHFYPNASPLVFQLLVRPLLGGAPDAAVVDKHAEQLAKVLDVY
EAHLARNKYLAGDEFTLADANHASYLLYLSKTPKAGLVAARPHVKAWWEAIVARPAFQKTVAAIP
LPPPP
>d1e6ba1 a.45.1.1 (A:88-220) Glutathione S-transferase {Mouse-ear cress (Arabidopsis thaliana), class zeta}
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PLLPRDLHKRAVNYQAMSIVLSGIQPHQNLAVIRYIEEKINVEEKTAWVNNAITKGFTALEKLLV
NCAGKHATGDEIYLADLFLAPQIHGAINRFQINMEPYPTLAKCYESYNELPAFQNALPEKQPDAP
SST
>d1a0fa1 a.45.1.1 (A:81-201) Glutathione S-transferase {Escherichia
coli}
QLLAPVNSISRYKTIEWLNYIATELHKGFTPLFRPDTPEEYKPTVRAQLEKKLQYVNEALKDEHW
ICGQRFTIADAYLFTVLRWAYAVKLNLEGLEHIAAFMQRMAERPEVQDALSAEGLK
>d1b8xa1 a.45.1.1 (A:81-260) Glutathione S-transferase {Escherichia
coli}
LGGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGD
HVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAWPLQGWQATFG
GGDHPPKSDLVPRGSRRASVGSRMHYPGAFTYSPTPVTSGIGIGMSAMGS
>d1pmt_1 a.45.1.1 (81-201) Glutathione S-transferase {Proteus
mirabilis}
NLIAPPKALERYHQIEWLNFLASEVHKGYSPLFSSDTPESYLPVVKNKLKSKFVYINDVLSKQKC
VCGDHFTVADAYLFTLSQWAPHVALDLTDLSHLQDYLARIAQRPNVHSALVTEGLI
>d1f2ea1 a.45.1.1 (A:81-201) Glutathione S-transferase {Sphingomonas
paucimobilis}
GLAPAEGSLDRYRLLSRLSFLGSEFHKAFVPLFAPATSDEAKAAAAESVKNHLAALDKELAGRDH
YAGNAFSVADIYLYVMLGWPAYVGIDMAAYPALGAYAGKIAQRPAVGAALKAEGLA
>d1g7oa1 a.45.1.1 (A:76-215) Glutaredoxin 2 {Escherichia coli}
PLLTGKRSPAIEEWLRKVNGYANKLLLPRFAKSAFDEFSTPAARKYFVDKKEASAGNFADLLAHS
DGLIKNISDDLRALDKLIVKPNAVNGELSEDDIQLFPLLRNLTLVAGINWPSRVADYRDNMAKQT
QINLLSSMAI
>d1k0da1 a.45.1.1 (A:201-351) Yeast prion protein ure2p, nitrogen
regulation fragment {Baker's yeast (Saccharomyces cerevisiae)}
LWSDDLADQSQINAWLFFQTSGHAPMIGQALHFRYFHSQKIASAVERYTDEVRRVYGVVEMALAE
RREALVMELDTENAAAYSAGTTPMSQSRFFDYPVWLVGDKLTIADLAFVPWNNVVDRIGINIKIE
FPEVYKWTKHMMRRPAVIKAL
>d1k0ma1 a.45.1.1 (A:92-240) Chloride intracellular channel 1 (clic1)
{Human (Homo sapiens)}
RYPKLAALNPESNTAGLDIFAKFSAYIKNSNPALNDNLEKGLLKALKVLDNYLTSPLPEGVDETS
AEDEGVSQRKFLDGNELTLADCNLLPKLHIVQVVCKKYRGFTIPEAFRGVHRYLSNAYAREEFAS
TCPDDEEIELAYEQVAKAL
>d1bmta1 a.46.1.1 (A:651-740) Methionine synthase domain {Escherichia
coli}
QAEWRSWEVNKRLEYSLVKGITEFIEQDTEEARQQATRPIEVIEGPLMDGMNVVGDLFGEGKMFL
PQVVKSARVMKQAVAYLEPFIEASK
>d2tpt_1 a.46.2.1 (1-70) Thymidine phosphorylase {Escherichia coli}
LFLAQEIIRKKRDGHALSDEEIRFFINGIRDNTISEGQIAALAMTIFFHDMTMPERVSLTMAMRD
SGTVL
>d1brwa1 a.46.2.1 (A:1-70) Pyrimidine nucleoside phosphorylase
{Bacillus stearothermophilus}
MRMVDLIAKKRDGKALTKEEIEWIVRGYTNGDIPDYQMSALAMAIYFRGMTEEETAALTMAMVQS
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GEMLD
>d1bf5a1 a.47.1.1 (A:136-316) STAT-1, coiled coil domain {Human (Homo
sapiens)}
LDKQKELDSKVRNVKDKVMCIEHEIKSLEDLQDEYDFKCKTLQNREHLLLKKMYLMLDNKRKEVV
HKIIELLNVTELTQNALINDELVEWKRRQQSACIGGPPNACLDQLQNWFTIVAESLQQVRQQLKK
LEELEQKYTYEHDPITKNKQVLWDRTFSLFQQLIQSS
>d1bg1a1 a.47.1.1 (A:136-321) STAT3b {Mouse (Mus musculus)}
VVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKM
QQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQIACIGGPPNICLDRLEN
WITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAF
>d1dn1b_ a.47.2.1 (B:) Syntaxin 1A N-terminal domain {Rat (Rattus
norvegicus)}
DRFMDEFFEQVEEIRGFIDKIAENVEEVKRKHSAILASPNPDEKTKEELEELMSDIKKTANKVRS
KLKSIEQSIEQEEGLNRSSADLRIRKTQHSTLSRKFVEVMSEYNATQSDYRERCKGRIQRQLEIT
GRTTTSEELEDMLESGNPAIFASGIIMDSSISKQALSEIETRHSEIIKLENSIRELHDMFMDMAM
LVESQGEMIDRIEYNVEHAVDYVERAV
>d1ez3a_ a.47.2.1 (A:) Syntaxin 1A N-terminal domain {Rat (Rattus
norvegicus)}
RDRFMDEFFEQVEEIRGFIDKIAENVEEVKRKHSAILASPNPDEKTKEELEELMSDIKKTANKVR
SKLKSIEQSIEQEEGLNRSSADLRIRKTQHSTLSRKFVEVMSEYNATQSDYRERCKGRI
>d1fioa_ a.47.2.1 (A:) Sso1 {Baker's yeast (Saccharomyces
cerevisiae)}
MHDFVGFMNKISQINRDLDKYDHTINQVDSLHKRLLTEVNEEQASHLRHSLDNFVAQATDLQFKL
KNEIKSAQRDGIHDTNKQAQAENSRQRFLKLIQDYRIVDSNYKEENKEQAKRQYMIIQPEATEDE
VEAAISDVGGQQIFSQALLNANRRGEAKTALAEVQARHQELLKLEKSMAELTQLFNDMEELVIEQ
Q
>d1hs7a_ a.47.2.1 (A:) Vam3p N-terminal domain {Baker's yeast
(Saccharomyces cerevisiae)}
TNQKTKELSNLIETFAEQSRVLEKECTKIGSKRDSKELRYKIETELIPNCTSVRDKIESNILIHQ
NGKLSADFKNLKTKYQSLQQSYNQRKSLFPLK
>d2cbla2 a.48.1.1 (A:47-177) N-terminal domain of cbl (N-cbl) {Human
(Homo sapiens)}
PPGTVDKKMVEKCWKLMDKVVRLCQNPKLALKNSPPYILDLLPDTYQHLRTILSRYEGKMETLGE
NEYFRVFMENLMKKTKQTISLFKEGKERMYEENSQPRRNLTKLSLIFSHMLAELKGIFPSGLFQG
D
>d1de4c1 a.48.2.1 (C:609-756) Transferrin receptor ectodomain,
C-terminal domain {Human (Homo sapiens)}
LDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFGNAEKTDRFVMKK
LNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQNNGAFNETLFRNQLALA
TWTIQGAANALSGDVWDI
>d1eo0a_ a.48.3.1 (A:) Transcription elongation factor TFIIS N-domain
{Baker's yeast (Saccharomyces cerevisiae)}
MDSKEVLVHVKNLEKNKSNDAAVLEILHVLDKEFVPTEKLLRETKVGVEVNKFKKSTNVEISKLV
KKMISSWKDAIN
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>d1f6va_ a.49.1.1 (A:) C-terminal domain of B transposition protein
{Bacteriophage mu}
GSRIAKRTAINKTKKADVKAIADAWQINGEKELELLQQIAQKPGALRILNHSLRLAAMTAHGKGE
RVNEDYLRQAFRELDLDVDISTLLRN
>d1i6ve_ a.143.1.1 (E:) RNA polymerase omega subunit {Thermus
aquaticus}
MAEPGIDKLFGMVDSKYRLTVVVAKRAQQLLRHRFKNTVLEPEERPKMRTLEGLYDDPNAVTWAM
KELLTGRLFFGENLVPEDRLQKEMERLYPTEEE
>d1cfaa_ a.50.1.1 (A:) C5a anaphylotoxin {Human (Homo sapiens)}
MLQKKIEEIAAKYKHSVVKKCCYDGASVNNDETCEQRAARISLGPRCIKAFTECCVVASQLRANI
SHKDMC
>d1c5a__ a.50.1.1 (-) C5a anaphylotoxin {Pig (Sus scrofa domestica)}
MLQKKIEEEAAKYKYAMLKKCCYDGAYRNDDETCEERAARIKIGPKCVKAFKDCCYIANQVRAEQ
S
>d0c3a__ a.50.1.1 (-) C3a anaphylotoxin {Human (Homo sapiens)}
SVQLTEKRMNKVGKYPKELRKCCEDGMRQNPMRFSCQRRTRFISLGEACKKVFLDCCNYITELRR
QHARASHLGLAR
>d1ocrh_ a.51.1.1 (H:) Cytochrome c oxidase subunit h {Cow (Bos
taurus)}
KIKNYQTAPFDSRFPNQNQTRNCWQNYLDFHRCEKAMTAKGGDVSVCEWYRRVYKSLCPISWVST
WDDRRAEGTFPGKI
>d1hyp__ a.52.1.1 (-) Soybean hydrophobic protein {Soybean (Glycine
max)}
PSCPDLSICLNILGGSLGTVDDCCALIGGLGDIEAIVCLCIQLRALGILNLNRNLQLILNSCGRS
YPSNATCPRT
>d1bwoa_ a.52.1.1 (A:) Plant non-specific lipid-transfer protein
(ns-LTP) {Wheat (Triticum aestivum), L. seeds}
IDCGHVDSLVRPCLSYVQGGPGPSGQCCDGVKNLHNQARSQSDRQSACNCLKGIARGIHNLNEDN
ARSIPPKCGVNLPYTISLNIDCSRV
>d1be2__ a.52.1.1 (-) Plant non-specific lipid-transfer protein
(ns-LTP) {Barley (Hordeum vulgare)}
LNCGQVDSKMKPCLTYVQGGPGPSGECCNGVRDLHNQAQSSGDRQTVCNCLKGIARGIHNLNLNN
AASIPSKCNVNVPYTISPDIDCSRIY
>d1fk5a_ a.52.1.1 (A:) Plant non-specific lipid-transfer protein
(ns-LTP) {Maize (Zea mays)}
AISCGQVASAIAPCISYARGQGSGPSAGCCSGVRSLNNAARTTADRRAACNCLKNAAAGVSGLNA
GNAASIPSKCGVSIPYTISTSTDCSRVN
>d1rzl__ a.52.1.1 (-) Plant non-specific lipid-transfer protein
(ns-LTP) {Rice (Oryza sativa)}
ITCGQVNSAVGPCLTYARGGAGPSAACCSGVRSLKAAASTTADRRTACNCLKNAARGIKGLNAGN
AASIPSKCGVSVPYTISASIDCSRVS
>d1hssa_ a.52.1.2 (A:) 0.19 alpha-amylase inhibitor {Wheat (Triticum
aestivum)}
MCYPGQAFQVPALPACRPLLRLQCNGSQVPEAVLRDCCQQLAHISEWCRCGALYSMLDSMYKEHG
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AQEGQAGTGAFPRCRREVVKLTAASITAVCRLPIVVDASGDGAYVCKDVAAYPDA

>d1tmqb_ a.52.1.2 (B:) Trypsin/alpha-amylase inhibitor RBI {Ragi (Elucine coracana gaertneri), seeds}

SVGTSCIPGMAIPHNPLDSCRWYVSTRTCGVGPRLATQEMKARCCRQLEAIPAYCRCEAVRILMDGVVTSSGQHEGRLLQDLPGCPRQVQRAFAPKLVTEVECNLATIHGGPFCLSL

>d1bea__ a.52.1.2 (-) Hageman factor/amylase inhibitor {Maize (Zea mays)}

SCVPGWAIPHNPLPSCRWYVTSRTCGIGPRLPWPELKRRCCRELADIPAYCRCTALSILMDGAIPPGPDAQLEGRLEDLPGCPREVQRGFAATLVTEAECNLATISGVAECPWILG

>g1pnb.1 a.52.1.3 (A:,B:) Napin BNIb {Rape (Brassica napus)}

QPQKCQREFQQEQHLRACQQWIRQQLAGSPFXQSGPQQGPWLREQCCNELYQEDQVCVCPTLKQAAKSVRVQGQHGPFQSTRIYQIAKNLPNVCNMKQIGTCPFIAI

>d1a1ua_ a.53.1.1 (A:) p53 tetramerization domain {Human (Homo sapiens)}

EYFTLQIRGRERFEKIREYNEALELKDAQ

>d1aie__ a.53.1.1 (-) p53 tetramerization domain {Human (Homo sapiens)}

EYFTLQIRGRERFEMFRELNEALELKDAQAG

>d1hs5a_ a.53.1.1 (A:) p53 tetramerization domain {Human (Homo sapiens)}

DGEYFTLQIRGRERFEQFRERNEALELKDAQAGK

>d1saia_ a.53.1.1 (A:) p53 tetramerization domain {Human (Homo sapiens)}

KKKPLDGEYFTLQIRGRERFEMFRELNEALELKDAQAGKEPG

>d1k1fa_ a.147.1.1 (A:) Bcr-Abl oncoprotein oligomerization domain {Human (Homo sapiens)}

MVDPVGFAEAWKAQFPDSEPPRMELRSVGDIEQELERAKASIRRLEQEVNQERFRMIYLQTLLAKEK

>d1adt_1 a.54.1.1 (176-265) Domain of early E2A DNA-binding protein, ADDBP {Human adenovirus type 5}

PIVSAWEKGMEAARALMDKYHVDNDLKANFKLLPDQVEALAAVCKTWLNEEHRGLQLTFTSNKTFVTMMGRFLQAYLQSFAEVTYKHHEP

>d1ihfa_ a.55.1.1 (A:) Integration host factor (IHF) {Escherichia coli}

ALTKAEMSEYLFDKLGLSKRDAKELVELFFEEIRRALENGEQVKLSGFGNFDLRDKNQRPGRNPKTGEDIPITARRVVTFRPGQKLKSRVENASPK

>d1ihfb_ a.55.1.1 (B:) Integration host factor (IHF) {Escherichia coli}

MTKSELIERLATQQSHIPAKTVEDAVKEMLEHMASTLAQGERIEIRGFGSFSLHYRAPRTGRNPKTGDKVELEGKYVPHFKPGKELRDRANIYG

>d1hns__ a.55.1.1 (-) DNA-binding domain of H1 protein, (H-NS) {Escherichia coli}

AQRPAKYSYVDENGETKTWTGQGRTPAVIKKAMDEQGKSLDDFLIKQ

>d1huua_ a.55.1.1 (A:) HU protein {Bacillus stearothermophilus}

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MNKTELINAVAETSGLSKKDATKAVDAVFDSITEALRKGDKVQLIGFGNFEVRERAARKGRNPQT
GEEMEIPASKVPAFKPGKALKDAVK
>d1b8za_ a.55.1.1 (A:) HU protein {Thermotoga maritima}
MNKKELIDRVAKKAGAKKKDVKLILDTILETITEALAKGEKVQIVGFGSFEVRKAAARKGVNPQT
RKPITIPERKVPKFKPGKALKEKVK
>d1exea_ a.55.1.1 (A:) Transcription factor 1, TF1 {Bacteriophage SPO1
(Bacillus subtilis)}
MNKTELIKAIAQDTGLTQVSVSKMLASFEKIITETVAKGDKVQLTGFLNIKPVARQARKGFNPQT
QEALEIAPSVGVSVKPGESLKKAAEGLKYEDFAK
>d1dp3a_ a.55.1.2 (A:) DNA-binding domain (fragment?) of the TraM
protein {Escherichia coli}
AKVQAYVSDEIVYKINKIVERRRAEGAKSTDVSFSSISTMLLELGLRVYEAQMER
>d1hlra1 a.56.1.1 (A:81-193) Aldehyde oxidoreductase, domain 2
{Desulfovibrio gigas}
QPENLHPLQKAWVLHGGAQCGFCSPGFIVSAKGLLDTNADPSREDVRDWFQKHRNACRCTGYKPL
VDAVMDAAAVINGKKPETDLEFKMPADGRIWGSKYPRPTAVAKVTGTL
>d1dgja1 a.56.1.1 (A:81-193) Aldehyde oxidoreductase, domain 2
{Desulfovibrio desulfuricans}
APDCLHPLQHAWIQHGAAQCGFCTPGFIVSAKALLDENVAPSREDVRDWFQKHHNICRCTGYKPL
VDAVMDAAAILRGEKTVEEISFKMPADGRIWGSSIPRPSAVAKVTGLA
>d1fo4a1 a.56.1.1 (A:93-165) Xanthine oxidase, domain 2 {Cow (Bos
taurus)}
STKTRLHPVQERIAKSHGSQCGFCTPGIVMSMYTLLRNQPEPTVEEIEDAFQGNLCRCTGYRPIL
QGFRTFAK
>d1jroa1 a.56.1.1 (A:85-166) Xanthine dehydrogenase chain A, domain
2 {Rhodobacter capsulatus}
DGRLHPVQQAMIDHHGSQCGFCTPGFIVSMAAAHDRDRKDYDDLLAGNLCRCTGYAPILRAAEAA
AGEPPADWLQADAAFTL
>d1qj2a1 a.56.1.1 (A:82-161) Carbon monoxide (CO) dehydrogenase
iron-sulfur protein, C-domain {Pseudomonas carboxydovorans}
APDGTLSALQEGFRMMHGLQCGYCTPGMIMRSHRLLQENPSPTEAEIRFGIGGNLCRCTGYQNIV
KAIQYAAAKINGVPF
>d1ffva1 a.56.1.1 (A:82-157) Carbon monoxide (CO) dehydrogenase
iron-sulfur protein, C-domain {Hydrogenophaga pseudoflava}
NKGVLHAVQEGFYKEHGLQCGFCTPGMLMRAYRFLQENPNPTEAEIRMGMTGNLCRCTGYQNIVK
AVQYAARKLQE
>d1dj8a_ a.57.1.1 (A:) Protein HNS-dependent expression A; HdeA
{Escherichia coli}
NKKPVNSWTCEDFLAVDESFQPTAVGFAEALNNKDKPEDAVLDVQGIATVTPAIVQACTQDKQAN
FKDKVKGEWDKIKK
>d1g9la_ a.144.1.1 (A:) poly(A) binding protein {Human (Homo sapiens)}
GPLGSAAAATPAVRTVPQYKYAAGVRNPQQHLNAQPQVTMQQPAVHVQGQEPLTASMLASAPPQE
QKQMLGERLFPLIQAMHPTLAGKITGMLLEIDNSELLHMLESPESLRSKVDEAVAVLQAHQAKEA
AQKAVNSATGVPTV
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>d1i2ta_ a.144.1.1 (A:) hyperplastic discs protein {Human (Homo
sapiens)}
HRQALGERLYPRVQAMQPAFASKITGMLLELSPAQLLLLLASEDSLRARVDEAMELIIAHG
>d1af7_1 a.58.1.1 (11-91) Chemotaxis receptor methyltransferase CheR,
N-terminal domain {Salmonella typhimurium}
SVLLQMTQRLALSDAHFRRICQLIYQRAGIVLADHKRDMVYNRLVRRLRALGLDDFGRYLSMLEA
NQNSAEWQAFINALTT
>d1e91a_ a.59.1.1 (A:) Sin3B {Mouse (Mus musculus)}
ESDSVEFNNAISYVNKIKTRFLDHPEIYRSFLEILHTYQKEQLHTKGRPFRGMSEEEVFTEVANL
FRGQEDLLSEFGQFLPEAKR
>d1g1eb_ a.59.1.1 (B:) Sin3A {Mouse (Mus musculus)}
SLQNNQPVEFNHAINYVNKIKNRFQGQPDIYKAFLEILHTYQKEQRNAKEAGGNYTPALTEQEVY
AQVARLFKNQEDLLSEFGQFLPDA
>d1bqv__ a.60.1.1 (-) Ets-1 transcription factor pointed domain {Mouse
(Mus musculus)}
MECADVPLLTPSSKEMMSQALKATFSGFTKEQQRLGIPKDPRQWTETHVRDWVMWAVNEFSLKGV
DFQKFCMSGAALCALGKECFLELAPDFVGDILWEHLEILQKEDVK
>d1b0xa_ a.60.1.2 (A:) EphA4 receptor tyrosine kinases {Mouse (Mus
musculus)}
FSAVVSVGDWLQAIKMDRYKDNFTAAGYTTLEAVVHMSQDDLARIGITAITHQNKILSSVQAMRT
QMQQMHG
>d1b4fa_ a.60.1.2 (A:) EphB2 receptor {Human (Homo sapiens)}
PDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFDVVSQMMMEDILRVGVTLAGHQKKILNSIQVM
RAQMNQIQS
>d1sgg__ a.60.1.2 (-) EphB2 receptor {Chicken (Gallus gallus)}
YTSFNTVDEWLDAIKMSQYKESFASAGFTTFDIVSQMTVEDILRVGVTLAGHQKKILNSIQVMRA
QM
>d1coka_ a.60.1.2 (A:) C-terminal domain of p73 {Human (Homo sapiens)}
YHADPSLVSFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMTIWRGLQDLKQG
HDY
>d1dxsa_ a.60.1.2 (A:) C-terminal domain of p73 {Human (Homo sapiens)}
SLVSFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMTIWRGLQDL
>d1cuk_2 a.60.2.1 (65-142) DNA helicase RuvA subunit, middle domain
{Escherichia coli}
NKQERTLFKELIKTNGVGPKLALAILSGMSAQQFVNAVEREEVGALVKLPGIGKKTAERLIVEMK
DRFKGLHGDLFTP
>d1bvsa2 a.60.2.1 (A:64-134) DNA helicase RuvA subunit, middle domain
{Mycobacterium leprae}
DAENRDLFLALLSVSGVGPRLAMATLAVHDAAALRQALADSDVASLTRVPGIGRRGAERIVLELA
DKVGPV
>d1dgsa1 a.60.2.2 (A:401-581) NAD+-dependent DNA ligase, domain 3
{Thermus filiformis}
RWPEACPECGHRLVKEGKVHRCPNPLCPAKRFEAIRHYASRKAMDIEGLGEKLIERLLEKGLVRD
VADLYHLRKEDLLGLERMGEKSAQNLLRQIEESKHRGLERLLYALGLPGVGEVLARNLARRFGTM
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DRLLEASLEELIEVEEVGELTARAILETLKDPAFRDLVRRLKEAGVSMESK
>d1coo__ a.60.3.1 (-) C-terminal domain of RNA polymerase alpha subunit {Escherichia coli}
FDPILLRPVDDLELTVRSANCLKAEAIHYIGDLVQRTEVELLKTPNLGKKSLTEIKDVLASRGLS
LGMRLENWPPASIADE
>d1doqa_ a.60.3.1 (A:) C-terminal domain of RNA polymerase alpha subunit {Thermus thermophilus}
EQEEELDLPLEELGLSTRVLHSLKEEGIESVRALLALNLKDLKNIPGIGERSLEEIKEALEKKGF
TLKE
>d1b22a_ a.60.4.1 (A:) DNA repair protein Rad51, N-terminal domain {Human (Homo sapiens)}
EEESFGPQPISRLEQCGINANDVKKLEEAGFHTVEAVAYAPKKELINIKGISEAKADKILAEAAK
LVPMG
>d1ci4a_ a.60.5.1 (A:) Barrier-to-autointegration factor, BAF {Human (Homo sapiens)}
MTTSQKHRDFVAEPMGEKPVGSLAGIGEVLGKKLEERGFDKAYVVLGQFLVLKKDEDLFREWLKD
TCGANAKQSRDCFGCLREWCDAFL
>d1bpya1 a.60.6.1 (A:10-91) DNA polymerase beta, N-terminal (8 kD)-domain {Human (Homo sapiens)}
TLNGGITDMLTELANFEKNVSQAIHKYNAYRKAASVIAKYPHKIKSGAEAKKLPGVGTKIAEKID
EFLATGKLRKLEKIRQD
>d1dk2a_ a.60.6.1 (A:) DNA polymerase beta, N-terminal (8 kD)-domain {Rat (Rattus norvegicus)}
SKRKAPQETLNGGITDMLVELANFEKNVSQAIHKYNAYRKAASVIAKYPHKIKSGAEAKKLPGVG
TKIAEKIDEFLATGKLRKLEK
>d1jmsa1 a.60.6.1 (A:148-242) Terminal deoxynucleotidyl transferase {Mouse (Mus musculus)}
KKISQYACQRRTTLNNYNQLFTDALDILAENDELRENEGSCLAFMRASSVLKSLPFPITSMKDTE
GIPCLGDKVKSIIEGIIEDGESSEAKAVLN
>d1tfr_1 a.60.7.1 (183-305) T4 RNase H {Bacteriophage T4}
GSAEIDCMTKILKGDKKDNVASVKVRSDFWFTRVEGERTPSMKTSIVEAIANDREQAKVLLTESE
YNRYKENLVLIDFDYIPDNIASNIVNYYNSYKLPPRGKIYSYFVKAGLSKLTNSINEF
>d1bgxt1 a.60.7.1 (T:174-289) 5' to 3' exonuclease domain of DNA polymerase Taq {Thermus aquaticus}
LRPDQWADYRALTGDESDNLPGVKGIGEKTARKLLEEWGSLEALLKNLDRLKPAIREKILAHMDD
LKLSWDLAKVRTDLPLEVDFAKRREPDRERLRAFLERLEFGSLLHEFGLLE
>d1xo1a1 a.60.7.1 (A:186-290) T5 5'-exonuclease {Bacteriophage T5}
VDDVEQFISLKAIMGDLGDNIRGVEGIGAKRGYNIIREFGNVLDIIDQLPLPGKQKYIQNLNASE
ELLFRNLILVDLPTYCVDAIAAVGQDVLDKFTKDILEIAE
>d1a77_1 a.60.7.1 (209-316) Flap endonuclease-1 {Archaeon Methanococcus jannaschii}
ISLDDLIDIAIFMGTDYNPGGVKGIGFKRAYELVRSGVAKDVLKKEVEYYDEIKRIFKEPKVTDN
YSLSLKLPDKEGIIKFLVDENDFNYDRVKKHVDKLYNLIANKT
>d1b43a1 a.60.7.1 (A:220-339) Fen-1 nuclease {Archaeon Pyrococcus

furiosus}
LTREKLIELAILVGTDYNPGGIKGIGLKKALEIVRHSKDPLAKFQKQSDVDLYAIKEFFLNPPVT
DNYNLVWRDPDEEGILKFLCDEHDFSEERVKNGLERLKKAIKSGKQSTLESWFKR
>d1d8ba_ a.60.8.1 (A:) HRDC domain from RecQ helicase {Baker's yeast (Saccharomyces cerevisiae)}
ELNNLRMTYERLRELSLNLGNRMVPPVGNFMPDSILKKMAAILPMNDSAFATLGTVEDKYRRRFK
YFKATIADLSKKRSSE
>d1go3f_ a.60.8.2 (F:) RNA polymerase II subunit RBP7 (RpoF) {Archaeon Methanococcus jannaschii}
MIGKKILGERYVTVSEAAEIMYNRAQIGELSYEQGCALDYLQKFAKLDKEEAKKLVEELISLGID
EKTAVKIADILPEDLDDLRAIYYKRELPENAEEILEIVRKYI
>d1f44a1 a.60.9.1 (A:20-129) Cre recombinase {Bacteriophage P1}
SDEVRKNLMDMFRDRQAFSEHTWKMLLSVCRSWAAWCKLNNRKWFPAEPEDVRDYLLYLQARGLA
VKTIQQHLGQLNMLHRRSGLPRPSDSNAVSLVMRRIRKENVDAGE
>d1a0p_1 a.60.9.1 (3-100) Recombinase XerD {Escherichia coli}
QDLARIEQFLDALWLEKNLAENTLNAYRRDLSMMVEWLHHRGLTLATAQSDDLQALLAERLEGGY
KATSSARLLSAVRRLFQYLYREKFREDDPSAHL
>d1floa1 a.60.9.1 (A:2-129) Flp recombinase {Baker's yeast (Saccharomyces cerevisiae)}
PQFDILCKTPPKVLVRQFVERFERPSGEKIALCAAELTYLCWMITHNGTAIKRATFMSYNTIISN
SLSFDIVNKSLQFKYKTQKATILEASLKKLIPAWEFTIIPYYGQKHQSDITDIVSSLQLQFES
>d1zyma1 a.60.10.1 (A:22-144) Enzyme I of the PEP:sugar phosphotransferase system HPr-binding (sub)domain {Escherichia coli}
DEIVIDRKKISADQVDQEVERFLSGRAKASAQLETIKTKAGETFGEEKEAIFEGHIMLLEDEELE
QEIIALIKDKHMTADAAAHEVIEGQASALEELDDEYLKERAADVRDIGKRLLRNILGL
>d1jyga_ a.60.11.1 (A:) Hypothetical protein YjbJ {Escherichia coli}
MNKDEAGGNWKQFKGKVKEQWGKLTDDDMTIIEGKRDQLVGKIQERYGYQKDQAEKEVVDWETRN
EYRW
>d1hiwa_ a.61.1.1 (A:) HIV-1 matrix protein (HIV-1 MA, HIVp17, p17, MA) {Human immunodeficiency virus type 1}
VLSGGELDKWEKIRLRPGGKKQYKLKHIVWASRELERFAVNPGLLETSEGCRQILGQLQPSLQTG
SEELRSLYNTIAVLYCVHQRIDVKDTKEALDKIEEEQNKSKKKAQQAAAD
>d1hiws_ a.61.1.1 (S:) HIV-1 matrix protein (HIV-1 MA, HIVp17, p17, MA) {Human immunodeficiency virus type 1}
VLSGGELDKWEKIRLRPGGKKQYKLKHIVWASRELERFAVNPGLLETSEGCRQILGQLQPSLQTG
SEELRSLYNTIAVLYCVHQRIDVKDTKEALDKIEEEQN
>d1tam__ a.61.1.1 (-) HIV-1 matrix protein (HIV-1 MA, HIVp17, p17, MA) {Human immunodeficiency virus type 1}
MGARASVLSGGELDRWEKIRLRPGGKKKYKLKHIVWASRELERFAVNPGLLETSEGCRQILGQLQ
PSLQTGSEELRSLYNTVATLYCVHQRIEIKDTKEALDKIEEEQNKSKKKAQQAAA
>d2hmx__ a.61.1.1 (-) HIV-1 matrix protein (HIV-1 MA, HIVp17, p17, MA) {Human immunodeficiency virus type 1}
HMGARASVLSGGELDKWEKIRLRPGGKKQYKLKHIVWASRELERFAVNPGLLETSEGCRQILGQL
QPSLQTGSEELRSLYNTIAVLYCVHQRIDVKDTKEALDKIEEEQNKSKKKAQQAAADTGNNSQVS

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QNY
>d1ed1a_ a.61.1.1 (A:) SIV matrix antigen {Simian immunodeficiency virus}
SVLSGKKADELEKIRLRPGGKKKYMLKHVVWAANELDRFGLAESLLENKEGCQKILSVLAPLVPT
GSENLKSLYNTVCVIWCIHAEEKVKHTEEAKQIVQRHLVVETGTAETMP
>d1jvr__ a.61.1.2 (-) HTLV-II matrix protein {Human T-cell leukemia virus type 2}
HMGQIHGLSPTPIPKAPRGLSTHHWLNFLQAAYRLQPGPSDFDFQQLRRFLKLALKTPIWLNPID
YSLLASLIPKGYPGRVVEIINILVKNQVSPSAPAAPVPTPICPTTTPPPPPPPSPEAHVPPPYVE
PTTTQCF
>d1bax__ a.61.1.3 (-) Mason-pfizer monkey virus matrix protein {Simian mason-pfizer virus}
MGQELSQHERYVEQLKQALKTRGVKVKYADLLKFFDFVKDTCPWFPQEGTIDIKRWRRVGDCFQD
YYNTFGPEKVPVTAFSYWNLIKELIDKKE
>d1a6s__ a.61.1.4 (-) GAG polyprotein M-domain {Rous sarcoma virus}
GEAVIKVISSACKTYCGKTSPSKKEIGAMLSLLQKEGLLMSPSDLYSPGSWDPITAALSQRAMIL
GKSGELKTWGLVLGALKAAREE
>d1heka_ a.61.1.5 (A:) EIAV matrix antigen {Equine infectious anemia virus, EIAV}
AMADIGSMGDPLTWSKALKKLEKVTVQGSQKLTTGNCNWALSLVDLFHDTNFVKEKDWQLRDVIP
LLEDVTQTLSGQEREAFERTWWAISAVKMGLQINNVVDGKASFQLLRAKYE
>d1qgta_ a.62.1.1 (A:) Hepatitis B viral capsid (hbcag) {Hepatitis B virus}
MDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAILCWGEL
MTLATWVGNNLEDPASRDLVVNYVNTNMGLKIRQLLWFHISCLTFGRETVLEYLVSFGVWIRTPP
AYRPPNAPILST
>d1aep__ a.63.1.1 (-) Apolipophorin-III {African locust (Locusta migratoria)}
NIAEAVQQLNHTIVNAAHELHETLGLPTPDEALNLLTEQANAFKTKIAEVTTSLKQEAEKHQGSV
AEQLNAFARNLNNSIHDAATSLNLQDQLNSLQSALTNVGHQWQDIATKTQASAQEAWAPVQSALQ
EAAEKTKEAAANLQNSIQSAVQK
>d1eq1a_ a.63.1.1 (A:) Apolipophorin-III {Manduca sexta}
DAPAGGNAFEEMEKHAKEFQKTFSEQFNSLVNSKNTQDFNKALKDGSDSVLQQLSAFSSSLQGAI
SDANGKAKEALEQARQNVEKTAEELRKAHPDVEKEANAFKDKLQAAVQTTVQESQKLAKEVASNM
EETNKKLAPKIKQAYDDFVKHAEEVQKKLHEAATKQ
>d1nkl__ a.64.1.1 (-) NK-lysin {Pig (Sus scrofa)}
GYFCESCRKIIQKLEDMVGPQPNEDTVTQAASQVCDKLKILRGLCKKIMRSFLRRISWDILTGKK
PQAICVDIKICKE
>d1qdma1 a.64.1.2 (A:1S-104S) (Pro)phytepsin {Barley (Hordeum vulgare)}
VVSQECKTIVSQYGQQILDLLLAETQPKKICSQVGLCTFDGTRGVSAGIRSVVDDEPVKSNGLRA
DPMCSACEMAVVWMQNQLAQNKTQDLILDYVNQLCNRLP
>d1e68a_ a.64.2.1 (A:) Bacteriocin AS-48 {Enterococcus faecalis}
MAKEFGIPAAVAGTVLNVVEAGGWVTTIVSILTAVGSGGLSLLAAAGRESIKAYLKKEIKKKGKR
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AVIAW
>d1ain__ a.65.1.1 (-) Annexin I {Human (Homo sapiens)}
GSAVSPYPTFNPSSDVAALHKAIMVKGVDEATIIDILTKRNNAQRQQIKAAYLQETGKPLDETLK
KALTGHLEEVVLALLKTPAQFDADELRAAMKGLGTDEDTLIEILASRTNKEIRDINRVYREELKR
DLAKDITSDTSGDFRNALLSLAKGDRSEDFGVNEDLADSDARALYEAGERRKGTDVNVFNTILTT
RSYPQLRRVFQKYTKYSKHDMNKVLDLELKGDIEKCLTAIVKCATSKPAFFAEKLHQAMKGVGTR
HKALIRIMVSRSEIDMNDIKAFYQKMYGISLCQAILDETKGDYEKILVALCGGN
>d1bo9a_ a.65.1.1 (A:) Annexin I {Human (Homo sapiens)}
TFNPSSDVAALHKAIMVKGVDEATIIDILTKRNNAQRQQIKAAYLQETGKPLDETLKKALTGHLE
EVVLALLK
>d1hm6a_ a.65.1.1 (A:) Annexin I {Pig (Sus scrofa)}
AMVSEFLKQAWFIDNEEQEYIKTVKGSKGGPGSAVSPYPTFNPSSDVEALHKAITVKGVDEATII
EILTKRTNAQRQQIKAAYLQEKGKPLDEALKKALTGHLEEVALALLKTPAQFDADELRAAMKGLG
TDEDTLNEILASRTNREIREINRVYKEELKRDLAKDITSDTSGDYQKALLSLAKGDRSEDLAIND
DLADTDARALYEAGERRKGTDLNVFITILTTRSYPHLRRVFQKYSKYSKHDMNKVLDLELKGDIE
NCLTVVVKCATSKPMFFAEKLHQAMKGIGTRHKTLIRIMVSRSEIDMNDIKACYQKLYGISLCQA
ILDETKGDYEKILVALCG
>d1axn__ a.65.1.1 (-) Annexin III {Human (Homo sapiens)}
SASIWVGHRGTVRDYPDFSPSVDAEAIQKAIRGIGTDEKMLISILTERSNAQRQLIVKEYQAAYG
KELKDDLKGDLSGHFEHLMVALVTPPAVFDAKQLKKSMKGAGTNEDALIEILTTRTSRQMKDISQ
AYYTVYKKSLGDDISSETSGDFRKALLTLADGRRDESLKVDEHLAKQDAQILYKAGENRWGTDED
KFTEILCLRSFPQLKLTFDEYRNISQKDIVDSIKGELSGHFEDLLLAIVNCVRNTPAFLAERLHR
ALKGIGTDEFTLNRIMVSRSEIDLLDIRTEFKKHYGYSLYSAIKSDTSGDYEITLLKICGGDD
>d1i4aa_ a.65.1.1 (A:) Annexin IV {Cow (Bos taurus)}
ASGFNAAEDAQTLRKAMKGLGTDEDAIINVLAYRSTAQRQEIRTAYKTTIGRDLMDDLKSELSGN
FEQVILGMMTPTVLYDVQELRKAMKGAGTDEGCLIEILASRTPEEIRRINQTYQLQYGRSLEDDI
RSDTSFMFQRVLVSLSAGGRDESNYLDDALMRQDAQDLYEAGEKKWGTDEVKFLTVLCSRNRNHL
LHVFDEYKRIAQKDIEQSIKSETSGSFEDALLAIVKCMRNKSAYFAERLYKSMKGLGTDDDTLIR
VMVSRAEIDMLDIRANFKRLYGKSLYSFIKGDTSGDYRKVLLILCGGDD
>d1ala__ a.65.1.1 (-) Annexin V {Chicken (Gallus gallus)}
KYTRGTVTAFSPFDARADAEALRKAMKGMGTDEETILKILTSRNNAQRQEIASAFKTLFGRDLVD
DLKSELTGKFETLMVSLMRPARIFDAHALKHAIKGAGTNEKVLTEILASRTPAEVQNIKQVYMQE
YEANLEDKITGETSGHFQRLLVVLLQANRDPDGRVEEALVEKDAQVLFRAGELKWGTDEETFITI
LGTRSVSHLRRVFDKYMTISGFQIEETIDRETSGDLEKLLLAVVKCIRSVPAYFAETLYYSMKGA
GTDDDTLIRVMVSRSEIDLLDIRHEFRKNFAKSLYQMIQKDTSGDYRKALLLLCGG
>d1hvd__ a.65.1.1 (-) Annexin V {Human (Homo sapiens)}
VLRGTVTDFPGFDGRADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDD
LKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQVYEEEY
GSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGELKWGTDEEKFITIF
GTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRSIPAYLAETLYYAMKGAG
TDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSGDYKKALLLLC
>d1g5na_ a.65.1.1 (A:) Annexin V {Rat (Rattus norvegicus)}
ALRGTVTDFSGFDGRADAEVLRKAMKGLGTDEDSILNLLTARSNAQRQQIAEEFKTLFGRDLVND
MKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTDEKVLTEIIASRTPEELRAIKQAYEEEY
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GSNLEDDVVGDTSGYYQRMLVVLLQANRDPDTAIDDAQVELDAQALFQAGELKWGTDEEKFITIL
GTRSVSHLRRVFDKYMTISGFQIEETIDRETSGNLENLLLAVVKSIRSIPAYLAETLYYAMKGAG
TDDHTLIRVIVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSGDYKKALLLLCGGEDD
>d1avc_1 a.65.1.1 (10-350) Annexin VI {Cow (Bos taurus)}
YRGSIRDFPDFNPSQDAETLYNAMKGFGSDKEAIINLITSRSNKQRQEICQNYKSLYGKDLIADL
KYELTGKFERLIVGLMRPPAYADAKEIKDAISGIGTDEKCLIEILASRTNEQIHQLVAAYKDAYE
RDLEADITGDTSGHFRKMLVVLLQGTREEDDVVSEDLVQQDVQDLYEAGELKWGTDEAQFIYILG
NRSKQHLRLVFDEYLKTTGKPIEASIRGELSGDFEKLMLAVVKCIRSTAEYFAERLFKAMKGLGT
RDNTLIRIMVSRSELDMLDIREIFRTKYEKSLYSMIKNDTSGEYKKTLLKLCGGDDDAAGQFFPE
AAQVAYQMWELSAVAR
>d1avc_2 a.65.1.1 (351-671) Annexin VI {Cow (Bos taurus)}
VELKGTVRPAGDFNPDADAKALRKAMKGLGTDEDTIIDIITHRSNAQRQQIRQTFKSHFGRDLMA
DLKSELSGDLARLILGLMMPPAHYDAKQLKKAMEGAGTDEKALIEILATRTNAEIQAINKAYKED
YHKTLEDALSSDTSGHFKRILISLATGNREEGGEDRERAREDAQVAAEILEIADTTSGDKSSLET
RFMMILCTRSYPDLRRVFQEFVKMTNYDVEHTIKKEMSGDVRDVFVAIVQSVKNKPLFFADKLYK
SMKGAGTEEKTLTRIMVSRSEIDLLNIRREFIEKYDKSLHQAIEGDTSGHFLKALLAICGG
>d1dm5a_ a.65.1.1 (A:) Annexin XII {Hydra vulgaris}
VVQGTVKPHASFNSREDAETLRKAMKGIGTDEKSITHILATRSNAQRQQIKTDYTTLFGKHLEDE
LKSELSGNYEAAALALLRKPDEFLAEQLHAAMKGLGTDKNALIDILCTQSNAQIHAIKAAFKLLY
KEDLEKEIISETSGNFQRLLVSMLQGGRKEDEPVNAAHAAEDAAAIYQAGEGQIGTDESRFNAVL
ATRSYPQLHQIFHEYSKISNKTILQAIENEFSGDIKNGLLAIVKSVENRFAYFAERLHHAMKGLG
TSDKTLIRILVSRSEIDLANIKETFQAMYGKSLYEFIADDCSGDYKDLLLQITGH
>d1dk5a_ a.65.1.1 (A:) Annexin 24(ca32) {Bell pepper (Capsicum annuum)}
HHHHMASLTVPAHVPSAAEDCEQLRSAFKGWGTNEKLIISILAHRTAAQRKLIRQTYAETFGEDL
LKELDRELTHDFEKLVLVWTLDPSERDAHLAKEATKRWTKSNFVLVELACTRSPKELVLAREAYH
ARYKKSLEEDVAYHTTGDHRKLLVPLVSSYRYGGEEVDLRLAKAESKILHEKISDKAYSDDEVIR
ILATRSKAQLNATLNHYKDEHGEDILKQLEDGDEFVALLRATIKGLVYPEHYFVEVLRDAINRRG
TEEDHLTRVIATRAEVDLKIIADEYQKRDSIPLGRAIAKDTRGDYESMLLALLGQE
>d1azsc1 a.66.1.1 (C:86-201) Transducin (alpha subunit), insertion domain {Cow (Bos taurus)}
GEKATKVQDIKNNLKEAIETIVAAMSNLVPPVELANPENQFRVDYILSVMNVPDFDFPPEFYEHA
KALWEDEGVRACYERSNEYQLIDCAQYFLDKIDVIKQDDYVPSDQDLLRCR
>d1tada1 a.66.1.1 (A:57-177) Transducin (alpha subunit), insertion domain {Cow (Bos taurus)}
YSLEECLEFIAIIYGNTLQSILAIVRAMTTLNIQYGDSARQDDARKLMHMADTIEEGTMPKEMSD
IIQRLWKDSGIQACFDRASEYQLNDSAGYYLSDLERLVTPGYVPTEQDVLRSRVKT
>d1cipa1 a.66.1.1 (A:61-181) Transducin (alpha subunit), insertion domain {Rat (Rattus norvegicus)}
YSEEECKQYKAVVYSNTIQSIIAIIRAMGRLKIDFGDAARADDARQLFVLAGAAEEGFMTAELAG
VIKRLWKDSGVQACFNRSREYQLNDSAAYYLNDLDRIAQPNYIPTQQDVLRTRVKT
>d1ej5a_ a.68.1.1 (A:) Wiscott-Aldrich syndrome protein, WASP, C-terminal domain {Human (Homo sapiens)}
SGFKHVSHVGWDPQNGFDVNNLDPDLRSLFSRAGISEAQLTDAETSKLIYDFIEDQGGLEAVRQE
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MRRQGGSGGSQSSEGLVGALMHVMQKRSRAIHSSDEGEDQAG
>d1e79a1 a.69.1.1 (A:380-510) C-terminal domain of alpha and beta
subunits of F1 ATP synthase {Cow (Bos taurus)}
TRAMKQVAGTMKLELAQYREVAAFAQFGSDLDAATQQLLSRGVRLTELLKQGQYSPMAIEEQVAV
IYAGVRGYLDKLEPSKITKFENAFLSHVISQHQALLGKIRTDGKISEESDAKLKEIVTNFLAGFE
A
>d1e79d1 a.69.1.1 (D:358-475) C-terminal domain of alpha and beta
subunits of F1 ATP synthase {Cow (Bos taurus)}
MDPNIVGSEHYDVARGVQKILQDYKSLQDIIAILGMDELSEEDKLTVSRARKIQRFLSQPFQVAE
VFTGHLGKLVPLKETIKGFQQILAGEYDHLPEQAFYMVGPIEEAVAKADKLAE
>d1skyb1 a.69.1.1 (B:372-502) C-terminal domain of alpha and beta
subunits of F1 ATP synthase {Bacillus sp., strain ps3}
IKAMKKVAGTLRLDLAAYRELEAFAQFGSDLDKATQANVARGARTVEVLKQDLHQPIPVEKQVLI
IYALTRGFLDDIPVEDVRRFEKEFYLWLDQNGQHLLEHIRTTKDLPNEDDLNQAIEAFKKTFVVS
Q
>d1skye1 a.69.1.1 (E:357-470) C-terminal domain of alpha and beta
subunits of F1 ATP synthase {Bacillus sp., strain ps3}
EIVGEEHYQVARKVQQTLERYKELQDIIAILGMDELSDEDKLVVHRARRIQFFLSQNFHVAEQFT
GQPGSYVPVKETVRGFKEILEGKYDHLPEDRFRLVGRIEEVVEKAKAMG
>d1fx0a1 a.69.1.1 (A:373-501) C-terminal domain of alpha and beta
subunits of F1 ATP synthase {Spinach (Spinacia oleracea), chloroplast}
IKAMKKVAGKLKLELAQFAELEAFAQFASDLDKATQNQLARGQRLRELLKQPQSAPLTVEEQVMT
IYTGTNGYLDSLELDQVRKYLVELRTYVKTNKPEFQEIISSTKTFTEEAEALLKEAIQEQMERF
>d1fx0b1 a.69.1.1 (B:378-485) C-terminal domain of alpha and beta
subunits of F1 ATP synthase {Spinach (Spinacia oleracea), chloroplast}
RIVGEEHYEIAQRVKETLQRYKELQDIIAILGLDELSEEDRLTVARARKIERFLSQPFFVAEVFT
GSPGKYVGLAETIRGFQLILSGELDSLPEQAFYLVGNIDEATA
>d1fkma1 a.69.2.1 (A:249-442) Ypt/Rab-GAP domain of gyp1p {Baker's
yeast (Saccharomyces cerevisiae)}
NSIIQRISKFDNILKDKTIINQQDLRQISWNGIPKIHRPVVWKLLIGYLPVNTKRQEGFLQRKRK
EYRDSLKHTFSDQHSRDIPTWHQIEIDIPRTNPHIPLYQFKSVQNSLQRILYLWAIRHPASGYVQ
GINDLVTPFFETFLTEYLPPSQIDDVEIKDPSTYMVDEQITDLEADTFWCLTKLLEQITDNYIH
>d1fkma2 a.69.2.1 (A:443-630) Ypt/Rab-GAP domain of gyp1p {Baker's
yeast (Saccharomyces cerevisiae)}
GQPGILRQVKNLSQLVKRIDADLYNHFQNEHVEFIQFAFRWMNCLLMREFQMGTVIRMWDTYLSE
TSQEVTSSYSMSSNDIKPPVTPTEPRVASFVTPTKDFQSPTTALSNMTPNNAVEDSGKMRQSSLN
EFHVFVCAAFLIKWSDQLMEMDFQETITFLQNPPTKDWTETDIEMLLSEAFIWQSLYK
>d1k5ha1   a.69.3.1   (A:301-398)   1-deoxy-D-xylulose-5-phosphate
reductoisomerase, C-terminal domain {Escherichia coli}
KLSALTFAAPDYDRYPCLKLAMEAFEQGQAATTALNAANEITVAAFLAQQIRFTDIAALNLSVLE
KMDMREPQCVDDVLSVDANAREVARKEVMRLAS
>d1abv__ a.70.1.1 (-) N-terminal domain of the delta subunit of the
F1F0-ATP synthase {Escherichia coli}
SEFITVARPYAKAAFDFAVEHQSVERWQDMLAFAAEVTKNEQMAELLSGALAPETLAESFIAVCG
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EQLDENGQNLIRVMAENGRLNALPDVLEQFIHLRAVSEAT
>d1g7da_ a.71.1.1 (A:) Endoplasmic reticulum protein ERP29, C-domain
{Rat (Rattus norvegicus)}
PGCLPAYDALAGQFIEASSREARQAILKQGQDGLSGVKETDKKWASQYLKIMGKILDQGEDFPAS
ELARISKLIENKMSEGKKEELQRSLNILTAFRKKGAEKEEL
>d1dvka_ a.72.1.1 (A:) Functional domain of the splicing factor Prp18
{Baker's yeast (Saccharomyces cerevisiae)}
MRIQEAIAQDKTISVIIDPSQIGSTEGKPLLSMKCNLYIHEILSRWKASLEAYHPELFLDTKKAL
FPLLLQLRRNQLAPDLLISLATVLYHLQQPKEINLAVQSYMKLSIGNVAWPIGVTSVGIHARSAH
SKIQGGRNAANIMIDERTRLWITSIKRLITFEEWYTSNH
>d1ak4c_ a.73.1.1 (C:) HIV-1 capsid protein {Human immunodeficiency
virus type 1}
PIVQNLQGQMVHQAISPRTLNAWVKVVEEKAFSPEVIPMFSALSEGATPQDLNTMLNTVGGHQAA
MQMLKETINEEAAEWDRLHPVHAGPIAPGQMREPRGSDIAGTTSTLQEQIGWMTHNPPIPVGEIY
KRWIILGLNKIVRMY
>d1e6jp2 a.73.1.1 (P:11-147) HIV-1 capsid protein {Human
immunodeficiency virus type 1}
VHQAISPRTLNAWVKVVEEKAFSPEVIPMFSALSEGATPQDLNTMLNTVGGHQAAMQMLKETINE
EAAEWDRVHPVHAGPIAPGQMREPRGSDIAGTTSTLQEQIGWMTNNPPIPVGEIYKRWIILGLNK
IVRMYSP
>d2eiaa2 a.73.1.1 (A:17-147) EIAV capsid protein p26 {Equine
infectious anemia virus}
PRGYTTWVNTIQTNGLLNEASQNLFGILSVDCTSEEMNAFLDVVPGQAGQKQILLDAIDKIADDW
DNRHPLPNAPLVAPPQGPIPMTARFIRGLGVPRERQMEPAFDQFRQTYRQWIIEAMSEGIKVMIG
K
>d1g03a_ a.73.1.1 (A:) HTLV-I capsid protein {Human T-cell leukemia
virus type 1}
PVMHPHGAPPNHRPWQMKDLQAIKQEVSQAAPGSPQFMQTIRLAVQQFDPTAKDLQDLLQYLCSS
LVASLHHQQLDSLISEAETRGITSYNPLAGPLRVQANNPQQQGLRREYQQLWLAAFAALPGSAKD
PSWA
>g1qrj.1 a.73.1.1 (A:,B:16-130) HTLV-I capsid protein {Human T-cell
leukemia virus type 1}
HHHHHSSGHIEGRHMXQMKDLQAIKQEVSQAAPGSPQFMQTIRLAVQQFDPTAKDLQDLLQYLCS
SLVASLHHQQLDSLISEAETRGITGYNPLAGPLRVQANNPQQQGLRREYQQLWLAAFAALPGSAK
D
>d1d1da2 a.73.1.1 (A:11-150) RSV capsid protein {Rous sarcoma virus}
WTPLEPKLITRLADTVRTKGLRSPITMAEVEALMSSPLLPHDVTNLMRVILGPAPYALWMDAWGV
QLQTVIAAATRDPRHPANGQGRGERTNLDRLKGLADGMVGNPQGQAALLRPGELVAITASALQAF
REVARLAEPA
>d1em9a_ a.73.1.1 (A:) RSV capsid protein {Rous sarcoma virus}
PVVIKTEGPAWTPLEPKLITRLADTVRTKGLRSPITMAEVEALMSSPLLPHDVTNLMRVILGPAP
YALWMDAWGVQLQTVIAAATRDPRHPANGQGRGERTNLNRLKGLADGMVGNPQGQAALLRPGELV
AITASALQAFREVARLA
>d1jsub2 a.74.1.1 (B:310-432) Cyclin A {Human (Homo sapiens)}
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TVNQFLTQYFLHQQPANCKVESLAMFLGELSLIDADPYLKYLPSVIAGAAFHLALYTVTGQSWPE
SLIRKTGYTLESLKPCLMDLHQTYLKAPQHAQQSIREKYKNSKYHGVSLLNPPETLNL
>d1vin_1 a.74.1.1 (181-308) Cyclin A {Cow (Bos taurus)}
DIHTYLREMEVKCKPKVGYMKKQPDITNSMRAILVDWLVEVGEEYKLQNETLHLAVNYIDRFLSS
MSVLRGKLQLVGTAAMLLASKFEEIYPPEVAEFVYITDDTYTKKQVLRMEHLVLKVLAFDLAA
>d1vin_2 a.74.1.1 (309-432) Cyclin A {Cow (Bos taurus)}
PTINQFLTQYFLHQQPANCKVESLAMFLGELSLIDADPYLKYLPSVIAAAAFHLALYTVTGQSWP
ESLVQKTGYTLETLKPCLLDLHQTYLRAPQHAQQSIREKYKNSKYHGVSLLNPPETLNL
>d1jkw_1 a.74.1.1 (11-161) Cyclin H (mcs2) {Human (Homo sapiens)}
WTFSSEEQLARLRADANRKFRCKAVANGKVLPNDPVFLEPHEEMTLCKYYEKRLLEFCSVFKPAM
PRSVVGTACMYFKRFYLNNSVMEYHPRIIMLTCAFLACKVDEFNVSSPQFVGNLRESPLGQEKAL
EQILEYELLLIQQLNFHLIVH
>d1jkw_2 a.74.1.1 (162-287) Cyclin H (mcs2) {Human (Homo sapiens)}
NPYRPFEGFLIDLKTRYPILENPEILRKTADDFLNRIALTDAYLLYTPSQIALTAILSSASRAGI
TMESYLSESLMLKENRTCLSQLLDIMKSMRNLVKKYEPPRSEEVAVLKQKLDRCHSAELAL
>d1bu2a1 a.74.1.1 (A:22-148) Viral cyclin {Herpes virus saimiri}
RVLNNLKLRELLLPKFTSLWEIQTEVTVDNRTILLTWMHLLCESFELDKSVFPLSVSILDRYLCK
KQGTKKTLQKIGAACVLIGSKIRTVKPMTVSKLTYLSCDCFTNLELINQEKDILEALKWDTE
>d1bu2a2 a.74.1.1 (A:149-250) Viral cyclin {Herpes virus saimiri}
AVLATDFLIPLCNALKIPEDLWPQLYEAASTTICKALIQPNIALLSPGLICAGGLLTTIETDNTN
CRPWTCYLEDLSSILNFSTNTVRTVKDQVSEAFSLYD
>d1f5qb1 a.74.1.1 (B:6-146) Viral cyclin {Murine herpes virus gamma
68}
FQGFLDSSLLNEEDCRQMIYRSEREHDARMVGVNVDQHFTSQYRKVLTTWMFCVCKDLRQDNNVF
PLAVALLDELFLSTRIDRENYQSTAAVALHIAGKVRAYMPIKATQLAYLCGGATTADKLLTLEVK
SLDTLSWVADR
>d1f5qb2 a.74.1.1 (B:147-252) Viral cyclin {Murine herpes virus gamma
68}
CLSTDLICYILHIMHAPREDYLNIYNLCRPKIFCALCDGRSAMKRPVLITLACMHLTMNQKYDYY
ENRIDGVCKSLYITKEELHQCCDLVDIAIVSFDENYFKINA
>d1g3nc1 a.74.1.1 (C:16-147) Viral cyclin {Kaposi sarcoma-associated
virus}
LCEDRIFYNILEIEPRFLTSDSVFGTFQQSLTSHMRKLLGTWMFSVCQEYNLEPNVVALALNLLD
RLLLIKQVSKEHFQKTGSACLLVASKLRSLTPISTSSLCYAAADSFSRQELIDQEKELLEKLAWR
TE
>d1g3nc2 a.74.1.1 (C:148-253) Viral cyclin {Kaposi sarcoma-associated
virus}
AVLATDVTSFLLLKLVGGSQHLDFWHHEVNTLITKALVDPLTGSLPASIISAAGCALLVPANVIP
QDTHSGGVVPQLASILGCDVSVLQAAVEQILTSVSDFDLRI
>d1vola1 a.74.1.2 (A:113-207) Transcription factor IIB (TFIIB), core
domain {Human (Homo sapiens)}
AMMNAFKEITTMADRINLPRNKVDRTNNLFRQAYEQKSLKGRANDAIASACLYIACRQEGVPRTF
KEICAVSRISKKEIGRCFKLILKALETSVD
>d1vola2 a.74.1.2 (A:208-316) Transcription factor IIB (TFIIB), core
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domain {Human (Homo sapiens)}
LITTGDFMSRFCSNLCLPKQVQMAATHIARKAVELDLVPGRSPISVAAAAIYMASQASAEKRTQK
EIGDIAGVADVTIRQSYRLIYPRAPDLFPTDFKFDTPVDKLPQL
>d1aisb1 a.74.1.2 (B:1108-1205) Transcription factor IIB (TFIIB),
core domain {Archaeon Pyrococcus woesei}
NLAFALSELDRITAQLKLPRHVEEEAARLYREAVRKGLIRGRSIESVMAACVYAACRLLKVPRTL
DEIADIARVDKKEIGRSYRFIARNLNLTPKKLF
>d1aisb2 a.74.1.2 (B:1206-1300) Transcription factor IIB (TFIIB),
core domain {Archaeon Pyrococcus woesei}
VKPTDYVNKFADELGLSEKVRRRAIEILDEAYKRGLTSGKSPAGLVAAALYIASLLEGEKRTQRE
VAEVARVTEVTVRNRYKELVEKLKIKVPIA
>d1guxa_ a.74.1.3 (A:) Retinoblastoma tumor suppressor domains {Human
(Homo sapiens)}
NTIQQLMMILNSASDQPSENLISYFNNCTVNPKESILKRVKDIGYIFKEKFAKAVGQGCVEIGSQ
RYKLGVRLYYRVMESMLKSEEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRSTSQNLDSG
TDLSFPWILNVLNLKAFDFYKVIESFIKAEGNLTREMIKHLERCEHRIMESLAWLSDSPLFDLIK
QSK
>d1guxb_ a.74.1.3 (B:) Retinoblastoma tumor suppressor domains {Human
(Homo sapiens)}
TSLSLFYKKVYRLAYLRLNTLCERLLSEHPELEHIIWTLFQHTLQNEYELMRDRHLDQIMMCSMY
GICKVKNIDLKFKIIVTAYKDLPHAVQETFKRVLIKEEEYDSIIVFYNSVFMQRLKTNILQYAST
RPPTLSPIPHI
>d1k8ke_ a.148.1.1 (E:) Arp2/3 complex 21 kDa subunit ARPC3 {Cow (Bos
taurus)}
PAYHSSLMDPDTKLIGNMALLPIRSQFKGPAPRETKDTDIVDEAIYYFKANVFFKNYEIKNEADR
TLIYITLYISECLKKLQKCNSKSQGEKEMYTLGITNFPIPGEPGFPLNAIYAKPANKQEDEVMRA
YLQQLRQETGLRLCEKVFDPQNDKPSKWWTCFVKRQFMNKSLSG
>d1jfza_ a.149.1.1 (A:) RNase III endonuclease domain {Aquifex
aeolicus}
GMKMLEQLEKKLGYTFKDKSLLEKALTHVSYSKKEHYETLEFLGDALVNFFIVDLLVQYSPNKRE
GFLSPLKAYLISEEFFNLLAQKLELHKFIRIKRGKINETIIGDVFEALWAAVYIDSGRDANFTRE
LFYKLFKEDILSAIKEGR
>d1hus__ a.75.1.1 (-) Ribosomal protein S7 {Bacillus
stearothermophilus}
RDVLPDPIYNSKLVTRLINKIMIDGKKSKAQKILYTAFDIIRERTGKDPMEVFEQALKNVMPVLE
VRARRVGGANYQVPVEVRPDRRVSLGLRWLVQYARLRNEKTMEERLANEIMDAANNTGAAVKKRE
DTHKMAEAN
>d1rss__ a.75.1.1 (-) Ribosomal protein S7 {Thermus thermophilus}
LQPDLVYGDVLVTAFINKIMRDGKKNLAARIFYDACKIIQEKTGQEPLKVFKQAVENVKPRMEVR
SRRVGGANYQVPMEVSPRRQQSLALRWLVQAANQRPERRAAVRIAHELMDAAEGKGGAVKKKEDV
ERMAEANRAYAHYRW
>d1iqva_ a.75.1.1 (A:) Ribosomal protein S7 {Archaeon Pyrococcus
horikoshii}
IKVMGRWSTEDVEVKDPSLKPYINLEPRLLPHTHGRHAKKHFGKANVHIVERLINKVMRSGGSHY
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KVAGHFMRREHRSLNSKKVRAYEVVKEAFKIIEKRTGKNPIQVLVWAIENAAPREDTTSVMFGGI
RYHVAVDISPLRRLDVALRNIALGASAKCYRTKMSFAEALAEEIILAANKDPKSYAYSKKLEIER
IAESSR
>d1jr3a1 a.80.1.1 (A:243-368) gamma subunit {Escherichia coli}
TLDDDQALSLVEAMVEANGERVMALINEAAARGIEWEALLVEMLGLLHRIAMVQLSPAALGNDMA
AIELRMRELARTIPPTDIQLYYQTLLIGRKELPYAPDRRMGVEMTLLRALAFHPRMPLPEP
>d1a5t_1 a.80.1.1 (208-330) delta prime subunit {Escherichia coli}
DNWQARETLCQALAYSVPSGDWYSLLAALNHEQAPARLHWLATLLMDALKRHHGAAQVTNVDVPG
LVAELANHLSPSRLQAILGDVCHIREQLMSVTGINRELLITDLLLRIEHYLQPGVVLP
>d1jr3d1 a.80.1.1 (D:212-338) delta subunit {Escherichia coli}
FTPFHWVDALLMGKSKRALHILQQLRLEGSEPVILLRTLQRELLLLVNLKRQSAHTPLRALFDKH
RVWQNRRGMMGEALNRLSQTQLRQAVQLLTRTELTLKQDYGQSVWAELEGLSLLLCHKPLAD
>d1iqpa1 a.80.1.1 (A:233-327) Replication factor C {Archaeon
Pyrococcus furiosus}
RARPEDIREMMLLALKGNFLKAREKLREILLKQGLSGEDVLVQMHKEVFNLPIEEPKKVLLADKI
GEYNFRLVEGANEIIQLEALLAQFTLIGKK
>d1jr5a_ a.150.1.1 (A:) Anti-sigma factor Asia {Bacteriophage T4}
MNKNIDTVREIITVASILIKFSREDIVENRANFIAFLNEIGVTHEGRKLNQNSFRKIVSELTQED
KKTLIDEFNEGFEGVYRYLEMYTNK
>d1f5ta2 a.76.1.1 (A:1065-1121) Diphtheria toxin repressor (DtxR)
{Corynebacterium diphtheriae}
TPTGRTLATAVMRKHRLAERLLTDIIGLDINKVHDEADRWEHVMSDEVERRLVKVLK
>d1g3sa2 a.76.1.1 (A:65-140) Diphtheria toxin repressor (DtxR)
{Corynebacterium diphtheriae}
TPTGRTLATAVMRKHRLAERLLTDIIGLDINKVHDEASRWEHVMSDEVERRLVKVLKDVSRSPFG
NPIPGLDELGV
>d1fx7a2 a.76.1.1 (A:65-144) Iron-dependent regulator {Mycobacterium
tuberculosis}
TEKGRALAIAVMRKHRLAERLLVDVIGLPWEEVHAEACRWEHVMSEDVERRLVKVLNNPTTSPFG
NPIPGLDELGVGPEP
>d1gpja1 a.151.1.1 (A:303-404) Glutamyl tRNA-reductase dimerization
domain {Archaeon Methanopyrus kandleri}
EIPKVEKLIEEELSTVEEELEKLKERRLVADVAKSLHEIKDRELERALRRLKTGDPENVLQDFAE
AYTKRLINVLTSAIMELPDEYRRAASRALRRASELNG
>d1ngr__ a.77.1.1 (-) p75 low affinity neurotrophin receptor {Rat
(Rattus norvegicus)}
GNLYSSLPLTKREEVEKLLNGDTWRHLAGELGYQPEHIDSFTHEACPVRALLASWGAQDSATLDA
LLAALRRIQRADIVESLCSE
>d1ddf__ a.77.1.1 (-) Fas {Human (Homo sapiens)}
METVAINLSDVDLSKYITTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNW
HQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLVLEHHHHHH
>d1a1w__ a.77.1.1 (-) FADD (Mort1) {Human (Homo sapiens)}
MDPFLVLLHSVSSSLSSSELTELKYLCLGRVGKRKLERVQSGLDLFSMLLEQNDLEPGHTELLRE
LLASLRRHDLLRRVDDFE
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>d1e41a_ a.77.1.1 (A:) FADD (Mort1) {Human (Homo sapiens)}
GSHMGEEDLCAAFNVICDNVGKDWRRLARQLKVSDTKIDSIEDRYPRNLTERVRESLRIWKNTEK
ENATVAHLVGALRSCQMNLVADLVQEVQQARDLQNRSGA
>d1fada_ a.77.1.1 (A:) FADD (Mort1) {Mouse (Mus musculus)}
AAPPGEAYLQVAFDIVCDNVGRDWKRLARELKVSEAKMDGIEEKYPRSLSERVRESLKVWKNAEK
KNASVAGLVKALRTCRLNLVADLVEEAQES
>d3crd__ a.77.1.1 (-) Raidd CARD domain {Human (Homo sapiens)}
MEARDKQVLRSLRLELGAEVLVEGLVLQYLYQEGILTENHIQEINAQTTGLRKTMLLLDILPSRG
PKAFDTFLDSLQEFPWVREKLKKAREEAMTDLPAG
>d1cy5a_ a.77.1.1 (A:) Apoptotic protease activating factor 1, APAF-1
{Human (Homo sapiens)}
MDAKARNCLLQHREALEKDIKTSYIMDHMISDGFLTISEEEKVRNEPTQQQRAAMLIKMILKKDN
DSYVSFYNALLHEGYKDLAALLHDGIPV
>d3ygsp_ a.77.1.1 (P:) Procaspase 9 prodomain {Human (Homo sapiens)}
SMDEADRRLLRRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQRAGSGSRRDQARQLIIDLET
RGSQALPLFISCLEDTGQDMLASFLRTNRQAG
>d1dgna_ a.77.1.1 (A:) Iceberg {Human (Homo sapiens)}
ADQLLRKKRRIFIHSVGAGTINALLDCLLEDEVISQEDMNKVRDENDTVMDKARVLIDLVTGKGP
KSCCKFIKHLCEEDPQLASKMGLH
>d1d2za_ a.77.1.1 (A:) Pelle death domain {Drosophila melanogaster}
LDNTMAIRLLPLPVRAQLCAHLDALDVWQQLATAVKLYPDQVEQISSQKQRGRSASNEFLNIWGG
QYNHTVQTLFALFKKLKLHNAMRLIKDYVSEDLHKYI
>d1d2zb_ a.77.1.1 (B:) Tube death domain {Drosophila melanogaster}
LSSKYSRNTELRRVEDNDIYRLAKILDENSCWRKLMSIIPKGMDVQACSGAGCLNFPAEIKKGFK
YTAQDVFQIDEAANRLPPDQSKSQMMIDEWKTSGKLNERPTVGVLLQLLVQAELFSAADFVALDF
LNESTPARPVDGPGALISLE
>d1hw1a2 a.78.1.1 (A:79-230) Fatty acid responsive transcription
factor FadR, C-terminal domain {Escherichia coli}
GLNILETLARLDHESVPQLIDNLLSVRTNISTIFIRTAFRQHPDKAQEVLATANEVADHADAFAE
LDYNIFRGLAFASGNPIYGLILNGMKGLYTRIGRHYFANPEARSLALGFYHKLSALCSEGAHDQV
YETVRRYGHESGEIWHRMQKNL
>d1eyva_ a.79.1.1 (A:) Antitermination factor NusB {Mycobacterium
tuberculosis}
GRHQARKRAVALLFEAEVRGISAAEVVDTRAALAEAKPDIARLHPYTAAVARGVSEHAAHIDDLI
TAHLRGWTLDRLPAVDRAILRVSVWELLHAADVPEPVVVDEAVQLAKELSTDDSPGFVNGVLGQV
M
>d1ey1a_ a.79.1.1 (A:) Antitermination factor NusB {Escherichia coli}
MKPAARRRARECAVQALYSWQLSQNDIADVEYQFLAEQDVKDVDVLYFRELLAGVATNTAYLDGL
MKPYLSRLLEELGQVEKAVLRIALYELSKRSDVPYKVAINEAIELAKSFGAEDSHKFVNGVLDKA
APVIRPNKK
>d1b79a_ a.81.1.1 (A:) N-terminal domain of DnaB helicase {Escherichia
coli}
PPHSIEAEQSVLGGLMLDNERWDDVAERVVADDFYTRPHRHIFTEMARLQESGSPIDLITLAESL
ERQGQLDSVGGFAYLAELSKNTPSAANISAYADIVRE
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>d1jwea_ a.81.1.1 (A:) N-terminal domain of DnaB helicase {Escherichia coli}
MKVPPHSIEAEQSVLGGLMLDNERWDDVAERVVADDFYTRPHRHIFTEMARLQESGSPIDLITLA
ESLERQGQLDSVGGFAYLAELSKNTPSAANISAYADIVRERAVVREMIS
>d1qc7a_ a.82.1.1 (A:) FliG C-terminal domain {Thermotoga maritima}
MFVFEDILKLDDRSIQLVLREVDTRDLALALKGASDELKEKIFKNMSKRAAALLKDELEYMGPVR
LKDVEEAQQKIINIIRRLEEAGEIVIARGGGEELIM
>d1qc7b_ a.82.1.1 (B:) FliG C-terminal domain {Thermotoga maritima}
MFVFEDILKLDDRSIQLVLREVDTRDLALALKGASDELKEKIFKNMSKRAAALLKDELEYMGPVR
LKDVEEAQQKIINIIRRLEEAGEIV
>d1crka1 a.83.1.1 (A:1-98) Creatine kinase, N-terminal domain {Chicken (Gallus gallus), mitochondria}
TVHEKRKLFPPSADYPDLRKHNNCMAECLTPAIYAKLRDKLTPNGYSLDQCIQTGVDNPGHPFIK
TVGMVAGDEESYEVFAEIFDPVIKARHNGYDPR
>d1qh4a1 a.83.1.1 (A:2-102) Creatine kinase, N-terminal domain {Chicken (Gallus gallus), brain-type}
PFSNSHNLLKMKYSVDDEYPDLSVHNNHMAKVLTLDLYKKLRDRQTSSGFTLDDVIQTGVDNPGH
PFIMTVGCVAGDEESYEVFKELFDPVIEDRHGGYKP
>d1qk1a1 a.83.1.1 (A:1-102) Creatine kinase, N-terminal domain {Human (Homo sapiens), mitochondria}
AASERRRLYPPSAEYPDLRKHNNCMASHLTPAVYARLCDKTTPTGWTLDQCIQTGVDNPGHPFIK
TVGMVAGDEETYEVFADLFDPVIQERHNGYDPRTMKH
>d2crka1 a.83.1.1 (A:8-102) Creatine kinase, N-terminal domain {Rabbit (Oryctolagus cuniculus)}
NKYKLNYKSEEEYPDLSKHNNHMAKVLTPDLYKKLRDKETPSGFTLDDVIQTGVDNPGHPFIMTV
GCVAGDEESYTVFKDLFDPIIQDRHGGFKP
>d1g0wa1 a.83.1.1 (A:2-102) Creatine kinase, N-terminal domain {Cow (Bos taurus), retinal isoform}
PFSNSHNTLKLRFPAEDEFPDLSGHNNHMAKVLTPELYAELRAKSTPSGFTVDDVIQTGVDNPGH
PYIMTVGCVAGDEESYDVFKELFDPIIEDRHGGYKP
>d1bg0_1 a.83.1.1 (2-95) Arginine kinase {Horseshoe crab (Limulus polyphemus)}
VDQATLDKLEAGFKKLQEASDCKSLLKKHLTKDVFDSIKNKKTGMGATLLDVIQSGVENLDSGVG
IYAPDAESYRTFGPLFDPIIDDYHGGFKL
>d1al01_ a.84.1.1 (1:) Scaffolding protein gpD of bacteriophage procapsid {Bacteriophage phi-X174}
EQSVRFQTALASIKLIQASAVLDLTEDDFDFLTSNKVWIATDRSRARRCVEACVYGTLDFVGYPR
FPAPVEFIAAVIAYYVHPVNIQTACLIMEGAEFTENIINGVERPVKAAELFAFTLRVRAGNTDVL
TDAEENVRQKLRA
>d1ll1_1 a.85.1.1 (1-109) Hemocyanin, N-terminal domain {Horseshoe crab (Limulus polyphemus)}
TLHDKQIRVCHLFEQLSSATVIRLKNVGKLQPGAIFSCFHPDHLEEARHLYEVFWEAGDFNDFIE
IAKEARTFVNEGLFAFAAEVAVLHRDDCKGLYVP
>d1lla_1 a.85.1.1 (2-109) Hemocyanin, N-terminal domain {Horseshoe

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crab (Limulus polyphemus)}
LHDKQIRICHLFEQLSSATVIGDGDKHKHSDRLKNVGKLQPGAIFSCFHPDHLEEARHLYEVFWE
AGDFNDFIEIAKEARTFVNEGLFAFAAEVAVLHRDDCKGLYVP
>d1hc2_1 a.85.1.1 (5-135) Hemocyanin, N-terminal domain {Spiny
lobster (Panulirus interruptus)}
TGNAQKQQDINHLLDKIYEPTKYPDLKDIAENFNPLGDTSIYNDHGAAVETLMKELNDHRLLEQR
HWYSLFNTRQRKEALMLFAVLNQCKEWYCFRSNAAYFRERMNEGEFVYALYVSVIHSKLGDGIVL
P
>d1lla_2 a.86.1.1 (110-379) Hemocyanin {Horseshoe crab (Limulus
polyphemus)}
PVQEIFPDKFIPSAAINEAFKKAHVRPEFDESPILVDVQDTGNILDPEYRLAYYREDVGINAHHW
HWHLVYPSTWNPKYFGKKKDRKGELFYYMHQQMCARYDCERLSNGMHRMLPFNNFDEPLAGYAPH
LTHVASGKYYSPRPDGLKLRDLGDIEISEMVRMRERILDSIHLGYVISEDGSHKTLDELHGTDIL
GALVESSYESVNHEYYGNLHNWGHVTMARIHDPDGRFHEEPGVMSDTSTSLRDPIFYNWHRFIDN
IFHEYKNTLK
>d1hc2_2 a.86.1.1 (136-398) Hemocyanin {Spiny lobster (Panulirus
interruptus)}
PLYQITPHMFTNSEVIDKAYSAKMTQKPGTFNVSFTGTKKNREQRVAYFGEDIGMNIHHVTWHMD
FPFWWEDSYGYHLDRKGELFFWVHHQLTARFDFERLSNWLDPVDELHWDRIIREGFAPLTSYKYG
GEFPVRPDNIHFEDVDGVAHVHDLEITESRIHEAIDHGYITDSDGHTIDIRQPKGIELLGDIIES
SKYSSNVQYYGSLHNTAHVMLGRQGDPHGKFNLPPGVMEHFETATRDPSFFRLHKYMDNIFKKHT
DSF
>d1js8a1 a.86.1.1 (A:2503-2791) Functional unit from octopus
hemocyanin {Giant octopus (Octopus dofleini)}
AIIRKNVNSLTPSDIKELRDAMAKVQADTSDNGYQKIASYHGIPLSCHYENGTAYACCQHGMVTF
PNWHRLLTKQMEDALVAKGSHVGIPYWDWTTTFANLPVLVTEEKDNSFHHAHIDVANTDTTRSPR
AQLFDDPDKGDKSFFYRQIALALEQTDFCDFEIQFEIGHNAIHSWVGGSSPYGMSTLHYTSYDPL
FYLHHSNTDRIWSVWQALQKYRGLPYNTANCEINKLVKPLKPFNLDTNPNAVTKAHSTGATSFDY
HKLGYDYDNLNFHGMTIPELEEHLKEIQH
>d1bt3a_ a.86.1.2 (A:) Catechol oxidase {Sweet potato (Ipomoea
batatas)}
APIQAPEISKCVVPPADLPPGAVVDNCCPPVASNIVDYKLPAVTTMKVRPAAHTMDKDAIAKFAK
AVELMKALPADDPRNFYQQALVHCAYCNGGYDQVNFPDQEIQVHNSWLFFPFHRWYLYFYERILG
KLIGDPSFGLPFWNWDNPGGMVLPDFLNDSTSSLYDSNRNQSHLPPVVVDLGYNGADTDVTDQQR
ITDNLALMYKQMVTNAGTAELFLGKAYRAGDAPSPGAGSIETSPHIPIHRWVGDPRNTNNEDMGN
FYSAGRDIAFYCHHSNVDRMWTIWQQLAGKPRKRDYTDSDWLNATFLFYDENGQAVKVRIGDSLD
NQKMGYKYAKTPLPWL
>d1dbha1 a.87.1.1 (A:198-404) Son of sevenless-1 (sos-1) {Human (Homo
sapiens)}
EQTYYDLVKAFMAEIRQYIRELNLIIKVFREPFVSNSKLFSANDVENIFSRIVDIHELSVKLLGH
IEDTVEMTDEGSPHPLVGSCFEDLAEELAFDPYESYARDILRPGFHDRFLSQLSKPGAALYLQSI
GEGFKEAVQYVLPRLLLAPVYHCLHYFELLKQLEEKSEDQEDKECLKQAITALLNVQSGMEKICS
KSLAKRRLSESA
>d1by1a_ a.87.1.1 (A:) beta-pix {Human (Homo sapiens)}
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MKGFDTTAINKSYYNVVLQNILETENEYSKELQTVLSTYLRPLQTSEKLSSANISYLMGNLEEIC
SFQQMLVQSLEECTKLPEAQQRVGGCFLNLMPQMKTLYLTYCANHPSAVNVLTEHSEELGEFMET
KGASSPGILVLTTGLSKPFMRLDKYPTLLKELERHMEDYHTDRQDIQKSMAAFKNLSAQCQEVRK
RKELELQILTEAIR
>d1f5xa_ a.87.1.1 (A:) RhoGEF Vav {Mouse (Mus musculus)}
MKGDEIYEDLMRLESVPTPPKMTEYDKRCCCLREIQQTEEKYTDTLGSIQQHFMKPLQRFLKPQD
METIFVNIEELFSVHTHFLKELKDALAGPGATTLYQVFIKYKERFLVYGRYCSQVESASKHLDQV
ATAREDVQMKLEECSQRANNGRFTLRDLLMVPMQRVLKYHLLLQELVKHTQDATEKENLRLALDA
MRDLAQCVNEVKR
>d1foea1 a.87.1.1 (A:1034-1239) GEF of TIAM1 (T-Lymphoma invasion and metastasis indusing protein 1) {Mouse (Mus musculus)}
QLSDADKLRKVICELLETERTYVKDLNCLMERYLKPLQKETFLTQDELDVLFGNLTEMVEFQVEF
LKTLEDGVRLVPDLEKLEKVDQFKKVLFSLGGSFLYYADRFKLYSAFCASHTKVPKVLVKAKTDT
AFKAFLDAQNPRQQHSSTLESYLIKPIQRVLKYPLLLRELFALTDAESEEHYHLDVAIKTMNKVA
SHINEMQKIHE
>d1boua_ a.88.1.1 (A:) LigA subunit of an aromatic-ring-opening dioxygenase LigAB {Sphingomonas paucimobilis, formerly Pseudomonas paucimobilis}
IDVHAYLAEFDDIPGTRVFTAQRARKGYNLNQFAMSLMKAENRERFKADESAYLDEWNLTPAAKA
AVLARDYNAMIDEGGNVYFLSKLFSTDGKSFQFAAGSMTGMTQEEYAQMMIDGGRSPAGVRSIKG
GY
>d1hbna1 a.89.1.1 (A:270-549) Alpha chain {Archaeon Methanobacterium thermoautotrophicum}
RRARGENEPGGVPFGYLADICQSSRVNYEDPVRVSLDVVATGAMLYDQIWLGSYMSGGVGFTQYA
TAAYTDNILDDFTYFGKEYVEDKYGLCEAPNNMDTVLDVATEVTFYGLEQYEEYPALLEDQFGGS
QRAAVVAAAAGCSTAFATGNAQTGLSGWYLSMYLHKEQHSRLGFYGYDLQDQCGASNVFSIRGDE
GLPLELRGPNYPNYAMNVGHQGEYAGISQAPHAARGDAFVFNPLVKIAFADDNLVFDFTNVRGEF
AKGALREFEPAGERALITPA
>d1e6va1 a.89.1.1 (A:273-552) Alpha chain {Archaeon Methanopyrus kandleri}
RRARGENEPGGVPFGVLADCVQTMRKYPDDPAKVALEVIAAGAMLYDQIWLGSYMSGGVGFTQYA
TAVYPDNILDDYVYYGLEYVEDKYGIAEAEPSMDVVKDVATEVTLYGLEQYERYPAAMETHFGGS
QRAAVCAAAAGCSTAFATGHAQAGLNGWYLSQILHKEGQGRLGFYGYALQDQCGAANSLSVRSDE
GLPLELRGPNYPNYAMNVGHLGEYAGIVQAAHAARGDAFCVHPVIKVAFADENLVFDFTEPRKEF
AKGALREFEPAGERDLIVPA
>d1e6ya1 a.89.1.1 (A:1284-1569) Alpha chain {Archaeon Methanosarcina barkeri}
RRARGPNEPGGLSFGHLSDIVQTSRVSEDPAKIALEVVGAGCMLYDQIWLGSYMSGGVGFTQYAT
AAYTDDILDNNTYYDVDYINDKYNGAATVGKDNKVKASLEVVKDIATESTLYGIETYEKFPTALE
DHFGGSQRATVLAAAAGVACSLATGNANAGLSGWYLSMYLHKEAWGRLGFFGFDLQDQCGATNVL
SYQGDEGLPDELRGPNYPNYAMNVGHQGGYAGIAQAAHSGRGDAFTVNPLLKVCFADDLLPFNFA
EPRREFGRGAIREFVPAGERSLVIPA
>d1hbnb1 a.89.1.1 (B:189-443) Beta chain {Archaeon Methanobacterium thermoautotrophicum}

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GYALRNIMVNHVVAATLKNTLQAAALSTILEQTAMFEMGDAVGAFERMHLLGLAYQGMNADNLVF
DLVKANGKEGTVGSVIADLVERALEDGVIKVEKELTDYKVYGTDDLAMWNAYAAAGLMAATMVNQ
GAARAAQGVSSTLLYYNDLIEFETGLPSVDFGKVEGTAVGFSFFSHSIYGGGGPGIFNGNHIVTR
HSKGFAIPCVAAAMALDAGTQMFSPEATSGLIKEVFSQVDEFREPLKYVVEAAAEIKNEI
>d1e6vb1 a.89.1.1 (B:190-442) Beta chain {Archaeon Methanopyrus kandleri}
GYALRNIMVNHIVAATRKNTMQAVCLAATLQQTAMFEMGDALGPFERLHLLGYAYQGLNADNMVY
DIVKKHGKEGTVGTVVREVVERALEDGVIEVKEELPSFKVYKANDMDLWNAYAAAGLVAAVMVNQ
GAARAAQGVSATILYYNDLLEYETGLPGVDFGRAEGTAVGFSFFSHSIYGGGGPGIFHGNHIVTR
HSKGFAIPPVAAAMALDAGTQMFSPEVTSKLIGDVFGEIDEFREPMKYITEAAAEEAK
>d1e6yb1 a.89.1.1 (B:2186-2433) Beta chain {Archaeon Methanosarcina barkeri}
GFSLRNIMANHVAAISNRNAMNASALSSIYEQSGIFEMGGAVGMFERHQLLGLAYQGLNANNLLY
DIVKENGKDGTIGTVIESVVRRAIEAGIISVDKTAPSGYNFYKANDVPKWNACAAVGTLAATLVN
CGAGRAAQNVSSTLLYFNDILEKETGLPGCDYGKVEGTAVGFSFFSHSIYGGGGPGVFNGNHVVT
RHSRGFAIPCVCAAVALDAGTQMFSIESTSGLIGDVFGAIPEFREPIKAVAGV
>d1bgf__ a.90.1.1 (-) Transcription factor STAT-4 N-domain {Mouse (Mus musculus)}
GGSQWNQVQQLEIKFLEQVDQFYDDNFPMEIRHLLAQWIETQDWEVASNNETMATILLQNLLIQL
DEQLGRVSKEKNLLLIHNLKRIRKVLQGKFHGNPMHVAVVISNCLREERRILAAANMPI
>d1agre_ a.91.1.1 (E:) Regulator of G-protein signalling 4, RGS4 {Rat (Rattus norvegicus)}
VSQEEVKKWAESLENLINHECGLAAFKAFLKSEYSEENIDFWISCEEYKKIKSPSKLSPKAKKIY
NEFISVQATKEVNLDSCTREETSRNMLEPTITCFDEAQKKIFNLMEKDSYRRFLKSRFYLDLT
>d1fqia_ a.91.1.1 (A:) RGS9, RGS domain {Cow (Bos taurus)}
KLVDIPTKMRVERWAFNFSELIRDPKGRQSFQHFLRKEFSGENLGFWEACEDLKYGDQSKVKEKA
EEIYKLFLAPGARRWINIDGKTMDITVKGLKHPHRYVLDAAQTHIYMLMKKDSYARYLKSPIYKE
MLAKAIEP
>d1cmza_ a.91.1.1 (A:) Galpha interacting protein, GaIP {Human (Homo sapiens)}
PSPEEVQSWAQSFDKLMHSPAGRSVFRAFLRTEYSEENMLFWLACEELKAEANQHVVDEKARLIY
EDYVSILSPKEVSLDSRVREGINKKMQEPSAHTFDDAQLQIYTLMHRDSYPRFLSSPTYRALL
>d1dk8a_ a.91.1.1 (A:) Axin RGS-homologous domain {Human (Homo sapiens)}
GSASPTPPYLKWAESLHSLLDDQDGISLFRTFLKQEGCADLLDFWFACTGFRKLEPCDSNEEKRL
KLARAIYRKYILDNNGIVSRQTKPATKSFIKGCIMKQLIDPAMFDQAQTEIQATMEENTYPSFLK
SDIYLEYTRTGSESPKV
>d1emua_ a.91.1.1 (A:) Axin RGS-homologous domain {Human (Homo sapiens)}
PPYLKWAESLHSLLDDQDGISLFRTFLKQEGCADLLDFWFACTGFRKLEPCDSNEEKRLKLARAI
YRKYILDNNGIVSRQTKPATKSFIKGCIMKQLIDPAMFDQAQTEIQATMEENTYPSFLKSDIYLE
YT
>d1iapa_ a.91.1.1 (A:) p115RhoGEF {Human (Homo sapiens)}
SQFQSLEQVKRRPAHLMALLQHVALQFEPGPLLCCLHADMLGSLGPKEAKKAFLDFYHSFLEKTA
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VLRVPVPPNVAFELDRTRADLISEDVQRRFVQEVVQSQQVAVGRQLEDFRSKRLMGMTPWEQELA
QLEAWVGRDRASYEARERHVAERLLMHLEEMQHTISTDEEKSAAVVNAIGLYMRHLGVRT
>d1htjf_ a.91.1.1 (F:) Pdz-RhoGEF RGS-like domain {Human (Homo
sapiens)}
ESDIIFQDLEKLKSRPAHLGVFLRYIFSQADPSPLLFYLCAEVYQQASPKDSRSLGKDIWNIFLE
KNAPLRVKIPEMLQAEIDSRLRNSEDARGVLCEAQEAAMPEIQEQIHDYRTKRTLGLGSLYGEND
LLDLDGDPLRERQVAEKQLAALGDILSAYAADRSAPMDFALNTYMSHAGIRL
>d1a9xa1 a.92.1.1 (A:403-555) Carbamoyl phosphate synthetase, large
subunit connection domain {Escherichia coli}
EVGATGFDPKVSLDDPEALTKIRRELKDAGADRIWYIADAFRAGLSVDGVFNLTNIDRWFLVQIE
ELVRLEEKVAEVGITGLNADFLRQLKRKGFADARLAKLAGVREAEIRKLRDQYDLHPVYKRVDTC
AAEFATDTAYMYSTYEEECEANP
>d1b80a_ a.93.1.1 (A:) Lignin peroxidase {White rot basidiomycete
(Phanerochaete chrysosporium)}
VIEKRATCSNGKTVGDASCCAWFDVLDDIQQNLFHGGQCGAEAHESIRLVFHDSIAISPAMEAQG
KFGGGGADGSIMIFDDIETAFHPNIGLDEIVKLQKPFVQKHGVTPGDFIAFAGAVALSNCPGAPQ
MNFFTGRAPATQPAPDGLVPEPFHTVDQIINRVNDAGEFDELELVWMLSAHSVAAVNDVDPTVQG
LPFDSTPGIFDSQFFVETQLRGTAFPGSGGNQGEVESPLPGEIRIQSDHTIARDSRTACEWQSFV
NNQSKLVDDFQFIFLALTQLGQDPNAMTDCSDVIPQSKPIPGNLPFSFFPAGKTIKDVEQACAET
PFPTLTTLPGPETSVQRIPPPPGA
>d1llp__ a.93.1.1 (-) Lignin peroxidase {White rot basidiomycete
(Phanerochaete chrysosporium)}
ATCANGKTVGDASCCAWFDVLDDIQANMFHGGQCGAEAHESIRLVFHDSIAISPAMEAKGKFGGG
GADGSIMIFDTIETAFHPNIGLDEVVAMQKPFVQKHGVTPGDFIAFAGAVALSNCPGAPQMNFFT
GRKPATQPAPDGLVPEPFHTVDQIIARVNDAGEFDELELVWMLSAHSVAAVNDVDPTVQGLPFDS
TPGIFDSQFFVETQFRGTLFPGSGGNQGEVESGMAGEIRIQTDHTLARDSRTACEWQSFVGNQSK
LVDDFQFIFLALTQLGQDPNAMTDCSDVIPLSKPIPGNGPFSFFPPGKSHSDIEQACAETPFPSL
VTLPGPATSVARIPPHKA
>d1qpaa_ a.93.1.1 (A:) Lignin peroxidase {White rot basidiomycete
(Phanerochaete chrysosporium)}
VACPDGVHTASNAACCAWFPVLDDIQQNLFHGGQCGAEAHEALRMVFHDSIAISPKLQSQGKFGG
GGADGSIITFSSIETTYHPNIGLDEVVAIQKPFIAKHGVTPGDFIAFAGAVGVSNCPGAPQMQFF
LGRPEATQAAPDGLVPEPFHTIDQVLARMLDAGGFDEIETVWLLSAHSIAAANDVDPTISGLPFD
STPGQFDSQFFVETQLRGTAFPGKTGIQGTVMSPLKGEMRLQTDHLFARDSRTACEWQSFVNNQT
KLQEDFQFIFTALSTLGHDMNAMIDCSEVIPAPKPVNFGPSFFPAGKTHADIEQACASTPFPTLI
TAPGPSASVARIPPPPSPN
>d1aru__ a.93.1.1 (-) Peroxidase {Arthromyces ramosus}
SVTCPGGQSTSNSQCCVWFDVLDDLQTNFYQGSKCESPVRKILRIVFHDAIGFSPALTAAGQFGG
GGADGSIIAHSNIELAFPANGGLTDTIEALRAVGINHGVSFGDLIQFATAVGMSNCPGSPRLEFL
TGRSNSSQPSPPSLIPGPGNTVTAILDRMGDAGFSPDEVVDLLAAHSLASQEGLNSAIFRSPLDS
TPQVFDTQFYIETLLKGTTQPGPSLGFAEELSPFPGEFRMRSDALLARDSRTACRWQSMTSSNEV
MGQRYRAAMAKMSVLGFDRNALTDCSDVIPSAVSNNAAPVIPGGLTVDDIEVSCPSEPFPEIATA
SGPLPSLAPAP
>d1jdra_ a.93.1.1 (A:) Cytochrome c peroxidase, CCP {Baker's yeast
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(Saccharomyces cerevisiae)}
TTPLVHVASVEKGRSYEDFQKVYNAIALKLREDDEYDNYIGYGPVLVRLAWHTSGTWDKHDNTGG
SYGGTYRFKKEFNDPSNAGLQNGFKFLEPIHKEFPWISSGDLFSLGGVTAVQEMQGPKIPWRCGR
VDTPEDTTPDNGRLPDADKDADYVRTFFQRLNMNDREVVALMGAHTLGKTHLKNSGYEGPWTANN
NVFDNSFYLNLLNEDWKLEKNDANNEQWDSKSGYMMLPTDYSLIQDPKYLSIVKEYANDQDKFFK
DFSKAFEKLLENGITFPKDAPSPFIFKTLEEQGL
>d1mn2__ a.93.1.1 (-) Manganese peroxidase {Basidomycetos fungus
(Phanerochaete chrysosporium)}
AVCPDGTRVSHAACCAFIPLAQDLQETIFQNECGQDAHEVIRLTFHDAIAISRSQGPKAGGGADG
SMLLFPTVEPNFSANNGIDDSVNNLIPFMQKHNTISAADLVQFAGAVALSNCPGAPRLEFLAGRP
NKTIAAVDGLIPEPQDSVTKILQRFEDAGGFTPFEVVSLLASHSVARANKVDQTIDAAPFDSTPF
TFDTQVFLEVLLKGVGFPGSANNTGEVASPLPLGSGSDTGEMRLQSDFALAHDPRTACIWQGFVN
EQAFMAASFRAAMSKLAVLGHNRNSLIDCSDVVPVPKPATGQPAMFPASTGPQDLELSCPSERFP
TLTTQPGASQSLIAHCPDGSMSCPGVQFNGPA
>d1apxa_ a.93.1.1 (A:) Ascorbate peroxidase {Pea (Pisum sativum)}
GKSYPTVSPDYQKAIEKAKRKLRGFIAEKKCAPLILRLAWHSAGTFDSKTKTGGPFGTIKHQAEL
AHGANNGLDIAVRLLEPIKEQFPIVSYADFYQLAGVVAVEITGGPEVPFHPGREDKPEPPPEGRL
PDATKGSDHLRDVFGKAMGLSDQDIVALSGGHTIGAAHKERSGFEGPWTSNPLIFDNSYFTELLT
GEKDGLLQLPSDKALLTDSVFRPLVEKYAADEDVFFADYAEAHLKLSELGFAEA
>d7atja_ a.93.1.1 (A:) Plant peroxidase {Horseradish (Armoracia
rusticana)}
QLTPTFYDNSCPNVSNIVRDTIVNELRSDPRIAASILRLHFHDCFVNGCDASILLDNTTSFRTEK
DAFGNANSARGFPVIDRMKAAVESACPRTVSCADLLTIAAQQSVTLAGGPSWRVPLGRRDSLQAF
LDLANANLPAPFFTLPQLKDSFRNVGLNRSSDLVALSGGHTFGKNQCRFIMDRLYNFSNTGLPDP
TLNTTYLQTLRGLCPLNGNLSALVDFDLRTPTIFDNKYYVNLEEQKGLIQSDQELFSSPNATDTI
PLVRSFANSTQTFFNAFVEAMDRMGNITPLTGTQGQIRLNCRVVN
>d1scha_ a.93.1.1 (A:) Plant peroxidase {Peanut (Arachis hypogaea)}
ELSSNFYATKCPNALSTIKSAVNSAVAKEARMGASLLRLHFHDCFVQGCDASVLLDDTSNFTGEK
TAGPNANSIRGFEVIDTIKSQVESLCPGVVSCADILAVAARDSVVALGGASWNVLLGRRDSTTAS
LSSANSDLPAPFFNLSGLISAFSNKGFTTKELVTLSGAHTIGQAQCTAFRTRIYNESNIDPTYAK
SLQANCPSVGGDTNLSPFDVTTPNKFDNAYYINLRNKKGLLHSDQQLFNGVSTDSQVTAYSNNAA
TFNTDFGNAMIKMGNLSPLTGTSGQIRTNCRKTN
>d1fhfa_ a.93.1.1 (A:) Plant peroxidase {Soybean (Glycine max)}
QLTPTFYRETCPNLFPIVFGVIFDASFTDPRIGASLMRLHFHDCFVQGCDGSVLLNNTDTIESEQ
DALPNINSIRGLDVVNDIKTAVENSCPDTVSCADILAIAAEIASVLGGGPGWPVPLGRRDSLTAN
RTLANQNLPAPFFNLTQLKASFAVQGLNTLDLVTLSGGHTFGRARCSTFINRLYNFSNTGNPDPT
LNTTYLEVLRARCPQNATGDNLTNLDLSTPDQFDNRYYSNLLQLNGLLQSDQELFSTPGADTIPI
VNSFSSNQNTFFSNFRVSMIKMGNIGVLTGDEGEIRLQCNFVNG
>d1bgp__ a.93.1.1 (-) Plant peroxidase {Barley (Hordeum vulgare),
peroxidase 1}
AEPPVAPGLSFDFYWQTCPRAESIVREFVQEAVRKDIGLAAGLLRLHFHDCFVQGCDASVLLDGS
ATGPGEQQAPPNLTLRPSAFKAVNDIRDRLERECRGAVVSCSDILALAARDSVVVSGGPDYRVPL
GRRDSRSFASTQDVLSDLPGPSSNVQSLLALLGRLGLDATDLVTISGGHTIGLAHCSSFEDRLFP
RPDPTISPTFLSRLKRTCPAKGTDRRTVLDVRTPNVFDNKYYIDLVNREGLFVSDQDLFTNAITR
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PIVERFAQSQQDFFEQFGVSIGKMGQMRVRTSDQGEVRRNCSVRNPGPG
>d1qgja_ a.93.1.1 (A:) Plant peroxidase {Mouse-ear cress (Arabidopsis
thaliana), peroxidase N}
QLSPDIYAKSCPNLVQIVRKQVAIALKAEIRMAASLIRLHFHDCFVNGCDASLLLDGADSEKLAI
PNINSARGFEVIDTIKAAVENACPGVVSCADILTLAARDSVVLSGGPGWRVALGRKDGLVANQNS
ANNLPSPFEPLDAIIAKFVAVNLNITDVVALSGAHTFGQAKCAVFSNRLFNFTGAGNPDATLETS
LLSNLQTVCPLGGNSNITAPLDRSTTDTFDNNYFKNLLEGKGLLSSDQILFSSDLAVNTTKKLVE
AYSRSQSLFFRDFTCAMIRMGNISNGASGEVRTNCRVINN
>d1pa2a_ a.93.1.1 (A:) Plant peroxidase {Mouse-ear cress (Arabidopsis
thaliana), peroxidase A2}
MQLNATFYSGTCPNASAIVRSTIQQALQSDTRIGASLIRLHFHDCFVNGCDASILLDDTGSIQSE
KNAGPNVNSARGFNVVDNIKTALENACPGVVSCSDVLALASEASVSLAGGPSWTVLLGRRDSLTA
NLAGANSSIPSPIESLSNITFKFSAVGLNTNDLVALSGAHTFGRARCGVFNNRLFNFSGTGNPDP
TLNSTLLSTLQQLCPQNGSASTITNLDLSTPDAFDNNYFANLQSNDGLLQSDQELFSTTGSSTIA
IVTSFASNQTLFFQAFAQSMINMGNISPLTGSNGEIRLDCKKVNGS
>g1cxp.1 a.93.1.2 (A:,C:) Myeloperoxidase {Human (Homo sapiens)}
CPEQDKYRTITGMCNNRRSPTLGASNRAFVRWLPAEYEDGFSLPYGWTPGVKRNGFPVALARAVS
NEIVRFPTDQLTPDQERSLMFMQWGQLLDHDLDFTPEPAXVNCETSCVQQPPCFPLKIPPNDPRI
KNQADCIPFFRSCPACPGSNITIRNQINALTSFVDASMVYGSEEPLARNLRNMSNQLGLLAVNQR
FQDNGRALLPFDNLHDDPCLLTNRSARIPCFLAGDTRSSEMPELTSMHTLLLREHNRLATELKSL
NPRWDGERLYQEARKIVGAMVQIITYRDYLPLVLGPTAMRKYLPTYRSYNDSVDPRIANVFTNAF
RYGHTLIQPFMFRLDNRYQPMEPNPRVPLSRVFFASWRVVLEGGIDPILRGLMATPAKLNRQNQI
AVDEIRERLFEQVMRIGLDLPALNMQRSRDHGLPGYNAWRRFCGLPQPETVGQLGTVLRNLKLAR
KLMEQYGTPNNIDIWMGGVSEPLKRKGRVGPLLACIIGTQFRKLRDGDRFWWENEGVFSMQQRQA
LAQISLPRIICDNTGITTVSKNNIFMSNSYPRDFVNCSTLPALNLASWREA
>d1eqga1 a.93.1.2 (A:74-583) Prostaglandin H2 synthase {Sheep (Ovis
aries)}
IWTWLRTTLRPSPSFIHFLLTHGRWLWDFVNATFIRDTLMRLVLTVRSNLIPSPPTYNIAHDYIS
WESFSNVSYYTRILPSVPRDCPTPMGTKGKKQLPDAEFLSRRFLLRRKFIPDPQGTNLMFAFFAQ
HFTHQFFKTSGKMGPGFTKALGHGVDLGHIYGDNLERQYQLRLFKDGKLKYQMLNGEVYPPSVEE
APVLMHYPRGIPPQSQMAVGQEVFGLLPGLMLYATIWLREHNRVCDLLKAEHPTWGDEQLFQTAR
LILIGETIKIVIEEYVQQLSGYFLQLKFDPELLFGAQFQYRNRIAMEFNQLYHWHPLMPDSFRVG
PQDYSYEQFLFNTSMLVDYGVEALVDAFSRQPAGRIGGGRNIDHHILHVAVDVIKESRVLRLQPF
NEYRKRFGMKPYTSFQELTGEKEMAAELEELYGDIDALEFYPGLLLEKCHPNSIFGESMIEMGAP
FSLKGLLGNPICSPEYWKASTFGGEVGFNLVKTATLKKLVCLNTKTCPYVSFHVP
>d1cvua1 a.93.1.2 (A:74-583) Prostaglandin H2 synthase {Mouse (Mus
musculus)}
FLTRIKLLLKPTPNTVHYILTHFKGVWNIVNNIPFLRSLIMKYVLTSRSYLIDSPPTYNVHYGYK
SWEAFSNLSYYTRALPPVADDCPTPMGVKGNKELPDSKEVLEKVLLRREFIPDPQGSNMMFAFFA
QHFTAQFFKTDHKRGPGFTRGLGHGVDLNHIYGETLDRQHKLRLFKDGKLKYQVIGGEVYPPTVK
DTQVEMIYPPHIPENLQFAVGQEVFGLVPGLMMYATIWLREHQRVCDILKQEHPEWGDEQLFQTS
KLILIGETIKIVIEDYVQHLSGYHFKLKFDPELLFNQQFQYQNRIASEFNTLYHWHPLLPDTFNI
EDQEYSFKQFLYNNSILLEHGLTQFVESFTRQIAGRVAGGRNVPIAVQAVAKASIDQSREMKYQS
LNEYRKRFSLKPYTSFEELTGEKEMAAELKALYSDIDVMELYPALLVEKPRPDAIFGETMVELGA
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PFSLKGLMGNPICSPQYWKPSTFGGEVGFKIINTASIQSLICNNVKGCPFTSFNVQ
>d1jj2o_ a.94.1.1 (O:) Ribosomal protein L19 (L19e) {Archaeon
Haloarcula marismortui}
TDLSAQKRLAADVLDVGKNRVWFNPERQGDIADAITREDVRELVDEGAIQAKDKKGNSRGRARER
QKKRAKGHQKGAGSRKGKAGARQNSKEDWESRIRAQRTKLRELRDEGTLSSSQYRDLYDKAGGGE
FDSVADLERYIDA
>d1aa7a_ a.95.1.1 (A:) Influenza virus matrix protein M1 {Influenza
virus}
MSLLTEVETYVLSIIPSGPLKAEIAQRLEDVFAGKNTDLEVLMEWLKTRPILSPLTKGILGFVFT
LTVPSERGLQRRRFVQNALNGNGDPNNMDKAVKLYRKLKREITFHGAKEISLSYSAGALASCMGL
IYNRMGAVTTEVAFGLVCATCEQIADSQ
>d2abk__ a.96.1.1 (-) Endonuclease III {Escherichia coli}
MNKAKRLEILTRLRENNPHPTTELNFSSPFELLIAVLLSAQATDVSVNKATAKLYPVANTPAAML
ELGVEGVKTYIKTIGLYNSKAENIIKTCRILLEQHNGEVPEDRAALEALPGVGRKTANVVLNTAF
GWPTIAVDTHIFRVCNRTQFAPGKNVEQVEEKLLKVVPAEFKVDCHHWLILHGRYTCIARKPRCG
SCIIEDLCEYKEKVDI
>d1mun__ a.96.1.2 (-) Catalytic domain of MutY {Escherichia coli}
MQASQFSAQVLDWYDKYGRKTLPWQIDKTPYKVWLSEVMLQQTQVATVIPYFERFMARFPTVTDL
ANAPLDEVLHLWTGLGYYARARNLHKAAQQVATLHGGKFPETFEEVAALPGVGRSTAGAILSLSL
GKHFPILNGNVKRVLARCYAVSGWPGKKEVENKLWSLSEQVTPAVGVERFNQAMMDLGAMICTRS
KPKCSLCPLQNGCIAAANNSWALYPGKKPK
>d1keaa_ a.96.1.2 (A:) Thymine-DNA glycosylase {Archaeon
Methanobacterium thermoformicicum}
DATNKKRKVFVSTILTFWNTDRRDFPWRHTRDPYVILITEILLRRTTAGHVKKIYDKFFVKYKCF
EDILKTPKSEIAKDIKEIGLSNQRAEQLKELARVVINDYGGRVPRNRKAILDLPGVGKYTCAAVM
CLAFGKKAAMVDANFVRVINRYFGGSYENLNYNHKALWELAETLVPGGKCRDFNLGLMDFSAIIC
APRKPKCEKCGMSKLCSYYEKC
>d1mpga1 a.96.1.3 (A:100-282) 3-Methyladenine DNA glycosylase II
(gene alkA or aidA) {Escherichia coli}
AARPGLRLPGCVDAFEQGVRAILGQLVSVAMAAKLTARVAQLYGERLDDFPEYICFPTPQRLAAA
DPQALKALGMPLKRAEALIHLANAALEGTLPMTIPGDVEQAMKTLQTFPGIGRWTANYFALRGWQ
AKDVFLPDDYLIKQRFPGMTPAQIRRYAERWKPWRSYALLHIWYTEGWQPDEA
>d1ko9a1 a.96.1.3 (A:136-323) 8-oxoguanine glycosylase {Human (Homo
sapiens)}
DPIECLFSFICSSNNNIARITGMVERLCQAFGPRLIQLDDVTYHGFPSLQALAGPEVEAHLRKLG
LGYRARYVSASARAILEEQGGLAWLQQLRESSYEEAHKALCILPGVGTKVADCICLMALDKPQAV
PVDVHMWHIAQRDYSWHPTTSQAKGPSPQTNKELGNFFRSLWGPYAGWAQAVLFSADL
>d1gln_1 a.97.1.1 (306-468) Anticodon-binding (C-terminal) domain of
glutamyl-tRNA synthetase (GluRS) {Thermus thermophilus}
DLEKLRWMNGKYIREVLSLEEVAERVKPFLREAGLSWESEAYLRRAVELMRPRFDTLKEFPEKAR
YLFTEDYPVSEKAQRKLEEGLPLLKELYPRLRAQEEWTEAALEALLRGFAAEKGVKLGQVAQPLR
AALTGSLETPGLFEILALLGKERALRRLERALA
>d1rlr_1 a.98.1.1 (10-221) R1 subunit of ribonucleotide reductase,
N-terminal domain {Escherichia coli}
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RDGSTERINLDKIHRVLDWAAEGLHNVSISQVELRSHIQFYDGIKTSDIHETIIKAAADLISRDA
PDYQYLAARLAIFHLRKKAYGQFEPPALYDHVVKMVEMGKYDNHLLEDYTEEEFKQMDTFIDHDR
DMTFSYAAVKQLEGKYLVQNRVTGEIYESAQFLYILVAACLFSNYPRETRLQYVKRFYDAVSTFK
ISLPTPIMSGVRTPTRQ
>d1dnpa1 a.99.1.1 (A:201-469) FAD-binding (C-terminal) domain of DNA photolyase {Escherichia coli}
PVEEKAAIAQLRQFCQNGAGEYEQQRDFPAVEGTSRLSASLATGGLSPRQCLHRLLAEQPQALDG
GAGSVWLNELIWREFYRHLITYHPSLCKHRPFIAWTDRVQWQSNPAHLQAWQEGKTGYPIVDAAM
RQLNSTGWMHNRLRMITASFLVKDLLIDWREGERYFMSQLIDGDLAANNGGWQWAASTGTDAAPY
FRIFNPTTQGEKFDHEGEFIRQWLPELRDVPGKVVHEPWKWAQKAGVTLDYPQPIVEHKEARVQT
LAAYEAARK
>d1iqra1 a.99.1.1 (A:172-416) FAD-binding (C-terminal) domain of DNA photolyase {Thermus thermophilus}
LPLPEPGEEAALAGLRAFLEAKLPRYAEERDRLDGEGGSRLSPYFALGVLSPRLAAWEAERRGGE
GARKWVAELLWRDFSYHLLYHFPWMAERPLDPRFQAFPWQEDEALFQAWYEGKTGVPLVDAAMRE
LHATGFLSNRARMNAAQFAVKHLLLPWKRCEEAFRHLLLDGDRAVNLQGWQWAGGLGVDAAPYFR
VFNPVLQGERHDPEGRWLKRWAPEYPSYAPKDPVVDLEEARRRYLRLARD
>d1qnf_1 a.99.1.1 (205-475) FAD-binding (C-terminal) domain of DNA photolyase {Anacystis nidulans}
PVEPGETAAIARLQEFCDRAIADYDPQRNFPAEAGTSGLSPALKFGAIGIRQAWQAASAAHALSR
SDEARNSIRVWQQELAWREFYQHALYHFPSLADGPYRSLWQQFPWENREALFTAWTQAQTGYPIV
DAAMRQLTETGWMHNRCRMIVASFLTKDLIIDWRRGEQFFMQHLVDGDLAANNGGWQWSASSGMD
PKPLRIFNPASQAKKFDATATYIKRWLPELRHVHPKDLISGEITPIERRGYPAPIVNHNLRQKQF
KALYNQLKAAI
>d2pgd_1 a.100.1.1 (177-473) 6-phosphogluconate dehydrogenase (6PGD) {Sheep (Ovis orientalis aries)}
GAGHFVKMVHNGIEYGDMQLICEAYHLMKDVLGLGHKEMAKAFEEWNKTELDSFLIEITASILKF
QDADGKHLLPKIRDSAGQKGTGKWTAISALEYGVPVTLIGEAVFARCLSSLKDERIQASKKLKGP
QNIPFEGDKKSFLEDIRKALYASKIISYAQGFMLLRQAATEFGWTLNYGGIALMWRGGCIIRSVF
LGKIKDAFDRNPGLQNLLLDDFFKSAVENCQDSWRRAISTGVQAGIPMPCFTTALSFYDGYRHAM
LPANLIQAQRDYFGAHTYELLAKPGQFIHTNWTGHGG
>d1pgja1 a.100.1.1 (A:179-478) 6-phosphogluconate dehydrogenase (6PGD) {Trypanosoma brucei}
GAGSCVKMYHNSGEYAILQIWGEVFDILRAMGLNNDEVAAVLEDWKSKNFLKSYMLDISIAAARA
KDKDGSYLTEHVMDRIGSKGTGLWSAQEALEIGVPAPSLNMAVVSRQFTMYKTERQANASNAPGI
TQSPGYTLKNKSPSGPEIKQLYDSVCIAIISCYAQMFQCLREMDKVHNFGLNLPATIATFRAGCI
LQGYLLKPMTEAFEKNPNISNLMCAFQTEIRAGLQNYRDMVALITSKLEVSIPVLSASLNYVTAM
FTPTLKYGQLVSLQRDVFGRHGYERVDKDGRESFQWPELQ
>d1qmga1 a.100.1.2 (A:308-595) Acetohydroxy acid isomeroreductase, ketoacid reductoisomerase (KARI) {Spinach (Spinacia oleracea)}
LEQEYKSDIFGERGILLGAVHGIVECLFRRYTESGMSEDLAYKNTVECITGVISKTISTKGMLAL
YNSLSEEGKKDFQAAYSASYYPSMDILYECYEDVASGSEIRSVVLAGRRFYEKEGLPAFPMGKID
QTRMWKVGEKVRSVRPAGDLGPLYPFTAGVYVALMMAQIEILRKKGHSYSEIINESVIEAVDSLN
PFMHARGVSFMVDNCSTTARLGSRKWAPRFDYILSQQALVAVDNGAPINQDLISNFLSDPVHEAI

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GVCAQLRPSVDISVTADADFVRPELRQA
>d1f0ya1 a.100.1.3 (A:204-302) Short chain L-3-hydroxyacyl CoA dehydrogenase {Human (Homo sapiens)}
GFIVNRLLVPYLMEAIRLYERGDASKEDIDTAMKLGAGYPMGPFELLDYVGLDTTKFIVDGWHEM
DAENPLHQPSPSLNKLVAENKFGKKTGEGFYKYK
>d3hdha1 a.100.1.3 (A:204-302) Short chain L-3-hydroxyacyl CoA dehydrogenase {Pig (Sus scrofa)}
GFIVNRLLVPYLIEAVRLYERGDASKEDIDTAMKLGAGYPMGPFELLDYVGLDTTKFIIDGWHEM
DSQNPLFQPSPAMNKLVAENKFGKKTGEGFYKYK
>d1dlja1 a.100.1.4 (A:197-294) UDP-glucose dehydrogenase (UDPGDH), middle domain {Streptococcus pyogenes}
ASEAEAVKLFANTYLALRVAYFNELDTYAESRKLNSHMIIQGISYDDRIGMHYNNPSFGYGGYSL
PKDTKQLLANYNNIPQTLIEAIVSSNNVRKSYI
>d1bg6_1 a.100.1.5 (188-359) N-(1-D-carboxylethyl)-L-norvaline dehydrogenase {Arthrobacter, strain 1c}
NVLHTSLTNVNAVMHPLPTLLNAARCESGTPFQYYLEGITPSVGSLAEKVDAERIAIAKAFDLNV
PSVCEWYKESYGQSPATIYEAVQGNPAYRGIAGPINLNTRYFFEDVSTGLVPLSELGRAVNVPTP
LIDAVLDLISSLIDTDFRKEGRTLEKLGLSGLTAAGIRSAVE
>d1evya1 a.100.1.6 (A:189-357) Glycerol-3-phosphate dehydrogenase {Trypanosome (Leishmania mexicana)}
DRSFVCWATTDTVGCEVASAVKNVLAIGSGVANGLGMGLNARAALIMRGLLEIRDLTAALGGDGS
AVFGLAGLGDLQLTCSSELSRNFTVGKKLGKGLPIEEIQRTSKAVAEGVATADPLMRLAKQLKVK
MPLCHQIYEIVYKKKNPRDALADLLSCGLQDEGLPPLFK
>d1ks9a1 a.100.1.7 (A:168-291) Ketopantoate reductase PanE {Escherichia coli}
NIRAELWRKLAVNCVINPLTAIWNCPNGELRHHPQEIMQICEEVAAVIEREGHHTSAEDLRDYVM
QVIDATAENISSMLQDIRALRHTEIDYINGFLLRRARAHGIAVPENTRLFEMVKRKESE
>d1utg__ a.101.1.1 (-) Uteroglobin {Rabbit (Oryctolagus cuniculus)}
GICPRFAHVIENLLLGTPSSYETSLKEFEPDDTMKDAGMQMKKVLDSLPQTTRENIMKLTEKIVK
SPLCM
>d1ccd__ a.101.1.1 (-) Clara cell 17kDa protein {Rat (Rattus norvegicus)}
SSDICPGFLQVLEALLLGSESNYEAALKPFNPASDLQNAGTQLKRLVDTLPQETRINIVKLTEKI
LTSPLCEQDLRV
>d1utra_ a.101.1.1 (A:) Clara cell 17kDa protein {Rat (Rattus norvegicus)}
ICPGFLQVLEALLLGSESNYEAALKPFNPASDLQNAGTQLKRLVDTLPQETRINIVKLTEKILTS
PLC
>d1gai__ a.102.1.1 (-) Glucoamylase {Aspergillus awamori, variant x100}
ATLDSWLSNEATVARTAILNNIGADGAWVSGADSGIVVASPSTDNPDYFYTWTRDSGLVIKTLVD
LFRNGDTDLLSTIEHYISSQAIIQGVSNPSGDLSSGGLGEPKFNVDETAYTGSWGRPQRDGPALR
ATAMIGFGQWLLDNGYTSAATEIVWPLVRNDLSYVAQYWNQTGYDLWEEVNGSSFFTIAVQHRAL
VEGSAFATAVGSSCSWCDSQAPQILCYLQSFWTGSYILANFDSSRSGKDTNTLLGSIHTFDPEAG
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CDDSTFQPCSPRALANHKEVVDSFRSIYTLNDGLSDSEAVAVGRYPEDSYYNGNPWFLCTLAAAE
QLYDALYQWDKQGSLEITDVSLDFFKALYSGAATGTYSSSSSTYSSIVSAVKTFADGFVSIVETH
AASNGSLSEQFDKSDGDELSARDLTWSYAALLTANNRRNSVVPPSWGETSASSVPGTCAATSASG
TYSSVTVTSWPSIVATG
>d1ayx__ a.102.1.1 (-) Glucoamylase {Baker's yeast (Saccharomycopsis
fibuligera)}
AYPSFEAYSNYKVDRTDLETFLDKQKEVSLYYLLQNIAYPEGQFNNGVPGTVIASPSTSNPDYYY
QWTRDSAITFLTVLSELEDNNFNTTLAKAVEYYINTSYNLQRTSNPSGSFDDENHKGLGEPKFNT
DGSAYTGAWGRPQNDGPALRAYAISRYLNDVNSLNEGKLVLTDSGDINFSSTEDIYKNIIKPDLE
YVIGYWDSTGFDLWEENQGRHFFTSLVQQKALAYAVDIAKSFDDGDFANTLSSTASTLESYLSGS
DGGFVNTDVNHIVENPDLLQQNSRQGLDSATYIGPLLTHDIGESSSTPFDVDNEYVLQSYYLLLE
DNKDRYSVNSAYSAGAAIGRYPEDVYNGDGSSEGNPWFLATAYAAQVPYKLAYDAKSASNDITIN
KINYDFFNKYIVDLSTINSAYQSSDSVTIKSGSDEFNTVADNLVTFGDSFLQVILDHINDDGSLN
EQLNRYTGYSTGAYSLTWSSGALLEAIRLRNKVKALA
>d1cem__ a.102.1.2 (-) CelA cellulase {Clostridium thermocellum}
AGVPFNTKYPYGPTSIADNQSEVTAMLKAEWEDWKSKRITSNGAGGYKRVQRDASTNYDTVSEGM
GYGLLLAVCFNEQALFDDLYRYVKSHFNGNGLMHWHIDANNNVTSHDGGDGAATDADEDIALALI
FADKQWGSSGAINYGQEARTLINNLYNHCVEHGSYVLKPGDRWGGSSVTNPSYFAPAWYKVYAQY
TGDTRWNQVADKCYQIVEEVKKYNNGTGLVPDWCTASGTPASGQSYDYKYDATRYGWRTAVDYSW
FGDQRAKANCDMLTKFFARDGAKGIVDGYTIQGSKISNNHNASFIGPVAAASMTGYDLNFAKELY
RETVAVKDSEYYGYYGNSLRLLTLLYITGNFPNPLSDL
>d1tf4a1 a.102.1.2 (A:1-460) Endo/exocellulase:cellobiose E-4,
N-terminal domain {Thermomonospora fusca}
EPAFNYAEALQKSMFFYEAQRSGKLPENNRVSWRGDSGLNDGADVGLDLTGGWYDAGDHVKFGFP
MAFTATMLAWGAIESPEGYIRSGQMPYLKDNLRWVNDYFIKAHPSPNVLYVQVGDGDADHKWWGP
AEVMPMERPSFKVDPSCPGSDVAAETAAAMAASSIVFADDDPAYAATLVQHAKQLYTFADTYRGV
YSDCVPAGAFYNSWSGYQDELVWGAYWLYKATGDDSYLAKAEYEYDFLSTEQQTDLRSYRWTIAW
DDKSYGTYVLLAKETGKQKYIDDANRWLDYWTVGVNGQRVPYSPGGMAVLDTWGALRYAANTAFV
ALVYAKVIDDPVRKQRYHDFAVRQINYALGDNPRNSSYVVGFGNNPPRNPHHRTAHGSWTDSIAS
PAENRHVLYGALVGGPGSPNDAYTDDRQDYVANEVATDYNAGFSSALAMLVEEYGGTPLADFPPT
EEPDG
>d1clc_1 a.102.1.2 (135-575) CelD cellulase {Clostridium
thermocellum}
AMNVYEDAFKTAMLGMYLLRCGTSVSATYNGIHYSHGPCHTNDAYLDYINGQHTKKDSTKGWHDA
GDYNKYVVNAGITVGSMFLAWEHFKDQLEPVALEIPEKNNSIPDFLDELKYEIDWILTMQYPDGS
GRVAHKVSTRNFGGFIMPENEHDERFFVPWSSAATADFVAMTAMAARIFRPYDPQYAEKCINAAK
VSYEFLKNNPANVFANQSGFSTGEYATVSDADDRLWAAAEMWETLGDEEYLRDFENRAAQFSKKI
EADFDWDNVANLGMFTYLLSERPGKNPALVQSIKDSLLSTADSIVRTSQNHGYGRTLGTTYYWGC
NGTVVRQTMILQVANKISPNNDYVNAALDAISHVFGRNYYNRSYVTGLGINPPMNPHDRRSGADG
IWEPWPGYLVGGGWPGPKDWVDIQDSYQTNEIAINWNAALIYALAGFVNYN
>d1faea_ a.102.1.2 (A:) Processive endocellulase CelF (Cel48F)
{Clostridium cellulolyticum}
ASSPANKVYQDRFESMYSKIKDPANGYFSEQGIPYHSIETLMVEAPDYGHVTTSEAMSYYMWLEA
MHGRFSGDFTGFDKSWSVTEQYLIPTEKDQPNTSMSRYDANKPATYAPEFQDPSKYPSPLDTSQP
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VGRDPINSQLTSAYGTSMLYGMHWILDVDNWYGFGARADGTSKPSYINTFQRGEQESTWETIPQP
CWDEHKFGGQYGFLDLFTKDTGTPAKQFKYTNAPDADARAVQATYWADQWAKEQGKSVSTSVGKA
TKMGDYLRYSFFDKYFRKIGQPSQAGTGYDAAHYLLSWYYAWGGGIDSTWSWIIGSSHNHFGYQN
PFAAWVLSTDANFKPKSSNGASDWAKSLDRQLEFYQWLQSAEGAIAGGATNSWNGRYEAVPSGTS
TFYGMGYVENPVYADPGSNTWFGMQVWSMQRVAELYYKTGDARAKKLLDKWAKWINGEIKFNADG
TFQIPSTIDWEGQPDTWNPTQGYTGNANLHVKVVNYGTDLGCASSLANTLTYYAAKSGDETSRQN
AQKLLDAMWNNYSDSKGISTVEQRGDYHRFLDQEVFVPAGWTGKMPNGDVIKSGVKFIDIRSKYK
QDPEWQTMVAALQAGQVPTQRLHRFWAQSEFAVANGVYAILFPD
>d1fp3a_ a.102.1.3 (A:) N-acyl-D-glucosamine 2-epimerase {Pig (Sus scrofa)}
MEKERETLQAWKERVGQELDRVMAFWLEHSHDREHGGFFTCLGRDGRVYDDLKYVWLQGRQVWMY
CRLYRKLERFHRPELLDAAKAGGEFLLRHARVAPPEKKCAFVLTRDGRPVKVQRSIFSECFYTMA
MNELWRVTAEARYQSEAVDMMDQIVHWVREDPSGLGRPQLPGAVASESMAVPMMLLCLVEQLGEE
DEELAGRYAQLGHWCARRILQHVQRDGQAVLENVSEDGEELSGCLGRHQNPGHALEAGWFLLRHS
SRSGDAKLRAHVIDTFLLLPFRSGWDADHGGLFYFQDADGLCPTQLEWAMKLWWPHSEAMIAFLM
GYSESGDPALLRLFYQVAEYTFRQFRDPEYGEWFGYLNREGKVALTIKGGPFKGCFHVPRCLAMC
EEMLSALLSRLA
>d1h54a1 a.102.1.4 (A:269-753) Lactobacillus maltose phosphorylase, central domain {Lactobacillus brevis}
DTQESLTAAMHQLSDKVAQSSYEDLLNAHTAIWAQRWEKSDVVIKGDDESQQGIRFNLFQLFSTY
YGEDARLNIGPKGFTGEKYGGATYWDTEAFAFPVYLGITDPKVTRNLLMYRYKQLDGAYINAQEQ
GLKGALFPMVTFDGIECHNEWEITFEEIHRNGDIAFAIYNYTRYTGDDSYVLHEGAKVLTEISRF
WADRVHFSKRNNQYMIHGVTGADEYENNVDNNWDTNMLAQWTLKYTLEILGKVDQDTAKQLDVSD
EEKTKWQDIVDRMYLPYDKDLNIFVQHDGFLDKDIEPVSSIPADQRPINQNWSWDKILRSPYIKQ
GDVLQGIWDFIDDYTPEQKKANFDFYEPLTVHESSLSPAIHSVLAADLHYEDKAVELYSRTARLD
LDNYNNDTTDGLHITSMTGAWIAVVQGFAGMRVRDGQLHYAPFLPKTWTSYTFRQVFRDRLIEVS
VHADGPHFKLLSGEPLTIDVAGAAAAAAAA
>d1dl2a_ a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {Baker's yeast (Saccharomyces cerevisiae)}
GAGEMRDRIESMFLESWRDYSKHGWGYDVYGPIEHTSHNMPRGNQPLGWIIVDSVDTLMLMYNSS
TLYKSEFEAEIQRSEHWINDVLDFDIDAEVNVFETTIRMLGGLLSAYHLSDVLEVGNKTVYLNKA
IDLGDRLALAFLSTQTGIPYSSINLHSGQAVKNHADGGASSTAEFTTLQMEFKYLAYLTGNRTYW
ELVERVYEPLYKNNDLLNTYDGLVPIYTFPDTGKFGASTIRFGSRGDSFYEYLLKQYLLTHETLY
YDLYRKSMEGMKKHLLAQSKPSSLWYIGEREQGLHGQLSPKMDHLVCFMGGLLASGSTEGLSIHE
ARRRPFFSKSDWDLAKGITDTCYQMYKQSSSGLAPEIVVFNDGNIKQDGWWRSSVGDFFVKPLDR
HNLQRPETVESIMFMYHLSHDHKYREWGAEIATSFFENTCVDCNDPKLRRFTSLSDCITLPTKKS
NNMESFWLAETLKYLYILFLDEFDLTKVVFNTEAHPFPVLDEEILKSQSLTTGWSL
>d1hcua_ a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {Trichoderma reesei}
KRGSPNPTRAAAVKAAFQTSWNAYHHFAFPHDDLHPVSNSFDDERNGWGSSAIDGLDTAILMGDA
DIVNTILQYVPQINFTTTAVANQGSSVFETNIRYLGGLLSAYDLLRGPFSSLATNQTLVNSLLRQ
AQTLANGLKVAFTTPSGVPDPTVFFNPTVRRSGASSNNVAEIGSLVLEWTRLSDLTGNPQYAQLA
QKGESYLLNPKGSPEAWPGLIGTFVSTSNGTFQDSSGSWSGLMDSFYEYLIKMYLYDPVAFAHYK
DRWVLGADSTIGHLGSHPSTRKDLTFLSSYNGQSTSPNSGHLASFGGGNFILGGILLNEQKYIDF

GIKLASSYFGTYTQTASGIGPEGFAWVDSVTGAGGSPPSSQSGFYSSAGFWVTAPYYILRPETLE
SLYYAYRVTGDSKWQDLAWEALSAIEDACRAGSAYSSINDVTQANGGGASDDMESFWFAEALKYA
YLIFAEESDVQVQATGGNKFVFNTEAHPFSIRS
>d1krea_ a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {Fungus (Penicillium citrinum)}
SNQAKADAVKEAFQHAWNGYMKYAFPHDELTPVSNGHADSRNGWGASAVDALSTAVIMGKADVVN
AILEHVADIDFSKTSDTVSLFETTIRYLAGMLSGYDLLQGPAKNLVDNQDLIDGLLDQSRNLADV
LKFAFDTPSGVPYNNINITSHGNDGATTNGLAVTGTLVLEWTRLSDLTGDEEYAKLSQKAESYLL
KPQPSSSEPFPGLVGSSININDGQFADSRVSWNGGDDSFYEYLIKMYVYDPKRFETYKDRWVLAA
ESTIKHLKSHPKSRPDLTFLSSYSNRNYDLSSQHLTCFDGGSFLLGGTVLDRQDFIDFGLELVDG
CEATYNSTLTKIGPDSWGWDPKKVPSDQKEFYEKAGFYISSGSYVLRPEVIESFYYAHRVTGKEI
YRDWVWNAFVAINSTCRTDSGFAAVSDVNKANGGSKYDNQESFLFAEVMKYSYLAHSEDAAWQVQ
KGGKNTFVYNTEAHPISVAR
>d1fo3a_ a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {Human (Homo sapiens)}
QGPVHLNYRQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRK
EFEEARKWVSKKLHFEKDVDVNLFESTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPS
KIPYSDVNIGTGVAHPPRWTSDSTVAEVTSIQLEFRELSRLTGDKKFQEAVEKVTQHIHGLSGKK
DGLVPMFINTHSGLFTHLGVFTLGARADSYYEYLLKQWIQGGKQETQLLEDYVEAIEGVRTHLLR
HSEPSKLTFVGELAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQMNRQMET
GLSPEIVHFNLYPQPGRRDVEVKPADRHNLLRPETVESLFYLYRVTGDRKYQDWGWEILQSFSRF
TRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLDAYVFNTEAHPLPI
WT
>d1qaza_ a.102.3.1 (A:) Alginate lyase A1-III {Sphingomonas sp., A1}
GSHPFDQAVVKDPTASYVDVKARRTFLQSGQLDDRLKAALPKEYDCTTEATPNPQQGEMVIPRRY
LSGNHGPVNPDYEPVVTLYRDFEKISATLGNLYVATGKPVYATCLLNMLDKWAKADALLNYDPKS
QSWYQVEWSAATAAFALSTMMAEPNVDTAQRERVVKWLNRVARHQTSFPGGDTSCCNNHSYWRGQ
EATIIGVISKDDELFRWGLGRYVQAMGLINEDGSFVHEMTRHEQSLHYQNYAMLPLTMIAETASR
QGIDLYAYKENGRDIHSARKFVFAAVKNPDLIKKYASEPQDTRAFKPGRGDLNWIEYQRARFGFA
DELGFMTVPIFDPRTGGSATLLAYKP
>d1cb8a1 a.102.3.2 (A:26-335) Chondroitinase AC {Pedobacter heparinus (Flavobacterium heparinum)}
GTAELIMKRVMLDLKKPLRNMDKVAEKNLNTLQPDGSWKDVPYKDDAMTNWLPNNHLLQLETIIQ
AYIEKDSHYYGDDKVFDQISKAFKYWYDSDPKSRNWWHNEIATPQALGEMLILMRYGKKPLDEAL
VHKLTERMKRGEPEKKTGANKTDIALHYFYRALLTSDEALLSFAVKELFYPVQFVHYEEGLQYDY
SYLQHGPQLQISSYGAVFITGVLKLANYVRDTPYALSTEKLAIFSKYYRDSYLKAIRGSYMDFNV
EGRGVSRPDILNKKAEKKRLLVAKMIDLKHTEEWADAIARTDSTVAAGYK
>d1egua1 a.102.3.2 (A:171-540) Hyaluronate lyase {Streptococcus pneumoniae}
KDTYTDRLDDWNGIIAGNQYYDSKNDQMAKLNQELEGKVADSLSSISSQADRIYLWEKFSNYKTS
ANLTATYRKLEEMAKQVTNPSSRYYQDETVVRTVRDSMEWMHKHVYNSEKSIVGNWWDYEIGTPR
AINNTLSLMKEYFSDEEIKKYTDVIEKFVPDPEHFRKTTDNPFKALGGNLVDMGRVKVIAGLLRK
DDQEISSTIRSIEQVFKLVDQGEGFYQDGSYIDHTNVAYTGAYGNVLIDGLSQLLPVIQKTKNPI
DKDKMQTMYHWIDKSFAPLLVNGELMDMSRGRSISRANSEGHVAAVEVLRGIHRIADMSEGETKQ

RLQSLVKTIVQSDSYYDVFKNLKTYKDISLMQSLLSDAGVASVPR
>d1f1sa1 a.102.3.2 (A:249-619) Hyaluronate lyase {Streptococcus agalactiae}
EDNFTKLLDKWNDVTIGNYVYDTNDSNMQKLNQKLDETNAKNIEAIKLDSNRTFLWKDLDNLNNS
AQLTATYRRLEDLAKQITNPHSTIYKNEKAIRTVKESLAWLHQNFYNVNKDIEGSANWWDFEIGV
PRSITGTLSLMNNYFTDAEIKTYTDPIEHFVPDAEYFRKTLVNPFKALGGNLVDMGRVKIIEGLL
RKDNTIIEKTSHSLKNLFTTATKAEGFYADGSYIDHTNVAYTGAYGNVLIDGLTQLLPIIQETDY
KISNQELDMVYKWINQSFLPLIVKGELMDMSRGRSISREAASSHAAAVEVLRGFLRLANMSNEER
NLDLKSTIKTIITSNKFYNVFNNLKSYSDIANMNKLLNDSTVATKP
>d5eau_1 a.102.4.1 (21-220) 5-Epi-aristolochene synthase, N-terminal domain {Tobacco (Nicotiana tabacum)}
SPSLWGDQFLSFSIDNQVAEKYAKEIEALKEQTRNMLLATGMKLADTLNLIDTIERLGISYHFEK
EIDDILDQIYNQNSNCNDLCTSALQFRLLRQHGFNISPEIFSKFQDENGKFKESLASDVLGLLNL
YEASHVRTHADDILEDALAFSTIHLESAAPHLKSPLREQVTHALEQCLHKGVPRVETRFFISSIY
DKEQS
>d2sqca1 a.102.4.2 (A:8-36,A:308-630) Squalene-hopene cyclase {Alicyclobacillus acidocaldarius}
APAYARTLDRAVEYLLSCQKDEGYWWGPLXISPVWDTGLAVLALRAAGLPADHDRLVKAGEWLLD
RQITVPGDWAVKRPNLKPGGFAFQFDNVYYPDVCDTAVVVWALNTLRLPDERRRRDAMTKGFRWI
VGMQSSNGGWGAYDVDNTSDLPNHIPFSDFGEVTDPPSEDVTAHVLECFGSFGYDDAWKVIRRAV
EYLKREQKPDGSWFGRWGVNYLYGTGAVVSALKAVGIDTREPYIQKALDWVEQHQNPDGGWGEDC
RSYEDPAYAGKGASTPSQTAWALMALIAGGRAESEAARRGVQYLVETQRPDGGWDEPYYTGTGFP
GDFYLGYTMYRHVFPTLALGRYKQAIER
>d2sqca2 a.102.4.2 (A:37-307) Squalene-hopene cyclase {Alicyclobacillus acidocaldarius}
LSNVTMEAEYVLLCHILDRVDRDRMEKIRRYLLHEQREDGTWALYPGGPPDLDTTIEAYVALKYI
GMSRDEEPMQKALRFIQSQGGIESSRVFTRMWLALVGEYPWEKVPMVPPEIMFLGKRMPLNIYEF
GSWARATVVALSIVMSRQPVFPLPERARVPELYETDVPPRRRGAKGGGGWIFDALDRALHGYQKL
SVHPFRRAAEIRALDWLLERQAGDGSWGGIQPPWFYALIALKILDMTQHPAFIKGWEGLELYGVE
LDYGGWMFQAS
>d1d8db_ a.102.4.3 (B:) Protein farnesyltransferase, beta-subunit {Rat (Rattus norvegicus)}
PVWSEPLYSLRPEHARERLQDDSVETVTSIEQAKVEEKIQEVFSSYKFNHLVPRLVLQREKHFHY
LKRGLRQLTDAYECLDASRPWLCYWILHSLELLDEPIPQIVATDVCQFLELCQSPDGGFGGGPGQ
YPHLAPTYAAVNALCIIGTEEAYNVINREKLLQYLYSLKQPDGSFLMHVGGEVDVRSAYCAASVA
SLTNIITPDLFEGTAEWIARCQNWEGGIGGVPGMEAHGGYTFCGLAALVILKKERSLNLKSLLQW
VTSRQMRFEGGFQGRCNKLVDGCYSFWQAGLLPLLHRALHAQGDPALSMSHWMFHQQALQEYILM
CCQCPAGGLLDKPGKSRDFYHTCYCLSGLSIAQHFGSGAMLHDVVMGVPENVLQPTHPVYNIGPD
KVIQATTHFLQKPVPGF
>d1dceb_ a.102.4.3 (B:) Rab geranylgeranyltransferase, beta subunit {Rat (Rattus norvegicus)}
TQQKDVTIKSDAPDTLLLEKHADYIASYGSKKDDYEYCMSEYLRMSGVYWGLTVMDLMGQLHRMN
KEEILVFIKSCQHECGGVSASIGHDPHLLYTLSAVQILTLYDSIHVINVDKVVAYVQSLQKEDGS
FAGDIWGEIDTRFSFCAVATLALLGKLDAINVEKAIEFVLSCMNFDGGFGCRPGSESHAGQIYCC

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TGFLAITSQLHQVNSDLLGWWLCERQLPSGGLNGRPEKLPDVCYSWWVLASLKIIGRLHWIDREK
LRSFILACQDEETGGFADRPGDMVDPFHTLFGIAGLSLLGEEQIKPVSPVFCMPEEVLQRVNVQP
ELVS
>d1c3d__ a.102.4.4 (-) C3D, a C3 fragment and ligand for complement
receptor 2 {Human (Homo sapiens)}
MLDAERLKHLIVTPSGAGEQNMIGMTPTVIAVHYLDETEQWEKFGLEKRQGALELIKKGYTQQLA
FRQPSSAFAAFVKRAPSTWLTAYVVKVFSLAVNLIAIDSQVLCGAVKWLILEKQKPDGVFQEDAP
VIHQEMIGGLRNNNEKDMALTAFVLISLQEAKDICEEQVNSLPGSITKAGDFLEANYMNLQRSYT
VAIAGYALAQMGRLKGPLLNKFLTTAKDKNRWEDPGKQLYNVEATSYALLALLQLKDFDFVPPVV
RWLNEQRYYGGGYGSTQATFMVFQALAQYQKDAP
>d1qqfa_ a.102.4.4 (A:) C3D, a C3 fragment and ligand for complement
receptor 2 {Rat (Rattus norvegicus)}
CGEQNMIGMTPTVIAVHYLDQTEQWEKFGLEKRQEALELIKKGYTQQLAFKQPISAYAAFNNRPP
STWLTAYVSRVFSLAANLIAIDSQVLCGAVKWLILEKQKPDGVFQEDGPVIHQEMIGGFRNTKEA
DVSLTAFVLIALQEARDICEGQVNSLPGSINKAGEYLEASYLNLQRPYTVAIAGYALALMNKLEE
PYLTKFLNTAKDRNRWEEPGQQLYNVEATSYALLALLLLKDFDSVPPVVRWLNDERYYGGGYGST
QATFMVFQALAQYRADV
>d1csc__ a.103.1.1 (-) Citrate synthase {Chicken (Gallus gallus)}
ASSTNLKDVLAALIPKEQARIKTFRQQHGGTALGQITVDMSYGGMRGMKGLVYETSVLDPDEGIR
FRGFSIPECQKLLPKGGXGGEPLPEGLFWLLVTGQIPTGAQVSWLSKEWAKRAALPSHVVTMLDN
FPTNLHPMSQLSAAITALNSESNFARAYAEGILRTKYWEMVYESAMDLIAKLPCVAAKIYRNLYR
AGSSIGAIDSKLDWSHNFTNMLGYTDAQFTELMRLYLTIHSDHEGGNVSAHTSHLVGSALSDPYL
SFAAAMNGLAGPLHGLANQEVLGWLAQLQKAXXXAGADASLRDYIWNTLNSGRVVPGYGHAVLRK
TDPRYTCQREFALKHLPGDPMFKLVAQLYKIVPNVLLEQGAAANPWPNVDAHSGVLLQYYGMTEM
NYYTVLFGVSRALGVLAQLIWSRALGFPLERPKSMSTDGLIAL
>d1csh__ a.103.1.1 (-) Citrate synthase {Chicken (Gallus gallus)}
STNLKDVLASLIPKEQARIKTFRQQHGNTAVGQITVDMSYGGMRGMKGLIYETSVLDPDEGIRFR
GFSIPECQKLLPKAGGGEEPLPEGLFWLLVTGQIPTPEQVSWVSKEWAKRAALPSHVVTMLDNFP
TNLHPMSQLSAAITALNSESNFARAYAEGINRTKYWEFVYEDAMDLIAKLPCVAAKIYRNLYRAG
SSIGAIDSKLDWSHNFTNMLGYTDPQFTELMRLYLTIHSDHEGGNVSAHTSHLVGSALSDPYLSF
AAAMNGLAGPLHGLANQEVLLWLSQLQKDLGADASDEKLRDYIWNTLNSGRVVPGYGHAVLRKTD
PRYTCQREFALKHLPSDPMFKLVAQLYKIVPNVLLEQGKAKNPWPNVDAHSGVLLQYYGMTEMNY
YTVLFGVSRALGVLAQLIWSRALGFPLERPKSMSTAGLEKLSAGG
>d2cts__ a.103.1.1 (-) Citrate synthase {Pig (Sus scrofa)}
ASSTNLKDILADLIPKEQARIKTFRQQHGNTAVGQITVDMMYGGMRGMKGLVYETSVLDPDEGIR
FRGYSIPECQKMLPKAKGGEEPLPEGLFWLLVTGQIPTEEQVSWLSKEWAKRAALPSHVVTMLDN
FPTNLHPMSQLSAAITALNSESNFARAYAEGIHRTKYWELIYEDCMDLIAKLPCVAAKIYRNLYR
EGSSIGAIDSKLDWSHNFTNMLGYTDAQFTELMRLYLTIHSDHEGGNVSAHTSHLVGSALSDPYL
SFAAAMNGLAGPLHGLANQEVLVWLTQLQKEVGKDVSDEKLRDYIWNTLNSGRVVPGYGHAVLRK
TDPRYTCQREFALKHLPHDPMFKLVAQLYKIVPNVLLEQGKAKNPWPNVDAHSGVLLQYYGMTEM
NYYTVLFGVSRALGVLAQLIWSRALGFPLERPKSMSTDGLIKLVDSK
>d1aj8a_ a.103.1.1 (A:) Citrate synthase {Archaeon Pyrococcus
furiosus}
LAKGLEDVYIDQTNICYIDGKEGKLYYRGYSVEELAELSTFEEVVYLLWWGKLPSLSELENFKKE
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LAKSRGLPKEVIEIMEALPKNTHPMGALRTIISYLGNIDDSGDIPVTPEEVYRIGISVTAKIPTI
VANWYRIKNGLEYVPPKEKLSHAANFLYMLHGEEPPKEWEKAMDVALILYAEHEINASTLAVMTV
GSTLSDYYSAILAGIGALKGPIHGGAVEEAIKQFMEIGSPEKVEEWFFKALQQKRKIMGAGHRVY
KTYDPRARIFKKYASKLGDKKLFEIAERLERLVEEYLSKKGISINVDYWSGLVFYGMKIPIELYT
TIFAMGRIAGWTAHLAEYVSHNRIIRPRLQYVGEIGKKYLPIELRR
>d1a59__ a.103.1.1 (-) Citrate synthase {Antarctic bacterium DS2-3R}
EPTIHKGLAGVTADVTAISKVNSDTNSLLYRGYPVQELAAKCSFEQVAYLLWNSELPNDSELKAF
VNFERSHRKLDENVKGAIDLLSTACHPMDVARTAVSVLGANHARAQDSSPEANLEKAMSLLATFP
SVVAYDQRRRRGEELIEPREDLDYSANFLWMTFGEEAAPEVVEAFNVSMILYAEHSFNASTFTAR
VITSTLADLHSAVTGAIGALKGPLHGGANEAVMHTFEEIGIRKDESLDEAATRSKAWMVDALAQK
KKVMGFGHRVYKNGDSRVPTMKSALDAMIKHYDRPEMLGLYNGLEAAMEEAKQIKPNLDYPAGPT
YNLMGFDTEMFTPLFIAARITGWTAHIMEQVADNALIRPLSEYNGPEQRQVP
>d1dz4a_ a.104.1.1 (A:) Cytochrome P450-CAM {Pseudomonas putida}
LAPLPPHVPEHLVFDFDMYNPSNLSAGVQEAWAVLQESNVPDLVWTRCNGGHWIATRGQLIREAY
EDYRHFSSECPFIPREAGEAYDFIPTSMDPPEQRQFRALANQVVGMPVVDKLENRIQELACSLIE
SLRPQGQCNFTEDYAEPFPIRIFMLLAGLPEEDIPHLKYLTDQMTRPDGSMTFAEAKEALYDYLI
PIIEQRRQKPGTDAISIVANGQVNGRPITSDEAKRMCGLLLVGGLDTVVNFLSFSMEFLAKSPEH
RQELIQRPERIPAACEELLRRFSLVADGRILTSDYEFHGVQLKKGDQILLPQMLSGLDERENACP
MHVDFSRQKVSHTTFGHGSHLCLGQHLARREIIVTLKEWLTRIPDFSIAPGAQIQHKSGIVSGVQ
ALPLVWDPATTKAV
>d1jpza_ a.104.1.1 (A:) Cytochrome P450 bm-3 {Bacillus megaterium}
TIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKEACDES
RFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMMVDIAVQLVQKW
ERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRALDEAMNKLQRANPDD
PAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSDDLLTHMLNGKDPETGEPLDDENIRYQIIT
FLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVDPVPSYKQVKQLKYVGMVLNEALRLW
PTAPAFSLYAKEDTVLGGEYPLEKGDELMVLIPQLHRDKTIWGDDVEEFRPERFENPSAIPQHAF
KPFGNGQRACIGQQFALHEATLVLGMMLKHFDFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPL
GGI
>d1jfba_ a.104.1.1 (A:) Cytochrome P450-NOR, nitric reductase {Fungus
(Fusarium oxysporum)}
APSFPFSRASGPEPPAEFAKLRATNPVSQVKLFDGSLAWLVTKHKDVCFVATSEKLSKVRTRQGF
PELSASGKQAAKAKPTFVDMDPPEHMHQRSMVEPTFTPEAVKNLQPYIQRTVDDLLEQMKQKGCA
NGPVDLVKEFALPVPSYIIYTLLGVPFNDLEYLTQQNAIRTNGSSTAREASAANQELLDYLAILV
EQRLVEPKDDIISKLCTEQVKPGNIDKSDAVQIAFLLLVAGNATMVNMIALGVATLAQHPDQLAQ
LKANPSLAPQFVEELCRYHTASALAIKRTAKEDVMIGDKLVRANEGIIASNQSANRDEEVFENPD
EFNMNRKWPPQDPLGFGFGDHRCIAEHLAKAELTTVFSTLYQKFPDLKVAVPLGKINYTPLNRDV
GIVDLPVIF
>d1jipa_ a.104.1.1 (A:) Cytochrome P450-ERYF {Saccaropolyspora
erythraea}
TTVPDLESDSFHVDWYRTYAELRETAPVTPVRFLGQDAWLVTGYDEAKAALSDLRLSSDPKKKYP
GVEVEFPAYLGFPEDVRNYFATNMGTSDPPTHTRLRKLVSQEFTVRRVEAMRPRVEQITAELLDE
VGDSGVVDIVDRFAHPLPIKVICELLGVDEKYRGEFGRWSSEILVMDPERAEQRGQAAREVVNFI
LDLVERRRTEPGDDLLSALIRVQDDDDGRLSADELTSIALVLLLAGFESSVSLIGIGTYLLLTHP
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DQLALVRRDPSALPNAVEEILRYIAPPETTTRFAAEEVEIGGVAIPQYSTVLVANGAANRDPKQF
PDPHRFDVTRDTRGHLSFGQGIHFCMGRPLAKLEGEVALRALFGRFPALSLGIDADDVVWRRSLL
LRGIDHLPVRLDG
>d1cpt__ a.104.1.1 (-) Cytochrome P450-TERP {Pseudomonas sp.}
MDARATIPEHIARTVILPQGYADDEVIYPAFKWLRDEQPLAMAHIEGYDPMWIATKHADVMQIGK
QPGLFSNAEGSEILYDQNNEAFMRSISGGCPHVIDSLTSMDPPTHTAYRGLTLNWFQPASIRKLE
ENIRRIAQASVQRLLDFDGECDFMTDCALYYPLHVVMTALGVPEDDEPLMLKLTQDFFGVEAARR
FHETIATFYDYFNGFTVDRRSCPKDDVMSLLANSKLDGNYIDDKYINAYYVAIATAGHDTTSSSS
GGAIIGLSRNPEQLALAKSDPALIPRLVDEAVRWTAPVKSFMRTALADTEVRGQNIKRGDRIMLS
YPSANRDEEVFSNPDEFDITRFPNRHLGFGWGAHMCLGQHLAKLEMKIFFEELLPKLKSVELSGP
PRLVATNFVGGPKNVPIRFTKA
>d1e9xa_ a.104.1.1 (A:) Cytochrome p450 14 alpha-sterol demethylase
(cyp51) {Mycobacterium tuberculosis}
MSAVALPRVSGGHDEHGHLEEFRTDPIGLMQRVRDECGDVGTFQLAGKQVVLLSGSHANEFFFRA
GDDDLDQAKAYPFMTPIFGEGVVFDASPERRKEMLHNAALRGEQMKGHAATIEDQVRRMIADWGE
AGEIDLLDFFAELTIYTSSACLIGKKFRDQLDGRFAKLYHELERGTDPLAYVDPYLPIESFRRRD
EARNGLVALVADIMNGRIANPPTDKSDRDMLDVLIAVKAETGTPRFSADEITGMFISMMFAGHHT
SSGTASWTLIELMRHRDAYAAVIDELDELYGDGRSVSFHALRQIPQLENVLKETLRLHPPLIILM
RVAKGEFEVQGHRIHEGDLVAASPAISNRIPEDFPDPHDFVPARYEQPRQEDLLNRWTWIPFGAG
RHRCVGAAFAIMQIKAIFSVLLREYEFEMAQPPESYRNDHSKMVVQLAQPACVRYRRRT
>d1io7a_ a.104.1.1 (A:) CYP119 {Archaeon Sulfolobus solfataricus}
MYDWFSEMRKKDPVYYDGNIWQVFSYRYTKEVLNNFSKFSSDLTGYHERLEDLRNGKIRFDIPTR
YTMLTSDPPLHDELRSMSADIFSPQKLQTLETFIRETTRSLLDSIDPREDDIVKKLAVPLPIIVI
SKILGLPIEDKEKFKEWSDLVAFRLGKPGEIFELGKKYLELIGYVKDHLNSGTEVVSRVVNSNLS
DIEKLGYIILLLIAGNETTTNLISNSVIDFTRFNLWQRIREENLYLKAIEEALRYSPPVMRTVRK
TKERVKLGDQTIEEGEYVRVWIASANRDEEVFHDGEKFIPDRNPNPHLSFGSGIHLCLGAPLARL
EARIAIEEFSKRFRHIEILDTEKVPNEVLNGYKRLVVRLKS
>d1dt6a_ a.104.1.1 (A:) Mammalian cytochrome p450 2c5 {Rabbit
(Oryctolagus cuniculus)}
PPGPTPFPIIGNILQIDAKDISKSLTKFSECYGPVFTVYLGMKPTVVLHGYEAVKEALVDLGEEF
AGRGSVPILEKVSKGLGIAFSNAKTWKEMRRFSLMTLRNFGMGKRSIEDRIQEEARCLVEELRKT
NASPCDPTFILGCAPCNVICSVIFHNRFDYKDEEFLKLMESLHENVELLGTPWLQVYNNFPALLD
YFPGIHKTLLKNADYIKNFIMEKVKEHQKLLDVNNPRDFIDCFLIKMEQENNLEFTLESLVIAVS
DLFGAGTETTSTTLRYSLLLLLKHPEVAARVQEEIERVIGRHRSPCMQDRSRMPYTDAVIHEIQR
FIDLLPTNLPHAVTRDVRFRNYFIPKGTDIITSLTSVLHDEKAFPNPKVFDPGHFLDESGNFKKS
DYFMPFSAGKRMCVGEGLARMELFLFLTSILQNFKLQSLVEPKDLDITAVVNGFVSVPPSYQLCF
IPIHH
>d1etob_ a.105.1.1 (B:) FIS protein {Escherichia coli}
MFEQRVNSDVLTVSTVNSQDQVTQKPLRDSVKQALKNYFAQLNGQDVNDLYELVLAEVEQPLLDM
VMQYTLGNQTRAALMMGINRGTLRKKLKKYGMN
>d1etxa_ a.105.1.1 (A:) FIS protein {Escherichia coli}
VLTVSTVNSQDQVTQKPLRDSVKQALKNYFAQLNGQDVNDLYELVLAEVEQPLLDMVMQYTRGNA
TRAALMMGINRGTLRKKLKKYGMN
>d1fipa_ a.105.1.1 (A:) FIS protein {Escherichia coli}
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PLRDSVKQALKNYFAQLNGQDVNDLYELVLAEVEQALLDMVMQYTRGNQTRAALMMGINRGTLRK
KLKKYGMN
>d1ntca_ a.105.1.1 (A:) DNA-binding domain of NTRC {Salmonella
typhimurium}
MDLPGELFEASTPDSPSHLPPDSWATLLAQWADRALRSGHQNLLSEAQPELERTLLTTALRHTQG
HKQEAARLLGWGAATLTAKLKELGME
>d1g8ea_ a.145.1.1 (A:) Flagellar transcriptional activator FlhD
{Escherichia coli}
MHTSELLKHIYDINLSYLLLAQRLIVQDKASAMFRLGINEEMATTLAALTLPQMVKLAETNQLVC
HFRFDSHQTITQLTQDSRVDDLQQIHTGIMLST
>d1g8eb_ a.145.1.1 (B:) Flagellar transcriptional activator FlhD
{Escherichia coli}
TSELLKHIYDINLSYLLLAQRLIVQDKASAMFRLGINEEMATTLAALTLPQMVKLAETNQLVCHF
RFDSHQTITQLTQDS
>d1jhga_ a.107.1.1 (A:) Trp repressor {Escherichia coli}
SAAMAEQRHQEWLRFVDLLKNAYQNDLHLPLLNLMLTPDEREALGTRVRIIEELLRGEMSQRELK
NELGAGIATITRGSNSLKAAPVELRQWLEEVLLKSD
>d1trra_ a.107.1.1 (A:) Trp repressor {Escherichia coli}
AQQSPYSAAMAEQRHEEWLRFVDLLKNAYQNDLHLPLLNLMLTPDEREALGTRVRIVEELLRGEM
SQRELKNELGAGIATITRGSNSLKAAPVELRQWLEEVLLK
>d1dd3a1 a.108.1.1 (A:1-57) Ribosomal protein L7/12, oligomerisation
(N-terminal) domain {Thermotoga maritima}
MTIDEIIEAIEKLTVSELAELVKKLEDKFGVTAAAPVAVAAAPVAGAAAGAAQEEKT
>d1dd3c1 a.108.1.1 (C:) Ribosomal protein L7/12, oligomerisation
(N-terminal) domain {Thermotoga maritima}
MTIDEIIEAIEKLTVSELAELVKKLEDKFGVT
>d1dd4d1 a.108.1.1 (D:) Ribosomal protein L7/12, oligomerisation
(N-terminal) domain {Thermotoga maritima}
MTIDEIIEAIEKLTVSELAELVKKLEDKFGVTAAAPVAVA
>d1iiea_ a.109.1.1 (A:) MHC class II-associated invariant chain
ectoplasmic trimerization domain {Human (Homo sapiens)}
YGNMTEDHVMHLLQNADPLKVYPPLKGSFPENLRHLKNTMETIDWKVFESWMHHWLLFEMSRHSL
EQKPTDAPPK
>d1aora1 a.110.1.1 (A:211-605) Aldehyde ferredoxin oxidoreductase
{Archaeon Pyrococcus furiosus}
IADKQKFMLVVREKVNKLRNDPVAGGGLPKYGTAVLVNIINENGLYPVKNFQTGVYPYAYEQSGE
AMAAKYLVRNKPCYACPIGCGRVNRLPTVGETEGPEYESVWALGANLGINDLASIIEANHMCDEL
GLDTISTGGTLATAMELYEKGHIKDEELGDAPPFRWGNTEVLHYYIEKIAKREGFGDKLAEGSYR
LAESYGHPELSMTVKKLELPAYDPRGAEGHGLGYATNNRGGCHIKNYMISPEILGYPYKMDPHDV
SDDKIKMLILFQDLTALIDSAGLCLFTTFGLGADDYRDLLNAALGWDFTTEDYLKIGERIWNAER
LFNLKAGLDPARDDTLPKRFLEEPMPEGPNKGHTVRLKEMLPRYYKLRGWTEDGKIPKEKLEELG
IAEFY
>d1b25a1 a.110.1.1 (A:211-619) Formaldehyde ferredoxin
oxidoreductase {Archaeon Pyrococcus furiosus}
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DKEELKKLSQEAYNEILNSPGYPFWKRQGTMAAVEWCNTNYALPTRNFSDGYFEFARSIDGYTME
GMKVQQRGCPYCNMPCGNVVLDAEGQESELDYENVALLGSNLGIGKLNEVSVLNRIADEMGMDTI
SLGVSIAHVMEAVERGILKEGPTFGDFKGAKQLALDIAYRKGELGNLAAEGVKAMAEKLGTHDFA
MHVKGLEVSGYNCYIYPAMALAYGTSAIGAHHKEAWVIAWEIGTAPIEGEKAEKVEYKISYDPIK
AQKVVELQRLRGGLFEMLTACRLPWVEVGLSLDYYPKLLKAITGVTYTWDDLYKAADRVYSLIRA
YWVREFNGKWDRKMDYPPKRWFTEGLKSGPHKGEHLDEKKYDELLSEYYRIRGWDERGIPKKETL
KELDLDFVIPELEKVTNLE
>d1d2ta_ a.111.1.1 (A:) Acid phosphatase {Escherichia blattae}
GNDTTTKPDLYYLKNSEAINSLALLPPPPAVGSIAFLNDQAMYEQGRLLRNTERGKLAAEDANLS
SGGVANAFSGAFGSPITEKDAPALHKLLTNMIEDAGDLATRSAKDHYMRIRPFAFYGVSTCNTTE
QDKLSKNGSYPSGHTSIGWATALVLAEINPQRQNEILKRGYELGQSRVICGYHWQSDVDAARVVG
SAVVATLHTNPAFQQQLQKAKAEFAQHQK
>d1qi9a_ a.111.1.2 (A:) Haloperoxidase (bromoperoxidase)
{Ascophyllum nodosum}
TCSTSDDADDPTPPNERDDEAFASRVAAAKRELEGTGTVCQINNGETDLAAKFHKSLPHDDLGQV
DADAFAALEDCILNGDLSICEDVPVGNSEGDPVGRLVNPTAAFAIDISGPAFSATTIPPVPTLPS
PELAAQLAEVYWMALARDVPFMQYGTDDITVTAAANLAGMEGFPNLDAVSIGSDGTVDPLSQLFR
ATFVGVETGPFISQLLVNSFTIDSITVEPKQETFAPDVNYMVDFDEWLNIQNGGPPAGPELLDDE
LRFVRNARDLARVTFTDNINTEAYRGALILLGLDAFNRAGVNGPFIDIDRQAGFVNFGISHYFRL
IGAAELAQRSSWYQKWQVHRFARPEALGGTLHLTIKGELNADFDLSLLENAELLKRVAAINAAQN
PNNEVTYLLPQAIQEGSPTHPSYPSGHATQNGAFATVLKALIGLDRGGDCYPDPVYPDDDGLKLI
DFRGSCLTFEGEINKLAVNVAFGRQMLGIHYRFDGIQGLLLGETITVRTLHQELMTFAEESTFEF
RLFTGEVIKLFQDGTFTIDGFKCPGLVYTGVENCV
>d1qhba_ a.111.1.2 (A:) Haloperoxidase (bromoperoxidase) {Red algae
(Corallina officinalis)}
GIPADNLQSRAKASFDTRVAAAELALARGAVPSFANGEELLYRNSETGDPSFIGSFTKGLPHDDN
GAIIDPDDFLAFVRAINSGDEKEIAALTLGPARDPETGLPIWRSDLANSLDLEVRGWENSSAGLT
FDLEGPDAQSVAMPPAPVLTSPELIAEMAELYLMALGRDIEFSEFDSPKNAAFIRSAIERLNGLE
WFNTPAKLGDPPAEIRRRRGEVTVGNLFRGILPGSEVGPYLSQFIIVGSKQIGSATVGNKTLVSP
NAADEFDGEIAYGSITISQRVRIATPGRDFMTDLKVFLDVQDAADFRGFESYEPGARLIRTIRDL
ATWVHFDSLYEAYLNACLILLANGVPFDPNLPFQQEDKLDNQDVFVNFGSAHVLSLVTEVATRAL
KAVRYQKFNIHRRLRPEATGGLISVNKNAFLKSESVFPEVDVLVEELSSILDDSASSNEKQNIAD
GDVSPGKSFLLPMAFAEGSPFHPSYGSGHAVVAGACVTILKAFFDANFQIDQVFEVDTDEDKLVK
SSFPGPLTVAGELNKLADNVAIGRNMAGVHYFSDQFESLLLGEQIAIGILEEQSLTYGENFFFNL
PKFDGTTIQI
>d1vns__ a.111.1.3 (-) Chloroperoxidase {Curvularia inaequalis}
VTPIPLPKIDEPEEYNTNYILFWNHVGLELNRVTHTVGGPLTGPPLSARALGMLHLAIHDAYFSI
CPPTDFTTFLSPDTENAAYRLPSPNGANDARQAVAGAALKMLSSLYMKPVEQPNPNPGANISDNA
YAQLGLVLDRSVLEAPGGVDRESASFMFGEDVADVFFALLNDPRGASQEGYHPTPGRYKFDDEPT
HPVVLIPVDPNNPNGPKMPFRQYHAPFYGKTTKRFATQSEHFLADPPGLRSNADETAEYDDAVRV
AIAMGGAQALNSTKRSPWQTAQGLYWAYDGSNLIGTPPRFYNQIVRRIAVTYKKEEDLANSEVNN
ADFARLFALVDVACTDAGIFSWKEKWEFEFWRPLSGVRDDGRPDHGDPFWLTLGAPATNTNDIPF
KPPFPAYPSGHATFGGAVFQMVRRYYNGRVGTWKDDEPDNIAIDMMISEELNGVNRDLRQPYDPT
APIEDQPGIVRTRIVRHFDSAWELMFENAISRIFLGVHWRFDAAAARDILIPTTTKDVYAVDNNG
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ATVFQNVEDIRYTTRGTREDEEGLFPIGGVPLGIEIADEIFNNGLKPTPPEIQP
>d1sig__ a.112.1.1 (-) sigma70 subunit fragment from RNA polymerase
{Escherichia coli}
MEGEIDIAKRIEDGINQVQCSVAEYPEAITYLLEQYNRVEAEEARLSDLITGFVDPNAEEDLAPT
ATHVGSELSQEDLDDDEDEDEEDGDDDSADDDNSIDPELAREKFAELRAQYVVTRDTIKAKGRSH
ATAQEEILKLSEVFKQFRLVPKQFDYLVNSMRVMMDRVRTQERLIMKLCVEQCKMPKKNFITLFT
GNETSDTWFNAAIAMNKPWSEKLHDVSEEVHRALQKLQQIEEETGLTIEQVKDINRRMSIGEAKA
RRAKKEMVEANLRLVISIAKKYTNRGLQFLDLIQEGNIGLMKAVDKFEYRRGYKFSTYATWWIRQ
AITRSIADQ
>d1ewqa1 a.113.1.1 (A:267-541) DNA repair protein MutS, domain III
{Thermus aquaticus}
RGQDTLFSVLDETRTAPGRRLLQSWLRHPLLDRGPLEARLDRVEGFVREGALREGVRRLLYRLAD
LERLATRLELGRASPKDLGALRRSLQILPELRALLGEEVGLPDLSPLKEELEAALVEDPPLKVSE
GGLIREGYDPDLDALRAAHREGVAYFLELEERERERTGIPTLKVGYNAVFGYYLEVTRPYYERVP
KEYRPVQTLKDRQRYTLPEMKEKEREVYRLEALIRRREEEVFLEVRERAKRQAEALREAARILAE
LDVYAALAEVAVRYG
>d1e3ma1 a.113.1.1 (A:270-566) DNA repair protein MutS, domain III
{Escherichia coli}
DAATRRNLEITQNLAGGAENTLASVLDCTVTPMGSRMLKRWLHMPVRDTRVLLERQQTIGALQDF
TAGLQPVLRQVGDLERILARLALRTARPRDLARMRHAFQQLPELRAQLETVDSAPVQALREKMGE
FAELRDLLERAIIDTPPVLVRDGGVIASGYNEELDEWRALADGATDYLERLEVRERERTGLDTLK
VGFNAVHGYYIQISRGQSHLAPINYMRRQTLKNAERYIIPELKEYEDKVLTSKGKALALEKQLYE
ELFDLLLPHLEALQQSASALAELDVLVNLAERAYTLN
>d1f5na1 a.114.1.1 (A:284-583) Interferon-induced guanylate-binding
protein 1 (GBP1), C-terminal domain {Human (Homo sapiens)}
GGIQVNGPRLESLVLTYVNAISSGDLPCMENAVLALAQIENSAAVQKAIAHYEQQMGQKVQLPTE
SLQELLDLHRDSEREAIEVFIRSSFKDVDHLFQKELAAQLEKKRDDFCKQNQEASSDRCSGLLQV
IFSPLEEEVKAGIYSKPGGYRLFVQKLQDLKKKYYEEPRKGIQAEEILQTYLKSKESMTDAILQT
DQTLTEKEKEIEVERVKAESAQASAKMLHEMQRKNEQMMEQKERSYQEHLKQLTEKMENDRVQLL
KEQERTLALKLQEQEQLLKEGFQKESRIMKNEIQDLQTKM
>d1bvp11 a.115.1.1 (1:1-120,1:255-349) Bluetongue virus capsid
protein vp7 (BTV-10 vp7) {Bluetongue virus}
MDTIAARALTVMRACATLQEARIVLEANVMEILGIAINRYNGLTLRGVTMRPTSLAQRNEMFFMC
LDMMLSAAGINVGPISPDYTQHMATIGVLATPEIPFTTEAANEIARVTGETSTWGXKTLNQYPAL
TAEIFNVYSFRDHTWHGLRTAILNRTTLPNMLPPIFPPNDRDSILTLLLLSTLADVYTVLRPEFA
IHGVNPMPGPLTRAIARAAYV
>d1qhda1 a.115.1.2 (A:1-148,A:333-397) vp6, the major capsid protein
of group A rotavirus {Bovine rotavirus}
MDVLYSLSKTLKDARDKIVEGTLYSNVSDLIQQFNQMIITMNGNEFQTGGIGNLPIRNWNFDFGL
LGTTLLNLDANYVETARNTIDYFVDFVDNVCMDEMVRESQRNGIAPQSDSLIKLSGIKFKRINFD
NSSEYIENWNLQNRRQRTXSVLADASETMLANVTSVRQEYAIPVGPVFPPGMNWTDLITNYSPSR
EDNLQRVFTVASIRSMLVK
>d1tx4a_ a.116.1.1 (A:) p50 RhoGAP domain {Human (Homo sapiens)}
PLPNQQFGVSLQHLQEKNPEQEPIPIVLRETVAYLQAHALTTEGIFRRSANTQVVREVQQKYNMG
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LPVDFDQYNALHLPAVILKTFLRELPEPLLTFDLYPHVVGFLNIDESQRVPATLQVLQTLPEENY
QVLRFLTAFLVQISAHSDQNKMTNTNLAVVFGPNLLWAKDAAITLKAINPINTFTKFLLDHQGEL
F
>d1pbwa_ a.116.1.1 (A:) p85 alpha subunit RhoGAP domain {Human (Homo
sapiens)}
LPDLAEQFAPPDIAPPLLIKLVEAIEKKGLECSTLYRTQSSSNLAELRQLLDCDTPSVDLEMIDV
HVLADAFKRYLLDLPNPVIPAAVYSEMISLAPEVQSSEEYIQLLKKLIRSPSIPHQYWLTLQYLL
KHFFKLSQTSSKNLLNARVLSEIFSPMLFRFSAASSDNTENLIKVIEILISTEW
>d1f7ca_ a.116.1.1 (A:) Graf {Chicken (Gallus gallus)}
AQLDSIGFSIIKKCIHAVETRGINEQGLYRIVGVNSRVQKLLSILMDPKTATETETEICAEWEIK
TITSALKTYLRMLPGPLMMYQFQRSFIKAAKLENQESRVSEIHSLVHRLPEKNRQMLHLLMNHLA
KVADNHKQNLMTVANLGVVFGPTLLRPQEETVAAIMDIKFQNIVIEILIENHEKIFNTVPE
>d1wer__ a.116.1.2 (-) p120GAP domain {Human (Homo sapiens)}
MPEEEYSEFKELILQKELHVVYALSHVCGQDRTLLASILLRIFLHEKLESLLLCTLNDREISMED
EATTLFRATTLASTLMEQYMKATATQFVHHALKDSILKIMESKQSCELSPSKLEKNEDVNTNLTH
LLNILSELVEKIFMASEILPPTLRYIYGCLQKSVQHKWPTNTTMRTRVVSGFVFLRLICPAILNP
RMFNIISDSPSPIAARTLILVAKSVQNLANLVEFGAKEPYMEGVNPFIKSNKHRMIMFLDELGNV
PELPDTTEHSRTDLSRDLAALHEICVAHSDELRTLSNERGAQQHVLKKLLAITELLQQKQNQYT
>d1nf1a_ a.116.1.2 (A:) GAP related domain of neurofibromin {Human
(Homo sapiens)}
ERLVELVTMMGDQGELPIAMALANVVPCSQWDELARVLVTLFDSRHLLYQLLWNMFSKEVELADS
MQTLFRGNSLASKIMTFCFKVYGATYLQKLLDPLLRIVITSSDWQHVSFEVDPTRLEPSESLEEN
QRNLLQMTEKFFHAIISSSSEFPPQLRSVCHCLYQVVSQRFPQNSIGAVGSAMFLRFINPAIVSP
YEAGILDKKPPPIIERGLKLMSKILQSIANHVLFTKEEHMRPFNDFVKSNFDAARRFFLDIASDC
PTSDAVNHSLSFISDGNVLALHRLLWNNQEKIGQYLSSNRDHKAVGRRPFDKMATLLAYLGPPE
>d1bkds_ a.117.1.1 (S:) Son of sevenless-1 (sos-1) {Human (Homo
sapiens)}
RLPSADVYRFAEPDSEENIIFEEGIPIIKAGTVIKLIERLTYHMYADPNFVRTFLTTYRSFCKPQ
ELLSLIIERFEIPEPRFRKEYIQPVQLRVLNVCRHWVEHHFYDFERDAYLLQRMEEFIGTVRGKA
MKKWVESITKIIQRKKITFQSSPPTVEWHISRPGHIETFDLLTLHPIEIARQLTLLESDLYRAVQ
PSELVGSVWTKEDKEINSPNLLKMIRHTTNLTLWFEKCIVETENLEERVAVVSRIIEILQVFQEL
NNFNGVLEVVSAMNSSPVYRLDHTFEQIPSRQKKILEEAHELSEDHYKKYLAKLRSINPPCVPFF
GIYLTNILKTEEGNPEVLKRHGKELINFSKRRKVAEITGEIQQYQNQPYCLRVESDIKRFFENLN
PMGNSMEKEFTDYLFNKSLEIEPRNPKPLPRFPKKYSYPLKSPGVRPSN
>d1h6oa_ a.146.1.1 (A:) TRF1 {Human (Homo sapiens)}
EDAGLVAEAEAVAAGWMLDFLCLSLCRAFRDGRSEDFRRTRNSAEAIIHGLSSLTACQLRTIYIC
QFLTRIAAGKTLDAQFENDERITPLESALMIWGSIEKEHDKLHEEIQNLIKIQAIAVCMENGNFK
EAEEVFERIFGDPNSHMPFKSKLLMIISQKDTFHSFFQHFSYNHMMEKIKSYVNYVLSEKSSTFL
MKAAAKVVE
>d1h6pa_ a.146.1.1 (A:) TRF2 {Human (Homo sapiens)}
AGEARLEEAVNRWVLKFYFHEALRAFRGSRYGDFRQIRDIMQALLVRPLGKEHTVSRLLRVMQCL
SRIEEGENLDCSFDMEAELTPLESAINVLEMIKTEFTLTEAVVESSRKLVKEAAVIICIKNKEFE
KASKILKKHMSKDPTTQKLRNDLLNIIREKNLAHPVIQNFSYETFQQKMLRFLESHLDDAEPYLL
TMAKKALK
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>d1g3jc_ a.118.1.1 (C:) beta-Catenin {Human (Homo sapiens)}
HHREGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLLLHQEGAKMAVRLAGGLQKMVALLN
KTNVKFLAITTDCLQILAYGNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSVCSS
NKPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSDAATKQEGMEGLLGTLVQLLGSDDINVV
TCAAGILSNLTCNNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTSRHQEAEMAQ
NAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLALCPANHAPLREQGAIPRLVQLLVRAHQDT
QRRTSMGGTQQQFVEGVRMEEIVEGCTGALHILARDVHNRIVIRGLNTIPLFVQLLYSPIENIQR
VAAGVLCELAQDKEAAEAIEAEGATAPLTELLHSRNEGVATYAAAVLFRMSE
>d1jdha_ a.118.1.1 (A:) beta-Catenin {Human (Homo sapiens)}
AVVNLINYQDDAELATRAIPELTKLLNDEDQVVVNKAAVMVHQLSKKEASRHAIMRSPQMVSAIV
RTMQNTNDVETARCTAGTLHNLSHHREGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLLL
HQEGAKMAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAYGNQESKLIILASGGPQALVNIMR
TYTYEKLLWTTSRVLKVLSVCSSNKPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSDAATK
QEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTCNNYKNKMMVCQVGGIEALVRTVLRAGDRED
ITEPAICALRHLTSRHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLALCPANH
APLREQGAIPRLVQLLVRAHQDTQRRTSMGGTQQQFVEGVRMEEIVEGCTGALHILARDVHNRIV
IRGLNTIPLFVQLLYSPIENIQRVAAGVLCELAQDKEAAEAIEAEGATAPLTELLHSRNEGVATY
AAAVLFRMS
>d1iala_ a.118.1.1 (A:) Importin alpha {Mouse (Mus musculus)}
DEQMLKRRNVSSFPDDATSPLQENRNNQGTVNWSVEDIVKGINSNNLESQLQATQAARKLLSREK
QPPIDNIIRAGLIPKFVSFLGKTDCSPIQFESAWALTNIASGTSEQTKAVVDGGAIPAFISLLAS
PHAHISEQAVWALGNIAGDGSAFRDLVIKHGAIDPLLALLAVPDLSTLACGYLRNLTWTLSNLCR
NKNPAPPLDAVEQILPTLVRLLHHNDPEVLADSCWAISYLTDGPNERIEMVVKKGVVPQLVKLLG
ATELPIVTPALRAIGNIVTGTDEQTQKVIDAGALAVFPSLLTNPKTNIQKEATWTMSNITAGRQD
QIQQVVNHGLVPFLVGVLSKADFKTQKEAAWAITNYTSGGTVEQIVYLVHCGIIEPLMNLLSAKD
TKIIQVILDAISNIFQAAEKLGETEKLSIMIEECGGLDKIEALQRHENESVYKASLNLIEKYF
>d1ibrb_ a.118.1.1 (B:) Importin beta {Human (Homo sapiens)}
ELITILEKTVSPDRLELEAAQKFLERAAVENLPTFLVELSRVLANPGNSQVARVAAGLQIKNSLT
SKDPDIKAQYQQRWLAIDANARREVKNYVLQTLGTETYRPSSASQCVAGIACAEIPVNQWPELIP
QLVANVTNPNSTEHMKESTLEAIGYICQDIDPEQLQDKSNEILTAIIQGMRKEEPSNNVKLAATN
ALLNSLEFTKANFDKESERHFIMQVVCEATQCPDTRVRVAALQNLVKIMSLYYQYMETYMGPALF
AITIEAMKSDIDEVALQGIEFWSNVCDEEMDLAIEASEAAEQGRPPEHTSKFYAKGALQYLVPIL
TQTLTKQDENDDDDDWNPCKAAGVCLMLLATCCEDDIVPHVLPFIKEHIKNPDWRYRDAAVMAFG
CILEGPEPSQLKPLVIQAMPTLIELMKDPSVVVRDTAAWTVGRICELLPEAAINDVYLAPLLQCL
IEG
>d1qgra_ a.118.1.1 (A:) Importin beta {Human (Homo sapiens)}
MELITILEKTVSPDRLELEAAQKFLERAAVENLPTFLVELSRVLANPGNSQVARVAAGLQIKNSL
TSKDPDIKAQYQQRWLAIDANARREVKNYVLHTLGTETYRPSSASQCVAGIACAEIPVNQWPELI
PQLVANVTNPNSTEHMKESTLEAIGYICQDIDPEQLQDKSNEILTAIIQGMRKEEPSNNVKLAAT
NALLNSLEFTKANFDKESERHFIMQVVCEATQCPDTRVRVAALQNLVKIMSLYYQYMETYMGPAL
FAITIEAMKSDIDEVALQGIEFWSNVCDEEMDLAIEASEAAEQGRPPEHTSKFYAKGALQYLVPI
LTQTLTKQDENDDDDDWNPCKAAGVCLMLLATCCEDDIVPHVLPFIKEHIKNPDWRYRDAAVMAF
GCILEGPEPSQLKPLVIQAMPTLIELMKDPSVVVRDTAAWTVGRICELLPEAAINDVYLAPLLQC
LIEGLSAEPRVASNVCWAFSSLAEAAYEAADVADDQEEPATYCLSSSFELIVQKLLETTDRPDGH
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QNNLRSSAYESLMEIVKNSAKDCYPAVQKTTLVIMERLQQVLQMESHIQSTSDRIQFNDLQSLLC
ATLQNVLRKVQHQDALQISDVVMASLLRMFQSTAGSGGVQEDALMAVSTLVEVLGGEFLKYMEAF
KPFLGIGLKNYAEYQVCLAAVGLVGDLCRALQSNIIPFCDEVMQLLLENLGNENVHRSVKPQILS
VFGDIALAIGGEFKKYLEVVLNTLQQASQAQVDKSDYDMVDYLNELRESCLEAYTGIVQGLKGDQ
ENVHPDVMLVQPRVEFILSFIDHIAGDEDHTDGVVACAAGLIGDLCTAFGKDVLKLVEARPMIHE
LLTEGRRSKTNKAKTLARWATKELRKLKNQA
>d1qbkb_ a.118.1.1 (B:) Karyopherin beta2 {Human (Homo sapiens)}
YEWKPDEQGLQQILQLLKESQSPDTTIQRTVQQKLEQLNQYPDFNNYLIFVLTKLKSEDEPTRSL
SGLILKNNVKAHFQNFPNGVTDFIKSECLNNIGDSSPLIRATVGILITTIASKGELQNWPDLLPK
LCSLLDSEDYNTCEGAFGALQKICEDSAEILDSDVLDRPLNIMIPKFLQFFKHSSPKIRSHAVAC
VNQFIISRTQALMLHIDSFTENLFALAGDEEPEVRKNVCRALVMLLEVRMDRLLPHMHNIVEYML
QRTQDQDENVALEACEFWLTLAEQPICKDVLVRHLPKLIPVLVNGMKYSDIDIILLKGDVEEDET
IPDSEQDIRPRFHRSRTVAQQHDEDGIEEEDDDDDEIDDDDTISDWNLRKCSAAALDVLANVYRD
ELLPHILPLLKELLFHHEWVVKESGILVLGAIAEGCMQGMIPYLPELIPHLIQCLSDKKALVRSI
TCWTLSRYAHWVVSQPPDTYLKPLMTELLKRILDSNKRVQEAACSAFATLEEEACTELVPYLAYI
LDTLVFAFSKYQHKNLLILYDAIGTLADSVGHHLNKPEYIQMLMPPLIQKWNMLKDEDKDLFPLL
ECLSSVATALQSGFLPYCEPVYQRCVNLVQKTLAQAMLNNAQPDQYEAPDKDFMIVALDLLSGLA
EGLGGNIEQLVARSNILTLMYQCMQDKMPEVRQSSFALLGDLTKACFQHVKPCIADFMPILGTNL
NPEFISVCNNATWAIGEISIQMGIEMQPYIPMVLHQLVEIINRPNTPKTLLENTAITIGRLGYVC
PQEVAPMLQQFIRPWCTSLRNIRDNEEKDSAFRGICTMISVNPSGVIQDFIFFCDAVASWINPKD
DLRDMFCKILHGFKNQVGDENWRRFSDQFPLPLKERLAAFYGV
>d1ee4a_ a.118.1.1 (A:) Karyopherin alpha {Baker's yeast (Saccharomyces cerevisiae)}
QELPQMTQQLNSDDMQEQLSATVKFRQILSREHRPPIDVVIQAGVVPRLVEFMRENQPEMLQLEA
AWALTNIASGTSAQTKVVVDADAVPLFIQLLYTGSVEVKEQAIWALGNVAGDSTDYRDYVLQCNA
MEPILGLFNSNKPSLIRTATWTLSNLCRGKKPQPDWSVVSQALPTLAKLIYSMDTETLVDACWAI
SYLSDGPQEAIQAVIDVRIPKRLVELLSHESTLVQTPALRAVGNIVTGNDLQTQVVINAGVLPAL
RLLLSSPKENIKKEACWTISNITAGNTEQIQAVIDANLIPPLVKLLEVAEDKTKKEACWAISNAS
SGGLQRPDIIRYLVSQGCIKPLCDLLEIADNRIIEVTLDALENILKMGEADKEARGLNINENADF
IEKAGGMEKIFNCQQNENDKIYEKAYKIIETYF
>d1b3ua_ a.118.1.2 (A:) Constant regulatory domain of protein phosphatase 2a, pr65alpha {Human (Homo sapiens)}
AAADGDDSLYPIAVLIDELRNEDVQLRLNSIKKLSTIALALGVERTRSELLPFLTDTIYDEDEVL
LALAEQLGTFTTLVGGPEYVHCLLPPLESLATVEETVVRDKAVESLRAISHEHSPSDLEAHFVPL
VKRLAGGDWFTSRTSACGLFSVCYPRVSSAVKAELRQYFRNLCSDDTPMVRRAAASKLGEFAKVL
ELDNVKSEIIPMFSNLASDEQDSVRLLAVEACVNIAQLLPQEDLEALVMPTLRQAAEDKSWRVRY
MVADKFTELQKAVGPEITKTDLVPAFQNLMKDCEAEVRAAASHKVKEFCENLSADCRENVIMSQI
LPCIKELVSDANQHVKSALASVIMGLSPILGKDNTIEHLLPLFLAQLKDECPEVRLNIISNLDCV
NEVIGIRQLSQSLLPAIVELAEDAKWRVRLAIIEYMPLLAGQLGVEFFDEKLNSLCMAWLVDHVY
AIREAATSNLKKLVEKFGKEWAHATIIPKVLAMSGDPNYLHRMTTLFCINVLSEVCGQDITTKHM
LPTVLRMAGDPVANVRFNVAKSLQKIGPILDNSTLQSEVKPILEKLTQDQDVDVKYFAQEALTVL
SLA
>d1hu3a_ a.118.1.2 (A:) Eukaryotic initiation factor eIF4G {Human (Homo sapiens)}
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SDPENIKTQELFRKVRSILNKLTPQMFNQLMKQVSGLTVDTEERLKGVIDLVFEKAIDEPSFSVA
YANMCRCLVTLKVPMADKPGNTVNFRKLLLNRCQKEFEKDKADDDVFEKKQKELEAASAPEERTR
LHDELEEAKDKARRRSIGNIKFIGELFKLKMLTEAIMHDCVVKLLKNHDEESLECLCRLLTTIGK
DLDFEKAKPRMDQYFNQMEKIVKERKTSSRIRFMLQDVIDLRLCNWVS
>d1h6ka1 a.118.1.2 (A:27-290) CBP80, 80KDa nuclear cap-binding
protein {Human (Homo sapiens)}
TEDHLESLICKVGEKSACSLESNLEGLAGVLEADLPNYKSKILRLLCTVARLLPEKLTIYTTLVG
LLNARNYNFGGEFVEAMIRQLKESLKANNYNEAVYLVRFLSDLVNCHVIAAPSMVAMFENFVSVT
QEEDVPQVRRDWYVYAFLSSLPWVGKELYEKKDAEMDRIFANTESYLKRRQKTHVPMLQVWTADK
PHPQEEYLDCLWAQIQKLKKDRWQERHILRPYLAFDSILCEALQHNLPPFTPPPHTEDSVYPMPR
VIFR
>d1h6ka2 a.118.1.2 (A:291-480) CBP80, 80KDa nuclear cap-binding
protein {Human (Homo sapiens)}
MFDYTDDPEGPVMPGSHSVERFVIEENLHCIIKSHWKERKTCAAQLVSYPGKNKIPLNYHIVEVI
FAELFQLPAPPHIDVMYTTLLIELCKLQPGSLPQVLAQATEMLYMRLDTMNTTCVDRFINWFSHH
LSNFQFRWSWEDWSDCLSQDPESPKPKFVREVLEKCMRLSYHQRILDIVPPTFSALCPSN
>d1h6ka3 a.118.1.2 (A:481-790) CBP80, 80KDa nuclear cap-binding
protein {Human (Homo sapiens)}
PTCIYKYGDESSNSLPGHSVALCLAVAFKSKATNDEIFSILKDVPNPNQDDDDDEGFSFNPLKIE
VFVQTLLHLAAKSFSHSFSALAKFHEVFKTLAESDEGKLHVLRVMFEVWRNHPQMIAVLVDKMIR
TQIVDCAAVANWIFSSELSRDFTRLFVWEILHSTIRKMNKHVLKIQKELEEAKEKLARQHDGVLE
EQIERLQEKVESAQSEQKNLFLVIFQRFIMILTEHLVRCETDGTSVLTPWYKNCIERLQQIFLQH
HQIIQQYMVTLENLLFTAELDPHILAVFQQFCALQA
>d1hs6a1 a.118.1.7 (A:461-610) Leukotriene A4 hydrolase C-terminal
domain {Human (Homo sapiens)}
DMTLTNACIALSQRWITAKEDDLNSFNATDLKDLSSHQLNEFLAQTLQRAPLPLGHIKRMQEVYN
FNAINNSEIRFRWLRLCIQSKWEDAIPLALKMATEQGRMKFTRPLFKDLAAFDKSHDQAVRTYQE
HKASMHPVTAMLVGKDLKVD
>d1b89a_ a.118.1.3 (A:) Clathrin heavy chain proximal leg segment {Cow
(Bos taurus)}
RLAELEEFINGPNNAHIQQVGDRCYDEKMYDAAKLLYNNVSNFGRLASTLVHLGEYQAAVDGARK
ANSTRTWKEVCFACVDGKEFRLAQMCGLHIVVHADELEELINYYQDRGYFEELITMLEAALGLER
AHMGMFTELAILYSKFKPQKMREHLELFWSRVNIPKVLRAAEQAHLWAELVFLYDKYEEYDNAII
TMMNHPTDAWKEGQFKDIITKVANVELYYRAIQFYLEFKPLLLNDLLMVLSPRLDHTRAVNYFSK
VKQLPLVKPYLRSVQNHNNKSVNESLNNLFITEEDYQALRTSIDAYDNFDNISLAQRLEKHELIE
FRRIAAYLFKG
>d1bpoa1 a.118.1.4 (A:331-487) Clathrin heavy-chain linker domain
{Rat (Rattus norvegicus)}
EENIIPYITNVLQNPDLALRMAVRNNLAGAEELFARKFNALFAQGNYSEAAKVAANAPKGILRTP
DTIRRFQSVPAQPGQTSPLLQYFGILLDQGQLNKYESLELCRPVLQQGRKQLLEKWLKEDKLECS
EELGDLVKSVDPTLALSVYLRANVPNK
>d1c9la1 a.118.1.4 (A:331-359) Clathrin heavy-chain linker domain
{Rat (Rattus norvegicus)}
EENIIPYITNVLQNPDLALRMAVRNNLAG
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>d1lrv__ a.118.1.5 (-) Leucine-rich repeat variant {Azotobacter vinelandii}
TPIGDCRVCSFRMSLLLTGRCTPGDACVAVESGRQIDRFFRNNPHLAVQYLADPFWERRAIAVRY
SPVEALTPLIRDSDEVVRRAVAYRLPREQLSALMFDEDREVRITVADRLPLEQLEQMAADRDYLV
RAYVVQRIPPGRLFRFMRDEDRQVRKLVAKRLPEESLGLMTQDPEPEVRRIVASRLRGDDLLELL
HDPDWTVRLAAVEHASLEALRELDEPDPEVRLAIAGRL
>d1e8xa1 a.118.1.6 (A:525-725) Phoshoinositide 3-kinase (PI3K) helical domain {Pig (Sus scrofa)}
HPIALPKHRPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAY
PKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDD
DVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEA
YLRGCG
>d1ib2a_ a.118.1.8 (A:) Pumilio 1 {Human (Homo sapiens)}
GRSRLLEDFRNNRYPNLQLREIAGHIMEFSQDQHGSRFIQLKLERATPAERQLVFNEILQAAYQL
MVDVFGNYVIQKFFEFGSLEQKLALAERIRGHVLSLALQMYGCRVIQKALEFIPSDQQNEMVREL
DGHVLKCVKDQNGNHVVQKCIECVQPQSLQFIIDAFKGQVFALSTHPYGCRVIQRILEHCLPDQT
LPILEELHQHTEQLVQDQYGNYVIQHVLEHGRPEDKSKIVAEIRGNVLVLSQHKFASNVVEKCVT
HASRTERAVLIDEVCTMNDGPHSALYTMMKDQYANYVVQKMIDVAEPGQRKIVMHKIRPHIA
>d1ho8a_ a.118.1.9 (A:) Regulatory subunit H of the V-type ATPase {Baker's yeast (Saccharomyces cerevisiae)}
GATKILMDSTHFNEIRSIIRSRSVAWDALARSEELSEIDASTAKALESILVKKNIGDGLSSSNNA
HSGFKVNGKTLIPLIHLLSTSDNEDCKKSVQNLIAELLSSDKYGDDTVKFFQEDPKQLEQLFDVS
LKGDFQTVLISGFNVVSLLVQNGLHNVKLVEKLLKNNNLINILQNIEQMDTCYVCIRLLQELAVI
PEYRDVIWLHEKKFMPTLFKILQRATDSQLATRIVATNSNHLGIQLQYHSLLLIWLLTFNPVFAN
ELVQKYLSDFLDLLKLVKITIKEKVSRLCISIILQCCSTRVKQHKKVIKQLLLLGNALPTVQSLS
ERKYSDEELRQDISNLKEILENEYQELTSFDEYVAELDSKLLCWSPPHVDNGFWSDNIDEFKKDN
YKIFRQLIELLQAKVRNGDVNAKQEKIIIQVALNDITHVVELLPESIDVLDKTGGKADIMELLNH
SDSRVKYEALKATQAIIGYTFK
>d1ycsb1 a.118.2.1 (B:327-456) 53BP2 {Human (Homo sapiens)}
PLALLLDSSLEGEFDLVQRIIYEVDDPSLPNDEGITALHNAVCAGHTEIVKFLVQFGVNVNAADS
DGWTPLHCAASCNNVQVCKFLVESGAAVFAMTYSDMQTAADKCEEMEEGYTQCSQFLYGVQEKMG
>d1awcb_ a.118.2.1 (B:) GA bindinig protein (GABP) beta 1 {Mouse (Mus musculus)}
DLGKKLLEAARAGQDDEVRILMANGAPFTTDWLGTSPLHLAAQYGHFSTTEVLLRAGVSRDARTK
VDRTPLHMAASEGHANIVEVLLKHGADVNAKDMLKMTALHWATEHNHQEVVELLIKYGADVHTQS
KFCKTAFDISIDNGNEDLAEILQ
>d1bd8__ a.118.2.1 (-) Cell cycle inhibitor p19ink4D {Human (Homo sapiens)}
RAGDRLSGAAARGDVQEVRRLLHRELVHPDALNRFGKTALQVMMFGSTAIALELLKQGASPNVQD
TSGTSPVHDAARTGFLDTLKVLVEHGADVNVPDGTGALPIHLAVQEGHTAVVSFLAAESDLHRRD
ARGLTPLELALQRGAQDLVDILQGHM
>d1blxb_ a.118.2.1 (B:) Cell cycle inhibitor p19ink4D {Mouse (Mus musculus)}
VCVGDRLSGAAARGDVQEVRRLLHRELVHPDALNRFGKTALQVMMFGSPAVALELLKQGASPNVQ
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DASGTSPVHDAARTGFLDTLKVLVEHGADVNALDSTGSLPIHLAIREGHSSVVSFLAPESDLHHR
DASGLTPLELARQRGAQNLMDILQGHMMIP
>d1ihba_ a.118.2.1 (A:) p18ink4C(ink6) {Human (Homo sapiens)}
WGNELASAAARGDLEQLTSLLQNNVNVNAQNGFGRTALQVMKLGNPEIARRLLLRGANPDLKDRT
GFAVIHDAARAGFLDTLQTLLEFQADVNIEDNEGNLPLHLAAKEGHLRVVEFLVKHTASNVGHRN
HKGDTACDLARLYGRNEVVSLMQANG
>d1a5e__ a.118.2.1 (-) Cell cycle inhibitor p16ink4A {Human (Homo
sapiens)}
MEPAAGSSMEPSADWLATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMMGSARVAELLLL
HGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYL
RAAAGGTRGSNHARIDAAEGPSDIPD
>d1bi7b_ a.118.2.1 (B:) Cell cycle inhibitor p16ink4A {Human (Homo
sapiens)}
EPSADWLATAAARGRVEEVRALLEAGANPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCAD
PATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAA
>d1iknd_ a.118.2.1 (D:) I-kappa-B-alpha {Human (Homo sapiens)}
DGDSFLHLAIIHEEKALTMEVIRQVKGDLAFLNFQNNLQQTPLHLAVITNQPEIAEALLGAGCDP
ELRDFRGNTPLHLACEQGCLASVGVLTQSCTTPHLHSILKATNYNGHTCLHLASIHGYLGIVELL
VSLGADVNAQEPCNGRTALHLAVDLQNPDLVSLLLKCGADVNRVTYQGYSPYQLTWGRPSTRIQQ
QLGQLTLENLQMLPESEDEESYDTES
>d1k1aa_ a.118.2.1 (A:) bcl-3 {Human (Homo sapiens)}
EDGDTPLHIAVVQGNLPAVHRLVNLFQQGGRELDIYNNLRQTPLHLAVITTLPSVVRLLVTAGAS
PMALDRHGQTAAHLACEHRSPTCLRALLDSAAPGTLDLEARNYDGLTALHVAVNTECQETVQLLL
ERGADIDAVDIKSGRSPLIHAVENNSLSMVQLLLQHGANVNAQMYSGSSALHSASGRGLLPLVRT
LVRSGADSSLKNCHNDTPLMVARSRRVIDILRG
>d1myo__ a.118.2.1 (-) Myotrophin {Rat (Rattus norvegicus)}
MCDKEFMWALKNGDLDEVKDYVAKGEDVNRTLEGGRKPLHYAADCGQLEILEFLLLKGADINAPD
KHHITPLLSAVYEGHVSCVKLLLSKGADKTVKGPDGLTALEATDNQAIKALLQ
>d1sw6a_ a.118.2.1 (A:) Swi6 ankyrin-repeat fragment {Baker's yeast
(Saccharomyces cerevisiae)}
GPIITFTHDLTSDFLSSPLKIMKALPSPVVNDNEQKMKLEAFLQRLLFPEIQEMPTSLNNDSSNR
NSEGGSSNQQQQHVSFDSLLQEVNDAFPNTQLNLNIPVDEHGNTPLHWLTSIANLELVKHLVKHG
SNRLYGDNMGESCLVKAVKSVNNYDSGTFEALLDYLYPCLILEDSMNRTILHHIIITSGMTGCSA
AAKYYLDILMGWIVKKQNRPIQSGTNEKESKPNDKNGERKDSILENLDLKWIIANMLNAQDSNGD
TCLNIAARLGNISIVDALLDYGADPFIANKSGLRPVDFGAG
>d1dcqa1 a.118.2.1 (A:369-522) Pyk2-associated protein beta {Mouse
(Mus musculus)}
ADTAAKLHSLCEAVKTRDIFGLLQAYADGVDLTEKIPLANGHEPDETALHLAVRSVDRTSLHIVD
FLVQNSGNLDKQTGKGSTALHYCCLTDNAECLKLLLRGKASIEIANESGETPLDIAKRLKHEHCE
ELLTQALSGRFNSHVHVEYEWRLL
>d1pbv__ a.118.3.1 (-) Exchange factor ARNO {Human (Homo sapiens)}
ANEGSKTLQRNRKMAMGRKKFNMDPKKGIQFLVENELLQNTPEEIARFLYKGEGLNKTAIGDYLG
EREELNLAVLHAFVDLHEFTDLNLVQALRQFLWSFRLPGEAQKIDRMMEAFAQRYCLCNPGVFQS
TDTCYVLSFAVIMLNTSLHNPNVRDKPGLERFVAMNRGINEGGDLPEELLRNLYDSIRNEPFKIP
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>d1bc9__ a.118.3.1 (-) Cytohesin-1/b2-1 {Human (Homo sapiens)}
MKNMQRNKQVAMGRKKFNMDPKKGIQFLIENDLLKNTCEDIAQFLYKGEGLNKTAIGDYLGERDE
FNIQVLHAFVELHEFTDLNLVQALRQFLWSFRLPGEAQKIDRMMEAFAQRYCQCNNGVFQSTDTC
YVLSFAIIMLNTSLHNPNVKDKPTVERFIAMNRGINDGGDLPEELLRNLYESIKNEPFKIPELEH
HHHHH
>d1qsaa1 a.118.5.1 (A:1-450) 70 KDa soluble lytic transglycosylase
(SLT70), superhelical domain {Escherichia coli}
DSLDEQRSRYAQIKQAWDNRQMDVVEQMMPGLKDYPLYPYLEYRQITDDLMNQPAVTVTNFVRAN
PTLPPARTLQSRFVNELARREDWRGLLAFSPEKPGTTEAQCNYYYAKWNTGQSEEAWQGAKELWL
TGKSQPNACDKLFSVWRASGKQDPLAYLERIRLAMKAGNTGLVTVLAGQMPADYQTIASAIISLA
NNPNTVLTFARTTGATDFTRQMAAVAFASVARQDAENARLMIPSLAQAQQLNEDQIQELRDIVAW
RLMGNDVTDEQAKWRDDAIMRSQSTSLIERRVRMALGTGDRRGLNTWLARLPMEAKEKDEWRYWQ
ADLLLERGREAEAKEILHQLMQQRGFYPMVAAQRIGEEYELKIDKAPQNVDSALTQGPEMARVRE
LMYWNLDNTARSEWANLVKSKSKTEQAQLARYAFNNQWWDLSVQATIAGKLWDHLEERFP
>d1d8da_ a.118.6.1 (A:) Protein farnesyltransferase alpha-subunit
{Rat (Rattus norvegicus)}
FLSLDSPTYVLYRDRAEWADIDPVPQNDGPSPVVQIIYSEKFRDVYDYFRAVLQRDERSERAFKL
TRDAIELNAANYTVWHFRRVLLRSLQKDLQEEMNYIIAIIEEQPKNYQVWHHRRVLVEWLKDPSQ
ELEFIADILNQDAKNYHAWQHRQWVIQEFRLWDNELQYVDQLLKEDVRNNSVWNQRHFVISNTTG
YSDRAVLEREVQYTLEMIKLVPHNESAWNYLKGILQDRGLSRYPNLLNQLLDLQPSHSSPYLIAF
LVDIYEDMLENQCDNKEDILNKALELCEILAKEKDTIRKEYWRYIGRSLQSKHSRESDIPASV
>d1jcqa_ a.118.6.1 (A:) Protein farnesyltransferase alpha-subunit
{Human (Homo sapiens)}
FVSLDSPSYVLYRDRAEWADIDPVPQNDGPNPVVQIIYSDKFRDVYDYFRAVLQRDERSERAFKL
TRDAIELNAANYTVWHFRRVLLKSLQKDLHEEMNYITAIIEEQPKNYQVWHHRRVLVEWLRDPSQ
ELEFIADILNQDAKNYHAWQHRQWVIQEFKLWDNELQYVDQLLKEDVRNNSVWNQRYFVISNTTG
YNDRAVLEREVQYTLEMIKLVPHNESAWNYLKGILQDRGLSKYPNLLNQLLDLQPSHSSPYLIAF
LVDIYEDMLENQCDNKEDILNKALELCEILAKEKDTIRKEYWRYIGRSLQSKH
>d1dcea1 a.118.6.1 (A:1-240,A:351-443) Rab geranylgeranyltransferase
alpha-subunit, N-terminal domain {Rat (Rattus norvegicus)}
MHGRLKVKTSEEQAEAKRLEREQKLKLYQSATQAVFQKRQAGELDESVLELTSQILGANPDFATL
WNCRREVLQHLETEKSPEESAALVKAELGFLESCLRVNPKSYGTWHHRCWLLSRLPEPNWARELE
LCARFLEADERNFHCWDYRRFVAAQAAVAPAEELAFTDSLITRNFSNYSSWHYRSCLLPQLHPQP
DSGPQGRLPENVLLKELELVQNAFFTDPNDQSAWFYHRWLLGRAEXLFRCELSVEKSTVLQSELE
SCKELQELEPENKWCLLTIILLMRALDPLLYEKETLQYFSTLKAVDPMRAAYLDDLRSKFLLENS
VLKMEYADV
>d1qjba_ a.118.7.1 (A:) zeta isoform {Human (Homo sapiens)}
MDKNELVQKAKLAEQAERYDDMAACMKSVTEQGAELSNEERNLLSVAYKNVVGARRSSWRVVSSI
EQKTEGAEKKQQMAREYREKIETELRDICNDVLSLLEKFLIPNASQAESKVFYLKMKGDYYRYLA
EVAAGDDKKGIVDQSQQAYQEAFEISKKEMQPTHPIRLGLALNFSVFYYEILNSPEKACSLAKTA
FDEAIAELDTLSEESYKDSTLIMQLLRDNLTLWTSDT
>d1a17__ a.118.8.1 (-) Protein phosphatase 5 {Human (Homo sapiens)}
PPADGALKRAEELKTQANDYFKAKDYENAIKFYSQAIELNPSNAIYYGNRSLAYLRTECYGYALG
DATRAIELDKKYIKGYYRRAASNMALGKFRAALRDYETVVKVKPHDKDAKMKYQECNKIVKQKAF
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ERAIAGDEHKRSVVDSLDIESMTIEDEYS
>d1elra_ a.118.8.1 (A:) Hop {Human (Homo sapiens)}
GKQALKEKELGNDAYKKKDFDTALKHYDKAKELDPTNMTYITNQAAVYFEKGDYNKCRELCEKAI
EVGRENREDYRQIAKAYARIGNSYFKEEKYKDAIHFYNKSLAEHRTPDVLKKCQQAEKILKEQ
>d1elwa_ a.118.8.1 (A:) Hop {Human (Homo sapiens)}
EQVNELKEKGNKALSVGNIDDALQCYSEAIKLDPHNHVLYSNRSAAYAKKGDYQKAYEDGCKTVD
LKPDWGKGYSRKAAALEFLNRFEEAKRTYEEGLKHEANNPQLKEGLQNMEAR
>d1qqea_ a.118.8.1 (A:) Vesicular transport protein sec17 {Baker's
yeast (Saccharomyces cerevisiae)}
ISDPVELLKRAEKKGVPSSGFMKLFSGSDSYKFEEAADLCVQAATIYRLRKELNLAGDSFLKAAD
YQKKAGNEDEAGNTYVEAYKCFKSGGNSVNAVDSLENAIQIFTHRGQFRRGANFKFELGEILEND
LHDYAKAIDCYELAGEWYAQDQSVALSNKCFIKCADLKALDGQYIEASDIYSKLIKSSMGNRLSQ
WSLKDYFLKKGLCQLAATDAVAAARTLQEGQSEDPNFADSRESNFLKSLIDAVNEGDSEQLSEHC
KEFDNFMRLDKWKITILNKIKESIQQQEDD
>d1hh8a_ a.118.8.1 (A:) Neutrophil cytosolic factor 2 (NCF-2, p67-phox)
{Human (Homo sapiens)}
SLVEAISLWNEGVLAADKKDWKGALDAFSAVQDPHSRICFNIGCMYTILKNMTEAEKAFTRSINR
DKHLAVAYFQRGMLYYQTEKYDLAIKDLKEALIQLRGNQLIDYKILGLQFKLFACEVLYNIAFMY
AKKEEWKKAEEQLALATSMKSEPRHSKIDKAMECVWKQKLYEPVVIPVGRLFRPNERQVAQL
>d1fcha_ a.118.8.1 (A:) Peroxin pex5 (peroxisomal targeting signal
1 (PTS1) receptor) {Human (Homo sapiens)}
SATYDKGYQFEEENPLRDHPQPFEEGLRRLQEGDLPNAVLLFEAAVQQDPKHMEAWQYLGTTQAE
NEQELLAISALRRCLELKPDNQTALMALAVSFTNESLQRQACEILRDWLRYTPAYAHLVTPAEEG
AGGAGLGPSKRILGSLLSDSLFLEVKELFLAAVRLDPTSIDPDVQCGLGVLFNLSGEYDKAVDCF
TAALSVRPNDYLLWNKLGATLANGNQSEEAVAAYRRALELQPGYIRSRYNLGISCINLGAHREAV
EHFLEALNMQRKSRGPRGEGGAMSENIWSTLRLALSMLGQSDAYGAADARDLSTLLTMFGLPQ
>d1hxia_ a.118.8.1 (A:) Peroxin pex5 (peroxisomal targeting signal
1 (PTS1) receptor) {Trypanosoma brucei}
NNTDYPFEANNPYMYHENPMEEGLSMLKLANLAEAALAFEAVCQKEPEREEAWRSLGLTQAENEK
DGLAIIALNHARMLDPKDIAVHAALAVSHTNEHNANAALASLRAWLL
>d1ihga1 a.118.8.1 (A:197-365) Cyclophilin 40 {Cow (Bos taurus)}
GSGDSHPDFPEDADVDLKDVDKILLISEDLKNIGNTFFKSQNWEMAIKKYTKVLRYVEGSRAAAE
DADGAKLQPVALSCVLNIGACKLKMSDWQGAVDSCLEALEIDPSNTKALYRRAQGWQGLKEYDQA
LADLKKAQEIAPEDKAIQAELLKVKQKIKAQKDKEKAAY
>d1iipa1 a.118.8.1 (A:197-298) Cyclophilin 40 {Cow (Bos taurus)}
GSGDSHPDFPEDADVDLKDVDKILLISEDLKNIGNTFFKSQNWEMAIKKYTKVLRYVEGSRAAAE
DADGAKLQPVALSCVLNIGACKLKMSDWQGAVDSCLE
>d1hz4a_ a.118.8.2 (A:) Transcription factor MalT domain III
{Escherichia coli}
EIKDIREDTMHAEFNALRAQVAINDGNPDEAERLAKLALEELPPGWFYSRIVATSVLGEVLHCKG
ELTRSLALMQQTEQMARQHDVWHYALWSLIQQSEILFAQGFLQTAWETQEKAFQLINEQHLEQLP
MHEFLVRIRAQLLWAWARLDEAEASARSGIEVLSSYQPQQQLQCLAMLIQCSLARGDLDNARSQL
NRLENLLGNGKYHSDWISNANKVRVIYWQMTGDKAAAANWLRHTAKPEFANNHFLQGQWRNIARA
QILLGEFEPAEIVLEELNENARSLRLMSDLNRNLLLLNQLYWQAGRKSDAQRVLLDALKLANRTG
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FISHFVIEGEAMAQQLRQLIQLNTLPELEQHRAQRILREIN
>d1eyha_ a.118.9.1 (A:) Epsin 1 {Rat (Rattus norvegicus)}
HNYSEAEIKVREATSNDPWGPSSSLMSEIADLTYNVVAFSEIMSMIWKRLNDHGKNWRHVYKAMT
LMEYLIKTGSERVSQQCKENMYAVQTLKDFQYVDRDGKDQGVNVREKAKQLVALLRDEDRLREER
AHALKTKEKLAQTA
>d1inza_ a.118.9.1 (A:) Epsin 1 {Human (Homo sapiens)}
GSSRMSTSSLRRQMKNIVHNYSEAEIKVREATSNDPWGPSSSLMSEIADLTYNVVAFSEIMSMIW
KRLNDHGKNWRHVYKAMTLMEYLIKTGSERVSQQCKENMYAVQTLKDFQYVDRDGKDQGVNVREK
AKQLVALLRDEDRLREER
>d1dvpa1 a.118.9.2 (A:1-145) Hrs {Fruit fly (Drosophila melanogaster)}
MFRSSFCKNLENATSHLRLEPDWPSILLICDEINQKDVTPKNAFAAIKKKMNSPNPHSSCYSLLV
LESIVKNCGAPVHEEVFTKENCEMFSSFLESTPHENVRQKMLELVQTWAYAFRSSDKYQAIKDTM
TILKAKGHTFPELRE
>d1elka_ a.118.9.2 (A:) Tom1 protein {Human (Homo sapiens)}
SDFLLGNPFSSPVGQRIEKATDGSLQSEDWALNMEICDIINETEEGPKDALRAVKKRIVGNKNFH
EVMLALTVLETCVKNCGHRFHVLVASQDFVESVLVRTILPKNNPPTIVHDKVLNLIQSWADAFRS
SPDLTGVVTIYEDLRRKGLEFPM
>d1juqa_ a.118.9.2 (A:) Gga3 {Human (Homo sapiens)}
ESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEGPQIAVRLLAHKIQSPQEWEALQALTVLEA
CMKNCGRRFHNEVGKFRFLNELIKVVSPKYLGDRVSEKVKTKVIELLYSWTMALPEEAKIKDAYH
MLKRQGIVQSDPPIPVDRTLI
>d1hf8a_ a.118.10.1 (A:) Clathrin assembly lymphoid myeloid leukaemia protein, Calm {Rat (Rattus norvegicus)}
GSAVSKTVCKATTHEIMGPKKKHLDYLIQCTNEMNVNIPQLADSLFERTTNSSWVVVFKSLITTH
HLMVYGNERFIQYLASRNTLFNLSNFLDKSGLQGYDMSTFIRRYSRYLNEKAVSYRQVAFDFTKV
KRGADGVMRTMNTEKLLKTVPIIQNQMDALLDFNVNSNELTNGVINAAFMLLFKDAIRLFAAYNE
GIINLLEKYFDMKKNQCKEGLDIYKKFLTRMTRISEFLKVAEQVGIDRGDIPDLSQAPSSLLDAL
EQH
>d1hx8a_ a.118.10.1 (A:) AP180 (Lap) {Fruit fly (Drosophila melanogaster)}
QGLAKSVCKATTEECIGPKKKHLDYLVHCANEPNVSIPHLANLLIERSQNANWVVVYKSLITTHH
LMAYGNERFMQYLASSNSTFNLSSFLDKGTVQDGGMGVPGGRMGYDMSPFIRRYAKYLNEKSLSY
RAMAFDFCKVKRGKEEGSLRSMNAEKLLKTLPVLQAQLDALLEFDCQSNDLSNGVINMSFMLLFR
DLIRLFACYNDGIINLLEKYFDMNKKHARDALDLYKKFLVRMDRVGEFLKVAENVGIDKGDIPDL
TKAPSSLLDALEQHLATL
>d1kpsb_ a.118.12.1 (B:) Ran-GTPase activating protein 1 (RanGAP1), C-terminal domain {Mouse (Mus musculus)}
TDLSTFLSFPSPEKLLRLGPKVSVLIVQQTDTSDPEKVVSAFLKVASVFRDDASVKTAVLDAIDA
LMKKAFSCSSFNSNTFLTRLLIHMGLLKSEDKIKAIPSLHGPLMVLNHVVRQDYFPKALAPLLLA
FVTKPNGALETCSFARHNLLQTLYNI
>d1k8kg_ a.118.13.1 (G:) Arp2/3 complex 16 kDa subunit ARPC5 {Cow (Bos taurus)}
ARFRKVDVDEYDENKFVDEDDGGDGQAGPDEGEVDSCLRQGNMTAALQAALKNPPINTKSQAVKD

RAGSIVLKVLISFKANDIEKAVQSLDKNGVDLLMKYIYKGFESPSDNSSAVLLQWHEKALAAGGV
GSIVRVLTARKTV
>d1ocre_ a.118.11.1 (E:) Cytochrome c oxidase subunit E {Cow (Bos taurus)}
SHGSHETDEEFDARWVTYFNKPDIDAWELRKGMNTLVGYDLVPEPKIIDAALRACRRLNDFASAV
RILEVVKDKAGPHKEIYPYVIQELRPTLNELGISTPEELGLDKV
>d1f8na1 a.119.1.1 (A:150-839) Lipoxigenase, C-terminal domain {Soybean (Glycine max), isozyme L1}
VPSETPAPLVSYREEELKSLRGNGTGERKEYDRIYDYDVYNDLGNPDKSEKLARPVLGGSSTFPY
PRRGRTGRGPTVTDPNTEKQGEVFYVPRDENLGHLKSKDALEIGTKSLSQIVQPAFESAFDLKST
PIEFHSFQDVHDLYEGGIKLPRDVISTIIPLPVIKELYRTDGQHILKFPQPHVVQVSQSAWMTDE
EFAREMIAGVNPCVIRGLEEFPPKSNLDPAIYGDQSSKITADSLDLDGYTMDEALGSRRLFMLDY
HDIFMPYVRQINQLNSAKTYATRTILFLREDGTLKPVAIELSLPHSAGDLSAAVSQVVLPAKEGV
ESTIWLLAKAYVIVNDSCYHQLMSHWLNTHAAMEPFVIATHRHLSVLHPIYKLLTPHYRNNMNIN
ALARQSLINANGIIETTFLPSKYSVEMSSAVYKNWVFTDQALPADLIKRGVAIKDPSTPHGVRLL
IEDYPYAADGLEIWAAIKTWVQEYVPLYYARDDDVKNDSELQHWWKEAVEKGHGDLKDKPWWPKL
QTLEDLVEVCLIIIWIASALHAAVNFGQYPYGGLIMNRPTASRRLLPEKGTPEYEEMINNHEKAY
LRTITSKLPTLISLSVIEILSTHASDEVYLGQRDNPHWTSDSKALQAFQKFGNKLKEIEEKLVRR
NNDPSLQGNRLGPVQLPYTLLYPSSEEGLTFRGIPNSISI
>d1ik3a1 a.119.1.1 (A:168-857) Lipoxigenase, C-terminal domain {Soybean (Glycine max), isozyme L3}
LPSETPAPLVKYREEELHNLRGDGTGERKEWERIYDYDVYNDLGDPDKGENHARPVLGGNDTFPY
PRRGRTGRKPTRKDPNSESRSNDVYLPRDEAFGHLKSSDFLTYGLKSVSQNVLPLLQSAFDLNFT
PREFDSFDEVHGLYSGGIKLPTDIISKISPLPVLKEIFRTDGEQALKFPPPKVIQVSKSAWMTDE
EFAREMLAGVNPNLIRCLKDFPPRSKLDSQVYGDHTSQITKEHLEPNLEGLTVDEAIQNKRLFLL
DHHDPIMPYLRRINATSTKAYATRTILFLKNDGTLRPLAIELSLPHPQGDQSGAFSQVFLPADEG
VESSIWLLAKAYVVVNDSCYHQLVSHWLNTHAVVEPFIIATNRHLSVVHPIYKLLHPHYRDTMNI
NGLARLSLVNDGGVIEQTFLWGRYSVEMSAVVYKDWVFTDQALPADLIKRGMAIEDPSCPHGIRL
VIEDYPYTVDGLEIWDAIKTWVHEYVFLYYKSDDTLREDPELQACWKELVEVGHGDKKNEPWWPK
MQTREELVEACAIIIWTASALHAAVNFGQYPYGGLILNRPTLSRRFMPEKGSAEYEELRKNPQKA
YLKTITPKFQTLIDLSVIEILSRHASDEVYLGERDNPNWTSDTRALEAFKRFGNKLAQIENKLSE
RNNDEKLRNRCGPVQMPYTLLLPSSKEGLTFRGIPNSISI
>d1lox_1 a.119.1.2 (113-663) 15-Lipoxygenase {Rabbit (Oryctolagus cuniculus)}
TGCTTVGDPQGLFQKHREQELEERRKLYQWGSWKEGLILNVAGSKLTDLPVDERFLEDKKIDFEA
SLAWGLAELALKNSLNILAPWKTLDDFNRIFWCGRSKLARRVRDSWQEDSLFGYQFLNGANPMLL
RRSVQLPARLVFPPGMEELQAQLEKELKAGTLFEADFALLDNIKANVILYCQQYLAAPLVMLKLQ
PDGKLMPMVIQLHLPKIGSSPPPLFLPTDPPMVWLLAKCWVRSSDFQVHELNSHLLRGHLMAEVF
TVATMRCLPSIHPVFKLIVPHLRYTLEINVRARNGLVSDFGIFDQIMSTGGGGHVQLLQQAGAFL
TYRSFCPPDDLADRGLLGVESSFYAQDALRLWEIISRYVQGIMGLYYKTDEAVRDDLELQSWCRE
ITEIGLQGAQKQGFPTSLQSVAQACHFVTMCIFTCTGQHSSIHLGQLDWFTWVPNAPCTMRLPPP
TTKDATLETVMATLPNLKQSSLQMSIVWQLGRDQPIMVPLGQHQEEYFSGPEPRAVLEKFREELA
IMDKEIEVRNEKLDIPYEYLRPSIVENSVAI
>d1c1ka_ a.120.1.1 (A:) gene 59 helicase assembly protein

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{Bacteriophage T4}
MIKLRMPAGGERYIDGKSVYKLYLMIKQHMNGKYDVIKYNWCMRVSDAAYQKRRDKYFFQKLSEK
YKLKELALIFISNLVANQDAWIGDISDADALVFYREYIGRLKQIKFKFEEDIRNIYYFSKKVEVS
AFKEIFEYNPKVQSSYIFKLLQSNIISFETFILLDSFLNIIDKHDEQTDNLVWNNYSIKLKAYRK
ILNIDSQKAKNVFIETVKSCKY
>d2tct_2 a.121.1.1 (68-208) Tetracyclin repressor (Tet-repressor,
TetR) {Escherichia coli}
LPAAGESWQSFLRNNAMSFRRALLRYRDGAKVHLGTRPDEKQYDTVETQLRFMTENGFSLRDGLY
AISAVSHFTLGAVLEQQEHTAALTDRPAAPDENLPPLLREALQIMDSDDGEQAFLHGLESLIRGF
EVQLTALLQIV
>d1jt6a2 a.121.1.1 (A:73-187) Multidrug binding protein QacR
{Staphylococcus aureus}
KTNREKFYLYNELSLTTEYYYPLQNAIIEFYTEYYKTNSINEKMNKLENKYIDAYHVIFKEGNLN
GEWSINDVNAVSKIAANAVNGIVTFTHEQNINERIKLMNKFSQIFLNGLS
>d1fqva1 a.122.1.1 (A:107-145) Skp1-Skp2 dimerisation domains {Human
(Homo sapiens)}
VSWDSLPDELLLGIFSCLCLPELLKVSGVCKRWYRLASD
>d1fqvb1 a.122.1.1 (B:85-160) Skp1-Skp2 dimerisation domains {Human
(Homo sapiens)}
IPVWDQEFLKVDQGTLFELILAANYLDIKGLLDVTCKTVANMIKGKTPEEIRKTFNIKNDFTEEE
EAQVRKENQWC
>d1fs1a1 a.122.1.1 (A:109-149) Skp1-Skp2 dimerisation domains {Human
(Homo sapiens)}
WDSLPDELLLGIFSCLCLPELLKVSGVCKRWYRLASDESLW
>d1fs1b1 a.122.1.1 (B:86-140) Skp1-Skp2 dimerisation domains {Human
(Homo sapiens)}
PVWDQEFLKVDQGTLFELILAANYLDIKGLLDVTCKTVANMIKGKTPEEIRKTFN
>d1fs2b1 a.122.1.1 (B:80-146) Skp1-Skp2 dimerisation domains {Human
(Homo sapiens)}
KRTDDIPVWDQEFLKVDQGTLFELILAANYLDIKGLLDVTCKTVANMIKGKTPEEIRKTFNIKND
FT
>d1g5ya_ a.123.1.1 (A:) Retinoid-X receptor (RXR-alpha) {Human (Homo
sapiens)}
PVERILEAELAVEPKTETYVEANMGLNPSSPNDPVTNICQAADKQLFTLVEWAKRIPHFSELPLD
DQVILLRAGWNELLIASFSHRSIAVKDGILLATGLHVHRNSAHSAGVGAIFDRVLTELVSKMRDM
QMDKTELGCLRAIVLFNPDSKGLSNPAEVEALREKVYASLEAYCKHKYPEQPGRFAKLLLRLPAL
RSIGLKCLEHLFFFKLIGDTPIDTFLMEMLEAP
>d1dkfb_ a.123.1.1 (B:) Retinoic acid receptor alpha (RAR-alpha)
{Human (Homo sapiens)}
PEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQL
PGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFA
FANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRPHMFPK
MLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLEN
>d1fcya_ a.123.1.1 (A:) Retinoic acid receptor gamma (RAR-gamma)
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{Human (Homo sapiens)}
ASPQLEELITKVSKAHQETFPSLCQLGKYTTNSSADHRVQLDLGLWDKFSELATKCIIKIVEFAK
RLPGFTGLSIADQITLLKAACLDILMLRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLV
FAFAGQLLPLEMDDTETGLLSAICLICGDRMDLEEPEKVDKLQEPLLEALRLYARRRRPSQPYMF
PRMLMKITDLRGISTKGAERAITLKMEIPGPMPPLIREMLE
>d1a28a_ a.123.1.1 (A:) Progesterone receptor {Human (Homo sapiens)}
QLIPPLINLLMSIEPDVIYAGHDNTKPDTSSSLLTSLNQLGERQLLSVVKWSKSLPGFRNLHIDD
QITLIQYSWMSLMVFGLGWRSYKHVSGQMLYFAPDLILNEQRMKESSFYSLCLTMWQIPQEFVKL
QVSQEEFLCMKVLLLLNTIPLEGLRSQTQFEEMRSSYIRELIKAIGLRQKGVVSSSQRFYQLTKL
LDNLHDLVKQLHLYCLNTFIQSRALSVEFPEMMSEVIAAQLPKILAGMVKPLLFHK
>d3erda_ a.123.1.1 (A:) Estrogen receptor alpha {Human (Homo sapiens)}
SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRVPGFVD
LTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEIFDMLLATSSR
FRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITDTLIHLMAKAGLTLQQ
QHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEMLDAHRLH
>d1qkma_ a.123.1.1 (A:) Estrogen receptor beta {Human (Homo sapiens)}
LDALSPEQLVLTLLEAEPPHVLISRPSAPFTEASMMMSLTKLADKELVHMISWAKKIPGFVELSL
FDQVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLATTSRFRE
LKLQHKEYLCVKAMILLNSSMYPLVTATQDADSSRKLAHLLNAVTDALVWVIAKSGISSQQQSMR
LANLLMLLSHVRHASNKGMEHLLNMKCKNVVPVYDLLLEMLNAHVL
>d1qkna_ a.123.1.1 (A:) Estrogen receptor beta {Rat (Rattus
norvegicus)}
TLSPEQLVLTLLEAEPPNVLVSRPSMPFTEASMMMSLTKLADKELVHMIGWAKKIPGFVELSLLD
QVRLLESCWMEVLMVGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLATTSRFRELK
LQHKEYLCVKAMILLNSSMYPLASANQEAESSRKLTHLLNAVTDALVWVIAKSGISSQQQSVRLA
NLLMLLSHVRHISNKGMEHLLSMKCKNVVPVYDLLLEMLNA
>d1i37a_ a.123.1.1 (A:) Androgen receptor {Rat (Rattus norvegicus)}
IFLNVLEAIEPGVVCAGHDNNQPDSFAALLSSLNELGERQLVHVVKWAKALPGFRNLHVDDQMAV
IQYSWMGLMVFAMGWRSFTNVNSRMLYFAPDLVFNEYRMHKSRMYSQCVRMRHLSQEFGWLQITP
QEFLCMKALLLFSIIPVDGLKNQKFFDELRMNYIKELDRIIACKRKNPTSCSRRFYQLTKLLDSV
QPIARELHQFTFDLLIKSHMVSVDFPEMMAEIISVQVPKILSGKVKPIYFH
>d1k7la_ a.123.1.1 (A:) Peroxisome proliferator activated receptor
alpha, PPAR-alpha {Human (Homo sapiens)}
DLKSLAKRIYEAYLKNFNMNKVKARVILSGKASNNPPFVIHDMETLCMAEKTLVAKLVANGIQNK
EAEVRIFHCCQCTSVETVTELTEFAKAIPGFANLDLNDQVTLLKYGVYEAIFAMLSSVMNKDGML
VAYGNGFITREFLKSLRKPFCDIMEPKFDFAMKFNALELDDSDISLFVAAIICCGDRPGLLNVGH
IEKMQEGIVHVLRLHLQSNHPDDIFLFPKLLQKMADLRQLVTEHAQLVQIIKKTESDAALHPLLQ
EIYRDMY
>d2prga_ a.123.1.1 (A:) Peroxisome proliferator activated receptor
gamma, PPAR-gamma {Human (Homo sapiens)}
ESADLRALAKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQ
EQSKEVAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNK
DGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLL
NVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLH
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PLLQEIYKDLY
>d2gwxa_ a.123.1.1 (A:) Peroxisome proliferator-activated receptor
delta, PPAR-DELTA {Human (Homo sapiens)}
LKAFSKHIYNAYLKNFNMTKKKARSILTGKASHTAPFVIHDIETLWQAEKGLVWKQLVNGLPPYK
EISVHVFYRCQCTTVETVRELTEFAKSIPSFSSLFLNDQVTLLKYGVHEAIFAMLASIVNKDGLL
VANGSGFVTREFLRSLRKPFSDIIEPKFEFAVKFNALELDDSDLALFIAAIILCGDRPGLMNVPR
VEAIQDTILRALEFHLQANHPDAQQLFPKLLQKMADLRQLVTEHAQMMQRIKKTETETSLHPLLQ
EIYKDM
>d1ilga_ a.123.1.1 (A:) Pregnane x receptor, PXR {Human (Homo sapiens)}
GLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCELPESLQAPSREEAAKWSQVRKDL
CSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKVISYFRDLPIED
QISLLKGAAFELCQLRFNTVFNAETGTWECGRLSYCLEDTAGGFQQLLLEPMLKFHYMLKKLQLH
EEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELR
SINAQHTQRLLRIQDIHPFATPLMQELFGI
>d1ie9a_ a.123.1.1 (A:) Vitamin D nuclear receptor {Human (Homo
sapiens)}
DSLRPKLSEEQQRIIAILLDAHHKTYDPTYSDFCQFRPPVRVNDGGGSVTLELSQLSMLPHLADL
VSYSIQKVIGFAKMIPGFRDLTSEDQIVLLKSSAIEVIMLRSNESFTMDDMSWTCGNQDYKYRVS
DVTKAGHSLELIEPLIKFQVGLKKLNLHEEEHVLLMAICIVSPDRPGVQDAALIEAIQDRLSNTL
QTYIRCRHPPPGSHLLYAKMIQKLADLRSLNEEHSKQYRCLSFQPECSMKLTPLVLEVFG
>d1bsxa_ a.123.1.1 (A:) Thyroid hormone receptor beta (TR-beta) {Human
(Homo sapiens)}
KPEPTDEEWELIKTVTEAHVATNAQGSHWKQKRKFLPEDIGQAPIVNAPEGGKVDLEAFSHFTKI
ITPAITRVVDFAKKLPMFCELPCEDQIILLKGCCMEIMSLRAAVRYDPESETLTLNGEMAVTRGQ
LKNGGLGVVSDAIFDLGMSLSSFNLDDTEVALLQAVLLMSSDRPGLACVERIEKYQDSFLLAFEH
YINYRKHHVTHFWPKLLMKVTDLRMIGACHASRFLHMKVECPTELFPPLFLEVFED
>d1hg4a_ a.123.1.1 (A:) Ultraspiracle protein, usp {Drosophila
melanogaster}
FSIERIIEAEQRAETQCGDRALTFLRVGPYSTVQPDYKGAVSALCQVVNKQLFQMVEYARMMPHF
AQVPLDDQVILLKAAWIELLIANVAWCSIVSLDDGGAGGGGGGLGHDGSFERRSPGLQPQQLFLN
QSFSYHRNSAIKAGVSAIFDRILSELSVKMKRLNLDRRELSCLKAIILYNPDIRGIKSRAEIEMC
REKVYACLDEHCRLEHPGDDGRFAQLLLRLPALRSISLKCQDHLFLFRITSDRPLEELFLEQLEA
PPPPG
>d1g2na_ a.123.1.1 (A:) Ultraspiracle protein, usp {Heliothis
virescens}
AAVQELSIERLLEMESLVADPSEEFQFLRVGPDSNVPPKFRAPVSSLCQIGNKQIAALVVWARDI
PHFSQLEMEDQILLIKGSWNELLLFAIAWRSMEFLTEERDGVDGTGNRTTSPPQLMCLMPGMTLH
RNSALQAGVGQIFDRVLSELSLKMRTLRVDQAEYVALKAIILLNPDVKGLKNRQEVEVLREKMFL
CLDEYCRRSRSSEEGRFAALLLRLPALRSISLKSFEHLFFFHLVADTSIAGYIRDALRNHA
>d1ah7__ a.124.1.1 (-) Bacterial phosholipase C {Bacillus cereus}
WSAEDKHKEGVNSHLWIVNRAIDIMSRNTTLVKQDRVAQLNEWRTELENGIYAADYENPYYDNST
FASHFYDPDNGKTYIPFAKQAKETGAKYFKLAGESYKNKDMKQAFFYLGLSLHYLGDVNQPMHAA
NFTNLSYPQGFHSKYENFVDTIKDNYKVTDGNGYWNWKGTNPEEWIHGAAVVAKQDYSGIVNDNT
KDWFVKAAVSQEYADKWRAEVTPMTGKRLMDAQRVTAGYIQLWFDTYGDR
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>d1ca1_1 a.124.1.1 (1-249) Alpha-toxin, N-terminal domain
{Clostridium perfringens}
WDGKIDGTGTHAMIVTQGVSILENDLSKNEPESVRKNLEILKENMHELQLGSTYPDYDKNAYDLY
QDHFWDPDTDNNFSKDNSWYLAYSIPDTGESQIRKFSALARYEWQRGNYKQATFYLGEAMHYFGD
IDTPYHPANVTAVDSAGHVKFETFAEERKEQYKINTVGCKTNEDFYADILKNKDFNAWSKEYARG
FAKTGKSIYYSHASMSHSWDDWDYAAKVTLANSQKGTAGYIYRFLHDVSEGNDP
>d1ak0__ a.124.1.2 (-) P1 nuclease {Penicillium citrinum}
WGALGHATVAYVAQHYVSPEAASWAQGILGSSSSSYLASIASWADEYRLTSAGKWSASLHFIDAE
DNPPTNCNVDYERDCGSSGCSISAIANYTQRVSDSSLSSENHAEALRFLVHFIGDMTQPLHDEAY
AVGGNKINVTFDGYHDNLHSDWDTYMPQKLIGGHALSDAESWAKTLVQNIESGNYTAQAIGWIKG
DNISEPITTATRWASDANALVCTVVMPHGAAALQTGDLYPTYYDSVIDTIELQIAKGGYRLANWI
NEIH
>d1f0ja_ a.125.1.1 (A:) Catalytic domain of cyclic nucleotide
phosphodiesterase 4b2b {Human (Homo sapiens)}
SISRFGVNTENEDHLAKELEDLNKWGLNIFNVAGYSHNRPLTCIMYAIFQERDLLKTFRISSDTF
ITYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPALDAVFTDLEILAAIFAAAIHDVDHPGV
SNQFLINTNSELALMYNDESVLENHHLAVGFKLLQEEHCDIFMNLTKKQRQTLRKMVIDMVLATD
MSKHMSLLADLKTMVETKKVTSSGVLLLDNYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIM
EEFFQQGDKERERGMEISPMCDKHTASVEKSQVGFIDYIVHPLWETWADLVQPDAQDILDTLEDN
RNWYQSMIPQAPAPPLDEQNRDCQGLMEKFQF
>d1gnia1 a.126.1.1 (A:3-196) Serum albumin {Human (Homo sapiens)}
HKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLH
TLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEE
TFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQ
>d1gnia2 a.126.1.1 (A:197-388) Serum albumin {Human (Homo sapiens)}
RLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA
KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVF
LGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLI
>d1gnia3 a.126.1.1 (A:389-584) Serum albumin {Human (Homo sapiens)}
KQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYL
SVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSE
KERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAAL
G
>d1j78a1 a.126.1.1 (A:13-198) Vitamin D binding protein {Human (Homo
sapiens)}
CKEFSHLGKEDFTSLSLVLYSRKFPSGTFEQVSQLVKEVVSLTEACCAEGADPDCYDTRTSALSA
KSCESNSPFPVHPGTAECCTKEGLERKLCMAALKHQPQEFPTYVEPTNDEICEAFRKDPKEYANQ
FMWEYSTNYGQAPLSLLVSYTKSYLSMVGSCCTSASPTVCFLKERLQLKHLSLLTT
>d1j78a2 a.126.1.1 (A:199-386) Vitamin D binding protein {Human (Homo
sapiens)}
LSNRVCSQYAAYGEKKSRLSNLIKLAQKVPTADLEDVLPLAEDITNILSKCCESASEDCMAKELP
EHTVKLCDNLSTKNSKFEDCCQEKTAMDVFVCTYFMPAAQLPELPDVELPTNKDVCDPGNTKVMD
KYTFELSRRTHLPEVFLSKVLEPTLKSLGECCDVEDSTTCFNAKGPLLKKELSSFIDK
>d1j78a3 a.126.1.1 (A:387-457) Vitamin D binding protein {Human (Homo
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sapiens)}
GQELCADYSENTFTEYKKKLAERLKAKLPDATPTELAKLVNKRSDFASNCCSINSPPLYCDSEID
AELKNI
>d1jswa_ a.127.1.1 (A:) L-aspartate ammonia lyase {Escherichia coli}
MSNNIRIEEDLLGTREVPADAYYGVHTLRAIENFYISNNKISDIPEFVRGMVMVKKAAAMANKEL
QTIPKSVANAIIAACDEVLNNGKCMDQFPVDVYQGGAGTSVNMNTNEVLANIGLELMGHQKGEYQ
YLNPNDHVNKCQSTNDAYPTGFRIAVYSSLIKLVDAINQLREGFERKAVEFQDILKMGRTQLQDA
VPMTLGQEFRAFSILLKEEVKNIQRTAELLLEVNLGATAIGTGLNTPKEYSPLAVKKLAEVTGFP
CVPAEDLIEATSDCGAYVMVHGALKRLAVKMSKICNDLRLLSSGPRAGLNEINLPELQAGSSIMP
AKVNPVVPEVVNQVCFKVIGNDTTVTMAAEAGQLQLNVMEPVIGQAMFESVHILTNACYNLLEKC
INGITANKEVCEGYVYNSIGIVTYLNPFIGHHNGDIVGKICAETGKSVREVVLERGLLTEAELDD
IFSV
>d1jswc_ a.127.1.1 (C:) L-aspartate ammonia lyase {Escherichia coli}
IRIEEDLLGTREVPADAYYGVHTLRAIENFYISNNKISDIPEFVRGMVMVKKAAAMANKELQTIP
KSVANAIIAACDEVLNNGKCMDQFPVDVYQGGAGTSVNMNTNEVLANIGLELMGHQKGEYQYLNP
NDHVNKCQSTNDAYPTGFRIAVYSSLIKLVDAINQLREGFERKAVEFQDILKMGRTQLQDAVPMT
LGQEFRAFSILLKEEVKNIQRTAELLLEVNLGATAIGTGLNTPKEYSPLAVKKLAEVTGFPCVPA
EDLIEATSDCGAYVMVHGALKRLAVKMSKICNDLRLLSSGPRAGLNEINLPELQAGSSIMPAKVN
PVVPEVVNQVCFKVIGNDTTVTMAAEAGQLQLNVMEPVIGQAMFESVHILTNACYNLLEKCINGI
TANKEVCEGYVYNSIGIVTYLNP
>d1fura_ a.127.1.1 (A:) Fumarase {Escherichia coli}
VRSEKDSMGAIDVPADKLWGAQTQRSLEHFRISTEKMPTSLIHALALTKRAAAKVNEDLGLLSEE
KASAIRQAADEVLAGQHDDEFPLAIWQTGSGTQSNMNMNEVLANRASELLGGVRGMERKVHPNDD
VNKSQSSNDVFPTAMHVAALLALRKQLIPQLKTLTQTLNEKSRAFADIVKIGRTNLQDATPLTLG
QEISGWVAMLEHNLKHIEYSLPHVAELALGGTAVGTGLNTHPEYARRVADELAVITCAPFVTAPN
KFEALATCDALVQAHGALKGLAASLMKIANDVRWLASGPRCGIGEISIPENEPGSSIMPGKVNPT
QCEALTMLCCQVMGNDVAINMGGASGNFELNVFRPMVIHNFLQSVRLLADGMESFNKHCAVGIEP
NRERINQLLNESLMLVTALNTHIGYDKAAEIAKKAHKEGLTLKAAALALGYLSEAEFDSWVRPEQ
M
>d1yfm__ a.127.1.1 (-) Fumarase {Baker's yeast (Saccharomyces
cerevisiae)}
SFRTETDAFGEIHVPADKYWGAQTQRSFQNFKIGGARERMPLPLVHAFGVLKKSAAIVNESLGGL
DPKISKAIQQAADEVASGKLDDHFPLVVFQTGSGTQSNMNANEVISNRAIEILGGKIGSKQVHPN
NHCNQSQSSNDTFPTVMHIAASLQIQNELIPELTNLKNALEAKSKEFDHIVKIGRTHLQDATPLT
LGQEFSGYVQQVENGIQRVAHSLKTLSFLAQGGTAVGTGLNTKPGFDVKIAEQISKETGLKFQTA
PNRFEALAAHDAIVECSGALNTLACSLFKIAQDIRYLGSGPRCGYHELMLPENEPGSSIMPGKVN
PTQNEALTQVCVQVMGNNAAITFAGSQGQFELNVFKPVMIANLLNSIRLITDAAYSFRVHCVEGI
KANEPRIHELLTKSLMLVTALNPKIGYDAASKVAKNAHKKGITLKESALELGVLTEKEFDEWVVP
EHML
>d1k62a_ a.127.1.1 (A:) Argininosuccinate lyase/delta-crystallin
{Human (Homo sapiens)}
GAVDPIMEKFNASIAYDRHLWEVDVQGSKAYSRGLEKAGLLTKAEMDQILHGLDKVAEEWAQGTF
KLNSNDEDIHTANERRLKELIGATAGKLHTGRSRNDQVVTDLRLWMRQTCSTLSGLLWELIRTMV
DRAEAERDVLFPGYTHLQRAQPIRWSHWILSHAVALTRDSERLLEVRKRINVLPLGSGAIAGNPL
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GVDRELLRAELNFGAITLNSMDATSERDFVAEFLFWRSLCMTHLSRMAEDLILYCTKEFSFVQLS
DAYSTGSSLMPRKKNPDSLELIRSKAGRVFGRCAGLLMTLKGLPSTYNKDLQEDKEAVFEVSDTM
SAVLQVATGVISTLQIHQENMGQALSPDMLATDLAYYLVRKGMPFRQAHEASGKAVFMAETKGVA
LNQLSLQELQTISPLFSGDVICVWDYRHSVEQYGALGGTARSSVDWQIRQVRALLQAQQA
>d1auwa_ a.127.1.1 (A:) Argininosuccinate lyase/delta-crystallin
{Domestic duck (Anas platyrhynchos), delta-crystallin}
TDPIMEKLNSSIAYDQRLSEVDIQGSMAYAKALEKAGILTKTELEKILSGLEKISEEWSKGVFVV
KQSDEDINTANERRLKELIGDIAGKLHTGRSRNDQVVTDLKLFMKNSLSIISTHLLQLIKTLVER
AAIEIDVILPGYTHLQKAQPIRWSQFLLSHAVALTRDSERLGEVKKRINVLPLGSGALAGNPLDI
DREMLRSELEFASISLNSMDAISERDFVVEFLSFATLLMIHLSKMAEDLIIYSTSEFGFLTDSDA
FSTGSSLMPQKKNPDSLELIRSKAGRVFGRLASILMVLKGLPSTYNKDLQEDKEAVFDVVDTLTA
VLQVATGVISTLQISKENMEKALTPEMLATDLALYLVRKGVPFRQAHTASGKAVHLAETKGITIN
KLSLEDLKSISPQFSSDVSQVFNFVNSVEQYTALGGTAKSSVTTQIEQLRELMKKQK
>d1dcnb_ a.127.1.1 (B:) Argininosuccinate lyase/delta-crystallin
{Domestic duck (Anas platyrhynchos), delta-crystallin}
DPIMAKLNSSIAYDQRLSEVDIQGSMAYAKALEKAGILTKTELAKILSGLEKISEEDIHTANERR
LKELIGDIAGKLNTGRSRNDQVVTDLKLFMKNSLSIISTHLLQLIKTLVERAAIEIDVILPGYTN
LQKAQPIRWSQFLLSHAVALTRDSERLGEVKKRINVLPLGSGALAGNPLDIDREMLRSELEFASI
SLNSMDAISERDFVVEFLSFATLLMIHLSKMAEDLIIYSTSEFGFLTLSPDSLELIRSKSGRVFG
RLASILMVLKGLPSTYNKDLQEDKEAVFDVVDTLTAVLQVATGVISTLQISKENMEKALTPEMLA
TDLALYLVRKGVPFRQAHTASGKAVHLAETKGITINNLSLEDLKSISPQFSSDVSQVFNFVNSVE
QYTALGGTAKSSVTTQIEQLRELMKKQK
>d1hy0a_ a.127.1.1 (A:) Argininosuccinate lyase/delta-crystallin
{Domestic duck (Anas platyrhynchos), delta-crystallin}
DPIMQMLSTSISTEQRLSEVDIQASIAYAKALEKAGILTKTELEKILSGLEKISEELSKGVIVVT
QSDEDIQTANERRLKELIGDIAGKLHTGRSRNEQVVTDLKLFMKNSLSIISTHLLQLIKTLVERA
AIEIDVILPGYTHLQKAQPIRWSQFLLSHAVALTRDSERLGEVKKRINVLPLGSGALAGNPLDID
REMLRSELEFASISLNSMDAISERDFVVEFLSVATLLLIHLSKMAEDLIIYSTSEFGFLTLSDAF
STGSSLMPQKKNPDSLELIRSKSGRVFGRLASILMVLKGLPSTYNKDLQEDKEAVIDVVDTLTAV
LQVATGVISTLQISKENMEKALTPEMLATDLALYLVRKGMPFRQAHTASGKAVHLAETKGIAINN
LTLEDLKSISPLFSSDVSQVFNFVNSVEQYTALGGTAKSSVTTQIEQLRELMKKQKE
>d1i0aa_ a.127.1.1 (A:) Argininosuccinate lyase/delta-crystallin
{Turkey (Meleagris gallopavo), delta-crystallin}
GRFVGSVDPIMEILSSSISTEQRLTEVDIQASMAYAKALEKASILTKTELEKILSGLEKISEESS
KGVLVMTQSDEDIQTAIERRLKELIGDIAGKLQTGRSRNEQVVTDLKLLLKSSISVISTHLLQLI
KTLVERAAIEIDIIMPGYTHLQKALPIRWSQFLLSHAVALTRDSERLGEVKKRITVLPLGSGVLA
GNPLEIDRELLRSELDMTSITLNSIDAISERDFVVELISVATLLMIHLSKLAEDLIIFSTTEFGF
VTLSDAYSTGSSLLPQKKNPDSLELIRSKAGRVFGRLAAILMVLKGIPSTFSKDLQEDKEAVLDV
VDTLTAVLQVATGVISTLQINKENMEKALTPELLSTDLALYLVRKGMPIRQAQTASGKAVHLAET
KGITINNLTLEDLKSISPLFASDVSQVFSVVNSVEQYTAVGGTAKSSVTAQIEQLRELLKKQK
>d1c3ca_ a.127.1.1 (A:) Adenylosuccinate lyase {Thermotoga maritima}
VERYSLSPMKDLWTEEAKYRRWLEVELAVTRAYEELGMIPKGVTERIRNNAKIDVELFKKIEEKT
NHDVVAFVEGIGSMIGEDSRFFHYGLTSSDVLDTANSLALVEAGKILLESLKEFCDVLWEVANRY
KHTPTIGRTHGVHAEPTSFGLKVLGWYSEMKRNVQRLERAIEEVSYGKISGAVGNYANVPPEVEE
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KALSYLGLKPEPVSTQVVPRDRHAFYLSTLAIVAAGIERIAVEIRHLQRTEVLEVEEPFRKGQRG
SSAMPHKKNPITCERLTGLSRMMRAYVDPSLENIALWHERDISHSSVERYVFPDATQTLYYMIVT
ATNVVRNMKVNEERMKKNIDLTKGLVFSQRVLLKLIEKGLTRKEAYDIVQRNALKTWNSEKHFLE
YLLEDEEVKKLVTKEELEELFDISYYLKHVDHIFERFEK
>d1dofa_ a.127.1.1 (A:) Adenylosuccinate lyase {Archaeon Pyrobaculum aerophilum}
HVSPFDWRYGSEEIRRLFTNEAIINAYLEVERALVCALEELGVAERGCCEKVNKASVSADEVYRL
ERETGHDILSLVLLLEQKSGCRYVHYGATSNDIIDTAWALLIRRALAAVKEKARAVGDQLASMAR
KYKTLEMVGRTHGQWAEPITLGFKFANYYYELYIACRQLALAEEFIRAKIGGAVGTMASWGELGL
EVRRRVAERLGLPHHVITTQVAPRESFAVLASALALMAAVFERLAVEIRELSRPEIGEVVEGGGG
SSAMPHKANPTASERIVSLARYVRALTHVAFENVALWHERDLTNSANERVWIPEALLALDEILTS
ALRVLKNVYIDEERITENLQKALPYILTEFHMNRMIKEGASRAEAYKKAKEVKALTFEYQKWPVE
RLIEDALSLKLC
>d1f1oa_ a.127.1.1 (A:) Adenylosuccinate lyase {Bacillus subtilis}
EMSAIWTDENRFQAWLEVEILACEAWAELGVIPKEDVKVMRENASFDINRILEIEKDTRHDVVAF
TRAVSESLGEERKWVHYGLTSTDVVDTALSYLLKQANDILLKDLERFVDIIKEKAKEHKYTVMMG
RTHGVHAEPTTFGLKLALWHEEMKRNLERFKQAKAGIEVGKISGAVGTYANIDPFVEQYVCEKLG
LKAAPISTQTLQRDRHADYMATLALIATSIEKFAVEIRGLQKSETREVEEFFAKGQKGSSAMPHK
RNPIGSENMTGMARVIRGYMMTAYENVPLWHERDISHSSAERIILPDATIALNYMLNRFSNIVKN
LTVFPENMKRNMDRTLGLIYSQRVLLALIDTGLTREEAYDTVQPKAMEAWEKQVPFRELVEAEEK
ITSRLSPEKIADCFDYNY
>d1gk2a_ a.127.1.2 (A:) Histidine ammonia-lyase (HAL) {Pseudomonas putida}
TELTLKPGTLTLAQLRAIHAAPVRLQLDASAAPAIDASVACVEQIIAEDRTAYGINTGFGLLAST
RIASHDLENLQRSLVLSHAAGIGAPLDDDLVRLIMVLKINSLSRGFSGIRRKVIDALIALVNAEV
YPHIPLKGSVGASGDLAPLAHMSLVLLGEGKARYKGQWLSATEALAVAGLEPLTLAAKEGLALLN
GTQASTAYALRGLFYAEDLYAAAIACGGLSVEAVLGSRSPFDARIHEARGQRGQIDTAACFRDLL
GDSSEVSLSHKNADKVQDPYSLRCQPQVMGACLTQLRQAAEVLGIEANAVSDNPLVFAAEGDVIS
GGNGHAEPVAMAADNLALAIAEIGSLSERRISLMMDKHMSQLPPFLVENGGVNSGFMIAQVTAAA
LASENKALSHPHSVDSLPTSANQEDHVSMAPAAGKRLWEMAENTRGVLAIEWLGACQGLDLRKGL
KTSAKLEKARQALRSEVAHYDRDRFFAPDIEKAVELLAKGSLTGLLPAGVLPSL
>d1uby__ a.128.1.1 (-) Farnesyl diphosphate synthase {Chicken (Gallus gallus)}
SPVVVEREREEFVGFFPQIVRDLTEDGIGHPEVGDAVARLKEVLQYNAPGGKCNRGLTVVAAYRE
LSGPGQKDAESLRCALAVGWCIELFQAASLVADDIMDQSLTRRGQLCWYKKEGVGLDAINDSFLL
ESSVYRVLKKYCRQRPYYVHLLELFLQTAYQTELGQMLDLITAPVSKVDLSHFSEERYKAIVKYK
TAFYSFYLPVAAAMYMVGIDSKEEHENAKAILLEMGEYFQIQDDYLDCFGDPALTGAVGTDIQDN
KCSWLVVQCLQRVTPEQRQLLEDNYGRKEPEKVAKVKELYEAVGMRAAFQQYEESSYRRLQELIE
KHSNRLPKEIFLGLAQKIYKRQK
>d1ezfa_ a.128.1.2 (A:) Squalene synthase {Human (Homo sapiens)}
NSLKTCYKYLNQTSRSFAAVIQALDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHS
FLYQPDWRFMESKEKDRQVLEDFPTISLEFRNLAEKYQTVIADICRRMGIGMAEFLDKHVTSEQE
WDKYCHYVAGLVGIGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDQQGGREFWP
QEVWSRYVKKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAI
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ATLAACYNNQQVFKGAVKIRKGQAVTLMMDATNMPAVKAIIYQYMEEIYHRIPDSDPSSSKTRQI
ISTIRTQN
>d5eau_2 a.128.1.3 (221-548) 5-Epi-aristolochene synthase, C-terminal domain {Tobacco (Nicotiana tabacum)}
KNNVLLRFAKLDFNLLQMLHKQELAQVSRWWKDLDFVTTLPYARDRVVECYFWALGVYFEPQYSQ
ARVMLVKTISMISIVDDTFDAYGTVKELEAYTDAIQRWDINEIDRLPDYMKISYKAILDLYKDYE
KELSSAGRSHIVCHAIERMKEVVRNYNVESTWFIEGYTPPVSEYLSNALATTTYYYLATTSYLGM
KSATEQDFEWLSKNPKILEASVIICRVIDDTATYEVEKSRGQIATGIECCMRDYGISTKEAMAKF
QNMAETAWKDINEGLLRPTPVSTEFLTPILNLARIVEVTYIHNLDGYTHPEKVLKPHIINLLVDS
IKI
>d1di1a_ a.128.1.4 (A:) Aristolochene synthase {Fungus (Penicillium roqueforti)}
TPPPTQWSYLCHPRVKEVQDEVDGYFLENWKFPSFKAVRTFLDAKFSEVTCLYFPLALDDRIHFA
CRLLTVLFLIDDVLEHMSFADGEAYNNRLIPISRGDVLPDRTKPEEFILYDLWESMRAHDAELAN
EVLEPTFVFMRAQTDRARLSIHELGHYLEYREKDVGKALLSALMRFSMGLRLSADELQDMKALEA
NCAKQLSVVNDIYSYDKEEEASRTGHKEGAFLCSAVKVLAEESKLGIPATKRVLWSMTREWETVH
DEIVAEKIASPDGCSEAAKAYMKGLEYQMSGNEQWSKTTR
>d1ps1a_ a.128.1.4 (A:) Pentalenene synthase {Streptomyces sp., UC5319}
QDVDFHIPLPGRQSPDHARAEAEQLAWPRSLGLIRSDAAAERHLRGGYADLASRFYPHATGADLD
LGVDLMSWFFLFDDLFDGPRGENPEDTKQLTDQVAAALDGPLPDTAPPIAHGFADIWRRTCEGMT
PAWCARSARHWRNYFDGYVDEAESRFWNAPCDSAAQYLAMRRHTIGVQPTVDLAERAGRFEVPHR
VFDSAVMSAMLQIAVDVNLLLNDIASLEKEEARGEQNNMVMILRREHGWSKSRSVSHMQNEVRAR
LEQYLLLESCLPKVGEIYQLDTAEREALERYRTDAVRTVIRGSYDWHRSSG
>d1jfaa_ a.128.1.5 (A:) Trichodiene synthase {Fusarium sporotrichioides}
MENFPTEYFLNTTVRLLEYIRYRDSNYTREERIENLHYAYNKAAHHFAQPRQQQLLKVDPKRLQA
SLQTIVGMVVYSWAKVSKECMADLSIHYTYTLVLDDSKDDPYPTMVNYFDDLQAGREQAHPWWAL
VNEHFPNVLRHFGPFCSLNLIRSTLDFFEGCWIEQYNFGGFPGSHDYPQFLRRMNGLGHCVGASL
WPKEQFNERSLFLEITSAIAQMENWMVWVNDLMSFYKEFDDERDQISLVKNYVVSDEISLHEALE
KLTQDTLHSSKQMVAVFSDKDPQVMDTIECFMHGYVTWHLCDRRYRLSEIYEKVKEEKTEDAQKF
CKFYEQAANVGAVSPSEWAYPPVAQLANV
>d1oela1 a.129.1.1 (A:2-136,A:410-525) GroEL {Escherichia coli}
AAKDVKFGNDAGVKMLRGVNVLADAVKVTLGPKGRNVVLDKSFGAPTITKDGVSVAREIELEDKF
ENMGAQMVKEVASKANDAAGDGTTTATVLAQAIITEGLKAVAAGMNPMDLKRGIDKAVTVAVEEL
KALSVXGVVAGGGVALIRVASKLADLRGQNEDQNVGIKVALRAMEAPLRQIVLNCGEEPSVVANT
VKGGDGNYGYNAATEEYGNMIDMGILDPTKVTRSALQYAASVAGLMITTECMVTDLP
>d1ioka1 a.129.1.1 (A:2-136,A:410-526) GroEL {Paracoccus denitrificans}
AAKEVKFNSDARDRMLKGVNILADAVKVTLGPKGRNVVIDKSFGAPRITKDGVSVAKEIELSDKF
ENMGAQMVREVASRTNDEAGDGTTTATVLAQAIVREGLKAVAAGMNPMDLKRGIDVATAKVVEAI
KSAARXGIVVGGGVALVQGAKVLEGLSGANSDQDAGIAIIRRALEAPMRQIAENAGVDGAVVAGK
VRESSDKAFGFNAQTEEYGDMFKFGVIDPAKVVRTALEDAASVAGLLITTEAMIAEKP
>d1a6da1 a.129.1.2 (A:17-145,A:404-519) Thermosome {Archaeon
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Thermoplasma acidophilum}
REQGKNAQRNNIEAAKAIADAVRTTLGPKGMDKMLVDSIGDIIISNDGATILKEMDVEHPTAKMI
VEVSKAQDTAVGDGTTTAVVLSGELLKQAETLLDQGVHPTVISNGYRLAVNEARKIIDEIAEKSX
FLWGGGAVEAELAMRLAKYANSVGGREQLAIEAFAKALEIIPRTLAENAGIDPINTLIKLKADDE
KGRISVGVDLDNNGVGDMKAKGVVDPLRVKTHALESAVEVATMILRIDDVI
>d1a6db1 a.129.1.2 (B:20-144,B:404-521) Thermosome {Archaeon Thermoplasma acidophilum}
KDAMKENIEAAIAISNSVRSSLGPRGMDKMLVDSLGDIVITNDGVTILKEMDVEHPAAKMMVEVS
KTQDSFVGDGTTTAVIIAGGLLQQAQGLINQNVHPTVISEGYRMASEEAKRVIDEISTKIXAYAA
GGGATAAEIAFRLRSYAQKIGGRQQLAIEKFADAIEEIPRALAENAGLDPIDILLKLRAEHAKGN
KTYGINVFTGEIEDMVKNGVIEPIRVGKQAIESATEAAIMILRIDDVIA
>d1ecma_ a.130.1.1 (A:) Chorismate mutase domain of P-protein {Escherichia coli}
NPLLALREKISALDEKLLALLAERRELAVEVGKAKLLSHRPVRDIDRERDLLERLITLGKAHHLD
AHYITRLFQLIIEDSVLTQQALLQQH
>d5csma_ a.130.1.2 (A:) Allosteric chorismate mutase {Baker's yeast (Saccharomyces cerevisiae)}
MDFTKPETVLNLQNIRDELVRMEDSIIFKFIERSHFATCPSVYEANHPGLEIPNFKGSFLDWALS
NLEIAHSRIRRFESPDETPFFPDKIQKSFLPSINYPQILAPYAPEVNYNDKIKKVYIEKIIPLIS
KRDGDDKNNFGSVATRDIECLQSLSRRIHFGKFVAEAKFQSDIPLYTKLIKSKDVEGIMKNITNS
AVEEKILERLTKKAEVYGVDPTERRIERRISPEYLVKIYKEIVIPITKEVEVEYLLRRLEE
>d1pprm1 a.131.1.1 (M:1-156) Peridinin-chlorophyll protein {Dinoflagellate (Amphidinium carterae)}
DEIGDAAKKLGDASYAFAKEVDWNNGIFLQAPGKLQPLEALKAIDKMIVMGAAADPKLLKAAAEA
HHKAIGSISGPNGVTSRADWDNVNAALGRVIASVPENMVMDVYDSVSKITDPKVPAYMKSLVNGA
DAEKAYEGFLAFKDVVKKSQVTSAAG
>d1pprm2 a.131.1.1 (M:157-312) Peridinin-chlorophyll protein {Dinoflagellate (Amphidinium carterae)}
PATVPSGDKIGVAAQQLSEASYPFLKEIDWLSDVYMKPLPGVSAQQSLKAIDKMIVMGAQADGNA
LKAAAEAHHKAIGSIDATGVTSAADYAAVNAALGRVIASVPKSTVMDVYNAMAGVTDTSIPLNMF
SKVNPLDANAAAKAFYTFKDVVQAAQ
>d1qq8a_ a.132.1.1 (A:) Heme oxygenase-1 (HO-1) {Human (Homo sapiens)}
PQDLSEALKEATKEVHTQAENAEFMRNFQKGQVTRDGFKLVMASLYHIYVALEEEIERNKESPVF
APVYFPEELHRKAALEQDLAFWYGPRWQEVIPYTPAMQRYVKRLHEVGRTEPELLVAHAYTRYLG
DLSGGQVLKKIAQKALDLPSSGEGLAFFTFPNIASATKFKQLYRSRMNSLEMTPAVRQRVIEEAK
TAFLLNIQLFEELQELLTH
>d1dvga_ a.132.1.1 (A:) Heme oxygenase-1 (HO-1) {Rat (Rattus norvegicus)}
SQDLSEALKEATKEVHIRAENSEFMRNFQKGQVSREGFKLVTASLYHIYTALEEEIERNKQNPVY
APLYFPEELHRRAALEQDLAFWYGPHWQEAIPYTPATQHYVKRLHEVGGTHPELLVAHAYTRYLG
DLSGGQVLKKIAQKALALPSSGEGLASFTFPSIDNPTKFKQLYRARMNTLELTPEVKHRVTEEAK
TAFLLNIELFEELQALLTE
>d1j77a_ a.132.1.2 (A:) Gram-negative bacterial heme oxygenase {Neisseria meningitidis}
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ALTFAKRLKADTTAVHDSVDNLVMSVQPFVSKENYIKFLKLQSVFHKAVDHIYKDAELNKAIPEL
EYMARYDAVTQDLKDLGEEPYKFDKELPYEAGNKAIGWLYCAEGSNLGAAFLFKHAQKLDYNGEH
GARHLAPHPDGRGKHWRAFVEHLNALNLTPEAEAEAIQGAREAFAFYKVVLRETFGLAADAEAPE
GMMPH
>d1knca_ a.152.1.1 (A:) Antioxidant defence protein AhpD {Mycobacterium tuberculosis}
SIEKLKAALPEYAKDIKLNLSSITRSSVLDQEQLWGTLLASAAATRNPQVLADIGAEATDHLSAA
ARHAALGAAAIMGMNNVFYRGRGFLEGRYDDLRPGLRMNIIANPGIPKANFELWSFAVSAINGCS
HCLVAHEHTLRTVGVDREAIFEALKAAAIVSGVAQALATIEALS
>d1poa__ a.133.1.2 (-) Snake phospholipase A2 {Taiwan cobra (Naja naja atra)}
NLYQFKNMIQCTVPSRSWWDFADYGCYCGRGGSGTPVDDLDRCCQVHDNCYNEAEKISGCWPYFK
TYSYECSQGTLTCKGGNNACAAAVCDCDRLAAICFAGAPYNDNDYNINLKARC
>d1pp2l_ a.133.1.2 (L:) Snake phospholipase A2 {Western diamondback rattlesnake (Crotalus atrox)}
SLVQFETLIMKIAGRSGLLWYSAYGCYCGWGGHGLPQDATDRCCFVHDCCYGKATDCNPKTVSYT
YSEENGEIICGGDDPCGTQICECDKAAAICFRDNIPSYDNKYWLFPPKDCREEPEPC
>d1bjja_ a.133.1.2 (A:) Snake phospholipase A2 {Chinese water moccasin (Agkistrodon halys pallas), different isoforms}
NLLQFNKMIKEETGKNAIPFYAFYGCYCGWGGQGKPKDGTDRCCFVHDCCYGRLVNCNTKSDIYS
YSLKEGYITCGKGTNCEEQICECDRVAAECFRRNLDTYNNGYMFYRDSKCTETSEEC
>d1jiaa_ a.133.1.2 (A:) Snake phospholipase A2 {Chinese water moccasin (Agkistrodon halys pallas), different isoforms}
HLLQFRKMIKKMTGKEPVVSYAFYGCYCGSGGRGKPKDATDRCCFVHDCCYEKVTGCDPKWDDYT
YSWKNGTIVCGGDDPCKKEVCECDKAAAICFRDNLKTYKKRYMAYPDILCSSKSEKC
>d1psj__ a.133.1.2 (-) Snake phospholipase A2 {Chinese water moccasin (Agkistrodon halys pallas), different isoforms}
SLIQFETLIMKVAKKSGMFWYSNYGCYCGWGGQGRPQDATDRCCFVHDCCYGKVTGCDPKMDVYS
FSEENGDIVCGGDDPCKKEICECDRAAAICFRDNLTLYNDKKYWAFGAKNCPQEESEPC
>d1ppa__ a.133.1.2 (-) Snake phospholipase A2 {Eastern cottonmouth snake (Agkistridon piscivorus)}
SVLELGKMILQETGKNAITSYGSYGCNCGWGHRGQPKDATDRCCFVHKCCYKKLTDCNHKTDRYS
YSWKNKAIICEEKNPCLKEMCECDKAVAICLRENLDTYNKKYKAYFKLKCKKPDTC
>d1vapa_ a.133.1.2 (A:) Snake phospholipase A2 {Eastern cottonmouth snake (Agkistridon piscivorus)}
NLFQFEKLIKKMTGKSGMLWYSAYGCYCGWGGQGRPKDATDRCCFVHDCCYGKVTGCNPKMDIYT
YSVDNGNIVCGGTNPCKKQICECDRAAAICFRDNLKTYDSKTYWKYPKKNCKEESEPC
>d1ijla_ a.133.1.2 (A:) Snake phospholipase A2 {Viper (Deinagkistrodon acutus)}
SLIQFETLIMKVVKKSGMFWYSAYGCYCGWGGHGRPQDATDRCCFVHDCCYGKVTGCDPKMDSYT
YSEENGDIVCGGDDPCKREICECDRVAADCFRDNLDTYNSDTYWRYPRQDCEESPEPC
>d1fe7a_ a.133.1.2 (A:) Snake phospholipase A2 {Snake (Daboia russelli pulchella)}
SLLEFGKMILEETGKLAIPSYSSYGCYCGWGGKGTPKDATDRCCFVHDCCYGNLPDCNPKSDRYK
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YKRVNGAIVCEKGTSCENRICECDKAAAICFRQNLNTYSKKYMLYPDFLCKGELKC
>d1ae7__ a.133.1.2 (-) Snake phospholipase A2 {Mainland tiger snake
(Notechis scutatus scutatus), notexin}
NLVQFSYLIQCANHGKRPTWHYMDYGCYCGAGGSGTPVDELDRCCKIHDDCYDEAGKKGCFPKMS
AYDYYCGENGPYCRNIKKKCLRFVCDCDVEAAFCFAKAPYNNANWNIDTKKRCQ
>d2nota_ a.133.1.2 (A:) Snake phospholipase A2 {Mainland tiger snake
(Notechis scutatus scutatus), notechis II-5}
NLVQFSYLIQCANHGRRPTRHYMDYGCYCGWGGSGTPVDELDRCCKIHDDCYSDAEKKGCSPKMS
AYDYYCGENGPYCRNIKKKCLRFVCDCDVEAAFCFAKAPYNNANWNIDTKKRCQ
>d1qlla_ a.133.1.2 (A:) Snake phospholipase A2 {Bothrops pirajai,
Piratoxin-II (PRTX-II)}
SLFELGKMILQETGKNPAKSYGAYGCNCGVLGRGKPKDATDRCCYVHKCCYKKLTGCNPKKDRYS
YSWKDKTIVCGENNPCLKELCECDKAVAICLRENLGTYNKKYRYHLKPFCKKADKC
>d1vip__ a.133.1.2 (-) Snake phospholipase A2 {Russell's viper (Vipera
russelli)}
NLFQFAEMIVKMTGKNPLSSYSDYGCYCGWGGKGKPQDATDRCCFVHDCCYEKVKSCKPKLSLYS
YSFQNGGIVCGDNHSCKRAVCECDRVAATCFRDNLNTYDKKYHNYPPSQCTGTEQC
>d1jlta_ a.133.1.2 (A:) Snake phospholipase A2 {Sand viper (Vipera
ammodytes meridionalis), vipoxin}
NLFQFGDMILQKTGKEAVHSYAIYGCYCGWGGQARAQDATDRCCFAQDCCYGRVNDCNPKTATYT
YSFENGDIVCGDNDLCLRAVCECDRAAAICLGENVNTYDKNYEYYSISHCTEESEQC
>d1jltb_ a.133.1.2 (B:) Snake phospholipase A2 {Sand viper (Vipera
ammodytes meridionalis), vipoxin}
NLFQFAKMINGKLGAFSVWNYISYGCYCGWGGQGTPKDATDRCCFVHDCCYGRVRGCNPKLAIYS
YSFKKGNIVCGKNNGCLRDICECDRVAANCFHQNKNTYNKNYKFLSSSRCRQTSEQC
>d1dpya_ a.133.1.2 (A:) Snake phospholipase A2 {Indian krait (Bungarus
caeruleus), different isoforms}
NLIQFKNMIQCAGTRIWTAYVAYGCYCGKGGSGTPVDELDRCCYTHDHCYNEAEKIPGCNPNIKT
YSYTCTQPNLTCTDSADTCAQFLCECDRTAAICFASAPYNSNNIMLSSSTSCQ
>d1fe5a_ a.133.1.2 (A:) Snake phospholipase A2 {Indian krait (Bungarus
caeruleus), different isoforms}
NLIQFKNMIQCAGTRPWTAYVNYGCYCGKGGSGTPVDELDRCCYTHDNCYNEAEKIPGCNPNIKT
YSYTCTEPNLTCTDTADTCARFLCNCDRTAAICFASAPYNSNNVMISSSTNCQ
>d1kvoa_ a.133.1.2 (A:) Phospholipase A2 {Human (Homo sapiens),
synovial fluid}
NLVNFHRMIKLTTGKEAALSYGFYGCHCGVGGRGSPKDATDRCCVTHDCCYKRLEKRGCGTKFLS
YKFSNSGSRITCAKQDSCRSQLCECDKAAATCFARNKTTYNKKYQYYSNKHCRGSTPRC
>d1g4ia_ a.133.1.2 (A:) Phospholipase A2 {Cow (Bos taurus), pancreas}
ALWQFNGMIKCKIPSSEPLLDFNNYGCYCGLGGSGTPVDDLDRCCQTHDNCYKQAKKLDSCKVLV
DNPYTNNYSYSCSNNEITCSSENNACEAFICNCDRNAAICFSKVPYNKEHKNLDKKNC
>d1hn4a_ a.133.1.2 (A:) Phospholipase A2 {Pig (Sus scrofa), pancreas}
GISSRALWQFRSMIKCAIPGSHPLMDFNNYGCYCGLGGSGTPVDELDRCCETHDNCYRDAKNLDS
CKFLVDNPYTESYSYSCSNTEITCNSKNNACEAFICNCDRNAAICFSKAPYNKEHKNLDTKKYC
>d5p2pa_ a.133.1.2 (A:) Phospholipase A2 {Pig (Sus scrofa), pancreas}
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ALFQFRSMIKCAIPGSHPLMDFNNYGCYCGWGGSGTPVDELDRCCETHDNCYRDAKNLSGCYPYT
ESYSYSCSNTEITCNSKNNACEAFICNCDRNAAICFSKAPYNKEHKNLDTKKYC
>d1buna_ a.133.1.2 (A:) beta2-bungarotoxin, phospholipase A2 chain {Many-banded krait (Bungarus multicinctus), elapid}
NLINFMEMIRYTIPCEKTWGEYADYGCYCGAGGSGRPIDALDRCCYVHDNCYGDAEKKHKCNPKT
QSYSYKLTKRTIICYGAAGTCARIVCDCDRTAALCFGNSEYIEGHKNIDTARFCQ
>d1goda_ a.133.1.2 (A:) Myotoxin II {Bothrops godmani}
SMYQLWKMILQETGKNAVPSYGLYGCNCGVGSRGKPKDATDRCCFVHKCCYKKLTDCSPKTDSYS
YSWKDKTIVCGDNNPCLQEMCECDKAVAICLRENLDTYNKNYKIYPKPLCKKADAC
>d1gmza_ a.133.1.2 (A:) Myotoxin II {Snake (Bothrops pirajai), piratoxin III}
DLWQFGKMILKETGKLPFPYYVTYGCYCGVGGRGGPKDATDRCCFVHDCCYGKLTSCKPKTDRYS
YSRKDGTIVCGENDPCRKEICECDKAAAVCFRENLDTYNKKYMSYLKSLCKKXADDC
>d1poc__ a.133.1.1 (-) Phospholipase A2 {European honeybee (Apis mellifera)}
IIYPGTLWCGHGNKSSGPNELGRFKHTDACCRTHDMCPDVMSAGESKHGLTNTASHTRLSCDCDD
KFYDCLKNSADTISSYFVGKMYFNLIDTKCYKLEHPVTGCGERTEGRCLHYTVDKSKPKVYQWFD
LRKY
>d1faza_ a.133.1.3 (A:) Prokaryotic phospholipase A2 {Streptomyces violaceoruber}
APADKPQVLASFTQTSASSQNAWLAANRNQSAWAAYEFDWSTDLCTQAPDNPFGFPFNTACARHD
FGYRNYKAAGSFDANKSRIDSAFYEDMKRVCTGYTGEKNTACNSTAWTYYQAVKIFG
>d1bxm__ a.134.1.1 (-) beta-cryptogein {Phytophthora cryptogea}
RGTCTATQQTAAYHTLVSILSDASFNQCSTDSGYSMLTAKALPTTAQYKLMCASTACNTMIKKIV
TLNPPNCDLTVPTSGLVLNVYSYANGFSNKCSSL
>d1g8qa_ a.135.1.1 (A:) CD81 extracellular domain {Human (Homo sapiens)}
FVNKDQIAKDVKQFYDQALQQAVVDDDANNAKAVVKTFHETLDCCGSSTLTALTTSVLKNNLCPS
GSNIISNLFKEDCHQKIDDLFSGKH
>d1dvoa_ a.136.1.1 (A:) Repressor of bacterial conjugation FinO {Escherichia coli}
PPKWKVKKQKLAEKAAREAELTAKKAQARQALSIYLNLPTLDEAVNTLKPWWPGLFDGDTPRLLA
CGIRDVLLEDVAQRNIPLSHKKLRRAMKAITRSESYLCAMKAGACRYDTEGYVTEHISQEEEVYA
AERLDKIRRQNRIKAELQAVLD
>d1jjsa_ a.153.1.1 (A:) Nuclear receptor coactivator CBP/p300 ibid domain {Mouse (Mus musculus)}
ALQDLLRTLKSPSSPQQQQQVLNILKSNPQLMAAFIKQRTAKYVAN
>d1kbhb_ a.153.1.1 (B:) Nuclear receptor coactivator CBP/p300 ibid domain {Mouse (Mus musculus)}
PNRSISPSALQDLLRTLKSPSSPQQQQQVLNILKSNPQLMAAFIKQRTAKYVANQPGMQ
>d1kbha_ a.153.1.1 (A:) Nuclear receptor coactivator ACTR {Human (Homo sapiens)}
EGQSDERALLDQLHTLLSNTDATGLEEIDRALGIPELVNQGQALEPK
>d1ffky_ a.137.1.1 (Y:) Ribosomal protein L39e {Archaeon Haloarcula
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marismortui}
GKKSKATKKRKAKLDNQNSRVPAYVMLKTDREVQRNHKRRHWRRNDTDE
>d1jj21_ a.137.1.1 (1:) Ribosomal protein L39e {Archaeon Haloarcula marismortui}
GKKSKATKKRLAKLDNQNSRVPAWVMLKTDEVQRNHKRRHWRRNDTDE
>d1g72b_ a.137.2.1 (B:) Methanol dehydrogenase, light chain {Methylophilus methylotrophus, w3a1}
YDGQNCKEPGNCWENKPGYPEKIAGSKYDPKHDPVELNKQEESIKAMDARNAKRIAN
>d4aahb_ a.137.2.1 (B:) Methanol dehydrogenase, light chain {Methylophilus methylotrophus, w3a1}
YDGQNCKEPGNCWENKPGYPEKIAGSKYDPKHDPVELNKQEESIKAMDARNAKRIANAKSSGNFVFDVK
>d1h4ib_ a.137.2.1 (B:) Methanol dehydrogenase, light chain {Methylobacterium extorquens}
YDGTKCKAAGNCWEPKPGFPEKIAGSKYDPKHDPKELNKQADSIKQMEERNKKRVENFKKTGKFEYDVAKISA
>d1gg2g_ a.137.3.1 (G:) Transducin (heterotrimeric G protein), gamma chain {Cow (Bos taurus)}
SIAQARKLVEQLKMEANIDRIKVSKAAADLMAYCEAHAKEDPLLTPVPASENPF
>d1gotg_ a.137.3.1 (G:) Transducin (heterotrimeric G protein), gamma chain {Cow (Bos taurus)}
LTEKDKLKMEVDQLKKEVTLERMLVSKCCEEFRDYVEERSGEDPLVKGIPEDKNPFKE
>d1tbge_ a.137.3.1 (E:) Transducin (heterotrimeric G protein), gamma chain {Cow (Bos taurus)}
APVINIEDLTEKDKLKMEVDQLKKEVTLERMLVSKCCEEFRDYVEERSGEDPLVKGIPEDKNPFKELK
>d1hfes_ a.137.4.1 (S:) Fe-only hydrogenase smaller subunit {Desulfovibrio desulfuricans}
VKQIKDYMLDRINGVYGADAKFPVRASQDNTQVKALYKSYLEKPLGHKSHDLLHTHWFDKSKGVKELTTAGKLPNPRASEFEGPYPYE
>d1ef1c_ a.137.5.1 (C:) Moesin tail domain {Human (Homo sapiens)}
AEASADLRADAMAKDRSEEERTTEAEKNERVQKHLKALTSELANARDESKKTANDMIHAENMRLGRDKYKTLRQIRQGNTKQRIDEFESM
>d2prgc_ a.137.6.1 (C:) Nuclear receptor coactivator Src-1 {Human (Homo sapiens)}
QTSHKLVQLLTTTAEQQLRHADIDTSCKDVLSCTGTSNSASANSSGGSCPSSHSSLTERHKILHRLLQEGSPSDIT
>d1dp5b_ a.137.7.1 (B:) Proteinase A inhibitor IA3 {Baker's yeast (Saccharomyces cerevisiae)}
NTDQQKVSEIFQSSKEKLQGDAKVVSDAFMM
>d1dpjb_ a.137.7.1 (B:) Proteinase A inhibitor IA3 {Baker's yeast (Saccharomyces cerevisiae)}
TDQQKVSEIFQSSKEKLQGDAKVVSDAFK
>d1e79i_ a.137.8.1 (I:) Epsilon subunit of mitochondrial F1F0-ATP
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synthase {Cow (Bos taurus)}
VAYWRQAGLSYIRYSQICAKAVRDALKTEFKANAMKTSGSTIKIVKV
>d1jjuc_ a.137.9.1 (C:) Quinohemoprotein amine dehydrogenase C chain
{Paracoccus denitrificans}
MNALVGCTTSFDPGWEVDAFGAVSNLCQPMEADLYGCADPCWXPAQVADTLNTYPNWSAGADDVM
QDWRKLQSVFPETK
>d1jmxg_ a.137.9.1 (G:) Quinohemoprotein amine dehydrogenase C chain
{Pseudomonas putida}
AVAGCTATTDPGWEVDAFGGVSSLCQPMEADLYGCSDPCWXPAQVPDMMSTYQDWNAQASNSAED
WRNLGTVFPKDK
>d1aqe__ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio desulfuricans,
different strains}
TFEIPESVTMSPKQFEGYTPKKGDVTFNHASHMDIACQQCHHTVPDTYTIESCMTEGCHDNIKER
TEISSVERTFHTTKDSEKSCVGCHRELKRQGPSDAPLACNSCHVQ
>d1i77a_ a.138.1.1 (A:) Cytochrome c3 {Desulfovibrio desulfuricans,
different strains}
APAAPDKPLEFKGSQKTVMFPHAVHAKVECVTCHHQVDGKESFAKCGSSGCHDDLAGKQGEKSLY
YVVHTKKELKHTNCIGCHSKVVEGKPELKKDLTACAKSKCHP
>d2cy3__ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio desulfuricans,
different strains}
ADAPGDDYVISAPEGMKAKPKGDKPGALQKTVPFPHTKHATVECVQCHHTLEADGGAVKKCTTSG
CHDSLEFRDKANAKDIKLVENAFHTQCIDCHKALKKDKKPTGPTACGKCHTTN
>d3cyr__ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio desulfuricans,
different strains}
APAVPNKPVEVKGSQKTVMFPHAPHEKVECVTCHHLVDGKESYAKCGSSGCHDDLTAKKGEKSLY
YVVHAKGELKHTSCLACHSKVVAEKPELKKDLTGCAKSKCHP
>d2cdv__ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio vulgaris}
APKAPADGLKMDKTKQPVVFNHSTHKAVKCGDCHHPVNGKENYQKCATAGCHDNMDKKDKSAKGY
YHAMHDKGTKFKSCVGCHLETAGADAAKKKELTGCKGSKCHS
>d2ctha_ a.138.1.1 (A:) Cytochrome c3 {Desulfovibrio vulgaris}
APKAPADGLKMEATKQPVVFNHSTHKSVKCGDCHHPVNGKEDYRKCGTAGCHDSMDKKDKSAKGY
YHVMHDKNTKFKSCVGCHVEVAGADAAKKKDLTGCKKSKCHE
>d1wad__ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio gigas}
VDVPADGAKIDFIAGGEKNLTVVFNHSTHKDVKCDDCHHDPGDKQYAGCTTDGCHNILDKADKSV
NSWYKVVHDAKGGAKPTCISCHKDKAGDDKELKKKLTGCKGSACHP
>d3caoa_ a.138.1.1 (A:) Cytochrome c3 {Desulfovibrio africanus}
EDMTHVPTDAFGKLERPAAVFNHDEHNEKAGIESCNACHHVWVNGVLAEDEDSVGTPCSDCHALE
QDGDTPGLQDAYHQQCWGCHEKQAKGPVMCGECHVKN
>d1hh5a_ a.138.1.1 (A:) Cytochrome c7 (cytochrome c551.5)
{Desulfuromonas acetoxidans}
ADVVTYENKKGNVTFDHKAHAEKLGCDACHEGTPAKIAIDKKSAHKDACKTCHKSNNGPTKCGGC
HIK
>d19hca_ a.138.1.1 (A:) Nine-haem cytochrome c {Desulfovibrio
desulfuricans, ATCC 27774}
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AALEPTDSGAPSAIVMFPVGEKPNPKGAAMKPVVFNHLIHEKKIADCETCHHTGDPVSCSTCHTV
EGKAEGDYITLDRAMHATDIAARAKGNTPTSCVSCHQSETKERRECAGCHAITTPKDDEAWCATC
HDITPSMTPSEMQKGIAGTLLPGDNEALAAETVLAEATVAPVSPMLAPYKVVIDALADKYEPSDF
THRRHLTSLMESIKDDKLAQAFHDKPEILCATCHHRSPLSLTPPKCGSCHTKEIDAADPGRPNLM
AAYHLECMGCHKGMAVARPRDTDCTTCHKAAA
>d1duwa_ a.138.1.1 (A:) Nine-haem cytochrome c {Desulfovibrio desulfuricans, ATCC 29577}
EPTDSGAPSAIVMFPVSAKPNPKGAAMKPAVFNHLAHEKKIANCETCHHTGDPVACSTCHTTEGK
AEGNFVTLDRAMHATNIAKRAKGNTPVSCVSCHEQQTKERRECAGCHAIVTPKRDQAWCATCHNV
TSSMTPEQMQQGIKGKLPPDQNEALAAETVLNHKPVQPLTAMQGPYKVSIDALADKYEPSNFTHR
RHMASLMERIKGDKLAEAFHNKPETLCATCHHRSPLSATPPKCGSCHTKEIDPANPNRPNLKAAY
HLQCMGCHQGMNVGRPKNTDCTTCHKARP
>d1dxrc_ a.138.1.2 (C:) Photosynthetic reaction centre (cytochrome subunit) {Rhodopseudomonas viridis}
CFEPPPATTTQTGFRGLSMGEVLHPATVKAKKERDAQYPPALAAVKAEGPPVSQVYKNVKVLGNL
TEAEFLRTMTAITEWVSPQEGCTYCHDENNLASEAKYPYVVARRMLEMTRAINTNWTQHVAQTGV
TCYTCHRGTPLPPYVRYLEPTLPLNNRETPTHVERVETRSGYVVRLAKYTAYSALNYDPFTMFLA
NDKRQVRVVPQTALPLVGVSRGKERRPLSDAYATFALMMSISDSLGTNCTFCHNAQTFESWGKKS
TPQRAIAWWGIRMVRDLNMNYLAPLNASLPASRLGRQGEAPQADCRTCHQGVTKPLFGASRLKDY
PELGPIK
>d1eysc_ a.138.1.2 (C:) Photosynthetic reaction centre (cytochrome subunit) {Thermochromatium tepidum}
CEGPPPGTEQIGYRGVGMENYYVKRQRALSIQANQPVESLPAADSTGPKASEVYQSVQVLKDLSV
GEFTRTMVAVTTWVSPKEGCNYCHVPGNWASDDIYTKVVSRRMFELVRAANSDWKAHVAETGVTC
YTCHRGNPVPKYAWVTDPGPKYPSGLKPTGQNYGSKTVAYASLPFDPLTPFLDQANEIRITGNAA
LAGSNPASLKQAEWTFGLMMNISDSLGVGCTSCHNTRAFNDWTQSTPKRTTAWYAIRHVRDINQN
YIWPLNDVLPASRKGPYGDPLRVSCMTCHQAVNKPLYGAQMAKDYPGLYK
>d1fgja_ a.138.1.3 (A:) Hydroxylamine oxidoreductase, HAO {Nitrosomonas europaea}
DISTVPDETYDALKLDRGKATPKETYEALVKRYKDPAHGAGKGTMGDYWEPIAISIYMDPNTFYK
PPVSPKEVAERKDCVECHSDETPVWVRAWKRSTHANLDKIRNLKSDDPLYYKKGKLEEVENNLRS
MGKLGEKETLKEVGCIDCHVDVNKKDKADHTKDIRMPTADTCGTCHLREFAERESERDTMVWPNG
QWPAGRPSHALDYTANIETTVWATMPQREVAEGCTMCHTNQNKCDNCHTRHEFSAAESRKPEACA
TCHSGVDHNNWEAYTMSKHGKLAEMNRDKWNWEVRLKDAFSKGGQNAPTCAACHMEYEGEYTHNI
TRKTRWANYPFVPGIAENITSDWSEARLDSWVLTCTQCHSERFARSYLDLMDKGTLEGLAKYQEA
NAIVHKMYEDGTLTGQKTNRPNPPEPEKPGFGIFTQLFWSKGNNPASLELKVLEMGENNLAKMHV
GLAHVNPGGWTYTEGWGPMNRAYVEIQDEYTKMQELSALQARVN
>d1ft5a_ a.138.1.3 (A:) Cytochrome c554 {Nitrosomonas europaea}
ADAPFEGRKKCSSCHKAQAQSWKDTAHAKAMESLKPNVKKEAKQKAKLDPAKDYTQDKDCVGCHV
DGFGQKGGYTIESPKPMLTGVGCESCHGPGRNFRGDHRKSGQAFEKSGKKTPRKDLAKKGQDFHF
EERCSACHLNYEGSPWKGAKAPYTPFTPEVDAKYTFKFDEMVKEVKAMHEHYKLEGVFEGEPKFK
FHDEFQASAKPAKKGK
>d1ddca_ a.138.1.3 (A:) Dimeric di-heme split-soret cytochrome c {Desulfovibrio desulfuricans, ATCC 27774}

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RFDQVGGAFGWKPHKLDPKECAQVAYDGYWYKGFGCGFGAFYSIVGLMGEKYGAPYNQFPFAMLE
ANKGGISDWGTIYGALYGAAATFSLFWGRKEVHPMVNELFRWYEVTKLPIFNPGDAAQGVKGDLP
MSASDSVLCHISVSKWCYENKIEATSKQRSERAGRLTADAAFKAAEIINTKIDQGKDFKSTFPMQ
ASVSSCGECHMTKGNDANWAKGIMDCTPCHSGTAATQNKFVNH
>d1qdba_ a.138.1.3 (A:) Cytochrome c nitrite reductase
{Sulfurospirillum deleyianum}
GIAGKEKSEEWAKYYPRQFDSWKKTKEYDSFTDMLAKDPALVIAWSGYAFSKDYNSPRGHYYALQ
DNVNSLRTGAPVDAKTGPLPTACWTCKSPDVPRLIEEDGELEYFTGKWAKYGSQIVNVIGCANCH
DDKTAELKVRVPHLNRGLQAAGLKTFEESTHQDKRTLVCAQCHVEYYFKKTEWKDAKGADKTAMV
VTLPWANGVGKDGNAGVEGMIKYYDEINFSDWTHNISKTPMLKAQHPGFEFWKSGIHGQKGVSCA
DCHMPYTQEGSVKYSDHQVKENPLDSMDQSCMNCHRESESKLRGIVHQKYERKEFLNKVAFDNIG
KAHLETGKAIEAGASDEELKEVRKLIRHGQFKADMAIAAHGNYFHAPEETLRLLAAGSDDAQKAR
LLLVKILAKHGVMDYIAPDFDTKDKAQKLAKVDIAALAAEKMKFKQTLEQEWKKEAKAKGRANPE
LYKDVDTINDGKSSWNKK
>d1fs7a_ a.138.1.3 (A:) Cytochrome c nitrite reductase {Wolinella
succinogenes}
KTAHSQGIEGKAMSEEWARYYPRQFDSWKKTKESDNITDMLKEKPALVVAWAGYPFSKDYNAPRG
HYYALQDNINTLRTGAPVDGKTGPLPSACWTCKSPDVPRIIEQDGELEYFTGKWAKYGDEIVNTI
GCYNCHDDKSAELKSKVPYLDRGLSAAGFKTFAESTHQEKRSLVCAQCHVEYYFKKTEWKDDKGV
DKTAMVVTLPWSKGISTEQMEAYYDEINFADWTHGISKTPMLKAQHPDWELYKTGIHGQKGVSCA
DCHMPYTQEGAVKYSDHKVGNPLDNMDKSCMNCHRESEQKLKDIVKQKFERKEFLQDIAFDNIGK
AHLETGKAMELGATDAELKEIRTHIRHAQWRADMAIAGHGSFFHAPEEVLRLLASGNEEAQKARI
KLVKVLAKYGAIDYVAPDFETKEKAQKLAKVDMEAFIAEKLKFKQTLEQEWKKQAIAKGRLNPES
LKGVDEKSSYYDKTKK
>d1e39a1 a.138.1.3 (A:1-102) Flavocytochrome c3 (respiratory fumarate
reductase), N-terminal domain {Shewanella frigidimarina}
ADNLAEFHVQNQECDSCHTPDGELSNDSLTYENTQCVSCHGTLAEVAETTKHEHYNAHASHFPGE
VACTSCHSAHEKSMVYCDSCHSFDFNMPYAKKWLRDE
>d1qo8a1 a.138.1.3 (A:2-102) Flavocytochrome c3 (respiratory fumarate
reductase), N-terminal domain {Shewanella frigidimarina}
TPDMGSFHADMGSCQSCHAKPIKVTDSETHENAQCKSCHGEYAELANDKLQFDPHNSHLGDINCT
SCHKGHEEPKFYCNECHSFDIKPMPFSDAKKKKSWD
>d1d4ca1 a.138.1.3 (A:1-102) Flavocytochrome c3 (respiratory fumarate
reductase), N-terminal domain {Shewanella putrefaciens}
APEVLADFHGEMGGCDSCHVSDKGGVTNDNLTHENGQCVSCHGDLKELAAAAPKDKVSPHKSHLI
GEIACTSCHKGHEKSVAYCDACHSFGFDMPFGGKWER
>d1neu__ b.1.1.1 (-) Myelin membrane adhesion molecule P0 {Rat (Rattus
norvegicus)}
IVVYTDREVYGAVGSQVTLHCSFWSSEWVSDDISFTWRYQPEGGRDAISIFHYAKGQPYIDEVGT
FKERIQWVGDPSWKDGSIVIHNLDYSDNGTFTCDVKNPPDIVGKTSQVTLYVFE
>d1eaja_ b.1.1.1 (A:) Coxsackie virus and adenovirus receptor (Car),
domain 1 {Human (Homo sapiens)}
FARSLSITTPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPADNQKVDQVIILYSGDKIY
DDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKKAPGVANKKIHLVVLV
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>d1qfoa_ b.1.1.1 (A:) N-terminal domain of sialoadhesin {Mouse (Mus musculus)}
TWGVSSPKNVQGLSGSCLLIPCIFSYPADVPVSNGITAIWYYDYSGKRQVVIHSGDPKLVDKRFR
GRAELMGNMDHKVCNLLLKDLKPEDSGTYNFRFEISDSNRWLDVKGTTVTVTT
>d1akjd_ b.1.1.1 (D:) CD8 {Human (Homo sapiens)}
SQFRVSPLDRTWNLGETVELKCQVLLSNPTSGCSWLFQPRGAAASPTFLLYLSQNKPKAAEGLDT
QRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPA
>d1bqhg_ b.1.1.1 (G:) CD8 {Mouse (Mus musculus)}
KPQAPELRIFPKKMDAELGQKVDLVCEVLGSVSQGCSWLFQNSSSKLPQPTFVVYMASSHNKITW
DEKLNSSKLFSAMRDTNNKYVLTLNKFSKENEGYYFCSVISNSVMYFSSVVPVLQKV
>d1cdy_1 b.1.1.1 (1-97) N-terminal domain of CD4 {Human (Homo sapiens)}
KKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKSPSKLNDRADSRRSLWDQG
NFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV
>d1wioa2 b.1.1.1 (A:179-291) N-terminal domain of CD4 {Human (Homo sapiens)}
FQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKRVTQ
DPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVV
>d1cid_1 b.1.1.1 (1-105) N-terminal domain of CD4 {Rat (Rattus rattus)}
TSITAYKSEGESAEFSFPLNLGEESLQGELRWKAEKAPSSQSWITFSLKNQKVSVQKSTSNPKFQ
LSETLPLTLQIPQVSLQFAGSGNLTLTLDRGILYQEVNLV
>d1hnf_1 b.1.1.1 (4-104) CD2, first domain {Human (Homo sapiens)}
TNALETWGALGQDINLDIPSFQMSDDIDDIKWEKTSDKKKIAQFRKEKETFKEKDTYKLFKNGTL
KIKHLKTDDQDIYKVSIYDTKGKNVLEKIFDLKIQE
>d1hnga1 b.1.1.1 (A:2-99) CD2, first domain {Rat (Rattus norvegicus)}
DSGTVWGALGHGINLNIPNFQMTDDIDEVRWERGSTLVAEFKRKMKPFLKSGAFEILANGDLKIK
NLTRDDSGTYNVTVYSTNGTRILNKALDLRILE
>d1ccza1 b.1.1.1 (A:1-93) CD2-binding domain of CD58, N-terminal domain {Human (Homo sapiens)}
FSQQIYGVVYGNVTFHVPSNVPLKEVLWKKQKDKVAELENSEFRAFSSFKNRVYLDTVSGSLTIY
NLTSSDEDEYEMESPNITDTMKFFLYVL
>d1qa9b_ b.1.1.1 (B:) CD2-binding domain of CD58, N-terminal domain {Human (Homo sapiens)}
SSQQIYGVKYGNVTFHVPSNQPLKEVLWKKQKDKVAELENSEFRAFSSFKNRVYLDTKSGSLTIY
NLTSSDEDEYEMESPNITDSMKFFLYVGES
>d1dr9a1 b.1.1.1 (A:1-105) CD80, N-terminal domain {Human (Homo sapiens)}
VIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKNRTIFDITNNL
SIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVK
>d1i85a_ b.1.1.1 (A:) CD86 (b7-2), N-terminal domain {Human (Homo sapiens)}
MLKIQAYFNETADLPCQFANSQNQSLSELVVFWQDQENLVLNEVYLGKEKFDSVHSKYMGRTSFD
SDSWTLRLHNLQIKDKGLYQCIIHHKKPTGMIRIHQMNSELSVLA
>d1f97a1 b.1.1.1 (A:27-128) Junction adhesion molecule, JAM, N-terminal domain {Mouse (Mus musculus)}
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KGSVYTAQSDVQVPENESIKLTCTYSGFSSPRVEWKFVQGSTTALVCYNSQITAPYADRVTFSSS
GITFSSVTRKDNGEYTCMVSEEGGQNYGEVSIHLTVL
>d1jmaa_ b.1.1.1 (A:) HSV glycoprotein D {Herpes simplex virus type
1}
KYALADASLKMADPNRFRGKDLPVLDQLTDPPGVRRVYHIQAGLPDPFQPPSLPITVYYAVLERA
CRSVLLNAPSEAPQIVRGASEDVRKQPYNLTIAWFRMGGNCAIPITVMEYTECSYNKSLGACPIR
TQPRWNYYDSFSAVSEDNLGFLMHAPAFETAGTYLRLVKINDWTEITQFILEHRAKGSCKYALPL
RIPPSACLSPQAYQQGVTVDSIGMLPRFIPENQRTVAVYSLKIAGWHGPKAPYTSTLLPPELSE
>d1igta1 b.1.1.1 (A:1-108) Immunoglobulin (variable domains of L and
H chains) {Intact IgG2a antibody Mab231 (mouse), kappa L chain}
DIVLTQSPSSLSASLGDTITITCHASQNINVWLSWYQQKPGNIPKLLIYKASNLHTGVPSRFSGS
GSGTGFTLTISSLQPEDIATYYCQQGQSYPLTFGGGTKLEIKR
>d1igtb1 b.1.1.1 (B:1-114) Immunoglobulin (variable domains of L and
H chains) {Intact IgG2a antibody Mab231 (mouse), kappa L chain}
EVKLQESGGGLVQPGGSLKLSCATSGFTFSDYYMYWVRQTPEKRLEWVAYISNGGGSTYYPDTVK
GRFTISRDNAKNTLYLQMSRLKSEDTAMYYCARHGGYYAMDYWGQGTTVTVSSA
>d1igya1 b.1.1.1 (A:2-107) Immunoglobulin (variable domains of L and
H chains) {Intact IgG1 antibody Mab61.1.3 (mouse), kappa L chain}
KCAHTVSKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPDRFTGSG
SATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK
>d1igyb1 b.1.1.1 (B:2-113) Immunoglobulin (variable domains of L and
H chains) {Intact IgG1 antibody Mab61.1.3 (mouse), kappa L chain}
VKLQESGAELARPGASVKMSCKASGYTFTTYTIHWIKQRPGQGLEWIGYINPSSVYTNYNQRFKD
KATLTRDRSSNTANIHLSSLTSDDSAVYYCVREGEVPYWGQGTTVTVSS
>d1hzhh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Intact IgG B12 antibody (human), kappa L chain}
QVQLVQSGAEVKKPGASVKVSCQASGYRFSNFVIHWVRQAPGQRFEWMGWINPYNGNKEFSAKFQ
DRVTFTADTSANTAYMELRSLRSADTAVYYCARVGPYSWDDSPQDNYYMDVWGKGTTVIVSS
>d1hzhl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Intact IgG B12 antibody (human), kappa L chain}
EIVLTQSPGTLSLSPGERATFSCRSSHSIRSRRVAWYQHKPGQAPRLVIHGVSNRASGISDRFSG
SGSGTDFTLTITRVEPEDFALYYCQVYGASSYTFGQGTKLERK
>d8faba1 b.1.1.1 (A:3-105) Immunoglobulin (variable domains of L and
H chains) {Fab HIL (human), lambda L chain}
ELTQPPSVSVSPGQTARITCSANALPNQYAYWYQQKPGRAPVMVIYKDTQRPSGIPQRFSSSTSG
TTVTLTISGVQAEDEADYYCQAWDNSASIFGGGTKLTV
>d8fabb1 b.1.1.1 (B:1-121) Immunoglobulin (variable domains of L and
H chains) {Fab HIL (human), lambda L chain}
AVKLVQAGGGVVQPGRSLRLSCIASGFTFSNYGMHWVRQAPGKGLEWVAVIWYNGSRTYYGDSVK
GRFTISRDNSKRTLYMQMNSLRTEDTAVYYCARDPDILTAFSFDYWGQGVLVTVSS
>d7fabh1 b.1.1.1 (H:1-116) Immunoglobulin (variable domains of L and
H chains) {Fab NEW (human), lambda L chain}
AVQLEQSGPGLVRPSQTLSLTCTVSGTSFDDYYWTWVRQPPGRGLEWIGYVFYTGTTLLDPSLRG
RVTMLVNTSKNQFSLRLSSVTAADTAVYYCARNLIAGGIDVWGQGSLVTVS
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>d7fabl1 b.1.1.1 (L:1-103) Immunoglobulin (variable domains of L and
H chains) {Fab NEW (human), lambda L chain}
ASVLTQPPSVSGAPGQRVTISCTGSSSNIGAGHNVKWYQQLPGTAPKLLIFHNNARFSVSKSGTS
ATLAITGLQAEDEADYYCQSYDRSLRVFGGGTKLTVLR
>d1bafh1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and
H chains) {Fab ANO2 (mouse), kappa L chain}
DVQLQESGPGLVKPSQSQSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYMSYSGSTRYNPSLR
SRISITRDTSKNQFFLQLKSVTTEDTATYFCARGWPLAYWGQGTQVSVSE
>d1bafl1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and
H chains) {Fab ANO2 (mouse), kappa L chain}
QIVLTQSPAIMSASPGEKVTMTCSASSSVYYMYWYQQKPGSSPRLLIYDTSNLASGVPVRFSGSG
SGTSYSLTISRMEAEDAATYYCQQWSSYPPITFGVGTKLELKR
>d1a3rh1 b.1.1.1 (H:2-119) Immunoglobulin (variable domains of L and
H chains) {Fab 8F5 (mouse), kappa L chain}
VQLQQSGAELVRPGASVKLSCTTSGFNIKDIYIHWVKQRPEQGLEWIGRLDPANGYTKYDPKFQG
KATITVDTSSNTAYLHLSSLTSEDTAVYYCDGYYSYYDMDYWGPGTSVTVSSAKTTAP
>d1a3rl1 b.1.1.1 (L:1-114) Immunoglobulin (variable domains of L and
H chains) {Fab 8F5 (mouse), kappa L chain}
DIVMTQSPSSLTVTTGEKVTMTCKSSQSLLNSRTQKNYLTWYQQKPGQSPKLLIYWASTRESGVP
DRFTGSGSGTDFTLSISGVQAEDLAVYYCQNNYNYPLTFGAGTKLELKRADAAPT
>d1bbjh1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and
H chains) {Fab B72.3 (mouse/human chimera), kappa L chain}
EVQLQQSDAELVKPGASVKISCKASGYTFTDHAIHWAKQKPEQGLEWIGYISPGNDDIKYNEKFK
GKATLTADKSSSTAYMQLNSLTSEDSAVYFCKRSYYGHWGQGTTLTVSSA
>d1bbjl1 b.1.1.1 (L:1-109) Immunoglobulin (variable domains of L and
H chains) {Fab B72.3 (mouse/human chimera), kappa L chain}
DIQMTQSPASLSVSVGETVTITCRASENIYSNLAWYQQKQGKSPQLLVYAATNLADGVPSRFSGS
GSGTQYSLKINSLQSEDFGSYYCQHFWGTPYTFGGGTRLEIKRA
>d1hila1 b.1.1.1 (A:1-108) Immunoglobulin (variable domains of L and
H chains) {Fab 17/9 (mouse), kappa L chain}
DIVMTQSPSSLTVTAGEKVTMSCTSSQSLFNSGKQKNYLTWYQQKPGQPPKVLIYWASTRESGVP
DRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSNPLTFGGGTKLELKR
>d1hilb1 b.1.1.1 (B:1-112) Immunoglobulin (variable domains of L and
H chains) {Fab 17/9 (mouse), kappa L chain}
EVQLVESGGDLVKPGGSLKLSCAASGFSFSSYGMSWVRQTPDKRLEWVATISNGGGYTYYPDSVK
GRFTISRDNAKNTLYLQMSSLKSEDSAMYYCARRERYDENGFAYWGQGTLVTVS
>d1dbbh1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and
H chains) {Fab DB3 (mouse), kappa L chain}
QIQLVQSGPELKKPGETVKISCKASGYAFTNYGVNWVKEAPGKELKWMGWINIYTGEPTYVDDFK
GRFAFSLETSASTAYLEINNLKNEDTATYFCTRGDYVNWYFDVWGAGTTVTVS
>d1dbbl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab DB3 (mouse), kappa L chain}
DVVMTQIPLSLPVNLGDQASISCRSSQSLIHSNGNTYLHWYLQKPGQSPKLLMYKVSNRFYGVPD
RFSGSGSGTDFTLKISRVEAEDLGIYFCSQSSHVPPTFGGGTKLEIK
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>d1dfbh1 b.1.1.1 (H:1-126) Immunoglobulin (variable domains of L and
H chains) {Fab 3D6 (human), kappa L chain}
EVQLVESGGGLVQPGRSLRLSCAASGFTFNDYAMHWVRQAPGKGLEWVSGISWDSSSIGYADSVK
GRFTISRDNAKNSLYLQMNSLRAEDMALYYCVKGRDYYDSGGYFTVAFDIWGQGTMVTVSS
>d1dfbl1 b.1.1.1 (L:1-106) Immunoglobulin (variable domains of L and
H chains) {Fab 3D6 (human), kappa L chain}
DIQMTQSPSTLSASVGDRVTITCRASQSISRWLAWYQQKPGKVPKLLIYKASSLESGVPSRFSGS
GSGTEFTLTISSLQPDDFATYYCQQYNSYSFGPGTKVDIKR
>d1igfh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Fab B13I2 (mouse), kappa L chain}
EVQLVESGGDLVKPGGSLKLSCAASGFTFSRCAMSWVRQTPEKRLEWVAGISSGGSYTFYPDTVK
GRFIISRNNARNTLSLQMSSLRSEDTAIYYCTRYSSDPFYFDYWGQGTTLTVSS
>d1igfl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab B13I2 (mouse), kappa L chain}
DVLMTQTPLSLPVSLGDQASISCRSNQTILLSDGDTYLEWYLQKPGQSPKLLIYKVSNRFSGVPD
RFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPPTFGGGTKLEIK
>d1igja1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab 26-10 (mouse), kappa L chain}
DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLNWYLQKAGQSPKLLIYKVSNRFSGVPD
RFSGSGSGTDFTLKISRVEAEDLGIYFCSQTTHVPPTFGGGTKLEIK
>d1igjb1 b.1.1.1 (B:2-114) Immunoglobulin (variable domains of L and
H chains) {Fab 26-10 (mouse), kappa L chain}
VQLQQSGPELVKPGASVRMSCKSSGYIFTDFYMNWVRQSHGKSLDYIGYISPYSGVTGYNQKFKG
KATLTVDKSSSTAYMELRSLTSEDSAVYYCAGSSGNKWAMDYWGHGASVTVSSA
>d1igmh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H
chains) {Fv POT (human) IgM, kappa L chain}
EVHLLESGGNLVQPGGSLRLSCAASGFTFNIFVMSWVRQAPGKGLEWVSGVFGSGGNTDYADAVK
GRFTITRDNSKNTLYLQMNSLRAEDTAIYYCAKHRVSYVLTGFDSWGQGTLVTVSSGSASAPTL
>d1igml_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H
chains) {Fv POT (human) IgM, kappa L chain}
DIQMTQSPSSLSASVGDRVTITCQASQDISNYLAWYQQKPGKAPELRIYDASNLETGVPSRFSGS
GSGTDFTFTISSLQPEDIATYYCQQYQNLPLTFGPGTKVDIKRTVAAPSV
>d1dqlh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H
chains) {Fv MEZ (human) IgM, kappa L chain}
EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISSDGGNKYYTDSVK
GRFTISRNDSKNTLYLQMNSLRTEDTAVFYCARGNPPYSSGWGGGDYWGQGTMVTVSS
>d1dqll_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H
chains) {Fv MEZ (human) IgM, kappa L chain}
DIQMTQSPSSLSASVGDRVTITCRASQDIRNDLGWYQQKPGKAPKKLIYAASSLQSGVPSRFSGS
GSGTDFTLTISSLQPEDFATYYCLQQNSNWTFGQGTKVDIK
>d1dn0a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab Kau cold agglutinin (human) IgM, kappa L chain}
EIVLTQSPATLSLSPGERATLSCGASQSVSSNYLAWYQQKPGQAPRLLIYDASSRATGIPDRFSG
SGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGGGTKVEI
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>d1dn0b1 b.1.1.1 (B:1-120) Immunoglobulin (variable domains of L and
H chains) {Fab Kau cold agglutinin (human) IgM, kappa L chain}
EVQLQQWGAGLLKPSETLSLTCAVYGGSFSDYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKS
RVTISVDTSKNQFSLKLSSVTAADTAVYYCARPPHDTSGHYWNYWGQGTLVTVSS
>d1indh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and
H chains) {Fab Cha255 (mouse), lambda L chain}
EVTLVESGGDSVKPGGSLKLSCAASGFTLSGETMSWVRQTPEKRLEWVATTLSGGGFTFYSASVK
GRFTISRDNAQNNLYLQLNSLRSEDTALYFCASHRFVHWGHGTLVTVSA
>d1faih1 b.1.1.1 (H:1-123) Immunoglobulin (variable domains of L and
H chains) {Fab R19.9 (mouse), kappa L chain}
QVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGVNWVKQRPGQGLEWIGYINPGKGYLSYNEKFK
GKTTLTVDRSSSTAYMQLRSLTSEDAAVYFCARSFYGGSDLAVYYFDSWGQGTTLTVS
>d1fail1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and
H chains) {Fab R19.9 (mouse), kappa L chain}
DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPSRFSGS
GSGTDYSLTISNLEHEDIATYFCQQGSTLPRTFGGGTKLEIKR
>d2fb4h1 b.1.1.1 (H:1-119) Immunoglobulin (variable domains of L and
H chains) {Fab KOL (human), lambda L chain}
EVQLVQSGGGVVQPGRSLRLSCSSSGFIFSSYAMYWVRQAPGKGLEWVAIIWDDGSDQHYADSVK
GRFTISRNDSKNTLFLQMDSLRPEDTGVYFCARDGGHGFCSSASCFGPDYWGQGTPVTVSSA
>d2fb4l1 b.1.1.1 (L:1-109) Immunoglobulin (variable domains of L and
H chains) {Fab KOL (human), lambda L chain}
QSVLTQPPSASGTPGQRVTISCSGTSSNIGSSTVNWYQQLPGMAPKLLIYRDAMRPSGVPDRFSG
SKSGASASLAIGGLQSEDETDYYCAAWDVSLNAYVFGTGTKVTVLG
>d2fbjh1 b.1.1.1 (H:1-118) Immunoglobulin (variable domains of L and
H chains) {Fab J539 (mouse), kappa L chain}
EVKLLESGGGLVQPGGSLKLSCAASGFDFSKYWMSWVRQAPGKGLEWIGEIHPDSGTINYTPSLK
DKFIISRDNAKNSLYLQMSKVRSEDTALYYCARLHYYGYNAYWGQGTLVTVSA
>d2fbjl1 b.1.1.1 (L:1-109) Immunoglobulin (variable domains of L and
H chains) {Fab J539 (mouse), kappa L chain}
EIVLTQSPAITAASLGQKVTITCSASSSVSSLHWYQQKSGTSPKPWIYEISKLASGVPARFSGSG
SGTSYSLTINTMEAEDAAIYYCQQWTYPLITFGAGTKLELKRAD
>d1fgvh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H
chains) {Fab H52 (synthetic, humanised version), kappa L chain}
EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYTMHWMRQAPGKGLEWVAGINPKNGGTSYADSVK
GRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGTLVTVSS
>d1fgvl_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H
chains) {Fab H52 (synthetic, humanised version), kappa L chain}
DIQMTQSPSSLSASVGDRVTITCRASQDINNYLNWYQQKPGKAPKLLIYYTSTLESGVPSRFSGS
GSGTDYTLTISSLQPEDFATYYCQQGNTLPPTFGAGTKVEIK
>d2fgwh1 b.1.1.1 (H:1-124) Immunoglobulin (variable domains of L and
H chains) {Fab H52 (synthetic, humanised version), kappa L chain}
EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYTMHWMRQAPGKGLEWVAGINPKNGGTSHNQRFM
DRFTISVDKSTSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGTLVTVSS
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>d1mcph1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and
H chains) {Fab MCPC603 (human), kappa L chain}
EVKLVESGGGLVQPGGSLRLSCATSGFTFSDFYMEWVRQPPGKRLEWIAASRNKGNKYTTEYSAS
VKGRFIVSRDTSQSILYLQMNALRAEDTAIYYCARNYYGSTWYFDVWGAGTTVTVS
>d2imn__ b.1.1.1 (-) Immunoglobulin (variable domains of L and H chains)
{Fab MCPC603 (human), kappa L chain}
DIVMTQSPSSLSVSAGERVTMSCKSSQSLLYKDGKNFLAWYQQKPGQPPKLLIYGASTRESGVPD
RFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHSYPLTFGAGTKLELKR
>d1fvca_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H
chains) {Fab 4D5 (synthetic, humanised version), kappa L chain}
DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGS
RSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRT
>d1fvcb_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H
chains) {Fab 4D5 (synthetic, humanised version), kappa L chain}
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVK
GRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSS
>d1ggbh1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and
H chains) {Fab 50.1 (mouse), kappa L chain}
QVQLQESGPGILQPSQTLSLTCSFSGFSLSTYGMGVSWIRQPSGKGLEWLAHIFWDGDKRYNPSL
KSRLKISKDTSNNQVFLKITSVDTADTATYYCVQEGYIYWGQGTSVTVS
>d1ggbl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab 50.1 (mouse), kappa L chain}
DIVLTQSPGSLAVSLGQRATISCRASESVDDDGNSFLHWYQQKPGQPPKLLIYRSSNLISGIPDR
FSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGAGTKLEIK
>d1ai1h1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and
H chains) {Fab 59.1 (mouse), kappa L chain}
QVKLQESGPAVIKPSQSLSLTCIVSGFSITRTNYCWHWIRQAPGKGLEWMGRICYEGSIYYSPSI
KSRSTISRDTSLNKFFIQLISVTNEDTAMYYCSRENHMYETYFDVWGQGTTVTVS
>d1ai1l1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and
H chains) {Fab 59.1 (mouse), kappa L chain}
DIVMTQSPASLVVSLGQRATISCRASESVDSYGKSFMHWYQQKPGQPPKVLIYIASNLESGVPAR
FSGSGSRTDFTLTIDPVEADDAATYYCQQNNEDPPTFGAGTKLEMRR
>d1mamh1 b.1.1.1 (H:1-119) Immunoglobulin (variable domains of L and
H chains) {Fab Yst9.1 (mouse), kappa L chain}
EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMSWVRQPPGKALEWLGFIRNKADGYTTEYSAS
VKGRFTISRDNSQSILYLQMNTLRAEDSATYYCTRDPYGPAAYWGQGTLVTVSA
>d1maml1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and
H chains) {Fab Yst9.1 (mouse), kappa L chain}
DIQMTQTTSSLSASLGDRVTISCRASQDIYNYLNWYQQKPDGTVKLLIYYTSRLHSGVPSRFSGS
GSGTDYSLTISNLNQEDMATYICQQGNTLPFTFGSGTKLEIKR
>d1mfa_1 b.1.1.1 (1L-111L) Immunoglobulin (variable domains of L and
H chains) {Fab SE155-4 (mouse), lambda L chain}
QIVVTQESALTTSPGETVTLTCRSSTGTVTSGNHANWVQEKPDHLFTGLIGDTNNRAPGVPARFS
GSLIGDKAALTITGAQPEDEAIYFCALWSNNHWIFGGGTKLTVLGQ
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>d1mfa_2 b.1.1.1 (251H-367H) Immunoglobulin (variable domains of L
and H chains) {Fab SE155-4 (mouse), lambda L chain}
EVQVQQSGTVVARPGASVKMSCKASGYTFTNYWMHWIKQRPGQGLEWIGAIYPGNSATFYNHKFR
AKTKLTAVTSTTTAYMELSSLTSEDSAVYYCTRGGHGYYGDYWGQGASLTVS
>d1nbvh1 b.1.1.1 (H:1-122) Immunoglobulin (variable domains of L and
H chains) {Fab BV04-01 (mouse), kappa L chain}
EVQPVETGGGLVQPKGSLKLSCAASGFSFNTNAMNWVRQAPGKGLEWVARIRSKSNNYATYYADS
VKDRFTISRDDSQNMLYLQMNNLKTEDTAMYYCVRDQTGTAWFAYWGQGTLVTVSAA
>d1teth1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and
H chains) {Fab TE33 (mouse), kappa L chain}
QIQLVQSGPELKTPGETVRISCKASGYTFTTYGMSWVKQTPGKGFKWMGWINTYSGVPTYADDFK
GRFAFSLETSASTAYLQINNLKNEDTATYFCARRSWYFDVWGTGTTVTVS
>d1tetl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab TE33 (mouse), kappa L chain}
DVLMTQTPLSLPVSLGDQASISCKSSQSIVHSSGNTYFEWYLQKPGQSPKLLIYKVSNRFSGVPD
RFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHIPFTFGSGTKLEIK
>d1flrh1 b.1.1.1 (H:1-118) Immunoglobulin (variable domains of L and
H chains) {Fab 4-4-20 (mouse), kappa L chain}
EVKLDETGGGLVQPGRPMKLSCVASGFTFSDYWMNWVRQSPEKGLEWVAQIRNKPYNYETYYSDS
VKGRFTISRDDSKSSVYLQMNNLRVEDMGIYYCTGSYYGMDYWGQGTSVTVSS
>d4fabl1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and
H chains) {Fab 4-4-20 (mouse), kappa L chain}
DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSQGNTYLRWYLQKPGQSPKVLIYKVSNRFSGVPD
RFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPWTFGGGTKLEIK
>d1jfqh1 b.1.1.1 (H:302-421) Immunoglobulin (variable domains of L
and H chains) {Fab 36-71 (mouse), kappa L chain}
VQLQQSGVELVRAGSSVKMSCKASGYTFTSNGINWVKQRPGQGLEWIGYNNPGNGYITYNEKFKG
KTTLTVDKSSNTAYMQLRSLTSEDSAVYFCARSEYYGGSYKFDYWGQGTTLTVSS
>d1jfql1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and
H chains) {Fab 36-71 (mouse), kappa L chain}
DIQMTQIPSSLSASLGDRVSISCRASQDINNFLNWYQQKPDGTIKLLIYFTSRSQSGVPSRFSGS
GSGTDYSLTISNLEQEDIATYFCQQGNALPRTFGGGTKLEIKR
>d1gigh1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and
H chains) {Fab HC19 (mouse), lambda L chain}
QVQLKESGPGLVAPSQSLSITCTVSGFLLISNGVHWVRQPPGKGLEWLGVIWAGGNTNYNSALMS
RVSISKDNSKSQVFLKMKSLQTDDTAMYYCARDFYDYDVFYYAMDYWGQGTSVTV
>d2cgrh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and
H chains) {Fab, anti-sweetener (mouse), kappa L chain}
RVQLLESGAELMKPGASVQISCKATGYTFSEYWIEWVKERPGHGLEWIGEILPGSGRTNYREKFK
GKATFTADTSSNTAYMQLSSLTSEDSAVYYCTRGYSSMDYWGQGTSVTVSAA
>d2cgrl1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and
H chains) {Fab, anti-sweetener (mouse), kappa L chain}
ELVMTQSPLSLPVSLGDQASISCRPSQSLVHSNGNTYLHWYLQKPGQSPKLLIYRVSNRFSGVPD
RFSGSGSGTAFTLKISRVEAEDLGVYFCSQGTHVPYTFGGGTKLELK
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>d1figh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Fab 1F7 (mouse), kappa L chain}
DVQLQQSGPELEKPGASVKISCKASGFSLPGHNINWIVQRNGKSLEWIGNIDPYYGGTNFNPKFK
GKATLTVDKSSSTLYMHLTSLQSEDSAVYYCARRRDGNYGFTYWGQGTLVTVSA
>d1figl1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and
H chains) {Fab 1F7 (mouse), kappa L chain}
ENVLTQSPAIMSASPGEKVTMACRASSSVSSTYLHWYQQKSGASPKLLIYSTSNLASGVPARFSG
SGSGTSYSLTISSVEAEDAATYYCQQYSGYPLTFGAGTKLELKR
>d1frgh1 b.1.1.1 (H:218-336) Immunoglobulin (variable domains of L
and H chains) {Fab 26/9 (mouse), kappa L chain}
EVLLVESGGDLVKPGGFLKLSCAASGFTFSSFGMSWVRHTPDKRLEWVATISNGGGYTYYQDSVK
GRFTISRDNAKNTLFLEMTSLKSEDAGLYYCARRERYDEKGFAYWGRGTLVTVS
>d1frgl1 b.1.1.1 (L:1-113) Immunoglobulin (variable domains of L and
H chains) {Fab 26/9 (mouse), kappa L chain}
DIVMTQSPSSLTVTAGEKVTMSCKSSQSLFNSGKRKNFLTWYHQKPGQPPKLLIYWASTRESGVP
DRFSGSGSGTDFTLTITSVQAEDLAIYYCQNDYSHPLTFGAGTKLELK
>d1a2ya_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H
chains) {Fab D1.3 (mouse), kappa L chain}
DIVLTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYYTTTLADGVPSRFSGS
GSGTQYSLKINSLQPEDFGSYYCQHFWSTPRTFGGGTKLEIK
>d1a2yb_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H
chains) {Fab D1.3 (mouse), kappa L chain}
QVQLQESGPGLVAPSQSLSITCTVSGFSLTGYGVNWVRQPPGKGLEWLGMIWGDGNTDYNSALKS
RLSISKDNSKSQVFLKMNSLHTDDTARYYCARERDYRLDYWGQGTTLTVSS
>d1a7ql_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H
chains) {Fab D1.3 (mouse), kappa L chain}
DIVLTQSPASLSASVGETVTITCRAGGNTHNYLAWYQQKQGKSPQLLVYYTTTLAAGVPSRFSGS
GSGTQYSLKINSLQPDDFGSYYCQHFWSTPRSFGGGTKLEI
>d1cica1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and
H chains) {Anti-idiotope (D1.3) Fab E225, (mouse), kappa L chain}
DIVMTQSHKFMSTSVGDRVSITCKASQDVRIAVAWYQQKPGQSPKLLIYWASTRHTGVPDRFTGS
GSGTDFTLTISNVQSEDLADYFCQHCGSYPFTFGSGTKLEIK
>d1cicb1 b.1.1.1 (B:1-117) Immunoglobulin (variable domains of L and
H chains) {Anti-idiotope (D1.3) Fab E225, (mouse), kappa L chain}
QVQLQQPGSELVRPGASVKLSCKASGYTFTNYWMHWVKQRPGQGLEWIGNIYPGSGDSNYDEKFK
SKATLTVDTSSSTAYMQLSGLTSEDSAVYYCARGLAFYFDHWGQGTTLTVSS
>d1jhlh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H
chains) {Fv D11.15 (mouse), kappa L chain}
QVQLQQSGAELVRPGASVKLSCKASGYTFISYWINWVKQRPGQGLEWIGNIYPSDSYTNYNQKFK
DKATLTVDKSSSTAYMQLSSPTSEDSAVYYCTRDDNYGAMDYWGQGTTVTV
>d1jhll_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H
chains) {Fv D11.15 (mouse), kappa L chain}
DIELTQSPSYLVASPGETITINCRASKSISKSLAWYQEKPGKTNNLLIYSGSTLQSGIPSRFSGS
GSGTDFTLTISSLEPEDFAMYICQQHNEYPWTFGGGTKLEIKR
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>d1bqlh1 b.1.1.1 (H:2-116) Immunoglobulin (variable domains of L and
H chains) {Fab HyHEL-5 (mouse), kappa L chain}
VQLQQSGAELMKPGASVKISCKASGYTFSDYWIEWVKQRPGHGLEWIGEILPGSGSTNYHERFKG
KATFTADTSSSTAYMQLNSLTSEDSGVYYCLHGNYDFDGWGQGTTLTVSS
>d1bqll1 b.1.1.1 (L:1-106) Immunoglobulin (variable domains of L and
H chains) {Fab HyHEL-5 (mouse), kappa L chain}
DIVLTQSPAIMSASPGEKVTMTCSASSSVNYMYWYQQKSGTSPKRWIYDTSKLASGVPVRFSGSG
SGTSYSLTISSMETEDAATYYCQQWGRNPTFGGGTKLEIKR
>d1ic7h_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H
chains) {Fab HyHEL-10 (mouse), kappa L chain}
DVQLQESGPSLVKPSQTLSLTCSVTGDSITSAYWSWIRKFPGNRLEYMGYVSYSGSTYYNPSLKS
RISITRDTSKNQYYLDLNSVTTEDTATYYCANWAGDYWGQGTLVTVSAA
>d2jelh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Fab JE142 (mouse), kappa L chain}
QVQLAQSGPELVRPGVSVKISCKGSGYTFTTYAMHWVKQSHAKSLEWIGLISTYSGYTNYNQKFK
GKATMTVDKSSSTAYMELARLTSEDSAIYYCARVMGEQYFDVWGAGTTVIVSS
>d1ncbh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Fab NC41 (mouse), kappa L chain}
QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLEWMGWINTNTGEPTYGEEFK
GRFAFSLETSASTANLQINNLKNEDKATFFCARGEDNFGSLSDYWGQGTTLTVSS
>d1ncbl1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and
H chains) {Fab NC41 (mouse), kappa L chain}
DIVMTQSPKFMSTSVGDRVTITCKASQDVSTAVVWYQQKPGQSPKLLIYWASTRHIGVPDRFAGS
GSGTDYTLTISSVQAEDLALYYCQQHYSPPWTFGGGTKLEIKR
>d1forh1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and
H chains) {Fab 17-Ia (mouse), kappa L chain}
QGQLQQSGAELVRPGSSVKISCKASGYAFSSFWVNWVKQRPGQGLEWIGQIYPGDGDNKYNGKFK
GKATLTADKSSTTAYMQLYSLTSEDSAVYFCARSGNYPYAMDYWGQGTSVTVSSA
>d1forl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab 17-Ia (mouse), kappa L chain}
QIVLTQSPAIMSAFPGEKVTITCSATSSVNYMHWFQQKPGTSPKLWIYSSSNLASGVPARFSGSG
SGTSYSLTISRMEAEDAATYYCQQRSSYPITFGSGTKLEIKR
>d1knoa1 b.1.1.1 (A:1-108) Immunoglobulin (variable domains of L and
H chains) {Fab CNJ206 (mouse), kappa L chain}
QIQMTQSPSSLSASLGERVSLTCRASQEISGYLSWLQQKPDGTIKRLIYAASTLDSGVPKRFSGS
RSGSDYSLTISSLESEDFADYYCLQYASSPYTFGGGTKLEILR
>d1knob1 b.1.1.1 (B:1-119) Immunoglobulin (variable domains of L and
H chains) {Fab CNJ206 (mouse), kappa L chain}
DVKLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYYADTVK
GRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARGDYYGSRGAYWGQGTLVTVSA
>d1eapb1 b.1.1.1 (B:1-124) Immunoglobulin (variable domains of L and
H chains) {Fab 17E8 (mouse), kappa L chain}
EVQLQESGTELVKPGASVKISCKASGYISTDHAIHWVKQRPEQGLEWIGYISPGNGDIKYNEKFK
VKATLTADQSSSTAYMQLNSLTSEDSAVYFCKRSYYGSSYVDYWGQGTTLTVSS
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>d1mrdh1 b.1.1.1 (H:2-115) Immunoglobulin (variable domains of L and
H chains) {Fab Jel 103 (mouse), kappa L chain}
VQLQQSGAELVKPGASVKLSCKASGYTFTSYWMQWVKQRPGQGLEWIGEIDPSDSYTNYNQKFKG
KATLTVDTSSSTAYMQLSSLTSEDSAVYYCANLRGYFDYWGQGTTLTVSSAK
>d1fbih1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and
H chains) {Fab F9.13.7 (mouse), kappa L chain}
QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQGPGQGLEWIGEIDPSDSYPNYNEKFK
GKATLTVDKSSSTAYMQLSSLTSEDSAVYYCASLYYYGTSYGVLDYWGQGTSVTVS
>d1fbil1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab F9.13.7 (mouse), kappa L chain}
DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQKKPDGTVKLLIYYTSRLHSGVPSRFSGS
GSGTDYSLTIRNLEQEDIATYFCQQGYTLPYTFGGGTKLEIK
>d1rmfh1 b.1.1.1 (H:1-119) Immunoglobulin (variable domains of L and
H chains) {Fab R6.5 (mouse), kappa L chain}
QVQLQQSGPELVRPGVSVKISCKGSGYTFIDYAIHWVKESHAKSLEWIGVISAYSGDTNYNQKFK
GKATMTVDKSSNTAYLELARLTSEDSAIYYCARGGWLLLSFDYWGQGTTLTVSS
>d1rmfl1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and
H chains) {Fab R6.5 (mouse), kappa L chain}
DVVMTQSPLSLPVSLGDQASISCRSSQSLVHSNGNNYLHWYLQKSGQAPKLLIYKVSNRFSGVPD
RFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPLTFGGGTKLEIK
>d1fpth1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Fab C3, neutralizing type 1 poliovirus, (mouse), kappa L
chain}
QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIQWIKQRPGQGLEWIGVINPGSGGTDYNANFK
GKATLTADKSSSIVYMQLSSLTSDDSAVYFCARDFYDYDVGFDYWGQGTTLTVSS
>d1fptl1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and
H chains) {Fab C3, neutralizing type 1 poliovirus, (mouse), kappa L
chain}
DVVMTQTPLSLPVSLGDQASISCSSSQSLVHSNGKTYLHWYLQKPGQSPKLLIYKVSNRFSGVPD
RFSGSGSGTYFTLKISRVEAEDLGVYFCSQSTHVPYTFGGGTKLEIKR
>d1ikfh1 b.1.1.1 (H:1-126) Immunoglobulin (variable domains of L and
H chains) {Fab, anti-cyclosporin A, (mouse), kappa L chain}
EVKLVESGGGLVQPGGSLKLSCATSGFTFSDYYMYWVRQNSEKRLEWVAFISNGGGSAFYADIVK
GRFTISRDNAKNTLYLQMSRLKSEDTAMYYCTRHTLYDTLYGNYPVWFADWGQGTLVTVSA
>d1ikfl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab, anti-cyclosporin A, (mouse), kappa L chain}
DIQMTQTTSSLSASLGDRVTISCRASQDISTYLNWYQQKPDGTVKLLIFYTSRLRSGVPSRFSGS
GSGTDYSLTISNLEQEDIATYFCQQGSRIPPTFGGGTKLEIL
>d1lmka1 b.1.1.1 (A:2-127) Immunoglobulin (variable domains of L and
H chains) {scFv dimer (L5MK16 diabody), based on: (mouse), kappa L
chain}
VQLQQSGTELMKPGRSLKISCKTTGYIFSNYWIEWVKQRPGHGLEWIGKILPGGGSNTYNDKFKG
KATFTADTSSNIAYMQLSSLTSEDSAVYYCARGEDYYAYWYVLDYWGQGTTVTVSSGGGGS
>d1lmka2 b.1.1.1 (A:201-312) Immunoglobulin (variable domains of L
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and H chains) {scFv dimer (L5MK16 diabody), based on: (mouse), kappa
L chain}
DIELTQSPLSLPVSLGDQASISCRSSQSLVHSNGNTSLHWYLKKPGQSPKLLIYKVSTRFSGVPD
RFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPFTFGSGTKLELK
>d1nqba2 b.1.1.1 (A:121-233) Immunoglobulin (variable domains of L
and H chains) {scFv trivalent antibody, based on: (mouse), kappa L
chain}
DIELTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFSGVPD
RFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGGGTKLEIKR
>d1igch1 b.1.1.1 (H:1-119) Immunoglobulin (variable domains of L and
H chains) {Fab MoPC21 (mouse), kappa L chain}
DVQLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTLHYADTVK
GRFTISRDNPKNTLFLQMTSLRSEDTGMYYCARWGNYPYYAMDYWGQGTSVTVS
>d1igcl1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and
H chains) {Fab MoPC21 (mouse), kappa L chain}
NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPDRFTGS
GSATDFTLTISSVQAEDLADYHCGQGNSYPYTFGGGTKLEIKR
>d1ibgh1 b.1.1.1 (H:2-113) Immunoglobulin (variable domains of L and
H chains) {Fab 40-50 (mouse), kappa L chain}
VHLVQSGPGLVAPSQSLSITCTVSGFSLTTYGVHWFRQPPGKGLEWLGLIWAGGNTDYNSALMSR
LSINKDNSKSQVFLKMNSLQADDTAMYYCARFRFASYYDYAVDYWGQGTSVTVSS
>d1ibgl1 b.1.1.1 (L:2-107) Immunoglobulin (variable domains of L and
H chains) {Fab 40-50 (mouse), kappa L chain}
IVLTQSPASLAVSLGQRATISCRASKSVSTSGYSHIHWYQQKPGQPPKLLIYLASILESGVPARF
SGSGSGTDFTLNIHPVEEEDAATYYCQHSREYPLTFGAGTELELK
>d1mlbb1 b.1.1.1 (B:1-118) Immunoglobulin (variable domains of L and
H chains) {Fab D44.1 (mouse), kappa L chain}
QVQLQESGAEVMKPGASVKISCKATGYTFSTYWIEWVKQRPGHGLEWIGEILPGSGSTYYNEKFK
GKATFTADTSSNTAYMQLSSLTSEDSAVYYCARGDGNYGYWGQGTTLTVSSAS
>d1a14h_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H
chains) {Fab NC10 (mouse), kappa L chain}
QVQLQQSGAELVKPGASVRMSCKASGYTFTNYNMYWVKQSPGQGLEWIGIFYPGNGDTSYNQKFK
DKATLTADKSSNTAYMQLSSLTSEDSAVYYCARSGGSYRYDGGFDYWGQGTTVTV
>d1a14l_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H
chains) {Fab NC10 (mouse), kappa L chain}
DIELTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQNPDGTVKLLIYYTSNLHSEVPSRFSGS
GSGTDYSLTISNLEQEDIATYFCQQDFTLPFTFGGGTAA
>d1nmbl_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H
chains) {Fab NC10 (mouse), kappa L chain}
DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQNPDGTVKLLIYYTSNLHSEVPSRFSGS
GSGTDYSLTISNLEQEDIATYFCQQDFTLPFTFGGGTKLEIRRA
>d1bm3h1 b.1.1.1 (H:1-125) Immunoglobulin (variable domains of L and
H chains) {Anti-integrin Fab OPG2 (mouse), kappa L chain}
EVQLVQSGGGLVNPGRSLKLSCAASGFTFSSYGMSWVRQTPEKRLEWVAAISGGGTYIHYPDSVK

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GRFTISRDNAKNNLYLQMSSLRSEDTALYYCTRHPFYRYDGGNYYAMDHWGQGTSVTVSA
>d1nsnh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and
H chains) {Fab N10 (mouse), kappa L chain}
DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYITYSGTTSYNPSLK
SRISISRDTSKNQFFMQLNSVTTEDTGTFYCTRGNGDWGQGTTLTVSSA
>d1nsnl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab N10 (mouse), kappa L chain}
DIVLTQSPSSLAVSLGQRATISCRASQSVSTSSFRYMHWYQQKPGQPPRLLIKYASNLESGVPAR
FSGSGSGTDFTLNIHPVEEEDTATYYCQHSWEIPYTFGGGTKLEIK
>d1iaih1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and
H chains) {Fab 730.1.4 (mouse), kappa L chain}
QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMAWINTYTGEPTYADDFK
GRFAFSLETSASTAYLQINNLKNEDTATYFCARDGYYENYYAMDYWGQGTSVTVSS
>d1iail1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and
H chains) {Fab 730.1.4 (mouse), kappa L chain}
DIVMTQSHKFMSTSVGDRVSITCKASQDVSTAVAWYQQKPGQSPKLLIYSASYQYTGVPDRFTGS
GSRTDFTFTINSVQAEDLAVYYCHQHYSTPFTFGSGTKLEIKR
>d1iaii1 b.1.1.1 (I:1-121) Immunoglobulin (variable domains of L and
H chains) {Fab 409.5.3 (mouse), kappa L chain}
EVKLQESGGGLVQPGGSMKLSCVASGFTFNNYWMSWVRQSPEKGLEWVAEIRLNSDNFATHYAES
VKGKFIISRDDSKSRLYLQMNSLRAEDTGIYYCVLRPLFYYAVDYWGQGTSVTVSS
>d1iaim1 b.1.1.1 (M:1-109) Immunoglobulin (variable domains of L and
H chains) {Fab 409.5.3 (mouse), kappa L chain}
DIQLTQSPAFMAASPGEKVTITCSVSSSISSSNLHWYQQKSETSPKPWIYGTSNLASGVPVRFSG
SGSGTSYSLTISSMEAEDAATYYCQQWNSYPYTFGGGTKLEIKR
>d1plgh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and
H chains) {Polysialic acid-binding Fab (mouse), kappa L chain}
QIQLQQSGPELVRPGASVKISCKASGYTFTDYYIHWVKQRPGEGLEWIGWIYPGSGNTKYNEKFK
GKATLTVDTSSSTAYMQLSSLTSEDSAVYFCARGGKFAMDYWGQGTSVTVSS
>d1plgl1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and
H chains) {Polysialic acid-binding Fab (mouse), kappa L chain}
DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLYWYLQKPGQSPKPLIYRVSNRFSGVPD
RFSGSGSGTDFTLKISRVEAEDLGVYFCFQGTHVPYTFGGGTRLEIK
>d1aj7h1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and
H chains) {Fab 48G7 (mouse/human), kappa L chain}
QVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKYDPKFQ
GKATITADTSSNTAYLQLSSLTSEDTAVYYCASYYGIYWGQGTTLTVSSA
>d1gafh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and
H chains) {Fab 48G7 (mouse/human), kappa L chain}
QVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPKQGLEWIGRIDPANVDTKYDPKFQ
DKATITADTSSKTTYLQLSSLTSEDTAVYYCASYYGIYWGQGTTLTVSS
>d1gafl1 b.1.1.1 (L:1-109) Immunoglobulin (variable domains of L and
H chains) {Fab 48G7 (mouse/human), kappa L chain}
DIQMTQSPSSLSASLGERVSLTCRASQEINGYLGWLQQKPDGTIKRLIYAASTLHSGVPKRFSGS
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RSGSDYSLTISSLESEDFADYYCLQYASYPRTFGGGTKVEIKRT
>d1vgeh1 b.1.1.1 (H:1-122) Immunoglobulin (variable domains of L and
H chains) {Fab TR1.9 (mouse/human), kappa L chain}
QVKLLEQSGAEVKKPGASVKVSCKASGYSFTSYGLHWVRQAPGQRLEWMGWISAGTGNTKYSQKF
RGRVTFTRDTSATTAYMGLSSLRPEDTAVYYCARDPYGGGKSEFDYWGQGTLVTVSS
>d1vgel1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab TR1.9 (mouse/human), kappa L chain}
ELVMTQSPSSLSASVGDRVNIACRASQGISSALAWYQQKPGKAPRLLIYDASNLESGVPSRFSGS
GSGTDFTLTISSLQPEDFAIYYCQQFNSYPLTFGGGTKVEIK
>d1yuhb1 b.1.1.1 (B:1-118) Immunoglobulin (variable domains of L and
H chains) {Fab anti-nitrophenol (mouse), lambda L chain}
QVQFQQSGAELVKPGASVKLSCKASGYTFTSYLMHWIKQRPGRGLEWIGRIDPNNVVTKFNEKFK
SKATLTVDKPSSTAYMELSSLTSEDSAVYYCARYAYCRPMDYWGQGTTVTVSS
>d1ucbh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Fab CBR96 (mouse/human), kappa L chain}
EVNLVESGGGLVQPGGSLKVSCVTSGFTFSDYYMYWVRQTPEKRLEWVAYISQGGDITDYPDTVK
GRFTISRDNAKNSLYLQMSRLKSEDTAMYYCARGLDDGAWFAYWGQGTLVTVSV
>d1ucbl1 b.1.1.1 (L:4-108) Immunoglobulin (variable domains of L and
H chains) {Fab CBR96 (mouse/human), kappa L chain}
MTQIPVSLPVSLGDQASISCRSSQIIVHNNGNTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFS
GSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPFTFGSGTKLEIKR
>d1dvfc_ b.1.1.1 (C:) Immunoglobulin (variable domains of L and H
chains) {Fv E5.2 (mouse), kappa L chain}
DIQLTQSPSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPSRFSGS
GSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGGGTKLEIK
>d1dvfd_ b.1.1.1 (D:) Immunoglobulin (variable domains of L and H
chains) {Fv E5.2 (mouse), kappa L chain}
QVQLQQSGTELVKSGASVKLSCTASGFNIKDTHMNWVKQRPEQGLEWIGRIDPANGNIQYDPKFR
GKATITADTSSNTAYLQLSLTSEDTAVYYCATKVIYYQGRGAMDYWGQGTTLTVS
>d1ghfh1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and
H chains) {Fab GH1002 (mouse), kappa L chain}
VQLQQSGPELKKPGETVKISCKLWYTFTDYGMNWVKQAPGKGLKWMGWIQTNTEEPTYGAEFKGR
FAFSLETSAFTAYKQINNLKNEDMATYFCARVEAGFDYWAQGTTLTVSS
>d1ghfl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab GH1002 (mouse), kappa L chain}
DIQMTQTTSSLSASLGDRVTISCRESQDISNSLNWYQQKPDGTVKLLIYYTSRLHSGVPSRFSGS
GTGTDYSLTISNLEQEDFATYFCQQGNTLPYTFGGGTKLEIK
>d1nldh1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and
H chains) {Fab 1583, against an epitope of gp41 of HIV-1, (mouse),
kappa L chain}
QVKLQQSGPGLVQPSQSLSITCTVSGFSLTCYGVHWVRQSPGKGLEWLGVIWSGGDTDYNAAFIS
RLSITKDNSKSQVFFKMNSLQPNDRAIYYCARRGGDFWGQGTTVTVS
>d1nldl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab 1583, against an epitope of gp41 of HIV-1, (mouse),
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kappa L chain}
DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDSGVPD
RFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPRTFGGGTKLEIK
>d1kelh1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and
H chains) {Fab 28B4 (mouse), kappa L chain}
EVKLVESGGGLGQPGGSLRLSCATSGFTFTDYYFNWARQPPGKALEWLGFIRNKAKGYTTEYSAS
VKGRFTISRDNSQGILYLQMNTLRAEDSATYYCARWGSYAMDYWGQGTSV
>d1kell1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and
H chains) {Fab 28B4 (mouse), kappa L chain}
DVLMTQTPLSLPVSLGDQASISCRFSQSIVHSNGNTYLEWYLQKSGQSPKLLIYKVSNRFSGVPD
RFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPRTFGGGTKLEIK
>d1osph1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and
H chains) {Fab 184.1 (mouse), kappa L chain}
EVQLQESGPSLVKPSQTLSLTCSVTGEPITSGFWDWIRKFPGNKLEFMGYIRYGGGTYYNPSLKS
PISITRDTSKNHYYLQLNSVVTEDTATYYCARSRDYYGSSGFAFWGEGTLVTVSA
>d1ospl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab 184.1 (mouse), kappa L chain}
DIQMSQSSSSFSVSLGDRVTITCKASEDIYSRLAWYQQKPGNAPRLLISGATSLETWVPSRFSGS
DSGKDYTLSITSLQTEDVATYFCQQYWSPPPTFGGGTKLEIK
>d1fj1a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab LA-2 (mouse), kappa L chain}
DIQMTQSPSSLSATLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGNPSRFSGS
GSGRDYSFSISNLEAEDIAIYYCLQYDNLQRTFGGGTKVEIK
>d1fj1b1 b.1.1.1 (B:1-114) Immunoglobulin (variable domains of L and
H chains) {Fab LA-2 (mouse), kappa L chain}
QIQLVQSGPELKKPGETVKISCKASGYTFTDYSMYWVKQAPGKGLKRMGWINTETGEPTYADDFK
GRFALSLDTSASTAYLHISNLKNEDTATYFCARGLDSWGQGTSVTVSSA
>d1cloh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Fab A5B7 (mouse), kappa L chain}
EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSAS
VKGRFTISRDKSQSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS
>d1clol1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab A5B7 (mouse), kappa L chain}
QTVLSQSPAILSASPGEKVTMTCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSG
SGTSYSLTISRVEAEDAATYYCQHWSSKPPTFGGGTKLEIK
>d1ad0a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab A5B7 (engineered human construct), kappa L chain}
QTVLTQSPSSLSVSVGDRVTITCRASSSVTYIHWYQQKPGLAPKSLIYATSNLASGVPSRFSGSG
SGTDYTFTISSLQPEDIATYYCQHWSSKPPTFGQGTKVEVKR
>d1ad0b1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and
H chains) {Fab A5B7 (engineered human construct), kappa L chain}
EVQLLESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKGLEWLGFIGNKANGYTTEYSAS
VKGRFTISRDKSKSTLYLQMNTLQAEDSAIYYCTRDRGLRFYFDYWGQGTLVTVSS
>d1mimh1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and
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H chains) {Fab CHI621 (mouse), kappa L chain}
QLQQSGTVLARPGASVKMSCKASGYSFTRYWMHWIKQRPGQGLEWIGAIYPGNSDTSYNQKFEGK
AKLTAVTSASTAYMELSSLTHEDSAVYYCSRDYGYYFDFWGQGTTLTVSS
>d1miml1 b.1.1.1 (L:1-105) Immunoglobulin (variable domains of L and
H chains) {Fab CHI621 (mouse), kappa L chain}
QIVSTQSPAIMSASPGEKVTMTCSASSSRSYMQWYQQKPGTSPKRWIYDTSKLASGVPARFSGSG
SGTSYSLTISSMEAEDAATYYCHQRSSYTFGGGTKLEIKR
>d1afvh1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and
H chains) {Fab 25.3 (mouse), kappa L chain}
QVQLQQPGSVLVRPGASVKLSCKASGYTFTSSWIHWAKQRPGQGLEWIGEIHPNSGNTNYNEKFK
GKATLTVDTSSSTAYVDLSSLTSEDSAVYYCARWRYGSPYYFDYWGQGTTLTVSS
>d1afvl1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and
H chains) {Fab 25.3 (mouse), kappa L chain}
DIVLTQSPASLAVSLGQRATISCRASESVDNYGISFMNWFQQKPGQPPKLLIYAASNLGSGVPAR
FSGSGSGTDFSLNIHPMEEEDTAMYFCQQSKEVPLTFGAGTKVELKR
>d2mpah1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and
H chains) {Bactericidal Fab MN12H2, (mouse), kappa L chain}
EVNLQQSGTVLARPGASVRMSCKASGYSFTSYWLHWIKQRPGQGLEWIGGIYPGNRDTRYTQRFK
DKAKLTAVTSANTAYMELSSLTNEDSAVYYCSIIYFDYADFIMDYWGQGTTVTVSS
>d2mpal1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and
H chains) {Bactericidal Fab MN12H2, (mouse), kappa L chain}
DIVMTQTPLSLPVSLGDKASISCRSSQALVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPD
RFSGSGSGTDFTLKISRVEAEDLGVFFCSQSTHVPRTFGGGTKLEIK
>d1qkzh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Fab MN14C11.6 (mouse), kappa L chain}
DVKLVESGGGLVKPGRSLKLSCAASGFTFSDYYMFWVRQTPEQRLEWVATISDGGAYTYYPDSVK
GRFTISRDNAKNNLYLQMNSLKSEDTGMYYCARDPLEYYGMDYWGQGTSVAVSS
>d1qkzl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab MN14C11.6 (mouse), kappa L chain}
NIVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYTVSNRFSGVPD
RFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHFPTFGGGTKLEIK
>d1pskh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and
H chains) {Fab against a ganglioside (mouse), kappa L chain}
EVQLQQSGPELVKPGASVKISCKTSGYTFTKYTMHWVKQSHGKSLEWIGDINPNNGGTNYNQKFK
GTATLTVHKSSTTAYMELRSLTSEDSAVYYCTSKSFDYWGQGTTLTVSS
>d1pskl1 b.1.1.1 (L:1-106) Immunoglobulin (variable domains of L and
H chains) {Fab against a ganglioside (mouse), kappa L chain}
QIVLTQSPAIMSASPGEKVTITCSASSSVSNIHWFQQKPGTFPKLWIYSTSTLASGVPGRFSGSG
SGTSYSLTISRMGAEDAATYYCQQRSGYPFTFGSGTKLEIK
>d1yejh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Fab D2.3 (mouse), kappa L chain}
EMQLQQSGAELLRPGTSVKLSCKTSGYIFTSYWIHWVKQRSGQGLEWIARIYPGTGSTYYNEKFK
GKATLTADKSSSTAYMQLSTLKSEDSAVYFCTRWGFIPVREDYVMDYWGQGTLVTVSS
>d1yejl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
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H chains) {Fab D2.3 (mouse), kappa L chain}
DIVMTQSPLTLSVTIGQPASISCKSSQSLLYSNGKTYLNWLLQRPGQSPKRLIHLVSKLDSGVPD
RITGSGSGTDFTLKISRVEAADLGVYYCVQGTHFPYTFGGGTKLEIL
>d1yedb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and
H chains) {Fab D2.4 (mouse), kappa L chain}
AVKLQQSGPELVRPGTSVKLSCKTSGYIFTSYWIHWLKQSSGQGLEWIARIYPGTGGTYYNEKFK
GKATLTADKSSSTAYMQLSSLKSEDSAVYFCTRWGFTTVRENYYAMDYWGQGTLVTVSS
>d1yeeh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Fab D2.5 (mouse), kappa L chain}
EVKLQESGAELVRPGASVKLSCKTSGYIFTSYWIHWVKQRAAAGLEWIARIYPGTGSSYYNVKFK
GKATLTADKSSSTAYMQLSSLKSDDSAVYFCVRWGFIPVREDYVLDYWGQGTLVTVSS
>d1cfvh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H
chains) {Fv 4155 (mouse), kappa L chain}
QVQLQESGGGLVNLGGSMTLSCVASGFTFNTYYMSWVRQTPEKTLELVAAINSDGEPIYYPDTLK
GRVTISRDNAKKTLYLQMSSLNFEDTALYYCARLNYAVYGMDYWGQGTTVTVSS
>d1cfvl_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H
chains) {Fv 4155 (mouse), kappa L chain}
DIELTQSPPSLPVSLGDQVSISCRSSQSLVSNNRRNYLHWYLQKPGQSPKLVIYKVSNRFSGVPD
RFSGSGSGTDFTLKISRVAAEDLGLYFCSQSSHVPLTFGSGTKLEIKR
>d1hyxh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Fab 6D9 (mouse), kappa L chain}
EVKLLESGGGLVKPGGSLKLSCAASGFTFSNYAMSWVRQTPEKRLEWVVSISSGGSIYYLDSVKG
RFTVSRDNARNILYLQMTSLRSEDTAMYFCARVSHYDGSRDWYFDVWGAGTSVTVSS
>d1hyxl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab 6D9 (mouse), kappa L chain}
ELVMTQTPLSLPVSLGDQASISCRSSQTIVHSNGDTYLDWFLQKPGQSPKLLIYKVSNRFSGVPD
RFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPPTFGGGTKLEIK
>d2hrph1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Fab F11.2.32 (mouse), kappa L chain}
DVQLVESGGGLVQPGGSRKLSCAASGFTFMRFGMHWVRQAPEKGLEWVAYISSGSSTIYYADTVK
GRFTISRDNPKNTLFLQMTSLRSEDTALYYCARSGGIERYDGTYYVMDYWGQGTSVTVSS
>d2hrpl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab F11.2.32 (mouse), kappa L chain}
DTVLTQSPASLAVSLGQRATISCRASESVDYYGKSFMNWFQQKPGQPPKLLIYAASNQGSGVPAR
FSGSGSGTDFSLHIHPMEEDDSAMYFCQQSKEVPWTFGGGTKLEIK
>d2ap2a_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H
chains) {scFv C219, (mouse sequence-based), kappa L chain}
FVRDIVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYWASTRES
GVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEP
>d2ap2b_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H
chains) {scFv C219, (mouse sequence-based), kappa L chain}
EVQLQQSGAELVRPGASVKLSCTASGFNIKDDFMHWVKQRPEQGLEWIGRIDPANDNTKYAPKFQ
DKATIIADTSSNTAYLQLSSLTSEDTAVYYCARREVYSYYSPLDVWGAGTTVTVPSG
>d1nfde1 b.1.1.1 (E:2-107) Immunoglobulin (variable domains of L and
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H chains) {Fab H57 (hamster), lambda L chain}
YELIQPSSASVTVGETVKITCSGDQLPKNFAYWFQQKSDKNILLLIYMDNKRPSGIPERFSGSTS
GTTATLTISGAQPEDEAAYYCLSSYGDNNDLVFGSGTQLTVLR
>d1nfdf1 b.1.1.1 (F:1-114) Immunoglobulin (variable domains of L and H chains) {Fab H57 (hamster), lambda L chain}
EVYLVESGGDLVQPGSSLKVSCAASGFTFSDFWMYWVRQAPGKGLEWVGRIKNIPNNYATEYADS
VRGRFTISRDDSRNSIYLQMNRLRVDDTAIYYCTRAGRFDHFDYWGQGTMVTVSSA
>d2h1ph1 b.1.1.1 (H:301-420) Immunoglobulin (variable domains of L and H chains) {Fab 2H1 (mouse), kappa L chain}
DVKLVESGGGLVKLGGSLKLSCAASGFTFSSYFLSWVRQTPEKRLELVATINSNGDKTYHPDTMK
GRFTISRDNAKNTLYLQMSSLKSEDTALYYCARRDSSASLYFDYWGQGTTLTVSS
>d2h1pl1 b.1.1.1 (L:1-113) Immunoglobulin (variable domains of L and H chains) {Fab 2H1 (mouse), kappa L chain}
DVVMTQTPLSLPVSLGDPASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPD
KFSGSGSGTDFTLKISRVEAEDQGVYFCSQSTHVPWTFGGGTKLEIKR
>d1aqkh1 b.1.1.1 (H:1-123) Immunoglobulin (variable domains of L and H chains) {Fab B7-15A2 (human), lambda L chain}
EVQLVESGGGVVQPGRSLRLSCAASGFTFNNYAIHWVRQAPGKGLEWVAFISYDGSKNYYADSVK
GRFTISRDNSKNTLFLQMNSLRPEDTAIYYCARVLFQQLVLYAPFDIWGQGTMVTVSS
>d1aqkl1 b.1.1.1 (L:1-111) Immunoglobulin (variable domains of L and H chains) {Fab B7-15A2 (human), lambda L chain}
ENVLTQPPSVSGAPGQRVTISCTGSNSNIGAGFTVHWYQHLPGTAPKLLIFANTNRPSGVPDRFS
GSKSGTSASLAITGLQAEDEADYYCQSYDSSLSARFGGGTRLTVLG
>d1axsa1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Oxy-cope catalytic Fab az-28, chimeric (mouse V domains/human C1 domains)}
ELVLTQSPSSMYASLGERVTITCKASQDINSYLNWFQQKPGKSPKTLIYRTNRLVDGVPSRFSGS
GSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGSGTKLEIK
>d1d5ih1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Oxy-cope catalytic Fab az-28, chimeric (mouse V domains/human C1 domains)}
QVQLQQSGAELMKPGASVKISCKATGYTFSSYWIEWVKQRPGHGLEWIGEILPGSGSTNYNEKFK
GKATFTADTSSNTAYMQLSSLTSEDSAVYYCARGHSYYFYDGDYWGQGTSVTVSS
>d1d5il1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Oxy-cope catalytic Fab az-28, chimeric (mouse V domains/human C1 domains)}
DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPSRFSGS
GSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGSGTKLEIK
>d1ar1c_ b.1.1.1 (C:) Immunoglobulin (variable domains of L and H chains) {Fv against Paracoccus denitrificans cytochrome c oxidase (mouse), kappa L chain}
EVKLQESGGDLVQPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVASINNGGGRTYYPDTVK
GRFTISRDNAKNTLYLQMSSLKSEDTAMYYCVRHEYYYAMDYWGQGTTVTVSS
>d1ar1d_ b.1.1.1 (D:) Immunoglobulin (variable domains of L and H

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chains) {Fv against Paracoccus denitrificans cytochrome c oxidase
(mouse), kappa L chain}
DIELTQTPVSLSASVGETVTITCRASENIYSYLAWYQQKQGKSPQFLVYNAKTLGEGVPSRFSGS
GSGTQFSLKINSLLPEDFGSYYCQHHYGTPPLTFGGGTKLEIK
>d1ae6h1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and
H chains) {Fab CTM01 (mouse), kappa L chain}
QIQLQQSGPELVKPGASVKISCKASGYTFTDYYINWMKQKPGQGLEWIGWIDPGSGNTKYNEKFK
GKATLTVDTSSSTAYMQLSSLTSEDTAVYFCAREKTTYYYAMDYWGQGTSVTVSAA
>d1ae6l1 b.1.1.1 (L:1-106A) Immunoglobulin (variable domains of L and
H chains) {Fab CTM01 (mouse), kappa L chain}
DIVMTQAAPSVPVTPGESLSISCRSSKSLLHSNGDTFLYWFLQRPGQSPQLLIYRMSNLASGVPD
RFSGSGSGTAFTLRVSRVEAEDVGVYYCMQHLEYPFTFGAGTKLELK
>d1ad9a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab CTM01 (human construct), kappa L chain}
DIQMTQSPSTLSASVGDRVTITCRSSKSLLHSNGDTFLYWFQQKPGKAPKLLMYRMSNLASGVPS
RFSGSGSGTEFTLTISSLQPDDFATYYCMQHLEYPFTFGQGTKVEVKR
>d1ad9b1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and
H chains) {Fab CTM01 (human construct), kappa L chain}
EIQLVQSGAEVKKPGSSVKVSCKASGYTFTDYYINWMRQAPGQGLEWIGWIDPGSGNTKYNEKFK
GRATLTVDTSTNTAYMELSSLRSEDTAFYFCAREKTTYYYAMDYWGQGTLVTVSS
>d1fgnh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and
H chains) {Anti-human tissue factor Fab 5G9 (mouse), kappa L chain}
EIQLQQSGAELVRPGALVKLSCKASGFNIKDYYMHWVKQRPEQGLEWIGLIDPENGNTIYDPKFQ
GKASITADTSSNTAYLQLSSLTSEDTAVYYCARDNSYYFDYWGQGTTLTVSS
>d1fgnl1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and
H chains) {Anti-human tissue factor Fab 5G9 (mouse), kappa L chain}
DIKMTQSPSSMYASLGERVTITCKASQDIRKYLNWYQQKPWKSPKTLIYYATSLADGVPSRFSGS
GSGQDYSLTISSLESDDTATYYCLQHGESPYTFGGGTKLEINR
>d1jpth1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and
H chains) {Anti-human tissue humanised factor Fab D3H44}
EVQLVESGGGLVQPGGSLRLSCAASGFNIKEYYMHWVRQAPGKGLEWVGLIDPEQGNTIYDPKFQ
DRATISADNSKNTAYLQMNSLRAEDTAVYYCARDTAAYFDYWGQGTLVTVSS
>d1jptl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Anti-human tissue humanised factor Fab D3H44}
DIQMTQSPSSLSASVGDRVTITCRASRDIKSYLNWYQQKPGKAPKVLIYYATSLAEGVPSRFSGS
GSGTDYTLTISSLQPEDFATYYCLQHGESPWTFGQGTKVEIK
>d1jrhh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Fab A6 (mouse), kappa L chain}
AVKLQESGPGILKPSQTLSLTCSFSGFSLTTYGMGVGWIRQSSGKGLEWLAHIWWDDDKYYNPSL
KSRLTISKDTSRNQVFLKITSVATADTATYYCARRAPFYGNHAMDYWGQGTTVTVSS
>d1jrhl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab A6 (mouse), kappa L chain}
SVEMTQSPSSFSVSLGDRVTITCKASEDIYNRLAWYQQKPGNAPRLLISGATSLETEVPSRFSGS
GSGKDYTLSITSLQTEDVATYYCQQYWSTWTFGGGTKLEIK
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>d1gpoh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Fab M41 (artificial design)}
EVKLQESGPSLVKPSQTLSLTCSVTGDSITSDFWSWIRQFPGNRLEYMGFVQYSGETAYNPSLKS
RISITRDTSKNQYYLDLNSVTTEDTAVYYCANWHGDYWGQGTTVTVSS
>d1gpol1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and
H chains) {Fab M41 (artificial design)}
DIELTQSPATLSVTPGNSVSISCRASQSLVNEDGNTYLFWYQQKSHESPRLLIKYASQSISGIPS
RFSGSGSGTDFTLSINSVETEDLAVYFCQQITDWPFTFGGGTKLEIK
>d1kb5h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Fab Desire-1 (mouse), kappa L chain}
EVQLQQSGPELEKPGASVKISCKASGYSFTGYNMNWVKQSNGKSLEWIGNIDPYYGGISYNQKFK
GRATLTVDKSSSTAYMQLKSLTSEDSAVYYCARSRTDLYYFDYWGQGTTLTVSS
>d1kb5l1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and
H chains) {Fab Desire-1 (mouse), kappa L chain}
DIQMTQSPASLSASVGETVTITCRASKNIYSYLAWYQQKQGKSPQLLVYNAKTLGEGVPSRFSGS
GSGTQFSLKINSLQPEDFGSYYCQHHYGTPYTFGGGTKLEIKR
>d1a4jb1 b.1.1.1 (B:1-119) Immunoglobulin (variable domains of L and
H chains) {Diels alder catalytic Fab (mouse), kappa L chain}
QVQLLESGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTYADDFK
GRFAFSLETSASTAYLQINNLKNEDTATYFCVQAERLRRTFDYWGAGTTVTVSS
>d1a4ka1 b.1.1.1 (A:1-112) Immunoglobulin (variable domains of L and
H chains) {Diels alder catalytic Fab (mouse), kappa L chain}
ELVMTQTPLSLPVSLGDQASISCRSSQSLLHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPD
RFSGSGSGTDFTLKISRVEAEDLGVYFCSQVTHVPPTFGGGTKLEIKRTVAA
>d1c1eh1 b.1.1.1 (H:1-119) Immunoglobulin (variable domains of L and
H chains) {Diels alder catalytic Fab 1E9 (mouse), kappa L chain}
QIQLVQSGPELKKPGETVKISCKASGYMFTNYGMNWVKQAPGKALKLMGWINPYTGESTFADDFK
GRFAFFLETSATTAYLQINNLKNEDMATYFCARGTTIVRAMDYWGQGTSLTVSSAKTTPP
>d1c1el1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and
H chains) {Diels alder catalytic Fab 1E9 (mouse), kappa L chain}
ELVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKFLIYKVSNRFSGVPD
RFGGSGSGTDFILKISRVEAEDLGVYFCFQSTHFFPTFGGGTKLEIKSADAA
>d1a3lh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Diels alder catalytic Fab 13G5 (mouse), kappa L chain}
EVQLEESGPELVRPGTSVKISCKASGYTFTNYWLGWVKQRPGHGFEWIGDIYPGGVYTTNNEKFR
GKAILTADTSSSTAYMQLSSLTSEDSAVYFCARAGGYYTGGDYWGQGTSVTVSS
>d1a3ll1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Diels alder catalytic Fab 13G5 (mouse), kappa L chain}
DIVLTQAAFSNPVTLGASASISCRSSKSLLNSNGIIHMYWYLQKPGQSPQLLIYQMSKLASGAPD
RFSGSGSGTDFTLRISRVEAEDVGVYYCAQNLELPYTFGGGTKLEIK
>d1ay1h1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and
H chains) {Fab TP7 (mouse), kappa L chain}
EVQLQESGPGLVKPYQSLSLSCTVTGYSITSDYAWNWIRQFPGNKLEWMGYITYSGTTDYNPSLK
SRISITRDTSKNQFFLQLNSVTTEDTATYYCARYYYGYWYFDVWGQGTTLTVSS
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>d1ay1l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab TP7 (mouse), kappa L chain}
DIQMTQSPAIMSASPGEKVTMTCSASSSVSYMYWYQQKPGSSPRLLIYDSTNLASGVPVRFSGSG
SGTSYSLTISRMEAEDAATYYCQQWSTYPLTFGAGTKLELK
>d1dsfh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H
chains) {Anticancer Fv B1 (mouse)}
QLVESGGGLVKPGGSLKLSCAASGFIFSDNYMYWVRQTPEKCLEWVATISDGGTYIDYSDSVKGR
FTISRDNAKNNLYLQMSSLRSEDTGMYYCGRSPIYYDYAPFTYWGQGTLVTVSA
>d1dsfl_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H
chains) {Anticancer Fv B1 (mouse)}
DVVMTQTPLSLPVSLGDQASISCRSSQNLVHSDGKTYLHWFLQKPGQSPTLLIYKVSNRFSGVPD
RFSGSGSGTDFILKISRVEAEDLGVYFCSQSTHVPLTFGCGTKLELK
>d1a6ta1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab Mab1-IA (mouse), kappa L chain}
QSVLSQSPAILSASPGEKVIMTCSPSSSVSYMQWYQQKPGSSPKPWIYSTSNLASGVPGRFSGGG
SGTSFSLTISGVEAEDAATYYCQQYSSHPLTFGGGTKLELK
>d1a6tb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and
H chains) {Fab Mab1-IA (mouse), kappa L chain}
EVQLQQSGPDLVKPGASVKISCKASGYSFSTYYMHWVKQSHGKSLEWIGRVDPDNGGTSFNQKFK
GKAILTVDKSSSTAYMELGSLTSEDSAVYYCARRDDYYFDFWGQGTSLTVSS
>d1a6wh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H
chains) {Fv B1-8 (mouse), lambda L chain}
QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKYNEKFK
SKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDYYGSSYFDYWGQGTTVTVSS
>d1a6wl_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H
chains) {Fv B1-8 (mouse), lambda L chain}
AVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPARFSG
SLIGNKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLE
>d1g9mh1 b.1.1.1 (H:1-129) Immunoglobulin (variable domains of L and
H chains) {HIV-1 neutralizing Fab 17B (human), kappa L chain}
QVQLLESGAEVKKPGSSVKVSCKASGDTFIRYSFTWVRQAPGQGLEWMGRIITILDVAHYAPHLQ
GRVTITADKSTSTVYLELRNLRSDDTAVYFCAGVYEGEADEGEYRNNGFLKHWGQGTLVTVTSA
>d1g9ml1 b.1.1.1 (L:1-109) Immunoglobulin (variable domains of L and
H chains) {HIV-1 neutralizing Fab 17B (human), kappa L chain}
ELELTQSPATLSVSPGERATLSCRASESVSSDLAWYQQKPGQAPRLLIYGASTRATGVPARFSGS
GSGAEFTLTISSLQSEDFAVYYCQQYNNWPPRYTFGQGTRLEIK
>d12e8h1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and
H chains) {Fab 2E8 (mouse), kappa L chain}
EVQLQQSGAEVVRSGASVKLSCTASGFNIKDYYIHWVKQRPEKGLEWIGWIDPEIGDTEYVPKFQ
GKATMTADTSSNTAYLQLSSLTSEDTAVYYCNAGHDYDRGRFPYWGQGTLVTVSAA
>d12e8l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab 2E8 (mouse), kappa L chain}
DIVMTQSQKFMSTSVGDRVSITCKASQNVGTAVAWYQQKPGQSPKLMIYSASNRYTGVPDRFTGS
GSGTDFTLTISNMQSEDLADYFCQQYSSYPLTFGAGTKLELK
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>d1adqh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {IgM rheumatoid factor Fab (human), lambda L chain}
EVQLVESGGGLVQPGRSLRLSCVTSGFTFDDYAMHWVRQSPGKGLEWVSGISWNTGTIIYADSVK
GRFIISRDNAKNSLYLQMNSLRVEDTALYYCAKTRSYVVAAEYYFHYWGQGILVTVSS
>d1adql1 b.1.1.1 (L:2-107) Immunoglobulin (variable domains of L and
H chains) {IgM rheumatoid factor Fab (human), lambda L chain}
YVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVVYDDSDRPPGIPERFSGSNS
GNTATLTISRVEAGDEADYYCQVWDSSSDHAVFGGGTKLTVLG
>d2hmic1 b.1.1.1 (C:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab 28 against HIV-1 RT (mouse), kappa L chain}
DIQMTQTTSSLSASLGDRVTISCSASQDISSYLNWYQQKPEGTVKLLIYYTSSLHSGVPSAFSGS
GSGTDYSLTISNLEPEDFATYYCQQYSKFPWTFGGGTKLEIK
>d2hmid1 b.1.1.1 (D:1-123) Immunoglobulin (variable domains of L and
H chains) {Fab 28 against HIV-1 RT (mouse), kappa L chain}
QITLKESGPGIVQPSQPFRLTCTFSGFSLSTSGIGVTWIRQPSGKGLEWLATIWWDDDNRYNPSL
KSRLTVSKDTSNNQAFLNMMTVETADTAIYYCAQSAITSVTDSAMDHWGQGTSVTVSS
>d1bvka_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H
chains) {Humanized anti-lysozyme Fv HuLys11 (mouse), kappa L chain}
DIQMTQSPSSLSASVGDRVTITCRASGNIHNYLAWYQQKPGKAPKLLIYYTTTLADGVPSRFSGS
GSGTDYTFTISSLQPEDIATYYCQHFWSTPRTFGQGTKVEIKR
>d1bvkb_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H
chains) {Humanized anti-lysozyme Fv HuLys11 (mouse), kappa L chain}
QVQLQESGPGLVRPSQTLSLTCTVSGFSLTGYGVNWVRQPPGRGLEWIGMIWGDGNTDYNSALKS
RVTMLKDTSKNQFSLRLSSVTAADTAVYYCARERDYRLDYWGQGSLVTVSS
>d1a0qh1 b.1.1.1 (H:2-114) Immunoglobulin (variable domains of L and
H chains) {Fab 29G11 (mouse), kappa L chain}
VQLQESDAELVKPGASVKISCKASGYTFTDHVIHWVKQKPEQGLEWIGYISPGNGDIKYNEKFKG
KATLTADKSSSTAYMQLNSLTSEDSAVYLCKRGYYGRSNVDYWGQGTTLTVSSA
>d1a0ql1 b.1.1.1 (L:2-108) Immunoglobulin (variable domains of L and
H chains) {Fab 29G11 (mouse), kappa L chain}
IELTQSPSSLSASLGGKVTITCKASQDIKKYIGWYQHKPGKQPRLLIHYTSTLLPGIPSRFRGSG
SGRDYSFSISNLEPEDIATYYCLQYYNLRTFGGGTKLEIKR
>d1fnsh1 b.1.1.1 (H:215-336) Immunoglobulin (variable domains of L
and H chains) {Fab NMC-4 (mouse), kappa L chain}
QVQLKESGPGLVAPSQSLSITCTVSGFSLTDYGVDWVRQPPGKGLEWLGMIWGDGSTDYNSALKS
RLSITKDNSKSQVFLKMNSLQTDDTARYYCVRDPADYGNYDYALDYWGQGTSVTVSS
>d1fnsl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab NMC-4 (mouse), kappa L chain}
DIQMTQSPSSLSASLGDRVTISCSASQDINKYLNWYQQKPDGAVKLLIFYTSSLHSGVPSRFSGS
GSGTDYSLTISNLEPEDIATYYCQQYEKLPWTFGGGTKLEVK
>d1qfuh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Influenza virus hemagglutinin-neutralizing Fab (mouse),
kappa L chain}
QVQLQQPGAELVRPGASVKLSCKASGYTLTTYWMNWFKQRPDQGLEWIGRIDPYDSETHYNQKFK
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DKAILTVDRSSSTAYMQLSSLTSEDSAVYYCTRFLQITTIIYGMDYWGQGTSVTVSS
>d1eo8h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Influenza virus hemagglutinin-neutralizing Fab BH151
(mouse), kappa L chain}
QVQLQQSGAELMKPGPSVKISCKATGYSFSTYFIEWIRQRPGHGLEWIGEILPGSDNTNFNEKFK
DRATFTADTPSNTAYMQLSSLTSEDSAVYYCARPTGRLWFSYWGQGTLVTVSA
>d1eo8l1 b.1.1.1 (L:1-106B) Immunoglobulin (variable domains of L and
H chains) {Influenza virus hemagglutinin-neutralizing Fab BH151
(mouse), kappa L chain}
QIILTQSPAIMSASPGEKVTMTCSASSDISYMHWYQQKSDTSPKIWIYDTSKLASGVPARFSGSG
SGTSYSLTISTMEAEDAATYYCHQRSSYPTFGGGTKLEIK
>d35c8h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Catalytic Fab 5C8 (mouse), kappa L chain}
EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQKPEQGLEWIAQIDPANGNTKYDPKFQ
GKATITADTSSNTAYLHLSSLTSEDSAVYYCAADPPYYGHGDYWGQGTTLTVSS
>d35c8l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Catalytic Fab 5C8 (mouse), kappa L chain}
DIVLTQSPAIMSASLGERVTMTCTASSSVSSSNLHWYQQKPGSSPKLWIYSTSNLASGVPARFSG
SGSGTSYSLTISSMEAEDAATYYCHQYHRSPYTFGGGTKLEIK
>d1a5fh1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and
H chains) {Anti-E-selectin Fab (mouse), kappa L chain}
EVALQQSGAELVKPGASVKLSCAASGFTIKDAYMHWVKQKPEQGLEWIGRIDSGSSNTNYDPTFK
GKATITADDSSNTAYLQMSSLTSEDTAVYYCARVGLSYWYAMDYWGQGTSVTVSS
>d1axth1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Catalytic Fab 33F12 (mouse), kappa L chain}
EVKLEESGGGLVQPGGSMKLSCVVSGLTFSRFWMSWVRQSPEKGLEWVAEIRLKSDNYATHYAES
VKGKFTISRDDSKSRLYLQMNSLRTEDTGIYYCKIYFYSFSYWGQGTLVTVSA
>d1axtl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Catalytic Fab 33F12 (mouse), kappa L chain}
ELVMTQTPLSLPVSLGDQASISCRSSQSLVHSYGNTFLNWYLQKSGQSPKLLIYKVSNRFSGVPD
RFSGSGSGTDFTLKISRVEAEDLGVYFCSQGTHVPYTFGGGTKLEIK
>d1b2wh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and
H chains) {Humanized and chimeric anti-gamma-interferon Fab}
EVQLVQSGGGVVQPGRSLKLSCLASGYIFTSSWINWVKQRPGRGLEWIGRIDPSDGEVHYNQDFK
DRFTISRDKSKNTLYLQMNSLRPEDTAVYYCARGFLPWFADWGQGTLVTVSS
>d1b2wl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Humanized and chimeric anti-gamma-interferon Fab}
DIQMTQSPSTLSASVGDRVTITCKASENVDTYVSWYQQKPGKAPKLLIYGASNRYTGVPSRFSGS
GSGTDFTLTISSLQPDDFATYYCGQSYNYPFTFGQGTKVEVK
>d1b4jh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and
H chains) {Humanized and chimeric anti-gamma-interferon Fab}
EVQLQQPGADLVMPGAPVKLSCLASGYIFTSSWINWVKQRPGRGLEWIGRIDPSDGEVHYNQDFK
DKATLTVDKSSSTAYIQLNSLTSEDSAVYYCARGFLPWFADWGQGTLVTVSA
>d1b4jl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
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H chains) {Humanized and chimeric anti-gamma-interferon Fab}
NIVMTQSPKSMYVSIGERVTLSCKASENVDTYVSWYQQKPEQSPKLLIYGASNRYTGVPDRFTGS
GSATDFTLTISSVQAEDLADYHCGQSYNYPFTFGSGTKLEIK
>d1bfoa1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and
H chains) {CAMPATH-1G igg2b monoclonal fab (rat), kappa L chain}
DIKMTQSPSFLSASVGDRVTLNCKASQNIDKYLNWYQQKLGESPKLLIYNTNNLQTGIPSRFSGS
GSGTDFTLTISSLQPEDVATYFCLQHISRPRTFGTGTKLELK
>d1bfob1 b.1.1.1 (B:1-121) Immunoglobulin (variable domains of L and
H chains) {CAMPATH-1G igg2b monoclonal fab (rat), kappa L chain}
EVKLLESGGGLVQPGGSMRLSCAGSGFTFTDFYMNWIRQPAGKAPEWLGFIRDKAKGYTTEYNPS
VKGRFTISRDNTQNMLYLQMNTLRAEDTATYYCAREGHTAAPFDYWGQGVMVTVSS
>d1ce1h1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and
H chains) {Therapeutic CAMPATH-1H humanized fab (rat), kappa L chain}
QVQLQESGPGLVRPSQTLSLTCTVSGFTFTDFYMNWVRQPPGRGLEWIGFIRDKAKGYTTEYNPS
VKGRVTMLVDTSKNQFSLRLSSVTAADTAVYYCAREGHTAAPFDYWGQGSLVTVSS
>d1ce1l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Therapeutic CAMPATH-1H humanized fab (rat), kappa L chain}
DIQMTQSPSSLSASVGDRVTITCKASQNIDKYLNWYQQKPGKAPKLLIYNTNNLQTGVPSRFSGS
GSGTDFTFTISSLQPEDIATYYCLQHISRPRTFGQGTKVEIK
>d1bj1h1 b.1.1.1 (H:1-123) Immunoglobulin (variable domains of L and
H chains) {VEGF neutralizing Fab-12 (mouse), kappa L chain}
EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWVRQAPGKGLEWVGWINTYTGEPTYAADFK
RRFTFSLDTSKSTAYLQMNSLRAEDTAVYYCAKYPHYYGSSHWYFDVWGQGTLVTVSS
>d1bj1j1 b.1.1.1 (J:1-107) Immunoglobulin (variable domains of L and
H chains) {VEGF neutralizing Fab-12 (mouse), kappa L chain}
DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKVLIYFTSSLHSGVPSRFSGS
GSGTDFTLTISSLQPEDFATYYCQQYSTVPWTFGQGTKVEIK
>d1blna1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and
H chains) {Anti-p-glycoprotein Fab MRK-16 (mouse), kappa L chain}
DVLMTQTPVSLSVSLGDQASISCRSSQSIVHSTGNTYLEWYLQKPGQSPKLLIYKISNRFSGVPD
RFSGSGSGTDFTLKISRVEAEDLGVYYCFQASHAPRTFGGGTKLEIK
>d1blnb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and
H chains) {Anti-p-glycoprotein Fab MRK-16 (mouse), kappa L chain}
EVILVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGGNTYYPDSVK
GRFTISRDNAKNNLYLQMSSLRSEDTALYYCARYYRYEAWFASWGQGTLVTVSA
>d1boga1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and
H chains) {Anti-p24 (HIV-1) Fab CB 4-1 (mouse), kappa L chain}
DIKMTQSPSSMYTSLGERVTITCKASQDINSFLTWFLQKPGKSPKTLIYRANRLMIGVPSRFSGS
GSGQTYSLTISSLEYEDMGIYYCLQYDDFPLTFGAGTKLDLK
>d1bogb1 b.1.1.1 (B:1-112) Immunoglobulin (variable domains of L and
H chains) {Anti-p24 (HIV-1) Fab CB 4-1 (mouse), kappa L chain}
QDQLQQSGAELVRPGASVKLSCKALGYIFTDYEIHWVKQTPVHGLEWIGGIHPGSSGTAYNQKFK
GKATLTADKSSTTAFMELSSLTSEDSAVYYCTRKDYWGQGTLVTVSA
>d1f58h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
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H chains) {Anti-gp120 (HIV-1) Fab 58.2, (mouse), kappa L chain}
DVQLQQSGPDLVKPSQSLSLTCTVTGYSITSGYSWHWIRQFPGNKLEWMGYIHYSAGTNYNPSLK
SRISITRDTSKNQFFLQLNSVTTEDTATYYCAREEAMPYGNQAYYYAMDCWGQGTTVTVSS
>d1f58l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Anti-gp120 (HIV-1) Fab 58.2, (mouse), kappa L chain}
DIVLTQSPASLAVSLGQRATISCKASQGVDFDGASFMNWYQQKPGQPPKLLIFAASTLESGIPAR
FSGRGSGTDFTLNIHPVEEEDAATYYCQQSHEDPLTFGAGTKLELK
>d1wejh1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and
H chains) {Anti-cytochrome c Fab E8, (mouse), kappa L chain}
EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEKGLEWIGRIDPASGNTKYDPKFQ
DKATITADTSSNTAYLQLSSLTSEDTAVYYCAGYDYGNFDYWGQGTT
>d1wejl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Anti-cytochrome c Fab E8, (mouse), kappa L chain}
DIQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNAKTLADGVPSRFSGS
GSGTQYSLKINSLQPEDFGSYYCQHFWSTPWTFGGGTKLEIK
>d1sbsh1 b.1.1.1 (H:1-123) Immunoglobulin (variable domains of L and
H chains) {Anti-HCG Fab 3A2, (mouse), kappa L chain}
EVNLEESGGGLVQPGGSMKLSCVASGFTFSNYWMNWVRQSPEKGLEWVADIRLKSNNYATLYAES
VKGRFTISRDDSKSSVYLQMNNLRAEDTGIYYCTRGAYYRYDYAMDYWGQGTSVTVSS
>d1sbsl1 b.1.1.1 (L:1-113) Immunoglobulin (variable domains of L and
H chains) {Anti-HCG Fab 3A2, (mouse), kappa L chain}
DIVMSQSPSSLAVSVGEKVTMTCKSSQSLLYSSNQMNYLAWYQQKPGQSPKLLIYWASTRESGVP
DRFTGSGSGTDFTLTISSVEAEDLAVYYCQQYHSYPFTFGSGTKLEIK
>d1sm3h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Tumor-specific Fab SM3, (mouse), lambda L chain}
QVQLQESGGGLVQPGGSMKLSCVASGFTFSNYWMNWVRQSPEKGLEWVAEIRLKSNNYATHYAES
VKGRFTISRDDSKSSVYLQMNNLRAEDTGIYYCTGVGQFAYWGQGTTVTVSS
>d2pcpa1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab 6B5, (mouse), kappa L chain}
DVLMTQTPLSLPVSLGDQASISCRSSQTIVHSNGNTYLEWYLQKPGQSPKLLIYKVTNRFSGVPD
RFSGSGSGTDFTLKISRVEAEDLGVYYCFQGTHAPYTFGGGTKLEIK
>d2pcpb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and
H chains) {Fab 6B5, (mouse), kappa L chain}
EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYIHWNKQSHGKSLEWIGYIYPNNGGNGYNHKFK
GKATLTVDKSSSTAYMDVRTLTSEDSAVYYCGRSTWDDFDYWGQGTTLTVSS
>d3fcta1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and
H chains) {Mature metal chelatase catalytic Fab, (human), kappa L
chain}
ELVMTQTPKFMSTTVGDRVSITCKASQNVGTPVAWYQQKPGQSPKLLIYSASNRYTGVPDRFTGS
GSGTDFTLTISNMQSEDLADYFCQQYSSYPLTFGGGTKVEIK
>d3fctb1 b.1.1.1 (B:1-114) Immunoglobulin (variable domains of L and
H chains) {Mature metal chelatase catalytic Fab, (human), kappa L
chain}
QVQLLESGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGMIDPNSGGTKYNEKFK
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SKATLTVDKPSNTAYMQLSSLTSEDSAVYYCTRRDMDYWGAGTTVTVSS
>d1cf8h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 19A4 (mouse), kappa L chain}
DVQLQESGPGLVKPSQSLSLTCTVTGYSITSGYAWNWIRQFPGNKLEWMGYIRYSGDTRYNPSLK
SRISITRDTSKNQFFLQLNSVTTEDTATYYCAIGYGNSDYWGQGTLVTVSA
>d1cf8l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 19A4 (mouse), kappa L chain}
DIVLTQSPTIMSVSPGEKVTLTCSASSSVSSNYVYWYQQKPGSSPKVWIYSTSNLASGVPARFSG
SGSGTSYSLTISSMEAEDAASYFCLQWSSFPYTFGGGTKLELK
>d1c12a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab directed agains the musk odorant traseolide, (mouse), kappa L chain}
DIELTQSPSSMSVSLGDTVSITCHASQGISSNIGWLQQKPGKSFKGLIYHGTNLEDGVPSRFSGS
GSGADYSLTISSLESEDFADYYCVQYVQFPFTFGSGTKLEIK
>d1c12b1 b.1.1.1 (B:301-413) Immunoglobulin (variable domains of L and H chains) {Fab directed agains the musk odorant traseolide, (mouse), kappa L chain}
QVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYISYSGSTSYSPSLK
SRISLTRDTSKNQFFLQLNSVTTEDTATYYCVTSLTWLLRRKRSYWGQGTTVTVSS
>d1dlfh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Anti-dansyl Fv, (mouse), kappa L chain}
EVKLEESGGGLVQPGGSMKLSCATSGFTFSDAWMDWVRQSPEKGLEWVAEIRNKANNHATYYAES
VKGRFTISRDDSKRRVYLQMNTLRAEDTGIYYCTGIYYHYPWFAYWGQGTLVTVS
>d1dlfl_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Anti-dansyl Fv, (mouse), kappa L chain}
DVVMTQTPLSLPVSLGNQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPD
RFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPFTFGSGTKLEIKR
>d43c9a_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Sterolytic and amidolytic Fv 43c9, (mouse), kappa L chain}
DVVMTQTPSSLAMSVGQKVTMSCKSSQSLLNISNQKNYLAWYQQKPGQSPKLLVYFASTRESGVP
DRFIGSGSGTDFTLTISSVQAEDQADYFCQQHYRAPRTFGGGTKLEIK
>d43c9b_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {Sterolytic and amidolytic Fv 43c9, (mouse), kappa L chain}
GQVQLVESGPGLVAPSQSLSITCTVSGISLSRYNVHWVRQSPGKGLEWLGMIWGGGSIEYNPALK
SRLSISKDNSKSQIFLKMNSLQTDDSAMYYCVSYGYGGDRFSYWGQGTLVTVS
>d1bz7a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab R24, (mouse), kappa L chain}
DIQMTQITSSLSVSLGDRVIISCRASQDIGNFLNWYQQKPDGSLKLLIYYTSRLQSGVPSRFSGW
GSGTDYSLTISNLEEEDIATFFCQQGKTLPYTFGGGTKLEIK
>d1bz7b1 b.1.1.1 (B:1-122) Immunoglobulin (variable domains of L and H chains) {Fab R24, (mouse), kappa L chain}
DVQLVESGGGLVQPGGSRKLSCAASGFTFSNFGMHWVRQAPEKGLEWVAYISSGGSSINYADTVK
GRFTISRDNPKNTLFLQMTSLRSEDTAIYYCTRGGTGTRSLYYFDYWGQGATLIVSS
>d1ct8a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and

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H chains) {Catalytic Fab 7C8, (mouse), kappa L chain}
ELVMTQTPATLSVTPGDSVSLSCRASQSVSNKLHWYQQKSHESPRLLIKFASQSIPGIPSRFSGS
GSGSDFTLSINSVETEDFGIYFCHQTHGRPLTFGAGTKLELK
>d1ct8b1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and
H chains) {Catalytic Fab 7C8, (mouse), kappa L chain}
QVKLLESGAVLVKPGASVKLSCKTSGFTFSSSYINWLKQKPGQSLEWIAWIYAGSGGTVYNQHFT
DKARLTVDTSSSTAYMQFSSLTTEDSAIYYCARYRYDEGFAYWGQGTLVTVSA
>d1c5da1 b.1.1.1 (A:1-106) Immunoglobulin (variable domains of L and
H chains) {Fab against the main immunogenic region of the human muscle
acetylcholine receptor, (rat), kappa L chain}
DIQMTQSPPSLSASLGDKVTITCQASQDINKYIAWYQQKPGKAPRQLIRYTSILVLGTPSRFSGS
GSGRDFSFSISNVASEDIASYYCLQYGNLYTFGAGTKLEIK
>d1c5db1 b.1.1.1 (B:1-117) Immunoglobulin (variable domains of L and
H chains) {Fab against the main immunogenic region of the human muscle
acetylcholine receptor, (rat), kappa L chain}
EVKLLESGPGLVQPSQTLSLTCTVSGFPLTTNGVSWVRQPPGKGLEWIAAISSGGSPYYNSALKS
RLSINRDTSKSQVFLKMNSLQTEDTAIYFCTREDGWNYFDYWGPGTMVTVSS
>d1f3rb2 b.1.1.1 (B:139-257) Immunoglobulin (variable domains of L
and H chains) {scFv MAB198, (rat), kappa L chain}
DIKLTQSPSLLSASVGDRVTLSCKGSQNINNYLAWYQQKLGEAPKLLIYNTNSLQTGIPSRFSGS
GSGTDYTLTISSLQPEDVATYFCYQYNNGYTFGAGTKLELKAAEQKLISEEDLN
>d1dqqa1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and
H chains) {Anti-lysozyme Fab HYHEL-63, (mouse), kappa L chain}
DIVLTQSPATLSVTPGDSVSLSCRASQSISNNLHWYQQKSHESPRLLIKYASQSISGIPSRFSGS
GSGTDFTLSINSVETEDFGMYFCQQSNSWPYTFGGGTKLEIK
>d1dqqb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and
H chains) {Anti-lysozyme Fab HYHEL-63, (mouse), kappa L chain}
EVQLQESGPSLVKPSQTLSLTCSVTGDSVTSDYWSWIRKFPGNKLEYMGYISYSGSTYYHPSLKS
RISITRDTSKNQYYLQLNSVTTEDTATYYCASWGGDVWGAGTTVTVSS
>d1ejoh1 b.1.1.1 (H:2501-2619) Immunoglobulin (variable domains of
L and H chains) {Anti-FMDV Fab 4C4, (mouse), kappa L chain}
QMLVESGGDLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGAYTYYPDSVKG
RFTISDDNAESTLYLQMSSLRSEDTAMYYCVRRAFDSDVGFASWGHRTLVTVSA
>d1ejol1 b.1.1.1 (L:2001-2111) Immunoglobulin (variable domains of
L and H chains) {Anti-FMDV Fab 4C4, (mouse), kappa L chain}
DIVLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYRASNLESGIPAR
FSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGAGTKLELK
>d1cr9h1 b.1.1.1 (H:1-110) Immunoglobulin (variable domains of L and
H chains) {Anti-prion Fab 3F4, (mouse), kappa L chain}
KVKLQQSGAELVRSGASVKLSCTASGFNIKDYYIQWVKQRPEQGLEWIGWIDPENGNSEYAPRFQ
GKATMTADTLSNTAYLQLSSLTSEDTAVYYCNADLHDYWGQGTTLTVSS
>d1cr9l1 b.1.1.1 (L:1-106A) Immunoglobulin (variable domains of L and
H chains) {Anti-prion Fab 3F4, (mouse), kappa L chain}
DVVMTQTPLSLSVTIGQPASISCKSSQSLLDSDGKTYLIWVFQRPGQSPKRLIFLVSKRDSGVPD
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RFTGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFPHTVGGGTKLEIA
>d1qfwh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Anti-[gonadotropin alpha subunit] Fv, kappa L chain}
QLQQSGAELVKPGASVKLSCKASDYTFTSYWMHWVKQRPGQGLEWIGEINPTNGRTYYNEKFKSK
ATLTVAASASTAAMQASSLTSEDSAVYYCARRYGNSFDYWGQGTTVTVSS
>d1qfwl_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Anti-[gonadotropin alpha subunit] Fv, kappa L chain}
DIELTQSPDSLAVSLGQRATISCRASESVDSYGNSFMQWYQQKPGQPPKLLIYRASNLESGIPAR
FSGTGSRTDFTLTINPVEADDVATYYCQQSDEYPYMYTFGGGTKLEIKR
>d1qfwi_ b.1.1.1 (I:) Immunoglobulin (variable domains of L and H chains) {Anti-[gonadotropin beta subunit] Fv, kappa L chain}
QVQLQESGGHLVKPGGSLKLSCAASGFAFSSFDMSWIRQTPEKRLEWVASITNVGTYTYYPGSVK
GRFSISRDNARNTLNLQMSSLRSEDTALYFCARQGTAAQPYWYFDVWGAGTTVTVS
>d1qfwm_ b.1.1.1 (M:) Immunoglobulin (variable domains of L and H chains) {Anti-[gonadotropin beta subunit] Fv, kappa L chain}
DIELTQSPKSMSMSVGERVTLSCKASETVDSFVSWYQQKPEQSPKLLIFGASNRFSGVPDRFTGS
GSATDFTLTISSVQAEDFADYHCGQTYNHPYTFGGGTKLEIKR
>d32c2a1 b.1.1.1 (A:1-110) Immunoglobulin (variable domains of L and H chains) {Fab 32C2 against P450-arom, (mouse), kappa L chain}
DIVLTQSPASLAVSLGQRATISCRASKSVSTSGYGYMHWNQQKPGQPPRLLIYLVSNLESGVPAR
FSGSGSGTDFTLNIHPVEEEDAATYYCQHIREPLTFGGGTKLEIK
>d32c2b1 b.1.1.1 (B:1-119) Immunoglobulin (variable domains of L and H chains) {Fab 32C2 against P450-arom, (mouse), kappa L chain}
DVQLQESGPGLVKPSQSLSLTCTVTGYSISSDYAWNWIRQFPGNKLEWMGYISYSGSTSYNPSLK
SRISITRDTSKNQFFLQLSSVTTEDTATYYCARGYYGSSHSPVWGAGTTVTVSS
>d1dqdh1 b.1.1.1 (H:1-122) Immunoglobulin (variable domains of L and H chains) {Fab HGR-2 F6, (mouse), kappa L chain}
EVQLQESGPSLVKPSQTLSLTCSVTGDSITSGYWNWIRKFPGNKLEYMGYISYSGSTYYNPSLKS
RLSITRDTSRNQYYLQLKSVTPEDTATYYCASPPGYYGSGPYAMDYWGQGTSVTVSS
>d1dqdl1 b.1.1.1 (L:1-106) Immunoglobulin (variable domains of L and H chains) {Fab HGR-2 F6, (mouse), kappa L chain}
DIVLSQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLCIYTTSNLASGVPARFSGSG
SGTSYSLTISRMEAEDAATYYCQQRSTYPPTFGSGTKLEIK
>d1deea1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab of human IgM RF 2A2}
DIQMTQSPSSLSASVGDRVTITCRTSQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS
GSGTDFTLTISSLQPEDFATYYCQQSYSAPRTFGQGTKVEIK
>d1deeb1 b.1.1.1 (B:501-621) Immunoglobulin (variable domains of L and H chains) {Fab of human IgM RF 2A2}
QVQLVESGGGVVQPGKSLRLSCAASGFTFSGYGMHWVRQAPGKGLEWVALISYDESNKYYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKVKFYDPTAPNDYWGQGTLVTVSS
>d1qnzh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Anti-HIV Fv 0.5B, (mouse), kappa L chain}
QVQLQQSGAELVKPGASVKMSCKASGYTFTTYPIEWMKQNHGKSLEWIGNFHPYSDDTNYNEKFK

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GKAKLTVEKSSSTVYLEFSRLTSDDSAVYYCAIHYGSAYAMDYWGQGTSVTVSS
>d1f4xh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and
H chains) {Anti-carbohydrate Fab S-20-4 (mouse), lambda L chain}
EVQLEESGGGLVTPGGSLRLSCAASGYVFSTYDMSWVRQTPEKRLEWVAFISSGGGRTSYPDTVK
GRFTISRDDAKNTLYLQMSSLQSEDTAMYYCTRHFYAVLDYWGRGTTLTVSS
>d1f4xl1 b.1.1.1 (L:1-110) Immunoglobulin (variable domains of L and
H chains) {Anti-carbohydrate Fab S-20-4 (mouse), lambda L chain}
QAVVTQESALTTSPGETVTLTCRSSTGTVTTSNYANWVQEKPDHLFTGLIGATNNRAAGVPVRFS
GSLIGGKAALTITGAQTEDEAIYFCALWYSGHWVFGGGTKLTVLG
>d1f11b1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and
H chains) {Anti-Pres2 Fab F124, (mouse), kappa L chain}
EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTGYNQKFK
GKATLTVDKSSSTAYMQLNSLTSEDSAVYYCANDYGSTYGFAYWGQGTLVTVSA
>d1f3dh1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and
H chains) {Catalytic Fab 4B2, (mouse), kappa L chain}
EIQLQQSGPELVKPGASVKVSCKASGYSFIDYNIHWVKQSHGKSLEWIGYIVPYSGGTTFNQKFK
GKATLTVDKSSSTAFMHLNSLTFEDSAVYYCANDYDGVYWGQGTTLTVSS
>d1f3dj1 b.1.1.1 (J:1-107) Immunoglobulin (variable domains of L and
H chains) {Catalytic Fab 4B2, (mouse), kappa L chain}
DVLMTQTPLSLPVSLGDQVSISCRSSQSIFHSDGKTYLEWHLQKPGQSPKLLIYKVSKRFSGVPD
RFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGGGTKLEIK
>d1fh5h1 b.1.1.1 (H:4-120) Immunoglobulin (variable domains of L and
H chains) {Fab MAK33, (human), kappa L chain}
SGGGLVKPAGSLKLSCAASGFTFSSYYMYWVRQTPDKRLEWVATISDGGSYTYYPDSVKGRFTIS
RDNAKNNLYLQMSSLKSEDTAMYYCARDAMDYWGQGTLVTVSA
>d1fskb1 b.1.1.1 (B:1-107) Immunoglobulin (variable domains of L and
H chains) {Anti bet v1 Fab BV16, (mouse), kappa L chain}
NIVLTQSPKSMSVSVGERVTLSCKASENVDTYVFWFQQKPDQSPKLLLYGPSNRYTGVPDRFTGS
GSTTDFTLTISSVQAEDLADYHCGQSYSYPYTFGGGTKLEIK
>d1fskc1 b.1.1.1 (C:1-118) Immunoglobulin (variable domains of L and
H chains) {Anti bet v1 Fab BV16, (mouse), kappa L chain}
QVQLQQPGTELVRPGASVILSCKASGYTFTSYWINWVKQRPGQGLEWVGNIFPSDSYTNYNQKFK
DKATLTVDKSSSTAYMQVNSPTSEDSAVYYCTRGARDTWFAYWGQGTLVTVSV
>d1c5ch1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Decarboxylase catalytic Fab 21D8, chimeric (mouse V
domains/human C1 domains)}
QVQLLEPGTELVKPGASVKLSCRASGYSFTSYWMHWVKQRPGQGLEWIGLIDPSNGRTNFNDKFK
SRATLTVDTSSSTAYMQLSSLTSEDSAVYYCVRIAYWGQGTLVTVSS
>d1c5cl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Decarboxylase catalytic Fab 21D8, chimeric (mouse V
domains/human C1 domains)}
EIQLTQSPSSLSASLGERVSLTCRTSQEISGYLSWLQQKPDGTIKRLIYDATKLDSGAPKRFSGS
RSGSDYSLTISSLESEDFADYYCLQYASFPRTFGGGTKLEIK
>d1etza1 b.1.1.1 (A:1-110) Immunoglobulin (variable domains of L and
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H chains) {Anti-sweetener Fab NC10.14, (mouse), lamba L chain}
FAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYAIWVQEKPDHLFSGLIGGTNNRVPGVPARFS
GSLIGDKAALTVTGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG
>d1etzb1 b.1.1.1 (B:1-126) Immunoglobulin (variable domains of L and
H chains) {Anti-sweetener Fab NC10.14, (mouse), lamba L chain}
QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVGWIRQPSGEGLEWLADIWWNDKKYYNPSL
KSRLTVSKDTSSNQVFLKITSVDTSDTATYHCARRTFSYYYGSSFYYFDNWGQGTTLTVSS
>d1emth1 b.1.1.1 (H:1-116) Immunoglobulin (variable domains of L and
H chains) {Anti-C60 fullerene Fab, (mouse), kappa L chain}
QVHLQESGPELVRPGASVKISCKTSGYVFSSSWMNWVKQRPGQGLKWIGRIYPGNGNTNYNEKFK
GKATLTADKSSNTAYMQLSSLTSVDSAVYFCATSSAYWGQGTLLTVSA
>d1emtl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Anti-C60 fullerene Fab, (mouse), kappa L chain}
DIQMTQTTSSLSASLGDRVTFSCSASQDISNYLNWYQQKPDGTIKLLIYYTSSLRSGVPSRFSGS
GSGTDYSLTINNLEPEDIATYFCQQYSRLPFTFGSGTKLEIK
>d1fl3a1 b.1.1.1 (A:2-116) Immunoglobulin (variable domains of L and
H chains) {Blue fluorescent Fab 19G2, (mouse), kappa L chain}
AALLESGGGLVKPGGSLKLSCTASGITFSRYIMSWVRQIPEKRLEWVASISSGGITYYPDSVAGR
FTISRDNVRNILYLQMSSLRSEDTALYYCARGQGRPYWGQGTSVTVSA
>d1fl3b1 b.1.1.1 (B:2-113) Immunoglobulin (variable domains of L and
H chains) {Blue fluorescent Fab 19G2, (mouse), kappa L chain}
AALTQSPVSNPVTLGTSASISCRSTKSLLHSNGITYLYWYLQKPGQSPQLLIYQMSNLASGVPNR
FSSSGSGTDFTLRINTVEAEDVGVYYCAQNLELPPTFGAGTKLELKR
>d1dzba1 b.1.1.1 (A:1-117) Immunoglobulin (variable domains of L and
H chains) {Anti-lysozyme scFv 1F9, (mouse), kappa L chain}
QVKLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKYDPKFQ
GKATITADTSSNTAYLQLSSLTSEDTAVYYCARWDWYFDVWGQGTTVTVSSG
>d1dzba2 b.1.1.1 (A:201-307) Immunoglobulin (variable domains of L
and H chains) {Anti-lysozyme scFv 1F9, (mouse), kappa L chain}
DIELTQSPSSMYTSLGERVTITCKASQDINSYLRWFQQKPGKSPKTLIYYATSLADGVPSRFSGS
GSGQDYSLTISSLESDDTTTYYCLQHGESPYTFGGGTKLEIK
>d1qoka1 b.1.1.1 (A:27-147) Immunoglobulin (variable domains of L and
H chains) {Anti-carcinoembryonic scFv MFE-23, (mouse), kappa L chain}
QVKLQQSGAELVRSGTSVKLSCTASGFNIKDSYMHWLRQGPEQGLEWIGWIDPENGDTEYAPKFQ
GKATFTTDTSSNTAYLQLSSLTSEDTAVYYCNEGTPTGPYYFDYWGQGTTVTVSSG
>d1qoka2 b.1.1.1 (A:162-267) Immunoglobulin (variable domains of L
and H chains) {Anti-carcinoembryonic scFv MFE-23, (mouse), kappa L
chain}
ENVLTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARFSGSG
SGTSYSLTISRMEAEDAATYYCQQRSSYPLTFGAGTKLELK
>d1e6oh1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and
H chains) {Fab 13B5 against HIV-1 capsid protein p24, (mouse), kappa
L chain}
EVQLQQSGAELARPGASVKMSCKASGYTFTSYTMHWVKQRPGQGLEWIGYINPSSGYSNYNQKFK
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DKATLTADKSSSTAYMQLSSLTSEDSAVYYCSRPVVRLGYNFDYWGQGSTLTVSS
>d1e6ol1 b.1.1.1 (L:1-105) Immunoglobulin (variable domains of L and
H chains) {Fab 13B5 against HIV-1 capsid protein p24, (mouse), kappa
L chain}
EIVLTQSPAITAASLGQKVTITCSASSSVSYMHWYQQKSGTSPKPWIYEISKLASGVPARFSGSG
SGTSYSLTISSMEAEDAAIYYCQQWNYPFTFGSGTKLEIK
>d1dl7h_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H
chains) {Fv M3C65, (human), lambda L chain}
QVQLKESGPGLVAPSQSLSITCTVSGFSLTGYGVNWVRQPPGKGLEWLGMIWGDGSTDYNSALKS
RLNISKDKSKSQVFLRMYSLQTDDTARYYCARDYGPYWGQGTLVTVS
>d1dl7l_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H
chains) {Fv M3C65, (human), lambda L chain}
QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTKHRTPGAPARFS
GSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVL
>d1egjh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Fab against cytokyne receptor common beta chain domain 4,
(mouse), kappa L chain}
EVQLQQSGPELVKPGTSVKMSCKASGYTFTDYYMKWVKHSHGKSLEWIGDINPSNGGTLYNQKFK
GKATLTVDKSSSTASMQLSRLTSEDSAVYYCSRGDGIHGGFAYWGQGTTVTVSS
>d1egjl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab against cytokyne receptor common beta chain domain 4,
(mouse), kappa L chain}
NIVLTQSPASLAVSLGQRATISCRANESVYSYGDSFMHWYQQKPGQPPKLLIYLASNLASGVPAR
FSGSGSRTDFTLTIDPVETDDAATYYCQQNNEDPWTFGGGTKLEIK
>d1ehlh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Anti-photoproduct Fab 64M-2, (mouse), kappa L chain}
EVQLQQSGTVLARPGASVKMSCKASGYSFTSFWMHWVKQRPGQGLEWIGTIYPGNSDTSYNQKFK
GKAKLTAVTSASTAYMEVSSLTNEDSAVYYCTRRSGYKYYALDYWGQGTSVTVSS
>d1fe8h1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and
H chains) {Fab RU5, (mouse), kappa L chain}
DVKLVQSGPGLVAPSQSLSITCTVSGFSLTTYGVSWVRQPPGKGLEWLGVIWGDGNTTYHSALIS
RLSISKDNSRSQVFLKLNSLHTDDTATYYCAGNYYGMDYWGQGTSVTVSS
>d1fe8l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab RU5, (mouse), kappa L chain}
DIAMTQTTSSLSASLGQKVTISCRASQDIGNYLNWYQQKPDGTVRLLIYYTSRLHSGVPSRFSGS
GSGTDYSLTISNLESEDIATYFCQNGGTNPWTFGGGTKLEVK
>d1ezvx_ b.1.1.1 (X:) Immunoglobulin (variable domains of L and H
chains) {Fv against Rieske protein from the yeast cytochrome bc1
complex, (mouse), kappa L chain}
EVKLQESGAGLVQPSQSLSLTCSVTGYSITSGYYWNWIRLFPGNKLEWVGYISNVGDNNYNPSLK
DRLSITRDTSKNQFFLKLNSVTTEDTATYYCARSEYYSVTGYAMDYWGQGTTVTVSSAWRHP
>d1ezvy_ b.1.1.1 (Y:) Immunoglobulin (variable domains of L and H
chains) {Fv against Rieske protein from the yeast cytochrome bc1
complex, (mouse), kappa L chain}
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DIELTQTPVSLAASLGDRVTISCRASQDINNFLNWYQQKPDGTIKLLIYYTSRLHAGVPSRFSGS
GSGTDYSLTISNLEPEDIATYFCQHHIKFPWTFGAGTKLEIK
>d1il1a1 b.1.1.1 (A:3-121) Immunoglobulin (variable domains of L and
H chains) {Anti-HIV Fab G3-519, (mouse), kappa L chain}
QLQQSGAELVRSGASVKLSCATSDFNIKDYYIHWVRQRPEQGLEWIGWLDPENGDTESAPKFQGK
ATMTADTSSNTAYLQLSSLTSEASAVYYCNAISTTRDYYALDYWGQGTSVTVSS
>d1il1b1 b.1.1.1 (B:1-112) Immunoglobulin (variable domains of L and
H chains) {Anti-HIV Fab G3-519, (mouse), kappa L chain}
DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSRNQMNYLSWYQQKPGQSPKLLIYWASTRESGVP
DRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYHYRTFGGGTRLEIR
>d1f8th1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Anti-IL2 Fab LNKB-2, (mouse), kappa L chain}
GVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYITYSGSTGYNPSLK
SRISITRDTSKNQFFLQLNSVTTEDTATYYCASYDDYTWFTYWGQGTLVTVSA
>d1f8tl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Anti-IL2 Fab LNKB-2, (mouse), kappa L chain}
DVQMTQTPLTLSVTIGQPASISCESSQSLLYSNGKTYLNWLLQRPGQSPKRLIYLVSKLDSGVPD
RFTGSGSGTDFTLRISRVEAEDLGVYYCVQGTHFPRTFGGGTKLEIK
>d1e4wh1 b.1.1.1 (H:1-110) Immunoglobulin (variable domains of L and
H chains) {Anti-TGFalpha Fab TAB2, (mouse), kappa L chain}
QVQLQQPGAELVKPGASVKLSCKASGFTFTNYWMHWVKQRPGQGLEWIGEILPSNGRTNYNEKFK
TKATLTVDKSSNTAYMQLSSLTSEDSAVYYCARSPSDYWGQGTTLTVSS
>d1e4wl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Anti-TGFalpha Fab TAB2, (mouse), kappa L chain}
DIQMTQTPSSLSASLGDRVTISCRASQDISHYLNWFQQKPDGTVKLLIYYTSTLHSGVPSRFSGS
GSGTDYSLTISNLEEEDIAFYFCQQGGALPFTFGSGTKLAIK
>d1h8na1 b.1.1.1 (A:3-109) Immunoglobulin (variable domains of L and
H chains) {Anti-ampicillin scFv, (mouse), kappa L chain}
KDIVLTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPDRFTG
SGSGTDFTLTISNVQSEDLADYFCQQYSSYPLTFGAGTKLEL
>d1h8na2 b.1.1.1 (A:132-243) Immunoglobulin (variable domains of L
and H chains) {Anti-ampicillin scFv, (mouse), kappa L chain}
QVQLQESGGELVRPGASVKLSCKASGYTFTSYWINWVKQRPGQGLEWIGNIYPSDSYTNYNQKFK
DKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARWGYWGQGTLVTVSA
>d1i7za1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab GNC92H2, (mouse/human chimera), kappa L chain}
DLVLTQSPASLAVSLGQRATISCRASKSVSTSGYNYMHWYQQKPGQPPKLLIYLASNLASGVPAR
FSGSGSGTDFTLNIHPVEEEDAATYYCLYSREFPPWTFGGGTKLEIK
>d1i7zb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and
H chains) {Fab GNC92H2, (mouse/human chimera), kappa L chain}
QVQLQQSGPELKKPGETVKISCKTSGYSFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTYADDFR
GRFAFSLATSASTAYLQIINLKNEDTATYFCETYDSPLGDYWGQGTTVTVSS
>d1iqda1 b.1.1.1 (A:2-108) Immunoglobulin (variable domains of L and
H chains) {Fab BO2C11 against the C2 domain of factor VIII, (human),

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kappa L chain}
IALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQKPGQAPRLLIYGASTRATGIPDRFSGS
GSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFGQGTRLEIK
>d1iqdb1 b.1.1.1 (B:1-114) Immunoglobulin (variable domains of L and
H chains) {Fab BO2C11 against the C2 domain of factor VIII, (human),
kappa L chain}
QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVRQAPGKGLEWVGSFDPESGESIYAREFQ
GSVTMTADTSTNIAYMELSSLRSDDTAVYYCAVPDPDAFDIWGQGTMVTVSS
>d1fn4a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab 198 against actylcholine receptor, (rat)}
DIKLTQSPSLLSASVGDRVTLSCKGSQNINNYLAWYQQKLGEAPKLLIYNTNSLQTGIPSRFSGS
GSGTDYTLTISSLQPEDVATYFCYQYNNGYTFGAGTKLELKR
>d1fn4b1 b.1.1.1 (B:1-106) Immunoglobulin (variable domains of L and
H chains) {Fab 198 against actylcholine receptor, (rat)}
QVQLLESGPGLVRPSETLSLTCTVSGFSLTSFSVSWVRHPSGKGPEWMGRMWYDGYTAYNSALKS
RLSISRDTSKNQVFLKMNSLQTDDTGTYYCTRDLYGGYPLGFWYFDFWGPG
>d1jglh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Anti-estradiol Fab 57-2, (mouse), kappa L chain}
QIQLVQSGPELKKPGETVRISCKASDYSFMTSGMQWVQQMPGKGLKWIGWLNTQSGVPEYAEDFK
GRFAFSLETSATTAYLQINNLKNEDTATYFCATWGGNSAYWGQGTTLTVSS
>d1jp5a1 b.1.1.1 (A:1-112) Immunoglobulin (variable domains of L and
H chains) {scFv 1695, (mouse), kappa L chain}
DILMTQTPLYLPVSLGDQASISCRSSQTIVHNNGNTYLEWYLQKPGQSPQLLIYKVSNRFSGVPD
RFSGSGSGTDFTLKISRVEAEDLGIYYCFQGSHFPPTFGGGTKLEIK
>d1jp5a2 b.1.1.1 (A:128-247) Immunoglobulin (variable domains of L
and H chains) {scFv 1695, (mouse), kappa L chain}
EVQLQQSGPELKKPGETVKISCKATNYAFTDYSMHWVKQAPGGDLKYVGWINTETDEPTFADDFK
GRFAFSLDTSTSTAFLQINNLKNEDTATYFCVRDRHDYGEIFTYWGQGTTVTVSS
>d1fl5b1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and
H chains) {Sulfide oxidase catalytic Fab 28b4 germline precursor,
(mouse/human?), kappa L chain}
QVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMSWVRQPPGKALEWLGFIRNKANGYTTEYSAS
VKGRFTISRDNSQSILYLQMNTLRAEDSATYYCARDGSYAMDYWGQGTSVTVSS
>d1k4ca1 b.1.1.1 (A:1-118) Immunoglobulin (variable domains of L and
H chains) {Fab against potassium channel KcsA, (mouse), kappa L chain}
QVQLQQPGAELVKPGASVKLSCKASGYTFTSDWIHWVKQRPGHGLEWIGEIIPSYGRANYNEKIQ
KKATLTADKSSSTAFMQLSSLTSEDSAVYYCARERGDGYFAVWGAGTTVTVSS
>d1k4cb1 b.1.1.1 (B:1-107) Immunoglobulin (variable domains of L and
H chains) {Fab against potassium channel KcsA, (mouse), kappa L chain}
DILLTQSPAILSVSPGERVSFSCRASQSIGTDIHWYQQRTNGSPRLLIKYASESISGIPSRFSGS
GSGTDFTLSINSVESEDIANYYCQQSNRWPFTFGSGTKLEIK
>d1jguh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and
H chains) {Catalytic Fab 1D4, (mouse), kappa L chain}
EVKLVESRGGLVKPGGSLQLSCAASGFTFSGYAMSWFRLTPEKRLEWVASIYNGFRIHYLDSVKG
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RFTISSDYARNILYLQMSTLRSEDTAMYYCSRGDAYSRYFDVWGAGTTVTVSA
>d1jgul1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Catalytic Fab 1D4, (mouse), kappa L chain}
EVVMTQSPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPD
RFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK
>d1i8ma1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and
H chains) {Anti ssDNA Fab, (mouse), kappa L chain}
ELQMTQSPASLSASVGETVTITCRASENIYSYLAWYQQKQGKSPQLLVYNAKTLAEGVPSRFSGS
GSGTQFSLKINSLQPEDFGSYYCQHHYGTPLTFGAGTKLELK
>d1i8mb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and
H chains) {Anti ssDNA Fab, (mouse), kappa L chain}
QVKLLESGPELVKPGASVKMSCKASGYTFTSYVMHWVKQKPGQGLEWIGYINPYNDGTKYNEKFK
GKATLTSDKSSSTAYMELSSLTSEDSAVYYCVRGGYRPYYAMDYWGQGTSVTVSS
>d1jv5b_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H
chains) {Anti-blood group A Fv, (human), kappa L chain}
QVQLQQPGAELVKPGTSVKLSCKASGYNFTSYWINWVKLRPGQGLEWIGDIYPGSGITNYNEKFK
SKATLTVDTSSSTAYMQLSSLASEDSALYYCAGQYGNLWFAYWGQGTLVTVS
>d1iqwh1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and
H chains) {Anti-human Fas Fab hfe7a, (mouse), kappa L chain}
QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMQWVKQRPGQGLEWIGEIDPSDSYTNYNQKFK
GKATLTVDTSSSTAYMQLSSLTSEDSAVYYCARNRDYSNNWYFDVWGTGTTVTVSS
>d1iqwl1 b.1.1.1 (L:1-111) Immunoglobulin (variable domains of L and
H chains) {Anti-human Fas Fab hfe7a, (mouse), kappa L chain}
DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLESGIPAR
FSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPRTFGGGTKLEIK
>d1jnha1 b.1.1.1 (A:1-108) Immunoglobulin (variable domains of L and
H chains) {Anti-estradiol Fab 10G6D6, (mouse), lambda L chain}
QAVVTQESALTTSPGETVTLTCRSSSGAITTSHYANWIQEKPDHLFTGLISGTNNRAPGVPARFS
GSLIGDKAALTITGAQTEDEAIYICALWFSNQFIFGSGTKVTV
>d1jnhb1 b.1.1.1 (B:1-117) Immunoglobulin (variable domains of L and
H chains) {Anti-estradiol Fab 10G6D6, (mouse), lambda L chain}
EVQLQQSGAELARPGASVKLSCRTSGYSFTTYWMQWVRQRPGQGLEWIAAIYPGDDDARYTQKFK
GKATLTADRSSSIVYLQLNSLTSEDSAVYSCSRGRSLYYTMDYWGQGTSVTV
>d1jnlh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and
H chains) {Anti-estradiol Fab 17E12E5, (mouse), kappa L chain}
EVQLQQSGAELVKPGASVRLSCSASGFNIKDTYMFWVKQRPEQGLDWIGRINPANGISKYDPRFQ
GKATLTADTSSNTAYLQLDNLTSEDTAVYYCAIEKDLPWGQGTLVTVSV
>d1jnll1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and
H chains) {Anti-estradiol Fab 17E12E5, (mouse), kappa L chain}
QIVMTQTPASLSASVGETVTITCRASGNIYNYLAWYQQKQGKSPQLLVYNAKTLVDGVPLRFSGS
GSGTQYSLKINSLQPEDFGNYYCHHFWNTPYTFGGGTKLEIK
>d1vhp__ b.1.1.1 (-) Immunoglobulin (variable domains of L and H chains)
{VH-P8 domain (human), camelized monomer}
EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKEREIVSAVSGSGGSTYYADSVK
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GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLKKYAFDYWGQGTLVTVSS
>d1jtpa_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H
chains) {Camel (Camelus dromedarius), anti-lysozyme antibody}
DVQLQASGGGSVQAGGSLRLSCAASGYTIGPYCMGWFRQAPGKEREGVAAINMGGGITYYADSVK
GRFTISQDNAKNTVYLLMNSLEPEDTAIYYCAADSTIYASYYECGHGLSTGGYGYDSWGQGTQVT
VSSRR
>d1bzqk_ b.1.1.1 (K:) Immunoglobulin (variable domains of L and H
chains) {Camel (Camelus dromedarius), anti-RNase A antibody}
QVQLVESGGGLVQAGGSLRLSCAASGYAYTYIYMGWFRQAPGKEREGVAAMDSGGGGTLYADSVK
GRFTISRDKGKNTVYLQMDSLKPEDTATYYCAAGGYELRDRTYGQWGQGTQVTVSSRGR
>d1f2xk_ b.1.1.1 (K:) Immunoglobulin (variable domains of L and H
chains) {Camel (Camelus dromedarius), antibody cab-ca05}
QVQLVESGGGSVQAGGSLRLSCAASGYTVSTYCMGWFRQAPGKEREGVATILGGSTYYGDSVKGR
FTISQDNAKNTVYLQMNSLKPEDTAIYYCAGSTVASTGWCSRLRPYDYHYRGQGTQVTVSS
>d1hcv__ b.1.1.1 (-) Immunoglobulin (variable domains of L and H chains)
{Llama (Lama glama), anti-gonadotropin alpha subunit VH domain}
VQLQESGGGLVQAGGSLRLSCAASGRTGSTYDMGWFRQAPGKERESVAAINWDSARTYYASSVRG
RFTISRDNAKKTVYLQMNSLKPEDTAVYTCGAGEGGTWDSWGQGTQVTVSS
>d1qd0a_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H
chains) {Llama (Lama glama), anti-RR6 VH domain}
QVQLQESGGGLVQAGGSLRLSCAASGRAASGHGHYGMGWFRQVPGKEREFVAAIRWSGKETWYKD
SVKGRFTISRDNAKTTVYLQMNSLKGEDTAVYYCAARPVRVADISLPVGFDYWGQGTQVTVSS
>d1i3ua_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H
chains) {Llama (Lama glama), the dye RR1-binding VHh domain}
VQLQESGGGLVQAGDSLKLSCEASGDSIGTYVIGWFRQAPGKERIYLATIGRNLVGPSDFYTRYA
DSVKGRFAVSRDNAKNTVNLQMNSLKPEDTAVYYCAAKTTTWGGNDPNNWNYWGQGTQVTV
>d1ivla_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H
chains) {VL domain (kappa) of antibody M29B, dimer synthetic}
DIELTQSPATLSVTPGNSVSISCRASQSIGNRLFWYQQKSHESPRLLIKYASQSISGIPSRFSGS
GSGTDFTLSINSVETEDLAVYFCQQVSEWPFTFGGGTKLEIK
>d1bwwa_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H
chains) {Bence-Jones VL (kappa) dimer REI (human)}
TPDIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQKPGKAPKLLIYEASNLQAGVPSRFS
GSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKLQIT
>d2rhe__ b.1.1.1 (-) Immunoglobulin (variable domains of L and H chains)
{Bence-Jones VL (lambda) dimer RHE (human)}
ESVLTQPPSASGTPGQRVTISCTGSATDIGSNSVIWYQQVPGKAPKLLIYYNDLLPSGVSDRFSA
SKSGTSASLAISGLESEDEADYYCAAWNDSLDEPGFGGGTKLTVLGQPK
>d1bjma1 b.1.1.1 (A:1-111) Immunoglobulin (variable domains of L and
H chains) {Bence-Jones lambda L chain dimer LOC (human)}
ESVLTQPPSASGTPGQRVTISCSGSSSNIGENSVTWYQHLSGTAPKLLIYEDNSRASGVSDRFSA
SKSGTSASLAISGLQPEDETDYYCAAWDDSLDVAVFGTGTKVTVLG
>d1wtla_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H
chains) {Bence-Jones VL (kappa) dimer WAT (human)}
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DIQMTQSPSSLSASVGDRVTITCRASQDITNYVNWFQQRPGQAPKVLIYGASILETGVPSRFSGS
GSGTDFTFTISSLQPEDIATYYCQQYDTLPLTFGGGTKVDIKR
>d1b0wa_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H
chains) {Bence-Jones VL (kappa) dimer BRE (human)}
DIQMTQSPSSLSASVGDRVTITCQASQDISDYLIWYQQKLGKAPNLLIYDASTLETGVPSRFSGS
GSGTEYTFTISSLQPEDIATYYCQQYDDLPYTFGQGTKVEIKR
>d1eeqa_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H
chains) {Bence-Jones VL (kappa) domain LEN (human)}
DIVLTQSPDSLAVSLGERATINCKSSQSVLDSSNSKNYLAWYQQKPGQPPKLLIYWASTRESGVP
DRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSHPYSFGQGTKLEIK
>d1lila1 b.1.1.1 (A:2-107) Immunoglobulin (variable domains of L and
H chains) {Bence-Jones lambda L chain dimer CLE (human)}
YEVTQPPSLSVSPGQTARITCSGEKLGDAYVCWYQQRPGQSPVVVIYQDNRRPSGIPERFSGSSS
GNTATLTISGTQTLDEADYYCQVWDSNASVVFGGGTKLTVLG
>d1cd0a_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H
chains) {Bence-Jones VL (lambda) dimer JTO (human)}
NFMLNQPHSVSESPGKTVTISCTRSSGNIDSNYVQWYQQRPGSAPITVIYEDNQRPSGVPDRFAG
SIDRSSNSASLTISGLKTEDEADYYCQSYDARNVVFGGGTRLTVLG
>d2cd0a_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H
chains) {Bence-Jones VL (lambda) dimer WIL (human)}
NFLLTQPHSVSESPGKTVTISCTRSSGSIANNYVHWYQQRPGSSPTTVIFEDDHRPSGVPDRFSG
SVDTSSNSASLTISGLKTEDEADYYCQSYDHNNQVFGGGTKLTVLG
>d1b6da1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and
H chains) {Bence-Jones kappa L chain DEL (human)}
DIQMTQSPSSLSASVGDRVTITCQASQDISSYLNWYQQKPGKAPKLLIHAASSLETGVPSRFSGS
GSGTDFSFTISSLQPEDLATYYCQQYDSLPLTFGGGTKVEIK
>d1ek3a_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H
chains) {Kappa-4 VL REC (human)}
DIVMTQSPDSLAVSPGERATINCKSSQNLLDSSFDTNTLAWYQQKPGQPPKLLIYWASSRESGVP
DRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPPTFGGGTKVEIKR
>d1mcoh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and
H chains) {Intact antibody (lambda) MCG (human)}
PLVLQESGPGLVKPSEALSLTCTVSGDSINTILYYWSWIRQPPGKGLEWIGYIYYSGSTYGNPSL
KSRVTISVNTSKNQFYSKLSSVTAADTAVYYCARVPLVVNPWGQGTLVTVSS
>d1dcla1 b.1.1.1 (A:1-111) Immunoglobulin (variable domains of L and
H chains) {Lambda L chain dimer MCG (human)}
PSALTQPPSASGSLGQSVTISCTGTSSNVGGYNYVSWYQQHAGKAPKVIIYEVNKRPSGVPDRFS
GSKSGNTASLTVSGLQAEDEADYYCSSYEGSDNFVFGTGTKVTVLG
>d1mcww1 b.1.1.1 (W:1-111) Immunoglobulin (variable domains of L and
H chains) {Heterologous L chain dimer MCG-WEIR hybrid (human)}
ESALTQPASVSGSPGQSITVSCAGHTSDVADSNSISWFQQHPDKAPKLLIYAVTFRPSGIPLRFS
GSKSGNTASLTISGLLPDDEADYFCMSYLSDASFVFGSGTKVTVLR
>d1ac6a_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus),
alpha-chain}
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DSVTQTEGQVALSEEDFLTIHCNYSASGYPALFWYVQYPGEGPQFLFRASRDKEKGSSRGFEATY
NKEATSFHLQKASVQESDSAVYYCALSGGNNKLTFGAGTKLTIKP
>d1b88a_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus),
alpha-chain}
MQQVRQSPQSLTVWEGETAILNCSYENSAFDYFPWYQQFPGEGPALLISILSVSNKKEDGRFTIF
FNKREKKLSLHIADSQPGDSATYFCAASASFGDNSKLIWGLGTSLVVNP
>d1d9ka_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus),
alpha-chain}
QVRQSPQSLTVWEGETTILNCSYEDSTFDYFPWYRQFPGKSPALLIAISLVSNKKEDGRFTIFFN
KREKKLSLHITDSQPGDSATYFCAATGSFNKLTFGAGTRLAVSPY
>d1fo0a_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus),
alpha-chain}
KVTQTQTSISVMEKTTVTMDCVYETQDSSYFLFWYKQTASGEIVFLIRQDSYKKENATVGHYSLN
FQKPKSSIGLIITATQIEDSAVYFCAMRGDYGGSGNKLIFGTGTLLSVKP
>d1h5ba_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus),
alpha-chain}
GDQVEQSPSALSLHEGTDSALRCNFTTTMRSVQWFRQNSRGSLISLFYLASGTKENGRLKSAFDS
ERARYSTLHIRDAQLEDSGTYFCAAEASSGSWQLIFGSGTQLTVMPVT
>d1i9ea_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus),
alpha-chain}
QSVTQPDARVTVSEGASLQLRCKYSYSATPYLFWYVQYPRQGLQLLLKYYSGDPVVQGVNGFEAE
FSKSNSSFHLRKASVHWSDSAVYFCAVSGFASALTFGSGTKVIVLPYIQN
>d1kb5a_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus),
alpha-chain}
QQVRQSPQSLTVWEGETAILNCSYEDSTFNYFPWYQQFPGEGPALLISIRSVSDKKEDGRFTIFF
NKREKKLSLHITDSQPGDSATYFCAARYQGGRALIFGTGTTVSVSPGSAD
>d1nfda1 b.1.1.1 (A:1-117) T-cell antigen receptor {Mouse (Mus
musculus), alpha-chain}
DSVTQTEGLVTVTEGLPVKLNCTYQTTYLTIAFFWYVQYLNEAPQVLLKSSTDNKRTEHQGFHAT
LHKSSSSFHLQKSSAQLSDSALYYCALSEGGNYKYVFGAGTRLKVIAH
>d1bd2d1 b.1.1.1 (D:1-117) T-cell antigen receptor {Human (Homo
sapiens), alpha-chain}
QQVKQNSPSLSVQEGRISILNCDYTNSMFDYFLWYKKYPAEGPTFLISISSIKDKNADGRFTVFL
NKSAKHLSLHIVPSQPGDSAVYFCAAMEGAQKLVFGQGTRLTINPN
>d1fytd1 b.1.1.1 (D:1-117) T-cell antigen receptor {Human (Homo
sapiens), alpha-chain}
QSVTQLGSHVSVSEGALVLLRCNYSSSVPPYLFWYVQYPNQGLQLLLKYTSAATLVKGINGFEAE
FKKSETSFHLTKPSAHMSDAAEYFCAVSESPFGNEKLTFGTGTRLTIIPN
>d1qrnd1 b.1.1.1 (D:1-117) T-cell antigen receptor {Human (Homo
sapiens), alpha-chain}
KEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMSIYSNGDKEDGRFTAQLN
KASQYVSLLIRDSQPSDSATYLCAVTTDSWGKLQFGAGTQVVVTPD
>d1bec_1 b.1.1.1 (3-117) T-cell antigen receptor {Mouse (Mus musculus),
beta-chain}
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AVTQSPRNKVAVTGGKVTLSCQQTNNHNNMYWYRQDTGHGLRLIHYSYGAGSTEKGDIPDGYKAS
RPSQEQFSLILELATPSQTSVYFCASGGGRGSYAEQFFGPGTRLTVLE
>d1fo0b_ b.1.1.1 (B:) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}
VTLLEQNPRWRLVPRGQAVNLRCILKNSQYPWMSWYQQDLQKQLQWLFTLRSPGDKEVKSLPGAD
YLATRVTDTELRLQVANMSQGRTLYCTCSADRVGNTLYFGEGSRLIV
>d1kb5b_ b.1.1.1 (B:) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}
VTLLEQNPRWRLVPRGQAVNLRCILKNSQYPWMSWYQQDLQKQLQWLFTLRSPGDKEVKSLPGAD
YLATRVTDTELRLQVANMSQGRTLYCTCSAAPDWGASAETLYFGSGTRLTVL
>d1nfdb1 b.1.1.1 (B:1-117) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}
DSGVVQSPRHIIKEKGGRSVLTCIPISGHSNVVWYQQTLGKELKFLIQHYEKVERDKGFLPSRFS
VQQFDDYHSEMNMSALELEDSAMYFCASSLRWGDEQYFGPGTRLTVLE
>d1tcrb1 b.1.1.1 (B:1-117) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}
EAAVTQSPRNKVAVTGGKVTLSCNQTNNHNNMYWYRQDTGHGLRLIHYSYGAGSTEKGDIPDGYK
ASRPSQENFSLILELATPSQTSVYFCASGGGGTLYFGAGTRLSVLE
>d1bd2e1 b.1.1.1 (E:3-118) T-cell antigen receptor {Human (Homo sapiens), beta-chain}
GVTQTPKFQVLKTGQSMTLQCAQDMNHEYMSWYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVS
RSTTEDFPLRLLSAAPSQTSVYFCASSYPGGGFYEQYFGPGTRLTVTE
>d1fyte1 b.1.1.1 (E:3-118) T-cell antigen receptor {Human (Homo sapiens), beta-chain}
KVTQSSRYLVKRTGEKVFLECVQDMDHENMFWYRQDPGLGLRLIYFSYDVKMKEKGDIPEGYSVS
REKKERFSLILESASTNQTSMYLCASSSTGLPYGYTFGSGTRLTVVE
>d1hxma1 b.1.1.1 (A:1-120) T-cell antigen receptor {Human (Homo sapiens), gamma-chain}
AIELVPEHQTVPVSIGVPATLRCSMKGEAIGNYYINWYRKTQGNTMTFIYREKDIYGPGFKDNFQ
GDIDIAKNLAVLKILAPSERDEGSYYCACDTLGMGGEYTDKLIFGKGTRVTVEPR
>d1hxmb1 b.1.1.1 (B:1-123) T-cell antigen receptor {Human (Homo sapiens), delta-chain}
AGHLEQPQISSTKTLSKTARLECVVSGITISATSVYWYRERPGEVIQFLVSISYDGTVRKESGIP
SGKFEVDRIPETSTSTLTIHNVEKQDIATYYCALWEAQQELGKKIKVFGPGTKLIITD
>d1tvda_ b.1.1.1 (A:) T-cell antigen receptor {Human (Homo sapiens), delta-chain}
DKVTQSSPDQTVASGSEVVLLCTYDTVYSNPDLFWYRIRPDYSFQFVFYGDDSRSEGADFTQGRF
SVKHILTQKAFHLVISPVRTEDSATYYCAFTLPPPTDKLIFGKGTRVTVEP
>d1ah1__ b.1.1.1 (-) Immunoreceptor CTLA-4 (CD152), N-terminal fragment {Human (Homo sapiens)}
AMHVAQPAVVLASSRGIASFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELTFLDDS
ICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPPPYYLGIGNGTQIYVIDPEPCPDSDQEPK
>d1i8lc_ b.1.1.1 (C:) Immunoreceptor CTLA-4 (CD152), N-terminal fragment {Human (Homo sapiens)}
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MHVAQPAVVLASSRGIASFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELTFLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPPPYYLGIGNGAQIYVIDPE

>d1dqta_ b.1.1.1 (A:) Immunoreceptor CTLA-4 (CD152), N-terminal fragment {Mouse (Mus musculus)}

IQVTQPSVVLASSHGVASFPCEYSPSHNTDEVRVTVLRQTNDQMTEVCATTFTEKNTVGFLDYPFCSGTFNESRVNLTIQGLRAVDTGLYLCKVELMYPPPYFVGMGNGTQIYVIDP

>d3frua1 b.1.1.2 (A:179-269) Fc (IgG) receptor, alpha-3 domain and beta subunit {Rat (Rattus norvegicus)}

KEPPSMRLKARPGNSGSSVLTCAAFSFYPPELKFRFLRNGLASGSGNCSTGPNGDGSFHAWSLLEVKRGDEHHYQCQVEHEGLAQPLTVDL

>d3frub1 b.1.1.2 (B:) Fc (IgG) receptor, alpha-3 domain and beta subunit {Rat (Rattus norvegicus)}

IQKTPQIQVYSRHPPENGKPNFLNCYVSQFHPPQIEIELLKNGKKIPNIEMSDLSFSKDWSFYILAHTEFTPTETDVYACRVKHVTLKEPKTVTWDRDM

>d1bmg__ b.1.1.2 (-) Class I MHC, beta2-microglobulin and alpha-3 domain {Cow (Bos taurus)}

IQRPPKIQVYSRHPPEDGKPNYLNCYVYGFHPPQIEIDLLKNGEKIKSEQSDLSFSKDWSFYLLSHAEFTPNSKDQYSCRVKHVTLEQPRIVKWDRDL

>d1i4fa1 b.1.1.2 (A:182-275) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), HLA-A2.1}

TDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTELVETRPAGDGTFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLRWE

>d1i4fb1 b.1.1.2 (B:) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), HLA-A2.1}

MIQRTPKIQVYSRHPAENGKSNFLNCYVSGFHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSQPKIVKWDRDM

>d1agda1 b.1.1.2 (A:182-276) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), HLA-B0801}

ADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTELVETRPAGDRTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWEP

>d1qqda1 b.1.1.2 (A:182-274) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), HLA-CW4}

AEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLPEPLTLRW

>d1mhea1 b.1.1.2 (A:182-274) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), HLA-E}

LEPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQQDGEGHTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLPEPVTLRW

>d1de4a1 b.1.1.2 (A:182-275) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), hemochromatosis protein Hfe}

QQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIW

>d1fzka1 b.1.1.2 (A:182-274) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), H-2KB}

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TDSPKAHVTHHSRPEDKVTLRCWALGFYPADITLTWQLNGEELIQDMELVETRPAGDGTFQKWAS
VVVPLGKEQYYTCHVYHQGLPEPLTLRW
>d1fzkb1 b.1.1.2 (B:) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), H-2KB}
IQKTPQIQVYSRHPPENGKPNILNCYVTQFHPPHIEIQMLKNGKKIPKVEMSDMSFSKDWSFYIL
AHTEFTPTETDTYACRVKHDSMAEPKTVYWDRDM
>d1jpfa1 b.1.1.2 (A:182-276) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), H-2DB}
TDSPKAHVTHHPRSKGEVTLRCWALGFYPADITLTWQLNGEELTQDMELVETRPAGDGTFQKWAS
VVVPLGKEQNYTCRVYHEGLPEPLTLRWEP
>d1mhca1 b.1.1.2 (A:182-276) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), H-2M3}
ADPPKAHVAHHPRPKGDVTLRCWALGFYPADITLTWQKDEEDLTQDMELVETRPSGDGTFQKWAA
VVVPSGEEQRYTCYVHHEGLTEPLALKWRS
>d1qo3a1 b.1.1.2 (A:182-275) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), H-2DD}
TDPPKAHVTHHRRPEGDVTLRCWALGFYPADITLTWQLNGEELTQEMELVETRPAGDGTFQKWAS
VVVPLGKEQKYTCHVEHEGLPEPLTLRWG
>d1k8da1 b.1.1.2 (A:182-274) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), IB QA-2}
TDPPKAHVTHHPRSYGAVTLRCWALGFYPADITLTWQLNGEELTQDMELVETRPAGDGTFQKWAS
VVVPLGKEQNYTCHVNHEGLPEPLTLRW
>d1ed3a1 b.1.1.2 (A:182-275) Class I MHC, beta2-microglobulin and alpha-3 domain {Rat (Rattus norvegicus), RT1-AA}
SDPPEAHVTLHPRPEGDVTLRCWALGFYPADITLTWQLNGEDLTQDMELVETRPAGDGTFQKWAS
VVVPLGKEQNYTCRVEHEGLPKPLSQRWE
>d1zaga1 b.1.1.2 (A:184-277) Zinc-alpha-2-glycoprotein, ZAG {Human (Homo sapiens)}
QDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAGEVQEPELRGDVLHNGNGTYQSWVVV
AVPPQDTAPYSCHVQHSSLAQPLVVPWEA
>d1hyrc1 b.1.1.2 (C:181-274) MHC I homolog {Human (Homo sapiens), Mic-a}
TVPPMVNVTRSEASEGNITVTCRASGFYPWNITLSWRQDGVSLSHDTQQWGDVLPDGNGTYQTWV
ATRICQGEEQRFTCYMEHSGNHSTHPVPS
>d1c16a1 b.1.1.2 (A:181-276) MHC I homolog {Mouse (Mus musculus), t22}
RSDPPKAHVTRHPRPEGDVTLRCWALGFYPADITLTWQLNGEELTQDMELVETRPAGDGTFQKWA
AVVVPLGKEQSYTCHVYHEGLPEPLILRWGG
>d1exua1 b.1.1.2 (A:177-267) MHC-related Fc receptor {Human (Homo sapiens)}
KEPPSMRLKARPSSPGFSVLTCSAFSFYPPELQLRFLRNGLAAGTGQGDFGPNSDGSFHASSSLT
VKSGDEHHYCCIVQHAGLAQPLRVEL
>d1igtb3 b.1.1.2 (B:236-361) Immunoglobulin (constant domains of L and H chains) {Intact IgG2a antibody Mab231 (mouse), kappa L chain}
PCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTA
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QTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKG
>d1igtb4 b.1.1.2 (B:363-474) Immunoglobulin (constant domains of L
and H chains) {Intact IgG2a antibody Mab231 (mouse), kappa L chain}
SVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFM
YSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSR
>d1igyb3 b.1.1.2 (B:236-361) Immunoglobulin (constant domains of L
and H chains) {Intact IgG1 antibody Mab61.1.3 (mouse), kappa L chain}
GCKPCICTVPEVSSVFIFPPKPKDTLLITVTPKVTCVVVDISKDDPEVQFSWFVDNVEVHTAQTQ
PREEQFNSTFRVVSALPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKG
>d1igyb4 b.1.1.2 (B:363-474) Immunoglobulin (constant domains of L
and H chains) {Intact IgG1 antibody Mab61.1.3 (mouse), kappa L chain}
KPRAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQSDGQAPENYKNTQPIMDTDGSYFV
YSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSH
>d1hzhh3 b.1.1.2 (H:236-359) Immunoglobulin (constant domains of L
and H chains) {Intact IgG B12 antibody (human), kappa L chain}
THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
>d8faba2 b.1.1.2 (A:106-208) Immunoglobulin (constant domains of L
and H chains) {Fab HIL (human), lambda L chain}
LGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPIKAGVETTTPSKQSNN
KYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAP
>d1dn0b2 b.1.1.2 (B:121-225) Immunoglobulin (constant domains of L
and H chains) {Fab Kau cold agglutinin (human) IgM, kappa L chain}
GSASAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGGKY
AATSQVLLPSKDVMAGTDEHVVCKVQHPNGNKEKNVPLPV
>d2fb4l2 b.1.1.2 (L:110-214) Immunoglobulin (constant domains of L
and H chains) {Fab KOL (human), lambda L chain}
QPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKY
AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
>d2ig2h2 b.1.1.2 (H:120-231) Immunoglobulin (constant domains of L
and H chains) {Fab KOL (human), lambda L chain}
STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPQPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS
SVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP
>d2fbjh2 b.1.1.2 (H:119-220) Immunoglobulin (constant domains of L
and H chains) {Fab J539 (mouse), kappa L chain}
ESARNPTIYPLTLPPALSSDPVIIGCLIHDYFPSGTMNVTWGKSGKDITTVNFPPALASGGRYTM
SNQLTLPAVECPEGESVKCSVQHDSNPVQELDVNCSG
>d1mfbl2 b.1.1.2 (L:112-212) Immunoglobulin (constant domains of L
and H chains) {Fab SE155-4 (mouse), lambda L chain}
PKSSPSVTLFPPSSEELETNKATLVCTITDFYPGVVTVDWKVDGTPVTQGMETTQPSKQSNNKYM
ASSYLTLTARAWERHSSYSCQVTHEGHTVEKSLSRA
>d1teth2 b.1.1.2 (H:113-213) Immunoglobulin (constant domains of L
and H chains) {Fab TE33 (mouse), kappa L chain}
SAKTTPPSVYPLAPGSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTV
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PSSPRPSETVTCNVAHPASSTKVDKKIVPR
>d2jelh2 b.1.1.2 (H:114-226) Immunoglobulin (constant domains of L
and H chains) {Fab JE142 (mouse), kappa L chain}
AATTPPSVYPLAPGSGGQGNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLAADLYTLS
SSVTVPSSPRPSETVTCNVAHPASSTKVDKKIAPG
>d2jell2 b.1.1.2 (L:109-212) Immunoglobulin (constant domains of L
and H chains) {Fab JE142 (mouse), kappa L chain}
ADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIGDGARQNGVLNSWTDQDSKDSTY
SMSSTLTLTKDEYERHNSYTCEATHKTSDSPIVKSFNRN
>d1eapb2 b.1.1.2 (B:125-221) Immunoglobulin (constant domains of L
and H chains) {Fab 17E8 (mouse), kappa L chain}
AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGGLSSSVHTFPALLQSGLYTMS
SSVTVPGGGWPSATVTCSVAHPASSTTVDKKL
>d1yuhb2 b.1.1.2 (B:119-218) Immunoglobulin (constant domains of L
and H chains) {Fab anti-nitrophenol (mouse/human), lambda L chain}
AATTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGALSSGVHTFPAVLQSDLYTLS
SSVTVPASTWPSGTVTCNVAHPASSTAVDKKIVPR
>d1clzh2 b.1.1.2 (H:115-231) Immunoglobulin (constant domains of L
and H chains) {Fab MBR96 (mouse), kappa L chain}
TTTAPSVYPLVPGCSDTSGSSVTLGCLVKGYFPEPVTVKWNYGALSSGVRTVSSVLQSGFYSLSS
LVTVPSSTWPSQTVICNVAHPASKTELIKRIEPR
>d1nldh2 b.1.1.2 (H:113-215) Immunoglobulin (constant domains of L
and H chains) {Fab 1583, against an epitope of gp41 of HIV-1, (mouse),
kappa L chain}
SASTTAPSVYPLAPVSGDQTNSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTL
SSSVTVTSSPWPSETITCNVAHPASSTKVDKKIEPRGC
>d1kelh2 b.1.1.2 (H:116-218) Immunoglobulin (constant domains of L
and H chains) {Fab 28B4 (mouse), kappa L chain}
TVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDL
YTLSSSVTVPSSPRPSETVTCNVAHPASSTKVDKKIVP
>d1osph2 b.1.1.2 (H:121-218) Immunoglobulin (constant domains of L
and H chains) {Fab 184.1 (mouse), kappa L chain}
AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSGLYTMS
SSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLE
>d1nfde2 b.1.1.2 (E:108-215) Immunoglobulin (constant domains of L
and H chains) {Fab H57 (hamster), lambda L chain}
GPKSSPKVTVFPPSPEELRTNKATLVCLVNDFYPGSATVTWKANGATINDGVKTTKPSKQGQNYM
TSSYLSLTADQWKSHNRVSCQVTHEGETVEKSLSPAECL
>d1nfdf2 b.1.1.2 (F:115-228) Immunoglobulin (constant domains of L
and H chains) {Fab H57 (hamster), lambda L chain}
TTTAPSVYPLAPACDSTTSTTDTVTLGCLVKGYFPEPVTVSWNSGALTSGVHTFPSVLHSGLYSL
SSSVTVPSSTWPKQPITCNVAHPASSTKVDKKIEPR
>d1aqkl2 b.1.1.2 (L:112-216) Immunoglobulin (constant domains of L
and H chains) {Fab B7-15A2 (human), lambda L chain}
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QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVNAGVETTKPSKQSNNKY
AASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPAECS
>d1a4kh2 b.1.1.2 (H:120-211) Immunoglobulin (constant domains of L
and H chains) {Diels alder catalytic Fab (mouse), kappa L chain}
SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV
PSSSLGTQTYICNVNHKPSNTKVDKKV
>d1c1eh2 b.1.1.2 (H:120-228) Immunoglobulin (constant domains of L
and H chains) {Diels alder catalytic Fab 1E9 (mouse), kappa L chain}
SVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVP
SSPRPSETVTCNVAHPASSTKVDKKIVPR
>d2hmic2 b.1.1.2 (C:108-214) Immunoglobulin (constant domains of L
and H chains) {Fab 28 against HIV-1 RT (mouse), kappa L chain}
RADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVAWAIDGSAAANGVLNSWTDQDSKDST
YSMSSTLTLTADEYEAANSYTCAATHKTSTSPIVKSFNANEC
>d1a5fh2 b.1.1.2 (H:121-217) Immunoglobulin (constant domains of L
and H chains) {Anti-E-selectin Fab (mouse), kappa L chain}
AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLS
SSVSVPTSTETVTCNVAHAPSSTKVDKKIVPR
>d1bfoa2 b.1.1.2 (A:108-214) Immunoglobulin (constant domains of L
and H chains) {CAMPATH-1G igg2b monoclonal fab (rat), kappa L chain}
RANAAPTVSIFPPSTEQLATGGASVVCLMNKFYPRDISVKWKIDGTERNGVLNSVTDQDSADSTY
SMSSTLSLTKADYQSHNLYTCQVVHKTSSSPVVAKNFNRNEC
>d1bogb2 b.1.1.2 (B:113-213) Immunoglobulin (constant domains of L
and H chains) {Anti-p24 (HIV-1) Fab CB 4-1 (mouse), kappa L chain}
AKTTAPSVYPLVPVCGGTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPALLQSGLYTLS
SSVTVTSNTWPSQTITCNVAHPASSTKVDKKIEPRV
>d1wejh2 b.1.1.2 (H:113-223) Immunoglobulin (constant domains of L
and H chains) {Anti-cytochrome c Fab E8, (mouse), kappa L chain}
LTVSSAETTPPSVYPLAPGTAALKSSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD
LYTLTSSVTVPSSTWPSQTVTCNVAHPASSTKVDKKIVPRNCGGDC
>d1sm3h2 b.1.1.2 (H:114-213) Immunoglobulin (constant domains of L
and H chains) {Tumor-specific Fab SM3, (mouse), lambda L chain}
AKTTPPTVYPLAPGSNAASQSMVTLGCLVKGYFPEPVTVTWNSGSLASGVHTFPAVLQSDLYTLS
SSVTVPSSTWPSETVTCNVAHPASSTKVDAKIVPR
>d1c12b2 b.1.1.2 (B:414-513) Immunoglobulin (constant domains of L
and H chains) {Fab directed agains the musk odorant traseolide, (mouse),
kappa L chain}
ASTKGPSVYPLAPGSKAAASMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSS
SVTVPSSPRPSETVTCNVAHPASSTKVDKKIVPE
>d1r24b2 b.1.1.2 (B:123-217) Immunoglobulin (constant domains of L
and H chains) {Fab R24, (mouse), kappa L chain}
ATTTAPSVYPLVPGCSDTSGSSVTLGCLVKGYFPGPVTVKWNYGALSSGVRTVSSVLQSGFYSLS
SLVTVPSSTWPSQTVICNVAHPASKTDLIK
>d1c5da2 b.1.1.2 (A:107-213) Immunoglobulin (constant domains of L
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and H chains) {Fab against the main immunogenic region of the human muscle acetylcholine receptor, (rat), kappa L chain}

RADAAPTVSIFPPSTEQLATGGASVVCLMNNFYPRDISVKWKIDGTERRDGVLDSVTDQDSKDSTYSMSSTLSLTKADYESHNLYTCEVVHKTSSSPVVKSFNRNEC

>d1c5db2 b.1.1.2 (B:118-215) Immunoglobulin (constant domains of L and H chains) {Fab against the main immunogenic region of the human muscle acetylcholine receptor, (rat), kappa L chain}

AQTTAPSVYPLAPGCGDTTSSTVTLGCLVKGYFPEPVTVTWNSGALSSDVHTFPAVLQSGLYTLTSSVTSSTWPSQTVTCNVAHPASSTKVDKKLERR

>d32c2b2 b.1.1.2 (B:120-218) Immunoglobulin (constant domains of L and H chains) {Fab 32C2 against P450-arom, (mouse), kappa L chain}

AKTTPPPVYPLVPGSLAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIEP

>d1deeb2 b.1.1.2 (B:622-723) Immunoglobulin (constant domains of L and H chains) {Fab of human IgM RF 2A2}

GSASAPTLFPLVSCENSNPSSTVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGGKYAATSQVLLPSKDVAQGTNEHVVCKVQHPNGNKEKDVPL

>d1f3dh2 b.1.1.2 (H:122-223) Immunoglobulin (constant domains of L and H chains) {Catalytic Fab 4B2, (mouse), kappa L chain}

AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDC

>d1fh5h2 b.1.1.2 (H:121-215) Immunoglobulin (constant domains of L and H chains) {Fab MAK33, (human), kappa L chain}

AKTTPPSVYPLAVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSETVTCNVAHPASSTKVDKKIVPR

>d1c5ch2 b.1.1.2 (H:114-230) Immunoglobulin (constant domains of L and H chains) {Decarboxylase catalytic Fab 21D8, chimeric (mouse V domains/human C1 domains)}

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC

>d1c5cl2 b.1.1.2 (L:108-214) Immunoglobulin (constant domains of L and H chains) {Decarboxylase catalytic Fab 21D8, chimeric (mouse V domains/human C1 domains)}

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>d1fe8h2 b.1.1.2 (H:116-216) Immunoglobulin (constant domains of L and H chains) {Fab RU5, (mouse), kappa L chain}

AETTAPSVYKLEPVSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG

>d1iqdb2 b.1.1.2 (B:115-212) Immunoglobulin (constant domains of L and H chains) {Fab BO2C11 against the C2 domain of factor VIII, (human), kappa L chain}

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTATYTCNVDHKPSNTKVDKRV

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>d1fn4b2 b.1.1.2 (B:107-208) Immunoglobulin (constant domains of L
and H chains) {Fab 198 against actylcholine receptor, (rat)}
TMVTVSSVFPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGALSSGVHTFPAVLQSGLYTLT
SSVTVPSSTWSSQAVTCNVAHPASSTKVDKKIVPRDC
>d1jguh2 b.1.1.2 (H:114-212) Immunoglobulin (constant domains of L
and H chains) {Catalytic Fab 1D4, (mouse), kappa L chain}
AKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLS
SSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEP
>d1jgul2 b.1.1.2 (L:108-214) Immunoglobulin (constant domains of L
and H chains) {Catalytic Fab 1D4, (mouse), kappa L chain}
RADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDST
YSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
>d1mcoh2 b.1.1.2 (H:118-219) Immunoglobulin (constant domains of L
and H chains) {Intact antibody (lambda) MCG (human)}
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPQPVTVSWNSGALTSGVHTFPAVLQSSGLYSL
SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVAPEL
>d1adqa1 b.1.1.2 (A:238-341) Immunoglobulin (constant domains of L
and H chains) {Fc (human) IgG1 class}
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPQVQFNWYVDGVQVHNAKTKPREQQFNSTYRV
VSVLTVLHQNWLDGKEYKCKVSNKGLPSSIEKTISKAKG
>d1dn2a1 b.1.1.2 (A:237-341) Immunoglobulin (constant domains of L
and H chains) {Fc (human) IgG1 class}
GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHENPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
>d1dn2a2 b.1.1.2 (A:342-443) Immunoglobulin (constant domains of L
and H chains) {Fc (human) IgG1 class}
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
>d1fc2d1 b.1.1.2 (D:238-341) Immunoglobulin (constant domains of L
and H chains) {Fc (human) IgG1 class}
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPQVKFNWYVDGVQVHNAKTKPREQQYNSTYRV
VSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKAKG
>d1fp5a1 b.1.1.2 (A:336-438) Immunoglobulin (constant domains of L
and H chains) {Fc (human) IgE}
VSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVT
STLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSG
>d1fp5a2 b.1.1.2 (A:439-543) Immunoglobulin (constant domains of L
and H chains) {Fc (human) IgE}
PRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGF
FVFSRLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSV
>d1i1ca1 b.1.1.2 (A:239-341) Immunoglobulin (constant domains of L
and H chains) {Fc (rat) IgG}
SVFIFPPKTKDVLGGGLTPKVTCVVVDISQNDPEVRFSWFIDDVEVHTAQTHAPEKQSNSTLRSV
SELPIVERDWLNGKTFKCKVNSGAFPAPIEKSISKPEG
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>d1i1ca2 b.1.1.2 (A:342-443) Immunoglobulin (constant domains of L
and H chains) {Fc (rat) IgG}
TPRGPQVYTMAPPKEEMTQSQVSITCMVKGFYPPDIYTEWKMNGQPQENYKNTPPTMDTDGSYFL
YSKLNVKKETWQQGNTFTCSVLHEGLENEHTEKSLSH
>d1pfc__ b.1.1.2 (-) Immunoglobulin (constant domains of L and H chains)
{Fc (guinea pig)}
RTISKAKGPPRIPEVYLLPPPRNELSKKKVSLTCMITGFYPADINVEWDSSEPSDYKNTPPVFDT
DGSFFLYSRLKVDTDAWNNGESFTCSVMHEALPNHVIQKSISRSPG
>d1cqka_ b.1.1.2 (A:) Immunoglobulin (constant domains of L and H
chains) {Fc MAK33 (mouse)}
PAAPQVYTIPPPLEQMAKDLVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVY
SKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSH
>d1g84a_ b.1.1.2 (A:) Immunoglobulin (constant domains of L and H
chains) {C epsilon2 domain from IgE (human)}
SRDFTPPTVKILQSSSDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE
LASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKSA
>d1tcra2 b.1.1.2 (A:118-213) T-cell antigen receptor {Mouse (Mus
musculus), alpha-chain}
IQNPEPAVYALKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDATVLDMKAMDSKSNGAIAWS
NQTSFTCQDIFKETNATYPSSDVPC
>d1bd2d2 b.1.1.2 (D:118-203) T-cell antigen receptor {Human (Homo
sapiens), alpha-chain}
IQNPDPAVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKDSDVYITDKTVLDMRSMDFKSNSAVAWS
NKSDFACANAFNNSIIPEDTF
>d1bec_2 b.1.1.2 (118-246) T-cell antigen receptor {Mouse (Mus
musculus), beta-chain}
DLRQVTPPKVSLFEPSKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVSTDPQAYKES
NYSYCLSSRLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVTQNISAEAWGRAD
>d1bd2e2 b.1.1.2 (E:119-247) T-cell antigen receptor {Human (Homo
sapiens), beta-chain}
DLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFYPDHVELSWWVNGKEVHSGVSTDPQPLKEQ
PALNDSRYALSSRLRVSATFWQDPRNHFRCQVQFYGLSENDEWTQDRAKPVTQIVSAEAWGRAD
>d1hxma2 b.1.1.2 (A:121-206) T-cell antigen receptor {Human (Homo
sapiens), gamma-chain}
SQPHTKPSVFVMKNGTNVACLVKEFYPKDIRINLVSSKKITEFDPAIVISPSGKYNAVKLGKYED
SNSVTCSVQHDNKTVHSTDFE
>d1hxmb2 b.1.1.2 (B:124-230) T-cell antigen receptor {Human (Homo
sapiens), delta-chain}
KQLDADVSPKPTIFLPSIAETKLQKAGTYLCLLEKFFPDVIKIHWEEKKSNTILGSQEGNTMKTN
DTYMKFSWLTVPEKSLDKEHRCIVRHENNKNGVDQEIIFPPI
>d1cd1a1 b.1.1.2 (A:186-279) CD1, beta2-microglobulin and alpha-3
domain {Mouse (Mus musculus)}
QEKPVAWLSSVPSSAHGHRQLVCHVSGFYPKPVWVMWMRGDQEQQGTHRGDFLPNADETWYLQAT
LDVEAGEEAGLACRVKHSSLGGQDIILYW
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>d1hdma1 b.1.1.2 (A:94-196) Class II MHC, C-terminal domains of alpha
and beta chains {Human (Homo sapiens), HLA-DM}
SRGFPIAEVFTLKPLEFGKPNTLVCFVSNLFPPMLTVNWHDHSVPVEGFGPTFVSAVDGLSFQAF
SYLNFTPEPSDIFSCIVTHEPDRYTAIAYWVPRNALPS
>d1hdmb1 b.1.1.2 (B:88-185) Class II MHC, C-terminal domains of alpha
and beta chains {Human (Homo sapiens), HLA-DM}
TRPPSVQVAKTTPFNTREPVMLACYVWGFYPAEVTITWRKNGKLVMHSSAHKTAQPNGDWTYQTL
SHLALTPSYGDTYTCVVEHIGAPEPILRDWTPG
>d1aqdb1 b.1.1.2 (B:93-190) Class II MHC, C-terminal domains of alpha
and beta chains {Human (Homo sapiens), HLA-DR1}
RRVEPKVTVYPSKTQPLQHHNLLVCSVSGFYPGSIEVRWFRNGQEEKAGVVSTGLIQNGDWTFQT
LVMLETVPRSGEVYTCQVEHPSVTSPLTVEWRA
>d1fv1a1 b.1.1.2 (A:82-181) Class II MHC, C-terminal domains of alpha
and beta chains {Human (Homo sapiens), HLA-DR2}
ITNVPPEVTVLTNSPVELREPNVLICFIDKFTPPVVNVTWLRNGKPVTTGVSETVFLPREDHLFR
KFHYLPFLPSTEDVYDCRVEHWGLDEPLLKHWEFD
>d1fv1b1 b.1.1.2 (B:93-190) Class II MHC, C-terminal domains of alpha
and beta chains {Human (Homo sapiens), HLA-DR2}
RRVEPKVTVYPARTQTLQHHNLLVCSVNGFYPGSIEVRWFRNSQEEKAGVVSTGLIQNGDWTFQT
LVMLETVPRSGEVYTCQVEHPSVTSPLTVEWRA
>d1d5zb1 b.1.1.2 (B:93-190) Class II MHC, C-terminal domains of alpha
and beta chains {Human (Homo sapiens), HLA-DR4}
RRVYPEVTVYPAKTQPLQHHNLLVCSVNGFYPGSIEVRWFRNGQEEKTGVVSTGLIQNGDWTFQT
LVMLETVPRSGEVYTCQVEHPSLTSPLTVEWRA
>d1jk8a1 b.1.1.2 (A:85-181) Class II MHC, C-terminal domains of alpha
and beta chains {Human (Homo sapiens), HLA-DQ8}
EVPEVTVFSKSPVTLGQPNTLICLVDNIFPPVVNITWLSNGHSVTEGVSETSFLSKSDHSFFKIS
YLTFLPSDDEIYDCKVEHWGLDEPLLKHWEPE
>d1jk8b1 b.1.1.2 (B:95-192) Class II MHC, C-terminal domains of alpha
and beta chains {Human (Homo sapiens), HLA-DQ8}
VEPTVTISPSRTEALNHHNLLVCSVTDFYPAQIKVRWFRNDQEETTGVVSTPLIRNGDWTFQILV
MLEMTPQRGDVYTCHVEHPSLQNPIIVEWRAQS
>d1iaka1 b.1.1.2 (A:82-181) Class II MHC, C-terminal domains of alpha
and beta chains {Mouse (Mus musculus), I-AK}
ATNEAPQATVFPKSPVLLGQPNTLICFVDNIFPPVINITWLRNSKSVTDGVYETSFFVNRDYSFH
KLSYLTFIPSDDDIYDCKVEHWGLEEPVLKHWEPE
>d1iakb1 b.1.1.2 (B:93-190) Class II MHC, C-terminal domains of alpha
and beta chains {Mouse (Mus musculus), I-AK}
RLEQPSVVISLSRTEALNHHNTLVCSVTDFYPAKIKVRWFRNGQEETVGVSSTQLIRNGDWTFQV
LVMLEMTPRRGEVYTCHVEHPSLTSPITVEWRA
>d1fnga1 b.1.1.2 (A:82-182) Class II MHC, C-terminal domains of alpha
and beta chains {Mouse (Mus musculus), I-EK}
DANVAPEVTVLSRSPVNLGEPNILICFIDKFSPPVVNVTWLRNGRPVTEGVSETVFLPRDDHLFR
KFHYLTFLPSTDDFYDCEVDHWGLEEPLRKHWEFEE
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>d1fngb1 b.1.1.2 (B:93-188) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-EK}
RRVEPTVTVYPTKTQPLEHHNLLVCSVSDFYPGNIEVRWFRNGKEEKTGIVSTGLVRNGDWTFQT
LVMLETVPQSGEVYTCQVEHPSLTDPVTVEW
>d2iada1 b.1.1.2 (A:83-186) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-AD}
TNEAPQATVFPKSPVLLGQPNTLICFVDNIFPPVINITWLRNSKSVTDGVYETSFLVNRDHSFHK
LSYLTFIPSDDDIYDCKVEHWGLEEPVLKHWEPEISSADLVPR
>d1es0a1 b.1.1.2 (A:83-180) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-A(G7)}
TNEAPQATVFPKSPVLLGQPNTLICFVDNIFPPVINITWLRNSKSVTDGVYETSFLVNRDHSFHK
LSYLTFIPSDDDIYDCKVEHWGLEEPVLKHWSS
>d1es0b1 b.1.1.2 (B:94-189) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-A(G7)}
RLEQPNVAISLSRTEALNHHNTLVCSVTDFYPAKIKVRWFRNGQEETVGVSSTQLIRNGDWTFQV
LVMLEMTPHQGEVYTCHVEHPSLKSPITVEWS
>d1k8ia1 b.1.1.2 (A:93-191) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), H2-DM}
VSRGLPVAEVFTLKPLEFGKPNTLVCFISNLFPPTLTVNWQLHSAPVEGASPTSISAVDGLTFQA
FSYLNFTPEPFDLYSCTVTHEIDRYTAIAYWVPQ
>d1k8ib1 b.1.1.2 (B:95-190) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), H2-DM}
APSVRVAQTTPFNTREPVMLACYVWGFYPADVTITWMKNGQLVPSHSNKEKTAQPNGDWTYQTVS
YLALTPSYGDVYTCVVQHSGTSEPIRGDWTP
>d1vcaa1 b.1.1.3 (A:91-199) Second domain of vascular cell adhesion molecule-1 (VCAM-1) {Human (Homo sapiens)}
FPKDPEIHLSGPLEAGKPITVKCSVADVYPFDRLEIDLLKGDHLMKSQEFLEDADRKSLETKSLE
VTFTPVIEDIGKVLVCRAKLHIDEMDSVPTVRQAVKELQVYISP
>d1iam_1 b.1.1.3 (83-185) Second domain of intercellular cell adhesion molecule-1 (ICAM-1) {Human (Homo sapiens)}
YWTPERVELAPLPSWQPVGKQLTLRCQVEGGAPRAQLTVVLLRGEKELKREPAVGEPAEVTTTVL
VRRDHHGAQFSCRTELDLRPQGLELFENTSAPYQLQTF
>d1ic1a1 b.1.1.3 (A:83-190) Second domain of intercellular cell adhesion molecule-1 (ICAM-1) {Human (Homo sapiens)}
YWTPERVELAPLPSWQPVGKNLTLRCQVEGGAPRANLTVVLLRGEKELKREPAVGEPAEVTTTVL
VRRDHHGANFSCRTELDLRPQGLELFENTSAPYQLQTFVLPAT
>d1zxq_1 b.1.1.3 (87-192) Second domain of intercellular cell adhesion molecule-2 (ICAM-2) {Human (Homo sapiens)}
PPRQVILTLQPTLVAVGKSFTIECRVPTVEPLDSLTLFLFRGNETLHYETFGKAAPAPQEATATF
NSTADREDGHRNFSCLAVLDLMSRGGNIFHKHSAPKMLEIY
>d1cdy_2 b.1.1.3 (98-178) CD4 {Human (Homo sapiens)}
FGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVL
QNQKKVEFKIDIVVLA
>d1wioa4 b.1.1.3 (A:292-363) CD4 {Human (Homo sapiens)}
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MRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKAVWVLNPEAGMWQCLLSDSGQVLLE
SNIKVLP
>d1cid_2 b.1.1.3 (106-177) CD4 {Rat (Rattus rattus)}
VMKVTQPDSNTLTCEVMGPTSPKMRLILKQENQEARVSRQEKVIQVQAPEAGVWQCLLSEGEEVK
MDSKIQV
>d1hnf_2 b.1.1.3 (105-182) CD2, second domain {Human (Homo sapiens)}
RVSKPKISWTCINTTLTCEVMNGTDPELNLYQDGKHLKLSQRVITHKWTTSLSAKFKCTAGNKVS
KESSVEPVSCPEK
>d1ccza2 b.1.1.3 (A:94-171) CD2-binding domain of CD58, second domain
{Human (Homo sapiens)}
EMVSKPMIYWECSNATLTCEVLEGTDVELKLYQGKEHLRSLRQKTMSYQWTNLRAPFKCKAVNRV
SQESEMEVVNCPE
>d1dr9a2 b.1.1.3 (A:106-200) CD80, second domain {Human (Homo
sapiens)}
ADFPTPSISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKL
DFNMTTNHSFMCLIKYGHLRVNQTFNWNTA
>d1vcaa2 b.1.1.4 (A:1-90) N-terminal domain of vascular cell adhesion
molecule-1 (VCAM-1) {Human (Homo sapiens)}
FKIETTPESRYLAQIGDSVSLTCSTTGCESPFFSWRTQIDSPLNGKVTNEGTTSTLTMNPVSFGN
EHSYLCTATCESRKLEKGIQVEIYS
>d1iam_2 b.1.1.4 (1-82) N-terminal domain of intracellular adhesion
molecule-1, ICAM-1 {Human (Homo sapiens)}
QTSVSPSKVILPRGGSVLVTCSTSCDQPKLLGIETPLPKKELLLPGNNRKVYELSNVQEDSQPMC
YSNCPDGQSTAKTFLTV
>d1zxq_2 b.1.1.4 (1-86) N-terminal domain of intracellular adhesion
molecule-2, ICAM-2 {Human (Homo sapiens)}
KVFEVHVRPKKLAVEPKGSLEVNCSTTCNQPEVGGLETSLNKILLDEQAQWKHYLVSNISHDTVL
QCHFTCSGKQESMNSNVSVYQ
>d1epfa1 b.1.1.4 (A:1-97) Neural cell adhesion molecule (NCAM) {Rat
(Rattus norvegicus)}
LQVDIVPSQGEISVGESKFFLCQVAGDAKDKDISWFSPNGEKLSPNQQRISVVWNDDDSSTLTIY
NANIDDAGIYKCVVTAEDGTQSEATVNVKIFQ
>d1epfa2 b.1.1.4 (A:98-189) Neural cell adhesion molecule (NCAM) {Rat
(Rattus norvegicus)}
KLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWKHKGRDVILKKDVRFIVLSNNYLQIRGIKK
TDEGTYRCEGRILARGEINFKDIQVIV
>d1ie5a_ b.1.1.4 (A:) Neural cell adhesion molecule (NCAM) {Chicken
(Gallus gallus)}
GKDIQVIVNVPPSVRARQSTMNATANLSQSVTLACDADGFPEPTMTWTKDGEPIEQEDNEEKYSF
NYDGSELIIKKVDKSDEAEYICIAENKAGEQDATIHLKVFAK
>d1gsma1 b.1.1.4 (A:1-90) Mucosal addressin cell adhesion molecule-1
(MADCAM-1) {Human (Homo sapiens)}
VKPLQVEPPEPVVAVALGASRQLTCRLACADRGASVQWRGLDTSLGAVQSDTGRSVLTVRNASLS
AAGTRVCVGSCGGRTFQHTVQLLVY
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>d1gsma2 b.1.1.4 (A:91-206) Mucosal addressin cell adhesion molecule-1 (MADCAM-1) {Human (Homo sapiens)}
AFPNQLTVSPAALVPGDPEVACTAHKVTPVDPNALSFSLLVGGQELEGAQALGPEVQEEEEEPQG
DEDVLFRVTERWRLPPLGTPVPPALYCQATMRLPGLELSHRQAIPVLIEGR
>d1fhga_ b.1.1.4 (A:) Telokin {Turkey (Meleagris gallopavo)}
AEEKPHVKPYFTKTILDMEVVEGSAARFDCKVEGYPDPEVMWFKDDNPVKESRHFQIDYDEEGNC
SLTISEVCGDDDAKYTCKAVNSLGEATCTAELLVETM
>d1g1ca_ b.1.1.4 (A:) Titin {Human (Homo sapiens), different modules}
SMEAPKIFERIQSQTVGQGSDAHFRVRVVGKPDPECEWYKNGVKIERSDRIYWYWPEDNVCELVI
RDVTGEDSASIMVKAINIAGETSSHAFLLVQAK
>d1nct__ b.1.1.4 (-) Titin {Human (Homo sapiens), different modules}
SKTTLAARILTKPRSMTVYEGESARFSCDTDGEPVPTVTWLRKGQVLSTSARHQVTTTKYKSTFE
ISSVQASDEGNYSVVVENSEGKQEAEFTLTIQK
>d1koa_1 b.1.1.4 (6265-6361) Twitchin {Nematode (Caenorhabditis elegans)}
QPRFIVKPYGTEVGEGQSANFYCRVIASSPPVVTWHKDDRELKQSVKYMKRYNGNDYGLTINRVK
GDDKGEYTVRAKNSYGTKEEIVFLNVTRHSEP
>d1wiu__ b.1.1.4 (-) Twitchin {Nematode (Caenorhabditis elegans)}
LKPKILTASRKIKIKAGFTHNLEVDFIGAPDPTATWTVGDSGAALAPELLVDAKSSTTSIFFPSA
KRADSGNYKLKVKNELGEDEAIFEVIVQ
>d1tiu__ b.1.1.4 (-) Twitchin {Human (Homo sapiens), Ig repeat 27}
LIEVEKPLYGVEVFVGETAHFEIELSEPDVHGQWKLKGQPLTASPDCEIIEDGKKHILILHNCQL
GMTGEVSFQAANAKSAANLKVKEL
>d1iray1 b.1.1.4 (Y:1-101) Type-1 interleukin-1 receptor {Human (Homo sapiens)}
DKCKEREEKIILVSSANEIDVRPCPLNPNEHKGTITWYKDDSKTPVSTEQASRIHQHKEKLWFVP
AKVEDSGHYYCVVRNSSYCLRIKISAKFVENEPNLC
>d1iray2 b.1.1.4 (Y:102-204) Type-1 interleukin-1 receptor {Human (Homo sapiens)}
YNAQAIFKQKLPVAGDGGLVCPYMEFFKNENNELPKLQWYKDCKPLLLDNIHFSGVKDRLIVMNV
AEKHRGNYTCHASYTYLGKQYPITRVIEFITLEENKPT
>d1iray3 b.1.1.4 (Y:205-311) Type-1 interleukin-1 receptor {Human (Homo sapiens)}
RPVIVSPANETMEVDLGSQIQLICNVTGQLSDIAYWKWNGSVIDEDDPVLGEDYYSVENPANKRR
STLITVLNISEIESRFYKHPFTCFAKNTHGIDAAYIQLIYPV
>d1cvsc1 b.1.1.4 (C:149-250) Fibroblast growth factor receptor, FGFR {Human (Homo sapiens), FGFR1}
MPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPQPTLRWLKNGKEFKPDHRIGGYKVRYATW
SIIMDSVVPSDKGNYTCIVENEYGSINHTYQLDVVER
>d1cvsc2 b.1.1.4 (C:251-359) Fibroblast growth factor receptor, FGFR {Human (Homo sapiens), FGFR1}
SPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAG
VNTTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVL
>d1ev2e1 b.1.1.4 (E:150-250) Fibroblast growth factor receptor, FGFR

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{Human (Homo sapiens), FGFR2}
NKRAPYWTNTEKMEKRLHAVPAANTVKFRCPAGGNPMPTMRWLKNGKEFKQEHRIGGYKVRNQHW
SLIMESVVPSDKGNYTCVVENEYGSINHTYHLDVVE
>d1ev2e2 b.1.1.4 (E:251-360) Fibroblast growth factor receptor, FGFR
{Human (Homo sapiens), FGFR2}
RSPHRPILQAGLPANASTVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYGPDGLPYLKVLKAA
GVNTTDKEIEVLYIRNVTFEDAGEYTCLAGNSIGISFHSAWLTVL
>d1biha1 b.1.1.4 (A:5-98) Hemolin {Moth (Hyalophora cecropia)}
KYPVLKDQPAEVLFRENNPTVLECIIEGNDQGVKYSWKKDGKSYNWQEHNAALRKDEGSLVFLRP
QASDEGHYQCFAETPAGVASSRVISFRKT
>d1biha2 b.1.1.4 (A:99-209) Hemolin {Moth (Hyalophora cecropia)}
YLIASPAKTHEKTPIEGRPFQLDCVLPNAYPKPLITWKKRLSGADPNADVTDFDRRITAGPDGNL
YFTIVTKEDVSDIYKYVCTAKNAAVDEEVVLVEYEIKGVTKDNSGY
>d1biha3 b.1.1.4 (A:210-306) Hemolin {Moth (Hyalophora cecropia)}
KGEPVPQYVSKDMMAKAGDVTMIYCMYGSNPMGYPNYFKNGKDVNGNPEDRITRHNRTSGKRLLF
KTTLPEDEGVYTCEVDNGVGKPQKHSLKLTVV
>d1biha4 b.1.1.4 (A:307-395) Hemolin {Moth (Hyalophora cecropia)}
SAPKYEQKPEKVIVVKQGQDVTIPCKVTGLPAPNVVWSHNAKPLSGGRATVTDSGLVIKGVKNGD
KGYYGCRATNEHGDKYFETLVQVN
>d1cs6a1 b.1.1.4 (A:7-103) Axonin-1 {Ckicken (Gallus gallus)}
RSYGPVFEEQPAHTLFPEGSAEEKVTLTCRARANPPATYRWKMNGTELKMGPDSRYRLVAGDLVI
SNPVKAKDAGSYQCVATNARGTVVSREASLRF
>d1cs6a2 b.1.1.4 (A:104-208) Axonin-1 {Ckicken (Gallus gallus)}
GFLQEFSAEERDPVKITEGWGVMFTCSPPPHYPALSYRWLLNEFPNFIPADGRRFVSQTTGNLYI
AKTEASDLGNYSCFATSHIDFITKSVFSKFSQLSLAAEDA
>d1cs6a3 b.1.1.4 (A:209-299) Axonin-1 {Ckicken (Gallus gallus)}
RQYAPSIKAKFPADTYALTGQMVTLECFAFGNPVPQIKWRKLDGSQTSKWLSSEPLLHIQNVDFE
DEGTYECEAENIKGRDTYQGRIIIHA
>d1cs6a4 b.1.1.4 (A:300-388) Axonin-1 {Ckicken (Gallus gallus)}
QPDWLDVITDTEADIGSDLRWSCVASGKPRPAVRWLRDGQPLASQNRIEVSGGELRFSKLVLEDS
GMYQCVAENKHGTVYASAELTVQA
>d1gl4b_ b.1.1.4 (B:) Perlecan Ig3 domain {Mouse (Mus musculus)}
PIMVTVEEQRSQSVRPGADVTFICTAKSKSPAYTLVWTRLHNGKLPSRAMDFNGILTIRNVQPSD
AGTYVCTGSNMFAMDQGTATLHVQ
>d1f97a2  b.1.1.4  (A:129-238)  Junction  adhesion  molecule,  JAM,
C-terminal domain {Mouse (Mus musculus)}
VPPSKPTISVPSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGISMLTADAKKTRAFMNSSFTIDPK
SGDLIFDPVTAFDSGEYYCQAQNGYGTAMRSEAAHMDAVELNVGG
>d1fltx_ b.1.1.4 (X:) Second domain of the Flt-1 receptor {Human (Homo
sapiens)}
GRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISN
ATYKEIGLLTCEATVNGHLYKTNYLTHRQT
>d1he7a_ b.1.1.4 (A:) NGF binding domain of trkA receptor {Human (Homo
sapiens)}
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SHMPASVQLHTAVEMHHWCIPFSVDGQPAPSLRWLFNGSVLNETSFIFTEFLEPAANETVRHGCL
RLNQPTHVNNGNYTLLAANPFGQASASIMAAFMDNPFEFNPE
>d1wwwx_ b.1.1.4 (X:) NGF binding domain of trkA receptor {Human (Homo
sapiens)}
VSFPASVQLHTAVEMHHWCIPFSVDGQPAPSLRWLFNGSVLNETSFIFTEFLEPAANETVRHGCL
RLNQPTHVNNGNYTLLAANPFGQASASIMAAFMDNP
>d1wwbx_ b.1.1.4 (X:) Ligand binding domain of trkB receptor {Human
(Homo sapiens)}
VHFAPTITFLESPTSDHHWCIPFTVKGNPKPALQWFYNGAILNESKYICTKIHVTNHTEYHGCLQ
LDNPTHMNNGDYTLIAKNEYGKDEKQISAHFMGWPGID
>d1wwca_ b.1.1.4 (A:) NT3 binding domain of trkC receptor {Human (Homo
sapiens)}
TVYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISEGCLL
FNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPVDE
>d1fcga1 b.1.1.4 (A:4-88) Fc gamma receptor ectodomain (CD32) {Human
(Homo sapiens), IIa}
APPKAVLKLEPPWINVLQEDSVTLTCQGARSPESDSIQWFHNGNLIPTHTQPSYRFKANNNDSGE
YTCQTGQTSLSDPVHLTVLF
>d1fcga2 b.1.1.4 (A:89-174) Fc gamma receptor ectodomain (CD32) {Human
(Homo sapiens), IIa}
EWLVLQTPHLEFQEGETIMLRCHSWKDKPLVKVTFFQNGKSQKFSHLDPTFSIPQANHSHSGDYH
CTGNIGYTLFSSKPVTITVQV
>d2fcba1 b.1.1.4 (A:6-90) Fc gamma receptor ectodomain (CD32) {Human
(Homo sapiens), IIb}
APPKAVLKLEPQWINVLQEDSVTLTCRGTHSPESDSIQWFHNGNLIPTHTQPSYRFKANNNDSGE
YTCQTGQTSLSDPVHLTVLS
>d2fcba2 b.1.1.4 (A:91-178) Fc gamma receptor ectodomain (CD32) {Human
(Homo sapiens), IIb}
EWLVLQTPHLEFQEGETIVLRCHSWKDKPLVKVTFFQNGKSKKFSRSDPNFSIPQANHSHSGDYH
CTGNIGYTLYSSKPVTITVQAPA
>d1fnla1 b.1.1.4 (A:3-86) Fc gamma receptor ectodomain (CD32) {Human
(Homo sapiens), III}
EDLPKAVVFLEPQWYSVLEKDSVTLKCQGAYSPEDNSTQWFHNESLISSQASSYFIDAATVNDSG
EYRCQTNLSTLSDPVQLEV
>d1fnla2 b.1.1.4 (A:87-175) Fc gamma receptor ectodomain (CD32) {Human
(Homo sapiens), III}
HIGWLLLQAPRWVFKEEDPIHLRCHSWKNTALHKVTYLQNGKDRKYFHHNSDFHIPKATLKDSGS
YFCRGLVGSKNVSSETVNITITQA
>d1f2qa1 b.1.1.4 (A:4-85) IgE high affinity receptor alpha subunit
{Human (Homo sapiens)}
KPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKFEDSGEYKC
QHQQVNESEPVYLEVFS
>d1f2qa2 b.1.1.4 (A:86-174) IgE high affinity receptor alpha subunit
{Human (Homo sapiens)}
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DWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYY
CTGKVWQLDYESEPLNITVIKAPR
>d1efxd1 b.1.1.4 (D:4-103) Killer cell inhibitory receptor {Human
(Homo sapiens), kir2dl3}
VHRKPSLLAHPGRLVKSEETVILQCWSDVRFEHFLLHREGKFKDTLHLIGEHHDGVSKANFSIGP
MMQDLAGTYRCYGSVTHSPYQLSAPSDPLDIVITG
>d1efxd2 b.1.1.4 (D:104-200) Killer cell inhibitory receptor {Human
(Homo sapiens), kir2dl3}
LYEKPSLSAQPGPTVLAGESVTLSCSSRSSYDMYHLSREGEAHECRFSAGPKVNGTFQADFPLGP
ATHGGTYRCFGSFRDSPYEWSNSSDPLLVSVI
>d1nkr_1 b.1.1.4 (6-101) Killer cell inhibitory receptor {Human (Homo
sapiens), p58-cl42 kir}
RKPSLLAHPGPLVKSEETVILQCWSDVMFEHFLLHREGMFNDTLRLIGEHHDGVSKANFSISRMT
QDLAGTYRCYGSVTHSPYQVSAPSDPLDIVI
>d1nkr_2 b.1.1.4 (102-200) Killer cell inhibitory receptor {Human
(Homo sapiens), p58-cl42 kir}
IGLYEKPSLSAQPGPTVLAGENVTLSCSSRSSYDMYHLSREGEAHERRLPAGPKVNGTFQADFPL
GPATHGGTYRCFGSFHDSPYEWSKSSDPLLVSVT
>d1g0xa1 b.1.1.4 (A:2-97) Ligand binding domain of lir-1 (ilt2) {Human
(Homo sapiens)}
HLPKPTLWAEPGSVITQGSPVTLRCQGGQETQEYRLYREKKTAPWITRIPQELVKKGQFPIPSIT
WEHAGRYRCYYGSDTAGRSESSDPLELVVTG
>d1g0xa2 b.1.1.4 (A:98-198) Ligand binding domain of lir-1 (ilt2)
{Human (Homo sapiens)}
AYIKPTLSAQPSPVVNSGGNVTLQCDSQVAFDGFILCKEGEDEHPQCLNSQPHARGSSRAIFSVG
PVSPSRRWWYRCYAYDSNSPYEWSLPSDLLELLVLG
>d1f42a1 b.1.1.4 (A:1-87) The p40 domain of interleukin-12 (IL-12 beta
chain), N-teminal domain {Human (Homo sapiens)}
IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQ
YTCHKGGEVLSHSLLLLHKKED
>d1jbja1 b.1.1.4 (A:101-186) CD3 gamma chain ectodomain fragment
{Mouse (Mus musculus)}
KKDGSQTNKAKNLVQVDGSRGDGSVLLTCGLTDKTIKWLKDGSIISPLNATKNTWNLGNNAKDPR
GTYQCQGAKETSNPLQVYYRM
>d1jbja2 b.1.1.4 (A:1-100) CD3 epsilon chain ectodomain fragment
{Mouse (Mus musculus)}
DDAENIEYKVSISGTSVELTCPLDSDENLKWEKNGQELPQKHDKHLVLQDFSEVEDSGYYVCYTP
ASNKNTYLYLKARVGSADDAKKDAAKKDDAKKDDA
>d1k3ia1 b.1.1.5 (A:538-639) Galactose oxidase, C-terminal domain
{Fungi (Fusarium spp)}
GNLATRPKITRTSTQSVKVGGRITISTDSSISKASLIRYGTATHTVNTDQRRIPLTLTNNGGNSY
SFQVPSDSGVALPGYWMLFVMNSAGVPSVASTIRVTQ
>d1qba_1 b.1.1.5 (781-885) Bacterial chitobiase, c-terminal domain
{Serratia marcescens}

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GETHFVDTQALEKDWLRFANILGQRELAKLDKGGVAYRLPVPGARVAGGKLEANIALPGLGIEYS
TDGGKQWQRYDAKAKPAVSGEVQVRSVSPDGKRYSRAEKV
>d1svb_1 b.1.1.5 (303-395) Envelope glycoprotein, domain III (C-terminal) {Tick-borne encephalitis virus}
TYTMCDKTKFTWKRAPTDSGHDTVVMEVTFSGTKPCRIPVRAVAHGSPDVNVAMLITPNPTIENN
GGGFIEMQLPPGDNIIYVGELSHQWFQK
>d1cgt_1 b.1.1.5 (495-579) Cyclodextrin glycosyltransferase, domain E {Bacillus circulans, different strains}
ETTPTIGHVGPVMGKPGNVVTIDGRGFGSTKGTVYFGTTAVTGAAITSWEDTQIKVTIPSVAAGN
YAVKVAASGVNSNAYNNFTI
>d1kcla1 b.1.1.5 (A:496-581) Cyclodextrin glycosyltransferase, domain E {Bacillus circulans, different strains}
TATPTIGHVGPMMAKPGVTITIDGRGFGSSKGTVYFGTTAVSGADITSWEDTQIKVKIPAVAGGN
YNIKVANAAGTASNVYDNFEV
>d1cyg_1 b.1.1.5 (492-574) Cyclodextrin glycosyltransferase, domain E {Bacillus stearothermophilus}
ESTPIIGHVGPMMGQVGHQVTIDGEGFGTNTGTVKFGTTAANVVSWSNNQIVVAVPNVSPGKYNI
TVQSSSGQTSAAYDNFEV
>d1qhoa1 b.1.1.5 (A:496-576) Cyclodextrin glycosyltransferase, domain E {Bacillus stearothermophilus, maltogenic alpha-amylase}
ASAPQIGSVAPNMGIPGNVVTIDGKGFGTTQGTVTFGGVTATVKSWTSNRIEVYVPNMAAGLTDV
KVTAGGVSSNLYSYNI
>d1pama1 b.1.1.5 (A:497-582) Cyclodextrin glycosyltransferase, domain E {Bacillus sp., strain 1011}
TTPIIGNVGPMMAKPGVTITIDGRGFGSGKGTVYFGTTAVTGADIVAWEDTQIQVKIPAVPGGIY
DIRVANAAGAASNIYDNFEVL
>d1ciu_1 b.1.1.5 (496-578) Cyclodextrin glycosyltransferase, domain E {Thermoanaerobacterium thermosulfurigenes, EM1}
SNSPLIGHVGPTMTKAGQTITIDGRGFGTTSGQVLFGSTAGTIVSWDDTEVKVKVPSVTPGKYNI
SLKTSSGATSNTYNNINI
>d1smaa1 b.1.1.5 (A:1-123) Maltogenic amylase, N-terminal domain {Thermus sp.}
MRKEAIHHRSTDNFAYAYDSETLHLRLQTKKNDVDHVELLFGDPYEWHDGAWQFQTMPMRKTGSD
GLFDYWLAEVKPPYRRLRYGFVLRAGGEKLVYTEKGFYHEAPSDDTAYYFCFPFLHRV
>d1bvza1 b.1.1.5 (A:1-120) Maltogenic amylase, N-terminal domain {Thermoactinomyces vulgaris, TVAII}
MLLEAIFHEAKGSYAYPISETQLRVRLRAKKGDVVRCEVLYADRYASPEEELAHALAGKAGSDER
FDYFEALLECSTKRVKYVFLLTGPQGEAVYFGETGFSAERSKAGVFQYAYIHRSE
>d1eh9a1 b.1.1.5 (A:1-90) Glycosyltrehalose trehalohydrolase, N-terminal domain {Archaeon Sulfolobus solfataricus, km1}
TFAYKIDGNEVIFTLWAPYQKSVKLKVLEKGLYEMERDEKGYFTITLNNVKVRDRYKYVLDDASE
IPDPASRYQPEGVHGPSQIIQESKE
>d1bf2_1 b.1.1.5 (1-162) Isoamylase, N-terminal domain {Pseudomonas amyloderamosa}
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AINSMSLGASYDAQQANITFRVYSSQATRIVLYLYSAGYGVQESATYTLSPAGSGVWAVTVPVSS
IKAAGITGAVYYGYRAWGPNWPYASNWGKGSQAGFVSDVDANGDRFNPNKLLLDPYAQEVSQDPL
NPSNQNGNVFASGASYRTTDSGIYAPKGVVLV
>d1lla_3 b.1.1.5 (380-628) Hemocyanin, C-terminal domain {Horseshoe crab (Limulus polyphemus)}
PYDHDVLNFPDIQVQDVTLHARVDNVVHTFMREQELELKHGINPGNARSIKARYYHLDHEPFSYA
VNVQNNSASDKHATVRIFLAPKYDELGNEIKADELRRTAIELDKFKTDLHPGKNTVVRHSLDSSV
TLSHQPTFEDLLHGVGLNEHKSEYCSCGWPSHLLVPKGNIKGMEYHLFVMLTDWDKDKVDGSESV
ACVDAVSYCGARDHKYPDKKPMGFPFDRPIHTEHISDFLTNNMFIKDIKIKFHE
>d1hc2_3 b.1.1.5 (399-653) Hemocyanin, C-terminal domain {Spiny lobster (Panulirus interruptus)}
PPYTHDNLEFSGMVVNGVAIDGELITFFDEFQYSLINAVDSGENIEDVEINARVHRLNHNEFTYK
ITMSNNNDGERLATFRIFLCPIEDNNGITLTLDEARWFCIELDKFFQKVPSGPETIERSSKDSSV
TVPDMPSFQSLKEQADNAVNGGHDLDLSAYERSCGIPDRMLLPKSKPEGMEFNLYVAVTDGDKDT
EGHNGGHDYGGTHAQCGVHGEAYPDNRPLGYPLERRIPDERVIDGVSNIKHVVVKIVHHL
>d1js8a2 b.1.1.5 (A:2792-2892) C-terminal domain of octopus hemocyanin {Giant octopus (Octopus dofleini)}
EDRVFAGFLLRTIGQSADVNFDVCTKDGECTFGGTFCILGGEHEMFWAFDRLFKYDITTSLKHLR
LDAHDDFDIKVTIKGIDGHVLSNKYLSPPTVFLAPA
>d1clc_2 b.1.1.5 (35-134) CelD cellulase, N-terminal domain {Clostridium thermocellum}
IETKVSAAKITENYQFDSRIRLNSIGFIPNHSKKATIAANCSTFYVVKEDGTIVYTGTATSMFDN
DTKETVYIADFSSVNEEGTYYLAVPGVGKSVNFKI
>d1f1sa2 b.1.1.5 (A:171-248) Hyaluronate lyase precatalytic domain {Streptococcus agalactiae}
SEHPQPVTTQIEKSVNTALNKNYVFNKADYQYTLTNPSLGKIVGGILYPNATGSTTVKISDKSGK
IIKEVPLSVTAST
>d1edqa1 b.1.1.5 (A:24-132) Chitinase A, N-terminal domain {Serratia marcescens}
AAPGKPTIAWGNTKFAIVEVDQAATAYNNLVKVKNAADVSVSWNLWNGDTGTTAKVLLNGKEAWS
GPSTGSSGTANFKVNKGGRYQMQVALCNADGCTASDATEIVVAD
>d1f13a1 b.1.1.5 (A:5-190) Transglutaminase N-terminal domain {Human (Homo sapiens)}
RTAFGGRRAVPPNNSNAAEDDLPTVELQGVVPRGVNLQEFLNVTSVHLFKERWDTNKVDHHTDKY
ENNKLIVRRGQSFYVQIDFSRPYDPRRDLFRVEYVIGRYPQENKGTYIPVPIVSELQSGKWGAKI
VMREDRSVRLSIQSSPKCIVGKFRMYVAVWTPYGVLRTSRNPETDTYILFNPWCED
>d1g0da1 b.1.1.5 (A:6-140) Transglutaminase N-terminal domain {Red sea bream (Chrysophrys major)}
GLIVDVNGRSHENNLAHRTREIDRERLIVRRGQPFSITLQCSDSLPPKHHLELVLHLGKRDEVVI
KVQKEHGARDKWWFNQQGAQDEILLTLHSPANAVIGHYRLAVLVMSPDGHIVERADKISFHMLFN
PWCRD
>d1eut_1 b.1.1.5 (403-505) Sialidase, "linker" domain {Micromonospora viridifaciens}
GICAPFTIPDVALEPGQQVTVPVAVTNQSGIAVPKPSLQLDASPDWQVQGSVEPLMPGRQAKGQV

TITVPAGTTPGRYRVGATLRTSAGNASTTFTVTVGLLD
>d1ksr__ b.1.1.5 (-) F-actin cross-linking gelation factor (ABP-120), one repeat (ROD 4) {Slime mold (Dictyostelium discoideum), different domains}
ADPEKSYAEGPGLDGGECFQPSKFKIHAVDPDGVHRTDGGDGFVVTIEGPAPVDPVMVDNGDGTY
DVEFEPKEAGDYVINLTLDGDNVNGFPKTVTVKPA
>d1qfha1 b.1.1.5 (A:646-749) F-actin cross-linking gelation factor (ABP-120), one repeat (ROD 4) {Slime mold (Dictyostelium discoideum), different domains}
KPAPSAEHSYAEGEGLVKVFDNAPAEFTIFAVDTKGVARTDGGDPFEVAINGPDGLVVDAKVTDN
NDGTYGVVYDAPVEGNYNVNVTLRGNPIKNMPIDVKCIE
>d1qfha2 b.1.1.5 (A:750-857) F-actin cross-linking gelation factor (ABP-120), one repeat (ROD 4) {Slime mold (Dictyostelium discoideum), different domains}
GANGEDSSFGSFTFTVAAKNKKGEVKTYGGDKFEVSITGPAEEITLDAIDNQDGTYTAAYSLVGN
GRFSTGVKLNGKHIEGSPFKQVLGNPGKKNPEVKSFTTTRTAN
>d1ds6b_ b.1.1.5 (B:) Rho GDP-dissociation inhibitor 1, RhoGDI {Human (Homo sapiens)}
GNYKPPPQKSLKELQEMDKDDESLIKYKKTLLGDGPVVTDPKAPNVVVTRLTLVCESAPGPITMD
LTGDLEALKKETIVLKEGSEYRVKIHFKVNRDIVSGLKYVQHTYRTGVKVDKATFMVGSYGPRPE
EYEFLTPVEEAPKGMLARGTYHNKSFFTDDDKQDHLSWEWNLSIKKEWG
>d1fsoa_ b.1.1.5 (A:) Rho GDP-dissociation inhibitor 1, RhoGDI {Human (Homo sapiens)}
MVPNVVVTGLTLVCSSAPGPLELDLTGDLESFKKQSFVLKEGVEYRIKISFRVNREIVSGMKYIQ
HTYRAGVAIDATDYMVGSYGPRAEEYEFLTPVEEAPKGMLARGSYSIKSRFTDDDKTDHLSWEWN
FTIKKDWK
>d1hh4e_ b.1.1.5 (E:) Rho GDP-dissociation inhibitor 1, RhoGDI {Human (Homo sapiens)}
HSVNYKPPAQKSIQEIQELDKDDESLRKYKEALLGRVAVSADPNVPNVVVTGLTLVCSSAPGPLE
LDLTGDLESFKKQSFVLKEGVEYRIKISFRVNREIVSGMKYIQHTYRKGVKIDKTDYMVGSYGPR
AEEYEFLTPVEEAPKGMLARGSYSIKSRFTDDDKTDHLSWEWNLTIKKDW
>d1rhoa_ b.1.1.5 (A:) Rho GDP-dissociation inhibitor 1, RhoGDI {Human (Homo sapiens)}
VAVSADPNVPNVVVTGLTLVCSSAPGPLELDLTGDLESFKKQSFVLKEGVEYRIKISFRVNREIV
SGMKYIEHTYRKGVKIDKTDYMVGSYGPRAEEYEFLTPVEEAPKGMLARGSYSIKSRFTDDDKTD
HLSWEWNLTIKKDWK
>d1ajw__ b.1.1.5 (-) Rho GDP-dissociation inhibitor 1, RhoGDI {Cow (Bos taurus)}
AVSADPNVPNVVVTRLTLVCSTAPGPLELDLTGDLESFKKQSFVLKEGVEYRIKISFRVNREIVS
GMKYIQHTYRKGVKIDKTDYMVGSYGPRAEEYEFLTPMEEAPKGMLARGSYNIKSRFTDDDRTDH
LSWEWNLTIKKEWKD
>d1doab_ b.1.1.5 (B:) Rho GDP-dissociation inhibitor 1, RhoGDI {Cow (Bos taurus)}
EPTAEQLAQIAAENEEDEHSVNYKPPAQKSIQEIQELDKDDESLRKYKEALLGRVAVSADPNVPN

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VVVTRLTLVCSTAPGPLELDLTGDLESFKKQSFVLKEGVEYRIKISFRVNREIVSGMKYIQHTYR
KGVKIDKTDYMVGSYGPRAEEYEFLTPMEEAPKGMLARGSYNIKSRFTDDDRTDHLSWEWNLTIK
KEWKD
>d1ayra2 b.1.1.5 (A:183-368) Arrestin {Cow (Bos taurus), visual
arrestin}
DMGPQPRAEASWQFFMSDKPLRLAVSLSKEIYYHGEPIPVTVAVTNSTEKTVKKIKVLVEQVTNV
VLYSSDYYIKTVAAEEAQEKVPPNSSLTKTLTLVPLLANNRERRGIALDGKIKHEDTNLASSTII
KEGIDKTVMGILVSYQIKVKLTVSGLLGELTSSEVATEVPFRLMHPQPEDPDTAKA
>d1cf1a1 b.1.1.5 (A:10-182) Arrestin {Cow (Bos taurus), visual
arrestin}
HVIFKKISRDKSVTIYLGKRDYIDHVERVEPVDGVVLVDPELVKGKRVYVSLTCAFRYGQEDIDV
MGLSFRRDLYFSQVQVFPPVGASGATTRLQESLIKKLGANTYPFLLTFPDYLPCSVMLQPAPQDV
GKSCGVDFEIKAFATHSTDVEEDKIPKKSSVRLLIRKVQHAPR
>d1cf1a2 b.1.1.5 (A:183-393) Arrestin {Cow (Bos taurus), visual
arrestin}
DMGPQPRAEASWQFFMSDKPLRLAVSLSKEIYYHGEPIPVTVAVTNSTEKTVKKIKVLVEQVTNV
VLYSSDYYIKTVAAEEAQEKVPPNSSLTKTLTLVPLLANNRERRGIALDGKIKHEDTNLASSTII
KEGIDKTVMGILVSYQIKVKLTVSGLLGELTSSEVATEVPFRLMHPQPEDPDTAKESFQDENFVF
EEFARQNLKDAGEYKE
>d1g4ma1 b.1.1.5 (A:5-175) Arrestin {Cow (Bos taurus), beta-arrestin
1}
GTRVFKKASPNGKLTVYLGKRDFVDHIDLVEPVDGVVLVDPEYLKERRVYVTLTCAFRYGREDLD
VLGLTFRKDLFVANVQSFPPAPEDKKPLTRLQERLIKKLGEHAYPFTFEIPPNLPCSVTLQPGPE
DTGKACGVDYEVKAFCAENLEEKIHKRNSVRLVIRKVQYAP
>d1g4ma2 b.1.1.5 (A:176-393) Arrestin {Cow (Bos taurus),
beta-arrestin 1}
ERPGPQPTAETTRQFLMSDKPLHLEASLDKEIYYHGEPISVNVHVTNNTNKTVKKIKISVRQYAD
ICLFNTAQYKCPVAMEEADDTVAPSSTFCKVYTLTPFLANNREKRGLALDGKLKHEDTNLASSTL
LREGANREILGIIVSYKVKVKLVVSRGGLLGDLASSDVAVELPFTLMHPKPKEEPPHREVPEHET
PVDTNLIELDTNDDDIVFEDFAR
>d1a02n1 b.1.1.5 (N:577-678) Transcription factor NFATC, C-terminal
domain {Human (Homo sapiens)}
LPMVERQDTDSCLVYGGQQMILTGQNFTSESKVVFTEKTTDGQQIWEMEATVDKDKSQPNMLFVE
IPEYRNKHIRTPVKVNFYVINGKRKRSQPQHFTYHPV
>d1imhc1 b.1.1.5 (C:368-468) Transcription factor TONEBP, C-terminal
domain {Human (Homo sapiens)}
VPEILKKSLHSCSVKGEEEVFLIGKNFLKGTKVIFQENVSDENSWKSEAEIDMELFHQNHLIVKV
PPYHDQHITLPVSVGIYVVTNAGRSHDVQPFTYTPD
>d1bfs__ b.1.1.5 (-) p50 subunit of NF-kappa B transcription factor,
C-terminal domain {Mouse (Mus musculus)}
ASNLKIVRMDRTAGCVTGGEEIYLLCDKVQKDDIQIRFYEEEENGGVWEGFGDFSPTDVHRQFAI
VFKTPKYKDVNITKPASVFVQLRRKSDLETSEPKPFLYYPE
>d1a3qa1 b.1.1.5 (A:227-327) p52 subunit of NF-kappa B (NFKB),
C-terminal domain {Human (Homo sapiens)}
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NLKISRMDKTAGSVRGGDEVYLLCDKVQKDDIEVRFYEDDENGWQAFGDFSPTDVHKQYAIVFRT
PPYHKMKIERPVTVFLQLKRKRGGDVSDSKQFTYYP
>d1bfta_ b.1.1.5 (A:) p65 subunit of NF-kappa B (NFKB), C-terminal
domain {Mouse (Mus musculus)}
TAELKICRVNRNSGSCLGGDEIFLLCDKVQKEDIEVYFTGPGWEARGSFSQADVHRQVAIVFRTP
PYADPSLQAPVRVSMQLRRPSDRELSEPMEFQYLPD
>d1ikna1 b.1.1.5 (A:192-303) p65 subunit of NF-kappa B (NFKB),
C-terminal domain {Mouse (Mus musculus)}
AELKICRVNRNSGSCLGGDEIFLLCDKVQKEDIEVYFTGPGWEARGSFSQADVHRQVAIVFRTPP
YADPSLQAPVRVSMQLRRPSDRELSEPMEFQYLPDTDDRHRIEEKRK
>d1nfia1 b.1.1.5 (A:190-314) p65 subunit of NF-kappa B (NFKB),
C-terminal domain {Human (Homo sapiens)}
NTAELKICRVNRNSGSCLGGDEIFLLCDKVQKEDIEVYFTGPGWEARGSFSQADVHRQVAIVFRT
PPYADPSLQAPVRVSMQLRRPSDRELSEPMEFQYLPDTDDRHRIEEKRKRTYETFKSIMK
>d1ahm__ b.1.1.5 (-) Major mite allergen {House-dust mite
(Dermatophagoides farinae), Der f 2}
DQVDVKDCANNEIKKVMVDGCHGSDPCIIHRGKPFTLEALFDANQNTKTAKIEIKASLDGLEIDV
PGIDTNACHFVKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKLIGDNGVLACAIATHGKIRD
>d1a9v__ b.1.1.5 (-) Major mite allergen {House-dust mite
(Dermatophagoides pteronyssinus), Der p 2}
SQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNTKTAKIEIKASIDGLEVDV
PGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGDDGVLACAIATHAKIRD
>d1soxa1 b.1.1.5 (A:344-466) Sulfite oxidase, C-terminal domain
{Chicken (Gallus gallus)}
ELPVQSAVTQPRPGAAVPPGELTVKGYAWSGGGREVVRVDVSLDGGRTWKVARLMGDKAPPGRAW
AWALWELTVPVEAGTELEIVCKAVDSSYNVQPDSVAPIWNLRGVLSTAWHRVRVSVQD
>d1cvra1 b.1.1.5 (A:351-432) Gingipain R (RgpB), C-terminal domain
{Porphyromonas gingivalis}
PTEMQVTAPANISASAQTFEVACDYNGAIATLSDDGDMVGTAIVKDGKAIIKLNESIADETNLTL
TVVGYNKVTVIKDVKVE
>d1h6ta1 b.1.1.6 (A:241-321) Internalin B {Listeria monocytogenes}
ECLNKPINHQSNLVVPNTVKNTDGSLVTPEIISDDGDYEKPNVKWHLPEFTNEVSFIFYQPVTIG
KAKARFHGRVTQPLKE
>d1h6ua1 b.1.1.6 (A:263-343) Internalin H {Listeria monocytogenes}
TITNQPVFYNNNLVVPNVVKGPSGAPIAPATISDNGTYASPNLTWNLTSFINNVSYTFNQSVTFK
NTTVPFSGTVTQPLTE
>d1ehxa_ b.1.1.6 (A:) Cellulosomal scaffoldin protein CipC, module
x2.1 {Clostridium cellulolyticum}
MQDPTINPTSISAKAGSFADTKITLTPNGNTFNGISELQSSQYTKGTNEVTLLASYLNTLPENTT
KTLTFDFGVGTKNPKLTITVLPKDIPGLE
>d1im3d_ b.1.1.6 (D:) Cytomegalovirus protein US2 {Human
cytomegalovirus}
PWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENLYVHADDVEFVPGESLKWNVR
NLDVMPIFETLALRLVLQGDVIWLRCVPEL
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>d1jjua3 b.1.1.6 (A:274-351) Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5 {Paracoccus denitrificans}

AAPQVLAVAPARLKIGEETQLRVAGTGLGSDLTLPEGVAGSVESAGNGVTVLKLTATGTPGPVSLELGGQKVDLVAYD

>d1jjua4 b.1.1.6 (A:352-489) Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5 {Paracoccus denitrificans}

RPDRISIVPDLTIARIGGNGGPIPKVPAQFEAMGWLNGPDGQPGTGDDIALGAFPASWATDNFDEEAEKMQDAKYAGSIDDTGLFTPAEAGPNPERPMQTNNAGNLKVIATVDAEGEPLSAEAHLYATVQRFVDAPIR

>d1jmxa3 b.1.1.6 (A:282-363) Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5 {Pseudomonas putida}

GKARLLAVQPAFIKAGGESEITLVGSGLAGKPDLGAGVEVTEVLEQTPTLVRLKARAAADAKPGQREVAVGTLKGVNLAVYD

>d1jmxa4 b.1.1.6 (A:364-494) Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5 {Pseudomonas putida}

KVEEVKVVPAFSIARIGENGASVPKVQGRFEAEAWGKDANGQPLRIGYLPASWKVEPFNERAVEDEDVKFAGKMQADGVFVPGGAGPNPERKMMTNNAGNLKVIATLADGGQTGEGHMIVTVQRWNNPPLP

>d2hft_1 b.1.2.1 (1-106) Extracellular region of human tissue factor {Human (Homo sapiens)}

SGTTNTVAAYNLTWKSTNFKTILEWEPKPVNQVYTVQISTKSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLET

>d2hft_2 b.1.2.1 (107-211) Extracellular region of human tissue factor {Human (Homo sapiens)}

NLGQPTIQSFEQVGTKVNVTVEDERTLVRRNNTFLSLRDVFGKDLIYTLYYWKSSSQEKGEFRSGKKTAKTNTNEFLIDVDKGENYCFSVQAVIPSRTVNRKSTDSPVECMG

>g1dan.1 b.1.2.1 (T:,U:91-106) Extracellular region of human tissue factor {Human (Homo sapiens)}

TVAAYNLTWKSTNFKTILEWEPKPVNQVYTVQISTKSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAXEPLYENSPEFTPYLET

>d1a21a1 b.1.2.1 (A:4-106) Extracellular region of human tissue factor {Rabbit (Oryctolagus cuniculus)}

TGRAYNLTWKSTNFKTILEWEPKSIDHVYTVQISTRLENWKSKCFLTAETECDLTDEVVKDVGQTYMARVLSYPARNGNTTGFPEEPPFRNSPEFTPYLDTNL

>d1a21a2 b.1.2.1 (A:107-208) Extracellular region of human tissue factor {Rabbit (Oryctolagus cuniculus)}

GQPTIQSFEQVGTKLNVTVQDARTLVRRNGTFLSLRAVFGKDLNYTLYYWRASSTGKKTATTNTNEFLIDVDKGENYCFSVQAVIPSRKRKQRSPESLTECT

>d1fna__ b.1.2.1 (-) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

RDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVDYTITVYAVTGRGDSPASSKPISINYRTEI

>d1fnf_1 b.1.2.1 (1142-1235) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

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PLSPPTNLHLEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVVHADQSSCTFDNL
SPGLEYNVSVYTVKDDKESVPISDTIIPA
>d1fnf_2 b.1.2.1 (1236-1326) Fibronectin, different Fn3 modules
{Human (Homo sapiens)}
VPPPTDLRFTNIGPDTMRVTWAPPPSIDLTNFLVRYSPVKNEEDVAELSISPSDNAVVLTNLLPG
TEYVVSVSSVYEQHESTPLRGRQKTG
>d1fnf_3 b.1.2.1 (1327-1415) Fibronectin, different Fn3 modules
{Human (Homo sapiens)}
LDSPTGIDFSDITANSFTVHWIAPRATITGYRIRHHPEHFSGRPREDRVPHSRNSITLTNLTPGT
EYVVSIVALNGREESPLLIGQQST
>d1fnha1 b.1.2.1 (A:3-92) Fibronectin, different Fn3 modules {Human
(Homo sapiens)}
PAPTDLKFTQVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSSSVVVSGLMVATK
YEVSVYALKDTLTSRPAQGVVTTLE
>d1fnha2 b.1.2.1 (A:93-182) Fibronectin, different Fn3 modules {Human
(Homo sapiens)}
NVSPPRRARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKPDVRSYTITGLQPGT
DYKIYLYTLNDNARSSPVVIDASTA
>d1fnha3 b.1.2.1 (A:183-271) Fibronectin, different Fn3 modules
{Human (Homo sapiens)}
IDAPSNLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRPRPGVTEATITGLEPGT
EYTIYVIALKNNQKSEPLIGRKKT
>d1j8ka_ b.1.2.1 (A:) Fibronectin, different Fn3 modules {Human (Homo
sapiens)}
NIDRPKGLAFTDVDVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTAELQGLRPG
SEYTVSVVALHDDMESQPLIGTQSTAIPA
>d2fnba_ b.1.2.1 (A:) Fibronectin, different Fn3 modules {Human (Homo
sapiens)}
MRGSEVPQLTDLSFVDITDSSIGLRWTPLNSSTIIGYRITVVAAGEGIPIFEDFVDSSVGYYTVT
GLEPGIDYDISVITLINGGESAPTTLTQQT
>d2mfn_1 b.1.2.1 (1-92) Fibronectin, different Fn3 modules {Mouse (Mus
musculus)}
GLDSPTGFDSSDITANSFTVHWVAPRAPITGYIIRHHAEHSVGRPRQDRVPPSRNSITLTNLNPG
TEYVVSIIAVNGREESPPLIGQQATVS
>d2mfn_2 b.1.2.1 (93-184) Fibronectin, different Fn3 modules {Mouse
(Mus musculus)}
DIPRDLEVIASTPTSLLISWEPPAVSVRYYRITYGETGGNSPVQEFTVPGSKSTATINNIKPGAD
YTITLYAVTGRGDSPASSKPVSINYKT
>d1qr4a1 b.1.2.1 (A:1-87) Tenascin {Chicken (Gallus gallus)}
DNPKDLEVSDPTETTLSLRWRRPVAKFDRYRLTYVSPSGKKNEMEIPVDSTSFILRGLDAGTEYT
ISLVAEKGRHKSKPTTIKGSTV
>d1qr4a2 b.1.2.1 (A:88-175) Tenascin {Chicken (Gallus gallus)}
VGSPKGISFSDITENSATVSWTPPRSRVDSYRVSYVPITGGTPNVVTVDGSKTRTKLVKLVPGVD
YNVNIISVKGFEESEPISGILKT
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>d1ten__ b.1.2.1 (-) Tenascin {Human (Homo sapiens)}
RLDAPSQIEVKDVTDTTALITWFKPLAEIDGIELTYGIKDVPGDRTTIDLTEDENQYSIGNLKPD
TEYEVSLISRRGDMSSNPAKETFTT
>d1cfb_1 b.1.2.1 (610-709) Neuroglian, two amino proximal Fn3 repeats
{Drosophila melanogaster}
IVQDVPNAPKLTGITCQADKAEIHWEQQGDNRSPILHYTIQFNTSFTPASWDAAYEKVPNTDSSF
VVQMSPWANYTFRVIAFNKIGASPPSAHSDSCTTQ
>d1cfb_2 b.1.2.1 (710-814) Neuroglian, two amino proximal Fn3 repeats
{Drosophila melanogaster}
PDVPFKNPDNVVGQGTEPNNLVISWTPMPEIEHNAPNFHYYVSWKRDIPAAAWENNNIFDWRQNN
IVIADQPTFVKYLIKVVAINDRGESNVAAEEVVGYSGEDR
>d1qg3a1 b.1.2.1 (A:1126-1217) Integin beta-4 subunit {Human (Homo
sapiens)}
DLGAPQNPNAKAAGSRKIHFNWLPPSGKPMGYRVKYWIQGDSESEAHLLDSKVPSVELTNLYPYC
DYEMKVCAYGAQGEGPYSSLVSCRTHQ
>d1qg3a2 b.1.2.1 (A:1218-1320) Integin beta-4 subunit {Human (Homo
sapiens)}
EVPSEPGRLAFNVVSSTVTQLSWAEPAETNGEITAYEVCYGLVNDDNRPIGPMKKVLVDNPKNRM
LLIENLRESQPYRYTVKARNGAGWGPEREAIINLATQP
>d1axib1 b.1.2.1 (B:32-130) Growth hormone receptor {Human (Homo
sapiens)}
EPKFTKCRSPERETFSCHWTDEVHHGTKNEGPIQLFYTRRNTQEWTQEWKECPDYVSAGENSCYF
NSSFTSIAIPYCIKLTSNGGTVDEKCFSVDEIVQ
>d1axib2 b.1.2.1 (B:131-236) Growth hormone receptor {Human (Homo
sapiens)}
PDPPIALNWTLLNVSLTGIHADIQVRWEAPRNADIQKGWMVLEYELQYKEVNETKWKMMDPILTT
SVPVYSLKVDKEYEVRVRSKQRNSGNYGEFSEVLYVTLPQM
>d1eerb1 b.1.2.1 (B:8-116) Erythropoietin (EPO) receptor {Human (Homo
sapiens)}
DPKFESKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVGPGQYSFSYQLEDEPWKLCRLHQA
PTARGAVRFWCSLPTADTSSFVPLELRVTAASGAPRYHRVIHIN
>d1eerb2 b.1.2.1 (B:117-220) Erythropoietin (EPO) receptor {Human
(Homo sapiens)}
EVVLLDAPVGLVARLADESGHVVLRWLPPPETPMTSHIRYEVDVSAGQGAGSVQRVEILEGRTEC
VLSNLRGRTRYTFAVRARMAEPSFGGFWSEWSEPVSLLT
>d1bp3b1 b.1.2.1 (B:202-300) Prolactin receptor {Human (Homo
sapiens)}
LPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNYSLTYHREGETLMHECPDYITGGPNSCHFGK
QYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYI
>d1bp3b2 b.1.2.1 (B:301-404) Prolactin receptor {Human (Homo
sapiens)}
VQPDPPLELAVEVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAAEWEIHFAGQQT
EFKILSLHPGQKYLVQVRCKPDHGYWSAWSPATFIQIPS
>d1f6fb1 b.1.2.1 (B:5-100) Prolactin receptor {Rat (Rattus

norvegicus)}

GKPEIHKCRSPDKETFTCWWNPGTDGGLPTNYSLTYSKEGEKTTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYI

>d1f6fb2 b.1.2.1 (B:101-203) Prolactin receptor {Rat (Rattus norvegicus)}

VEPEPPRNLTLEVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEWEIHFTGHQTQFKVFDLYPGQKYLVQTRCKPDHGYWSRWSQESSVEMP

>d1iarb1 b.1.2.1 (B:1-96) Interleukin-4 receptor alpha chain {Human (Homo sapiens)}

FKVLQEPTCVSDYMSISTCEWKMNGPTNCSTELRLLYQLVFLLSEAHTCIPENNGGAGCVCHLLMDDVVSADNYTLDLWAGQQLLWKGSFKPSEHV

>d1iarb2 b.1.2.1 (B:97-197) Interleukin-4 receptor alpha chain {Human (Homo sapiens)}

KPRAPGNLTVHTNVSDTLLLTWSNPYPPDNYLYNHLTYAVNIWSENDPADFRIYNVTYLEPSLRIAASTLKSGISYRARVRAWAQAYNTTWSEWSPSTKWH

>d1egja_ b.1.2.1 (A:) Common beta-chain in the GM-CSF, IL-3 and IL-5 receptors {Human (Homo sapiens)}

IQMAPPSLNVTKDGDSYSLRWETMKMRYEHIDHTFEIQYRKDTATWKDSKTETLQNAHSMALPALEPSTRYWARVRVRTSRTGYNGIWSEWSEARSWDTES

>d1gh7a1 b.1.2.1 (A:1-103) Common beta-chain in the GM-CSF, IL-3 and IL-5 receptors {Human (Homo sapiens)}

EETIPLQTLRCYNDYTSHITCRWADTQDAQRLVNVTLIRRVNEDLLEPVSCDLSDDMPWSACPHPRCVPRRCVIPCQSFVVTDVDYFSFQPDRPLGTRLTVTL

>d1gh7a2 b.1.2.1 (A:104-217) Common beta-chain in the GM-CSF, IL-3 and IL-5 receptors {Human (Homo sapiens)}

TQHVQPPEPRDLQISTDQDHFLLTWSVALGSPQSHWLSPGDLEFEVVYKRLQDSWEDAAILLSNTSQATLGPEHLMPSSTYVARVRTRLAPGSRLSGRPSKWSPEVCWDSQPGD

>d1gh7a3 b.1.2.1 (A:218-316) Common beta-chain in the GM-CSF, IL-3 and IL-5 receptors {Human (Homo sapiens)}

EAQPQNLECFFDGAAVLSCSWEVRKEVASSVSFGLFYKPSPDAGSAVLLREEECSPVLREGLGSLHTRHHCQIPVPDPATHGQYIVSVQPRRAEKHIKS

>d1cd9b1 b.1.2.1 (B:1-107) Granulocyte colony-stimulating factor (GC-SF) receptor {Mouse (Mus musculus)}

AGYPPASPSNLSCLMHLTTNSLVCQWEPGPETHLPTSFILKSFRSRADCQYQGDTIPDCVAKKRQNNCSIPRKNLLLYQYMAIWVQAENMLGSSESPKLCLDPMDVV

>d1cd9b2 b.1.2.1 (B:108-213) Granulocyte colony-stimulating factor (GC-SF) receptor {Mouse (Mus musculus)}

KLEPPMLQALDIGPDVVSHQPGCLWLSWKPWKPSEYMEQECELRYQPQLKGANWTLVFHLPSSKDQFELCGLHQAPVYTLQMRCIRSSLPGFWSPWSPGLQLRPTM

>d1fyhb1 b.1.2.1 (B:12-109) Interferon-gamma receptor alpha chain {Human (Homo sapiens)}

VPTPTNVTIESYNMNPIVYWEYQIMPQVPVFTVEVKNYGVKNSEWIDACINISHHYCNISDHVGDPSNSLWVRVKARVGQKESAYAKSEEFAVCRDGK

>d1fyhb2 b.1.2.1 (B:110-223) Interferon-gamma receptor alpha chain

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{Human (Homo sapiens)}
IGPPKLDIRKEEKQIMIDIFHPSVFVNGDEQEVDYDPETTCYIRVYNVYVRMNGSEIQYKILTQK
EDDCDEIQCQLAIPVSSLNSQYCVSAEGVLHVWGVTTEKSKEVCITIFN
>d1bqua1 b.1.2.1 (A:5-99) Cytokyne receptor gp130 cytokine-binding
domains {Human (Homo sapiens)}
GLPPEKPKNLSCIVNEGKKMRCEWDGGRETHLETNFTLKSEWATHKFADCKAKRDTPTSCTVDYS
TVYFVNIEVWVEAENALGKVTSDHINFDPV
>d1bqua2 b.1.2.1 (A:100-214) Cytokyne receptor gp130 cytokine-binding
domains {Human (Homo sapiens)}
YKVKPNPPHNLSVINSEELSSILKLTWTNPSIKSVIILKYNIQYRTKDASTWSQIPPEDTASTRS
SFTVQDLKPFTEYVFRIRCMKEDGKGYWSDWSEEASGITYEDRPSKEPSF
>d1i1ra1 b.1.2.1 (A:2-101) Cytokyne receptor gp130 cytokine-binding
domains {Human (Homo sapiens)}
LLDPCGYISPESPVVQLHSNFTAVCVLKEKCMDYFHVNANYIVWKTNHFTIPKEQYTIINRTASS
VTFTDIASLNIQLTCNILTFGQLEQNVYGITIISG
>d1j7vr1 b.1.2.1 (R:2-100) Interleukin-10 receptor 1, IL-10R1 {Human
(Homo sapiens)}
GTELPSPPSVWFEAEFFHHILHWTPIPQQSESTCYEVALLRYGIESWNSISQCSQTLSYDLTAVT
LDLYHSNGYRARVRAVDGSRHSQWTVTNTRFSVD
>d1j7vr2 b.1.2.1 (R:101-206) Interleukin-10 receptor 1, IL-10R1
{Human (Homo sapiens)}
EVTLTVGSVNLEIHNGFILGKIQLPRPKMAPAQDTYESIFSHFREYEIAIRKVPGQFTFTHKKVK
HEQFSLLTSGEVGEFCVQVKPSVASRSNKGMWSKEECISLT
>d1bpv__ b.1.2.1 (-) Type I titin module {Human (Homo sapiens)}
SPIDPPGKPVPLNITRHTVTLKWAKPEYTGGFKITSYIVEKRDLPNGRWLKANFSNILENEFTVS
GLTEDAAYEFRVIAKNAAGAISPPSEPSDAITCRDDVEA
>d1f42a2 b.1.2.1 (A:88-211) The p40 domain of interleukin-12 (IL-12
beta chain), domains 2 and 3 {Human (Homo sapiens)}
GIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAAT
LSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDII
>d1f42a3 b.1.2.1 (A:212-306) The p40 domain of interleukin-12 (IL-12
beta chain), domains 2 and 3 {Human (Homo sapiens)}
KPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATV
ICRKNASISVRAQDRYYSSSWSEWASVPCS
>d1b4ra_ b.1.3.1 (A:) Polycystein-1, PKD-1 {Human (Homo sapiens)}
ATLVGPHGPLASGQLAAFHIAAPLPVTATRWDFGDGSAEVDAAGPAASHRYVLPGRYHVTAVLAL
GAGSALLGTDVQVEA
>d1jz8a1 b.1.4.1 (A:220-333) beta-Galactosidase, domains 2 and 4
{Escherichia coli}
TQISDFHVATRFNDDFSRAVLEAEVQMCGELRDYLRVTVSLWQGETQVASGTAPFGGEIIDERGG
YADRVTLRLNVENPKLWSAEIPNLYRAVVELHTADGTLIEAEACDVGFR
>d1jz8a2 b.1.4.1 (A:626-730) beta-Galactosidase, domains 2 and 4
{Escherichia coli}
FFQFRLSGQTIEVTSEYLFRHSDNELLHWMVALDGKPLASGEVPLDVAPQGKQLIELPELPQPES
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AGQLWLTVRVVQPNATAWSEAGHISAWQQWRLAENLSVTL
>d1bhga1 b.1.4.1 (A:226-328) beta-Glucuronidase {Human (Homo
sapiens)}
TYIDDITVTTSVEQDSGLVNYQISVKGSNLFKLEVRLLDAENKVVANGTGTQGQLKVPGVSLWWP
YLMHERPAYLYSLEVQLTAQTSLGPVSDFYTLPVGIRT
>d1f13a2 b.1.5.1 (A:516-627) Transglutaminase, two C-terminal domains
{Human (Homo sapiens)}
SNVDMDFEVENAVLGKDFKLSITFRNNSHNRYTITAYLSANITFYTGVPKAEFKKETFDVTLEPL
SFKKEAVLIQAGEYMGQLLEQASLHFFVTARINETRDVLAKQKSTVL
>d1f13a3 b.1.5.1 (A:628-728) Transglutaminase, two C-terminal domains
{Human (Homo sapiens)}
TIPEIIIKVRGTQVVGSDMTVTVEFTNPLKETLRNVWVHLDGPGVTRPMKKMFREIRPNSTVQWE
EVCRPWVSGHRKLIASMSSDSLRHVYGELDVQIQRR
>d1g0da2 b.1.5.1 (A:472-583) Transglutaminase, two C-terminal domains
{Red sea bream (Chrysophrys major)}
RLQLSIKHAQPVFGTDFDVIVEVKNEGGRDAHAQLTMLAMAVTYNSLRRGECQRKTISVTVPAHK
AHKEVMRLHYDDYVRCVSEHHLIRVKALLDAPGENGPIMTVANIPLS
>d1g0da3 b.1.5.1 (A:584-684) Transglutaminase, two C-terminal domains
{Red sea bream (Chrysophrys major)}
TPELLVQVPGKAVVWEPLTAYVSFTNPLPVPLKGGVFTLEGAGLLSATQIHVNGAVAPSGKVSVK
LSFSPMRTGVRKLLVDFDSDRLKDVKGVTTVVVHKK
>d1ncia_ b.1.6.1 (A:) N-cadherin (neural) {Mouse (Mus musculus)}
GSDWVIPPINLPENSRGPFPQELVRIRSGRDKNLSLRYSVTGPGADQPPTGIFIINPISGQLSVT
KPLDRELIARFHLRAHAVDINGNQVENPIDIVINVID
>d1ncja2 b.1.6.1 (A:102-215) N-cadherin (neural) {Mouse (Mus
musculus)}
NDNRPEFLHQVWNGSVPEGSKPGTYVMTVTAIDADDPNALNGMLRYRIVSQAPSTPSPNMFTINN
ETGDIITVAAGLDREKVQQYTLIIQATDMEGNPTYGLSNTATAVITVTD
>d1edha1 b.1.6.1 (A:3-101) E-cadherin (epithelial) {Mouse (Mus
musculus)}
VIPPISCPENEKGEFPKNLVQIKSNRDKETKVFYSITGQGADKPPVGVFIIERETGWLKVTQPLD
REAIAKYILYSHAVSSNGEAVEDPMEIVITVTDQ
>d1edha2 b.1.6.1 (A:102-213) E-cadherin (epithelial) {Mouse (Mus
musculus)}
NDNRPEFTQEVFEGSVAEGAVPGTSVMKVSATDADDDVNTYNAAIAYTIVSQDPELPHKNMFTVN
RDTGVISVLTSGLDRESYPTYTLVVQAADLQGEGLSTTAKAVITVKD
>d2mcm__ b.1.7.1 (-) Macromycin {Streptomyces macromomyceticus}
APGVTVTPATGLSNGQTVTVSATGLTPGTVYHVGQCAVVEPGVIGCDATTSTDVTADAAGKITAQ
LKVHSSFQAVVGADGTPWGTVNCKVVSCSAGLGSDSGEGAAQAITFA
>d1noa__ b.1.7.1 (-) Neocarzinostatin {Streptomyces carzinostaticus}
AAPTATVTPSSGLSDGTVVKVAGAGLQAGTAYDVGQCAWVDTGVLACNPADFSSVTADANGSAST
SLTVRRSFEGFLFDGTRWGTVDCTTAACQVGLSDAAGNGPEGVAISFN
>d1acx__ b.1.7.1 (-) Actinoxanthin {Actinomyces globisporus, number
1131}
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APAFSVSPASGASDGQSVSVSVAAAGETYYIAQCAPVGGQDACNPATATSFTTDASGAASFSFTV
RKSYAGQTPSGTPVGSVDCATDACNLGAGNSGLNLGHVALTFG
>d1hzka_ b.1.7.1 (A:) Antitumor antibiotic C-1027 apoprotein
{Streptomyces globisporus}
APAFSVSPASGLSDGQSVSVSVSGAAAGETYYIAQCAPVGGQDACNPATATSFTTDASGAASFSF
VVRKSYTGSTPEGTPVGSVDCATAACNLGAGNSGLDLGHVALTFG
>d1akp__ b.1.7.1 (-) Kedarcidin (apo form) {Actimomycete, strain
L585-6}
ASAAVSVSPATGLADGATVTVSASGFATSTSATALQCAILADGRGACNVAEFHDFSLSGGEGTTS
VVVRRSFTGYVMPDGPEVGAVDCDTAPGGCEIVVGGNTGEYGNAAISFG
>d1cbja_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Cow (Bos
taurus)}
ATKAVCVLKGDGPVQGTIHFEAKGDTVVVTGSITGLTEGDHGFHVHQFGDNTQGCTSAGPHFNPL
SKKHGGPKDEERHVGDLGNVTADKNGVAIVDIVDPLISLSGEYSIIGRTMVVHEKPDDLGRGGNE
ESTKTGNAGSRLACGVIGIAK
>d1azva_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Human (Homo
sapiens)}
ATKAVCVLKGDGPVQGIINFEQKESNGPVKVWGSIKRLTEGLHGFHVHEFGDNTAGCTSAGPHFN
PLSRKHGGPKDEERHVGDLGNVTADKDGVADVSIEDSVISLSGDHCIIGRTLVVHEKADDLGKGG
NEESTKTGNAGSRLACGVIGIAQ
>d1xsoa_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {African clawed
frog (Xenopus laevis)}
VKAVCVLAGSGDVKGVVHFEQQDEGAVSVEGKIEGLTDGLHGFHIHVFGDNTNGCMSAGSHFNPE
NKNHGAPGDTDRHVGDLGNVTAEGGVAQFKITDSLISLKGPNSIIGRTAVVHEKADDLGKGGNDE
SLKTGNAGGRLACGVIGYSP
>d1srda_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Spinach
(Spinacia oleracea)}
ATKKAVAVLKGTSNVEGVVTLTQEDDGPTTVNVRISGLAPGKHGFHLHEFGDTTNGCMSTGPHFN
PDKKTHGAPEDEVRHAGDLGNIVANTDGVAEATIVDNQIPLTGPNSVVGRALVVHELEDDLGKGG
HELSPTTGNAGGRLACGVVGLTPV
>d1jcv__ b.1.8.1 (-) Cu,Zn superoxide dismutase, SOD {Baker's yeast
(Saccharomyces cerevisiae)}
VQAVAVLKGDAGVSGVVKFEQASESEPTTVSYEIAGNSPNAERGFHIHEFGDATNGCVSAGPHFN
PFKKTHGAPTDEVRHVGDMGNVKTDENGVAKGSFKDSLIKLIGPTSVVGRSVVIHAGQDDLGKGD
TEESLKTGNAGPRPACGVIGLTN
>d1yaia_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Photobacterium
leiognathi}
QDLTVKMTDLQTGKPVGTIELSQNKYGVVFTPELADLTPGMHGFHIHQNGSCASSEKDGKVVLGG
AAGGHYDPEHTNKHGFPWTDDNHKGDLPALFVSANGLATNPVLAPRLTLKELKGHAIMIHAGGDN
HSDMPKALGGGGARVACGVIQ
>d1eso__ b.1.8.1 (-) Cu,Zn superoxide dismutase, SOD {Escherichia
coli}
ASEKVEMNLVTSQGVGQSIGSVTITETDKGLEFSPDLKALPPGEHGFHIHAKGSCQPATKDGKAS
AAESAGGHLDPQNTGKHEGPEGAGHLGDLPALVVNNDGKATDAVIAPRLKSLDEIKDKALMVHVG
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GDNMSDQPKPLGGGGERYACGVIK
>d1eqwa_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Salmonella
typhimurium}
NTLTVKMNDALSSGTGENIGEITVSETPYGLLFTPHLNGLTPGIHGFHVHTNPSCMPGMKDGKEV
PALMAGGHLDPEKTGKHLGPYNDKGHLGDLPGLVVNADGTATYPLLAPRLKSLSELKGHSLMIHK
GGDNYSDKPAPLGGGGARFACGVIE
>d2apsa_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Actinobacillus
pleuropneumoniae}
EKLVVQVQQLDPVKGNKDVGTVEITESAYGLVFTPHLHGLAQGLHGFHIHQNPSCEPKEKDGKLV
AGLGAGGHWDPKETKQHGYPWSDNAHLGDLPALFVEHDGSATNPVLAPRLKKLDEVKGHSLMIHE
GGDNHSDHPAPLGGGGPRMACGVIK
>d1ej8a_ b.1.8.1 (A:) Copper chaperone for superoxide dismutase,
C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
SSAVAILETFQKYTIDQKKDTAVRGLARIVQVGENKTLFDITVNGVPEAGNYHASIHEKGDVSKG
VESTGKVWHKFDEPIECFNESDLGKNLYSGKTFLSAPLPTWQLIGRSFVISKSLNHPENEPSSVK
DYSFLGVIAR
>d1jk9b1 b.1.8.1 (B:74-245) Copper chaperone for superoxide dismutase,
C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
GKPNSSAVAILETFQKYTIDQKKDTAVRGLARIVQVGENKTLFDITVNGVPEAGNYHASIHEKGD
VSKGVESTGKVWHKFDEPIECFNESDLGKNLYSGKTFLSAPLPTWQLIGRSFVISKSLNHPENEP
SSVKDYSFLGVIARSAGVWENNKQVCACTGKTVWEERKDALA
>d1do5a_ b.1.8.1 (A:) Copper chaperone for superoxide dismutase,
C-terminal domain {Human (Homo sapiens)}
QNLGAAVAILGGPGTVQGVVRFLQLTPERCLIEGTIDGLEPGLHGLHVHQYGDLTNNCNSCGNHF
NPDGASHGGPQDSDRHRGDLGNVRADADGRAIFRMEDEQLKVWDVIGRSLIIDEGEDDLGRGGHP
LSKITGNSGERLACGIIARSAGLF
>d1d7ca_ b.1.9.1 (A:) Cytochrome domain of cellobiose dehydrogenase
{Fungus (Phanerochaete chrysosporium)}
ESASQFTDPTTGFQFTGITDPVHDVTYGFVFPPLATSGAQSTEFIGEVVAPIASKWIGIALGGAM
NNDLLLVAWANGNQIVSSTRWATGYVQPTAYTGTATLTTLPETTINSTHWKWVFRCQGCTEWNNG
GGIDVTSQGVLAWAFSNVAVDDPSDPQSTFSEHTDFGFFGIDYSTAHSANYQNYLNGDSG
>d1i8aa_ b.1.9.2 (A:) Xylanase 10A {Thermotoga maritima}
MVATAKYGTPVIDGEIDEIWNTTEEIETKAVAMGSLDKNATAKVRVLWDENYLYVLAIVKDPVLN
KDNSNPWEQDSVEIFIDENNHKTGYYEDDDAQFRVNYMNEQTFGTGGSPARFKTAVKLIEGGYIV
EAAIKWKTIKPTPNTVIGFNIQVNDANEKGQRVGIISWSDPTNNSWRDPSKFGNLRLIK
>d1qtsa1 b.1.10.1 (A:692-824) Alpa-adaptin AP2, N-terminal subdomain
{Mouse (Mus musculus)}
GSPGIRLGSSEDNFARFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFLNFTPTL
ICADDLQTNLNLQTKPVDPTVDGGAQVQQVVNIECISDFTEAPVLNIQFRYGGTFQNVSVKLPIT
LNK
>d1e42a1 b.1.10.1 (A:705-824) Beta2-adaptin AP2, N-terminal subdomain
{Human (Homo sapiens)}
GGYVAPKAVWLPAVKAKGLEISGTFTHRQGHIYMEMNFTNKALQHMTDFAIQFNKNSFGVIPSTP
LAIHTPLMPNQSIDVSLPLNTLGPVMKMEPLNNLQVAVKNNIDVFYFSCLIPLNV
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>d1jv2a1 b.1.15.1 (A:439-598) Thigh, calf-1 and calf-2 domains of integrin alpha {Human (Homo sapiens)}
PVITVNAGLEVYPSILNQDNKTCSLPGTALKVSCFNVRFCLKADGKGVLPRKLNFQVELLLDKLK
QKGAIRRALFLYSRSPSHSKNMTISRGGLMQCEELIAYLRDESEFRDKLTPITIFMEYRLDYRTA
ADTTGLQPILNQFTPANISRQAHILLDCGE
>d1jv2a2 b.1.15.1 (A:599-737) Thigh, calf-1 and calf-2 domains of integrin alpha {Human (Homo sapiens)}
DNVCKPKLEVSVDSDQKKIYIGDDNPLTLIVKAQNQGEGAYEAELIVSIPLQADFIGVVRNNEAL
ARLSCAFKTENQTRQVVCDLGNPMKAGTQLLAGLRFSVHQQSEMDTSVKFDLQIQSSNLFDKVSP
VVSHKVDLA
>d1jv2a3 b.1.15.1 (A:738-956) Thigh, calf-1 and calf-2 domains of integrin alpha {Human (Homo sapiens)}
VLAAVEIRGVSSPDHVFLPIPNWEHKENPETEEDVGPVVQHIYELRNNGPSSFSKAMLHLQWPYK
YNNNTLLYILHYDIDGPMNCTSDMEINPLRIKISSLQTTEKNDTVAGQGERDHLITKRDLALSEG
DIHTLGCGVAQCLKIVCQVGRLDRGKSAILYVKSLLWTETFMNKENQNHSYSLKSSASFNVIEFP
YKNLPIEDITNSTLVTTNVTWGIQ
>d1jv2b1 b.1.15.1 (B:55-106,B:355-434) Hybrid domain of integrin beta {Human (Homo sapiens)}
EFPVSEARVLEDRPLSDKGSGDSSQVTQVSPQRIALRLRPDDSKNFSIQVRQXVELEVRDLPEEL
SLSFNATCLNNEVIPGLKSCMGLKIGDTVSFSIEAKVRGCPQEKEKSFTIKPVGFKDSLIVQVTF
DCD
>d1qpxa1 b.1.11.1 (A:1-124) Pilus chaperone PapD, N-domain {Escherichia coli}
AVSLDRTRAVFDGSEKSMTLDISNDNKQLPYLAQAWIENENQEKIITGPVIATPPVQRLDPGAKS
MVRLSTTPDISKLPQDRESLFYFNLREIPPRSEKANVVQIALCTKIKLFYRPAAIKTRP
>d1quna1 b.1.11.1 (A:1-121) Periplasmic chaperone FimC {Escherichia coli}
GVALGATRVIYPAGQKQVQLAVTNNDENSTYLIQSWVENADGVKDGRFIVTPPLFAMKGKKENTL
RILDATNNQLPQDRESLFWMNVKAIPSMDKSKLTENTLQLAIISRIKLYYRPAKLA
>d1mspa_ b.1.11.2 (A:) Major sperm protein, alpha isoform (recombinant), ph 4.6 {Pig roundworm (Ascaris suum)}
SVPPGDINTQPSQKIVFNAPYDDKHTYHIKITNAGGRRIGWAIKTTNMRRLSVDPPCGVLDPKEK
VLMAVSCDTFNAATEDLNNDRITIEWTNTPDGAAKQFRREWFQGDGMVRRKNLPIEYNL
>d4kbpa1 b.1.12.1 (A:9-120) Purple acid phosphatase, N-terminal domain {Kidney bean (Phaseolus vulgaris)}
RDMPLDSDVFRVPPGYNAPQQVHITQGDLVGRAMIISWVTMDEPGSSAVRYWSEKNGRKRIAKGK
MSTYRFFNYSSGFIHHTTIRKLKYNTKYYYEVGLRNTTRRFSFITPP
>d1dqia_ b.1.13.1 (A:) Superoxide reductase (SOR) {Archaeon Pyrococcus furiosus}
MISETIRSGDWKGEKHVPVIEYEREGELVKVKVQVGKEIPHPNTTEHHIRYIELYFLPEGENFVY
QVGRVEFTAHGESVNGPNTSDVYTEPIAYFVLKTKKKGKLYALSYCNIHGLWENEVTLE
>d1dfx_1 b.1.13.1 (37-125) Desulfoferrodoxin C-terminal domain {Desulfovibrio desulfuricans}
VEGSTDGAMEKHVPVIEKVDGGYLIKVGSVPHPMEEKHWIEWIELLADGRSYTKFLKPGDAPEAF
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FAIDASKVTAREYCNLHGHWKAEN
>d1f00i1 b.1.14.1 (I:658-752) Intimin {Escherichia coli}
ASITEIKADKTTAVANGQDAITYTVKVMKGDKPVSNQEVTFTTTLGKLSNSTEKTDTNGYAKVTL
TSTTPGKSLVSARVSDVAVDVKAPEVEFFT
>d1f00i2 b.1.14.1 (I:753-841) Intimin {Escherichia coli}
TLTIDDGNIEIVGTGVKGKLPTVWLQYGQVNLKASGGNGKYTWRSANPAIASVDASSGQVTLKEK
GTTTISVISSDNQTATYTIATPNS
>d1cwva1 b.1.14.1 (A:503-596) Invasin {Yersinia pseudotuberculosis}
LTLTAAVIGDGAPANGKTAITVEFTVADFEGKPLAGQEVVITTNNGALPNKITEKTDANGVARIA
LTNTTDGVTVVTAEVEGQRQSVDTHFVKG
>d1cwva2 b.1.14.1 (A:597-692) Invasin {Yersinia pseudotuberculosis}
TIAADKSTLAAVPTSIIADGLMASTITLELKDTYGDPQAGANVAFDTTLGNMGVITDHNDGTYSA
PLTSTTLGVATVTVKVDGAAFSVPSVTVNFT
>d1cwva3 b.1.14.1 (A:693-795) Invasin {Yersinia pseudotuberculosis}
ADPIPDAGRSSFTVSTPDILADGTMSSTLSFVPVDKNGHFISGMQGLSFTQNGVPVSISPITEQP
DSYTATVVGNSVGDVTITPQVDTLILSTLQKKISLFPV
>d1cwva4 b.1.14.1 (A:796-886) Invasin {Yersinia pseudotuberculosis}
PTLTGILVNGQNFATDKGFPKTIFKNATFQLQMDNDVANNTQYEWSSSFTPNVSVNDQGQVTITY
QTYSEVAVTAKSKKFPSYSVSYRFYP
>d1f0la1 b.2.1.1 (A:381-535) Diphtheria toxin, C-terminal domain
{Corynebacterium diphtheriae}
SPGHKTQPFLHDGYAVSWNTVEDSIIRTGFQGESGHDIKITAENTPLPIAGVLLPTIPGKLDVNK
SKTHISVNGRKIRMRCRAIDGDVTFCRPKSPVYVGNGVHANLHVAFHRSSSEKIHSNEISSDSIG
VLGYQKTVDHTKVNSKLSLFFEIKS
>d1exh__ b.2.2.1 (-) Exo-1,4-beta-D-glycanase (cellulase, xylanase),
cellulose-binding domain, CBD {Cellulomonas fimi}
ASSGPAGCQVLWGVNQWNTGFTANVTVKNTSSAPVDGWTLTFSFPSGQQVTQAWSSTVTQSGSAV
TVRNAPWNGSIPAGGTAQFGFNGSHTGTNAAPTAFSLNGTPCTVG
>d1e5ba_ b.2.2.1 (A:) Endo-1,4-beta xylanase D, xylan binding domain,
XBD {Cellulomonas fimi}
TGCSVTATRAEEWSDGFNVTYSVSGSSAWTVNLALNGSQTIQASWNANVTGSGSTRTVTPNGSGN
TFGVTVMKNGSSTTPAATCAGS
>d1hejc_ b.2.2.1 (C:) Endo-1,4-beta xylanase D, xylan binding domain,
XBD {Cellulomonas fimi}
TGSCSVSAVRGEEWADRFNVTYSVSGSSSWVVTLGLNGGQSVQSSWNAALTGSSGTVTARPNGSG
NSFGVTFYKNGSSATPGATCATG
>d1nbca_ b.2.2.2 (A:) Cellusomal scaffolding protein A, scafoldin
{Clostridium thermocellum}
NLKVEFYNSNPSDTTNSINPQFKVTNTGSSAIDLSKLTLRYYYTVDGQKDQTFWCDHAAIIGSNG
SYNGITSNVKGTFVKMSSSTNNADTYLEISFTGGTLEPGAHVQIQGRFAKNDWSNYTQSNDYSFK
SASQFVEWDQVTAYLNGVLVWGKEP
>d1g43a_ b.2.2.2 (A:) Cellusomal scaffolding protein A, scafoldin
{Clostridium cellulolyticum}
AGTGVVSVQFNNGSSPASSNSIYARFKVTNTSGSPINLADLKLRYYYTQDADKPLTFWCDHAGYM
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SGSNYIDATSKVTGSFKAVSPAVTNADHYLEVALNSDAGSLPAGGSIEIQTRFARNDWSNFDQSN
DWSYTAAGSYMDWQKISAFVGGTLAYGSTP

>d1tf4a2 b.2.2.2 (A:461-605) Endo/exocellulase:cellobiose E-4, C-terminal domain {Thermomonospora fusca}

PEIFVEAQINTPGTTFTEIKAMIRNQSGWPARMLDKGTFRYWFTLDEGVDPADITVSSAYNQCAT
PEDVHHVSGDLYYVEIDCTGEKIFPGGQSEHRREVQFRIAGGPGWDPSNDWSFQGIGNELAPAPY
IVLYDDGVPVWGTAP

>d1anu__ b.2.2.2 (-) Cohesin domain {Clostridium thermocellum, cellulosome, various modules}

VVVEIGKVTGSVGTTVEIPVYFRGVPSKGIANCDFVFRYDPNVLEIIGIDPGDIIVDPNPTKSFD
TAIYPDRKIIVFLFAEDSGTGAYAITKDGVFAKIRATVKSSAPGYITFDEVGGFADNDLVEQKVS
FIDGGVNV

>d1aoha_ b.2.2.2 (A:) Cohesin domain {Clostridium thermocellum, cellulosome, various modules}

AVRIKVDTVNAKPGDTVRIPVRFSGIPSKGIANCDFVYSYDPNVLEIIEIEPGELIVDPNPTKSF
DTAVYPDRKMIVFLFAEDSGTGAYAITEDGVFATIVAKVKSGAPNGLSVIKFVEVGGFANNDLVE
QKTQFFDGGVNVG

>d1g1ka_ b.2.2.2 (A:) Cohesin domain {Clostridium thermocellum, cellulosome, various modules}

ASLKVTVGTANGKPGDTVTVPVTFADVAKMKNVGTCNFYLGYDASLLEVVSVDAGPIVKNAAVNF
SSSASNGTISFLFLDNTITDELITADGVFANIKFKLKSVTAKTTTPVTFKDGGAFGDGTMSKIAS
VTKTNGSVTIDPG

>d1qba_2 b.2.2.3 (28-200) Bacterial chitobiase, n-terminal domain {Serratia marcescens}

DQQLVDQLSQLKLNVKMLDNRAGENGVDCAALGADWASCNRVLFTLSNDGQAIDGKDWVIYFHSP
RQTLRVDNDQFKIAHLTGDLYKLEPTAKFSGFPAGKAVEIPVVAEYWQLFRNDFLPRWYATSGDA
KPKMLANTDTENLDQFVAPFTGDQWKRTKDDKNILMTPASRFV

>d1amx__ b.2.3.1 (-) Collagen-binding domain of adhesin {Staphylococcus aureus}

TSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVSKDITIKDQIQGGQQLDLSTLNINVTGTHSNY
YSGQSAITDFEKAFPGSKITVDNTKNTIDVTIPQGYGSYNSFSINYKTKITNEQQKEFVNNSQAW
YQEHGKEEVNGKSFNHTVHN

>d1qunb1 b.2.3.2 (B:1-158) Mannose-specific adhesin FimH {Escherichia coli}

FACKTANGTAIPIGGGSANVYVNLAPVVNVGQNLVVDLSTQIFCHNDYPETITDYVTLQRGSAYG
GVLSNFSGTVKYSGSSYPFPTTSETPRVVYNSRTDKPWPVALYLTPVSSAGGVAIKAGSLIAVLI
LRQTNNYNSDDFQFVWNIYANNDVVVPT

>d1qunb2 b.2.3.2 (B:159-279) Mannose-specific adhesin FimH {Escherichia coli}

GGCDVSARDVTVTLPDYPGSVPIPLTVYCAKSQNLGYYLSGTTADAGNSIFTNTASFSPAQGVGV
QLTRNGTIIPANNTVSLGAVGTSAVSLGLTANYARTGGQVTAGNVQSIIGVTFVYQ

>d1pdkb_ b.2.3.2 (B:) PapK pilus subunit {Escherichia coli}

LLDRPCHVSGDSLNKHVVFKTRASRDFWYPPGRSPTESFVIRLENCHATAVGKIVTLTFKGTEEA
ALPGHLKVTGVNAGRLGIALLDTDGSSLLKPGTSHNKGQGEKVTGNSLELPFGAYVVATPEALRT

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KSVVPGDYEATATFELTYR
>d1j8ra_ b.2.3.3 (A:) PapG adhesin receptor-binding domain {Escherichia coli}
WNNIVFYSLGDVNSYQGGNVVITQRPQFITSWRPGIATVTWNQCNGPEFADGFWAYYREYIAWVV
FPKKVMTQNGYPLFIEVHNKGSWSEENTGDNDSYFFLKGYKWDERAFDAGNLCQKPGEITRLTEK
FDDIIFKVALPADLPLGDYSVKIPYTSGMQRHFASYLGARFKIPYNVAKTLPRENEMLFLFKNIG
G
>d1edya_ b.2.4.1 (A:) alpha-1-macroglobulin {Rat (Rattus norvegicus)}
EAPFTLKVNTLPLNFDKAEHHRKFQIHINVSYIGERPNSNMVIVDVKMVSGFIPVKPSVKKLQDQ
SNIQRTEVNTNHVLIYIEKLTNQTMGFSFAVEQDIPVKNLKPAPVKVYDYYETDEFAIEEYSAPF
SSDS
>d1bv8a_ b.2.4.1 (A:) alpha-2-macroglobulin {Human (Homo sapiens)}
EEFPFALGVQTLPQTCDEPKAHTSFQISLSVSYTGSRSASNMAIVDVKMVSGFIPLKPTVKMLER
SNHVSRTEVSSNHVLIYLDKVSNQTLSLFFTVLQDVPVRDLKPAIVKVYDYYETDEFAIAEYNAP
CSKDLGNA
>d1ayoa_ b.2.4.1 (A:) alpha-2-macroglobulin {Cow (Bos taurus)}
EFPFALEVQTLPQTCDGPKAHTSFQISLSVSYIGSRPASNMAIVDVKMVSGFIPLKPTVKMLERS
NVSRTEVSNNHVLIYLDKVTNETLTLTFTVLQDIPVRDLKPAIVKVYDYYETDEFAVAEYSAPCS
>d1ycsa_ b.2.5.1 (A:) p53 tumor suppressor, DNA-binding domain {Human (Homo sapiens)}
VPSQKTYQGSYGFRLGFLHSGTAKSVTCTYSPALNKMFCQLAKTCPVQLWVDSTPPPGTRVRAMA
IYKQSQHMTEVVRRCPHHERCSDSDGLAPPQHLIRVEGNLRVEYLDDRNTFRHSVVVPYEPPEVG
SDCTTIHYNYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGRDRRTEEE
>d1hu8a_ b.2.5.1 (A:) p53 tumor suppressor, DNA-binding domain {Mouse (Mus musculus)}
TYQGNYGFHLGFLQSGTAKSVMCTYSPPLNKLFCQLAKTCPVQLWVSATPPAGSRVRAMAIYKKS
QHMTEVVRRCPHHERCSDGDGLAPPQHLIRVEGNLAPEYLEDRQTFRHSVVVPYEPPEAGSEYTT
IHYKYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVRVCACPGRDRRTEEE
>d1a02n2 b.2.5.1 (N:399-576) Transcription factor NFATC, DNA-binding domain {Human (Homo sapiens)}
WPLSSQSGSYELRIEVQPKPHHRAHYETEGSRGAVKAPTGGHPVVQLHGYMENKPLGLQIFIGTA
DERILKPHAFYQVHRITGKTVTTTSYEKIVGNTKVLEIPLEPKNNMRATIDCAGILKLRNADIEL
RKGETDIGRKNTRVRLVFRVHIPESSGRIVSLQTASNPIECSQRSAHE
>d1a66a_ b.2.5.1 (A:) Transcription factor NFATC, DNA-binding domain {Human (Homo sapiens)}
MKDWQLPSHSGPYELRIEVQPKSHHRARYETEGSRGAVKASAGGHPIVQLHGYLENEPLMLQLFI
GTADDRLLRPHAFYQVHRITGKTVSTTSHEAILSNTKVLEIPLLPENSMRAVIDCAGILKLRNSD
IELRKGETDIGRKNTRVRLVFRVHVPQPSGRTLSLQVASNPIECSQRS
>d1imhc2 b.2.5.1 (C:188-367) Transcription factor TONEBP, DNA-binding domain {Human (Homo sapiens)}
KKSPMLCGQYPVKSEGKELKIVVQPETQHRARYLTEGSRGSVKDRTQQGFPTVKLEGHNEPVVLQ
VFVGNDSGRVKPHGFYQACRVTGRNTTPCKEVDIEGTTVIEVGLDPSNNMTLAVDCVGILKLRNA
DVEARIGIAGSKKKSTRARLVFRVNIMRKDGSTLTLQTPSSPILCTQPAG
>d1nfka2 b.2.5.1 (A:39-250) p50 subunit of NF-kappa B (NFKB),
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N-terminal domain {Mouse (Mus musculus)}
GPYLQILEQPKQRGFRFRYVCEGPSHGGLPGASSEKNKKSYPQVKICNYVGPAKVIVQLVTNGKN
IHLHAHSLVGKHCEDGVCTVTAGPKDMVVGFANLGILHVTKKKVFETLEARMTEACIRGYNPGLL
VHSDLAYLQAEGGGDRQLTDREKEIIRQAAVQQTKEMDLSVVRLMFTAFLPDSTGSFTRRLEPVV
SDAIYDSKAPNASNLKI
>d1a3qa2 b.2.5.1 (A:37-226) p52 subunit of NF-kappa B (NFKB),
N-terminal domain {Human (Homo sapiens)}
GPYLVIVEQPKQRGFRFRYGCEGPSHGGLPGASSEKGRKTYPTVKICNYEGPAKIEVDLVTHSDP
PRAHAHSLVGKQCSELGICAVSVGPKDMTAQFNNLGVLHVTKKNMMGTMIQKLQRQRLRSRPQGL
TEAEQRELEQEAKELKKVMDLSIVRLRFSAFLRSLPLKPVISQPIHDSKSPGAS
>d1ikna2 b.2.5.1 (A:19-191) p65 subunit of NF-kappa B (NFKB),
N-terminal domain {Mouse (Mus musculus)}
PYVEIIEQPKQRGMRFRYKCEGRSAGSIPGERSTDTTKTHPTIKINGYTGPGTVRISLVTKDPPH
RPHPHELVGKDCRDGYYEADLCPDRSIHSFQNLGIQCVKKRDLEQAISQRIQTNNNPFHVPIEEQ
RGDYDLNAVRLCFQVTVRDPAGRPLLLTPVLSHPIFDNRAPNT
>d1nfia2 b.2.5.1 (A:20-189) p65 subunit of NF-kappa B (NFKB),
N-terminal domain {Human (Homo sapiens)}
YVEIIEQPKQRGMRFRYKCEGRSAGSIPGERSTDTTKTHPTIKINGYTGPGTVRISLVTKDPPHR
PHPHELVGKDCRDGFYEAELCPDRCIHSFQNLGIQCVKKRDLEQAISQRIQTNNNPFQVPIEEQR
GDYDLNAVRLCFQVTVRDPSGRPLRLPPVLPHPIFDNRAP
>d1bvoa_ b.2.5.1 (A:) Dorsal homologue Gambif1 {African malaria
mosquito (Anopheles gambiae)}
PYVEITEQPHPKALRFRYECEGRSAGSIPGVNTTAEQKTFPSIQVHGYRGRAVVVVSCVTKEGPE
HKPHPHNLVGKEGCKKGVCTVEINSTTMSYTFNNLGIQCVKKKDVEEALRLRQEIRVDPFRTGFG
HAKEPGSIDLNAVRLCFQVFLEGQQRGRFTEPLTPVVSDIIYDKK
>d1xbra_ b.2.5.1 (A:) T domain from Brachyury transcription factor
{African clawed frog (Xenopus laevis)}
ELKVSLEERDLWTRFKELTNEMIVTKNGRRMFPVLKVSMSGLDPNAMYTVLLDFVAADNHRWKYV
NGEWVPGGKPEPQAPSCVYIHPDSPNFGAHWMKDPVSFSKVKLTNKMNGGGQIMLNSLHKYEPRI
HIVRVGGTQRMITSHSFPETQFIAVTAYQNEEITALKIKHNPFAKAFLDAKERN
>d1bf5a2 b.2.5.1 (A:317-568) STAT-1, DNA-binding domain {Human (Homo
sapiens)}
FVVERQPCMPTHPQRPLVLKTGVQFTVKLRLLVKLQELNYNLKVKVLFDKDVNERNTVKGFRKFN
ILGTHTKVMNMEESTNGSLAAEFRHLQLKEQKNAGTRTNEGPLIVTEELHSLSFETQLCQPGLVI
DLETTSLPVVVISNVSQLPSGWASILWYNMLVAEPRNLSFFLTPPCARWAQLSEVLSWQFSSVTK
RGLNVDQLNMLGEKLLGPNASPDGLIPWTRFCKENINDKNFPFWLWIESILELIKKH
>d1bg1a2 b.2.5.1 (A:322-575) STAT3b {Mouse (Mus musculus)}
VVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAALRGSRKFNI
LGTNTKVMNMEESNNGSLSAEFKHLTLREQRCGNGGRANCDASLIVTEELHLITFETEVYHQGLK
IDLETHSLPVVVISNICQMPNAWASILWYNMLTNNPKNVNFFTKPPIGTWDQVAEVLSWQFSSTT
KRGLSIEQLTTLAEKLLGPGVNYSGCQITWAKFCKENMAGKGFSFWVWLDNIIDLVKKY
>d1e50q_ b.2.5.1 (Q:) Acute myeloid leukemia 1 protein (AML1), RUNT
domain {Human (Homo sapiens)}
LVRTDSPNFLCSVLPTHWRCNKTLPIAFKVVALGDVPDGTLVTVMAGNDENYSAELRNATAAMKN
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QVARFNDLRFVGRSGRGKSFTLTITVFTNPPQVATYHRAIKITVD
>d1h9da_ b.2.5.1 (A:) Acute myeloid leukemia 1 protein (AML1), RUNT domain {Human (Homo sapiens)}
VLADHPGELVRTDSPNFLCSVLPTHWRCNKTLPIAFKVVALGDVPDGTLVTVMAGNDENYSAELR
NATAAMKNQVARFNDLRFVGRSGRGKSFTLTITVFTNPPQVATYHRAIKITVDGPREPRR
>d1hcz_1 b.2.6.1 (1-167,231-250) Cytochrome f, large domain {Turnip (Brassica rapa)}
YPIFAQQNYENPREATGRIVCANCHLASKPVDIEVPQAVLPDTVFEAVVKIPYDMQLKQVLANGK
KGALNVGAVLILPEGFELAPPDRISPEMKEKIGNLSFQNYRPNKKNILVIGPVPGQKYSEITFPI
LAPDPATNKDVHFLKYPIYVGGNRGRGQIYPDGSKSNXPNVGGFGQGDAEIVLQDPLR
>d1e2wa1 b.2.6.1 (A:1-168,A:233-251) Cytochrome f, large domain {Chlamydomonas reinhardtii}
YPVFAQQNYANPREANGRIVCANCHLAQKAVEIEVPQAVLPDTVFEAVIELPYDKQVKQVLANGK
KGDLNVGMVLILPEGFELAPPDRVPAEIKEKVGNLYYQPYSPEQKNILVVGPVPGKKYSEMVVPI
LSPDPAKNKNVSYLKYPIYFGGNRGRGQVYPDGKKSNFXNVGGFGQAETEIVLQNPAR
>d1ci3m1 b.2.6.1 (M:1-169,M:232-249) Cytochrome f, large domain {Phormidium laminosum}
YPFWAQQNYANPREATGRIVCANCHLAAKPAEIEVPQAVLPDSVFKAVVKIPYDHSVQQVQADGS
KGPLNVGAVLMLPEGFTIAPEDRIPEEMKEEVGPSYLFQPYADDKQNIVLVGPLPGDEYEEIVFP
VLSPNPATNKSVAFGKYSIHLGANRGRGQIYPTGEKSNNXNVGGFGQKDTEIVLQSPN
>d1i31a_ b.2.7.1 (A:) Second domain of Mu2 adaptin subunit (ap50) of ap2 adaptor {Rat (Rattus norvegicus)}
IGWRREGIKYRRNELFLDVLESVNLLMSPQGQVLSAHVSGRVVMKSYLSGMPECKFGMNDKIVIE
KQGKGTADETSKSGKQSIAIDDCTFHQCVRLSKFDSERSISFIPPDGEFELMRYRTTKDIILPFR
VIPLVREVGRTKLEVKVVIKSNFKPSLLAQKIEVRIPTPLNTSGVQVICMKGKAKYKASENAIVW
KIKRMAGMKESQISAEIELLPTNDKKKWARPPISMNFEVPFAPSGLKVRYLKVFEPKLNYSDHDV
IKWVRYIGRSGIYETRC
>d1cgt_2 b.3.1.1 (580-684) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus circulans, different strains}
LTGDQVTVRFVVNNASTTLGQNLYLTGNVAELGNWSTGSTAIGPAFNQVIHQYPTWYYDVSVPAG
KQLEFKFFKKNGSTITWESGSNHTFTTPASGTATVTVNWQ
>d1kcla2 b.3.1.1 (A:582-686) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus circulans, different strains}
LSGDQVSVRFVVNNATTALGQNVYLTGSVSELGNWDPAKAIGPMYNQVVYQYPNWYYDVSVPAGK
TIEFKFLKKQGSTVTWEGGSNHTFTAPSSGTATINVNWQP
>d1cyg_2 b.3.1.1 (575-680) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus stearothermophilus}
LTNDQVSVRFVVNNATTNLGQNIYIVGNVYELGNWDTSKAIGPMFNQVVYSYPTWYIDVSVPEGK
TIEFKFIKKDSQGNVTWESGSNHVYTTPTNTTGKIIVDWQN
>d1qhoa2 b.3.1.1 (A:577-686) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus stearothermophilus, maltogenic alpha-amylase}
LSGTQTSVVFTVKSAPPTNLGDKIYLTGNIPELGNWSTDTSGAVNNAQGPLLAPNYPDWFYVFSV
PAGKTIQFKFFIKRADGTIQWENGSNHVATTPTGATGNITVTWQN

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>d1pama2 b.3.1.1 (A:583-686) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus sp., strain 1011}
TGDQVTVRFVINNATTALGQNVFLTGNVSELGNWDPNNAIGPMYNQVVYQYPTWYYDVSVPAGQT
IEFKFLKKQGSTVTWEGGANRTFTTPTSGTATVNVNWQP
>d1ciu_2 b.3.1.1 (579-683) Cyclodextrin glycosyltransferase, C-terminal domain {Thermoanaerobacterium thermosulfurigenes, EM1}
LTGNQICVRFVVNNASTVYGENVYLTGNVAELGNWDTSKAIGPMFNQVVYQYPTWYYDVSVPAGT
TIQFKFIKKNGNTITWEGGSNHTYTVPSSSTGTVIVNWQQ
>d1acz__ b.3.1.1 (-) Glucoamilase, granular starch-binding domain {Aspergillus niger}
CTTPTAVAVTFDLTATTTYGENIYLVGSISQLGDWETSDGIALSADKYTSSDPLWYVTVTLPAGE
SFEYKFIRIESDDSVEWESDPNREYTVPQACGTSTATVTDTWR
>d1cqya_ b.3.1.1 (A:) beta-amylase {Bacillus cereus}
TPVMQTIVVKNVPTTIGDTVYITGNRAELGSWDTKQYPIQLYYDSHSNDWRGNVVLPAERNIEFK
AFIKSKDGTVKSWQTIQQSWNPVPLKTTSHTSSW
>d1h8la1 b.3.2.1 (A:305-383) Carboxypeptidase D, a regulatory domain {Crested duck (Lophonetta specularioides)}
GIWGFVLDATDGRGILNATISVADINHPVTTYKDGDYWRLLVQGTYKVTASARGYDPVTKTVEVD
SKGGVQVNFTLSRT
>d1vcbc_ b.3.3.1 (C:) VHL {Human (Homo sapiens)}
LRSVNSREPSQVIFCNRSPRVVLPVWLNFDGEPQPYPTLPPGTGRRIHSYRGHLWLFRDAGTHDG
LLVNQTELFVPSLNVDGQPIFANITLPVYTLKERCLQVVRSLVKPENYRRLDIVRSLYEDLEDHP
NVQKDLERLTQE
>d1f86a_ b.3.4.1 (A:) Transthyretin (synonym: prealbumin) {Human (Homo sapiens)}
CPLMVKVLDAVRGSPAINVAVHVFRKAADDTWEPFASGKTSESGELHGLTTEEEFVEGIYKVEID
TKSYWKALGISPFHEHAEVVFTANDSGPRRYTIAALLSPYSYSTMAVVTN
>d1ttba_ b.3.4.1 (A:) Transthyretin (synonym: prealbumin) {Human (Homo sapiens)}
GPTGTGESKCPLMVKVLDAVRGSPAINVAVHVFRKAADDTWEPFASGKTSESGELHGLTTEEEFV
EGIYKVEIDTKSYWKALGISPFHEHAEVVFTANDSGPRRYTIATLLSPYSYSTTAVVTNPKE
>d1gkea_ b.3.4.1 (A:) Transthyretin (synonym: prealbumin) {Rat (Rattus norvegicus)}
SKCPLMVKVLDAVRGSPAVDVAVKVFKKTADGSWEPFASGKTAESGELHGLTTDEKFTEGVYRVE
LDTKSYWKALGISPFHEYAEVVFTANDSGHRHYTIAALLSPYSYSTTAVVSNPQN
>d1tfpa_ b.3.4.1 (A:) Transthyretin (synonym: prealbumin) {Chicken (Gallus gallus)}
CPLMVKVLDAVRGSPAANVAVKVFKKAADGTWQDFATGKTTEFGEIHELTTEEQFVEGVYRVEFD
TSSYWKGLGLSPFHEYADVVFTANDSGHRHYTIAALLSPFSYSTTAVVS
>d1d2oa1 b.3.5.1 (A:535-624) B repeat unit of collagen binding surface protein (cna) {Staphylococcus aureus}
ETTSSIGEKVWDDKDNQDGKRPEKVSVNLLANGEKVKTLDVTSETNWKYEFKDLPKYDEGKKIEY
TVTEDHVKDYTTDINGTTITNKYTP
>d1d2oa2 b.3.5.1 (A:625-721) B repeat unit of collagen binding surface
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protein (cna) {Staphylococcus aureus}
GETSATVTKNWDDNNNQDGKRPTEIKVELYQDGKATGKTAILNESNNWTHTWTGLDEKAKGQQVK
YTVEELTKVKGYTTHVDNNDMGNLITTNKYTP
>d1dmha_ b.3.6.1 (A:) Catechol 1,2-dioxygenase {Acinetobacter calcoaceticus}
VKIFNTQDVQDFLRVASGLEQEGGNPRVKQIIHRVLSDLYKAIEDLNITSDEYWAGVAYLNQLGA
NQEAGLLSPGLGFDHYLDMRMDAEDAALGIENATPRTIEGPLYVAGAPESVGYARMDDGSDPNGH
TLILHGTIFDADGKPLPNAKVEIWHANTKGFYSHFDPTGEQQAFNMRRSIITDENGQYRVRTILP
AGYGCPPEGPTQQLLNQLGRHGNRPAHIHYFVSADGHRKLTTQINVAGDPYTYDDFAYATREGLV
VDAVEHTDPEAIKANDVEGPFAEMVFDLKLTRLVDGVDNQVVDRPRLAV
>d3pcca_ b.3.6.1 (A:) Protocatechuate-3,4-dioxygenase, alpha chain {Pseudomonas aeruginosa}
PIELLPETPSQTAGPYVHIGLALEAAGNPTRDQEIWNRLAKPDAPGEHILLLGQVYDGNGHLVRD
SFLEVWQADANGEYQDAYNLENAFNSFGRTATTFDAGEWTLHTVKPGVVNNAAGVPMAPHINISL
FARGINIHLHTRLYFDDEAQANAKCPVLNLIEQPQRRETLIAKRCEVDGKTAYRFDIRIQGEGET
VFFDF
>d1eo9a_ b.3.6.1 (A:) Protocatechuate-3,4-dioxygenase, alpha chain {Acinetobacter calcoaceticus, adp1}
ELKETPSQTGGPYVHIGLLPKQANIEVFEHNLDNNLVQDNTQGQRIRLEGQVFDGLSLPLRDVLI
EIWQADTNGVYPSQADTQGKQVDPNFLGWGRTGADFGTGFWSFNTIKPGAVPGRKGSTQAPHISL
IIFARGINIGLHTRVYFDDEAEANAKDPVLNSIEWATRRQTLVAKREERDGEVVYRFDIRIQGEN
ETVFFDI
>d3pccm_ b.3.6.1 (M:) Protocatechuate-3,4-dioxygenase, beta chain {Pseudomonas aeruginosa}
PAQDNSRFVIRDRNWHPKALTPDYKTSIARSPRQALVSIPQSISETTGPNFSHLGFGAHDHDLLL
NFNNGGLPIGERIIVAGRVVDQYGKPVPNTLVEMWQANAGGRYRHKNDRYLAPLDPNFGGVGRCL
TDSDGYYSFRTIKPGPYPWRNGPNDWRPAHIHFGISGPSIATKLITQLYFEGDPLIPMCPIVKSI
ANPEAVQQLIAKLDMNNANPMDCLAYRFDIVLRGQRKTHFE
>d1eo9b_ b.3.6.1 (B:) Protocatechuate-3,4-dioxygenase, beta chain {Acinetobacter calcoaceticus, adp1}
IIWGAYAQRNTEDHPPAYAPGYKTSVLRSPKNALISIAETLSEVTAPHFSADKFGPKDNDLILNY
AKDGLPIGERVIVHGYVRDQFGRPVKNALVEVWQANASGRYRHPNDQYIGAMDPNFGGCGRMLTD
DNGYYVFRTIKPGPYPWRNRINEWRPAHIHFSLIADGWAQRLISQFYFEGDTLIDSCPILKTIPS
EQQRRALIALEDKSNFIEADSRCYRFDITLRGRRATYFENDLT
>d1c3ga1 b.4.1.1 (A:180-259) Heat shock protein 40 Sis1 {Baker's yeast (Saccharomyces cerevisiae)}
ETVQVNLPVSLEDLFVGKKKSFKIGRKGPHGASEKTQIDIQLKPGWKAGTKITYKNQGDYNPQTG
RRKTLQFVIQEKSHP
>d1c3ga2 b.4.1.1 (A:260-349) Heat shock protein 40 Sis1 {Baker's yeast (Saccharomyces cerevisiae)}
NFKRDGDDLIYTLPLSFKESLLGFSKTIQTIDGRTLPLSRVQPVQPSQTSTYPGQGMPTPKNPSQ
RGNLIVKYKVDYPISLNDAQKRAID
>d1hd8a1 b.105.1.1 (A:263-356) Penicillin-binding protein 5, C-terminal domain {Escherichia coli}

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FETVNPLKVGKEFASEPVWFGDSDRASLGVDKDVYLTIPRGRMKDLKASYVLNSSELHAPLQKNQ
VVGTINFQLDGKTIEQRPLVVLQEIPEGN
>d1hoe__ b.5.1.1 (-) alpha-Amylase inhibitor tendamistat
{Streptomyces tendae}
DTTVSEPAPSCVTLYQSWRYSQADNGCAETVTVKVVYEDDTEGLCYAVAPGQITTVGDGYIGSHG
HARYLARCL
>d1aac__ b.6.1.1 (-) Amicyanin {Paracoccus denitrificans}
DKATIPSESPFAAAEVADGAIVVDIAKMKYETPELHVKVGDTVTWINREAMPHNVHFVAGVLGEA
ALKGPMMKKEQAYSLTFTEAGTYDYHCTPHPFMRGKVVVE
>d1id2a_ b.6.1.1 (A:) Amicyanin {Paracoccus versutus (Thiobacillus
versutus)}
QDKITVTSEKPVAAADVPADAVVVGIEKMKYLTPEVTIKAGETVYWVNGEVMPHNVAFKKGIVGE
DAFRGEMMTKDQAYAITFNEAGSYDYFCTPHPFMRGKVIVE
>d1plc__ b.6.1.1 (-) Plastocyanin {Poplar (Populus nigra), variant
italica}
IDVLLGADDGSLAFVPSEFSISPGEKIVFKNNAGFPHNIVFDEDSIPSGVDASKISMSEEDLLNA
KGETFEVALSNKGEYSFYCSPHQGAGMVGKVTVN
>d9pcy__ b.6.1.1 (-) Plastocyanin {French bean (Phaseolus vulgaris)}
LEVLLGSGDGSLVFVPSEFSVPSGEKIVFKNNAGFPHNVVFDEDEIPAGVDAVKISMPEEELLNA
PGETYVVTLDTKGTYSFYCSPHQGAGMVGKVTVN
>d1pla__ b.6.1.1 (-) Plastocyanin {Parsley (Petroselinum crispum)}
AEVKLGSDDGGLVFSPSSFTVAAGEKITFKNNAGFPHNIVFDEDEVPAGVNAEKISQPEYLNGAG
ETYEVTLTEKGTYKFYCEPHAGAGMKGEVTVN
>d1ag6__ b.6.1.1 (-) Plastocyanin {Spinach (Spinacia oleracea)}
VEVLLGGDDGSLAFLPGDFSVASGEEIVFKNNAGFPHNVVFDEDEIPSGVDAAKISMSEEDLLNA
PGETYKVTLTEKGTYKFYCSPHQGAGMVGKVTVN
>d1bypa_ b.6.1.1 (A:) Plastocyanin {White campion (Silene pratensis)}
AEVLLGSSDGGLAFVPSDLSIASGEKITFKNNAGFPHNDLFDKKEVPAGVDVTKISMPEEDLLNA
PGEEYSVTLTEKGTYKFYCAPHAGAGMVGKVTVN
>d1iuz__ b.6.1.1 (-) Plastocyanin {Sea lettuce (Ulva pertusa)}
AQIVKLGGDDGSLAFVPSKISVAAGEAIEFVNNAGFPHNIVFDEDAVPAGVDADAISYDDYLNSK
GETVVRKLSTPGVYGVYCEPHAGAGMKMTITVQ
>d2plt__ b.6.1.1 (-) Plastocyanin {Green alga (Chlamydomonas
reinhardtii)}
DATVKLGADSGALEFVPKTLTIKSGETVNFVNNAGFPHNIVFDEDAIPSGVNADAISRDDYLNAP
GETYSVKLTAAGEYGYYCEPHQGAGMVGKIIVQ
>d7pcy__ b.6.1.1 (-) Plastocyanin {Green alga (Enteromorpha
prolifera)}
AAIVKLGGDDGSLAFVPNNITVGAGESIEFINNAGFPHNIVFDEDAVPAGVDADAISAEDYLNSK
GQTVVRKLTTPGTYGVYCDPHSGAGMKMTITVQ
>d1kdj__ b.6.1.1 (-) Plastocyanin {Fern (Adiantum capillus-veneris)}
AKVEVGDEVGNFKFYPDSITVSAGEAVEFTLVGETGHNIVFDIPAGAPGTVASELKAASMDENDL
LSEDEPSFKAKVSTPGTYTFYCTPHKSANMKGTLTVK
>d1nin__ b.6.1.1 (-) Plastocyanin {Anabaena variabilis}
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ETYTVKLGSDKGLLVFEPAKLTIKPGDTVEFLNNKVPPHNVVFDAALNPAKSADLAKSLSHKQLL
MSPGQSTSTTFPADAPAGEYTFYCEPHRGAGMVGKITVAG
>d1bawa_ b.6.1.1 (A:) Plastocyanin {Cyanobacterium (Phormidium
laminosum)}
ETFTVKMGADSGLLQFEPANVTVHPGDTVKWVNNKLPPHNILFDDKQVPGASKELADKLSHSQLM
FSPGESYEITFSSDFPAGTYTYYCAPHRGAGMVGKITVEG
>d1pcs__ b.6.1.1 (-) Plastocyanin {Cyanobacterium (Synechocystis sp.),
pcc 6803}
ANATVKMGSDSGALVFEPSTVTIKAGEEVKWVNNKLSPHNIVFDADGVPADTAAKLSHKGLLFAA
GESFTSTFTEPGTYTYYCEPHRGAGMVGKVVVE
>d1bxva_ b.6.1.1 (A:) Plastocyanin {Cyanobacterium (Synechocystis
sp.), pcc 7942}
QTVAIKMGADNGMLAFEPSTIEIQAGDTVQWVNNKLAPHNVVVEGQPELSHKDLAFSPGETFEAT
FSEPGTYTYYCEPHRGAGMVGKIVVQ
>d2b3ia_ b.6.1.1 (A:) Plastocyanin {Photosynthetic prokaryote
(Prochlorothrix hollandica)}
ASVQIKMGTDKYAPLYEPKALSISAGDTVEFVMNKVGPHNVIFDKVPAGESAPALSNTKLAIAPG
SFYSVTLGTPGTYSFYCTPHRGAGMVGTITVE
>d1paz__ b.6.1.1 (-) Pseudoazurin {Alcaligenes faecalis, strain s-6}
ENIEVHMLNKGAEGAMVFEPAYIKANPGDTVTFIPVDKGHNVESIKDMIPEGAEKFKSKINENYV
LTVTQPGAYLVKCTPHYAMGMIALIAVGDSPANLDQIVSAKKPKIVQERLEKVIA
>d1pmy__ b.6.1.1 (-) Pseudoazurin {Methylobacterium extorquens,
strain am1}
DEVAVKMLNSGPGGMMVFDPALVRLKPGDSIKFLPTDKGHNVETIKGMAPDGADYVKTTVGQEAV
VKFDKEGVYGFKCAPHYMMGMVALVVVGDKRDNLEAAKSVQHNKLTQKRLDPLFAQIQ
>d1bqk__ b.6.1.1 (-) Pseudoazurin {Achromobacter cycloclastes}
ADFEVHMLNKGKDGAMVFEPASLKVAPGDTVTFIPTDKGHNVETIKGMIPDGAEAFKSKINENYK
VTFTAPGVYGVKCTPHYGMGMVGVVQVGDAPANLEAVKGAKNPKKAQERLDAALAALGN
>d1adwa_ b.6.1.1 (A:) Pseudoazurin {Thiosphaera pantotropha}
ATHEVHMLNKGESGAMVFEPAFVRAEPGDVINFVPTDKSHNVEAIKEILPEGVESFKSKINESYT
LTVTEPGLYGVKCTPHFGMGMVGLVQVGDAPENLDAAKTAKMPKKARERMDAELAQVN
>d2cbp__ b.6.1.1 (-) Plantacyanin {Cucumber (Cucumis sativus)}
AVYVVGGSGGWTFNTESWPKGKRFRAGDILLFNYNPSMHNVVVVNQGGFSTCNTPAGAKVYTSGR
DQIKLPKGQSYFICNFPGHCQSGMKIAVNAL
>d1f56a_ b.6.1.1 (A:) Plantacyanin {Spinach (Spinacia oleracea)}
AVYNIGWSFNVNGARGKSFRAGDVLVFKYIKGQHNVVAVNGRGYASCSAPRGARTYSSGQDRIKL
TRGQNYFICSFPGHCGGGMKIAINAK
>d1azca_ b.6.1.1 (A:) Azurin {Alcaligenes denitrificans}
AQCEATIESNDAMQYNLKEMVVDKSCKQFTVHLKHVGKMAKVAMGHNWVLTKEADKQGVATDGMN
AGLAQDYVKAGDTRVIAHTKVIGGGESDSVTFDVSKLTPGEAYAYFCSFPGHWAMMKGTLKLSN
>d1dyza_ b.6.1.1 (A:) Azurin {Alcaligenes xylosoxidans, NCIMB (11015),
different isoforms}
AQCEATVESNDAMQYNVKEIVVDKSCKQFTMHLKHVGKMAKVAMGHNLVLTKDADKQAVATDGMG
AGLAQDYVKAGDTRVIAHTKVIGGGESDSVTFDVSKIAAGENYAYFCSFPGHWAMMKGTLKLGS
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>d1rkra_ b.6.1.1 (A:) Azurin {Alcaligenes xylosoxidans, NCIMB (11015),
different isoforms}
AECSVDIAGNDGMQFDKKEITVSKSCKQFTVNLKHPGKLAKNVMGHNWVLTKQADMQGAVNDGMA
AGLDNNYVKKDDARVIAHTKVIGGGETDSVTFDVSKLAAGEDYAYFCSFPGHFALMKGVLKLVD
>d1cc3a_ b.6.1.1 (A:) Azurin {Pseudomonas aeruginosa}
AECSVDIQGNDQMQFNTNAITVDKSCKQFTVNLSHPGNLPKNVMGHNWVLSTAADMQGVVTDGMA
SGLDKDYLKPDDSRVIAHTKLIGSGEKDSVTFDVSKLKEGEQYMFFCSELCGINHALMKGTLTLK
>d1jzga_ b.6.1.1 (A:) Azurin {Pseudomonas aeruginosa}
AECSVDIQGNDQMQFNTNAITVDKSCKQFTVNLSHPGNLPKNVMGHNWVLSTAADMQGVVTDGMA
SGLDKDYLKPDDSRVIAHTKLIGSGEKDSVTFDVSKLKEGEQYMFFCTFPGHSALMKGTLTLK
>d1joi__ b.6.1.1 (-) Azurin {Pseudomonas fluorescens}
AECKVTVDSTDQMSFNTKAIEIDKSCKTFTVELTHSGSLPKNVMGHNWVLSSAADMPGIASDGMA
AGIDKNYLKEGDTRVIAHTKIIGAGEKDSVTFDVSKLAAGTDYAFFCSFPGHISMMKGTVTVK
>d1nwpa_ b.6.1.1 (A:) Azurin {Pseudomonas putida}
AECKVTVDSTDQMSFNTKDIAIDKSCKTFTVELTHSGSLPKNVMGHNLVISKEADMQPIATDGLS
AGIDKQYLKDGDARVIAHTKVIGAGEKDSVTFDVSKLAAGEKYGFFCSFPGHISMMKGTVTLK
>d1cuoa_ b.6.1.1 (A:) Azurin {Methylomonas sp. j}
ASCETTVTSGDTMTYSTRSISVPASCAEFTVNFEHKGHMPKTGMGHNWVLAKSADVGDVAKEGAH
AGADNNFVTPGDKRVIAFTPIIGGGEKTSVKFKVSALSKDEAYTYFCSYPGHFSMMRGTLKLEE
>d1qhqa_ b.6.1.1 (A:) Auracyanin {Chloroflexus aurantiacus}
ANAPGGSNVVNETPAQTVEVRAAPDALAFAQTSLSLPANTVVRLDFVNQNNLGVQHNWVLVNGGD
DVAAAVNTAAQNNADALFVPPPDTPNALAWTAMLNAGESGSVTFRTPAPGTYLYICTFPGHYLAG
MKGTLTVTP
>d1e30a_ b.6.1.1 (A:) Rusticyanin {Thiobacillus ferrooxidans}
LDTTWKEATLPQVKAMLEKDTGKVSGDTVTYSGKTVHVVAAAVLPGFPFPSFEVHDKKNPTLEIP
AGATVDVTFINTNKGFGHSFDITKKGPPYAVMPVIDPIVAGTGFSPVPKDGKFGYTNFTWHPTAG
TYYYVCQIPGHAATGQFGKIVVK
>d1jer__ b.6.1.1 (-) Stellacyanin {Cucumber (Cucumis sativus)}
MQSTVHIVGDNTGWSVPSSPNFYSQWAAGKTFRVGDSLQFNFPANAHNVHEMETKQSFDACNFVN
SDNDVERTSPVIERLDELGMHYFVCTVGTHCSNGQKLSINVVAAN
>d1ibya_ b.6.1.4 (A:) Red copper protein nitrosocyanin {Nitrosomonas
europaea}
EHNFNVVINAYDTTIPELNVEGVTVKNIRAFNVLNEPETLVVKKGDAVKVVVENKSPISEGFSID
AFGVQEVIKAGETKTISFTADKAGAFTIWCQLHPKNIHLPGTLNVVE
>d1qnia1 b.6.1.4 (A:451-581) Nitrous oxide reductase, C-terminal
domain {Pseudomonas nautica}
KIYERNDPYFASCRAQAEKDGVTLESDNKVIRDGNKVRVYMTSVAPQYGMTDFKVKEGDEVTVYI
TNLDMVEDVTHGFCMVNHGVSMEISPQQTASVTFTAGKPGVYWYYCNWFCHALHMEMVGRMLVEA
A
>d1fwxa1 b.6.1.4 (A:452-581) Nitrous oxide reductase, C-terminal
domain {Paracoccus denitrificans}
SVWDRNDPMWAETRAQAEADGVDIDNWTEEVIRDGNKVRVYMSSVAPSFSIESFTVKEGDEVTVI
VTNLDEIDDLTHGFTMGNYGVAMEIGPQMTSSVTFVAANPGVYWYYCQWFCHALHMEMRGRMLVE
PK
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>d1cyx__ b.6.1.2 (-) Quinol oxidase (CyoA) {Escherichia coli}
KPITIEVVSMDWKWFFIYPEQGIATVNEIAFPANTPVYFKVTSNSVMHSFFIPRLGSQIYAMAGM
QTRLHLIANEPGTYDGICAEICGPGHSGMKFKAIATPDRAAFDQWVAKAKQSPNTMSDMAAFEKL
AAPSEYNQVEYFSNVKPDLFADVINKFM
>d1fftb1 b.6.1.2 (B:118-283) Quinol oxidase (CyoA) {Escherichia coli}
KPLAHDEKPITIEVVSMDWKWFFIYPEQGIATVNEIAFPANTPVYFKVTSNSVMNSFFIPRLGSQ
IYAMAGMQTRLHLIANEPGTYDGISASYSGPGFSGMKFKAIATPDRAAFDQWVAKAKQSPNTMSD
MAAFEKLAAPSEYNQVEYFSNVKPDLFADVINKFMA
>d1ocrb1 b.6.1.2 (B:91-227) Cytochrome c oxidase {Cow (Bos taurus)}
NNPSLTVKTMGHQWYWSYEYTDYEDLSFDSYMIPTSELKPGELRLLEVDNRVVLPMEMTIRMLVS
SEDVLHSWAVPSLGLKTDAIPGRLNQTTLMSSRPGLYYGQCSEICGSNHSFMPIVLELVPLKYFE
KWSASML
>d1ar1b1 b.6.1.2 (B:108-252) Cytochrome c oxidase {Paracoccus denitrificans}
NDPDLVIKAIGHQWYWSYEYPNDGVAFDALMLEKEALADAGYSEDEYLLATDNPVVVPVGKKVLV
QVTATDVIHAWTIPAFAVKQDAVPGRIAQLWFSVDQEGVYFGQCSELCGINHAYMPIVVKAVSQE
KYEAWLAGAKEEFAA
>d2cuaa_ b.6.1.2 (A:) Cytochrome c oxidase {Thermus thermophilus, ba3 type}
AGKLERVDPTTVRQEGPWADPAQAVVQTGPNQYTVYVLAFAFGYQPNPIEVPQGAEIVFKITSPD
VIHGFHVEGTNINVEVLPGEVSTVRYTFKRPGEYRIICNQYCGLGHQNMFGTIVVKE
>d2cuab_ b.6.1.2 (B:) Cytochrome c oxidase {Thermus thermophilus, ba3 type}
AYTLATHTAGVIPAGKLERVDPTTVRQEGPWADPAQAVVQTGPNQYTVYVLAFAFGYQPNPIEVP
QGAEIVFKITSPDVIHGFHVEGTNINVEVLPGEVSTVRYTFKRPGEYRIICNQYCGLGHQNMFGT
IVVKE
>d1nif_1 b.6.1.3 (8-166) Nitrite reductase, NIR {Achromobacter cycloclastes}
DISTLPRVKVDLVKPPFVHAHDQVAKTGPRVVEFTMTIEEKKLVIDREGTEIHAMTFNGSVPGPL
MVVHENDYVELRLINPDTNTLLHNIDFHAATGALGGGALTQVNPGEETTLRFKATKPGVFVYHCA
PEGMVPWHVTSGMNGAIMVLPRDGLKDEK
>d1nif_2 b.6.1.3 (167-340) Nitrite reductase, NIR {Achromobacter cycloclastes}
GQPLTYDKIYYVGEQDFYVPKDEAGNYKKYETPGEAYEDAVKAMRTLTPTHIVFNGAVGALTGDH
ALTAAVGERVLVVHSQANRDTRPHLIGGHGDYVWATGKFRNPPDLDQETWLIPGGTAGAAFYTFR
QPGVYAYVNHNLIEAFELGAAGHFKVTGEWNDDLMTSVVKPASM
>d1j9qa1 b.6.1.3 (A:4-166) Nitrite reductase, NIR {Alcaligenes faecalis, strain s-6}
ATAAEIAALPRQKVELVDPPFVHAHSQVAEGGPKVVEFTMVIEEKKIVIDDAGTEVHAMAFNGTV
PGPLMVVHQDDYLELTLINPETNTLMHNINFHAATGALGGGGLTEINPGEKTILRFKATKPGVFV
YHCAPPGMVPWHVVSGMNGAIMVLPREGLHDGK
>d1j9qa2 b.6.1.3 (A:167-339) Nitrite reductase, NIR {Alcaligenes faecalis, strain s-6}
GKALTYDKIYYVGEQDFYVPRDENGKYKKYEAPGDAYEDTVKVMRTLTPTHVVFNGAVGALTGDK
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AMTAAVGEKVLIVHSQANRDTRPHLIGGHGDYVWATGKFNTPPDVDQETWFIPGGAAGAAFYTFQ
QPGIYAYVNHNLIEAFELGAAAHFKVTGEWNDDLMTSVLAPSG
>d1gs7a1 b.6.1.3 (A:1-159) Nitrite reductase, NIR {Alcaligenes
xylosoxidans}
QDADKLPHTKVTLVAPPQVHPHEQATKSGPKVVEFTMTIEEKKMVIDDKGTTLQAMTFNGSMPGP
TLVVHEGDYVQLTLVNPATNAMPHNVDFHGATGALGGAKLTNVNPGEQATLRFKADRSGTFVYHC
APEGMVPWHVVSGMSGTLMVLPRDGLKDP
>d1gs7a2 b.6.1.3 (A:160-336) Nitrite reductase, NIR {Alcaligenes
xylosoxidans}
QGKPLHYDRAYTIGEFDLYIPKGPDGKYKDYATLAESYGDTVQVMRTLTPSHIVFNGKVGALTGA
NALTAKVGETVLLIHSQANRDTRPHLIGGFGDWVWETGKFANPPQRDLETWFIRGGSAGAALYTF
KQPGVYAYLNHNLIEAFELGAAGHIKVEGKWNDDLMKQIKAPAPIPR
>d1ndsa1 b.6.1.3 (A:11-166) Nitrite reductase, NIR {Alcaligenes
xylosoxidans}
GLPRVAVDLVAPPLVHPHSQVAAGAPKVVQFRMSIEEKKMVADDDGTTAQAMTFNGSVPGPTLVV
HEGDYIELTLVNPATNSMPHNVDFHAATGALGGAGLTQVVPGQEAVLRFKADRSGTFVYHCAPAG
MVPWHVVSGMNGALMVLPRDGLRDAA
>d1ndsa2 b.6.1.3 (A:167-340) Nitrite reductase, NIR {Alcaligenes
xylosoxidans}
GAALAYDRVYTIGESDLYVPKAADGNYSDYPALASAYADTVAVMRTLTPSHAVFNGAVGALTGAN
ALTAAVGESVLIIHSQANRDSRPHLIGGHGDWVWTTGKFANPPQLNMETWFIPGGSAAAALYTFK
QPGTYAYLSHNLIEAMELGAAAQASVEGQWDDDLMTSVAAPGPA
>d1kbva1 b.6.1.3 (A:13-163) Nitrite reductase, NIR {Neisseria
gonorrhoeae, AniA}
ELPVIDAVTTHAPEVPPAIDRDYPAKVRVKMETVEKTMKMDDGVEYRYWTFDGDVPGRMIRVREG
DTVEVEFSNNPSSTVPHNVDFHAATGQGGGAAATFTAPGRTSTFSFKALQPGLYIYHCAVAPVGM
HIANGMYGLILVEPKEGLPKV
>d1kbva2 b.6.1.3 (A:164-314) Nitrite reductase, NIR {Neisseria
gonorrhoeae, AniA}
DKEFYIVQGDFYTKGKKGAQGLQPFDMDKAVAEQPEYVVFNGHVGALTGDNALKAKAGETVRMYV
GNGGPNLVSSFHVIGEIFDKVYVEGGKLINENVQSTIVPAGGSAIVEFKVDIPGNYTLVDHSIFR
AFNKGALGQLKVEGAENPEIM
>d1kv7a1 b.6.1.3 (A:31-170) multi-copper oxidase CueO {Escherichia
coli}
RPTLPIPDLLTTDARNRIQLTIGAGQSTFGGKTATTWGYNGNLLGPAVKLQRGKAVTVDIYNQLT
EETTLHWHGLEVPGEVDGGPQGIIPPGGKRSVTLNVDQPAATCWFHPHQHGKTGRQVAMGLAGLV
VIEDDEILKL
>d1kv7a2 b.6.1.3 (A:171-335) multi-copper oxidase CueO {Escherichia
coli}
MLPKQWGIDDVPVIVQDKKFSADGQIDYQLDVMTAAVGWFGDTLLTNGAIYPQHAAPRGWLRLRL
LNGCNARSLNFATSDNRPLYVIASDGGLLPEPVKVSELPVLMGERFEVLVEVNDNKPFDLVTLPV
SQMGMAIAPFDKPHPVMRIQPIAISASGALPDTLS
>d1kv7a3 b.6.1.3 (A:336-516) multi-copper oxidase CueO {Escherichia
coli}
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SLPALPSLEGLTVRKLQLSMDPMLDMMGMQMLMEKYGDQAMAGMDHSQMMGHMGHGNMNHMNHGG
KFDFHHANKINGQAFDMNKPMFAAAKGQYERWVISGVGDMMLHPFHIHGTQFRILSENGKPPAAH
RAGWKDTVKVEGNVSEVLVKFNHDAPKEHAYMAHCHLLEHEDTGMMLGFTV
>d1aoza1 b.6.1.3 (A:1-129) Ascorbate oxidase {Zucchini (Cucurbita
pepo medullosa)}
SQIRHYKWEVEYMFWAPNCNENIVMGINGQFPGPTIRANAGDSVVVELTNKLHTEGVVIHWHGIL
QRGTPWADGTASISQCAINPGETFFYNFTVDNPGTFFYHGHLGMQRSAGLYGSLIVDPPQGKKE
>d1aoza2 b.6.1.3 (A:130-338) Ascorbate oxidase {Zucchini (Cucurbita
pepo medullosa)}
PFHYDGEINLLLSDWWHQSIHKQEVGLSSKPIRWIGEPQTILLNGRGQFDCSIAAKYDSNLEPCK
LKGSESCAPYIFHVSPKKTYRIRIASTTALAALNFAIGNHQLLVVEADGNYVQPFYTSDIDIYSG
ESYSVLITTDQNPSENYWVSVGTRARHPNTPPGLTLLNYLPNSVSKLPTSPPPQTPAWDDFDRSK
NFTYRITAAMGSPK
>d1aoza3 b.6.1.3 (A:339-552) Ascorbate oxidase {Zucchini (Cucurbita
pepo medullosa)}
PPVKFNRRIFLLNTQNVINGYVKWAINDVSLALPPTPYLGAMKYNLLHAFDQNPPPEVFPEDYDI
DTPPTNEKTRIGNGVYQFKIGEVVDVILQNANMMKENLSETHPWHLHGHDFWVLGYGDGKFSAEE
ESSLNLKNPPLRNTVVIFPYGWTAIRFVADNPGVWAFHCHIEPHLHMGMGVVFAEGVEKVGRIPT
KALACGGTAKSLINNPKNP
>d1hfua1 b.6.1.3 (A:1-131) Laccase {Inky cap fungus (Coprinus
cinereus)}
AIVNSVDTMTLTNANVSPDGFTRAGILVNGVHGPLIRGGKNDNFELNVVNDLDNPTMLRPTSIHW
HGLFQRGTNWADGADGVNQCPISPGHAFLYKFTPAGHAGTFWYHSHFGTQYCDGLRGPMVIYDDN
D
>d1hfua2 b.6.1.3 (A:132-303) Laccase {Inky cap fungus (Coprinus
cinereus)}
PHAALYDEDDENTIITLADWYHIPAPSIQGAAQPDATLINGKGRYVGGPAAELSIVNVEQGKKYR
MRLISLSCDPNWQFSIDGHELTIIEVDGELTEPHTVDRLQIFTGQRYSFVLDANQPVDNYWIRAQ
PNKGRNGLAGTFANGVNSAILRYAGAANADPTTSANPNPAQL
>d1hfua3 b.6.1.3 (A:304-503) Laccase {Inky cap fungus (Coprinus
cinereus)}
NEADLHALIDPAAPGIPTPGAADVNLRFQLGFSGGRFTINGTAYESPSVPTLLQIMSGAQSANDL
LPAGSVYELPRNQVVELVVPAGVLGGPHPFHLHGHAFSVVRSAGSSTYNFVNPVKRDVVSLGVTG
DEVTIRFVTDNPGPWFFHCHIEFHLMNGLAIVFAEDMANTVDANNPPVEWAQLCEIYDDLPPEAT
SIQTV
>d1kcw_1 b.6.1.3 (1-192) Ceruloplasmin {Human (Homo sapiens)}
KEKHYYIGIIETTWDYASDHGEKKLISVDTEHSNIYLQNGPDRIGRLYKKALYLQYTDETFRTTI
EKPVWLGFLGPIIKAETGDKVYVHLKNLASRPYTFHSHGITYYKEHEGAIYPDNTTDFQRADDKV
YPGEQYTYMLLATEEQSPGEGDGNCVTRIYHSHIDAPKDIASGLIGPLIICKKDSLDKEKEK
>d1kcw_2 b.6.1.3 (193-338) Ceruloplasmin {Human (Homo sapiens)}
HIDREFVVMFSVVDENFSWYLEDNIKTYCSEPEKVDKDNEDFQESNRMYSVNGYTFGSLPGLSMC
AEDRVKWYLFGMGNEVDVHAAFFHGQALTNKNYRIDTINLFPATLFDAYMVAQNPGEWMLSCQNL
NHLKAGLQAFFQVQEC
>d1kcw_3 b.6.1.3 (347-553) Ceruloplasmin {Human (Homo sapiens)}
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IRGKHVRHYYIAAEEIIWNYAPSGIDIFTKENLTAPGSDSAVFFEQGTTRIGGSYKKLVYREYTD
ASFTNRKERGPEEEHLGILGPVIWAEVGDTIRVTFHNKGAYPLSIEPIGVRFNKNNEGTYYSPNY
NPQSRSVPPSASHVAPTETFTYEWTVPKEVGPTNADPVCLAKMYYSAVDPTKDIFTGLIGPMKIC
KKGSLHANGRQK
>d1kcw_4 b.6.1.3 (554-705) Ceruloplasmin {Human (Homo sapiens)}
DVDKEFYLFPTVFDENESLLLEDNIRMFTTAPDQVDKEDEDFQESNKMHSMNGFMYGNQPGLTMC
KGDSVVWYLFSAGNEADVHGIYFSGNTYLWRGERRDTANLFPQTSLTLHMWPDTEGTFNVECLTT
DHYTGGMKQKYTVNQCRRQSED
>d1kcw_5 b.6.1.3 (706-884) Ceruloplasmin {Human (Homo sapiens)}
STFYLGERTYYIAAVEVEWDYSPQREWEKELHHLQEQNVSNAFLDKGEFYIGSKYKKVVYRQYTD
STFRVPVERKAEEEHLGILGPQLHADVGDKVKIIFKNMATRPYSIHAHGVQTESSTVTPTLPGET
LTYVWKIPERSGAGTEDSACIPWAYYSTVDQVKDLYSGLIGPLIVCRRP
>d1kcw_6 b.6.1.3 (892-1040) Ceruloplasmin {Human (Homo sapiens)}
RRKLEFALLFLVFDENESWYLDDNIKTYSDHPEKVNKDDEEFIESNKMHAINGRMFGNLQGLTMH
VGDEVNWYLMGMGNEIDLHTVHFHGHSFQYKHRGVYSSDVFDIFPGTYQTLEMFPRTPGIWLLHC
HVTDHIHAGMETTYTVLQN
>d1qasa2 b.7.1.1 (A:626-756) PI-specific phospholipase C isozyme D1
(PLC-D1), C-terminal domain {Rat (Rattus norvegicus)}
WRPERLRVRIISGQQLPKVNKNKNSIVDPKVIVEIHGVGRDTGSRQTAVITNNGFNPRWDMEFEF
EVTVPDLALVRFMVEDYDSSSKNDFIGQSTIPWNSLKQGYRHVHLLSKNGDQHPSATLFVKISIQ
D
>d1rlw__ b.7.1.1 (-) Domain from cytosolic phospholipase A2 {Human
(Homo sapiens)}
SSHKFTVVVLRATKVTKGAFGDMLDTPDPYVELFISTTPDSRKRTRHFNNDINPVWNETFEFILD
PNQENVLEITLMDANYVMDETLGTATFTVSSMKVGEKKEVPFIFNQVTEMVLEMSLEVASS
>d1d5ra1 b.7.1.1 (A:188-351) Pten tumor suppressor (Phoshphoinositide
phosphatase), C-terminal domain {Human (Homo sapiens)}
YRPVALLFHKMMFETIPMFSGGTCNPQFVVCQLKVKIYSSNSGPTRREDKFMYFEFPQPLPVCGD
IKVEFFHKQNKMLKKDKMFHFWVNTFFIPGPEEVDNDKEYLVLTLTKNDLDKANKDKANRYFSPN
FKVKLYFTKTV
>d1e8xa2 b.7.1.1 (A:357-522) Phoshoinositide 3-kinase (PI3K) {Pig
(Sus scrofa)}
CDRKFRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLWNVWLEFSIKIK
DLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEYVLHMWQ
LSGKGEDQGSFNADKLTSATNPDKENSMSISILLDN
>d1e8ya2 b.7.1.1 (A:357-522) Phoshoinositide 3-kinase (PI3K) {Human
(Homo sapiens)}
CDRKFRVKIRGIDIPVLPRNTDLTVFVEANIQHGQQVLCQRRTSPKPFTEEVLWNVWLEFSIKIK
DLPKGALLNLQIYCGKAPALSSKASAESPSSESKGKVRLLYYVNLLLIDHRFLLRRGEYVLHMWQ
ISGKGEDQGSFNADKLTSATNPDKENSMSISILLDN
>d1bdya_ b.7.1.1 (A:) Domain from protein kinase C delta {Rat (Rattus
norvegicus)}
MAPFLRISFNSYELGSLQAEDDASQPFCAVKMKEALTTDRGKTLVQKKPTMYPEWKSTFDAHIYE
GRVIQIVLMRAAEDPMSEVTVGVSVLAERCKKNNGKAEFWLDLQPQAKVLMCVQYFLE
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>d1gmia_ b.7.1.1 (A:) Domain from protein kinase C epsilon {Rat (Rattus
rattus)}
MVVFNGLLKIKICEAVSLKPTAWSLRDAVGPRPQTFLLDPYIALNVDDSRIGQTATKQKTNSPAW
HDEFVTDVCNGRKIELAVFHDAPIGYDDFVANCTIQFEELLQNGSRHFEDWIDLEPEGKVYVIID
LSGSSG
>d1byna_ b.7.1.2 (A:) Synaptogamin I {Rat (Rattus norvegicus)}
EKLGKLQYSLDYDFQNNQLLVGIIQAAELPALDMGGTSDPYVKVFLLPDKKKKFETKVHRKTLNP
VFNEQFTFKVPYSELGGKTLVMAVYDFDRFSKHDIIGEFKVPMNTVDFGHVTEEWRDLQSAEK
>d1dqva1 b.7.1.2 (A:295-424) Synaptogamin I {Rat (Rattus norvegicus)}
GAPCGRISFALRYLYGSDQLVVRILQALDLPAKDSNGFSDPYVKIYLLPDRKKKFQTKVHRKTLN
PIFNETFQFSVPLAELAQRKLHFSVYDFDRFSRHDLIGQVVLDNLLELAEQPPDRPLWRDILEGG
>d1dqva2 b.7.1.2 (A:425-569) Synaptogamin I {Rat (Rattus norvegicus)}
SEKADLGELNFSLCYLPTAGLLTVTIIKASNLKAMDLTGFSDPYVKASLISEGRRLKKRKTSIKK
NTLNPTYNEALVFDVAPESVENVGLSIAVVDYDCIGHNEVIGVCRVGPEAADPHGREHWAEMLAN
PRKPVEHWHQLVEEK
>d1k5wa_ b.7.1.2 (A:) Synaptogamin I {Rat (Rattus norvegicus)}
KLGDICFSLRYVPTAGKLTVVILEAKNLKKMDVGGLSDPYVKIHLMQNGKRLKKKKTTIKKNTLN
PYYNESFSFEVPFEQIQKVQVVVTVLDYDKIGKNDAIGKVFVGYNSTGAELRHWSDMLANPRRPI
AQWHTLQVEEEVDAMLAV
>d1rsy__ b.7.1.2 (-) Synaptogamin I {Rat (Rattus norvegicus)}
GGGILDSMVEKEEPKEEEKLGKLQYSLDYDFQNNQLLVGIIQAAELPALDMGGTSDPYVKVFLLP
DKKKKFETKVHRKTLNPVFNEQFTFKVPYSELGGKTLVMAVYDFDRFSKHDIIGEFKVPMNTVDF
GHVTEEWRDLQSA
>d1dsya_ b.7.1.2 (A:) C2 domain from protein kinase c (alpha) {Rat
(Rattus norvegicus)}
TEKRGRIYLKAEVTDEKLHVTVRDAKNLIPMDPNGLSDPYVKLKLIPDPKNESKQKTKTIRSTLN
PQWNESFTFKLKPSDKDRRLSVEIWDWDRTTRNDFMGSLSFGVSELMKMPASGWYKLLNQEEGEY
YNVPIPE
>d1a25a_ b.7.1.2 (A:) C2 domain from protein kinase c (beta) {Rat
(Rattus norvegicus)}
ERRGRIYIQAHIDREVLIVVVRDAKNLVPMDPNGLSDPYVKLKLIPDPKSESKQKTKTIKCSLNP
EWNETFRFQLKESDKDRRLSVEIWDWDLTSRNDFMGSLSFGISELQKAGVDGWFKLLSQEEGEYF
NV
>d3rpba_ b.7.1.2 (A:) C2b-domain of rabphilin {Rat (Rattus
norvegicus)}
RGKILVSLMYSTQQGGLIVGIIRCVHLAAMDANGYSDPFVKLWLKPDMGKKAKHKTQIKKKTLNP
EFNEEFFYDIKHSDLAKKSLDISVWDYDIGKSNDYIGGCQLGISAKGERLKHWYECLKNKDKKIE
RWHQLQNENH
>d1qpxa2 b.7.2.1 (A:125-215) PapD {Escherichia coli}
NEVWQDQLILNKVSGGYRIENPTPYYVTVIGLGGSEKQAEEGEFETVMLSPRSEQTVKSANYNTP
YLSYINDYGGRPVLSFICNGSRCSVK
>d1quna2 b.7.2.1 (A:122-205) FimC {Escherichia coli}
LPPDQAAEKLRFRRSANSLTLINPTPYYLTVTELNAGTRVLENALVPPMGESAVKLPSDAGSNIT
YRTINDYGALTPKMTGVME
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>d1who__ b.7.3.1 (-) Pollen allergen PHL P 2 {Timothy grass (Phleum pratense)}
VPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELREHGSDEWVAMTKGEGGVWTFDSEEPLQGPFN
FRFLTEKGMKNVFDDVVPEKYTIGATYAP
>d1dcea2 b.7.4.1 (A:241-350) Rab geranylgeranyltransferase alpha-subunit, insert domain {Rat (Rattus norvegicus)}
PHDVLCCVHVSREEACLSVCFSRPLTVGSRMGTLLLMVDEAPLSVEWRTPDGRNRPSHVWLCDLP
AASLNDQLPQHTFRVIWTGSDSQKECVLLKDRPECWCRDSATDEQ
>d1czya1 b.8.1.1 (A:350-501) TNF receptor associated factor 2 (TRAF2) {Human (Homo sapiens)}
YDGVFIWKISDFPRKRQEAVAGRIPAIFSPAFYTSRYGYKMCLRIYLNGDGTGRGTHLSLFFVVM
KGPNDALLRWPFNQKVTLMLLDQNNREHVIDAFRPDVTSSSFQRPVNDMNIASGCPLFCPVSKME
AKNSYVRDDAIFIKAIVDLTGL
>d1flka1 b.8.1.1 (A:350-504) TNF receptor associated factor 3 (TRAF3) {Human (Homo sapiens)}
YNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIM
RGEYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQTVL
ENGTYIKDDTIFIKVIVDTSDLPDP
>d1k2fa_ b.8.1.2 (A:) SIAH, seven in absentia homolog {Mouse (Mus musculus)}
SVLFPCKYASSGCEITLPHTEKAEHEELCEFRPYSCPCPGASCKWQGSLDAVMPHLMHQHKSITT
LQGEDIVFLATDINLPGAVDWVMMQSCFGFHFMLVLEKQEKYDGHQQFFAIVQLIGTRKQAENFA
YRLELNGHRRRLTWEATPRSIHEGIATAIMNSDCLVFDTSIAQLFAENGNLGINVTISMC
>d2bn2a_ b.9.1.1 (A:) Neurophysin II {Cow (Bos taurus)}
AMSDLELRQCLPCGPGGKGRCFGPSICCGDELGCFVGTAEALRCQEENYLPSPCQSGQKPCGSGG
RCAAAGICCNDESCVTEPEC
>d1kvp__ b.10.1.1 (-) Bacteriophage capsid proteins {Bacteriophage phi-X174}
SNIQTGAERMPHDLSHLGFLAGQIGRLITISTTPVIAGDSFEMDAVGALRLSPLRRGLAIDSTVD
IFTFYVPHRHVYGEQWIKFMKDGVNATPLPTVNTTGYIDHAAFLGTINPDTNKIPKHLFQGYLNI
YNNYFKAPWMPDRTEANPNELNQDDARYGFRCCHLKNIWTAPLPPETELSRQMTTSTGMAPVTTK
FRDVPNLSGTPLIFRDNKGRTIKTGQLGIGPVDAGFLVAQNTAQAANGERAIPSNLWADLSNATS
IDIMGLQAAYANLHTDQERDYFMQRYRDVISSFGGKTSYDADNRPLLVMRSNLWASGYDVDGTDQ
TSLGQFSGRVQQTYKHSVPRFFVPEHGTMFTLALVRFPPTATKEIQYLNAKGALTYTDIAGDPVL
YGNLPPREISMKDVFRSGDSSKKFKIAEGQWYRYAPSYVSPAYHLLEGFPFIQEPPSGDLQERVL
IRHHDYDQCFQSVQLLQWNSQVKFNVTVYRNLPTTRDSIMTS
>d2bpa1_ b.10.1.1 (1:) Bacteriophage capsid proteins {Bacteriophage phi-X174}
SNIQTGAERMPHDLSHLGFLAGQIGRLITISTTPVIAGDSFEMDAVGALRLSPLRRGLAIDSTVD
IFTFYVPHRHVYGEQWIKFMKDGVNATPLPTVNTTGYIDHAAFLGTINPDTNKIPKHLFQGYLNI
YNNYFKAPWMPDRTEANPNELNQDDARYGFRCCHLKNIWTAPLPPETELSRQMTTSTTSIDIMGL
QAAYANLHTDQERDYFMQRYRDVISSFGGKTSYDADNRPLLVMRSNLWASGYDVDGTDQTSLGQF
SGRVQQTYKHSVPRFFVPEHGTMFTLALVRFPPTATKEIQYLNAKGALTYTDIAGDPVLYGNLPP
REISMKDVFRSGDSSKKFKIAEGQWYRYAPSYVSPAYHLLEGFPFIQEPPSGDLQERVLIRHHDY

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DQCFQSVQLLQWNSQVKFNVTVYRNLPTTRDSIMTS
>d2bpa2_ b.10.1.1 (2:) Bacteriophage capsid proteins {Bacteriophage
phi-X174}
MFQTFISRHNSNFFSDKLVLTSVTPASSAPVLQTPKATSSTLYFDSLTVNAGNGGFLHCIQMDTS
VNAANQVVSVGADIAFDADPKFFACLVRFESSSVPTTLPTAYDVYPLNGRHDGGYYTVKDCVTID
VLPRTPGNNVYVGFMVWSNFTATKCRGLVSLNQVIKEIICLQPLK
>d1gff1_ b.10.1.1 (1:) Bacteriophage capsid proteins {Bacteriophage
G4}
VPHDLSHLVFEAGKIGRLKTISWTPVVAGDSFECDMVGAIRLSPLRRGLAVDSRVDIFSFYIPHR
HIYGQQWINFMKDGVNASPLPPVTCSSGWDSAAYLGTIPSSTLKVPKFLHQGYLNIYNNYFKPPW
SDDLTYANPSNMPSEDYKWGVRVANLKSIWTAPLPPDTRTSENMTTGTSTIDIMGLQAAYAKLHT
EQERDYFMTRYRDIMKEFGGHTSYDGDNRPLLLMRSEFWASGYDVDGTDQSSLGQFSGRVQQTFN
HKVPRFYVPEHGVIMTLAVTRFPPTHEMEMHYLVGKENLTYTDIACDPALMANLPPREVSLKEFF
HSSPDSAKFKIAEGQWYRTQPDRVAFPYNALDGFPFYSALPSTDLKDRVLVNTNNYDEIFQSMQL
AHWNMQTKFNINVYRHMPTTRDSIMTS
>d1gff2_ b.10.1.1 (2:) Bacteriophage capsid proteins {Bacteriophage
G4}
MFQKFISKHNAPINSTQLAATKTPAVAAPVLSVPNLSRSTILINATTTAVTTHSGLCHVVRIDET
NPTNHHALSIAGSLSNVPADMIAFAIRFEVADGVVPTAVPALYDVYPIETFNNGKAISFKDAVTI
DSHPRTVGNDVYAGIMLWSNAWTASTISGVLSVNQVNREATVLQPLK
>d1stma_ b.10.1.2 (A:) SPMV coat protein {Satellite panicum mosaic
virus}
AAATSLVYDTCYVTLTERATTSFQRQSFPTLKGMGDRAFQVVAFTIQGVSAAPLMYNARLYNPGD
TDSVHATGVQLMGTVPRTVRLTPRVGQNNWFFGNTEEAETILAIDGLVSTKGANAPSNTVIVTGC
FRLAPSELQSS
>d1a34a_ b.10.1.2 (A:) STMV coat protein {Satellite tobacco mosaic
virus}
TGDNSNVVTMIRAGSYPKVNPTPTWVRAIPFEVSVQSGIAFKVPVGSLFSANFRTDSFTSVTVMS
VRAWTQLTPPVNEYSFVRLKPLFKTGDSTEEFEGRASNINTRASVGYRIPTNLRQNTVAADNVCE
VRSNCRQVALVISCCFN
>d2stv__ b.10.1.2 (-) STNV coat protein {Satellite tobacco necrosis
virus}
TMRAVKRMINTHLEHKRFALINSGNTNATAGTVQNLSNGIIQGDDINQRSGDQVRIVSHKLHVRG
TAITVSQTFRFIWFRDNMNRGTTPTVLEVLNTANFMSQYNPITLQQKRFTILKDVTLNCSLTGES
IKDRIINLPGQLVNYNGATAVAASNGPGAIFMLQIGDSLVGLWDSSYEAVYTDA
>d1smva_ b.10.1.2 (A:) SMV coat potein {Sesbania mosaic virus}
GAITVLHCELTAEIGVTDSIVVSSELVMPYTVGTWLRGVADNWSKYSWLSVRYTYIPSCPSSTAG
SIHMGFQYDMADTVPVSVNKLSNLRGYVSGQVWSGSAGLCFINNSRCSDTSTAISTTLDVSELGK
KWYPYKTSADYATAVGVDVNIATDLVPARLVIALLDGSSSTAVAAGRIYDTYTIQMIEPTASALN
L
>d1smvc_ b.10.1.2 (C:) SMV coat potein {Sesbania mosaic virus}
QAGISMAPSAQGAMVRIRNPAVSSSRGAITVLHCELTAEIGVTDSIVVSSELVMPYTVGTWLRGV
ADNWSKYSWLSVRYTYIPSCPSSTAGSIHMGFQYDMADTVPVSVNKLSNLRGYVSGQVWSGSAGL
CFINNSRCSDTSTAISTTLDVSELGKKWYPYKTSADYATAVGVDVNIATDLVPARLVIALLDGSS
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STAVAAGRIYDTYTIQMIEPTASALNL
>d1f2na_ b.10.1.2 (A:) RYMV capsid protein {Rice yellow mottle virus}
LSSNTWPLHSVEFLADFKRSSTSADATTYDCVPFNLPRVWSLARCYSMWKPTRWDVVYLPEVSAT
VAGSIEMCFLYDYADTIPRYTGKMSRTAGFVTSSVWYGAEGCHLLSGGSARNAVVASMDCSRVGW
KRVTSSIPSSVDPNVVNTILPARLAVRSSIKPTVSDTPGKLYVIASMVLRDPVDPTLNT
>d1f2nc_ b.10.1.2 (C:) RYMV capsid protein {Rice yellow mottle virus}
AEPQLQRAPVAQASRISGTVPGPLSSNTWPLHSVEFLADFKRSSTSADATTYDCVPFNLPRVWSL
ARCYSMWKPTRWDVVYLPEVSATVAGSIEMCFLYDYADTIPRYTGKMSRTAGFVTSSVWYGAEGC
HLLSGGSARNAVVASMDCSRVGWKRVTSSIPSSVDPNVVNTILPARLAVRSSIKPTVSDTPGKLY
VIASMVLRDPVDPTLNT
>d1bmv1_ b.10.1.2 (1:) BPMV coat protein {Bean pod mottle virus}
SISQQTVWNQMATVRTPLNFDSSKQSFCQFSVDLLGGGISVDKTGDWITLVQNSPISNLLRVAAW
KKGCLMVKVVMSGNAAVKRSDWASLVQVFLTNSNSTEHFDACRWTKSEPHSWELIFPIEVCGPNN
GFEMWSSEWANQTSWHLSFLVDNPKQSTTFDVLLGISQNFEIAGNTLMPAFSVPQ
>d1bmv2_ b.10.1.2 (2:) BPMV coat protein {Bean pod mottle virus}
METNLFKLSLDDVETPKGSMLDLKISQSKIALPKNTVGGTILRSDLLANFLTEGNFRASVDLQRT
HRIKGMIKMVATVGIPENTGIALACAMNSSIRGRASSDIYTICSQDCELWNPACTKAMTMSFNPN
PCSDAWSLEFLKRTGFHCDIICVTGWTATPMQDVQVTIDWFISSQECVPRTYCVLNPQNPFVLNR
WMGKLTFPQGTSRSVKRMPLSIGGGAGAKSAILMNMPNAVLSMWRYFVGDLVFEVSKMTSPYIKC
TVSFFIAFGNLADDTINFEAFPHKLVQFGEIQEKVVLKFSQEEFLTAWSTQVRPATTLLADGCPY
LYAMVHDSSVSTIPGDFVIGVKLTIIENMCAYGLNPGISGSRLLGTIPQ
>d1a6ca1 b.10.1.2 (A:1-176) TRSV capsid protein {Tobacco ringspot virus}
AVTVVPDPTCCGTLSFKVPKDAKKGKHLGTFDIRQAIMDYGGLHSQEWCAKGIVNPTFTVRMHAP
RNAFAGLSIACTFDDYKRIDLPALGNECPPSEMFELPTKVFMLKDADVHEWQFNYGELTGHGLCN
WANVATQPTLYFFVASTNQVTMAADWQCIVTMHVDMGPVIDRFELN
>d1a6ca2 b.10.1.2 (A:177-348) TRSV capsid protein {Tobacco ringspot virus}
PTMTWPIQLGDTFAIDRYYEAKEIKLDGSTSMLSISYNFGGPVKHSKKHAISYSRAVMSRNLGWS
GTISGSVKSVSSLFCTASFVIFPWECEAPPTLRQVLWGPHQIMHGDGQFEIAIKTRLHSAATTEE
GFGRLGILPLSGPIAPDAHVGSYEFIVHINTWRPDSQVHPPM
>d1a6ca3 b.10.1.2 (A:349-513) TRSV capsid protein {Tobacco ringspot virus}
FSSSELYNWFTLTNLKPDANTGVVNFDIPGYIHDFASKDATVTLASNPLSWLVAATGWHYGEVDL
CISWSRSKQAQAQEGSVSITTNYRDWGAYWQGQARIYDLRRTEAEIPIFLGSYAGATPSGALGKQ
NYVRISIVNAKDIVALRVCLRPKSIKFWGRSATLF
>d4sbva_ b.10.1.2 (A:) SBMV coat protein {Southern bean mosaic virus, cow pea strain}
SSMDVTILSHCELSTELAVTVTIVVTSELVMPFTVGTWLRGVAQNWSKYAWVAIRYTYLPSCPTT
TSGAIHMGFQYDMADTLPVSVNQLSNLKGYVTGPVWEGQSGLCFVNNTKCPDTSRAITIALDTNE
VSEKRYPFKTATDYATAVGVNANIGNILVPARLVTAMEGGSSKTAVNTGRLYASYTIRLIEPIAA
ALNL
>d4sbvc_ b.10.1.2 (C:) SBMV coat protein {Southern bean mosaic virus, cow pea strain}
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QAGVSMAPIAQGTMVKLRPPMLRSSMDVTILSHCELSTELAVTVTIVVTSELVMPFTVGTWLRGV
AQNWSKYAWVAIRYTYLPSCPTTTSGAIHMGFQYDMADTLPVSVNQLSNLKGYVTGPVWEGQSGL
CFVNNTKCPDTSRAITIALDTNEVSEKRYPFKTATDYATAVGVNANIGNILVPARLVTAMEGGSS
KTAVNTGRLYASYTIRLIEPIAAALNL
>d2tbva_ b.10.1.2 (A:) TBSV coat protein {Tomato bushy stunt virus}
GGVTVTSHREYLTQVNNSSGFVVNGGIVGNSLQLNPSNGTLFSWLPALASNFDQYSFNSVVLDYV
PLCGTTEVGRVALYFDKDSQDPEPADRVELANFGVLKETAPWAEAMLRIPTDKVKRYCNDSATVD
QKLIDLGQLGIATYGGAGADAVGELFLARSVTLYFPQPTNTLLSSKRLDLTGSLADATGPGYLVL
TRTPTVLTHTFRATGTFNLSGGLRCLTSLTLGATGAVVINDILAIDNVGTASDYFLNCTVSSLPA
TVTFTVSGVAAGILLVGRARANVVNLL
>d2tbvc_ b.10.1.2 (C:) TBSV coat protein {Tomato bushy stunt virus}
IITHVGGVGGSIMAPVAVSRQLVGSKPKFTGRTSGGVTVTSHREYLTQVNNSSGFVVNGGIVGNS
LQLNPSNGTLFSWLPALASNFDQYSFNSVVLDYVPLCGTTEVGRVALYFDKDSQDPEPADRVELA
NFGVLKETAPWAEAMLRIPTDKVKRYCNDSATVDQKLIDLGQLGIATYGGAGADAVGELFLARSV
TLYFPQPTNTLLSSKRLDLTGSLADATGPGYLVLTRTPTVLTHTFRATGTFNLSGGLRCLTSLTL
GATGAVVINDILAIDNVGTASDYFLNCTVSSLPATVTFTVSGVAAGILLVGRARANVVNLL
>d1cwpa_ b.10.1.2 (A:) Cowpea chlorotic mottle virus {Host: cowpea
(Vigna unguiculta), (L.)}
KAIKAWTGYSVSKWTASCAAAEAKVTSAITISLPNELSSERNKQLKVGRVLLWLGLLPSVSGTVK
SCVTETQTTAAASFQVALAVADNSKDVVAAMYPEAFKGITLEQLAADLTIYLYSSAALTEGDVIV
HLEVEHVRPTFDDSFTPVY
>d1c8na_ b.10.1.2 (A:) TNV coat protein {Tobacco necrosis virus}
NSTVVSNSELILNLTPIALAYTVQSLPLIATQPAWLGTIADNYSKWRWVSLRIIYSPKCPTTTSG
TVAMCLSYDRNDVAPGSRVQLSQTYKAINFPPYAGYDGAAILNTDVTPTSAIYVDVDVTRFDKAW
YSTIGTAAFAALTAFDQNQFCPCTVHIGSDGGPAVAVPPGDIFFKYVIELIEPINPTMN
>d1c8nc_ b.10.1.2 (C:) TNV coat protein {Tobacco necrosis virus}
GVSRAGGFVTAPVIGAMVTRPTVPRFGMRGNSTVVSNSELILNLTPIALAYTVQSLPLIATQPAW
LGTIADNYSKWRWVSLRIIYSPKCPTTTSGTVAMCLSYDRNDVAPGSRVQLSQTYKAINFPPYAG
YDGAAILNTDVTPTSAIYVDVDVTRFDKAWYSTIGTAAFAALTAFDQNQFCPCTVHIGSDGGPAV
AVPPGDIFFKYVIELIEPINPTMN
>d1auya_ b.10.1.2 (A:) TYMV coat protein {Turnip yellow mosaic virus}
SPLTIKQPFQSEVLFAGTKDAEASLTIANIDSVSTLTTFYRHASLESLWVTIHPTLQAPTFPTTV
GVCWVPAQSPVTPAQITKTYGGQIFCIGGAIQTLSPLIVKCPLEMMQPRVKDSIQYLDSPKLLIS
ITAQPTAPPASTCIITVSGTLSMHSPLITDTST
>d1auyb_ b.10.1.2 (B:) TYMV coat protein {Turnip yellow mosaic virus}
MEIDKELAPQDRTVTVATVLPAVPGPSPLTIKQPFQSEVLFAGTKDAEASLTIANIDSVSTLTTF
YRHASLESLWVTIHPTLQAPTFPTTVGVCWVPAQSPVTPAQITKTYGGQIFCIGGAIQTLSPLIV
KCPLEMMQPRVKDSIQYLDSPKLLISITAQPTAPPASTCIITVSGTLSMHSPLITDTST
>d1e57a_ b.10.1.2 (A:) PHMV coat protein {Physalis mottle virus}
SPAIVLPFQFEATTFGTAETAAQVSLQTADPITKLTAPYRHAQIVECKAILTPTDLAVSNPLTVY
LAWVPANSPATPTQILRVYGGQSFVLGGAISAAKTIEVPLNLDSVNRMLKDSVTYTDTPKLLAYS
RAPTNPSKIPTASIQISGRIRLSKPMLIAN
>d1e57b_ b.10.1.2 (B:) PHMV coat protein {Physalis mottle virus}
VVKVKQASIPAPGSILSQPNTEQSPAIVLPFQFEATTFGTAETAAQVSLQTADPITKLTAPYRHA
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QIVECKAILTPTDLAVSNPLTVYLAWVPANSPATPTQILRVYGGQSFVLGGAISAAKTIEVPLNL
DSVNRMLKDSVTYTDTPKLLAYSRAPTNPSKIPTASIQISGRIRLSKPMLIAN
>d1ddla_ b.10.1.2 (A:) DYMV coat protein {Desmodium yellow mottle
tymovirus}
MEQDKILAHQASLNTKPSLLPPPVGNPPPVISYPFQITLASLGTEDAADSVSIASNSVLATYTAL
YRHAQLKHLKATIHPTYMAPKYPTSVALVWVPANSTATSTQVLDTYGGLHFCIGGSVNSVKPIDV
EANLTNLNPIIKASTTFTDTPKLLYYSKAQATAPTSPTCYLTIQGQIELSSPLLQASS
>d1f15a_ b.10.1.2 (A:) CMV coat protein {Cucumber mosaic virus, strain
fny}
ERCRPGYTFTSITLKPPKIDRGSYYGKRLLLPDSVTEYDKKLVSRLQIRVNPLPKFDSTVWVTVR
KVPASSDLSVAAISAMFADGASPVLVYQYAASGVQANNKLLYDLSAMRADIGDMRKYAVLVYSKD
DALETDELVLHVDIEHQRIPTSGVLPV
>d1f15b_ b.10.1.2 (B:) CMV coat protein {Cucumber mosaic virus, strain
fny}
DANFRVLSQQLSRLNKTLAAGRPTINHPTFVGSERCRPGYTFTSITLKPPKIDRGSYYGKRLLLP
DSVTEYDKKLVSRLQIRVNPLPKFDSTVWVTVRKVPASSDLSVAAISAMFADGASPVLVYQYAAS
GVQANNKLLYDLSAMRADIGDMRKYAVLVYSKDDALETDELVLHVDIEHQRIPTSGVLPV
>d2bbva_ b.10.1.3 (A:) Nodavirus capsid protein {Black beetle virus}
LTRLSQPGLAFLKCAFAPPDFNTDPGKGIPDRFEGKVVTRKDVLNQSINFTANRDTFILIAPTPG
VAYWVADVPAGTFPISTTTFNAVNFPGFNSMFGNAAASRSDQVSSFRYASMNVGIYPTSNLMQFA
GSITVWKCPVKLSNVQFPVATTPATSALVHTLVGLDGVLAVGPDNFSESFIKGVFSQSVCNEPDF
EFSDILEGIQTLPPANVTVATSGQPFNLAAGAEAVSGIVGWGNMDTIVIRVSAPTGAVNSAILKT
WACLEYRPNPNAMLYQFGHDSPPCDEVALQEYRTVARSLPVAVIAAQN
>d2bbvc_ b.10.1.3 (C:) Nodavirus capsid protein {Black beetle virus}
TQTAPVPQQNVPKQPRRRRNRARRNRRQGRAMNMGALTRLSQPGLAFLKCAFAPPDFNTDPGKGI
PDRFEGKVVTRKDVLNQSINFTANRDTFILIAPTPGVAYWVADVPAGTFPISTTTFNAVNFPGFN
SMFGNAAASRSDQVSSFRYASMNVGIYPTSNLMQFAGSITVWKCPVKLSNVQFPVATTPATSALV
HTLVGLDGVLAVGPDNFSESFIKGVFSQSVCNEPDFEFSDILEGIQTLPPANVTVATSGQPFNLA
AGAEAVSGIVGWGNMDTIVIRVSAPTGAVNSAILKTWACLEYRPNPNAMLYQFGHDSPPCDEVAL
QEYRTVARSLPVAVIAAQN
>d1nova_ b.10.1.3 (A:) Nodavirus capsid protein {Nodamura virus}
NMLKMSAPGLDFLKCAFASPDFSTDPGKGIPDKFQGLVLPKKHCLTQSITFTPGKQTMLLVAPIP
GIACLKAEANVGASFSGVPLASVEFPGFDQLFGTSATDTAANVTAFRYASMAAGVYPTSNLMQFA
GSIQVYKIPLKQVLNSYSQTVATVPPTNLAQNTIAIDGLEALDALPNNNYSGSFIEGCYSQSVCN
EPEFEFHPIMEGYASVPPANVTNAQASMFTNLTFSGARYTGLGDMDAIAILVTTPTGAVNTAVLK
VWACVEYRPNPNSTLYEFARESPANDEYALAAYRKIARDIPIAVACKDN
>d1novc_ b.10.1.3 (C:) Nodavirus capsid protein {Nodamura virus}
RRRAAPRQQQRQQSNRASNQPRRRRARRTRRQQRMAATNNMLKMSAPGLDFLKCAFASPDFSTDP
GKGIPDKFQGLVLPKKHCLTQSITFTPGKQTMLLVAPIPGIACLKAEANVGASFSGVPLASVEFP
GFDQLFGTSATDTAANVTAFRYASMAAGVYPTSNLMQFAGSIQVYKIPLKQVLNSYSQTVATVPP
TNLAQNTIAIDGLEALDALPNNNYSGSFIEGCYSQSVCNEPEFEFHPIMEGYASVPPANVTNAQA
SMFTNLTFSGARYTGLGDMDAIAILVTTPTGAVNTAVLKVWACVEYRPNPNSTLYEFARESPAND
EYALAAYRKIARDIPIAVACKDN
>g1f8v.1 b.10.1.3 (A:,D:) Nodavirus capsid protein {Pariacoto virus}
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NRRNKARKVVSRSTALVPMAPASQRTGPAPRKPRKRNQALVRNPRLTDAGLAFLKCAFAAPDFSV
DPGKGIPDNFHGRTLAIKDCNTTSVVFTPNTDTYIVVAPVPGFAYFRAEVAVGAQPTTFVGVPYP
TYATNFGAGSQNGLPAVNNYSKFRYASMACGLYPTSNMMQFSGSVQVWRVDLNLSEAVNPAVTAI
TPAPGVFANFVDKRINGLRGIRPLAPRDNYSGNFIDGAYTFAFDKSTDFEWCDFVRSLEFSESNV
LGAATAMKLLAPGGGTDTTLTGLGNVNTLVYKISTPTGAVNTAILRTWNCIELQPYTDSALFQFS
GVSPPFDPLALECYHNLKMRFPVAVSSRENXSKFWEGVLRVLNQISGTLSVIPGPVGTISAGVHQ
LTGMYM
>g1f8v.2 b.10.1.3 (B:,E:) Nodavirus capsid protein {Pariacoto virus}
NPRLTDAGLAFLKCAFAAPDFSVDPGKGIPDNFHGRTLAIKDCNTTSVVFTPNTDTYIVVAPVPG
FAYFRAEVAVGAQPTTFVGVPYPTYATNFGAGSQNGLPAVNNYSKFRYASMACGLYPTSNMMQFS
GSVQVWRVDLNLSEAVNPAVTAITPAPGVFANFVDKRINGLRGIRPLAPRDNYSGNFIDGAYTFA
FDKSTDFEWCDFVRSLEFSESNVLGAATAMKLLAPGGGTDTTLTGLGNVNTLVYKISTPTGAVNT
AILRTWNCIELQPYTDSALFQFSGVSPPFDPLALECYHNLKMRFPVAVSSRENXSKFWEGVLRVL
NQISGTLSVIP
>d1dnv__ b.10.1.3 (-) Galleria mellonella densovirus capsid protein
{Wax moth (Galleria mellonella), densovirus}
VYIIPRPFSNFGKKLSTYTKSHKFMIFGLANNVIGPTGTGTTAVNRLLTTCLAEIPWQKLPLYMN
QSEFDLLPPGSRVVECNVKVIFRTNRIAFETSSTVTKQATLNQISNVQTAIGLNKLGWGINRAFT
AFQSDQPMIPTATTAPKYEPVTGDTGYRGMIADYYGADSTNDTAFGNAGNYPHHQVSSFTFLQNY
YCMYQQTNQGTGGWPCLAEHLQQFDSKTVNNQCLIDVTYKPKMGLIKSPLNYKIIGQPTVKGTIS
VGDNLVNMRGAVVTNPPEATQNVAESTHNLTRNFPADLFNIYSDIEKSQVLHKGPWGHENPQIQP
SVHIGIQAVPALTTGALLINSSPLNSWTDSMGYIDVMSSCTVMEAQPTHFPFSTEANTNPGNTIY
RINLTPNSLTSAFNGLYGNGATLGN
>d1b35a_ b.10.1.3 (A:) Cricket paralysis virus (CRPV) {Host:
australian black field cricket (Teleogryllus commodus)}
VMGEDQQIPRNEAQHGVHPISIDTHRISNNWSPQAMCIGEKVVSIRQLIKRFGIFGDANTLQADG
SSFVVAPFTVTSPTKTLTSTRNYTQFDYYYYLYAFWRGSMRIKMVAETQDGTGTPRKKTNFTWFV
RMFNSLQDSFNSLISTSSSAVTTTVLPSGTINMGPSTQVIDPTVEGLIEVEVPYYNISHITPAVT
IDDGTPSMEDYLKGHSPPCLLTFSPRDSISATNHIITASFMRALGDDFSFMYLLGVPPLVNVARA
>d1b35b_ b.10.1.3 (B:) Cricket paralysis virus (CRPV) {Host:
australian black field cricket (Teleogryllus commodus)}
ENSHIENEDKRLTSEQKEIVHFVSEGVTPSTTALPDIVNLSTNYLDKNTREDRIHSIKDFLSRPI
IIATNLWSVSDPVEKQLYTANFPEVLISNAMYQDKLKGFVGLRATLVVKVQVNSQPFQQGRLMLQ
YIPYAQYMPNRVTLINETLQGRSGCPRTDLELSVGTEVEMRIPYVSPHLYYNLITGQGSFGSIYV
VVYSQLHDQVSGTGSIEYTVWAHLEDVDVQYPTGANIFTGNEAYIKGTSRYDAAQKAHAA
>d1b35c_ b.10.1.3 (C:) Cricket paralysis virus (CRPV) {Host:
australian black field cricket (Teleogryllus commodus)}
SKPTVQGKIGECKLRGQGRMANFDGMDMSHKMALSSTNEIETNEGLAGTSLDVMDLSRVLSIPNY
WDRFTWKTSDVINTVLWDNYVSPFKVKPYSATITDRFRCTHMGKVANAFTYWRGSMVYTFKFVKT
QYHSGRLRISFIPYYYNTTISTGTPDVSRTQKIVVDLRTSTAVSFTVPYIGSRPWLYCIRPESSW
LSKDNTDGALMYNCVSGIVRVEVLNQLVAAQNVFSEIDVICEVNGGPDLEFAGPTCPRYVPYAGD
FTLADTRKIEAERTQEYSNNED
>d1sida_ b.10.1.4 (A:) Murine polyomavirus coat protein vp1 {Murine
polyoma virus, strain small-plaque 16}
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KACPRPAPVPKLLIKGGMEVLDLVTGPDSVTEIEAFLNPRMGQPPTPESLTEGGQYYGWSRGINL
ATSDTEDSPGNNTLPTWSMAKLQLPMLNEDLTCDTLQMWEAVSVKTEVVGSGSLLDVHGFNKPTD
TVNTKGISTPVEGSQYHVFAVGGEPLDLQGLVTDARTKYKEEGVVTIKTITKKDMVNKDQVLNPI
SKAKLDKDGMYPVEIWHPDPAKNENTRYFGNYTGGTTTPPVLQFTNTLTTVLLDENGVGPLCKGE
GLYLSCVDIMGWRVTRNYDVHHWRGLPRYFKITLRKRWVKNPYPMASLISSLFNNMLPQVQGQPM
EGENTQVEEVRVYDGTEPVPGDPDMTRYVDRFGKTKTVFPG
>d1vpsa_ b.10.1.4 (A:) Murine polyomavirus coat protein vp1 {Murine
polyoma virus, strain small-plaque 16}
GGMEVLDLVTGPDSVTEIEAFLNPRMGQPPTPESLTEGGQYYGWSRGINLATSDTEDSPGNNTLP
TWSMAKLQLPMLNEDLTCDTLQMWEAVSVKTEVVGSGSLLDVHGFNKPTDTVNTKGISTPVEGSQ
YHVFAVGGEPLDLQGLVTDARTKYKEEGVVTIKTITKKDMVNKDQVLNPISKAKLDKDGMYPVEI
WHPDPAKNENTRYFGNYTGGTTTPPVLQFTNTLTTVLLDENGVGPLCKGEGLYLSCVDIMGWRVT
RNYDVHHWRGLPRYFKITLRKRWVK
>d1fmd1_ b.10.1.4 (1:) Foot-and-mouth desease virus {Foot-and-mouth
disease virus, (strain bfs, 1860)}
TTTTGESADPVTTTVENYGGETQVQRRHHTDVAFVLDRFVKVTVSDNQHTLDVMQAHKDNIVGAL
LRAATYYFSDLEIAVTHTGKLTWVPNGAPVSALNNTTNPTAYHKGPVTRLALPYTAPHRVLATAY
TGTTTYTASARGDLAHLTTTHAAHLPTSFNFGAVKAETITELLVRMKRAELYCPRPILPIQPTGD
RHKQPLVAPAKQ
>d1fmd2_ b.10.1.4 (2:) Foot-and-mouth desease virus {Foot-and-mouth
disease virus, (strain bfs, 1860)}
DKKTEETTLLEDRILTTRNGHTTSTTQSSVGVTFGYATAEDSTSGPNTSALETRVHQAERFFKMA
LFDWVPSQNFGHMHKVVLPHEPKGVYGGLVKSYAYMRNGWDVEVTAVGNQFNGGCLLVALVPEMG
DISDREKYQLTLYPHQFINPRTNMTAHITVPYVGVNRYDQYKQHRPWTLVVMVVAPLTTNTAGAQ
QIKVYANIAPTNVHVAGELPSKE
>d1fmd3_ b.10.1.4 (3:) Foot-and-mouth desease virus {Foot-and-mouth
disease virus, (strain bfs, 1860)}
GIFPVACSDGYGNMVTTDPKTADPAYGKVYNPPRTALPGRFTNYLDVAEACPTFLMFENVPYVST
RTDGQRLLAKFDVSLAAKHMSNTYLAGLAQYYTQYTGTINLHFMFTGPTDAKARYMVAYVPPGMD
APDNPEEAAHCIHAEWDTGLNSKFTFSIPYISAADYTYTASHEAETTCVQGWVCVYQITHGKADA
DALVVSASAGKDFELRLPVDARQQ
>d1qqp1_ b.10.1.4 (1:) Foot-and-mouth desease virus {Foot-and-mouth
disease virus, (strain bfs, 1860)}
TTSAGESADPVTTTVENYGGETQIQRRQHTDVSFIMDRFVKVTPQNQINILDLMQVPSHTLVGAL
LRASTYYFSDLEIAVKHEGDLTWVPNGAPEKALDNTTNPTAYHKAPLTRLALPYTAPHRVLATVY
NGECRYSRNAVPNLRGDLQVLAQKVARTLPTSFNYGAIKATRVTELLYRMKRAETYCPRPLLAIH
PTEARHKQKIVAPVK
>d1qqp2_ b.10.1.4 (2:) Foot-and-mouth desease virus {Foot-and-mouth
disease virus, (strain bfs, 1860)}
DKKTEETTLLEDRILTTRNGHTTSTTQSSVGVTYGYATAEDFVSGPNTSGLETRVVQAERFFKTH
LFDWVTSDSFGRCHLLELPTDHKGVYGSLTDSYAYMRNGWDVEVTAVGNQFNGGCLLVAMVPELC
SIQKRELYQLTLFPHQFINPRTNMTAHITVPFVGVNRYDQYKVHKPWTLVVMVVAPLTVNTEGAP
QIKVYANIAPTNVHVAGEFPSKE
>d1qqp3_ b.10.1.4 (3:) Foot-and-mouth desease virus {Foot-and-mouth
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disease virus, (strain bfs, 1860)}
GIFPVACSDGYGGLVTTDPKTADPVYGKVFNPPRNQLPGRFTNLLDVAEACPTFLRFEGGVPYVT
TKTDSDRVLAQFDMSLAAKHMSNTFLAGLAQYYTQYSGTINLHFMFTGPTDAKARYMVAYAPPGM
EPPKTPEAAAHCIHAEWDTGLNSKFTFSIPYLSAADYTYTASDVAETTNVQGWVCLFQITHGKAD
GDALVVLASAGKDFELRLPVDARAE
>d1c8da_ b.10.1.4 (A:) Parvovirus (panleukopenia virus) capsid {Host:
dog (Canis familiaris)}
GVGISTGTFNNQTEFKFLENGWVYITANSSRLVHLNMPESENYRRVVVNNMDKTAVNGNMALDDI
HAEIVTPWSLVDANAWGVWFNPGDWQLIVNTMSELHLVSFEQEIFNVVLKTVSESATQPPTKVYN
NDLTASLMVALDSNNTMPFTPAAMRSETLGFYPWKPTIPTPWRYYFQWDRTLIPSHTGTSGTPTN
IYHGTDPDDVQFYTIENSVPVHLLRTGDEFATGTFFFDCKPCRLTHTWQTNRALGLPPFLNSLPQ
SEGDTNFGDIGVQQDKRRGVTQMGNTNYITEATIMRPAEVGYSAPYYSFEASTQGPFKTPIAAGR
GGAQTDENQAADGNPRYAFGRQHGQKTTTTGETPERFTYIAHQDTGRYPEGDWIQNINFNLPVTN
DNVLLPTDPIGGKTGINYTNIFNTYGPLTALNNVPPVYPNGQIWDKEFDTDLKPRLHVNAPFVCQ
NNCPGQLFVKVAPNLTNQYDPDASANMSRIVTYSDFWWKGKLVFKAKLRASHTWNPIQQMSINVD
NQFNYVPSNIGGMKIVYEKSQLAPRKLY
>d1k3va_ b.10.1.4 (A:) Parvovirus (panleukopenia virus) capsid {Host:
pig (Sus scrofa)}
GVGVSTGTFNNQTEFQYLGEGLVRITAHASRLIHLNMPEHETYKRIHVLNSESGVAGQMVQDDAH
TQMVTPWSLIDANAWGVWFNPADWQLISNNMTEINLVSFEQEIFNVVLKTITESATSPPTKIYNN
DLTASLMVALDTNNTLPYTPAAPRSETLGFYPWLPTKPTQYRYYLSCIRNLNPPTYTGQSQQITD
SIQTGLHSDIMFYTIENAVPIHLLRTGDEFSTGIYHFDTKPLKLTHSWQTNRSLGLPPKLLTEPT
TEGDQHPGTLPAANTRKGYHQTINNSYTEATAIRPAQVGYNTPYMNFEYSNGGPFLTPIVPTADT
QYNDDEPNGAIRFTMDYQHGHLTTSSQELERYTFNPQSKCGRAPKQQFNQQAPLNLENTNNGTLL
PSDPIGGKSNMHFMNTLNTYGPLTALNNTAPVFPNGQIWDKELDTDLKPRLHVTAPFVCKNNPPG
QLFVKIAPNLTDDFNADSPQQPRIITYSNFWWKGTLTFTAKMRSSNMWNPIQQHTTTAENIGNYI
PTNIGGIRMFPEYSQLIPRKLY
>d1mvma_ b.10.1.4 (A:) MVM coat protein {Murine minute virus, strain
i}
GVGVSTGSYDNQTHYRFLGDGWVEITALATRLVHLNMPKSENYCRIRVHNTTDTSVKGNMAKDDA
HEQIWTPWSLVDANAWGVWLQPSDWQYICNTMSQLNLVSLDQEIFNVVLKTVTEQDSGGQAIKIY
NNDLTACMMVAVDSNNILPYTPAANSMETLGFYPWKPTIASPYRYYFCVDRDLSVTYENQEGTIE
HNVMGTPKGMNSQFFTIENTQQITLLRTGDEFATGTYYFDTNPVKLTHTWQTNRQLGQPPLLSTF
PEADTDAGTLTAQGSRHGATQMEVNWVSEAIRTRPAQVGFCQPHNDFEASRAGPFAAPKVPADVT
QGMDREANGSVRYSYGKQHGENWAAHGPAPERYTWDETNFGSGRDTRDGFIQSAPLVVPPPLNGI
LTNANPIGTKNDIHFSNVFNSYGPLTTFSHPSPVYPQGQIWDKELDLEHKPRLHITAPFVCKNNA
PGQMLVRLGPNLTDQYDPNGATLSRIVTYGTFFWKGKLTMRAKLRANTTWNPVYQVSVEDNGNSY
MSVTKWLPTATGNMQSVPLITRPVARNTY
>d1hxs1_ b.10.1.4 (1:) Poliovirus {Poliovirus type 1, strain Mahoney}
GSSSTDNTVRETVGAATSRDALPNTEASGPTHSKEIPALTAVETGATNPLVPSDTVQTRHVVQHR
SRSESSIESFFARGACVTIMTVDNPASTTNKDKLFAVWKITYKDTVQLRRKLEFFTYSRFDMELT
FVVTANFTETNNGHALNQVYQIMYVPPGAPVPEKWDDYTWQTSSNPSIFYTYGTAPARISVPYVG
ISNAYSHFYDGFSKVPLKDQSAALGDSLYGAASLNDFGILAVRVVNDHNPTKVTSKIRVYLKPKH
IRVWCPRPPRAVAYYGPGVDYKDGTLTPLSTKDLTTY
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>d1hxs2_ b.10.1.4 (2:) Poliovirus {Poliovirus type 1, strain Mahoney}
ACGYSDRVLQLTLGNSTITTQEAANSVVAYGRWPEYLRDSEANPVDQPTEPDVAACRFYTLDTVS
WTKESRGWWWKLPDALRDMGLFGQNMYYHYLGRSGYTVHVQCNASKFHQGALGVFAVPEMCLAGD
SNTTTMHTSYQNANPGEKGGTFTGTFTPDNNQTSPARRFCPVDYLLGNGTLLGNAFVFPHQIINL
RTNNCATLVLPYVNSLSIDSMVKHNNWGIAILPLAPLNFASESSPEIPITLTIAPMCCEFNGLRN
ITLPRLQ
>d1hxs3_ b.10.1.4 (3:) Poliovirus {Poliovirus type 1, strain Mahoney}
GLPVMNTPGSNQYLTADNFQSPCALPEFDVTPPIDIPGEVKNMMELAEIDTMIPFDLSATKKNTM
EMYRVRLSDKPHTDDPILCLSLSPASDPRLSHTMLGEILNYYTHWAGSLKFTFLFCGSMMATGKL
LVSYAPPGADPPKKRKEAMLGTHVIWDIGLQSSCTMVVPWISNTTYRQTIDDSFTEGGYISVFYQ
TRIVVPLSTPREMDILGFVSACNDFSVRLLRDTTHIEQKA
>d1pov0_ b.10.1.4 (0:) Poliovirus {Poliovirus type 1, strain Mahoney}
GAQVSSQKVGAHENSNRAYGGSTINYTTINYYRDSASNAASKQDFSQDPSKFTEPIKDVLIKTAP
MLNSPNIEACGYSDRVLQLTLGNSTITTQEAANSVVAYGRWPEYLRDSEANPVDQPTEPDVAACR
FYTLDTVSWTKESRGWWWKLPDALRDMGLFGQNMYYHYLGRSGYTVHVQCNASKFHQGALGVFAV
PEMCLAGDSNTTTMHTSYQNANPGEKGGTFTGTFTPDNNQTSPARRFCPVDYLLGNGTLLGNAFV
FPHQIINLRTNNCATLVLPYVNSLSIDSMVKHNNWGIAILPLAPLNFASESSPEIPITLTIAPMC
CEFNGLRNITLPRLQ
>d1pov1_ b.10.1.4 (1:) Poliovirus {Poliovirus type 1, strain Mahoney}
QHRSRSESSIESFFARGACVTIMTVDNPASTTNKDKLFAVWKITYKDTVQLRRKLEFFTYSRFDM
ELTFVVTANFTETNNGHALNQVYQIMYVPPGAPVPEKWDDYTWQTSSNPSIFYTYGTAPARISVP
YVGISNAYSHFYDGFSKVPLKDQSAALGDSLYGAASLNDFGILAVRVVNDHNPTKVTSKIRVYLK
PKHIRVWCPRPPRAVAYYGPGVDYKDGTLTPLSTKDLTTY
>d1eah1_ b.10.1.4 (1:) Poliovirus {Poliovirus type 2, strain Lansing}
ANNLPDTQSSGPAHSKETPALTAVETGATNPLVPSDTVQTRHVIQKRTRSESTVESFFARGACVA
IIEVDNDAPTKRASKLFSVWKITYKDTVQLRRKLEFFTYSRFDMEFTFVVTSNYTDANNGHALNQ
VYQIMYIPPGAPIPGKWNDYTWQTSSNPSVFYTYGAPPARISVPYVGIANAYSHFYDGFAKVPLA
GQASTEGDSLYGAASLNDFGSLAVRVVNDHNPTKLTSKIRVYMKPKHVRVWCPRPPRAVPYYGPG
VDYKDGLAPLPGKGLTTY
>d1eah2_ b.10.1.4 (2:) Poliovirus {Poliovirus type 2, strain Lansing}
SVRVMQLTLGNSTITTQEAANSVVAYGRWPEYIKDSEANPVDQPTEPDVAACRFYTLDTVTWRKE
SRGWWWKLPDALKDMGLFGQNMFYHYLGRAGYTVHVQCNASKFHQGALGVFAVPEMCLAGDSTTH
MFTKYENANPGEKGGEFKGSFTLDTNATNPARNFCPVDYLFGSGVLAGNAFVYPHQIINLRTNNC
ATLVLPYVNSLSIDSMTKHNNWGIAILPLAPLDFATESSTEIPITLTIAPMCCEFNGLRNITVPR
TQ
>d1eah3_ b.10.1.4 (3:) Poliovirus {Poliovirus type 2, strain Lansing}
GLPVLNTPGSNQYLTADNYQSPCAIPEFDVTPPIDIPGEVRNMMELAEIDTMIPLNLTNQRKNTM
DMYRVELNDAAHSDTPILCLSLSPASDPRLAHTMLGEILNYYTHWAGSLKFTFLFCGSMMATGKL
LVSYAPPGAEAPKSRKEAMLGTHVIWDIGLQSSCTMVVPWISNTTYRQTINDSFTEGGYISMFYQ
TRVVVPLSTPRKMDILGFVSACNDFSVRLLRDTTHISQEA
>d1pvc1_ b.10.1.4 (1:) Poliovirus {Poliovirus type 3, strain Sabin}
QDSLPDTKASGPAHSKEVPALTAVETGATNPLAPSDTVQTRHVVQRRSRSESTIESFFARGACVA
IIEVDNEQPTTRAQKLFAMWRITYKDTVQLRRKLEFFTYSRFDMEFTFVVTANFTNANNGHALNQ
VYQIMYIPPGAPTPKSWDDYTWQTSSNPSIFYTYGAAPARISVPYVGLANAYSHFYDGFAKVPLK
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TDANDQIGDSLYSAMTVDDFGVLAVRVVNDHNPTKVTSKVRIYMKPKHVRVWCPRPPRAVPYYGP
GVDYRNNLDPLSEKGLTTY
>d1pvc2_ b.10.1.4 (2:) Poliovirus {Poliovirus type 3, strain Sabin}
ACGYSDRVLQLTLGNSTITTQEAANSVVAYGRWPEFIRDDEANPVDQPTEPDVATCRFYTLDTVM
WGKESKGWWWKLPDALRDMGLFGQNMYYHYLGRSGYTVHVQCNASKFHQGALGVFAIPEYCLAGD
SDKQRYTSYANANPGERGGKFYSQFNKDNAVTSPKREFCPVDYLLGCGVLLGNAFVYPHQIINLR
TNNSATIVLPYVNALAIDSMVKHNNWGIAILPLSPLDFAQDSSVEIPITVTIAPMCSEFNGLRNV
TAPKFQ
>d1pvc3_ b.10.1.4 (3:) Poliovirus {Poliovirus type 3, strain Sabin}
GLPVLNTPGSNQYLTSDNHQSPCAIPEFDVTPPIDIPGEVKNMMELAEIDTMIPLNLESTKRNTM
DMYRVTLSDSADLSQPILCLSLSPAFDPRLSHTMLGEVLNYYTHWAGSLKFTFLFCGSMMATGKI
LVAYAPPGAQPPTSRKEAMLGTHVIWDLGLQSSCTMVVPWISNVTYRQTTQDSFTEGGYISMFYQ
TRIVVPLSTPKSMSMLGFVSACNDFSVRLLRDTTHISQSA
>d4rhv1_ b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 14}
TVASISSGPKHTQKVPILTANETGATMPVLPSDSIETRTTYMHFNGSETDVECFLGRAACVHVTE
IQNKDATGIDNHREAKLFNDWKINLSSLVQLRKKLELFTYVRFDSEYTILATASQPDSANYSSNL
VVQAMYVPPGAPNPKEWDDYTWQSASNPSVFFKVGDTSRFSVPYVGLASAYNCFYDGYSHDDAET
QYGITVLNHMGSMAFRIVNEHDEHKTLVKIRVYHRAKHVEAWIPRAPRALPYTSIGRTNYPKNTE
PVIKKRKGDIKSY
>d4rhv2_ b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 14}
GYSDRVQQITLGNSTITTQEAANAVVCYAEWPEYLPDVDASDVNKTSKPDTSVCRFYTLDSKTWT
TGSKGWCWKLPDALKDMGVFGQNMFFHSLGRSGYTVHVQCNATKFHSGCLLVVVIPEHQLASHEG
GNVSVKYTFTHPGERGIDLSSANEVGGPVKDVLYNMNGTLLGNLLIFPHQFINLRTNNTATIVIP
YINSVPIDSMTRHNNVSLMVIPIAPLTVPTGATPSLPITVTIAPMCTEFSGIRSKSIVPQ
>d4rhv3_ b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 14}
GLPTTTLPGSGQFLTTDDRQSPSALPNYEPTPRIHIPGKVHNLLEIIQVDTLIPMNNTHTKDEVN
SYLIPLNANRQNEQVFGTNLFIGDGVFKTTLLGEIVQYYTHWSGSLRFSLMYTGPALSSAKLILA
YTPPGARGPQDRREAMLGTHVVWDIGLQSTIVMTIPWTSGVQFRYTDPDTYTSAGFLSCWYQTSL
ILPPETTGQVYLLSFISACPDFKLRLMKDTQTISQTVALTE
>d1aym1_ b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 16}
NPVERYVDEVLNEVLVVPNINQSHPTTSNAAPVLDAAETGHTNKIQPEDTIETRYVQSSQTLDEM
SVESFLGRSGCIHESVLDIVDNYNDQSFTKWNINLQEMAQIRRKFEMFTYARFDSEITMVPSVAA
KDGHIGHIVMQYMYVPPGAPIPTTRDDYAWQSGTNASVFWQHGQPFPRFSLPFLSIASAYYMFYD
GYDGDTYKSRYGTVVTNDMGTLCSRIVTSEQLHKVKVVTRIYHKAKHTKAWCPRPPRAVQYSHTH
TTNYKLSSEVHNDVAIRPRTNLTTV
>d1aym2_ b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 16}
SDRIIQITRGDSTITSQDVANAVVGYGVWPHYLTPQDATAIDKPTQPDTSSNRFYTLDSKMWNST
SKGWWWKLPDALKDMGIFGENMFYHFLGRSGYTVHVQCNASKFHQGTLLVVMIPEHQLATVNKGN
VNAGYKYTHPGEAGREVGTQVENEKQPSDDNWLNFDGTLLGNLLIFPHQFINLRSNNSATLIVPY
VNAVPMDSMVRHNNWSLVIIPVCQLQSNNISNIVPITVSISPMCAEFSGARAKTVVQ
>d1aym3_ b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 16}
GLPVYVTPGSGQFMTTDDMQSPCALPWYHPTKEIFIPGEVKNLIEMCQVDTLIPINSTQSNIGNV
SMYTVTLSPQTKLAEEIFAIKVDIASHPLATTLIGEIASYFTHWTGSLRFSFMFCGTANTTLKVL
LAYTPPGIGKPRSRKEAMLGTHVVWDVGLQSTVSLVVPWISASQYRFTTPDTYSSAGYITCWYQT
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NFVVPPNTPNTAEMLCFVSGCKDFCLRMARDTDLHKQTGPITQ
>d1r1a1_ b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 1A}
NYIDEVLNEVLVVPNIKESHHTTSNSAPLLDAAETGHTSNVQPEDAIETRYVITSQTRDEMSIES
FLGRSGCVHISRIKVDYTDYNGQDINFTKWKITLQEMAQIRRKFELFTYVRFDSEITLVPCIAGR
GDDIGHIVMQYMYVPPGAPIPSKRNDFSWQSGTNMSIFWQHGQPFPRFSIPFLSIASAYYMFYDG
YDGDNTSSKYGSVVTNDMGTICSRIVTEKQKLSVVITTHIYHKAKHTKAWCPRPPRAVPYTHSHV
TNYMPETGDVTTAIVRRNTITTA
>d1r1a2_ b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 1A}
DRIMQITRGDSTISSDDVANAVVGYGVWPHYLTPQDATAINKPTQPDTSSNRFYTLESKHWNGSS
KGWWWKLPDALKDMGIFGENMYYHFLGRSGYTVHVQCNASKFHQGTLLVAMIPEHQLASAKHGSV
TAGYKLTHPGEAGRDVSQERDASLRQPSDDSWLNFDGTLLGNLLIFPHQFINLRSNNSATLIVPY
VNAVPMDSMLRHNNWCLVIIPISPLRSETTSSNIVPITVSISPMCAEFSGARAKNIKQ
>d1r1a3_ b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 1A}
GLPVYITPGSGQFMTTDDMQSPCALPWYHPTKEISIPGEVKNLIEMCQVDTLIPVNNVGNNVGNV
SMYTVQLGNQTGMAQKVFSIKVDITSTPLATTLIGEIASYYTHWTGSLRFSFMFCGTANTTLKLL
LAYTPPGIDEPTTRKDAMLGTHVVWDVGLQSTISLVVPWVSASHFRLTADNKYSMAGYITCWYQT
NLVVPPSTPQTADMLCFVSACKDFCLRMARDTDLHIQSGPIEQ
>d1fpn1_ b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 2}
LVVPNINSSNPTTSNSAPALDAAETGHTSSVQPEDVIETRYVQTSQTRDEMSLESFLGRSGCIHE
SKLEVTLANYNKENFTVWAINLQEMAQIRRKFELFTYTRFDSEITLVPCISALSQDIGHITMQYM
YVPPGAPVPNSRDDYAWQSGTNASVFWQHGQAYPRFSLPFLSVASAYYMFYDGYDEQDQNYGTAN
TNNMGSLCSRIVTEKHIHKVHIMTRIYHKAKHVKAWCPRPPRALEYTRAHRTNFKIEDRSIQTAI
VTRPIITTA
>d1fpn2_ b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 2}
RIIQITRGDSTITSQDVANAIVAYGVWPHYLSSKDASAIDKPSQPDTSSNRFYTLRSVTWSSSSK
GWWWKLPDALKDMGIFGENMFYHYLGRSGYTIHVQCNASKFHQGTLIVALIPEHQIASALHGNVN
VGYNYTHPGETGREVKAETRLNPDLQPTEEYWLNFDGTLLGNITIFPHQFINLRSNNSATIIAPY
VNAVPMDSMRSHNNWSLVIIPICPLETSSAINTIPITISISPMCAEFSGARAKRQ
>d1fpn3_ b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 2}
GLPVFITPGSGQFLTTDDFQSPCALPWYHPTKEISIPGEVKNLVEICQVDSLVPINNTDTYINSE
NMYSVVLQSSINAPDKIFSIRTDVASQPLATTLIGEISSYFTHWTGSLRFSFMFCGTANTTVKLL
LAYTPPGIAEPTTRKDAMLGTHVIWDVGLQSTISMVVPWISASHYRNTSPGRSTSGYITCWYQTR
LVIPPQTPPTARLLCFVSGCKDFCLRMARDTNLHLQSGAIAQ
>d1rhi1_ b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 3}
QTLASVSSGPKHTQSVPALTANETGATLPTRPSDNVETRTTYMHFNGSETDVESFLGRAACVHVT
EIKNKNAAGLDNHRKEGLFNDWKINLSSLVQLRKKLELFTYVRFDSEYTILATASQPEASSYSSN
LTVQAMYVPPGAPNPKEWDDYTWQSASNPSVFFKVGETSRFSVPFVGIASAYNCFYDGYSHDDPD
TPYGITVLNHMGSMAFRVVNEHDVHTTIVKIRVYHRAKHVEAWIPRAPRALPYVSIGRTNYPRDS
KTIVKKRTNIKTY
>d1rhi2_ b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 3}
GYSDRVQQITLGNSTITTQEARNAIVCYAEWPEYLSDNDASDVNKTSKPDISVCRFYTLDSKTWK
ATSKGWCWKLPDALKDMGVFGQNMFYHSLGRTGYTIHVQCNATKFHSGCLLVVVIPEHQLASHEG
GTVSVKYKYTHPGDRGIDLDTVEVAGGPTSDAIYNMDGTLLGNLLIFPHQFINMRTNNTATIVVP
YINSVPIDSMTRHNNVSLMVVPIAPLNAPTGSSPTLPVTVTIAPMCTEFTGIRSRSIVPQ
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>d1rhi3_ b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 3}
GLPTTTLPGSGQFLTTDDRQSPSALPSYEPTPRIHIPGKVRNLLEIIQVGTLIPMNNTGTNDNVT
NYLIPLHADRQNEQIFGTKLYIGDGVFKTTLLGEIAQYYTHWSGSLRISLMYTGPALSSAKIILA
YTPPGTRGPEDKKEAMLGTHVVWDIGLQSTIVMTIPWTSGVQFRYTDPDTYTSAGYLSCWYLTSL
ILPPQTSGQVYLLSFISACPDFKLRLMKDTQTISQTDALTE
>d1bev1_ b.10.1.4 (1:) Bovine enterovirus coat protein {Bovine
enterovirus, VG-5-27}
QAAGALVAGTSTSTHSVATDSTPALQAAETGATSTARDESMIETRTIVPTHGIHETSVESFFGRS
SLVGMPLLATGTSITHWRIDFREFVQLRAKMSWFTYMRFDVEFTIIATSSTGQNVTTEQHTTYQV
MYVPPGAPVPSNQDSFQWQSGCNPSVFADTDGPPAQFSVPFMSSANAYSTVYDGYARFMDTDPDR
YGILPSNFLGFMYFRTLEDAAHQVRFRIYAKIKHTSCWIPRAPRQAPYKKRYNLVFSGDSDRICS
NRASLTSY
>d1bev2_ b.10.1.4 (2:) Bovine enterovirus coat protein {Bovine
enterovirus, VG-5-27}
EACGYSDRVAQLTLGNSTITTQEAANICVAYGCWPAKLSDTDATSVDKPTEPGVSADRFYTLRSK
PWQADSKGWYWKLPDALNNTGMFGQNAQFHYLYRGGWAVHVQCNATKFHQGTLLVLAIPEHQIAT
QEQPAFDRTMPGSEGGTFQEPFWLEDGTSLGNSLIYPHQWINLRTNNSATLILPYVNAIPMDSAI
RHSNWTLAIIPVAPLKYAAETTPLVPITVTIAPMETEYNGLRRAIASNQ
>d1bev3_ b.10.1.4 (3:) Bovine enterovirus coat protein {Bovine
enterovirus, VG-5-27}
GLPTKPGPGSYQFMTTDEDCSPCILPDFQPTPEIFIPGKVNNLLEIAQVESILEANNREGVEGVE
RYVIPVSVQDALDAQIYALRLELGGSGPLSSSLLGTLAKHYTQWSGSVEITCMFTGTFMTTGKVL
LAYTPPGGDMPRNREEAMLGTHVIWDFGLQSSITLVIPWISASHFRGVSNDDVLNYQYYAAGHVT
IWYQTNMVIPPGFPNTAGIIMMIAAQPNFSFRIQKDREDMTQTAILQ
>d2mev1_ b.10.1.4 (1:) Mengo virus {Host: monkey brain; middle size
plaque variant}
GVENAEKGVTENTDATADFVAQPVYLPENQTKVAFFYDRSSPIGAFAVKSGSLESGFAPFSNKAC
PNSVILTPGPQFDPAYDQLRPQRLTEIWGNGNEETSEVFPLKTKQDYSFCLFSPFVYYKCDLEVT
LSPHTSGAHGLLVRWCPTGTPTKPTTQVLHEVSSLSEGRTPQVYSAGPGTSNQISFVVPYNSPLS
VLPAVWYNGHKRFDNTGDLGIAPNSDFGTLFFAGTKPDIKFTVYLRYKNMRVFCPRPTVFFPWPT
SGDKIDMT
>d2mev2_ b.10.1.4 (2:) Mengo virus {Host: monkey brain; middle size
plaque variant}
ENLSDRVSQDTAGNTVTNTQSTVGRLVGYGTVHDGEHPASCADTASEKILAVERYYTFKVNDWTS
TQKPFEYIRIPLPHVLSGEDGGVFGATLRRHYLVKTGWRVQVQCNASQFHAGSLLVFMAPEYPTL
DVFAMDNRWSKDNLPNGTRTQTNRKGPFAMDHQNFWQWTLYPHQFLNLRTNTTVDLEVPYVNIAP
TSSWTQHASWTLVIAVVAPLTYSTGASTSLDITASIQPVRPVFNGLRHEVLSRQ
>d2mev3_ b.10.1.4 (3:) Mengo virus {Host: monkey brain; middle size
plaque variant}
SPIPVTIREHAGTWYSTLPDSTVPIYGKTPVAPANYMVGEYKDFLEIAQIPTFIGNKVPNAVPYI
EASNTAVKTQPLAVYQVTLSCSCLANTFLAALSRNFAQYRGSLVYTFVFTGTAMMKGKFLIAYTP
PGAGKPTSRDQAMQATYAIWDLGLNSSYSFTVPFISPTHFRMVGTDQANITNVDGWVTVWQLTPL
TYPPGCPTSAKILTMVSAGKDFSLKMPISPAPWSPQ
>d1cov1_ b.10.1.4 (1:) Coxsackievirus B3 {Host: human (Homo sapiens)}
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RVADTVGTGPTNSEAIPALTAAETGHTSQVVPSDTMQTRHVKNYHSRSESTIENFLCRSACVYFT
EYENSGAKRYAEWVITPRQAAQLRRKLEFFTYVRFDLELTFVITSTQQPSTTQNQDAQILTHQIM
YVPPGGPVPDKVDSYVWQTSTNPSVFWTEGNAPPRMSVPFLSIGNAYSNFYDGWSEFSRNGVYGI
NTLNNMGTLYARHVNAGSTGPIKSTIRIYFKPKHVKAWIPRPPRLCQYEKAKNVNFQPSGVTTTR
QSITTMTNT
>d1cov2_ b.10.1.4 (2:) Coxsackievirus B3 {Host: human (Homo sapiens)}
GYSDRVRSITLGNSTITTQECANVVVGYGVWPDYLKDSEATAEDQPTQPDVATCRFYTLDSVQWQ
KTSPGWWWKLPDALSNLGLFGQNMQYHYLGRTGYTIHVQCNASKFHQGCLLVVCVPEAEMGCATL
NNTPSSAELLGGDTAKEFADKPVASGSNKLVQRVVYNAGMGVGVGNLTIFPHQWINLRTNNSATI
VMPYTNSVPMDNMFRHNNVTLMVIPFVPLDYCPGSTTYVPITVTIAPMCAEYNGLRLAGHQ
>d1cov3_ b.10.1.4 (3:) Coxsackievirus B3 {Host: human (Homo sapiens)}
GLPTMNTPGSCQFLTSDDFQSPSAMPQYDVTPEMRIPGEVKNLMEIAEVDSVVPVQNVGEKVNSM
EAYQIPVRSNEGSGTQVFGFPLQPGYSSVFSRTLLGEILNYYTHWSGSIKLTFMFCGSAMATGKF
LLAYSPPGAGAPTKRVDAMLGTHVVWDVGLQSSCVLCIPWISQTHYRYVASDEYTAGGFITCWYQ
TNIVVPADAQSSCYIMCFVSACNDFSVRLLKDTPFISQENFFQ
>d1d4m1_ b.10.1.4 (1:) Coxsackievirus A9 {Host: human (Homo sapiens)}
GDVEEAIERAVVHVADTMRSGPSNSASVPALTAVETGHTSQVTPSDTMQTRHVKNYHSRSESTVE
NFLGRSACVYMEEYKTTDNDVNKKFVAWPINTKQMVQMRRKLEMFTYLRFDMEVTFVITSRQDPG
TTLAQDMPVLTHQIMYVPPGGPIPAKVDDYAWQTSTNPSIFWTEGNAPARMSIPFISIGNAYSNF
YDGWSNFDQRGSYGYNTLNNLGHIYVRHVSGSSPHPITSTIRVYFKPKHTRAWVPRPPRLCQYKK
AFSVDFTPTPITDTRKDINTVTTV
>d1d4m2_ b.10.1.4 (2:) Coxsackievirus A9 {Host: human (Homo sapiens)}
SDRVRSITLGNSTITTQECANVVVGYGRWPTYLRDDEATAEDQPTQPDVATCRFYTLDSIKWEKG
SVGWWWKFPEALSDMGLFGQNMQYHYLGRAGYTIHVQCNASKFHQGCLLVVCVPEAEMGGAVVGQ
AFSATAMANGDKAYEFTSATQSDQTKVQTAIHNAGMGVGVGNLTIYPHQWINLRTNNSATIVMPY
INSVPMDNMFRHYNFTLMVIPFVKLDYADTASTYVPITVTVAPMCAEYNGLRLAQAQ
>d1d4m3_ b.10.1.4 (3:) Coxsackievirus A9 {Host: human (Homo sapiens)}
GLPTMNTPGSTQFLTSDDFQSPCALPQFDVTPSMNIPGEVKNLMEIAEVDSVVPVNNVQDTTDQM
EMFRIPVTINAPLQQQVFGLRLQPGLDSVFKHTLLGEILNYYAHWSGSMKLTFVFCGSAMATGKF
LIAYSPPGANPPKTRKDAMLGTHIIWDIGLQSSCVLCVPWISQTHYRLVQQDEYTSAGYVTCWYQ
TGMIVPPGTPNSSSIMCFASACNDFSVRMLRDTPFISQDNKLQ
>d1ev11_ b.10.1.4 (1:) Echovirus type 1 {Host: human (Homo sapiens)}
GDVQNAVEGAMVRVADTVQTSATNSERVPNLTAVETGHTSQAVPGDTMQTRHVINNHVRSESTIE
NFLARSACVFYLEYKTGTKEDSNSFNNWVITTRRVAQLRRKLEMFTYLRFDMEITVVITSSQDQS
TSQNQNAPVLTHQIMYVPPGGPIPVSVDDYSWQTSTNPSIFWTEGNAPARMSIPFISIGNAYSNF
YDGWSHFSQAGVYGFTTLNNMGQLFFRHVNKPNPAAITSVARIYFKPKHVRAWVPRPPRLCPYIN
STNVNFEPKPVTEVRTNIITT
>d1ev12_ b.10.1.4 (2:) Echovirus type 1 {Host: human (Homo sapiens)}
GYSDRVRSITLGNSTITTQECANVVVGYGEWPEYLSDNEATAEDQPTQPDVATCRFYTLDSVQWE
NGSPGWWWKFPDALRDMGLFGQNMYYHYLGRAGYTIHVQCNASKFHQGCILVVCVPEAEMGSAQT
SGVVNYEHISKGEIASRFTTTTTAEDHGVQAAVWNAGMGVGVGNLTIFPHQWINLRTNNSATIVM
PYVNSVPMDNMYRHHNFTLMIIPFVPLDFSAGASTYVPITVTVAPMCAEYNGLRLAGHQ
>d1ev13_ b.10.1.4 (3:) Echovirus type 1 {Host: human (Homo sapiens)}
GLPTMNTPGSNQFLTSDDFQSPSAMPQFDVTPEMHIPGEVRNLMEIAEVDSVMPINNDSAAKVSS
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MEAYRVELSTNTNAGTQVFGFQLNPGAESVMNRTLMGEILNYYAHWSGSIKITFVFCGSAMTTGK
FLLSYAPPGAGAPKTRKDAMLGTHVVWDVGLQSSCVLCIPWISQTHYRFVEKDPYTNAGFVTCWY
QTSVVSPASNQPKCYMMCMVSACNDFSVRMLRDTKFIEQTSFYQ
>d1tme1_ b.10.1.4 (1:) Theiler's murine encephalomyelitis virus
{Theiler's murine encephalomyelitis virus, strain da}
GSDNAEKGKVSNDDASVDFVAEPVKLPENQTRVAFFYDRAVPIGMLRPGQNIESTFVYQENDLRL
NCLLLTPLPSFCPDSTSGPVKTKAPVQWRWVRSGGTTNFPLMTKQDYAFLCFSPFTYYKCDLEVT
VSALGTDTVASVLRWAPTGAPADVTDQLIGYTPSLGETRNPHMWLVGAGNTQISFVVPYNSPLSV
LPAAWFNGWSDFGNTKDFGVAPNADFGRLWIQGNTSASVRIRYKKMKVFCPRPTLFFPWPV
>d1tme2_ b.10.1.4 (2:) Theiler's murine encephalomyelitis virus
{Theiler's murine encephalomyelitis virus, strain da}
DRVASDKAGNSATNTQSTVGRLCGYGEAHHGEHPASCADTATDKVLAAERYYTIDLASWTTTQEA
FSHIRIPLPHVLAGEDGGVFGATLRRHYLCKTGWRVQVQCNASQFHAGSLLVFMAPEFYTGKGTK
TGDMEPTDPFTMDTTWRAPQGAPTGYRYDSRTGFFAMNHQNQWQWTVYPHQILNLRTNTTVDLEV
PYVNIAPTSSWTQHANWTLVVAVFSPLQYASGSSSDVQITASIQPVNPVFNGLRHETVIA
>d1tme3_ b.10.1.4 (3:) Theiler's murine encephalomyelitis virus
{Theiler's murine encephalomyelitis virus, strain da}
SPIAVTVREHKGCFYSTNPDTTVPIYGKTISTPNDYMCGEFSDLLELCKLPTFLGNPNSNNKRYP
YFSATNSVPTTSLVDYQVALSCSCMCNSMLAAVARNFNQYRGSLNFLFVFTGAAMVKGKFLIAYT
PPGAGKPTTRDQAMQATYAIWDLGLNSSFVFTAPFISPTHYRQTSYTSATIASVDGWVTVWQLTP
LTYPSGTPVNSDILTLVSAGDDFTLRMPISPTKWVPQ
>d1tmf1_ b.10.1.4 (1:) Theiler's murine encephalomyelitis virus
{Theiler's murine encephalomyelitis virus, strain da}
GVDNAEKGKVSNDDASVDFVAEPVKLPENQTRVAFFYDRAVPIGMLRPGQNMETTFNYQENDYRL
NCLLLTPLPSFCPDSSSGPQKTKAPVQWRWVRSGGVNGANFPLMTKQDYAFLCFSPFTFYKCDLE
VTVSALGTDTVASVLRWAPTGAPADVTDQLIGYTPSLGETRNPHMWLVGAGNSQVSFVVPYNSPL
SVLPAAWFNGWSDFGNTKDFGVAPNADFGRLWIQGNTSASVRIRYKKMKVFCPRPTLFFPWPTPT
TTKINADNPVPILELE
>d1tmf2_ b.10.1.4 (2:) Theiler's murine encephalomyelitis virus
{Theiler's murine encephalomyelitis virus, strain da}
DQNTEEMENLSDRVASDKAGNSATNTQSTVGRLCGYGKSHHGEHPASCADTATDKVLAAERYYTI
DLASWTTSQEAFSHIRIPLPHVLAGEDGGVFGATLRRHYLCKTGWRVQVQCNASQFHAGSLLVFM
APEFYTGKGTKTGTMEPSDPFTMDTEWRSPQGAPTGYRYDSRTGFFATNHQNQWQWTVYPHQILN
LRTNTTVDLEVPYVNVAPSSSWTQHANWTLVVAVLSPLQYATGSSPDVQITASLQPVNPVFNGLR
HETVIAQ
>d1sva1_ b.10.1.4 (1:) Simian virus 40 (SV40) coat protein {Simian
virus 40}
PKKPKEPVQVPKLVIKGGIEVLGVKTGVDSFTEVECFLNPQMGNPDEHQKGLSKSLAAEKQFTDD
SPDKEQLPCYSVARIPLPNINEDLTCGNILMWEAVTVKTEVIGVTAMLNLHSGTQKTHENGAGKP
IQGSNFHFFAVGGEPLELQGVLANYRTKYPAQTVTPKNATVDSQQMNTDHKAVLDKDNAYPVECW
VPDPSKNENTRYFGTYTGGENVPPVLHITNTATTVLLDEQGVGPLCKADSLYVSAVDICGLFTNT
SGTQQWKGLPRYFKITLRKRSVKNPYPISFLLSDLINRRTQRVDGQPMIGMSSQVEEVRVYEDTE
ELPGDPDMIRYIDEFGQTTTRMQ
>d1dzla_ b.10.1.4 (A:) L1 protein {Human papillomavirus type 16}
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KVVSTDEYVARTNIYYHAGTSRLLAVGHPYFPIKKPNNNKILVPKVSGLQYRVFRIHLPDPNKFG
FPDTSFYNPDTQRLVWACVGVEVGRGQPLGVGISGHPLLNKLDDTENASAYAANAGVDNRECISM
DYKQTQLCLIGCKPPIGEHWGKGSPCTQVAVQPGDCPPLELINTVIQDGDMVDTGFGAMDFTTLQ
ANKSEVPLDICTSICKYPDYIKMVSEPYGDSLFFYLRREQMFVRHLFNRAGTVGENVPDDLYIKG
SGSTANLASSNYFPTPSGSMVTSDAQIFNKPYWLQRAQGHNNGICWGNQLFVTVVDTTRSTNMSL
CAAISTSETTYKNTNFKEYLRHGEEYDLQFIFQLCKITLTADVMTYIHSMNSTILEDWNFGLQPP
PGGTLEDTYRFVTSQAIACQKHTPPAPKEDPLKKYTFWEVNLKEKFSADLDQFPLGRKFLLQLGL
>d1ihma_ b.10.1.4 (A:) Calcivirus capsid protein {Norwalk virus}
DPLAMDPVAGSSTAVATAGQVNPIDPWIINNFVQAPQGEFTISPNNTPGDVLFDLSLGPHLNPFL
LHLSQMYNGWVGNMRVRIMLAGNAFTAGKIIVSCIPPGFGSHNLTIAQATLFPHVIADVRTLDPI
EVPLEDVRNVLFHNNDRNQQTMRLVCMLYTPLRTGGGTGDSFVVAGRVMTCPSPDFNFLFLVPPT
VEQKTRPFTLPNLPLSSLSNSRAPLPISSMGISPDNVQSVQFQNGRCTLDGRLVGTTPVSLSHVA
KIRGTSNGTVINLTELDGTPFHPFEGPAPIGFPDLGGCDWHINMTQFGHSSQTQYDVDTTPDTFV
PHLGSIQANGIGSGNYVGVLSWISPPSHPSGSQVDLWKIPNYGSSITEATHLAPSVYPPGFGEVL
VFFMSKMPGPGAYNLPCLLPQEYISHLASEQAPTVGEAALLHYVDPDTGRNLGEFKAYPDGFLTC
VPNGASSGPQQLPINGVFVFVSWVSRFYQLKPVGTAS
>d1amm_1 b.11.1.1 (1-85) gamma-Crystallin {Cow (Bos taurus), isoform II (B)}
GKITFYEDRGFQGHCYECSSDCPNLQPYFSRCNSIRVDSGCWMLYERPNYQGHQYFLRRGDYPDY
QQWMGFNDSIRSCRLIPQHT
>d1amm_2 b.11.1.1 (86-174) gamma-Crystallin {Cow (Bos taurus), isoform II (B)}
GTFRMRIYERDDFRGQMSEITDDCPSLQDRFHLTEVHSLNVLEGSWVLYEMPSYRGRQYLLRPGE
YRRYLDWGAMNAKVGSLRRVMDFY
>d1elpa1 b.11.1.1 (A:1-85) gamma-Crystallin {Cow (Bos taurus), isoform IIIb (D)}
GKITFYEDRGFQGRHYECSSDHSNLQPYLGRCNSVRVDSGCWMIYEQPNYLGPQYFLRRGDYPDY
QQWMGLNDSIRSCRLIPHAG
>d1elpa2 b.11.1.1 (A:87-174) gamma-Crystallin {Cow (Bos taurus), isoform IIIb (D)}
SHRLRLYEREDYRGQMIEITEDCSSLQDRFHFNEIHSLNVLEGSWVLYELPNYRGRQYLLRPGEY
RRYHDWGAMNAKVGSLRRVIDIY
>d1a7ha_ b.11.1.1 (A:) gamma-Crystallin {Cow (Bos taurus), isoform S}
MYKIQIFEKGDFNGQMHETTEDCPSIMEQFHMREVHSCKVLEGAWIFYELPNYRGRQYLLDKKEY
RKPVDWGAASPAVQSFRRIVE
>d1ha4a_ b.11.1.1 (A:) gamma-Crystallin {Human (Homo sapiens)}
GQYKIQIFEKGDFSGQMYETTEDCPSIMEQFHMREIHSCKVLEGVWIFYELPNYRGRQYLLDKKE
YRKPIDWGAASPAVQSFRRIVE
>d1a45_1 b.11.1.1 (1-84) gamma-Crystallin {Cow (Bos taurus), isoform F}
GKITFYEDRGFQGRHYECSSDHSNLQPYFSRCNSIRVDSGCWMLYEQPNFQGPQYFLRRGDYPDY
QQWMGLNDSIRSCRLIPHT
>d1a45_2 b.11.1.1 (86-174) gamma-Crystallin {Cow (Bos taurus),
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isoform F}
GSHRLRIYEREDYRGQMVEITEDCSSLHDRFHFSEIHSFNVLEGWWVLYEMTNYRGRQYLLRPGD
YRRYHDWGATNARVGSLRRAVDFY
>d2bb2_1 b.11.1.1 (-2-85) beta-Crystallin {Cow (Bos taurus)}
LNPKIIIFEQENFQGHSHELNGPCPNLKETGVEKAGSVLVQAGPWVGYEQANCKGEQFVFEKGEY
PRWDSWTSSRRTDSLSSLRPIKVDS
>d2bb2_2 b.11.1.1 (86-175) beta-Crystallin {Cow (Bos taurus)}
QEHKITLYENPNFTGKKMEVIDDDVPSFHAHGYQEKVSSVRVQSGTWVGYQYPGYRGLQYLLEKG
DYKDSGDFGAPQPQVQSVRRIRDMQW
>d1a5da1 b.11.1.1 (A:1-84) beta-Crystallin {Rat (Rattus norvegicus),
isoform E}
GKITFYEDRGFQGRHYECSTDHSNLQPYFSRCNSVRVDSGCWMLYEQPNFTGCQYFLRRGDYPDY
QQWMGFSDSVRSCRLIPHS
>d1a5da2 b.11.1.1 (A:85-174) beta-Crystallin {Rat (Rattus norvegicus),
isoform E}
SSHRIRIYEREDYRGQMVEITDDCPHLQDRFHFSDFHSFHVMEGYWVLYEMPNYRGRQYLLRPGE
YRRYHDWGAMNARVGSLRRIMDFY
>d1bd7a_ b.11.1.1 (A:) beta-Crystallin {Rat (Rattus norvegicus),
isoform E}
EHKIILYENPNFTGKKMEIVDDDVPSFHAHGYQEKVSSVRVQSGTWVGYQYPGYRGLQYLLEKGD
YKDNSDFGAPHPQVQSVRRIRDMQGNPKIIIFEQENFQGHSHELSGPCPNLKETGMEKAGSVLVQ
AGPWVGYEQANCKGEQFVFEKGEYPRWDSWTSSRRTDSLSSLRPIK
>d1npsa_ b.11.1.1 (A:) Protein S {Myxococcus xanthus}
ANITVFYNEDFQGKQVDLPPGNYTRAQLAALGIENNTISSVKVPPGVKAILYQNDGFAGDQIEVV
ANAEELGPLNNNVSSIRVISVPV
>d1prr_2 b.11.1.1 (91-173) Protein S {Myxococcus xanthus}
PRARFFYKEQFDGKEVDLPPGQYTQAELERYGIDNNTISSVKPQGLAVVLFKNDNFSGDTLPVNS
DAPTLGAMNNNTSSIRIS
>d1hdfa_ b.11.1.1 (A:) Spherulin 3a (S3a) {Slime mold (Physarum
polycephalum)}
SVCKGVSGNPAKGEVFLYKHVNFQGDSWKVTGNVYDFRSVSGLNDVVSSVKVGPNTKAFIFKDDR
FNGNFIRLEESSQVTDLTTRNLNDAISSMIVATFE
>d1wkt__ b.11.1.2 (-) Yeast killer toxin {Williopsis mrakii}
GDGYLIMCKNCDPNTGSCDWKQNWNTCVGIGANVHWMVTGGSTDGKQGCATIWEGSGCVGRSTTM
CCPANTCCNINTGFYIRSYRRVE
>d1bhu__ b.11.1.3 (-) Streptomyces metalloproteinase inhibitor, SMPI
{Streptomyces nigrescens}
APSCPAGSLCTYSGTGLSGARTVIPASDMEKAGTDGVKLPASARSFANGTHFTLRYGPARKVTCV
RFPCYQYATVGKVAPGAQLRSLPSPGATVTVGQDLGD
>d1f53a_ b.11.1.4 (A:) Killer toxin-like protein SKLP {Streptomyces
sp.}
IDHVPCRGGENFLKIWSHSGGQQSVDCYANRGRIDFGGWWVDKISTGNNDLIYYDANGDSVRVDR
WHDITYPNRPPKVNSIEIL
>d1g6ea_ b.11.1.6 (A:) Antifungal protein AFP1 {Streptomyces tendae,
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tu901}
MINRTDCNENSYLEIHNNEGRDTLCFANAGTMPVAIYGVNWVESGNNVVTLQFQRNLSDPRLETI
TLQKWGSWNPGHIHEILSIRIY
>d1c01a_ b.11.1.5 (A:) Plant antimicrobial protein MIAMP1 {Macadamia
nut (Macadamia integrifolia)}
SAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQAGCSGVAHTRFGSSARACN
PFGWKSIFIQC
>d1f8na2 b.12.1.1 (A:6-149) Plant lipoxigenase {Soybean (Glycine max),
isozyme L1}
HKIKGTVVLMPKNELEVNPDGSAVDNLNAFLGRSVSLQLISATKADAHGKGKVGKDTFLEGINTS
LPTLGAGESAFNIHFEWDGSMGIPGAFYIKNYMQVEFFLKSLTLEAISNQGTIRFVCNSWVYNTK
LYKSVRIFFANHTY
>d1ik3a2 b.12.1.1 (A:9-167) Plant lipoxigenase {Soybean (Glycine max),
isozyme L3}
GHKIKGTVVLMRKNVLDVNSVTSVGGIIGQGLDLVGSTLDTLTAFLGRSVSLQLISATKADANGK
GKLGKATFLEGIITSLPTLGAGQSAFKINFEWDDGSGIPGAFYIKNFMQTEFFLVSLTLEDIPNH
GSIHFVCNSWIYNAKLFKSDRIFFANQTY
>d1lox_2 b.12.1.1 (2-112) 15-Lipoxygenase {Rabbit (Oryctolagus
cuniculus)}
GVYRVCVSTGASIYAGSKNKVELWLVGQHGEVELGSCLRPTRNKEEEFKVNVSKYLGSLLFVRLR
KKHFLKEDAWFCNWISVQALGAAEDKYWFPCYRWVVGDGVQSLPVG
>d1hpla1 b.12.1.2 (A:337-449) Pancreatic lipase, C-terminal domain
{Horse (Equus caballus)}
RWRYRVDVTLSGKKVTGHVLVSLFGNKGNSRQYEIFQGTLKPDNTYSNEFDSDVEVGDLEKVKFI
WYNNVINLTLPKVGASKITVERNDGSVFNFCSEETVREDVLLTLTAC
>d1etha1 b.12.1.2 (A:337-448) Pancreatic lipase, C-terminal domain
{Pig (Sus scrofa)}
ARWRYKVSVTLSGKKVTGHILVSLFGNEGNSRQYEIYKGTLQPDNTHSDEFDSDVEVGDLQKVKF
IWYNVINPTLPRVGASKITVERNDGKVYDFCSQETVREEVLLTLNPC
>d1gpl_1 b.12.1.2 (337-449) Pancreatic lipase, C-terminal domain
{Guinea pig (Cavia porcellus)}
RWRYKVSVTLSGKKVTGHILVSLFGNKGNSKQYEIFKGTLKPDSTHSNEFDSDVDVGDLQMVKFI
WYNNVINPTLPRVGASKIIVETNVGKQFNFCSPETVREEVLLTLTPC
>d1rp1_1 b.12.1.2 (337-449) Pancreatic lipase, C-terminal domain {Dog
(Canis familiaris)}
RWRYGVSITLSGKRATGQAKVALFGSKGNTHQFNIFKGILKPGSTHSNEFDAKLDVGTIEKVKFL
WNNNNPTFPKVGAAKITVQKGEEKTVHSFCSESTVREDVLLTLTPC
>d1bu8a1 b.12.1.2 (A:337-449) Pancreatic lipase, C-terminal domain
{Rat (Rattus norvegicus)}
RWRYKVSVTLSGAKKLSGYILVALYGNNGNSKQYEIFKGSLKPEARHVRDIDVDINVGEIQKVKF
LWNNKVINLFRPTLGASQITVQSGVDGKEYNFCSSDTVREDVLQSLYPC
>d1ca1_2 b.12.1.3 (250-370) Alpha-toxin, C-terminal domain
{Clostridium perfringens}
SVGKNVKELVAYISTSGEKDAGTDDYMYFGIKTKDGKTQEWEMDNPGNDFMTGSKDTYTFKLKDE
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NLKIDDIQNMWIRKRKYTAFPDAYKPENIKVIANGKVVVDKDINEWISGNSTYNIK
>d1k5ja_ b.13.3.1 (A:) Nucleoplasmin core {Xenopus laevis}
VSLIWGCELNEQNKTFEFKVEDDEEKCEHQLALRTVCLGDKAKDEFHIVEIVTQEEGAEKSVPIA
TLKPSILPMATMVGIELTPPVTFRLKAGSGPLYISGQHVA
>d1pgs_1 b.13.1.1 (4-140) Peptide:N-glycosidase F, PNGase F
{Flavobacterium meningosepticum}
DNTVNIKTFDKVKNAFGDGLSQSAEGTFTFPADVTTVKTIKMFIKNECPNKTCDEWDRYANVYVK
NKTTGEWYEIGRFITPYWVGTEKLPRGLEIDVTDFKSLLSGNTELKIYTETWLAKGREYSVDFDI
VYGTPDY
>d1pgs_2 b.13.1.1 (141-314) Peptide:N-glycosidase F, PNGase F
{Flavobacterium meningosepticum}
KYSAVVPVIQYNKSSIDGVPYGKAHTLGLKKNIQLPTNTEKAYLRTTISGWGHAKPYDAGSRGCA
EWCFRTHTIAINNANTFQHQLGALGCSANPINNQSPGNWTPDRAGWCPGMAVPTRIDVLNNSLTG
STFSYEYKFQSWTNNGTNGDAFYAISSFVIAKSNTPISAPVVTN
>d1phm_1 b.13.1.2 (45-198) Peptidylglycine alpha-hydroxylating
monooxygenase, PHM {Rat (Rattus norvegicus)}
NECLGTIGPVTPLDASDFALDIRMPGVTPKESDTYFCMSMRLPVDEEAFVIDFKPRASMDTVHHM
LLFGCNMPSSTGSYWFCDEGTCTDKANILYAWARNAPPTRLPKGVGFRVGGETGSKYFVLQVHYG
DISAFRDNHKDCSGVSVHLTRVPQ
>d1phm_2 b.13.1.2 (199-354) Peptidylglycine alpha-hydroxylating
monooxygenase, PHM {Rat (Rattus norvegicus)}
PLIAGMYLMMSVDTVIPPGEKVVNADISCQYKMYPMHVFAYRVHTHHLGKVVSGYRVRNGQWTLI
GRQNPQLPQAFYPVEHPVDVTFGDILAARCVFTGEGRTEATHIGGTSSDEMCNLYIMYYMEAKYA
LSFMTCTKNVAPDMFRTIPAEANIPI
>d1hx6a1 b.13.2.1 (A:15-244) Coat protein p3 {Bacteriophage prd1}
LRNQQAMAANLQARQIVLQQSYPVIQQVETQTFDPANRSVFDVTPANVGIVKGFLVKVTAAITNN
HATEAVALTDFGPANLVQRVIYYDPDNQRHTETSGWHLHFVNTAKQGAPFLSSMVTDSPIKYGDV
MNVIDAPATIAAGATGELTMYYWVPLAYSETDLTGAVLANVPQSKQRLKLEFANNNTAFAAVGAN
PLEAIYQGAGAADCEFEEISYTVYQSYLDQLPVGQ
>d1hx6a2 b.13.2.1 (A:245-384) Coat protein p3 {Bacteriophage prd1}
NGYILPLIDLSTLYNLENSAQAGLTPNVDFVVQYANLYRYLSTIAVFDNGGSFNAGTDINYLSQR
TANFSDTRKLDPKTWAAQTRRRIATDFPKGVYYCDNRDKPIYTLQYGNVGFVVNPKTVNQNARLL
MGYEYFTSRT
>d1dhx_1 b.13.2.2 (44-650) Adenovirus hexon {Human adenovirus type
2}
FRNPTVAPTHDVTTDRSQRLTLRFIPVDREDTAYSYKARFTLAVGDNRVLDMASTYFDIRGVLDR
GPTFKPYSGTAYNALAPKGAPNSCEWEQTEDSGRAVAEDEEEDEDEEEEEEEQNARDQATKKTH
VYAQAPLSGETITKSGLQIGSDNAETQAKPVYADPSYQPEPQIGESQWNEADANAAGGRVLKKTT
PMKPCYGSYARPTNPFGGQSVLVPDEKGVPLPKVDLQFFSNTTSLNDRQGNATKPKVVLYSEDVN
METPDTHLSYKPGKGDENSKAMLGQQSMPNRPNYIAFRDNFIGLMYYNSTGNMGVLAGQASQLNA
VVDLQDRNTELSYQLLLDSIGDRTRYFSMWNQAVDSYDPDVRIIENHGTEDELPNYCFPLGGIGV
TDTYQAIKANGNGSGDNGDTTWTKDETFATRNEIGVGNNFAMEINLNANLWRNFLYSNIALYLPD
KLKYNPTNVEISDNPNTYDYMNKRVVAPGLVDCYINLGARWSLDYMDNVNPFNHHRNAGLRYRSM
LLGNGRYVPFHIQVPQKFFAIKNLLLLPGSYTYEWNFRKDVNMVLQSSLGNDLRVDGASIKFDSI
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CLYATFFPMAHNTASTLEAMLR
>d1ruxa1 b.13.2.2 (A:5-636) Adenovirus hexon {Human adenovirus type 5}
MMPQWSYMHISGQDASEYLSPGLVQFARATETYFSLNNKFRNPTVAPTHDVTTDRSQRLTLRFIP
VDREDTAYSYKARFTLAVGDNRVLDMASTYFDIRGVLDRGPTFKPYSGTAYNALAPKGAPNPCEW
DEAATALEINLEEEDDDNEDEVDEQAEQQKTHVFGQAPYSGINITKEGIQIGVEGQTPKYADKTF
QPEPQIGESQWYETEINHAAGRVLKKTTPMKPCYGSYAKPTNENGGQGILVKQQNGKLESQVEMQ
FFSTTEATAGNGDNLTPKVVLYSEDVDIETPDTHISYMPTIKEGNSRELMGQQSMPNRPNYIAFR
DNFIGLMYYNSTGNMGVLAGQASQLNAVVDLQDRNTELSYQLLLDSIGDRTRYFSMWNQAVDSYD
PDVRIIENHGTEDELPNYCFPLGGVINTETLTKVKPKTGQENGWEKDATEFSDKNEIRVGNNFAM
EINLNANLWRNFLYSNIALYLPDKLKYSPSNVKISDNPNTYDYMNKRVVAPGLVDCYINLGARWS
LDYMDNVNPFNHHRNAGLRYRSMLLGNGRYVPFHIQVPQKFFAIKNLLLLPGSYTYEWNFRKDVN
MVLQSSLGNDLRVDGASIKFDSICLYATFFPMAHNTASTLEAMLRND
>d1ruxa2 b.13.2.2 (A:637-946) Adenovirus hexon {Human adenovirus type 5}
TNDQSFNDYLSAANMLYPIPANATNVPISIPSRNWAAFRGWAFTRLKTKETPSLGSGYDPYYTYS
GSIPYLDGTFYLNHTFKKVAITFDSSVSWPGNDRLLTPNEFEIKRSVDGEGYNVAQCNMTKDWFL
VQMLANYNIGYQGFYIPESYKDRMYSFFRNFQPMSRQVVDDTKYKDYQQVGILHQHNNSGFVGYL
APTMREGQAYPANFPYPLIGKTAVDSITQKKFLCDRTLWRIPFSSNFMSMGALTDLGQNLLYANS
AHALDMTFEVDPMDEPTLLYVLFEVFDVVRVHRPHRGVIETVYLRTPFSA
>d1kful2 b.14.1.1 (L:356-514) Calpain large subunit, middle domain (domain III) {Human (Homo sapiens)}
WKLTKMDGNWRRGSTAGGCRNYPNTFWMNPQYLIKLEEEDEDEEDGESGCTFLVGLIQKHRRRQR
KMGEDMHTIGFGIYEVPEELSGQTNIHLSKNFFLTNRARERSDTFINLREVLNRFKLPPGEYILV
PSTFEPNKDGDFCIRVFSEKKADYQAVDD
>d1df0a2 b.14.1.1 (A:356-514) Calpain large subunit, middle domain (domain III) {Rat (Rattus norvegicus)}
WKLTKMDGNWRRGSTAGGCRNYPNTFWMNPQYLIKLEEEDEDDEDGERGCTFLVGLIQKHRRRQR
KMGEDMHTIGFGIYEVPEELTGQTNIHLSKNFFLTTRARERSDTFINLREVLNRFKLPPGEYVLV
PSTFEPHKNGDFCIRVFSEKKADYQTVDD
>d1f35a_ b.94.1.1 (A:) Olfactory marker protein {Mouse (Mus musculus)}
AEDGPQKQQLEMPLVLDQDLTQQMRLRVESLKQRGEKKQDGEKLIRPAESVYRLDFIQQQKLQFD
HWNVVLDKPGKVTITGTSQNWTPDLTNLMTRQLLDPAAIFWRKEDSDAMDWNEADALEFGERLSD
LAKIRKVMYFLITFGEGVEPANLKASVVFNQL
>d1shsa_ b.15.1.1 (A:) Small heat shock protein {Archaeon Methanococcus jannaschii}
TGIQISGKGFMPISIIEGDQHIKVIAWLPGVNKEDIILNAVGDTLEIRAKRSPLMITESERIIYS
EIPEEEEIYRTIKLPATVKEENASAKFENGVLSVILPKAESSIKKGINIE
>d1gmea_ b.15.1.1 (A:) Small heat shock protein {Wheat (Triticum aestivum)}
SIVRRSNVFDPFADLWADPFDTFRSIVPAISGGGSETAAFANARMDWKETPEAHVFKADLPGVKK
EEVKVEVEDGNVLVVSGERTKEKEDKNDKWHRVERSSGKFVRRFRLLEDAKVEEVKAGLENGVLT
VTVPKAEVKKPEVKAIQISG
>d1gmeb_ b.15.1.1 (B:) Small heat shock protein {Wheat (Triticum

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aestivum)}
NARMDWKETPEAHVFKADLPGVKKEEVKVEVEDGNVLVVSGERTKEKEDKNDKWHRVERSSGKFV
RRFRLLEDAKVEEVKAGLENGVLTVTVPKAEVKKPEVKAIQISG
>d1ejfa_ b.15.1.2 (A:) Co-chaperone p23 {Human (Homo sapiens)}
MQPASAKWYDRRDYVFIEFCVEDSKDVNVNFEKSKLTFSCLGGSDNFKHLNEIDLFHCIDPNDSK
HKRTDRSILCCLRKGESGQSWPRLTKERAKLNWLSVDFNNWKDWE
>d1ezsa_ b.16.1.1 (A:) Ecotin, trypsin inhibitor {Escherichia coli}
PYPQAEKGMKRQVIQLTPQEDESTLKVELLIGQTLEVDCNLHRLGGKLENKTLEGAAAAYYVFDK
VSSPVSTRMACPDGKKEKKFVTAYLGDAGMLRYNSKLPIVVYTPDNVDVKYRVWKAEEKIDNAVV
R
>d1slua_ b.16.1.1 (A:) Ecotin, trypsin inhibitor {Escherichia coli}
IAPYPQAEKGMKRQVIQLTPQEDESTLKVELLIGQTLEVDCNLHRLGGKLENKTLEGWGYDYYVF
DKVSSPVSTMMHCPDGKKEKKFVTAYLGDAGMLRYNSKLPIVVYTPDNVDVKYRVWKAEEKIDNA
VVR
>g1fi8.1 b.16.1.1 (C:,D:) Ecotin, trypsin inhibitor {Escherichia
coli}
PLEKIAPYPQAEKGMKRQVIQLTPQEDESTLKVELLIGQTLEVDCNLHRLGGKLENKTLEGWGYD
YYVFDKVSSPIEPDXKFVTAYLGDAGMLRYNSKLPIVVYTPDNVDVKYRVWKAEEKIDNAVVR
>d1beha_ b.17.1.1 (A:) Phosphatidylethanolamine binding protein, PEBP
{Human (Homo sapiens)}
VDLSKWSGPLSLQEVDEQPQHPLHVTYAGAAVDELGKVLTPTQVKNRPTSISWDGLDSGKLYTLV
LTDPDAPSRKDPKYREWHHFLVVNMKGNDISSGTVLSDYVGSGPPKGTGLHRYVWLVYEQDRPLK
CDEPILSNRSGDHRGKFKVASFRKKYELRAPVAGTCYQAEWDDYVPKLYEQLSG
>d1a44__ b.17.1.1 (-) Phosphatidylethanolamine binding protein, PEBP
{Cow (Bos taurus)}
PVDLSKWSGPLSLQEVDERPQHPLQVKYGGAEVDELGKVLTPTQVKNRPTSITWDGLDPGKLYTL
VLTDPDAPSRKDPKYREWHHFLVVNMKGNNISSGTVLSDYVGSGPPKGTGLHRYVWLVYEQEGPL
KCDEPILSNRSGDHRGKFKVASFRKKYELGAPVAGTCYQAEWDDYVPKLYEQLSG
>d1qoua_ b.17.1.1 (A:) Centroradialis protein Cen {Garden snapdragon
(Antirrhinum majus)}
GRVIGDVVDHFTSTVKMSVIYNSNNSIKHVYNGHELFPSAVTSTPRVEVHGGDMRSFFTLIMTDP
DVPGPSDPYLREHLHWIVTDIPGTTDSSFGKEVVSYEMPRPNIGIHRFVFLLFKQKKRGQAMLSP
PVVCRDGFNTRKFTQENELGLPVAAVFFNCQRET
>d1fjja_ b.17.1.2 (A:) Hypothetical protein YbhB {Escherichia coli}
AMKLISNDLRDGDKLPHRHVFNGMGYDGDNISPHLAWDDVPAGTKSFVVTCYDPDAPTGSGWWHW
VVVNLPADTRVLPQGFGSGLVAMPDGVLQTRTDFGKTGYDGAAPPKGETHRYIFTVHALDIERID
VDEGASGAMVGFNVHFHSLASASITAMFS
>d1fuxa_ b.17.1.2 (A:) Hypothetical protein YbcL {Escherichia coli}
EFQVTSNEIKTGEQLTTSHVFSGFGCEGGNTSPSLTWSGVPEGTKSFAVTVYDPDAPTGSGWWHW
TVVNIPATVTYLPVDAGRRDGTKLPTGAVQGRNDFGYAGFGGACPPKGDKPHHYQFKVWALKTEK
IPVDSNSSGALVGYMLNANKIATAEITPVYEIKLE
>d1g13a_ b.95.1.1 (A:) Ganglioside M2 (gm2) activator {Human (Homo
sapiens)}
SSFSWDNCDEGKDPAVIRSLTLEPDPIIVPGNVTLSVMGSTSVPLSSPLKVDLVLEKEVAGLWIK
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IPCTDYIGSCTFEHFCDVLDMLIPTGEPCPEPLRTYGLPCHCPFKEGTYSLPKSEFVVPDLELPS
WLTTGNYRIESVLSSSGKRLGCIKIAASLKGI
>d1i9ba_ b.96.1.1 (A:) Acetylcholine binding protein (ACHBP) {Great
pond snail (Lymnaea stagnalis)}
FDRADILYNIRQTSRPDVIPTQRDRPVAVSVSLKFINILEVNEITNEVDVVFWQQTTWSDRTLAW
NSSHSPDQVSVPISSLWVPDLAAYNAISKPEVLTPQLARVVSDGEVLYMPSIRQRFSCDVSGVDT
ESGATCRIKIGSWTHHSREISVDPTTENSDDSEYFSQYSRFEILDVTQKKNSVTYSCCPEAYEDV
EVSLNFRKKG
>d1k3ia2 b.18.1.1 (A:-12-150) Galactose oxidase, N-terminal domain
{Fungi (Fusarium spp)}
IPEGSLQFLSLRASAPIGSAISRNNWAVTCDSAQSGNECNKAIDGNKDTFWHTFYGANGDPKPPH
TYTIDMKTTQNVNGLSMLPRQDGNQNGWIGRHEVYLSSDGTNWGSPVASGSWFADSTTKYSNFET
RPARYVRLVAITEANGQPWTSIAEINVFQASS
>d1eut_2 b.18.1.1 (506-647) Sialidase, C-terminal domain
{Micromonospora viridifaciens}
QARMSIADVDSEETAREDGRASNVIDGNPSTFWHTEWSRADAPGYPHRISLDLGGTHTISGLQYT
RRQNSANEQVADYEIYTSLNGTTWDGPVASGRFTTSLAPQRAVFPARDARYIRLVALSEQTGHKY
AAVAELEVEGQR
>d1czsa_ b.18.1.2 (A:) C2 domain of factor V {Human (Homo sapiens)}
GCSTPLGMENGKIENKQITASSFKKSWWGDYWEPFRARLNAQGRVNAWQAKANNNKQWLEIDLLK
IKKITAIITQGCKSLSSEMYVKSYTIHYSEQGVEWKPYRLKSSMVDKIFEGNTNTKGHVKNFFNP
PIISRFIRVIPKTWNQSITLRLELFGCDIY
>d1d7pm_ b.18.1.2 (M:) C2 domain of factor VIII {Human (Homo sapiens)}
LNSCSMPLGMESKAISDAQITASSYFTNMFATWSPSKARLHLQGRSNAWRPQVNNPKEWLQVDFQ
KTMKVTGVTTQGVKSLLTSMYVKEFLISSSQDGHQWTLFFQNGKVKVFQGNQDSFTPVVNCLDPP
LLTRYLRIHPQSWVHQIALRMEVLGCEAQ
>d1jhja_ b.18.1.9 (A:) APC10/DOC1 subunit of the anaphase-promoting
complex {Human (Homo sapiens)}
ATPNKTPPGADPKQLERTGTVREIGSQAVWSLSSCKPGFGVDQLRDDNLETYWQSDGSQPHLVNI
QFRRKTTVKTLCIYADYKSDESYTPSKISVRVGNNFHNLQEIRQLELVEPSGWIHVPLTDNHKKP
TRTFMIQIAVLANHQNGRDTHMRQIKIYTPV
>d1dlc_1 b.18.1.3 (500-644) delta-Endotoxin, C-terminal domain
{Bacillus thuringiensis tenebrionis, CRYIIIA (BT13)}
FFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQCTENGSAATIYVTPDVSYSQKYRAR
IHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLTYNSFNLASFSTPFELSGNNLQIGVTGLSA
GDKVYIDKIEFIPVN
>d1ji6a1 b.18.1.3 (A:503-652) delta-Endotoxin, C-terminal domain
{Bacillus thuringiensis, CRY3bb1}
FFNTIDAEKITQLPVVKAYALSSGASIIEGPGFTGGNLLFLKESSNSIAKFKVTLNSAALLQRYR
VRIRYASTTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAE
SFVSNEKIYIDKIEFIPVQL
>d1ciy_1 b.18.1.3 (462-609) delta-Endotoxin, C-terminal domain
{Bacillus thuringiensis, CRYIA (A)}
NNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVRI
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RYASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFTTPFNFSNGSSVFTLSAHVFN
SGNEVYIDRIEFVPAEVT
>d1i5pa1 b.18.1.3 (A:473-633) delta-Endotoxin, C-terminal domain
{Bacillus thuringiensis subsp. kurstaki, CRY2AA}
NIYAANENGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNTTARYTLR
GNGNSYNLYLRVSSIGNSTIRVTINGRVYTVSNVNTTTNNDGVNDNGARFSDINIGNIVASDNTN
VTLDINVTLNSGTPFDLMNIMFVPTNLPPLY
>d1nuka_ b.18.1.4 (A:) Ligand-binding domain of the ephb2 receptor
tyrosine kinase {Mouse (Mus musculus)}
EETLMDSTTATAELGWMVHPPSGWEEVSGYDENMNTIRTYQVCNVFESSQNNWLRTKFIRRRGAH
RIHVEMKFSVRDCSSIPSVPGSCKETFNLYYYEADFDLATKTFPNWMENPWVKVDTIAADESFSQ
VDLGGRVMKINTEVRSFGPVSRNGFYLAFQDYGGCMSLIAVRVFYR
>d1jz8a3 b.18.1.5 (A:13-219) beta-Galactosidase {Escherichia coli}
RRDWENPGVTQLNRLAAHPPFASWRNSEEARTDRPSQQLRSLNGEWRFAWFPAPEAVPESWLECD
LPEADTVVVPSNWQMHGYDAPIYTNVTYPITVNPPFVPTENPTGCYSLTFNVDESWLQEGQTRII
FDGVNSAFHLWCNGRWVGYGQDSRLPSEFDLSAFLRAGENRLAVMVLRWSDGSYLEDQDMWRMSG
IFRDVSLLHKPT
>d1bhga2 b.18.1.5 (A:22-225) beta-Glucuronidase {Human (Homo
sapiens)}
GLQGGMLYPQESPSRECKELDGLWSFRADFSDNRRRGFEEQWYRRPLWESGPTVDMPVPSSFNDI
SQDWRLRHFVGWVWYEREVILPERWTQDLRTRVVLRIGSAHSYAIVWVNGVDTLEHEGGYLPFEA
DISNLVQVGPLPSRLRITIAINNTLTPTTLPPGTIQYLTDTSKYPKGYFVQNTYFDFFNYAGLQR
SVLLYTTPT
>d1cx1a_ b.18.1.6 (A:) Cellulose-binding domain {Cellulomonas fimi}
ASLDSEVELLPHTSFAESLGPWSLYGTSEPVFADGRMCVDLPGGQGNPWDAGLVYNGVPVGEGES
YVLSFTASATPDMPVRVLVGEGGGAYRTAFEQGSAPLTGEPATREYAFTSNLTFPPDGDAPGQVA
FHLGKAGAYEFCISQVSLTTSAT
>d1ulo__ b.18.1.6 (-) Cellulose-binding domain {Cellulomonas fimi}
ASPIGEGTFDDGPEGWVAYGTDGPLDTSTGALCVAVPAGSAQYGVGVVLNGVAIEEGTTYTLRYT
ATASTDVTVRALVGQNGAPYGTVLDTSPALTSEPRQVTETFTASATYPATPAADDPEGQIAFQLG
GFSADAWTLCLDDVALDSEVEL
>d1gmma_ b.18.1.10 (A:) Carbohydrate binding module from xylanase U
{Clostridium thermocellum}
FSKIESEEYNSLKSSTIQTIGTSDGGSGIGYIESGDYLVFNKINFGNGANSFKARVASGADTPTN
IQLRLGSPTGTLIGTLTVASTGGWNNYEEKSCSITNTTGQHDLYLVFSGPVNIDYFIFDSN
>d1gnya_ b.18.1.11 (A:) Xylan-binding module from xylanase 10c
{Pseudomonas cellulosa}
GNVVIEVDMANGWRGNASGSTSHSGITYSADGVTFAALGDGVGAVFDIARPTTLEDAVIAMVVNV
SAEFKASEANLQIFAQLKEDWSKGEWDCLAGSSELTADTDLTLTCTIDEDDDKFNQTARDVQVGI
QAKGTPAGTITIKSVTITLAQEA
>d1j83a_ b.18.1.12 (A:) Endo-1,4-beta glucanase EngF {Clostridium
cellulovorans}
QPTAPKDFSSGFWDFNDGTTQGFGVNPDSPITAINVENANNALKISNLNSKGSNDLSEGNFWANV
RISADIWGQSINIYGDTKLTMDVIAPTPVNVSIAAIPQSSTHGWGNPTRAIRVWTNNFVAQTDGT
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YKATLTISTNDSPNFNTIATDAADSVVTNMILFVGSNSDNISLDNIKFTK
>d1dyoa_ b.18.1.7 (A:) Xylan-binding domain {Clostridium thermocellum}
PDAGYYYHDTFEGSVGQWTARGPAEVLLSGRTAYKGSESLLVRNRTAAWNGAQRALNPRTFVPGN
TYCFSVVASFIEGASSTTFCMKLQYVDGSGTQRYDTIDMKTVGPNQWVHLYNPQYRIPSDATDMY
VYVETADDTINFYIDEAIGAVAGTVI
>d1xnaa_ b.18.1.8 (A:) N-terminal domain of xrcc1 {Human (Homo sapiens)}
MPEIRLRHVVSCSSQDSTHCAENLLKADTYRKWRAAKAGEKTISVVLQLEKEEQIHSVDIGNDGS
AFVEVLVGSSAGGAGEQDYEVLLVTSSFMSPSESRSGSNPNRVRMFGPDKLVRAAAEKRWDRVKI
VCSQPYSKDSPFGLSFVRFHS
>d1ju3a1 b.18.1.13 (A:352-574) Bacterial cocaine esterase C-terminal domain {Rhodococcus sp. mb1}
PLPDTAYTPFYLGGSGAANTSTGGGTLSTSISGTESADTYLYDPADPVPSLGGTLLFHNGDNGPA
DQRPIHDRDDVLCYSTEVLTDPVEVTGTVSARLFVSSSAVDTDFTAKLVDVFPDGRAIALCDGIV
RMRYRETLVNPTLIEAGEIYEVAIDMLATSNVFLPGHRIMVQVSSSNFPKYDRNSNTGGVIAREQ
LEEMCTAVNRIHRGPEHPSHIVLPIIKR
>d1bvp12 b.19.1.1 (1:121-254) Virus capsid protein vp7 (BTV-10 vp7), central (top) domain {Bluetongue virus}
PARQPYGFFLETEETFQPGRWFMRAAQAVTAVVCGPDMIQVSLNAGARGDVQQIFQGRNDPMMIY
LVWRRIENFAMAQGNSQQTQAGVTVSVGGVDMRAGRIIAWDGQAALHVHNPTQQNAMVQIQVVFY
ISMD
>d1ahsa_ b.19.1.1 (A:) Virus capsid protein vp7 (BTV-10 vp7), central (top) domain {African horse sickness virus}
TGPYAGAVEVQQSGRYYVPQGRTRGGYINSNIAEVCMDAGAAGQVNALLAPRRGDAVMIYFVWRP
LRIFCDPQGASLESAPGTFVTVDGVNVAAGDVVAWNTIAPVNVGNPGARRSILQFEVLWYT
>d1qhda2 b.19.1.1 (A:149-332) vp6, the major capsid protein of group A rotavirus {Bovine rotavirus}
GFTFHKPNIFPYSASFTLNRSQPAHDNLMGTMWLNAGSEIQVAGFDYSCAINAPANTQQFEHIVQ
LRRVLTTATITLLPDAERFSFPRVITSADGATTWYFNPVILRPNNVEIEFLLNGQIINTYQARFG
TIIARNFDTIRLSFQLMRPPNMTPAVAALFPNAQPFEHHATVGLTLRIESAVCE
>d1jsda_ b.19.1.2 (A:) Hemagglutinin {Influenza A virus, different strains}
DKICIGYQSTNSTETVDTLTETNVPVTHAKELLHTSHNGMLCATNLGHPLILDTCTIEGLIYGNP
SCDLLLGGREWSYIVERPSAVNGMCYPGNVENLEELRSLFSSASSYQRIQIFPDTIWNVSYSGTS
SACSDSFYRSMRWLTQKNNAYPIQDAQYTNNRGKSILFMWGINHPPTDTVQTNLYTRTDTTTSVT
TEDINRTFKPVIGPRPLVNGLHGRIDYYWSVLKPGQTLRVRSNGNLIAPWYGHILSGESHGRILK
TDLNSGNCVVQCQTERGGLNTTLPFHNVSKYAFGNCPKYVGVKSLKLAVGLRNVPAR
>d1jsma_ b.19.1.2 (A:) Hemagglutinin {Influenza A virus, different strains}
DQICIGYHANNSTEQVDTIMEKNVTVTHAQDILEKTHNGKLCDLNGVKPLILRDCSVAGWLLGNP
MCDEFLNVPEWSYIVEKDNPVNGLCYPENFNDYEELKHLLSSTNHFEKIRIIPRSSWSNHDASSG
VSSACPYNGRSSFFRNVVWLIKKNNAYPTIKRSYNNTNQEDLLILWGIHHPNDAAEQTKLYQNPT
TYVSVGTSTLNQRSVPEIATRPKVNGQSGRMEFFWTILKPNDAINFESNGNFIAPEYAYKIVKKG
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GSAIMKSGLEYGNCNTKCQTPMGAINSSMPFHNIHPLTIGECPKYVKSGRLVLATGLRNVP
>d2visc_ b.19.1.2 (C:) Hemagglutinin {Influenza A virus, different
strains}
VQSSSTGKICNNPHRILDGIDCTLIDALLGDPHCDVFQNETWDLFVERSKAFSNCYPYDVPDYAS
LRSLVASSGTLEFITEGFTWTGVIQNGGSNACKRGPGSGFFSRLNWLTKSGSTYPVLNVTMPNND
NFDKLYIWGIHHPSTNQEQTSLYVQASGRVTVSTRRSQQTIIPNIGSRPWVRGLSSRISIYWTIV
KPGDVLVINSNGNLIAPRGYFKMRTGKSSIMRSDAPIDTCISECITPNGSIPNDKPFQNVNKITY
GACPKYV
>d2viua_ b.19.1.2 (A:) Hemagglutinin {Influenza A virus, different
strains}
STATLCLGHHAVPNGTLVKTITDDQIEVTNATELVQSSSTGKICNNPHRILDGIDCTLIDALLGD
PHCDVFQNETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFITEGFTWTGVIQNGGSNA
CKRGPGSGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYIWGIHHPSTNQEQTSLYVQASGRVT
VSTRRSQQTIIPNIGSRPWVRGLSSRISIYWTIVKPGDVLVINSNGNLIAPRGYFKMRTGKSSIM
RSDAPIDTCISECITPNGSIPNDKPFQNVNKITYGACPKYVKQNTLKLATGMRNVPEKQT
>d1flca1 b.19.1.3 (A:151-306) Hemagglutinin domain of
haemagglutinin-esterase-fusion glycoprotein HEF1 {Influenza C virus}
CMSLVNALDKTIPLQVTAGTAGNCNNSFLKNPALYTQEVKPSENKCGKENLAFFTLPTQFGTYEC
KLHLVASCYFIYDSKEVYNKRGCDNYFQVIYDSFGKVVGGLDNRVSPYTGNSGDTPTMQCDMLQL
KPGRYSVRSSPRFLLMPERSYCFDMK
>d1aol__ b.20.1.1 (-) F-MuLV receptor-binding domain {Friend murine
leukemia virus}
QVYNITWEVTNGDRETVWAISGNHPLWTWWPVLTPDLCMLALSGPPHWGLEYQAPYSSPPGPPCC
SGSSGSSAGCSRDCDEPLTSLTPRCNTAWNRLKLDQVTHKSSEGFYVCPGSHRPREAKSCGGPDS
FYCASWGCETTGRVYWKPSSSWDYITVDNNLTTSQAVQVCKDNKWCNPLAIQFTNAGKQVTSWTT
GHYWGLRLYVSGRDPGLTFGIRLRYQNLGPRVP
>d1knb__ b.21.1.1 (-) Adenovirus fiber protein head domain (knob domain)
{Human adenovirus type 5}
NDKLTLWTTPAPSPNCRLNAEKDAKLTLVLTKCGSQILATVSVLAVKGSLAPISGTVQSAHLIIR
FDENGVLLNNSFLDPEYWNFRNGDLTEGTAYTNAVGFMPNLSAYPKSHGKTAKSNIVSQVYLNGD
KTKPVTLTITLNGTQETGDTTPSAYSMSFSWDWSGHNYINEIFATSSYTFSYIAQE
>d1qhva_ b.21.1.1 (A:) Adenovirus fiber protein head domain (knob
domain) {Human adenovirus type 2}
AITIGNKNDDKLTLWTTPDPSPNCRIHSDNDCKFTLVLTKCGSQVLATVAALAVSGDLSSMTGTV
ASVSIFLRFDQNGVLMENSSLKKHYWNFRNGNSTNANPYTNAVGFMPNLLAYPKTQSQTAKNNIV
SQVYLHGDKTKPMILTITLNGTSESTETSEVSTYSMSFTWSWESGKYTTETFATNSYTFSYIAQE
>d1h7za_ b.21.1.1 (A:) Adenovirus fiber protein head domain (knob
domain) {Human adenovirus type 3}
KNNTLWTGPKPEANCIIEYGKQNPDSKLTLILVKNGGIVNGYVTLMGASDYVNTLFKNKNVSINV
ELYFDATGHILPDSSSLKTDLELKYKQTADFSARGFMPSTTAYPFVLPNAGTHNENYIFGQCYYK
ASDGALFPLEVTVMLNKRLPDSRTSYVMTFLWSLNAGLAPETTQATLITSPFTFSYIREDD
>d1kaca_ b.21.1.1 (A:) Adenovirus fiber protein head domain (knob
domain) {Human adenovirus type 12}
TPYDPLTLWTTPDPPPNCSLIQELDAKLTLCLTKNGSIVNGIVSLVGVKGNLLNIQSTTTTVGVH
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LVFDEQGRLITSTPTALVPQASWGYRQGQSVSTNTVTNGLGFMPNVSAYPRPNASEAKSQMVSLT
YLQGDTSKPITMKVAFNGITSLNGYSLTFMWSGLSNYINQPFSTPSCSFSYITQE
>d1kkea1 b.21.1.2 (A:250-312) Reovirus attachment protein sigma 1
{Reovirus}
EQSYVASAVTPLRLNSSTKVLDMLIDSSTLEINSSGQLTVRSTSPNLRYPIADVSGGIGMSPN
>d1aly__ b.22.1.1 (-) Extracellular domain of CD40 ligand {Human (Homo
sapiens)}
GDQNPQIAAHVISEASSKTTSVLQWAEKGYYTMSNNLVTLENGKQLTVKRQGLYYIYAQVTFCSN
REASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQQSIHLGGVFELQPGASVFVNVTDPS
QVSHGTGFTSFGLLKL
>d1c28a_ b.22.1.1 (A:) 30 kd adipocyte complement-related protein
{Mouse (Mus musculus)}
MYRSAFSVGLETRVTVPNVPIRFTKIFYNQQNHYDGSTGKFYCNIPGLYYFSYHITVYMKDVKVS
LFKKDKAVLFTYDQYQEKNVDQASGSVLLHLEVGDQVWLQVYGDGDHNGLYADNVNDSTFTGFLL
YHDT
>d1tnra_ b.22.1.1 (A:) Tumor necrosis factor (TNF) {Human (Homo
sapiens)}
KPAAHLIGDPSKQNSLLWRANTDRAFLQDGFSLSNNSLLVPTSGIYFVYSQVVFSGKAYSPKATS
SPLYLAHEVQLFSSQYPFHVPLLSSQKMVYPGLQEPWLHSMYHGAAFQLTQGDQLSTHTDGIPHL
VLSPSTVFFGAFAL
>d4tsva_ b.22.1.1 (A:) Tumor necrosis factor (TNF) {Human (Homo
sapiens)}
DKPVAHVVANPQAEGQLQWSNRRANALLANGVELRDNQLVVPIEGLFLIYSQVLFKGQGCPSTHV
LLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYLGGVFQLEKGDRLSAEINRP
DYLDFAESGQVYFGIIAL
>d2tnfa_ b.22.1.1 (A:) Tumor necrosis factor (TNF) {Mouse (Mus
musculus)}
SDKPVAHVVANHQVEEQLEWLSQRANALLANGMDLKDNQLVVPADGLYLVYSQVLFKGQGCPDYV
LLTHTVSRFAISYQEKVNLLSAVKSPCPKDTPEGAELKPWYEPIYLGGVFQLEKGDQLSAEVNLP
KYLDFAESGQVYFGVIAL
>d1dg6a_ b.22.1.1 (A:) Apoptosis-2 ligand, apo2l/TRAIL {Human (Homo
sapiens)}
QRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYI
YSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPAPILLMKSARNSCWSKDAEYGLYSIYQGGIFE
LKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
>d1jtzx_ b.22.1.1 (X:) TRANCE/RANKL cytokine {Mouse (Mus musculus)}
QPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHET
SGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQ
VSNPSLLDPDQDATYFGAFKVQDID
>d1jh5a_ b.22.1.1 (A:) Soluble part of TALL-1, sTALL-1 {Human (Homo
sapiens)}
VTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKILVKETGYFFIYGQVLYTDKTY
AMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCYSAGIAKLEEGDELQLAIPRENAQIS
LDGDVTFFGALKLL
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>d1gr3a_ b.22.1.1 (A:) Collagen X NC1 trimerisation domain {Human (Homo
sapiens)}
MPVSAFTVILSKAYPAIGTPIPFDKILYNRQQHYDPRTGIFTCQIPGIYYFSYHVHVKGTHVWVG
LYKNGTPVMYTYDEYTKGYLDQASGSAIIDLTENDQVWLQLPNAESNGLYSSEYVHSSFSGFLVA
PM
>d1sfp__ b.23.1.1 (-) Acidic seminal fluid protein (ASFP) {Cow (Bos
taurus)}
LPRNTNCGGILKEESGVIATYYGPKTNCVWTIQMPPEYHVRVSIQYLQLNCNKESLEIIDGLPGS
PVLGKICEGSLMDYRSSGSIMTVKYIREPEHPASFYEVLYFQDPQA
>d1sppa_ b.23.1.1 (A:) Major seminal plasma glycoprotein PSP-I {Pig
(Sus scrofa)}
LDYHACGGRLTDDYGTIFTYKGPKTECVWTLQVDPKYKLLVSIPTLNLTCGKEYVEVLEGAPGSK
SLGKFCEGLSILNRGSSGMTVKYKRDSGHPASPYEIIFLRDSQG
>d1sppb_ b.23.1.1 (B:) Major seminal plasma glycoprotein PSP-II {Pig
(Sus scrofa)}
ARINGPDECGRVIKDTSGSISNTDRQKNLCTWTILMKPDQKVRMAIPYLNLACGKEYVEVFDGLL
SGPSYGKLCAGAAIVFLSTANTMTIKYNRISGNSSSPFLIYFYGSSP
>d1cb8a2 b.24.1.1 (A:600-700) Chondroitinase AC {Pedobacter heparinus
(Flavobacterium heparinum)}
PKVLANTNQLQAVYHQQLDMVQAIFYTAGKLSVAGIEIETDKPCAVLIKHINGKQVIWAADPLQK
EKTAVLSIRDLKTGKTNRVKIDFPQQEFAGATVELK
>d1egua2 b.24.1.1 (A:815-893) Hyaluronate lyase {Streptococcus
pneumoniae}
SSLIENNETLQSVYDAKQGVWGIVKYDDSVSTISNQFQVLKRGVYTIRKEGDEYKIAYYNPETQE
SAPDQEVFKKLEQH
>d1f1sa3 b.24.1.1 (A:920-984) Hyaluronate lyase {Streptococcus
agalactiae}
SKQQVIYDKNSQTWAVIKHDNQESLINNQFKMNKAGLYLVQKVGNDYQNVYYQPQTMTKTDQLAI
>d1iaza_ b.97.1.1 (A:) Equinatoxin II (eqtII, tenebrosin C) {European
sea anemone (Actinia equina)}
AGAVIDGASLSFDILKTVLEALGNVKRKIAVGVDNESGKTWTALNTYFRSGTSDIVLPHKVPHGK
ALLYNGQKDRGPVATGAVGVLAYLMSDGNTLAVLFSVPYDYNWYSNWWNVRIYKGKRRADQRMYE
ELYYNLSPFRGDNGWHTRNLGYGLKSRGFMNSSGHAILEIHVSKA
>d1aun__ b.25.1.1 (-) Pathogenesis-related protein 5d {Common tobacco
(Nicotiana tabacum)}
SGVFEVHNNCPYTVWAAATPVGGGRRLERGQSWWFWAPPGTKMARIWGRTNCNFDGAGRGWCQTG
DCGGVLECKGWGKPPNTLAEYALNQFSNLDFWDISVIDGFNIPMSFGPTKPGPGKCHGIQCTANI
NGECPGSLRVPGGCNNPCTTFGGQQYCCTQGPCGPTELSRWFKQRCPDAYSYPQDDPTSTFTCTS
WTTDYKVMFCPYG
>d1du5a_ b.25.1.1 (A:) Zeamatin {Maize (Zea mays)}
AVFTVVNQCPFTVWAASVPVGGGRQLNRGESWRITAPAGTTAARIWARTGCKFDASGRGSCRTGD
CGGVLQCTGYGRAPNTLAEYALKQFNNLDFFDISLIDGFNVPMSFLPDGGSGCSRGPRCAVDVNA
RCPAELRQDGVCNNACPVFKKDEYCCVGSAANDCHPTNYSRYFKGQCPDAYSYPKDDATSTFTCP
AGTNYKVVFCP
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>d1thw__ b.25.1.1 (-) Thaumatin {Ketemfe (Thaumatococcus daniellii)}
ATFEIVNRCSYTVWAAASKGDAALDAGGRQLNSGESWTINVEPGTKGGKIWARTDCYFDDSGSGI
CKTGDCGGLLRCKRFGRPPTTLAEFSLNQYGKDYIDISNIKGFNVPMDFSPTTRGCRGVRCAADI
VGQCPAKLKAPGGGCNDACTVFQTSEYCCTTGKCGPTEYSRFFKRLCPDAFSYVLDKPTTVTCPG
SSNYRVTFCPTA
>d1dd1a_ b.26.1.1 (A:) Smad4 tumor suppressor C-terminal domain {Human
(Homo sapiens)}
NGHLQHHPPMPPHPGHYWPVHNELAFQPPISNHPAPEYWCSIAYFEMDVQVGETFKVPSSCPIVT
VDGYVDPSGGDRFCLGQLSNVHRTEAIERARLHIGKGVQLECKGEGDVWVRCLSDHAVFVQSYYL
DREAGRAPGDAVHKIYPSAYIKVFDLRQCHRQMQQQAATAQAAAAAQAAAVAGNIPGPGSVGGIA
PAISLSAAAGIGVDDLRRLCILRMSFVKGWGPDYPRQSIKETPCWIEIHLHRALQLLDEVLHTMP
I
>d1ygs__ b.26.1.1 (-) Smad4 tumor suppressor C-terminal domain {Human
(Homo sapiens)}
APEYWCSIAYFEMDVQVGETFKVPSSCPIVTVDGYVDPSGGDRFCLGQLSNVHRTEAIERARLHI
GKGVQLECKGEGDVWVRCLSDHAVFVQSYYLDREAGRAPGDAVHKIYPSAYIKVFDLRQCHRQMQ
QQAATAQAAAAAQAAAVAGNIPGPGSVGGIAPAISLSAAAGIGVDDLRRLCILRMSFVKGWGPDY
PRQSIKETPCWIEIHLHRALQLLDEVLHTM
>d1khxa_ b.26.1.1 (A:) Smad2 MH2 domain {Human (Homo sapiens)}
PVTYSEPAFWCSIAYYELNQRVGETFHASQPSLTVDGFTDPSNSERFCLGLLSNVNRNATVEMTR
RHIGRGVRLYYIGGEVFAECLSDSAIFVQSPNCNQRYGWHPATVCKIPPGCNLKIFNNQEFAALL
AQSVNQGFEAVYQLTRMCTIRMSFVKGWGAEYRRQTVTSTPCWIELHLNGPLQWLDKVLTQMGSP
SVRCSSMS
>d1khua_ b.26.1.1 (A:) Smad1 {Human (Homo sapiens)}
PKHWCSIVYYELNNRVGEAFHASSTSVLVDGFTDPSNNKNRFCLGLLSNVNRNSTIENTRRHIGK
GVHLYYVGGEVYAECLSDSSIFVQSRNCNYHHGFHPTTVCKIPSGCSLKIFNNQEFAQLLAQSVN
HGFETVYELTKMCTIRMSFVKGWGAEYHRQDVTSTPCWIEIHLHGPLQWLDKVLTQMGSPHNPIS
SVS
>d1dmza_ b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53
{Baker's yeast (Saccharomyces cerevisiae)}
GNGRFLTLKPLPDSIIQESLEIQQGVNPFFIGRSEDCNCKIEDNRLSRVHCFIFKKRHAVGKSMY
ESPAQGLDDIWYCHTGTNVSYLNNNRMIQGTKFLLQDGDEIKIIWDKNNKFVIGFKVEINDTTGL
FNEGLGMLQEQRVVLKQTAEEKDLVKKL
>d1g6ga_ b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53
{Baker's yeast (Saccharomyces cerevisiae)}
GENIVCRVICTTGQIPIRDLSADISQVLKEKRSIKKVWTFGRNPACDYHLGNISRLSNKHFQILL
GEDGNLLLNDISTNGTWLNGQKVEKNSNQLLSQGDEITVGVGVESDILSLVIFINDKFKQCL
>d1k3ja_ b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53
{Baker's yeast (Saccharomyces cerevisiae)}
ATQRFLIEKFSQEQIGENIVCRVICTTGQIPIRDLSADISQVLKEKRSIKKVWTFGRNPACDYHL
GNISRLSNKHFQILLGEDGNLLLNDISTNGTWLNGQKVEKNSNQLLSQGDEITVGVGVESDILSL
VIFINDKFKQCLEQNKVDRIR
>d1qu5a_ b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53
{Baker's yeast (Saccharomyces cerevisiae)}
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EAETREQKLLHSNNTENVKSSKKKGNGRFLTLKPLPDSIIQESLEIQQGVNPFFIGRSEDCNCKI
EDNRLSRVHCFIFKKRHAVGKSMYESPAQGLDDIWYCHTGTNVSYLNNNRMIQGTKFLLQDGDEI
KIIWDKNNKFVIGFKVEINDTTGLFNEGLGMLQEQRVVLKQTAEEKDLVKKL
>d1cq3a_ b.27.1.1 (A:) Soluble secreted chemokine inhibitor, VCCI
{Cowpox virus}
SFSSSSSCTEEENKHHMGIDVIIKVTKQDQTPTNDKICQSVTEVTESEDESEEVVKGDPTTYYTV
VGGGLTMDFGFTKCPKISSISEYSDGNTVNARLSSVSPGQGKDSPAITREEALSMIKDCEMSINI
KCSEEEKDSNIKTHPVLGSNISHKKVSYEDIIGSTIVDTKCVKNLEISVRIGDMCKESSELEVKD
GFKYVDGSASEDAADDTSLINSAKLIACV
>d1p35a_ b.28.1.1 (A:) Paculovirus p35 {Nuclear polyhedrosis virus
(Autographa californica), ACMNPV}
CVIFPVEIDVSQTIIRDCQVDKQTRELVYINKIMNTQLTKPVLMMFNISGPIRSVTRKNNNLRDR
IKSKVDEQFDQLERDYSDQMDGFHDSIKYFKDEHYSVSCQNGSVLKSKFAKILKSHDYTDKKSIE
AYEKYCLPKLVDERNDYYVAVCVLKPGFENGSNQVLSFEYNPIGNKVIVPFAHEINDTGLYEYDV
VAYVDSVQFDGEQFEEFVQSLILPSSFKNSEKVLYYNEASKNKSMIYKALEFTTESSWGKSEKYN
WKIFCNGFIYDKKSKVLYVKLHNVTSALNKNVILNTIKA
>d1nls__ b.29.1.1 (-) Concanavalin A {Jack bean (Canavalia
ensiformis)}
ADTIVAVELDTYPNTDIGDPSYPHIGIDIKSVRSKKTAKWNMQNGKVGTAHIIYNSVDKRLSAVV
SYPNADSATVSYDVDLDNVLPEWVRVGLSASTGLYKETNTILSWSFTSKLKSNSTHETNALHFMF
NQFSKDQKDLILQGDATTGTDGNLELTRVSSNGSPQGSSVGRALFYAPVHIWESSAVVASFEATF
TFLIKSPDSHPADGIAFFISNIDSSIPSGSTGRLLGLFPDAN
>d2cna__ b.29.1.1 (-) Concanavalin A {Jack bean (Canavalia
ensiformis)}
ADTIVAVELDTYPNTDIGDPSYPHIGIDIKSVRSKKTAKWNMQDGKVGTAHIIYNSVDKRLSAVV
SYPNADATSVSYDVDLNDVLPEWVRVGLSASTGLYKETNTILSWSFTSKLKSNSTHQTDALHFMF
NQFSKDQKDLILQGDATTGTDGNLELTRVSSNGSPEGSSVGRALFYAPVHIWESSATVSAFEATF
AFLIKSPDSHPADGIAFFISNIDSSIPSGSTGRLLGLFPDAN
>g2ltn.1 b.29.1.1 (A:,B:) Legume lectin {Garden pea (Pisum sativum)}
TETTSFLITKFSPDQQNLIFQGDGYTTKEKLTLTKAVKNTVGRALYSSPIHIWDRETGNVANFVT
SFTFVINAPNSYNVADGFTFFIAPVDTKPQTGGGYLGVFNSAEYDKTTQTVAVEFDTFYNAAWDP
SNRDRHIGIDVNSIKSVNTKSWKLQNGEEANVVIAFNAATNVLTVSLTYPNXVTSYTLSDVVSLK
DVVPEWVRIGFSATTGAEYAAHEVLSWSFHSELSG
>g1len.1 b.29.1.1 (A:,B:) Legume lectin {Common lentil (Lens
culinaris)}
TETTSFSITKFSPDQQNLIFQGDGYTTKGKLTLTKAVKSTVGRALYSTPIHIWDRDTGNVANFVT
SFTFVIDAPSSYNVADGFTFFIAPVDTKPQTGGGYLGVFNSKEYDKTSQTVAVEFDTFYNAAWDP
SNKERHIGIDVNSIKSVNTKSWNLQNGERANVVIAFNAATNVLTVTLTYPNXVTSYTLNEVVPLK
DVVPEWVRIGFSATTGAEFAAQEVHSWSFNSQLG
>d1led__ b.29.1.1 (-) Legume lectin {West-central african legume
(Griffonia simplicifolia)}
ENTVNFTYPDFWSYSLKNGTEITFLGDATRIPGALQLTKTDANGNPVRSSAGQASYSEPVFLWDS
TGKAASFYTSFTFLLKNYGAPTADGLAFFLAPVDSSVKDYGGFLGLFRHETAADPSKNQVVAVEF
DTWINKDWNDPPYPHIGIDVNSIVSVATTRWENDDAYGSSIATAHITYDARSKILTVLLSYEHGR
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DYILSHVVDLAKVLPQKVRIGFSAGVGYDEVTYILSWHFFSTLDGTNK
>d1hqla_ b.29.1.1 (A:) Legume lectin {Griffonia simplicifolia, lectin
I-b4}
SVSFTFPNFWSDVEDSIIFQGDANTTAGTLQLCKTNQYGTPLQWSAGRALYSDPVQLWDNKTESV
ASFYTEFTFFLKITGNGPADGLAFFLAPPDSDVKDAGEYLGLFNKSTATQPSKNQVVAVEFDTWT
NPNFPEPSYRHIGINVNSIVSVATKRWEDSDIFSGKIATARISYDGSAEILTVVLSYPDGSDYIL
SHSVDMRQNLPESVRVGISASTGNNQFLTVYILSWRFSSNL
>d1ax0__ b.29.1.1 (-) Legume lectin {Coral tree (Erythrina
corallodendron)}
VETISFSFSEFEPGNDNLTLQGAALITQSGVLQLTKINQNGMPAWDSTGRTLYAKPVHIWDMTTG
TVASFETRFSFSIEQPYTRPLPADGLVFFMGPTKSKPAQGYGYLGIFNNSKQDNSYQTLGVEFDT
FSNPWDPPQVPHIGIDVNSIRSIKTQPFQLDNGQVANVVIKYDASSKILHAVLVYPSSGAIYTIA
EIVDVKQVLPEWVDVGLSGATGAQRDAAETHDVYSWSFQASLPE
>d1wbfa_ b.29.1.1 (A:) Legume lectin {Winged bean (Psophocarpus
tetragonolobus), basic agglutinin}
KTISFNFNQFHQNEEQLKLQRDARISSNSVLELTKVVNGVPTWNSTGRALYAKPVQVWDSTTGNV
ASFETRFSFSIRQPFPRPHPADGLVFFIAPPNTQTGEGGGYFGIYNPLSPYPFVAVEFDTFRNTW
DPQIPHIGIDVNSVISTKTVPFTLDNGGIANVVIKYDASTKILHVVLVFPSLGTIYTIADIVDLK
QVLPESVNVGFSAATGDPSGKQRNATETHDILSWSFSASLPG
>d1f9ka_ b.29.1.1 (A:) Legume lectin {Winged bean (Psophocarpus
tetragonolobus), acidic lectin}
ETQSFNFDHFEENSKELNLQRQASIKSNGVLELTKLTKNGVPVWKSTGRALYAEPIKIWDSTTGN
VASFETRFSFNITQPYAYPEPADGLTFFMVPPNSPQGEDGGNLGVFKPPEGDNAFAVEFDTFQNT
WDPQVPHIGIDVNSIVSSKTLHFQLENGGVANVVIKYDSPTKILNVVLAFHSVGTVYTLSNIVDL
KQEFPNSEWVNVGLSATTGYQKNAVETHEIISWSFTSSL
>g1loe.1 b.29.1.1 (A:,B:) Legume lectin {Lathyrus ochrus, isolectin
I}
TETTSFSITKFGPDQQNLIFQGDGYTTKERLTLTKAVRNTVGRALYSSPIHIWDSKTGNVANFVT
SFTFVIDAPNSYNVADGFTFFIAPVDTKPQTGGGYLGVFNSKDYDKTSQTVAVEFDTFYNTAWDP
SNGDRHIGIDVNSIKSINTKSWALQNGKEANVVIAFNAATNVLTVSLTYPXTSYTLNEVVPLKEF
VPEWVRIGFSATTGAEFAAHEVLSWYFHSELA
>d2pela_ b.29.1.1 (A:) Legume lectin {Peanut (Arachis hypogaea)}
AETVSFNFNSFSEGNPAINFQGDVTVLSNGNIQLTNLNKVNSVGRVLYAMPVRIWSSATGNVASF
LTSFSFEMKDIKDYDPADGIIFFIAPEDTQIPAGSIGGGTLGVSDTKGAGHFVGVEFDTYSNSEY
NDPPTDHVGIDVNSVDSVKTVPWNSVSGAVVKVTVIYDSSTKTLSVAVTNDNGDITTIAQVVDLK
AKLPERVKFGFSASGSLGGRQIHLIRSWSFTSTLITT
>d1g9fa_ b.29.1.1 (A:) Legume lectin {Soybean (Glycine max)}
AETVSFSWNKFVPKQPNMILQGDAIVTSSGKLQLNKVDENGTPKPSSLGRALYSTPIHIWDKETG
SVASFAASFNFTFYAPDTKRLADGLAFFLAPIDTKPQTHAGYLGLFNENESGDQVVAVEFDTFRN
SWDPPNPHIGINVNSIRSIKTTSWDLANNKVAKVLITYDASTSLLVASLVYPSQRTSNILSDVVD
LKTSLPEWVRIGFSAATGLDIPGESHDVLSWSFASNLPHASSNIDPLDLTSFVLHE
>g1qmo.1 b.29.1.1 (A:,E:) Legume lectin {Field bean (Dolichos lab lab),
Fril}
AQSLSFSFTKFDPNQEDLIFQGHATSTNNVLQVTKLDSAGNPVSSSAGRVLYSAPLRLWEDSAVL
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TSFDTIINFEISTPYTSRIADGLAFFIAPPDSVISYHGGFLGLFPNANXSNVVAVEFDTYLNPDY
GDPNYIHIGIDVNSIRSKVTAKWDWQNGKIATAHISYNSVSKRLSVTSYYAGSKPATLSYDIELH
TVLPEWVRVGLSASTGQDKERNTVHSWSFTSSLWTN
>d1g7ya_ b.29.1.1 (A:) Legume lectin {Horse gram (Dolichos biflorus),
different isoforms}
ADIQSFSFKNFNSSSFILQGDATVSSSKLRLTKVKGNGLPTLSSLGRAFYSSPIQIYDKSTGAVA
SWATSFTANIFAPNKSSSADGIAFALVPVGSEPKSNSGFLGVFDSDVYDNSAQTVAVEFDTFSNT
DWDPTSRHIGIDVNSIKSIRTASWGLANGQNAEILITYNAATSLLVASLVHPSRRTSYIVSERVD
ITNELPEYVSIGFSATTGLSEGYTETHDVLSWSFASKLPDDSTTEPLDIASYLVRNVL
>d1lu1__ b.29.1.1 (-) Legume lectin {Horse gram (Dolichos biflorus),
different isoforms}
ANIQSFSFKNFNSPSFILQGDATVSSGKLQLTKVKENGIPTPSSLGRAFYSSPIQIYDKSTGAVA
SWATSFTVKISAPSKASFADGIAFALVPVGSEPRRNGGYLGVFDSDVYNNSAQTVAVEFDTLSNS
GWDPSMKHIGIDVNSIKSIATVSWDLANGENAEILITYNAATSLLVASLVHPSRRTSYILSERVD
ITNELPEYVSVGFSATTGLSEGYIETHDVLSWSFASKLPDDSTAEPLDLASYLVRNVL
>d1h9wa_ b.29.1.1 (A:) Legume lectin {Duke (Dioclea guianensis)}
ADTIVAVELDSYPNTDIGDPSYPHIGIDIKSIRSKSTARWNMQTGKVGTAHISYNSVAKRLSAVV
SYTGSSSTTVSYDVDLNNVLPEWVRVGLSATTGLYKETNTILSWSFTSKLKTNSIADANSLHFSF
NQFSQNPKDLILQGDATTDSDGNLELTKVSSSGDPQGSSVGRALFYAPVHIWEKSAVVASFDATF
TFLIKSPDRDPADGITFFIANTDTSIPSGSGGRLLGLFPDAN
>d1fx5a_ b.29.1.1 (A:) Legume lectin {Furze (Ulex europaeus), UEA-I}
SDDLSFKFKNFSQNGKDLSFQGNASVIETGVLQLNKVGNNLPDETGGIARYIAPIHIWNCNTGEL
ASFITSFSFFMETSANPKAATDGLTFFLAPPDSPLRRAGGYFGLFNDTKCDSSYQTVAVEFDTIG
SPVNFWDPGFPHIGIDVNCVKSINAERWNKRYGLNNVANVEIIYEASSKTLTASLTYPSDQTSIS
VTSIVDLKEILPEWVSVGFSGSTYIGRQATHEVLNWYFTSTFINT
>d1qnwa_ b.29.1.1 (A:) Legume lectin {Furze (Ulex europaeus), UEA-II}
SDDLSFNFDKFVPNQKNIIFQGDASVSTTGVLQVTKVSKPTTTSIGRALYAAPIQIWDSITGKVA
SFATSFSFVVKADKSDGVDGLAFFLAPANSQIPSGSSAGMFGLFSSSDSKSSNQIIAVEFDTYFG
KAYNPWDPDFKHIGIDVNSIKSIKTVKWDWRNGEVADVVITYRAPTKSLTVCLSYPSDGTSNIIT
ASVDLKAILPEWVSVGFSGGVGNAAEFETHDVLSWYFTSNLE
>d1dbna_ b.29.1.1 (A:) Legume lectin {Maackia amurensis,
leukoagglutinin}
SDELSFTINNFVPNEADLLFQGEASVSSTGVLQLTKVENGQPQKYSVGRALYAAPVRIWGNTTGS
VASFSTSFTFVVKAPNPDITSDGLAFYLAPPDSQIPSGSVSKYLGLFNNSNSDSSNQIVAVEFDT
YFAHSYDPWDPNYRHIGIDVNGIESIKTVQWDWINGGVAFATITYLAPNKTLIASLVYPSNQTTF
SVAASVDLKEILPEWVRVGFSAATGYPTEVETHDVLSWSFTSTL
>d1fnya_ b.29.1.1 (A:) Legume lectin {Black locust (Robinia
pseudoacacia)}
TGSLSFSFPKFAPNQPYLINQGDALVTSTGVLQLTNVVNGVPSSKSLGRALYAAPFQIWDSTTGN
VASFVTSFTFIIQAPNPATTADGLAFFLAPVDTQPLDLGGMLGIFKDGYFNKSNQIVAVEFDTFS
NGDWDPKGRHLGINVNSIESIKTVPWNWTNGEVANVFISYEASTKSLTASLVYPSLETSFIIDAI
VDVKIVLPEWVRFGFSATTGIDKGYVQTNDVLSWSFESNLPG
>d1avba_ b.29.1.1 (A:) Phytohemagglutinin-L, PHA-L, also arcelin
{Kidney bean (Phaseolus vulgaris)}
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SNDASFNVETFNKTNLILQGDATVSSEGHLLLTNVKGNEEDSMGRAFYSAPIQINDRTIDNLASF
STNFTFRINAKNIENSAYGLAFALVPVGSRPKLKGRYLGLFNTTNYDRDAHTVAVVFDTVSNRIE
IDVNSIRPIATESCNFGHNNGEKAEVRITYDSPKNDLRVSLLYPSSEEKCHVSATVPLEKEVEDW
VSVGFSATSGSKKETTETHNVLSWSFSSNFI
>d1dhkb_ b.29.1.1 (B:) Phytohemagglutinin-L, PHA-L, also arcelin
{Kidney bean (Phaseolus vulgaris)}
ATETSFIIDAFNKTNLILQGDATVSSNGNLQLSYNSYDSMSRAFYSAPIQIRDSTTGNVASFDTN
FTMNIRTHRQANSAVGLDFVLVPVQPESKGDTVTVEFDTFLSRISIDVNNNDIKSVPWDVHDYDG
QNAEVRITYNSSTKVFSVSLSNPSTGKSNNVSTTVELEKEVYDWVSVGFSATSGAYQWSYETHDV
LSWSFSSKF
>d1g8wa_ b.29.1.1 (A:) Phytohemagglutinin-L, PHA-L, also arcelin
{Kidney bean (Phaseolus vulgaris)}
SNDIYFNFQRFNETNLILQRDASVSSSGQLRLTNLNGNGEPRVGSLGRAFYSAPIQIWDNTTGTV
ASFATSFTFNIQVPNNAGPADGLAFALVPVGSQPKDKGGFLGLFDGSNSNFHTVAVEFDTLYNKD
WDPTERHIGIDVNSIRSIKTTRWDFVNGENAEVLITYDSSTNLLVASLVYPSQKTSFIVSDTVDL
KSVLPEWVSVGFSATTGINKGNVETNDVLSWSFASKLS
>d1ioaa_ b.29.1.1 (A:) Phytohemagglutinin-L, PHA-L, also arcelin
{Kidney bean (Phaseolus vulgaris), G02771, arcelin-5a}
ATETSFNFPNFHTDDKLILQGNATISSKGQLQLTGVGSNELPRVDSLGRAFYSDPIQIKDSNNVA
SFNTNFTFIIRAKNQSISAYGLAFALVPVNSPPQKKQEFLGIFNTNNPEPNARTVAVVFNTFKNR
IDFDKNFIKPYVNENCDFHKYNGEKTDVQITYDSSNNDLRVFLHFTVSQVKCSVSATVHLEKEVD
EWVSVGFSPTSGLTEDTTETHDVLSWSFSSKFR
>d1gbg__ b.29.1.2 (-) Bacillus 1-3,1-4-beta-glucanase {Bacillus
licheniformis}
QTGGSFYEPFNNYNTGLWQKADGYSNGNMFNCTWRANNVSMTSLGEMRLSLTSPSYNKFDCGENR
SVQTYGYGLYEVNMKPAKNVGIVSSFFTYTGPTDGTPWDEIDIEFLGKDTTKVQFNYYTNGVGNH
EKIVNLGFDAANSYHTYAFDWQPNSIKWYVDGQLKHTATTQIPQTPGKIMMNLWNGAGVDEWLGS
YNGVTPLYAHYNWVRYTKR
>d2ayh__ b.29.1.2 (-) Bacillus 1-3,1-4-beta-glucanase {Hybrid protein:
residues 1-16 from Bacillus amyloliquefaciens and Bacillus macerans}
QTGGSFFEPFNSYNSGTWEKADGYSNGGVFNCTWRANNVNFTNDGKLKLGLTSSAYNKFDCAEYR
STNIYGYGLYEVSMKPAKNTGIVSSFFTYTGPAHGTQWDEIDIEFLGKDTTKVQFNYYTNGVGGH
EKVISLGFDASKGFHTYAFDWQPGYIKWYVDGVLKHTATANIPSTPGKIMMNLWNGTGVDDWLGS
YNGANPLYAEYDWVKYTSN
>d1ajka_ b.29.1.2 (A:) Bacillus 1-3,1-4-beta-glucanase {Bacillus
macerans}
NTGIVSSFFTYTGPAHGTQWDEIDIEFLGKDTTKVQFNYYTNGVGGHEKVISLGFDASKGFHTYA
FDWQPGYIKWYVDGVLKHTATANIPSTPGKIMMNLWNGTGVDDWLGSYNGANPLYAEYDWVKYTS
NQTGGSFFEPFNSYNSGTWEKADGYSNGGVFNCTWRANNVNFTNDGKLKLGLTSSAYNKFDCAEY
RSTNIYGYGLYEVSMKPAK
>d1ajoa_ b.29.1.2 (A:) Bacillus 1-3,1-4-beta-glucanase {Bacillus
macerans}
GHEKVISLGFDASKGFHTYAFDWQPGYIKWYVDGVLKHTATANIPSTPGKIMMNLWNGTGVDDWL
GSYNGANPLYAEYDWVKYTSNQTGGSFFEPFNSYNSGTWEKADGYSNGGVFNCTWRANNVNFTND
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GKLKLGLTSSAYNKFDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGPAHGTQWDEIDIE
FLGKDTTKVQFNYYTNG
>d1cpm__ b.29.1.2 (-) Bacillus 1-3,1-4-beta-glucanase {Bacillus macerans}
FDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGPAHGTQWDEIDIEFLGKDTTKVQFNYY
TNGVGGHEKVISLGFDASKGFHTYAFDWQPGYIKWYVDGVLKHTATANIPSTPGKIMMNLWNGTG
VDDWLGSYNGANPLYAEYDWVKYTSNQTGGSFFEPFNSYNSGTWEKADGYSNGGVFNCTWRANNV
NFTNDGKLKLGLTSSAYNA
>d1cpn__ b.29.1.2 (-) Bacillus 1-3,1-4-beta-glucanase {Bacillus macerans}
FDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGPAHGTQWDEIDIEFLGKDTTKVQFNYY
TNGVGGHEKVISLGFDASKGFHTYAFDWQPGYIKWYVDGVLKHTATANIPSTPGKIMMNLWNGTG
VDDWLGSYNGANPLYAEYDWVKYTSNGSVFWEPKSYFNPSTWEKADGYSNGGVFNCTWRANNVNF
TNDGKLKLGLTSS
>d1dypa_ b.29.1.2 (A:) kappa-Carrageenase, catalytic {Pseudoalteromonas carrageenovora}
SMQPPIAKPGETWILQAKRSDEFNVKDATKWNFQTENYGVWSWKNENATVSKGKLKLTTKRESHQ
RTFWDGCNQQQVANYPLYYTSGVAKSRATGNYGYYEARIKGASTFPGVSPAFWMYSTIDRSLTKE
GDVQYSEIDVVELTQKSAVRESDHDLHNIVVKNGKPTWMRPGSFPQTNHNGYHLPFDPRNDFHTY
GVNVTKDKITWYVDGEIVGEKDNLYWHRQMNLTLSQGLRAPHTQWKCNQFYPSANKSAEGFPTSM
EVDYVRTWVKV
>d1slta_ b.29.1.3 (A:) S-lectin, different isoforms {Cow (Bos taurus)}
CGLVASNLNLKPGECLRVRGEVAADAKSFLLNLGKDDNNLCLHFNPRFNAHGDVNTIVCNSKDAG
AWGAEQRESAFPFQPGSVVEVCISFNQTDLTIKLPDGYEFKFPNRLNLEAINYLSAGGDFKIKCV
AFE
>d1bkza_ b.29.1.3 (A:) S-lectin, different isoforms {Human (Homo sapiens)}
SNVPHKSSLPEGIRPGTVLRIRGLVPPNASRFHVNLLCGEEQGSDAALHFNPRLDTSEVVFNSKE
QGSWGREERGPGVPFQRGQPFEVLIIASDDGFKAVVGDAQYHHFRHRLPLARVRLVEVGGDVQLD
SVRIF
>d1hlca_ b.29.1.3 (A:) S-lectin, different isoforms {Human (Homo sapiens)}
ELEVKNMDMKPGSTLKITGSIADGTDGFVINLGQGTDKLNLHFNPRFSESTIVCNSLDGSNWGQE
QREDHLCFSPGSEVKFTVTFESDKFKVKLPDGHELTFPNRLGHSHLSYLSVRGGFNMSSFKLKE
>d1qmja_ b.29.1.3 (A:) S-lectin, different isoforms {Chicken (Gallus gallus)}
QGLVVTQLDVQPGECVKVKGKILSDAKGFSVNVGKDSSTLMLHFNPRFDCHGDVNTVVCNSKEDG
TWGEEDRKADFPFQQGDKVEICISFDAAEVKVKVPEVEFEFPNRLGMEKIQYLAVEGDFKVKAIK
FS
>d1a78a_ b.29.1.3 (A:) S-lectin, different isoforms {Toad (Bufo arenarum)}
ASAGVAVTNLNLKPGHCVEIKGSIPPDCKGFAVNLGEDASNFLLHFNARFDLHGDVNKIVCNSKE
ADAWGSEQREEVFPFQQGAEVMVCFEYQTQKIIIKFSSGDQFSFPVRKVLPSIPFLSLEGLAFKS
ITTE
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>d1hdka_ b.29.1.3 (A:) Charcot-Leyden crystal (CLC) protein {Human
(Homo sapiens)}
SLLPVPYTEAASLSTGSTVTIKGRPLVCFLNEPYLQVDFHTEMKEESDIVFHFQVCFGRRVVMNS
REYGAWKQQVESKNMPFQDGQEFELSISVLPDKYQVMVNGQSSYTFDHRIKPEAVKMVQVWRDIS
LTKFNVSYL
>d1a3k__ b.29.1.3 (-) Galectin-3 CRD {Human (Homo sapiens)}
LIVPYNLPLPGGVVPRMLITILGTVKPNANRIALDFQRGNDVAFHFNPRFNENNRRVIVCNTKLD
NNWGREERQSVFPFESGKPFKIQVLVEPDHFKVAVNDAHLLQYNHRVKKLNEISKLGISGDIDLT
SASYTMI
>d1c1la_ b.29.1.3 (A:) Congerin I {Conger eel (Conger myriaster)}
GGLQVKNFDFTVGKFLTVGGFINNSPQRFSVNVGESMNSLSLHLDHRFNYGADQNTIVMNSTLKG
DNGWETEQRSTNFTLSAGQYFEITLSYDINKFYIDILDGPNLEFPNRYSKEFLPFLSLAGDARLT
LVKLE
>d1d2sa_ b.29.1.4 (A:) Sex hormone-binding globulin {Human (Homo
sapiens)}
PPAVHLSNGPGQEPIAVMTFDLTKITKTSSSFEVRTWDPEGVIFYGDTNPKDDWFMLGLRDGRPE
IQLHNHWAQLTVGAGPRLDDGRWHQVEVKMEGDSVLLEVDGEEVLRLRQVSGHPIMRIALGGLLF
PASNLRLPLVPALDGCLRRDSWLDKQAEISASAPTSLRSC
>d1dyka1 b.29.1.4 (A:2744-2932) Laminin alpha2 chain {Mouse (Mus
musculus)}
HGPCVAESEPALLTGSKQFGLSRNSHIAIAFDDTKVKNRLTIELEVRTEAESGLLFYMARINHAD
FATVQLRNGFPYFSYDLGSGDTSTMIPTKINDGQWHKIKIVRVKQEGILYVDDASSQTISPKKAD
ILDVVGILYVGGLPINYTTRRIGPVTYSLDGCVRNLHMEQAPVDLDQPTSSFHVGTCFA
>d1dyka2 b.29.1.4 (A:2933-3117) Laminin alpha2 chain {Mouse (Mus
musculus)}
NAESGTYFDGTGFAKAVGGFKVGLDLLVEFEFRTTRPTGVLLGVSSQKMDGMGIEMIDEKLMFHV
DNGAGRFTAIYDAEIPGHMCNGQWHKVTAKKIKNRLELVVDGNQVDAQSPNSASTSADTNDPVFV
GGFPGGLNQFGLTTNIRFRGCIRSLKLTKGTGKPLEVNFAKALELRGVQPVSCPT
>d1c4ra_ b.29.1.4 (A:) Ligand-binding domain of neurexin 1beta {Rat
(Rattus norvegicus)}
HAGTTYIFSKGGGQITYKWPPNDRPSTRADRLAIGFSTVQKEAVLVRVDSSSGLGDYLELHIHQG
KIGVKFNVGTDDIAIEESNAIINDGKYHVVRFTRSGGNATLQVDSWPVIERYPAGRQLTIFNSQA
TIIIGGKEQGQPFQGQLSGLYYNGLKVLNMAAENDANIAIVGNVRLVGEV
>d1saca_ b.29.1.5 (A:) Serum amyloid P component (SAP) {Human (Homo
sapiens)}
HTDLSGKVFVFPRESVTDHVNLITPLEKPLQNFTLCFRAYSDLSRAYSLFSYNTQGRDNELLVYK
ERVGEYSLYIGRHKVTSKVIEKFPAPVHICVSWESSSGIAEFWINGTPLVKKGLRQGYFVEAQPK
IVLGQEQDSYGGKFDRSQSFVGEIGDLYMWDSVLPPENILSAYQGTPLPANILDWQALNYEIRGY
VIIKPLVWV
>d1b09a_ b.29.1.5 (A:) C-reactive protein (CRP) {Human (Homo sapiens)}
QTDMSRKAFVFPKESDTSYVSLKAPLTKPLKAFTVCLHFYTELSSTRGYSIFSYATKRQDNEILI
FWSKDIGYSFTVGGSEILFEVPEVTVAPVHICTSWESASGIVEFWVDGKPRVRKSLKKGYTVGAE
ASIILGQEQDSFGGNFEGSQSLVGDIGNVNMWDFVLSPDEINTIYLGGPFSPNVLNWRALKYEVQ
GEVFTKPQLWP
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>d1jhna1 b.29.1.12 (A:61-262) Calnexin {Dog (Canis familiaris)}
YKAPVPSGEVYFADSFDRGTLSGWILSKAKKDDTDDEIAKYDGKWEVDEMKETKLPGDKGLVLMS
RAKHHAISAKLNKPFLFDTKPLIVQYEVNFQNGIECGGAYVKLLSKTPELNLDQFHDKTPYTIMF
GPDKCGEDYKLHFIFRHKNPKTGVYEEKHAKRPDADLKTYFTDKKTHLYTLILNPDNSFEILVDQ
SIVNSGN
>d1jhna2 b.29.1.12 (A:412-458) Calnexin {Dog (Canis familiaris)}
LEPFKMTPFSAIGLELWSMTSDIFFDNFIVCGDRRVVDDWANDGWGL
>d1a8d_1 b.29.1.6 (1-247) Tetanus neurotoxin {Clostridium tetani}
MKNLDCWVDNEEDIDVILKKSTILNLDINNDIISDISGFNSSVITYPDAQLVPGINGKAIHLVNN
ESSEVIVHKAMDIEYNDMFNNFTVSFWLRVPKVSASHLEQYGTNEYSIISSMKKHSLSIGSGWSV
SLKGNNLIWTLKDSAGEVRQITFRDLPDKFNAYLANKWVFITITNDRLSSANLYINGVLMGSAEI
TGLGAIREDNNITLKLDRCNNNNQYVSIDKFRIFCKALNPKEIEKLYTSYLS
>d3btaa1 b.29.1.6 (A:872-1078) Botulinum neurotoxin {Clostridium
botulinum, serotype A}
IINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSM
YENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYS
QMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYI
WIKYFNLFDKEL
>d1epwa1 b.29.1.6 (A:862-1079) Botulinum neurotoxin {Clostridium
botulinum, serotype B}
NIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFS
VSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIR
EDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMK
YFSIFNTELSQSNIEERYKIQSY
>d1ikpa1 b.29.1.7 (A:2-251) Exotoxin A, N-terminal domain
{Pseudomonas aeruginosa}
EEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIADTNGQGVLHYSMVLEGGNDALKLAIDNALSI
TSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSP
IYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVSVVMAQAQPRREKRWSEWASGKVL
CLLDQLDGVYNYLAQQRCNLDDTWEGKIYRVLAGNPAKHDLDIKPTVISHRLHFP
>d1kit_1 b.29.1.8 (25-216) Vibrio cholerae sialidase, N-terminal and
insertion domains {Vibrio cholerae}
ALFDYNATGDTEFDSPAKQGWMQDNTNNGSGVLTNADGMPAWLVQGIGGRAQWTYSLSTNQHAQA
SSFGWRMTTEMKVLSGGMITNYYANGTQRVLPIISLDSSGNLVVEFEGQTGRTVLATGTAATEYH
KFELVFLPGSNPSASFYFDGKLIRDNIQPTASKQNMIVWGNGSSNTDGVAAYRDIKFEIQGD
>d1kit_2 b.29.1.8 (347-543) Vibrio cholerae sialidase, N-terminal and
insertion domains {Vibrio cholerae}
DVTDQVKERSFQIAGWGGSELYRRNTSLNSQQDWQSNAKIRIVDGAANQIQVADGSRKYVVTLSI
DESGGLVANLNGVSAPIILQSEHAKVHSFHDYELQYSALNHTTTLFVDGQQITTWAGEVSQENNI
QFGNADAQIDGRLHVQKIVLTQQGHNLVEFDAFYLAQQTPEVEKDLEKLGWTKIKTGNTMSLYGN
AS
>d2sli_1 b.29.1.9 (81-276) Leech intramolecular trans-sialidase,
N-terminal domain {North american leech (Macrobdella decora)}
IPEGILMEKNNVDIAEGQGYSLDQEAGAKYVKAMTQGTIILSYKSTSENGIQSLFSVGNSTAGNQ
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DRHFHIYITNSGGIGIELRNTDGVFNYTLDRPASVRALYKGERVFNTVALKADAANKQCRLFANG
ELLATLDKDAFKFISDITGVDNVTLGGTKRQGKIAYPFGGTIGDIKVYSNALSDEELIQATGVTT
Y
>d6cel__ b.29.1.10 (-) Cellobiohydrolase I (cellulase, Endoglucanase
I, CBH1) {Trichoderma reesei, Cel7A}
ESACTLQSETHPPLTWQKCSSGGTCTQQTGSVVIDANWRWTHATNSSTNCYDGNTWSSTLCPDNE
TCAKNCCLDGAAYASTYGVTTSGNSLSIDFVTQSAQKNVGARLYLMASDTTYQEFTLLGNEFSFD
VDVSQLPCGLNGALYFVSMDADGGVSKYPTNTAGAKYGTGYCDSQCPRDLKFINGQANVEGWEPS
SNNANTGIGGHGSCCSQMDIWEANSISEALTPHPCTTVGQEICEGDGCGGTYSDNRYGGTCDPDG
CDWNPYRLGNTSFYGPGSSFTLDTTKKLTVVTQFETSGAINRYYVQNGVTFQQPNAELGSYSGNE
LNDDYCTAEEAEFGGSSFSDKGGLTQFKKATSGGMVLVMSLWDDYYANMLWLDSTYPTNETSSTP
GAVRGSCSTSSGVPAQVESQSPNAKVTFSNIKFGPIGSTGNPSG
>d1eg1a_ b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase
I, CBH1) {Trichoderma reesei, Endoglucanase I}
EQPGTSTPEVHPKLTTYKCTKSGGCVAQDTSVVLDWNYRWMHDANYNSCTVNGGVNTTLCPDEAT
CGKNCFIEGVDYAASGVTTSGSSLTMNQYMPSSSGGYSSVSPRLYLLDSDGEYVMLKLNGQELSF
DVDLSALPCGENGSLYLSQMDENGGANQYNTAGANYGSGYCDAQCPVQTWRNGTLNTSHQGFCCN
EMDILEGNSRANALTPHSCTATACDSAGCGFNPYGSGYKSYYGPGDTVDTSKTFTIITQFNTDNG
SPSGNLVSITRKYQQNGVDIPSAQPGGDTISSCPSASAYGGLATMGKALSSGMVLVFSIWNDNSQ
YMNWLDSGNAGPCSSTEGNPSNILANNPNTHVVFSNIRWGDIGSTT
>d3ovwa_ b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase
I, CBH1) {Fusarium oxysporum}
ETPDKAKEQHPKLETYRCTKASGCKKQTNYIVADAGIHGIRQKNGAGCGDWGQKPNATACPDEAS
CAKNCILSGMDSNAYKNAGITTSGNKLRLQQLINNQLVSPRVYLLEENKKKYEMLHLTGTEFSFD
VEMEKLPCGMNGALYLSEMPQDGGKSTSRNSKAGAYYGAGYCDAQCYVTPFINGVGNIKGQGVCC
NELDIWEANSRATHIAPHPCSKPGLYGCTGDECGSSGICDKAGCGWNHNRINVTDFYGRGKQYKV
DSTRKFTVTSQFVANKQGDLIELHRHYIQDNKVIESAVVNISGPPKINFINDKYCAATGANEYMR
LGGTKQMGDAMSRGMVLAMSVWWSEGDFMAWLDQGVAGPCDATEGDPKNIVKVQPNPEVTFSNIR
IGEIGSTSSV
>d1dyma_ b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase
I, CBH1) {Humicola insolens, Cel7b}
EKPGETKEVHPQLTTFRCTKRGGCKPATNFIVLDSLSHPIHRAEGLGPGGCGDWGNPPPKDVCPD
VESCAKNCIMEGIPDYSQYGVTTNGTSLRLQHILPDGRVPSPRVYLLDKTKRRYEMLHLTGFEFT
FDVDATKLPCGMNSALYLSEMHPTGAKSKYNPGGAYYGTGYCDAQCFVTPFINGLGNIEGKGSCC
NAMDIWEANSRASHVAPHTCNKKGLYLCEGEECAFEGVCDKNGCGWNNYRVNVTDYYGRGEEFKV
NTLKPFTVVTQFLANRRGKLEKIHRFYVQDGKVIESFYTNKEGVPYTNMIDDEFCEATGSRKYME
LGATQGMGEALTRGMVLAMSIWWDQGGNMEWLDHGEAGPCAKGEGAPSNIVQVEPFPEVTYTNLR
WGEIGSTY
>d1gpia_ b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase
I, CBH1) {Phanerochaete chrysosporium, Cel7d}
EQAGTNTAENHPQLQSQQCTTSGGCKPLSTKVVLDSNWRWVHSTSGYTNCYTGNEWDTSLCPDGK
TCAANCALDGADYSGTYGITSTGTALTLKFVTGSNVGSRVYLMADDTHYQLLKLLNQEFTFDVDM
SNLPCGLNGALYLSAMDADGGMSKYPGNKAGAKYGTGYCDSQCPKDIKFINGEANVGNWTETGSN
TGTGSYGTCCSEMDIWEANNDAAAFTPHPCTTTGQTRCSGDDCARNTGLCDGDGCDFNSFRMGDK
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TFLGKGMTVDTSKPFTVVTQFLTNDNTSTGTLSEIRRIYIQNGKVIQNSVANIPGVDPVNSITDN
FCAQQKTAFGDTNWFAQKGGLKQMGEALGNGMVLALSIWDDHAANMLWLDSDYPTDKDPSAPGVA
RGTCATTSGVPSDVESQVPNSQVVFSNIKFGDIGSTFSGTS
>d1xnb__ b.29.1.11 (-) Xylanase II {Bacillus circulans}
ASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGY
LTLYGWTRSPLIEYYVVDSWGTYRPTGTYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWS
VRQSKRPTGSNATITFTNHVNAWKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW
>d1qh7a_ b.29.1.11 (A:) Xylanase II {Bacillus agaradhaerens}
EIVTDNSIGNHDGYDYEFWKDSGGSGTMILNHGGTFSAQWNNVNNILFRKGKKFNETQTHQQVGN
MSINYGANFQPNGNAYLCVYGWTVDPLVEYYIVDSWGNWRPPGATPKGTITVDGGTYDIYETLRV
NQPSIKGIATFKQYWSVRRSKRTSGTISVSNHFRAWENLGMNMGKMYEVALTVEGYQSSGSANVY
SNTLRINGNPLS
>d1hixa_ b.29.1.11 (A:) Xylanase II {Streptomyces sp. s38, xyl1}
ITTNQTGTNNGYYYSFWTDGGGSVSMNLASGGSYGTSWTNCGNFVAGKGWANGARRTVNYSGSFN
PSGNAYLTLYGWTANPLVEYYIVDNWGTYRPTGTYKGTVTSDGGTYDVYQTTRVNAPSVEGTKTF
NQYWSVRQSKRTGGSITAGNHFDAWARYGMPLGSFNYYMIMATEGYQSSGSSSIS
>d1xnd__ b.29.1.11 (-) Xylanase II {Trichoderma harzianum}
QTIGPGTGYSNGYYYSYWNDGHAGVTYTNGGGGSFTVNWSNSGNFVAGKGWQPGTKNKVINFSGS
YNPNGNSYLSIYGWSRNPLIEYYIVENFGTYNPSTGATKLGEVTSDGSVYDIYRTQRVNQPSIIG
TATFYQYWSVRRNHRSSGSVNTANHFNAWASHGLTLGTMDYQIVAVEGYFSSGSASITVS
>d1xyn__ b.29.1.11 (-) Xylanase II {Trichoderma reesei, xynI}
ASINYDQNYQTGGQVSYSPSNTGFSVNWNTQDDFVVGVGWTTGSSAPINFGGSFSVNSGTGLLSV
YGWSTNPLVEYYIMEDNHNYPAQGTVKGTVTSDGATYTIWENTRVNEPSIQGTATFNQYISVRNS
PRTSGTVTVQNHFNAWASLGLHLGQMNYQVVAVEGWGGSGSASQSVSN
>d1enxa_ b.29.1.11 (A:) Xylanase II {Trichoderma reesei, xynII}
ETIQPGTGYNNGYFYSYWNDGHGGVTYTNGPGGQFSVNWSNSGNFVGGKGWQPGTKNKVINFSGS
YNPNGNSYLSVYGWSRNPLIEYYIVENFGTYNPSTGATKLGEVTSDGSVYDIYRTQRVNQPSIIG
TATFYQYWSVRRNHRSSGSVNTANHFNAWAQQGLTLGTMDYQIVAVEGYFSSGSASITVS
>d1yna__ b.29.1.11 (-) Xylanase II {Thermomyces lanuginosus}
ETTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGV
YQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDG
TQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITVADVG
>d1bk1__ b.29.1.11 (-) Xylanase II {Aspergillus kawachii}
AGINYVQNYNGNLGDFTYDESAGTFSMYWEDGVSSDFVVGLGWTTGSSNAITYSAEYSASGSSSY
LAVYGWVNYPQAEYYIVEDYGDYNPCSSATSLGTVYSDGSTYQVCTDTRTNEPSITGTSTFTQYF
SVRESTRTSGTVTVANHFNFWAQHGFGNSDFNYQVMAVEAWSGAGSASVTIS
>d1pvxa_ b.29.1.11 (A:) Xylanase II {Paecilomyces variotii bainier}
GTTPNSEGWHDGYYYSWWSDGGGDSTYTNNSGGTYEITWGNGGNLVGGKGWNPGLNARAIHFTGV
YQPNGTSYLSVYGWTRNPLVEYYIVENFGSSNPSSGSTDLGTVSCDGSTYTLGQSTRYNAPSIDG
TQTFNQYWSVRQDKRSSGTVQTGCHFDAWASAGLNVTGDHYYQIVATEGYFSSGYARITVADVG
>d1f5ja_ b.29.1.11 (A:) Xylanase II {Dictyoglomus thermophilum}
ALTSNASGTFDGYYYELWKDTGNTTMTVYTQGRFSCQWSNINNALFRTGKKYNQNWQSLGTIRIT
YSATYNPNGNSYLCIYGWSTNPLVEFYIVESWGNWRPPGATSLGQVTIDGGTYDIYRTTRVNQPS
IVGTATFDQYWSVRTSKRTSGTVTVTDHFRAWANRGLNLGTIDQITLCVEGYQSSGSANITQNTF
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SQSS
>d2nlra_ b.29.1.11 (A:) Endo-1,4-beta-glucanase (cellulase) catalytic domain {Streptomyces lividans, CelB2}
DTTICEPFGTTTIQGRYVVQNNRWGSTAPQCVTATDTGFRVTQADGSAPTNGAPKSYPSVFNGCH
YTNCSPGTDLPVRLDTVSAAPSSISYGFVDGAVYNASYDIWLDPTARTDGVNQTEIMIWFNRVGP
IQPIGSPVGTASVGGRTWEVWSGGNGSNDVLSFVAPSAISGWSFDVMDFVRATVARGLAENDWYL
TSVQAGFEPWQNGAGLAVNSFSSTVET
>d1h8va_ b.29.1.11 (A:) Endo-1,4-beta-glucanase (cellulase) catalytic domain {Trichoderma reesei, Cel12A}
ETSCDQWATFTGNGYTVSNNLWGASAGSGFGCVTAVSLSGGASWHADWQWSGGQNNVKSYQNSQI
AIPQKRTVNSISSMPTTASWSYSGSNIRANVAYDLFTAANPNHVTYSGDYELMIWLGKYGDIGPI
GSSQGTVNVGGQSWTLYYGYNGAMQVYSFVAQTNTTNYSGDVKNFFNYLRDNKGYNAAGQYVLSY
QFGTEPFTGSGTLNVASWTASIN
>d1jz8a4 b.30.1.1 (A:731-1023) beta-Galactosidase, domain 5 {Escherichia coli}
PAASHAIPHLTTSEMDFCIELGNKRWQFNRQSGFLSQMWIGDKKQLLTPLRDQFTRAPLDNDIGV
SEATRIDPNAWVERWKAAGHYQAEAALLQCTADTLADAVLITTAHAWQHQGKTLFISRKTYRIDG
SGQMAITVDVEVASDTPHPARIGLNCQLAQVAERVNWLGLGPQENYPDRLTAACFDRWDLPLSDM
YTPYVFPSENGLRCGTRELNYGPHQWRGDFQFNISRYSQQQLMETSHRHLLHAEEGTWLNIDGFH
MGIGGDDSWSPSVSAEFQLSAGRYHYQLVWCQK
>d1oaca1 b.30.2.1 (A:301-724) Copper amine oxidase, domain 3 (catalytic) {Escherichia coli}
PAVKPMQIIEPEGKNYTITGDMIHWRNWDFHLSMNSRVGPMISTVTYNDNGTKRKVMYEGSLGGM
IVPYGDPDIGWYFKAYLDSGDYGMGTLTSPIARGKDAPSNAVLLNETIADYTGVPMEIPRAIAVF
ERYAGPEYKHQEMGQPNVSTERRELVVRWISTVGNADYIFDWIFHENGTIGIDAGATGIEAVKGV
KAKTMHDETAKDDTRYGTLIDHNIVGTTHQHIYNFRLDLDVDGENNSLVAMDPVVKPNTAGGPRT
STMQVNQYNIGNEQDAAQKFDPGTIRLLSNPNKENRMGNPVSYQIIPYAGGTHPVAKGAQFAPDE
WIYHRLSFMDKQLWVTRYHPGERFPEGKYPNRSTHDTGLGQYSKDNESLDNTDAVVWMTTGTTHV
ARAEEWPIMPTEWVHTLLKPWNFFDETPTLGALK
>d1ksia1 b.30.2.1 (A:207-647) Copper amine oxidase, domain 3 (catalytic) {Pea seedling (Pisum sativum)}
VSKQSPPFGPKQHSLTSHQPQGPGFQINGHSVSWANWKFHIGFDVRAGIVISLASIYDLEKHKSR
RVLYKGYISELFVPYQDPTEEFYFKTFFDSGEFGFGLSTVSLIPNRDCPPHAQFIDTYVHSANGT
PILLKNAICVFEQYGNIMWRHTENGIPNESIEESRTEVNLIVRTIVTVGNADNVIDWEFKASGSI
KPSIALSGILEIKGTNIKHKDEIKEDLHGKLVSANSIGIYHDHFYIYYLDFDIDGTHNSFEKTSL
KTVRIKDGSSKRKSYWTTETQTAKTESDAKITIGLAPAELVVVNPNIKTAVGNEVGYRLIPAIPA
HPLLTEDDYPQIRGAFTNYNVWVTAYNRTEKWAGGLYVDHSRGDDTLAVWTKQNREIVNKDIVMW
HVVGIHHVPAQEDFPIMPLLSTSFELRPTNFFERNPVLKTLSPRDVAWPGC
>d1av4_1 b.30.2.1 (212-628) Copper amine oxidase, domain 3 (catalytic) {Arthrobacter globiformis}
PLRTTQKPISITQPEGPSFTVTGGNHIEWEKWSLDVGFDVREGVVLHNIAFRDGDRLRPIINRAS
IAEMVVPYGDPSPIRSWQNYFDTGEYLVGQYANSLELGCDCLGDITYLSPVISDAFGNPREIRNG
ICMHEEDWGILAKHSDLWSGINYTRRNRRMVISFFTTIGNADYGFYWYLYLDGTIEFEAKATGVV
FTSAFPEGGSDNISQLAPGLGAPFHQHIFSARLDMAIDGFTNRVEEEDVVRQTMGPGNERGNAFS
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RKRTVLTRESEAVREADARTGRTWIISNPESKNRLNEPVGYKLHAHNQPTLLADPGSSIARRAAF
ATKDLWVTRYADDERYPTGDFVNQHSGGAGLPSYIAQDRDIDGQDIVVWHTFGLTHFPRVEDWPI
MPVDTVGFKLRPEGFFDRSPVLDVPAN
>d1a2va1 b.30.2.1 (A:237-672) Copper amine oxidase, domain 3 (catalytic) {Yeast (Hansenula polymorpha)}
PEAPPINVTQPEGVSFKMTGNVMEWSNFKFHIGFNYREGIVLSDVSYNDHGNVRPIFHRISLSEM
IVPYGSPEFPHQRKHALDIGEYGAGYMTNPLSLGCDCKGVIHYLDAHFSDRAGDPITVKNAVCIH
EEDDGLLFKHSDFRDNFATSLVTRATKLVVSQIFTAANAEYCLYWVFMQDGAIRLDIRLTGILNT
YILGDDEEAGPWGTRVYPNVNAHNHQHLFSLRIDPRIDGDGNSAAACDAKSSPYPLGSPENMYGN
AFYSEKTTFKTVKDSLTNYESATGRSWDIFNPNKVNPYSGKPPSYKLVSTQCPPLLAKEGSLVAK
RAPWASHSVNVVPYKDNRLYPSGDHVPQWSGDGVRGMREWIGDGSENIDNTDILFFHTFGITHFP
APEDFPLMPAEPITLMLRPRHFFTENPGLDIQPSYAMTTSEAKRAV
>d1cb8a3 b.30.3.1 (A:336-599) Chondroitinase AC {Pedobacter heparinus (Flavobacterium heparinum)}
IEPYHHQFWNGDYVQHLRPAYSFNVRMVSKRTRRSESGNKENLLGRYLSDGATNIQLRGPEYYNI
MPVWEWDKIPGITSRDYLTDRPLTKLWGEQGSNDFAGGVSDGVYGASAYALDYDSLQAKKAWFFF
DKEIVCLGAGINSNAPENITTTLNQSWLNGPVISTAGKTGRGKITTFKAQGQFWLLHDAIGYYFP
EGANLSLSTQSQKGNWFHINNSHSKDEVSGDVFKLWINHGARPENAQYAYIVLPGINKPEEIKKY
NGTA
>d1egua3 b.30.3.1 (A:541-814) Hyaluronate lyase {Streptococcus pneumoniae}
TSYLSAFNKMDKTAMYNAEKGFGFGLSLFSSRTLNYEHMNKENKRGWYTSDGMFYLYNGDLSHYS
DGYWPTVNPYKMPGTTETDAKRADSDTGKVLPSAFVGTSKLDDANATATMDFTNWNQTLTAHKSW
FMLKDKIAFLGSNIQNTSTDTAATTIDQRKLESSNPYKVYVNDKEASLTEQEKDYPETQSVFLES
SDSKKNIGYFFFKKSSISMSKALQKGAWKDINEGQSDKEVENEFLTISQAHKQNGDSYGYMLIPN
VDRATFNQMIKELE
>d1f1sa4 b.30.3.1 (A:620-919) Hyaluronate lyase {Streptococcus agalactiae}
LKSNLSTFNSMDRLAYYNAKKDFGFALSLHSKRTLNYEGMNDENTRGWYTGDGMFYIYNSDQSHY
SNHFWPTVNPYKMAGTTEKDAKREDTTKEFMSKHSKDAKEKTGQVTGTSDFVGSVKLNDHFALAA
MDFTNWDRTLTAQKGWVILNDKIVFLGSNIKNTNGIGNVSTTIDQRKDDSKTPYTTYVNGKTIDL
KQASSQQFTDTKSVFLESKEPGRNIGYIFFKNSTIDIERKEQTGTWNSINRTSKNTSIVSNPFIT
ISQKHDNKGDSYGYMMVPNIDRTSFDKLANSKEVELLENS
>d1h54a2 b.30.4.1 (A:1-268) Lactobacillus maltose phosphorylase, N-terminal domain {Lactobacillus brevis}
MKRIFEVQPWNVITHTFDPKDKRLQESMTSLGNGYMGMRGDFEEGYSGDSLQGIYLGGVWYPDKT
RVGWWKNGYPKYFGKVVNAVNFIKLPIEINGEPVDLAKDKISDFTLDLDMHQGVLNRSFVVERGA
VRVALNFQRFLSVAQPELSVQKVTVKNLSDAEVDVTLKPSIDADVMNEEANYDERFWDVLATDQQ
ADRGSIVAKTTPNPFGTPRFTSGMEMRLVTDLKNVAITQPNEKEVTTAYTGKLAPQASAELEKRV
IVVTSRDY
>d1hs6a2 b.98.1.1 (A:1-208) Leukotriene A4 hydrolase N-terminal domain {Human (Homo sapiens)}
PEIVDTCSLASPASVCRTKHLHLRCSVDFTRRTLTGTAALTVQSQEDNLRSLVLDTKDLTIEKVV
INGQEVKYALGERQSYKGSPMEISLPIALSKNQEIVIEISFETSPKSSALQWLTPEQTSGKEHPY

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LFSQCQAIHCRAILPCQDTPSVKLTYTAEVSVPKELVALMSAIRDGETPDPEDPSRKIYKFIQKV
PIPCYLIALVVGA
>d1es6a_ b.31.1.1 (A:) EV matrix protein {Ebola virus}
GDTPSNPLRPIADDTIDHASHTPGSVSSAFILEAMVNVISGPKVLMKQIPIWLPLGVADQKTYSF
DSTTAAIMLASYTITHFGKATNPLVRVNRLGPGIPDHPLRLLRIGNQAFLQEFVLPPVQLPQYFT
FDLTALKLITQPLPAATWTDDTPTGSNGALRPGISFHPKLRPILLPNKSGKKGNSADLTSPEKIQ
AIMTSLQDFKIVPIDPTKNIMGIEVPETLVLKLTGKKVTSKNGQPIIPVLLPKYIGLDPVAPGDL
TMVITQDCDTCHSPASLP
>d1qexa_ b.32.1.1 (A:) gp9 {Bacteriophage T4}
MFIQEPKKLIDTGEIGNASTGDILFDGGNKINSDFNAIYNAFGDQRKMAVANGTGADGQIIHATG
YYQKHSITEYATPVKVGTRHDIDTSTVGVKVIIERGELGDCVEFINSNGSISVTNPLTIQAIDSI
KGVSGNLVVTSPYSKVTLRCISSDNSTSVWNYSIESMFGQKESPAEGTWNISTSGSVDIPLFHRT
EYNMAKLLVTCQSVDGRKIKTAEINILVDTVNSEVISSEYAVMRVGNETEEDEIANIAFSIKENY
VTATISSSTVGMRAAVKVIATQKIGVAQ
>d1rie__ b.33.1.1 (-) ISP subunit of the mitochondrial cytochrome
bc1-complex, watersoluble domain {Cow (Bos taurus)}
AMSKIEIKLSDIPEGKNMAFKWRGKPLFVRHRTKKEIDQEAAVEVSQLRDPQHDLERVKKPEWVI
LIGVCTHLGCVPIANAGDFGGYYCPCHGSHYDASGRIRKGPAPLNLEVPSYEFTSDDMVIVG
>d1ezve1 b.33.1.1 (E:87-215) ISP subunit of the mitochondrial
cytochrome bc1-complex, watersoluble domain {Baker's yeast
(Saccharomyces cerevisiae)}
DVLAMAKVEVNLAAIPLGKNVVVKWQGKPVFIRHRTPHEIQEANSVDMSALKDPQTDADRVKDPQ
WLIMLGICTHLGCVPIGEAGDFGGWFCPCHGSHYDISGRIRKGPAPLNLEIPAYEFDGDKVIVG
>d1rfs__ b.33.1.1 (-) ISP subunit from chloroplast cytochrome bf
complex {Spinach (Spinacia oleracea)}
TIAKDALGNDVIAAEWLKTHAPGDRTLTQGLKGDPTYLVVESDKTLATFGINAVCTHLGCVVPFN
AAENKFICPCHGSQYNNQGRVVRGPAPLSLALAHCDVDDGKVVFVPWTETDFRTGEAPWWSA
>d1g8kb_ b.33.1.1 (B:) Arsenite oxidase Rieske subunit {Alcaligenes
faecalis}
RTTLAYPATAVSVAKNLAANEPVSFTYPDTSSPCVAVKLGAPVPGGVGPDDDIVAYSVLCTHMGC
PTSYDSSSKTFSCPCHFTEFDAEKAGQMICGEATADLPRVLLRYDAASDALTAVGVDGLIYGRQA
NVI
>d1fqta_ b.33.1.1 (A:) Rieske-type ferredoxin associated with
biphenyl dioxygenase {Burkholderia cepacia}
MKFTRVCDRRDVPEGEALKVESGGTSVAIFNVDGELFATQDRCTHGDWSLSDGGYLEGDVVECSL
HMGKFCVRTGKVKSPPPCEALKIFPIRIEDNDVLVDFEAGYLAP
>d1eg9a1 b.33.1.2 (A:1-154) Naphthalene 1,2-dioxygenase alpha subunit,
N-domain {Pseudomonas putida}
MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVI
VSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNK
KCLGLKEVARVESFHGFIYGCFDQ
>d1bia_2 b.34.1.1 (271-317) Biotin repressor/biotin holoenzyme
synthetase, C-terminal domain {Escherichia coli}
FINRPVKLIIGDKEIFGISRGIDKQGALLLEQDGIIKPWMGGEISLR
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>d1byma_ b.34.1.2 (A:) Diphtheria toxin repressor (DtxR)
{Corynebacterium diphtheriae}
NPIPGLDELGVGNSDAAAPGTRVIDAATSMPRKVRIVQINEIFQVETDQFTQLLDADIRVGSEVE
IVDRDGHITLSHNGKDVELLDDLAHTIRIEEL
>d1c0wa3 b.34.1.2 (A:165-223) Diphtheria toxin repressor (DtxR)
{Corynebacterium diphtheriae}
IVQINEIFQVETDQFTQLLDADIRVGSEVEIVDRDGHITLSHNGKDVELLDDLAHTIRI
>d1g3sa3 b.34.1.2 (A:148-225) Diphtheria toxin repressor (DtxR)
{Corynebacterium diphtheriae}
PGTRVIDAATSMPRKVRIVQINEIFQVETDQFTQLLDADIRVGSEVEIVDRDGHITLSHNGKDVE
LLDDLAHTIRIEE
>d1fx7a3 b.34.1.2 (A:145-230) Iron-dependent regulator IdeR
{Mycobacterium tuberculosis}
GADDANLVRLTELPAGSPVAVVVRQLTEHVQGDIDLITRLKDAGVVPNARVTVETTPGGGVTIVI
PGHENVTLPHEMAHAVKVEKV
>d1igqa_ b.34.1.3 (A:) Transcriptional repressor protein KorB
{Escherichia coli}
KKAIVQVEHDERPARLILNRRPPAEGYAWLKYEDDGQEFEANLADVKLVALIEG
>d1igub_ b.34.1.3 (B:) Transcriptional repressor protein KorB
{Escherichia coli}
PDPDKLKKAIVQVEHDERPARLILNRRPPAEGYAWLKYEDDGQEFEANLADVKLVALIEG
>d1ckaa_ b.34.2.1 (A:) C-Crk, N-terminal SH3 domain {Mouse (Mus
musculus)}
AEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEGKRGMIPVPYVEKY
>d1efna_ b.34.2.1 (A:) Fyn proto-oncogene tyrosine kinase, SH3 domain
{Human (Homo sapiens)}
ALFVALYDYEAITEDDLSFHKGEKFQILNSSEGDWWEARSLTTGETGYIPSNYVAPV
>d1shfa_ b.34.2.1 (A:) Fyn proto-oncogene tyrosine kinase, SH3 domain
{Human (Homo sapiens)}
VTLFVALYDYEARTEDDLSFHKGEKFQILNSSEGDWWEARSLTTGETGYIPSNYVAPVD
>d1neb__ b.34.2.1 (-) SH3 domain from nebulin {Human (Homo sapiens)}
TAGKIFRAMYDYMAADADEVSFKDGDAIINVQAIDEGWMYGTVQRTGRTGMLPANYVEAI
>d1bbza_ b.34.2.1 (A:) Abl tyrosine kinase, SH3 domain {Human (Homo
sapiens)}
NLFVALYDFVASGDNTLSITKGEKLRVLGYNHNGEWCEAQTKNGQGWVPSNYITPVNS
>d2abl_1 b.34.2.1 (75-139) Abl tyrosine kinase, SH3 domain {Human (Homo
sapiens)}
MGPSENDPNLFVALYDFVASGDNTLSITKGEKLRVLGYNHNGEWCEAQTKNGQGWVPSNYITPVN
>d1pht__ b.34.2.1 (-) Phosphatidylinositol 3-kinase (p85-alpha
subunit, pi3k), SH3 domain {Human (Homo sapiens)}
AEGYQYRALYDYKKEREEDIDLHLGDILTVNKGSLVALGFSDGQEARPEEIGWLNGYNETTGERG
DFPGTYVEYIGRKKISPP
>d1g2ba_ b.34.2.1 (A:) alpha-Spectrin, SH3 domain {Chicken (Gallus
gallus)}
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MDRQGFVPAAYVKKLDSGTGKELVLALYDYQEKSPREVTMKKGDILTLLNSTNKDWWKVEVN
>d1pwt__ b.34.2.1 (-) alpha-Spectrin, SH3 domain {Chicken (Gallus gallus)}
MGTGKELVLALYDYQEKSPREVTMKKGDILTLLNSTNKDWWKVEVNDRQGFVPAAYVKKLD
>d1qkwa_ b.34.2.1 (A:) alpha-Spectrin, SH3 domain {Chicken (Gallus gallus)}
KELVLALYDYQEKSPREVTMKKGDILTLLNSTNKDWWKVEVGDRQGFVPAAYVKKLD
>d1tuc__ b.34.2.1 (-) alpha-Spectrin, SH3 domain {Chicken (Gallus gallus)}
MGPREVTMKKGDILTLLNSTNKDWWKVEVNDRQGFVPAAYVKKLDSGTGKELVLALYDYQE
>d1awj__ b.34.2.1 (-) IL-2 inducible T-cell (Itc) kinase {Mouse (Mus musculus)}
KKPLPPTPEDNRRSFQEPEETLVIALYDYQTNDPQELALRCDEEYYLLDSSEIHWWRVQDKNGHEGYAPSSYLVEKS
>d1bu1a_ b.34.2.1 (A:) Hemapoetic cell kinase Hck {Human (Homo sapiens)}
IIVVALYDYEAIHHEDLSFQKGDQMVVLEESGEWWKARSLATRKEGYIPSNYVARVD
>d1qcfa1 b.34.2.1 (A:80-145) Hemapoetic cell kinase Hck {Human (Homo sapiens)}
SGIRIIVVALYDYEAIHHEDLSFQKGDQMVVLEESGEWWKARSLATRKEGYIPSNYVARVDSLET
>d1cska_ b.34.2.1 (A:) c-src tyrosine kinase {Human (Homo sapiens)}
GTECIAKYNFHGTAEQDLPFCKGDVLTIVAVTKDPNWYKAKNKVGREGIIPANYVQKR
>d1fmk_1 b.34.2.1 (82-145) c-src tyrosine kinase {Human (Homo sapiens)}
MVTTFVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLSTGQTGYIPSNYVAPSDSIQA
>d1nloc_ b.34.2.1 (C:) c-src tyrosine kinase {Chicken (Gallus gallus)}
TFVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLTTGQTGYIPSNYVAPS
>d1awx__ b.34.2.1 (-) Bruton's tyrosine kinase {Human (Homo sapiens)}
GSMSTSELKKVVALYDYMPMNANDLQLRKGDEYFILEESNLPWWRARDKNGQEGYIPSNYVTEAEDS
>d1qlya_ b.34.2.1 (A:) Bruton's tyrosine kinase {Human (Homo sapiens)}
LKKVVALYDYMPMNANDLQLRKGDEYFILEESNLPWWRARDKNGQEGYIPSNYVTEAE
>d1gl5a_ b.34.2.1 (A:) tyrosine kinase tec {Mouse (Mus musculus)}
GSEIVVAMYDFQATEAHDLRLERGQEYIILEKNDLHWWRARDKYGSEGYIPSNYVTGKKSNNLDQYD
>d1gcqa_ b.34.2.1 (A:) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal domains {Human (Homo sapiens)}
STYVQALFDFDPQEDGELGFRRGDFIHVMDNSDPNWWKGACHGQTGMFPRNYVTPV
>d1gria1 b.34.2.1 (A:1-56) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal domains {Human (Homo sapiens)}
MEAIAKYDFKATADDELSFKRGDILKVLNEECDQNWYKAELNGKDGFIPKNYIEMK
>d1gria2 b.34.2.1 (A:157-217) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal domains {Human (Homo sapiens)}
QPTYVQALFDFDPQEDGELGFRRGDFIHVMDNSDPNWWKGACHGQTGMFPRNYVTPVNRNV
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>d1gbra_ b.34.2.1 (A:) Growth factor receptor-bound protein 2 (GRB2),
N- and C-terminal domains {Mouse (Mus musculus)}
GSRRASVGSMEAIAKYDFKATADDELSFKRGDILKVLNEECDQNWYKAELNGKDGFIPKNYIEMK
PHPEFIVTD
>d1sema_ b.34.2.1 (A:) Growth factor receptor-bound protein 2 (GRB2),
N- and C-terminal domains {Caenorhabditis elegans, SEM-5}
ETKFVQALFDFNPQESGELAFKRGDVITLINKDDPNWWEGQLNNRRGIFPSNYVCPYN
>d2hsp__ b.34.2.1 (-) Phospholipase C, SH3 domain {Human (Homo
sapiens)}
GSPTFKCAVKALFDYKAQREDELTFIKSAIIQNVEKQEGGWWRGDYGGKKQLWFPSNYVEEMVNP
EGIHRD
>d1h92a_ b.34.2.1 (A:) p56-lck tyrosine kinase, SH3 domain {Human (Homo
sapiens)}
GSPLQDNLVIALHSYEPSHDGDLGFEKGEQLRILEQSGEWWKAQSLTTGQEGFIPFNFVAKAN
>d1lcka1 b.34.2.1 (A:63-116) p56-lck tyrosine kinase, SH3 domain
{Human (Homo sapiens)}
DNLVIALHSYEPSHDGDLGFEKGEQLRILEQSGEWWKAQSLTTGQEGFIPFNFV
>d1ycsb2 b.34.2.1 (B:457-519) 53BP2 {Human (Homo sapiens)}
IMNKGVIYALWDYEPQNDDELPMKEGDCMTIIHREDEDEIEWWWARLNDKEGYVPRNLLGLYP
>d1bb9__ b.34.2.1 (-) Amphiphysin 2 {Rat (Rattus norvegicus)}
TTGRLDLPPGFMFKVQAQHDYTATDTDELQLKAGDVVLVIPFQNPEEQDEGWLMGVKESDWNQHK
ELEKCRGVFPENFTERVQ
>d1i07a_ b.34.2.1 (A:) EPS8 SH3 domain {Mouse (Mus musculus)}
KKYAKSKYDFVARNSSELSVMKDDVLEILDDRRQWWKVRNASGDSGFVPNNILDIMRTP
>d1gcqc_ b.34.2.1 (C:) Vav N-terminal SH3 domain {Mouse (Mus musculus)}
GSHMPKMEVFQEYYGIPPPPGAFGPFLRLNPGDIVELTKAEAEHNWWEGRNTATNEVGWFPCNRV
HPYV
>d1k1za_ b.34.2.1 (A:) Vav N-terminal SH3 domain {Mouse (Mus musculus)}
RAQDKKRNELGLPKMEVFQEYYGIPPPPGAFGGFLRLNPGDIVELTKAEAEHNWWEGRNTATNEV
GWFPCNRVHPYVH
>d1i1ja_ b.34.2.1 (A:) Melanoma inhibitory activity protein {Human
(Homo sapiens)}
GPMPKLADRKLCADQECSHPISMAVALQDYMAPDCRFLTIHRGQVVYVFSKLKGRGRLFWGGSVQ
GDYYGDLAARLGYFPSSIVREDQTLKPGKVDVKTDKWDFYC
>d1kjwa1 b.34.2.1 (A:430-525) Psd-95 {Rat (Rattus norvegicus)}
GFYIRALFDYDKTKDCGFLSQALSFRFGDVLHVIDAGDEEWWQARRVHSDSETDDIGFIPSKRRV
ERREWSRLKAKDWGSSSGSQGREDSVLSYET
>d1br2a1 b.34.3.1 (A:34-79) Myosin S1 fragment, N-terminal domain
{Chicken (Gallus gallus), pectoral muscle}
LVWVPSEKHGFEAASIKEEKGDEVTVELQENGKKVTLSKDDIQKMN
>d2mysa1 b.34.3.1 (A:34-79) Myosin S1 fragment, N-terminal domain
{Chicken (Gallus gallus), pectoral muscle}
AKSSVFVVHPKQSFVKGTIQSKEGGKVTVKTEGGETLTVKEDQVFS
>d1b7ta1 b.34.3.1 (A:29-76) Myosin S1 fragment, N-terminal domain {Bay
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scallop (Aequipecten irradians)}
DGKKNCWVPDEKEGFASAEIQSSKGDEITVKIVADSSTRTVKKDDIQS
>d1jwya1 b.34.3.1 (A:36-79) Myosin S1 fragment, N-terminal domain
{Slime mold (Dictyostelium discoideum)}
FKLTVSDKRYIWYNPDPKERDSYECGEIVSETSDSFTFKTVDGQ
>d1lvk_1 b.34.3.1 (34-79) Myosin S1 fragment, N-terminal domain {Slime
mold (Dictyostelium discoideum)}
YIWYNPDPKERDSYECGEIVSETSDSFTFKTSDGQDRQVKKDDANQ
>d1g5va_ b.34.9.1 (A:) Survival motor neuron protein 1, smn {Human
(Homo sapiens)}
QQWKVGDKCSAIWSEDGCIYPATIASIDFKRETCVVVYTGYGNREEQNLSDLLSPI
>d1khca_ b.34.9.2 (A:) DNA methyltransferase DNMT3B {Mouse (Mus
musculus)}
TEYQDDKEFGIGDLVWGKIKGFSWWPAMVVSWKATSKRQAMPGMRWVQWFGDGKFSEISADKLVA
LGLFSQHFNLATFNKLVSYRKAMYHTLEKARVRAGKTFSSSPGESLEDQLKPMLEWAHGGFKPTG
IEGLKPN
>d1vie__ b.34.4.1 (-) R67 dihydrofolate reductase {Escherichia coli,
plasmid PLZ1}
PSNATFGMGDRVRKKSGAAWQGQIVGWYCTNLTPEGYAVESEAHPGSVQIYPVAALERIN
>d1psf__ b.34.4.2 (-) Photosystem I accessory protein E (PsaE)
{Cyanobacterium (Synechococcus sp.), pcc 7002}
AIERGSKVKILRKESYWYGDVGTVASIDKSGIIYPVIVRFNKVNYNGFSGSAGGLNTNNFAEHEL
EVVG
>d1qp2a_ b.34.4.2 (A:) Photosystem I accessory protein E (PsaE)
{Cyanobacterium (Nostoc sp.), strain pcc8009}
MVQRGSKVRILRPESYWFQDVGTVASVDQSGIKYPVIVRFEKVNYSGINTNNFAEDELVEVEAPK
AKPKK
>d1jb0e_ b.34.4.2 (E:) Photosystem I accessory protein E (PsaE)
{Synechococcus elongatus}
VQRGSKVKILRPESYWYNEVGTVASVDQTPGVKYPVIVRFDKVNYTGYSGSASGVNTNNFALHEV
QEVA
>d1dj7b_ b.34.4.3 (B:) Ferredoxin thioredoxin reductase (FTR), alpha
(variable) chain {Synechocystis sp.}
MNVGDRVRVTSSVVVYHHPEHKKTAFDLQGMEGEVAAVLTEWQGRPISANLPVLVKFEQRFKAHF
RPDEVTLI
>d2ahjb_ b.34.4.4 (B:) Nitrile hydratase beta chain {Rhodococcus
erythropolis}
MDGVHDLAGVQGFGKVPHTVNADIGPTFHAEWEHLPYSLMFAGVAELGAFSVDEVRYVVERMEPR
HYMMTPYYERYVIGVATLMVEKGILTQDELESLAGGPFPLSRPSESEGRPAPVETTTFEVGQRVR
VRDEYVPGHIRMPAYCRGRVGTISHRTTEKWPFPDAIGHGRNDAGEEPTYHVKFAAEELFGSDTD
GGSVVVDLFEGYLEPA
>d1jj2s_ b.34.5.1 (S:) Ribosomal proteins L24 (L24p) {Archaeon
Haloarcula marismortui}
SKQPDKQRKSQRRAPLHERHKQVRATLSADLREEYGQRNVRVNAGDTVEVLRGDFAGEEGEVINV
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DLDKAVIHVEDVTLEKTDGEEVPRPLDTSNVRVTDLDLEDEKREARLESEDDSA
>d1jj2p_ b.34.5.1 (P:) Ribosomal proteins L21e {Archaeon Haloarcula
marismortui}
PSSNGPLEGTRGKLKNKPRDRGTSPPQRAVEEFDDGEKVHLKIDPSVPNGRFHPRFDGQTGTVEG
KQGDAYKVDIVDGGKEKTIIVTAAHLRRQE
>d2eifa1 b.34.5.2 (A:1-73) N-terminal domain of eukaryotic initiation
translation factor 5a {Archaeon Methanococcus jannaschii}
VIIMPGTKQVNVGSLKVGQYVMIDGVPCEIVDISVSKPGKHGGAKARVVGIGIFEKVKKEFVAPT
SSKVEVPI
>d1bkb_1 b.34.5.2 (4-74) N-terminal domain of eukaryotic initiation
translation factor 5a {Archaeon Pyrobaculum aerophilum}
KWVMSTKYVEAGELKEGSYVVIDGEPCRVVEIEKSKTGKHGSAKARIVAVGVFDGGKRTLSLPVD
AQVEVP
>d1rl2a1 b.34.5.3 (A:126-195) C-terminal domain of ribosomal protein
L2 {Bacillus stearothermophilus}
GNALPLENIPVGTLVHNIELKPGRGGQLVRAAGTSAQVLGKEGKYVIVRLASGEVRMILGKCRAT
VGEVG
>d1jj2a1 b.34.5.3 (A:91-237) C-terminal domain of ribosomal protein
L2 {Archaeon Haloarcula marismortui}
GNTLPLAEIPEGVPVCNVESSPGDGGKFARASGVNAQLLTHDRNVAVVKLPSGEMKRLDPQCRAT
IGVVGGGGRTDKPFVKAGNKHHKMKARGTKWPNVRGVAMNAVDHPFGGGGRQHPGKPKSISRNAP
PGRKVGDIASKRTGRGG
>d3vub__ b.34.6.1 (-) CcdB {Escherichia coli}
MQFKVYTYKRESRYRLFVDVQSDIIDTPGRRMVIPLASARLLSDKVSRELYPVVHIGDESWRMMT
TDMASVPVSVIGEEVADLSHRENDIKNAINLMFWGI
>d1hyoa1 b.34.8.1 (A:1-118) Fumarylacetoacetate hydrolase, FAH,
N-terminal domain {Mouse (Mus musculus)}
MSFIPVAEDSDFPIQNLPYGVFSTQSNPKPRIGVAIGDQILDLSVIKHLFTGPALSKHQHVFDET
TLNNFMGLGQAAWKEARASLQNLLSASQARLRDDKELRQRAFTSQASATMHLP
>d1ex4a1 b.34.7.1 (A:223-270) DNA-binding domain of retroviral
integrase {Human immunodeficiency virus type 1}
FRVYYRDSRNSLWKGPAKLLWKGEGAVVIQDNSDIKVVPRRKAKIIRD
>d1ihva_ b.34.7.1 (A:) DNA-binding domain of retroviral integrase
{Human immunodeficiency virus type 1}
MIQNFRVYYRDSRDPVWKGPAKLLWKGEGAVVIQDNSDIKVVPRRKAKIIRD
>d1c0ma1 b.34.7.1 (A:217-269) DNA-binding domain of retroviral
integrase {Rous sarcoma virus (RSV, avian sarcoma virus)}
VLTEGPPVKIRIETGEWEKGWNVLVWGRGYAAVKNRDTDKVIWVPSRKVKPDI
>d1c6vx_ b.34.7.1 (X:) DNA-binding domain of retroviral integrase
{Simian immunodeficiency virus}
KNSKFKNFRVYYREGRDQLWKGPGELLWKGEGAVLLKVGTDIKVVPRRKAKIIKD
>d1aono_ b.35.1.1 (O:) Chaperonin-10 (GroES) {Escherichia coli}
MNIRPLHDRVIVKRKEVETKSAGGIVLTGSAAAKSTRGEVLAVGNGRILENGEVKPLDVKVGDIV
IFNDGYGVKSEKIDNEEVLIMSESDILAIVEA
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>d1jh2a_ b.35.1.1 (A:) Chaperonin-10 (GroES) {Mycobacterium
tuberculosis}
AKVNIKPLEDKILVQANEAETTTASGLVIPDTAKEKPQEGTVVAVGPGRWDEDGEKRIPLDVAEG
DTVIYSKYGGTEIKYNGEEYLILSARDVLAVVSK
>d1lepa_ b.35.1.1 (A:) Chaperonin-10 (GroES) {Mycobacterium leprae}
AKVKIKPLEDKILVQAGEAETMTPSGLVIPENAKEKPQEGTVVAVGPGRWDEDGAKRIPVDVSEG
DIVIYSKYGGTEIKYNGEEYLILSARDVLAVVSK
>d1g31a_ b.35.1.1 (A:) GP31 co-chaperonin {Bacteriophage T4}
QQLPIRAVGEYVILVSEPAQAGDEEVTESGLIIGKRVQGEVPELCVVHSVGPDVPEGFCEVGDLT
SLPVGQIRNVPHPFVALGLKQPKEIKQKFVTCHYKAIPCLYK
>d1heta1 b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Horse
(Equus caballus)}
STAGKVIKCKAAVLWEEKKPFSIEEVEVAPPKAHEVRIKMVATGICRSDDHVVSGTLVTPLPVIA
GHEAAGIVESIGEGVTTVRPGDKVIPLFTPQCGKCRVCKHPEGNFCLKNDLSMPRGTMQDGTSRF
TCRGKPIHHFLGTSTFSQYTVVDEISVAKIDAASPLEKVCLIGCXKDSVPKLVADFMAKKFALDP
LITHVLPFEKINEGFDLLRSGESIRTILTF
>d1d1ta1 b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Human
(Homo sapiens), different isozymes}
GTAGKVIKCKAAVLWEQKQPFSIEEIEVAPPKTKEVRIKILATGICRTDDHVIKGTMVSKFPVIV
GHEATGIVESIGEGVTTVKPGDKVIPLFLPQCRECNACRNPDGNLCIRSDITGRGVLADGTTRFT
CKGKPVHHFLNTSTFTEYTVVDESSVAKIDDAAPPEKVCLIGCXRDDVPKLVTEFLAKKFDLDQL
ITHVLPFKKISEGFELLNSGQSIRTVLTF
>d1hsoa1 b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Human
(Homo sapiens), different isozymes}
STAGKVIKCKAAVLWELKKPFSIEEVEVAPPKAHEVRIKMVAVGICGTDDHVVSGTMVTPLPVIL
GHEAAGIVESVGEGVTTVKPGDKVIPLAIPQCGKCRICKNPESNYCLKNDVSNPQGTLQDGTSRF
TCRRKPIHHFLGISTFSQYTVVDENAVAKIDAASPLEKVCLIGCXKECVPKLVADFMAKKFSLDA
LITHVLPFEKINEGFDLLHSGKSIRTILMF
>d1hsza1 b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Human
(Homo sapiens), different isozymes}
STAGKVIKCKAAVLWEVKKPFSIEDVEVAPPKAYEVRIKMVAVGICRTDDHVVSGNLVTPLPVIL
GHEAAGIVESVGEGVTTVKPGDKVIPLFTPQCGKCRVCKNPESNYCLKNDLGNPRGTLQDGTRRF
TCRGKPIHHFLGTSTFSQYTVVDENAVAKIDAASPLEKVCLIGCXKEGIPKLVADFMAKKFSLDA
LITHVLPFEKINEGFDLLHSGKSIRTVLTF
>d1ht0a1 b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Human
(Homo sapiens), different isozymes}
STAGKVIKCKAAVLWELKKPFSIEEVEVAPPKAHEVRIKMVAAGICRSDEHVVSGNLVTPLPVIL
GHEAAGIVESVGEGVTTVKPGDKVIPLFTPQCGKCRICKNPESNYCLKNDLGNPRGTLQDGTRRF
TCSGKPIHHFVGVSTFSQYTVVDENAVAKIDAASPLEKVCLIGCXKESVPKLVADFMAKKFSLDA
LITNVLPFEKINEGFDLLRSGKSIRTVLTF
>d1teha1 b.35.1.2 (A:3-174,A:325-374) Alcohol dehydrogenase {Human
(Homo sapiens), different isozymes}
ANEVIKCKAAVAWEAGKPLSIEEIEVAPPKAHEVRIKIIATAVCHTDAYTLSGADPEGCFPVILG
HEGAGIVESVGEGVTKLKAGDTVIPLYIPQCGECKFCLNPKTNLCQKIRVTQGKGLMPDGTSRFT
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CKGKTILHYMGTSTFSEYTVVADISVAKIDPLAPLDKVCLLGCXVESVPKLVSEYMSKKIKVDEF
VTHNLSFDEINKAFELMHSGKSIRTVVKI
>d1e3ia1 b.35.1.2 (A:1-174,A:325-376) Alcohol dehydrogenase {Mouse
(Mus musculus), class II}
GTQGKVIKCKAAIAWKTGSPLCIEEIEVSPPKACEVRIQVIATCVCPTDINATDPKKKALFPVVL
GHECAGIVESVGPGVTNFKPGDKVIPFFAPQCKRCKLCLSPLTNLCGKLRNFKYPTIDQELMEDR
TSRFTCKGRSIYHFMGVSSFSQYTVVSEANLARVDDEANLERVCXKSVDSVPNLVSDYKNKKFDL
DLLVTHALPFESINDAIDLMKEGKSIRTILTF
>d1cdoa1 b.35.1.2 (A:1-175,A:325-374) Alcohol dehydrogenase {Cod
(Gadus callarias)}
ATVGKVIKCKAAVAWEANKPLVIEEIEVDVPHANEIRIKIIATGVCHTDLYHLFEGKHKDGFPVV
LGHEGAGIVESVGPGVTEFQPGEKVIPLFISQCGECRFCQSPKTNQCVKGWANESPDVMSPKETR
FTCKGRKVLQFLGTSTFSQYTVVNQIAVAKIDPSAPLDTVCLLGCXKDGVPKMVKAYLDKKVKLD
EFITHRMPLESVNDAIDLMKHGKCIRTVLSL
>d1keva1 b.35.1.2 (A:1-150,A:315-351) Bacterial secondary alcohol
dehydrogenase {Clostridium beijerinckii}
MKGFAMLGINKLGWIEKERPVAGSYDAIVRPLAVSPCTSDIHTVFEGALGDRKNMILGHEAVGEV
VEVGSEVKDFKPGDRVIVPCTTPDWRSLEVQAGFQQHSNGMLAGWKFSNFKDGVFGEYFHVNDAD
MNLAILPKDMPLENAVMITDXDLSKLVTHVYHGFDHIEEALLLMKDKPKDLIKAVVIL
>d1ykfa1 b.35.1.2 (A:1-150,A:315-352) Bacterial secondary alcohol
dehydrogenase {Thermoanaerobacter brockii}
MKGFAMLSIGKVGWIEKEKPAPGPFDAIVRPLAVAPCTSDIHTVFEGAIGERHNMILGHEAVGEV
VEVGSEVKDFKPGDRVVVPAITPDWRTSEVQRGYHQHSGGMLAGWKFSNVKDGVFGEFFHVNDAD
MNLAHLPKEIPLEAAVMIPDXDPSKLVTHVFRGFDNIEKAFMLMKDKPKDLIKPVVILA
>d1e3ja1 b.35.1.2 (A:4-150,A:314-351) Ketose reductase (sorbitol
dehydrogenase) {Silverleaf whitefly (Bemisia argentifolii)}
DNLSAVLYKQNDLRLEQRPIPEPKEDEVLLQMAYVGICGSDVHYYEHGRIADFIVKDPMVIGHEA
SGTVVKVGKNVKHLKKGDRVAVEPGVPCRRCQFCKEGKYNLCPDLTFCATPPDDGNLARYYVHAA
DFCHKLPDNVSLEEGALXNVKQLVTHSFKLEQTVDAFEAARKKADNTIKVMISCRQ
>d1qora1 b.35.1.2 (A:2-135,A:266-327) Quinone oxidoreductase
{Escherichia coli}
ATRIEFHKHGGPEVLQAVEFTPADPAENEIQVENKAIGINFIDTYIRSGLYPPPSLPSGLGTEAA
GIVSKVGSGVKHIKAGDRVVYAQSALGAYSSVHNIIADKAAILPAAISFEQAAASFLKGLTVYYL
LRKTXLQGYITTREELTEASNELFSLIASGVIKVDVAEQQKYPLKDAQRAHEILESRATQGSSLL
IP
>d1auua_ b.35.2.1 (A:) SacY {Bacillus subtilis}
MKIKRILNHNAIVVKDQNEEKILLGAGIAFNKKKNDIVDPSKIEKTFIRKDTPDY
>d1pdr__ b.36.1.1 (-) Discs large protein homolog {Human (Homo
sapiens)}
ITREPRKVVLHRGSTGLGFNIVGGEDGEGIFISFILAGGPADLSGELRKGDRIISVNSVDLRAAS
HEQAAAALKNAGQAVTIVAQYRPEEYSRQHA
>d1kwaa_ b.36.1.1 (A:) Cask/Lin-2 {Human (Homo sapiens)}
RSRLVQFQKNTDEPMGITLKMNELNHCIVARIMHGGMIHRQGTLHVGDEIREINGISVANQTVEQ
LQKMLREMRGSITFKIVPSYREF
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>d1be9a_ b.36.1.1 (A:) Synaptic protein PSD-95 {Rat (Rattus norvegicus)}
FLGEEDIPREPRRIVIHRGSTGLGFNIIGGEDGEGIFISFILAGGPADLSGELRKGDQILSVNGV
DLRNASHEQAAIALKNAGQTVTIIAQYKPEEYSRFEANSRVNSSGRIVTN
>d1qlca_ b.36.1.1 (A:) Synaptic protein PSD-95 {Rat (Rattus norvegicus)}
AEKVMEIKLIKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAAHKDGRLQIGDKILAVNSVG
LEDVMHEDAVAALKNTYDVVYLKVAKPSNA
>d1qava_ b.36.1.1 (A:) Syntrophin {Mouse (Mus musculus)}
GSLQRRRVTVRKADAGGLGISIKGGRENKMPILISKIFKGLAADQTEALFVGDAILSVNGEDLSS
ATHDEAVQALKKTGKEVVLEVKYMK
>d1b8qa_ b.36.1.1 (A:) Neuronal nitric oxide synthase, NNOS {Rat (Rattus norvegicus)}
GSHMIEPNVISVRLFKRKVGGLGFLVKERVSKPPVIISDLIRGGAAEQSGLIQAGDIILAVNDRP
LVDLSYDSALEVLRGIASETHVVLILRGPEGFTTHLETTFTGDGTPKTIRVTQPLGPPTKAV
>d1qaua_ b.36.1.1 (A:) Neuronal nitric oxide synthase, NNOS {Rat (Rattus norvegicus)}
NVISVRLFKRKVGGLGFLVKERVSKPPVIISDLIRGGAAEQSGLIQAGDIILAVNDRPLVDLSYD
SALEVLRGIASETHVVLILRGPEGFTTHLETTFTGDGTPKTIRVTQP
>d3pdza_ b.36.1.1 (A:) Phosphatase hPTP1e {Human (Homo sapiens)}
PKPGDIFEVELAKNDNSLGISVTGGVNTSVRHGGIYVKAVIPQGAAESDGRIHKGDRVLAVNGVS
LEGATHKQAVETLRNTGQVVHLLLEKGQSPT
>d1g9oa_ b.36.1.1 (A:) Na+/H+ exchanger regulatory factor, NHERF {Human (Homo sapiens)}
RMLPRLCCLEKGPNGYGFHLHGEKGKLGQYIRLVEPGSPAEKAGLLAGDRLVEVNGENVEKETHQ
QVVSRIRAALNAVRLLVVDPETDEQL
>d1ihja_ b.36.1.1 (A:) Inad {Fruit fly (Drosophila melanogaster)}
GELIHMVTLDKTGKKSFGICIVRGEVKDSPNTKTTGIFIKGIVPDSPAHLCGRLKVGDRILSLNG
KDVRNSTEQAVIDLIKEADFKIELEIQTF
>d1fc6a3 b.36.1.3 (A:157-248) Photosystem II D1 C-terminal processing protease {Algae (Scenedesmus obliquus)}
AGSVTGVGLEITYDGGSGKDVVVLTPAPGGPAEKAGARAGDVIVTVDGTAVKGMSLYDVSDLLQG
EADSQVEVVLHAPGAPSNTRTLQLTRQ
>d1k32a1 b.36.1.3 (A:763-853) Tricorn protease {Archaeon Thermoplasma acidophilum}
GRIACDFKLDGDHYVVAKAYAGDYSNEGEKSPIFEYGIDPTGYLIEDIDGETVGAGSNIYRVLSE
KAGTSARIRLSGKGGDKRDLMIDILD
>d1i16__ b.36.1.2 (-) Interleukin 16 {Human (Homo sapiens)}
MPDLNSSTDSAASASAASDVSVESTAEATVCTVTLEKMSAGLGFSLEGGKGSLHGDKPLTINRIF
KGAASEQSETVQPGDEILQLGGTAMQGLTRFEAWNIIKALPDGPVTIVIRRKSLQSKETTAAGDS
>d1g3p_1 b.37.1.1 (1-65) N-terminal domains of the minor coat protein g3p {Bacteriophage M13}
AETVESCLAKSHTENSFTNVWKDDKTLDRYANYEGCLWNATGVVVCTGDETQCYGTWVPIGLAIP
>d1g3p_2 b.37.1.1 (91-217) N-terminal domains of the minor coat protein

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g3p {Bacteriophage M13}
EYGDTPIPGYTYINPLDGTYPPGTEQNPANPNPSLEESQPLNTFMFQNNRFRNRQGALTVYTGTV
TQGTDPVKTYYQYTPVSSKAMYDAYWNGKFRDCAFHSGFNEDIFVCEYQGQSSDLPQPPVNA
>d1fgp__ b.37.1.1 (-) N-terminal domains of the minor coat protein
g3p {Bacteriophage fd}
ETVESCLAKPHTENSFTNVWKDDKTLDRYANYEGCLWNATGVVVCTGDETQCYGTWVPIGLAIPE
NAAAH
>d1b34a_ b.38.1.1 (A:) D1 core SNRNP protein {Human (Homo sapiens)}
KLVRFLMKLSHETVTIELKNGTQVHGTITGVDVSMNTHLKAVKMTLKNREPVQLETLSIRGNNIR
YFILPDSLPLDTLLV
>d1b34b_ b.38.1.1 (B:) D2 core SNRNP protein {Human (Homo sapiens)}
TGPLSVLTQSVKNNTQVLINCRNNKKLLGRVKAFDRHCNMVLENVKEMWTEVPKSGKGKKKSKPV
NKDRYISKMFLRGDSVIVVLRNPLIAGK
>d1d3ba_ b.38.1.1 (A:) D3 core SNRNP protein {Human (Homo sapiens)}
GVPIKVLHEAEGHIVTCETNTGEVYRGKLIEAEDNMNCQMSNITVTYRDGRVAQLEQVYIRGCKI
RFLILPD
>d1d3bb_ b.38.1.1 (B:) B core SNRNP protein {Human (Homo sapiens)}
SKMLQHIDYRMRCILQDGRIFIGTFKAFDKHMNLILCDCDEFRKIKPKNSKQAEREEKRVLGLVL
LRGENLVSMTVEGPPP
>d1d3bl_ b.38.1.1 (L:) B core SNRNP protein {Human (Homo sapiens)}
TVGKSSKMLQHIDYRMRCILQDGRIFIGTFKAFDKHMNLILCDCDEFRKIKPKNSKQAEREEKRV
LGLVLLRGENLVSMTVEGPPPKDTG
>d1i81a_ b.38.1.1 (A:) Archaeal homoheptameric Sm protein {Archaeon
Methanobacterium thermoautotrophicum}
RVNVQRPLDALGNSLNSPVIIKLKGDREFRGVLKSFDLHMNLVLNDAEELEDGEVTRRLGTVLIR
GDNIVYISP
>d1jria_ b.38.1.1 (A:) Archaeal homoheptameric Sm protein {Archaeon
Methanobacterium thermoautotrophicum}
QRPLDALGNSLNSPVIIKLKGDREFRGVLKSFDLHMNLVLNDAEELEDGEVTRRLGTVLIRGDNI
VYISRGK
>d1i8fa_ b.38.1.1 (A:) Archaeal homoheptameric Sm protein {Archaeon
Pyrobaculum aerophilum}
ATLGATLQDSIGKQVLVKLRDSHEIRGILRSFDQHVNLLLEDAEEIIDGNVYKRGTMVVRGENVL
FISPVP
>d1i4k1_ b.38.1.1 (1:) Archaeal homoheptameric Sm protein {Archaeon
Archaeoglobus fulgidus}
PPRPLDVLNRSLKSPVIVRLKGGREFRGTLDGYDIHMNLVLLDAEEIQNGEVVRKVGSVVIRGDT
VVFVSPA
>d1h5pa_ b.99.1.1 (A:) Nuclear autoantigen Sp100b {Human (Homo
sapiens)}
MDENINFKQSELPVTCGEVKGTLYKERFKQGTSKKCIQSEDKKWFTPREFEIEGDRGASKNWKLS
IRCGGYTLKVLMENKFLPEPPSTRKKVTIK
>d1whi__ b.39.1.1 (-) Ribosomal protein L14 {Bacillus
stearothermophilus}
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MIQQESRLKVADNSGAREVLVIKVLGGSGRRYANIGDVVVATVKDATPGGVVKKGQVVKAVVVRT
KRGVRRPDGSYIRFDENACVIIRDDKSPRGTRIFGPVARELRDKDFMKIISLAPEVI
>d1jj2j_ b.39.1.1 (J:) Ribosomal protein L14 {Archaeon Haloarcula marismortui}
MEALGADVTQGLEKGSLITCADNTGARELKVISVHGYSGTKNRHPKAGLGDKITVSVTKGTPEMR
RQVLEAVVVRQRKPIRRPDGTRVKFEDNAAVIVDENEDPRGTELKGPIAREVAQRFGSVASAATM
IV
>d1ez6a_ b.40.1.1 (A:) Staphylococcal nuclease {Staphylococcus aureus}
LHKEPATLIKAIDGDTVKLMYKGQPMVFRLLLVDIPETKHPKKGVEKYGPEAAAFTKKMVENAKK
IEVEFDKGQRTDKYGRGLAYIYADGKMVNEALVRQGLAKVAYVYKGNNTHEQLLRKAEAQAKKEK
LNIWS
>d1joqa_ b.40.1.1 (A:) Staphylococcal nuclease {Staphylococcus aureus}
ATSTKKLHKEPATLIKAIDGDTVKLMYKGQPMTFRLLLVDTPETKHPKKGVEKYGPEASAFTKKM
VENAKKIEVEFDKGQRTDKYGRGLAYIYADGKMVNEALVRQGLAKVAYVYKPNNTHEQLLRKSEA
QAKKEKLNIWSEDNADSGQ
>d1sty__ b.40.1.1 (-) Staphylococcal nuclease {Staphylococcus aureus}
KLHKEPATLIKAIDGDTVKLMYKGQPMTFRLLLVDTPETKHPKKGVEKYGPEASAFTKKMVENAK
KIEVEFDKGQRTDKYGRGLAYIYADGKMVNEALVRQGLAKVAYVYKPNNTHEQHLRGKSEAQAKK
EKLNIWS
>d2sob__ b.40.1.1 (-) Staphylococcal nuclease {Staphylococcus aureus}
ATSTKKLHKEPATLIKAIDGDTVKLMYKGQPMTFRLLLVDTPETKHPKKGVEKYGPEASAFTKKM
LENAKKIEVEFDKGQRTDKYGRVLAYIYADGKMVNEAL
>d1djrd_ b.40.2.1 (D:) Heat-labile toxin {Escherichia coli, type IB}
APQTITELCSEYRNTQIYTINDKILSYTESMAGKREMVIITFKSGETFQVEVPGSQHIDSQKKAI
ERMKDTLRITYLTETKIDKLCVWNNKTPNSIAAISMKN
>d1ltrd_ b.40.2.1 (D:) Heat-labile toxin {Escherichia coli, type IB}
APQSITELCSEYHNTQIYTINDKILSYTESMAGKREMVIITFKSGATFQVEVPGSQHIDSQKKAI
ERMKDTLRITYLTETKIDKLCVWNNKTPNSIAAISMEKLYAGA
>d1tiid_ b.40.2.1 (D:) Heat-labile toxin {Escherichia coli, type IIB}
GASQFFKDNCNRTTASLVEGVELTKYISDINNNTDGMYVVSSTGGVWRISRAKDYPDNVMTAEMR
KIAMAAVLSGMRVNMCASPASSPNVIWAIELEA
>d3chbd_ b.40.2.1 (D:) Cholera toxin {Vibrio cholerae}
TPQNITDLCAEYHNTQIHTLNDKIFSYTESLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAI
ERMKDTLRIAYLTEAKVEKLCVWNNKTPRAIAAISMAN
>d1c4qa_ b.40.2.1 (A:) Verotoxin-1/shiga-toxin, B-pentamer {Escherichia coli}
TPDCVTGKVEYTKYNDDDTFTVKVGDKELATNRANLQSLLLSAQITGMTVTIKTNACHNGGGFSE
VIFR
>d2bosa_ b.40.2.1 (A:) Verotoxin-1/shiga-toxin, B-pentamer {Escherichia coli}
ADCAKGKIEFSKYNEDNTFTVKVSGREYWTNRWNLQPLLQSAQLTGMTVTIISNTCSSGSGFAEV
QFN

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>d1prtb1 b.40.2.1 (B:90-199) Pertussis toxin S2/S3 subunits, C-terminal domain {Bordetella pertussis}
TTRNTGQPATDHYYSNVTATRLLSSTNSRLCAVFVRSGQPVIGACTSPYDGKYWSMYSRLRKMLY
LIYVAGISVRVHVSKEEQYYDYEDATFETYALTGISICNPGSSLC
>d1prtc1 b.40.2.1 (C:90-199) Pertussis toxin S2/S3 subunits, C-terminal domain {Bordetella pertussis}
TIYKTGQPAADHYYSKVTATRLLASTNSRLCAVFVRDGQSVIGACASPYEGRYRDMYDALRRLLY
MIYMSGLAVRVHVSKEEQYYDYEDATFQTYALTGISLCNPAASIC
>d1prtd_ b.40.2.1 (D:) Pertussis toxin S4 subunit {Bordetella pertussis}
DVPYVLVKTNMVVTSVAMKPYEVTPTRMLVCGIAAKLGAAASSPDAHVPFCFGKDLKRPGSSPME
VMLRAVFMQQRPLRMFLGPKQLTFEGKPALELIRMVECSGKQDCP
>d1prtf_ b.40.2.1 (F:) Pertussis toxin S5 subunit {Bordetella pertussis}
LPTHLYKNFTVQELALKLKGKNQEFCLTAFMSGRSLVRACLSDAGHEHDTWFDTMLGFAISAYAL
KSRIALTVEDSPYPGTPGDLLELQICPLNGYCE
>d1esfa1 b.40.2.2 (A:1-120) Staphylococcal enterotoxin A, SEA {Staphylococcus aureus}
SEKSEEINEKDLRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFLQHTILFKGFFTDHSWYN
DLLVDFDSKDIVDKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT
>d1i4pa1 b.40.2.2 (A:1-120) Staphylococcal enterotoxin C2, SEC2 {Staphylococcus aureus}
ESQPDPTPDELHKSSEFTGTMGNMKYLYDDHYVSATKVMSVDKFLAHDLIYNISDKKLKNYDKVK
TELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGITKHEG
>d3tss_1 b.40.2.2 (5-93) Toxic shock syndrome toxin-1 (TSST-1) {Staphylococcus aureus}
NIKDLLDWYSSGSDTFTNSEVLDNSLGSMRIKNTDGSISLIIFPSPYYSPAFTKGEKVDLNTKRI
KKSQHTSEGTWIHFQISGVTNTEK
>d1sebd1 b.40.2.2 (D:2-121) Staphylococcal enterotoxin B, SEB {Staphylococcus aureus}
SQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTYDNVRVEFKN
KDLADKYKDKYVDVFGANYYYQCYFSKKKTCMYGGVTEH
>d3seb_1 b.40.2.2 (1-121) Staphylococcal enterotoxin B, SEB {Staphylococcus aureus}
ESQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNYDNVR
VEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTCMYGGVTEH
>d1jckb1 b.40.2.2 (B:1-121) Staphylococcal enterotoxin C3, SEC3 {Staphylococcus aureus}
ESQPDPMPDDLHKSSEFTGTMGNMKYLYDDHYVSATKVKSVDKFLAHDLIYNINDKKLNNYDKVK
TELLNEDLANKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTSGKTCMYGGITKHEGN
>d1enfa1 b.40.2.2 (A:2-101) Staphylococcal enterotoxin H, SEH {Staphylococcus aureus}
DLHDKSELTDLALANAYGQYNHPFIKENIKSDEISGEKDLIFRNQGDSGNDLRVKFATADLAQKF
KNKNVDIYGASFYYKCEKISENISECLYGGTTLNS
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>d1an8_1 b.40.2.2 (3-95) Streptococcal superantigen Spe-C {Streptococcus pyogenes}
KKDISNVKSDLLYAYTITPYDYKDCRVNFSTTHTLNIDTQKYRGKDYYISSEMSYEASQKFKRDD
HVDVFGLFYILNSHTGEYIYGGITPAQN
>d1et9a1 b.40.2.2 (A:1-95) Streptococcal superantigen Spe-H {Streptococcus pyogenes}
NSYNTTNRHNLESLYKHDSNLIEADSIKNSPDIVTSHMLKYSVKDKNLSVFFEKDWISQEFKDKE
VDIYALSAQEVCECPGKRYEAFGGITLTNS
>d1eu3a1 b.40.2.2 (A:2A-96) Streptococcal superantigen Smez-2 {Streptococcus pyogenes}
GLEVDNNSLLRNIYSTIVYEYSDIVIDFKTSHNLVTKKLDVRDARDFFINSEMDEYAANDFKTGD
KIAVFSVPFDWNYLSKGKVTAYTYGGITPYQK
>d1bxta1 b.40.2.2 (A:1-119) Streptococcal superantigen SSA {Streptococcus pyogenes}
SSQPDPTPEQLNKSSQFTGVMGNLRCLYDNHFVEGTNVRSTGQLLQHDLIFPIKDLKLKNYDSVK
TEFNSKDLATKYKNKDVDIFGSNYYYNCYYSEGNSCKNAKKTCMYGGVTEHHRN
>d1fnua1 b.40.2.2 (A:1-107) Streptococcal pyrogenic exotoxin A1 {Streptococcus pyogenes}
QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHDLIYNVSGPNYDKLKTELKNQ
EMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHE
>d1d2ba_ b.40.3.1 (A:) TIMP-1 {Human (Homo sapiens)}
CTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDAADIRFVYTPA
MESVCGYFHRSHNRSEEFLIAGKLQDGLLHITTCSFVAPWNSLSLAQRRGFTKTYTVGCEE
>d1ueab_ b.40.3.1 (B:) TIMP-1 {Human (Homo sapiens)}
CTCVPPHPQTAFCNSDLVIRAKFVGTPEVAQTTLYQRYEIKMTKMYKGFQALGDAADIRFVYTPA
MESVCGYFHRSHARSEEFLIAGKLQDGLLHITTCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVF
PCLSIPCKLQSGTHCLWTDQLLQGSEKGFQSRHLACLPREPGLCTWQSLRS
>d1br9__ b.40.3.1 (-) TIMP-2 {Human (Homo sapiens)}
CSCSPVHPQQAFCNADVVIRAKAVSEKEVDSGNDIYGNPIKRIQYEIKQIKMFKGPEKDIEFIYT
APSSAVCGVSLDVGGKKEYLIAGKAEGDGKMHITLCDFIVPWDTLSTTQKKSLNHRYQMGCECKI
TRCPMIPCYISSPDECLWMDWVTEKNINGHQAKFFACIKRSDGSCAWYRGAA
>d2tmp__ b.40.3.1 (-) TIMP-2 {Human (Homo sapiens)}
CSCSPVHPQQAFCNADVVIRTKAVSEKEVDSGNDIYGNPIKRIQYEIKQIKMFKGPEKDIEFIYT
APSSAVCGVSLDVGGKKEYLIAGKAEGDGKMHITLCDFIVPWDTLSTTQKKSLNHRYQMGCE
>d1bqqt_ b.40.3.1 (T:) TIMP-2 {Cow (Bos taurus)}
CSCSPVHPQQAFCNADIVIRAKAVNKKEVDSGNDIYGNPIKRIQYEIKQIKMFKGPDQDIEFIYT
APAAAVCGVSLDIGGKKEYLIAGKAEGNGNMHITLCDFIVPWDTLSATQKKSLNHRYQMGCECKI
TRCPMIPCYISSPDECLWMDWVTEKNINGHQAKFFACIKRSDGSCAWYRGAAPP
>d1jb3a_ b.40.3.2 (A:) The laminin-binding domain of agrin {Chicken (Gallus gallus)}
ELQRREEEANVVLTGTVEEIMNVDPVHHTYSCKVRVWRYLKGKDIVTHEILLDGGNKVVIGGFGD
PLICDNQVSTGDTRIFFVNPAPQYMWPAHRNELMLNSSLMRITLRNLEEVEHCVEEHRKLLA
>d1k28a1 b.40.8.1 (A:6-129) Tail-associated lysozyme gp5, N-terminal domain {Bacteriophage T4}

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NNLNWFVGVVEDRMDPLKLGRVRVRVVGLHPPQRAQGDVMGIPTEKLPWMSVIQPITSAAMSGIG
GSVTGPVEGTRVYGHFLDKWKTNGIVLGTYGGIVREKPNRLEGFSDPTGQYPRRLGNDT
>d1eova1 b.40.4.1 (A:71-204) Aspartyl-tRNA synthetase (AspRS)
{Baker's yeast (Saccharomyces cerevisiae)}
AKDNYGKLPLIQSRDSDRTGQKRVKFVDLDEAKDSDKEVLFRARVHNTRQQGATLAFLTLRQQAS
LIQGLVKANKEGTISKNMVKWAGSLNLESIVLVRGIVKKVDEPIKSATVQNLEIHITKIYTISET
PEAL
>d1b8aa1 b.40.4.1 (A:1-103) Aspartyl-tRNA synthetase (AspRS)
{Archaeon Pyrococcus kodakaraensis}
MYRTHYSSEITEELNGQKVKVAGWVWEVKDLGGIKFLWIRDRDGIVQITAPKKKVDPELFKLIPK
LRSEDVVAVEGVVNFTPKAKLGFEILPEKIVVLNRAET
>d1c0aa1 b.40.4.1 (A:1-106) Aspartyl-tRNA synthetase (AspRS)
{Escherichia coli}
MRTEYCGQLRLSHVGQQVTLCGWVNRRRDLGSLIFIDMRDREGIVQVFFDPDRADALKLASELRN
EFCIQVTGTVRARDEKNINRDMATGEIEVLASSLTIINRAD
>d1g51a1 b.40.4.1 (A:1-104) Aspartyl-tRNA synthetase (AspRS) {Thermus
thermophilus}
MRRTHYAGSLRETHVGEEVVLEGWVNRRRDLGGLIFLDLRDREGLVQLVAHPASPAYATAERVRP
EWVVRAKGLVRLRPEPNPRLATGRVEVELSALEVLAEAK
>d1bbua1 b.40.4.1 (A:11-154) Lysyl-tRNA synthetase (LysRS)
{Escherichia coli, gene lysS}
VVDLNNELKTRREKLANLREQGIAFPNDFRRDHTSDQLHAEFDGKENEELEALNIEVAVAGRMMT
RRIMGKASFVTLQDVGGRIQLYVARDDLPEGVYNEQFKKWDLGDILGAKGKLFKTKTGELSIHCT
ELRLLTKALRPLPD
>d1krs__ b.40.4.1 (-) Lysyl-tRNA synthetase (LysRS) {Escherichia coli,
gene lysS}
FRRDHTSDQLHAEFDGKENEELEALNIEVAVAGRMMTRRIMGKASFVTLQDVGGRIQLYVARDDL
PEGVYNEQFKKWDLGDILGAKGKLFKTKTGELSIHCTELRLLTKA
>d1e1oa1 b.40.4.1 (A:11-153) Lysyl-tRNA synthetase (LysRS)
{Escherichia coli, gene lysU}
AIDFNDELRNRREKLAALRQQGVAFPNDFRRDHTSDQLHEEFDAKDNQELESLNIEVSVAGRMMT
RRIMGKASFVTLQDVGGRIQLYVARDSLPEGVYNDQFKKWDLGDIIGARGTLFKTQTGELSIHCT
ELRLLTKALRPLP
>d1gm5a2 b.40.4.9 (A:106-285) RecG "wedge" domain {Thermotoga
maritima}
CSGEEVDLSTDIQYAKGVGPNRKKKLKKLGIETLRDLLEFFPRDYEDRRKIFKLNDLLPGEKVTT
QGKIVSVETKKFQNMNILTAVLSDGLVHVPLKWFNQDYLQTYLKQLTGKEVFVTGTVKSNAYTGQ
YEIHNAEVTPKEGEYVRRILPIYRLTSGISQKQMRKIFEENIPSLCCSLK
>d1cuk_3 b.40.4.2 (1-64) DNA helicase RuvA subunit, N-terminal domain
{Escherichia coli}
MIGRLRGIIIEKQPPLVLIEVGGVGYEVHMPMTCFYELPEAGQEAIVFTHFVVREDAQLLYGFN
>d1bvsa3 b.40.4.2 (A:1-63) DNA helicase RuvA subunit, N-terminal
domain {Mycobacterium leprae}
MIFSVRGEVLEVALDHAVIEAAGIGYRVNATPSALATLNQGSQARLVTAMVVREDSMTLYGFS
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>d3ulla_ b.40.4.3 (A:) ssDNA-binding protein {Human (Homo sapiens),
mitochondria}
LERSLNRVHLLGRVGQDPVLRQVEGKNPVTIFSLATNEMWRSGDSEVYQLGDVSQKTTWHRISVF
RPGLRDVAYQYVKKGSRIYLEGKIDYGEYMDKNNVRRQATTIIADNIIFL
>d1kawa_ b.40.4.3 (A:) ssDNA-binding protein {Escherichia coli}
RGVNKVILVGNLGQDPEVRYMPNGGAVANITLATSESWRDKATGEMKEQTEWHRVVLFGKLAEVA
SEYLRKGSQVYIEGQLRTRKWTDQSGQDRYTTEVVVNVGGTMQML
>d1qvca_ b.40.4.3 (A:) ssDNA-binding protein {Escherichia coli}
ASRGVNKVILVGNLGQDPEVRYMPNGGAVANITLATSESWRDKATGEMKEQTEWHRVVLFGKLAE
VASEYLRKGSQVYIEGQLRTRKWTDQSGQDRYTTEVVVNVGGTMQMLGGRQGGGAPAGGNIGGGQ
PQGGWGQPQQPQGGN
>d1ewia_ b.40.4.3 (A:) Replication protein A 70 KDa subunit (RPA70)
fragment {Human (Homo sapiens)}
MVGQLSEGAIAAIMQKGDTNIKPILQVINIRPITTGNSPPRYRLLMSDGLNTLSSFMLATQLNPL
VEEEQLSSNCVCQIHRFIVNTLKDGRRVVILMELEVLKSAEAVGVKIGN
>d1fgua1 b.40.4.3 (A:181-298) Replication protein A 70 KDa subunit
(RPA70) fragment {Human (Homo sapiens)}
MSKVVPIASLTPYQSKWTICARVTNKSQIRTWSNSRGEGKLFSLELVDESGEIRATAFNEQVDKF
FPLIEVNKVYYFSKGTLKIANKQFTAVKNDYEMTFNNETSVMPCEDDHHLPTV
>d1fgua2 b.40.4.3 (A:299-426) Replication protein A 70 KDa subunit
(RPA70) fragment {Human (Homo sapiens)}
QFDFTGIDDLENKSKDSLVDIIGICKSYEDATKITVRSNNREVAKRNIYLMDTSGKVVTATLWGE
DADKFDGSRQPVLAIKGARVSDFGGRSLSVLSSSTIIANPDIPEAYKLRGWFDAEGQALDGVS
>d1quqa_ b.40.4.3 (A:) Replication protein A 32 KDa subunit (RPA32)
fragment {Human (Homo sapiens)}
HIVPCTISQLLSATLVDEVFRIGNVEISQVTIVGIIRHAEKAPTNIVYKIDDMTAAPMDVRQWVD
TDDTSSENTVVPPETYVKVAGHLRSFQNKKSLVAFKIMPLEDMNEFTTHILEVINAHMVLSK
>d1quqb_ b.40.4.3 (B:) Replication protein A 14 KDa (RPA14) subunit
{Human (Homo sapiens)}
DMMDLPRSRINAGMLAQFIDKPVCFVGRLEKIHPTGKMFILSDGEGKNGTIELMEPLDEEISGIV
EVVGRVTAKATILCTSYVQFKEDSHPFDLGLYNEAVKIIHDFPQFYPLG
>d1jb7a1 b.40.4.3 (A:36-204) Telomere end binding protein alpha
subunit {Oxytricha nova}
YEYVELAKASLTSAQPQHFYAVVIDATFPYKTNQERYICSLKIVDPTLYLKQQKGAGDASDYATL
VLYAKRFEDLPIIHRAGDIIRVHRATLRLYNGQRQFNANVFYSSSWALFSTDKRSVTQEINNQDA
VSDTTPFSFSSKHATIEKNEISILQNLRKWANQYFSSYS
>d1jb7a2 b.40.4.3 (A:205-328) Telomere end binding protein alpha
subunit {Oxytricha nova}
VISSDMYTALNKAQAQKGDFDVVAKILQVHELDEYTNELKLKDASGQVFYTLSLKLKFPHVRTGE
VVRIRSATYDETSTQKKVLILSHYSNIITFIQSSKLAKELRAKIQDDHSVEVASLKKNV
>d1jb7a3 b.40.4.3 (A:329-495) Telomere end binding protein alpha
subunit {Oxytricha nova}
SLNAVVLTEVDKKHAALPSTSLQDLFHHADSDKELQAQDTFRTQFYVTKIEPSDVKEWVKGYDRK
TKKSSSLKGASGKGDNIFQVQFLVKDASTQLNNNTYRVLLYTQDGLGANFFNVKADNLHKNADAR
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KKLEDSAELLTKFNSYVDAVVERRNGFYLIKDTKLIY
>d1k8ga2 b.40.4.3 (A:205-315) Telomere end binding protein alpha
subunit {Oxytricha nova}
VISSDMYTALNKAQAQKGDFDVVAKILQVHELDEYTNELKLKDASGQVFYTLSLKLKFPHVRTGE
VVRIRSATYDETSTQKKVLILSHYSNIITFIQSSKLAKELRAKIQD
>d1jb7b_ b.40.4.3 (B:) Core domain of telomere end binding protein
beta subunit {Oxytricha nova}
QQQSAFKQLYTELFNNEGDFSKVSSNLKKPLKCYVKESYPHFLVTDGYFFVAPYFTKEAVNEFHA
KFPNVNIVDLTDKVIVINNWSLELRRVNSAEVFTSYANLEARLIVHSFKPNLQERLNPTRYPVNL
FRDDEFKTTIQHFRHTALQAAINKTVKGDNLVDISKVADAAGKKGKVDAGIVKASASKGDEFSDF
SFKEGNTATLKIADIFVQEKG
>d1jjcb3 b.40.4.4 (B:39-151) Domain B2 of PheRS-beta, PheT {Thermus
thermophilus (Thermus aquaticus)}
FPIPRGVVFARVLEAHPIPGTRLKRLVLDAGRTVEVVSGAENARKGIGVALALPGTELPGLGQKV
GERVIQGVRSFGMALSPRELGVGEYGGGLLEFPEDALPPGTPLSEAWP
>d1fl0a_ b.40.4.4 (A:) EMAP II {Human (Homo sapiens)}
IDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLK
PAKMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLH
TNDECVATYKGVPFEVKGKGVCRAQTMSNSGIKL
>d1gd7a_ b.40.4.4 (A:) CsaA {Thermus thermophilus}
MTPLEAFQILDLRVGRVLRAEPHEKARKPSYKLWVDLGPLGVKQSSAQITELYRPEDLVGRLVVC
AVNLGAKRVAGFLSEVLVLGVPDEAGRVVLLAPDREVPLGGKVF
>d1mjc__ b.40.4.5 (-) Major cold shock protein {Escherichia coli}
SGKMTGIVKWFNADKGFGFITPDDGSKDVFVHFSAIQNDGYKSLDEGQKVSFTIESGAKGPAAGN
VTSL
>d1csp__ b.40.4.5 (-) Major cold shock protein {Bacillus subtilis}
MLEGKVKWFNSEKGFGFIEVEGQDDVFVHFSAIQGEGFKTLEEGQAVSFEIVEGNRGPQAANVTK
EA
>d1c9oa_ b.40.4.5 (A:) Major cold shock protein {Bacillus
caldolyticus}
MQRGKVKWFNNEKGYGFIEVEGGSDVFVHFTAIQGEGFKTLEEGQEVSFEIVQGNRGPQAANVVK
L
>d1g6pa_ b.40.4.5 (A:) Major cold shock protein {Thermotoga maritima}
MRGKVKWFDSKKGYGFITKDEGGDVFVHWSAIEMEGFKTLKEGQVVEFEIQEGKKGPQAAHVKVV
E
>d1h95a_ b.40.4.5 (A:) Y-box protein 1 cold shock domain (YB1-CSD)
{Human (Homo sapiens)}
MKKVIATKVLGTVKWFNVRNGYGFINRNDTKEDVFVHQTAIKKNNPRKYLRSVGDGETVEFDVVE
GEKGAEAANVTGPG
>d1sro__ b.40.4.5 (-) S1 RNA-binding domain of polyribonucleotide
phosphorylase, PNPase {Escherichia coli}
AEIEVGRVYTGKVTRIVDFGAFVAIGGGKEGLVHISQIADKRVEKVTDYLQMGQEVPVKVLEVDR
QGRIRLSIKEA
>d1e3pa2 b.40.4.5 (A:656-717) S1 RNA-binding domain of
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polyribonucleotide phosphorylase, PNPase {Streptomyces antibioticus}
GSVVKTTTFGAFVSLLPGKDGLLHISQIRKLAGGKRVENVEDVLGVGQKVQVEIAEIDSRGK
>d1hh2p1 b.40.4.5 (P:127-198) S1 domain of NusA {Thermotoga maritima}
FEKYSELKGTVTTAEVIRVMGEWADIRIGKLETRLPKKEWIPGEEIKAGDLVKVYIIDVVKTTKG
PKILVSR
>d1k0ra1 b.40.4.5 (A:108-183) S1 domain of NusA {Mycobacterium
tuberculosis}
STREGEIVAGVIQRDSRANARGLVVVRIGTETKASEGVIPAAEQVPGESYEHGNRLRCYVVGVTR
GAREPLITLSR
>d1go3e_ b.40.4.5 (E:) RNA polymerase II subunit RBP4 (RpoE) {Archaeon
Methanococcus jannaschii}
MYKILEIADVVKVPPEEFGKDLKETVKKILMEKYEGRLDKDVGFVLSIVDVKDIGEGKVVHGDGS
AYHPVVFETLVYIPEMYELIEGEVVDVVEFGSFVRLGPLDGLIHVSQIMDDYVSYDPKREAIIGK
ETGKVLEIGDYVRARIVAISLKAERKRGSKIALTMRQPYLGKLEWIEEEKAKKQ
>d1ah9__ b.40.4.5 (-) Translational initiation factor 1, IF1
{Escherichia coli}
AKEDNIEMQGTVLETLPNTMFRVELENGHVVTAHISGKMRKNYIRILTGDKVTVELTPYDLSKGR
IVFRSR
>d1hr0w_ b.40.4.5 (W:) Translational initiation factor 1, IF1
{Escherichia coli}
AKEKDTIRTEGVVTEALPNATFRVKLDSGPEILAYISGKMRMHYIRILPGDRVVVEITPYDPTRG
RIVYRK
>d1jt8a_ b.40.4.5 (A:) Archaeal initiation factor-1a, aIF1a {Archaeon
Methanococcus jannaschii}
MAEQQQEQQIRVRIPRKEENEILGIIEQMLGASRVRVRCLDGKTRLGRIPGRLKNRIWVREGDVV
IVKPWEVQGDQKCDIIWRYTKTQVEWLKRKGYLDELL
>d1d7qa_ b.40.4.5 (A:) Translation initiation factor-1a, eIF1a {Human
(Homo sapiens)}
PKNKGKGGKNRRRGKNENESEKRELVFKEDGQEYAQVIKMLGNGRLEAMCFDGVKRLCHIRGKLR
KKVWINTSDIILVGLRDYQDNKADVILKYNADEARSLKAYGELPEHAKINETDTFGPGDDDEIQF
DDIGDDDEDIDDI
>d1a62_2 b.40.4.5 (48-125) Rho termination factor, RNA-binding domain
{Escherichia coli}
DIFGDGVLEILQDGFGFLRSADSSYLAGPDDIYVSPSQIRRFNLRTGDTISGKIRPPKEGERYFA
LLKVNEVNFDKPE
>d2eifa2 b.40.4.5 (A:74-132) C-terminal domain of eukaryotic
initiation translation factor 5a {Archaeon Methanococcus jannaschii}
IDRRKGQVLAIMGDMVQIMDLQTYETLELPIPEGIEGLEPGGEVEYIEAVGQYKITRVI
>d1bkb_2 b.40.4.5 (75-139) C-terminal domain of eukaryotic initiation
translation factor 5a {Archaeon Pyrobaculum aerophilum}
IIEKFTAQILSVSGDVIQLMDMRDYKTIEVPMKYVEEEAKGRLAPGAEVEVWQILDRYKIIRVKG
>d1rl2a2 b.40.4.5 (A:60-125) N-terminal domain of ribosomal protein
L2 {Bacillus stearothermophilus}
QYRIIDFKRDKDGIPGRVATIEYDPNRSANIALINYADGEKRYIIAPKNLKVGMEIMSGPDADIK
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I
>d1jj2a2 b.40.4.5 (A:1-90) N-terminal domain of ribosomal protein L2 {Archaeon Haloarcula marismortui}
GRRIQGQRRGRGTSTFRAPSHRYKADLEHRKVEDGDVIAGTVVDIEHDPARSAPVAAVEFEDGDR
RLILAPEGVGVGDELQVGVDAEIAP
>d1fjgl_ b.40.4.5 (L:) Ribosomal protein S12 {Thermus thermophilus}
PTINQLVRKGREKVRKKSKVPALKGAPFRRGVCTVVRTVTPKKPNSALRKVAKVRLTSGYEVTAY
IPGEGHNLQEHSVVLIRGGRVKDLPGVRYHIVRGVYDAAGVKDRKKSRSKYGTKKPKEAA
>d1fjgq_ b.40.4.5 (Q:) Ribosomal protein S17 {Thermus thermophilus}
PKKVLTGVVVSDKMQKTVTVLVERQFPHPLYGKVIKRSKKYLAHDPEEKYKLGDVVEIIESRPIS
KRKRFRVLRLVESGRMDLVEKYLIRRQNYQSLSKRGGKA
>d1i94q_ b.40.4.5 (Q:) Ribosomal protein S17 {Thermus thermophilus}
PKKVLTGVVVSDKMQKTVTVLVERQFPHPLYGKVIKRSKKYLAHDPEERYKVGDVVEIIEARPIS
KRKRFRVLRLVEEGRLDLVEKYLVRRQNYASLSKRGGKA
>d1rip__ b.40.4.5 (-) Ribosomal protein S17 {Bacillus stearothermophilus}
QRKVYVGRVVSDKMDKTITVLVETYKKHPLYGKRVKYSKKYKAHDEHNEAKVGDIVKIMETRPLS
ATKRFRLVEIVEKAVR
>d1ckma1 b.40.4.6 (A:239-327) RNA guanylyltransferase (mRNA capping enzyme) {Chlorella virus, PBCV-1}
THHTIDFIIMSEDGTIGIFDPNLRKNVPVGKLDGYYNKGSIVECGFADGTWKYIQGRSDKNQAND
RLTYEKTLLNIEENITIDELLDLF
>d1a0i_1 b.40.4.6 (241-349) ATP-dependent DNA ligase {Bacteriophage T7}
PENEADGIIQGLVWGTKGLANEGKVIGFEVLLESGRLVNATNISRALMDEFTETVKEATLSQWGF
FSPYGIGDNDACTINPYDGWACQISYMEETPDGSLRHPSFVMFR
>d1fvia1 b.40.4.6 (A:190-293) ATP-dependent DNA ligase {Chlorella virus, PBCV-1}
FKDAEATIISMTALFKNTNTKTKDNFGYSKRSTHKSGKVEEDVMGSIEVDYDGVVFSIGTGFDAD
QRRDFWQNKESYIGKMVKFKYFEMGSKDCPRFPVFIGIR
>d1dgsa2 b.40.4.6 (A:315-400) NAD+-dependent DNA ligase {Thermus filiformis}
AEEKETRLLDVVFQVGRTGRVTPVGVLEPVFIEGSEVSRVTLHNESYIEELDIRIGDWVLVHKAG
GVIPEVLRVLKERRTGKERPI
>d1gvp__ b.40.4.7 (-) Gene V protein {Filamentous bacteriophage (f1, M13)}
MIKVEIKPSQAQFTTRSGVSRQGKPYSLNEQLCYVDLGNEYPVLVKITLDEGQPAYAPGLYTVHL
SSFKVGQFGSLMIDRLRLVPAK
>d1pfsa_ b.40.4.7 (A:) Gene V protein {Pseudomonas bacteriophage pf3}
MNIQITFTDSVRQGTSAKGNPYTFQEGFLHLEDKPHPLQCQFFVESVIPAGSYQVPYRINVNNGR
PELAFDFKAMKRA
>d1gpc__ b.40.4.7 (-) Gene 32 protein (gp32) core {Bacteriophage T4}
GFSSEDKGEWKLKLDNAGNGQAVIRFLPSKNDEQAPFAILVNHGFKKNGKWYIETCSSTHGDYDS
CPVCQYISKNDLYNTDNKEYSLVKRKTSYWANILVVKDPAAPENEGKVFKYRFGKKIWDKINAMI
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AVDVEMGETPVDVTCPWEGANFVLKVKQVSGFSNYDESKFLNQSAIPNIDDESFQKELFEQMVDL
SEMTSKDKFKSFEELNTKFGQVM
>d1je5a_ b.40.4.7 (A:) gp2.5 {Bacteriophage T7}
MAKKIFTSALGTAEPYAYIAKPDYGNEERGFGNPRGVYKVDLTIPNKDPRCQRMVDEIVKCHEEA
YAAAVEEYEANPPAVARGKKPLKPYEGDMPFFDNGDGTTTFKFKCYASFQDKKTKETKHINLVVV
DSKGKKMEDVPIIGGGSKLKVKYSLVPYKWNTAVGASVKLQLESVMLVELATFGGGEDDWADEVE
EN
>d1i50h_ b.40.4.8 (H:) RNA polymerase subunit RBP8 {Baker's yeast (Saccharomyces cerevisiae)}
SNTLFDDIFQVSEVDPGRYNKVCRIEAASTTQDQCKLTLDINVELFPVAAQDSLTVTIASSLNLE
DTPANDSSATRSWRPPQAGDRSLADDYDYVMYGTAYKFEEVSKDLIAVYYSFGGLLMRLEGNYRN
LNNLKQENAYLLIRR
>d1e9ga_ b.40.5.1 (A:) Inorganic pyrophosphatase {Baker's yeast (Saccharomyces cerevisiae)}
TYTTRQIGAKNTLEYKVYIEKDGKPVSAFHDIPLYADKENNIFNMVVEIPRWTNAKLEITKEETL
NPIIQDTKKGKLRFVRNCFPHHGYIHNYGAFPQTWEDPNVSHPETKAVGDNDPIDVLEIGETIAY
TGQVKQVKALGIMALLDEGETDWKVIAIDINDPLAPKLNDIEDVEKYFPGLLRATNEWFRIYKIP
DGKPENQFAFSGEAKNKKYALDIIKETHDSWKQLIAGKSSDSKGIDLTNVTLPDTPTYSKAASDA
IPPASLKADAPIDKSIDKWFFISG
>d1qeza_ b.40.5.1 (A:) Inorganic pyrophosphatase {Archaeon Sulfolobus acidocaldarius}
KLSPGKNAPDVVNVLVEIPQGSNIKYEYDDEEGVIKVDRVLYTSMNYPFNYGFIPGTLEEDGDPL
DVLVITNYQLYPGSVIEVRPIGILYMKDEEGEDAKIVAVPKDKTDPSFSNIKDINDLPQATKNKI
VHFFEHYKELEPGKYVKISGWGSATEAKNRIQLAIKRVSG
>d1i40a_ b.40.5.1 (A:) Inorganic pyrophosphatase {Escherichia coli}
SLLNVPAGKDLPEDIYVVIEIPANADPIKYEIDKESGALFVDRFMSTAMFYPCNYGYINHTLSLD
GDPVDVLVPTPYPLQPGSVTRCRPVGVLKMTDEAGEDAKLVAVPHSKLSKEYDHIKDVNDLPELL
KAQIAHFFEHYKDLEKGKWVKVEGWENAEAAKAEIVASFERAKNK
>d2prd__ b.40.5.1 (-) Inorganic pyrophosphatase {Thermus thermophilus}
ANLKSLPVGDKAPEVVHMVIEVPRGSGNKYEYDPDLGAIKLDRVLPGAQFYPGDYGFIPSTLAED
GDPLDGLVLSTYPLLPGVVVEVRVVGLLLMEDEKGGDAKVIGVVAEDQRLDHIQDIGDVPEGVKQ
EIQHFFETYKALEAKKGKWVKVTGWRDRKAALEEVRACIARYKG
>d1fr3a_ b.40.6.1 (A:) Molybdate/tungstate binding protein MOP {Sporomusa ovata}
MKISGRNKLEATVKEIVKGTVMAKIVMDYKGTELVAAITIDSVADLDLVPGDKVTALVKATEMEV
LK
>d1guta_ b.40.6.1 (A:) Molybdate/tungstate binding protein MOP {Clostridium pasteurianum, MOP II}
SISARNQLKGKVVGLKKGVVTAEVVLEIAGGNKITSIISLDSVEELGVKEGAELTAVVKSTDVMI
LA
>d1h9ma1 b.40.6.2 (A:1-73) Cytoplasmic molybdate-binding protein ModG {Azotobacter vinelandii}
MKISARNVFKGTVSALKEGAVNAEVDILLGGGDKLAAVVTLESARSLQLAAGKEVVAVVKAPWVL
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LMTDSSGY
>d1h9ma2 b.40.6.2 (A:74-141) Cytoplasmic molybdate-binding protein
ModG {Azotobacter vinelandii}
RLSARNILTGTVKTIETGAVNAEVTLALQGGTEITSMVTKEAVAELGLKPGASASAVIKASNVIL
GVP
>d1h9ra1    b.40.6.2    (A:123-199)    C-terminal    domain    of
molybdate-dependent  transcriptional  regulator  ModE  {Escherichia
coli}
MQTSARNQWFGTITARDHDDVQQHVDVLLADGKTRLKVAITAQSGARLGLDEGKEVLILLKAPWV
GITQDEAVAQNA
>d1h9ra2    b.40.6.2    (A:200-261)    C-terminal    domain    of
molybdate-dependent  transcriptional  regulator  ModE  {Escherichia
coli}
DNQLPGIISHIERGAEQCEVLMALPDGQTLCATVPVNEATSLQQGQNVTAYFNADSVIIATL
>d1g2913  b.40.6.3  (1:241-301)  Maltose  transport  protein  MalK,
C-terminal domain {Archaeon Thermococcus litoralis}
GSPPMNFLDAIVTEDGFVDFGEFRLKLLPDQFEVLGELGYVGREVIFGIRPEDLYDAMFAQ
>d1g2914  b.40.6.3  (1:302-372)  Maltose  transport  protein  MalK,
C-terminal domain {Archaeon Thermococcus litoralis}
VRVPGENLVRAVVEIVENLGSERIVRLRVGGVTFVGSFRSESRVREGVEVDVVFDMKKIHIFDKT
TGKAIF
>d1b3qa2  b.40.7.1  (A:540-671)  Histidine  kinase  CheA,  C-terminal
domain {Thermotoga maritima}
TLAIICALLVKVNNLVYAIPIANIDTILSISKEDIQRVQDRDVIVIRGEVIPVYRLWEVLQIEHK
EELEEMEAVIVRVGNRKYGIVVDDLLGQDDIVIKSLGKVFSEVKEFSGAAILGDGSIALIINVSG
IV
>d1k0sa_ b.40.7.1 (A:) Chemotaxis protein CheW {Thermotoga maritima}
MKTLADALKEFEVLSFEIDEQALAFDVDNIEMVIEKSDITPVPKSRHFVEGVINLRGRIIPVVNL
AKILGISFDEQKMKSIIVARTKDVEVGFLVDRVLGVLRITENQLDLTNVSDKFGKKSKGLVKTDG
RLIIYLDIDKIIEEITVKEGV
>d1dxrh1   b.41.1.1   (H:37-258)   Photosynthetic   reaction   centre
{Rhodopseudomonas viridis}
RREGYPLVEPLGLVKLAPEDGQVYELPYPKTFVLPHGGTVTVPRRRPETRELKLAQTDGFEGAPL
QPTGNPLVDAVGPASYAERAEVVDATVDGKAKIVPLRVATDFSIAEGDVDPRGLPVVAADGVEAG
TVTDLWVDRSEHYFRYLELSVAGSARTALIPLGFCDVKKDKIVVTSILSEQFANVPRLQSRDQIT
LREEDKVSAYYAGGLLYATPERAESLL
>d1qovh1   b.41.1.1   (H:36-250)   Photosynthetic   reaction   centre
{Rhodobacter sphaeroides}
MREGYPLENEDGTPAANQGPFPLPKPKTFILPHGRGTLTVPGPESEDRPIALARTAVSEGFPHAP
TGDPMKDGVGPASWVARRDLPELDGHGHNKIKPMKAAAGFHVSAGKNPIGLPVRGCDLEIAGKVV
DIWVDIPEQMARFLEVELKDGSTRLLPMQMVKVQSNRVHVNALSSDLFAGIPTIKSPTEVTLLEE
DKICGYVAGGLMYAAPKRKS
>d1eysh1   b.41.1.1   (H:59-259)   Photosynthetic   reaction   centre
{Thermochromatium tepidum}
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PDLPDPKTFVLPHNGGTVVAPRVEAPVAVNATPFSPAPGSPLVPNGDPMLSGFGPAASPDRPKHC
DLTFEGLPKIVPMRVAKEFSIAEGDPDPRGMTVVGLDGEVAGTVSDVWVDRSEPQIRYLEVEVAA
NKKKVLLPIGFSRFDKKARKVKVDAIKAAHFANVPTLSNPDQVTLYEEDKVCAYYAGGKLYATAE
RAGPLL
>d1bfg__ b.42.1.1 (-) Basic FGF (FGF2) {Human (Homo sapiens)}
DPKRLYCKNGGFFLRIHPDGRVDGVREKSDPHIKLQLQAEERGVVSIKGVSANRYLAMKEDGRLL
ASKSVTDECFFFERLESNNYNTYRSRKYTSWYVALKRTGQYKLGSKTGPGQKAILFLPMSA
>d1bla__ b.42.1.1 (-) Basic FGF (FGF2) {Human (Homo sapiens)}
MAEGEITTLPALPEDGGSGAFPPGHFKDPKRLYCKNGGFFLRIHPDGRVDGVREKSDPHIKLQLQ
AEERGVVSIKGVSANRYLAMKEDGRLLASKSVTDECFFFERLESNNYNTYRSRKYTSWYVALKRT
GQYKLGSKTGPGQKAILFLPMSAKS
>d1bara_ b.42.1.1 (A:) Acidic FGF (FGF1) {Cow (Bos taurus)}
PKLLYCSNGGYFLRILPDGTVDGTKDRSDQHIQLQLAAESIGEVYIKSTETGQFLAMDTDGLLYG
SQTPNEECLFLERLEENGYNTYISKKHAEKHWFVGLKKNGRSKLGPRTHFGQKAILFLPLPV
>d1jqza_ b.42.1.1 (A:) Acidic FGF (FGF1) {Human (Homo sapiens)}
HHHHFNLPPGNYKKPKLLYCSNGGHFLRILPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTET
GQYLAMDTDGLLYGSQTPNEECLFLERLEENHYNTYISKKHAEKNWFVGLKKNGSCKRGPRTHYG
QKAILFLPLPV
>d2afga_ b.42.1.1 (A:) Acidic FGF (FGF1) {Human (Homo sapiens)}
KPKLLYCSNGGHFLRILPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTETGQYLAMDTDGLLY
GSQTPNEECLFLERLEENHYNTYISKKHAEKNWFVGLKKNGSCKRGPRTHYGQKAILFLPLPVS
>d1fmms_ b.42.1.1 (S:) Acidic FGF (FGF1) {Eastern newt (Notophthalmus
viridescens)}
QKPKLLYCSNGGYFLRIFPDGKVDGTRDRSDPYIQLQFYAESVGEVYIKSLETGQYLAMDSDGQL
YASQSPSEECLFLERLEENNYNTYKSKVHADKDWFVGIKKNGKTKPGSRTHFGQKAILFLPLPVS
SD
>d1ijta_ b.42.1.1 (A:) Fibroblast growth factor 4 (FGF4) {Human (Homo
sapiens)}
GIKRLRRLYCNVGIGFHLQALPDGRIGGAHADTRDSLLELSPVERGVVSIFGVASRFFVAMSSKG
KLYGSPFFTDECTFKEILLPNNYNAYESYKYPGMFIALGKNGKTKKGNRVSPTMKVTHFLPRL
>d1qqka_ b.42.1.1 (A:) Keratinocyte growth factor, FGF7 {Rat (Rattus
norvegicus)}
DIRVRRLFCRTQWYLRIDKRGKVKGTQEMRNSYNIMEIRTVAVGIVAIKGVESEYYLAMNKEGKL
YAKKECNEDCNFKELILENHYNTYASAKWTHSGGEMFVALNQKGLPVKGKKTKKEQKTAHFLPMA
IT
>d1qqla_ b.42.1.1 (A:) Keratinocyte growth factor, FGF7 {Rat (Rattus
norvegicus)}
DIRVRRLFCRTQWYLRIDKRGKVKGTQEMRNSYNIMEIRTVAVGIVAIKGVESEYYLAMNKEGKL
YAKQTPNEECLFLERLEENHYNTYISKKHAEKNWFVGLKKNGSCKRGPRTHYGQKAILFLPLPVS
S
>d1ihka_ b.42.1.1 (A:) Fibroblast growth factor 9, FGF9 {Human (Homo
sapiens)}
TDLDHLKGILRRRQLYCRTGFHLEIFPNGTIQGTRKDHSRFGILEFISIAVGLVSIRGVDSGLYL
GMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTPREGTRTKRH
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QKFTHFLPRPVDPDKVPELYKDILSQS
>d1i1b__ b.42.1.2 (-) Interleukin-1beta {Human (Homo sapiens)}
VRSLNCTLRDSQQKSLVMSGPYELKALHLQGQDMEQQVVFSMSFVQGEESNDKIPVALGLKEKNL
YLSCVLKDDKPTLQLESVDPKNYPKKKMEKRFVFNKIEINNKLEFESAQFPNWYISTSQAENMPV
FLGGTKGGQDITDFTMQFVSS
>d8i1b__ b.42.1.2 (-) Interleukin-1beta {Mouse (Mus musculus)}
QLHYRLRDEQQKSLVLSDPYELKALHLNGQNINQQVIFSMSFVQGEPSNDKIPVALGLKGKNLYL
SCVMKDGTPTLQLESVDPKQYPKKKMEKRFVFNKIEVKSKVEFESAEFPNWYISTSQAEHKPVFL
GNNSGQDIIDFTMESV
>d1ilr1_ b.42.1.2 (1:) Interleukin-1 receptor antagonist protein
{Human (Homo sapiens)}
SKMQAFRIWDVNQKTFYLRNNQLVAGYLQGPNVNLEEKIDVVPIEPHALFLGIHGGKMCLSCVKS
GDETRLQLEAVNITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWFLCTAMEADQPVSLTNMP
DEGVMVTKFYFQEDE
>d2ila__ b.42.1.2 (-) Interleukin-1alpha {Human (Homo sapiens)}
NVKYNFMRIIKYEFILNDALNQSIIRANAQYLTAAALHNLDEAVKFDMGAYKSSKDDAKITVILR
ISKTQLYVTAQDEDQPVLLKEMPEIPKTITGSETNLLFFWETHGTKNYFTSVAHPNLFIATKQDY
WVCLAGGPPSITDFQILE
>d2aaib1 b.42.2.1 (B:1-135) Plant cytotoxin B-chain (lectin) {Castor
bean (Ricinus communis), Ricin}
ADVCMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDANQLWTLKRDNTIRSNGKCLT
TYGYSPGVYVMIYDCNTAATDATRWQIWDNGTIINPRSSLVLAATSGNSGTTLTVQTNIYAVSQG
WLPTN
>d2aaib2 b.42.2.1 (B:136-262) Plant cytotoxin B-chain (lectin)
{Castor bean (Ricinus communis), Ricin}
NTQPFVTTIVGLYGLCLQANSGQVWIEDCSSEKAEQQWALYADGSIRPQQNRDNCLTSDSNIRET
VVKILSCGPASSGQRWMFKNDGTILNLYSGLVLDVRASDPSLKQIILYPLHGDPNQIWLPLF
>d1abrb1 b.42.2.1 (B:1-140) Plant cytotoxin B-chain (lectin) {Abrus
precatorius}
IVEKSKICSSRYEPTVRIGGRDGMCVDVYDNGYHNGNRIIMWKCKDRLEENQLWTLKSDKTIRSN
GKCLTTYGYAPGSYVMIYDCTSAVAEATYWEIWDNGTIINPKSALVLSAESSSMGGTLTVQTNEY
LMRQGWRTGN
>d1abrb2 b.42.2.1 (B:141-267) Plant cytotoxin B-chain (lectin) {Abrus
precatorius}
NTSPFVTSISGYSDLCMQAQGSNVWMADCDSNKKEQQWALYTDGSIRSVQNTNNCLTSKDHKQGS
TILLMGCSNGWASQRWVFKNDGSIYSLYDDMVMDVKGSDPSLKQIILWPYTGKPNQIWLTLF
>d1ce7b1 b.42.2.1 (B:1-133) Plant cytotoxin B-chain (lectin)
{European mistletoe (Viscum album)}
CSASEPTVRIVGRNGMNVDVRDDDFHDGNQIQLWPSKSNNDPNQLWTIKRDGTIRSNGSCLTTYG
YTAGVYVMIFDCATAVGEATVWQIWGNGTIINPRSNLVLAASSGIKGTTLTVQTLDYTLGQGWLA
GND
>d1ce7b2 b.42.2.1 (B:134-255) Plant cytotoxin B-chain (lectin)
{European mistletoe (Viscum album)}
TAPREVTIYGFNDLCMESGGGSVTVETCSSGKADKWALYGDGSIRPEQNQAQCLTSGGDSVAGVN
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IVSCSGAASGQRWVFTNEGAILNLKNGLAMDVANPGGGRIIIYPATGKPNQMWLPVF
>d1hwmb1 b.42.2.1 (B:3-135) Plant cytotoxin B-chain (lectin)
{Sambucus ebulus, ebulin}
ETCAIPAPFTRRIVGRDGLCVDVRNGYDTDGTPIQLWPCGTQRNQQWTFYNDKTIRSMGKCMTAN
GLNSGSYIMITDCSTAAEDATKWEVLIDGSIINPSSGLVMTAPSGASRTTLLLENNIHAASQGWT
VSN
>d1hwmb2 b.42.2.1 (B:136-266) Plant cytotoxin B-chain (lectin)
{Sambucus ebulus, ebulin}
DVQPIATLIVGYNEMCLQANGENNNVWMEDCDVTSVQQQWALFDDRTIRVNNSRGLCVTSNGYVS
KDLIVIRKCQGLATQRWFFNSDGSVVNLKSTRVMDVKESDVSLQEVIIFPATGNPNQQWRTQVPQ
I
>d1xyfa1 b.42.2.1 (A:313-436) Endo-1,4-beta-xylanase C-terminal
domain {Streptomyces olivaceoviridis}
GQIKGVGSGRCLDVPNASTTDGTQVQLYDCHSATNQQWTYTDAGELRVYGDKCLDAAGTGNGTKV
QIYSCWGGDNQKWRLNSDGSIVGVQSGLCLDAVGGGTANGTLIQLYSCSNGSNQRWTRT
>d1dqga_ b.42.2.2 (A:) Mannose receptor {Mouse (Mus musculus)}
DARQFLIYNEDHKRCVDALSAISVQTATCNPEAESQKFRWVSDSQIMSVAFKLCLGVPSKTDWAS
VTLYACDSKSEYQKWECKNDTLFGIKGTELYFNYGNRQEKNIKLYKGSGLWSRWKVYGTTDDLCS
RGYE
>d1jlxa1 b.42.3.1 (A:1-153) Agglutinin {Love-lies-bleeding
(Amaranthus caudatus)}
AGLPVIMCLKSNNHQKYLRYQSDNIQQYGLLQFSADKILDPLAQFEVEPSKTYDGLVHIKSRYTN
KYLVRWSPNHYWITASANEPDENKSNWACTLFKPLYVEEGNMKKVRLLHVQLGHYTQNYTVGGSF
VSYLFAESSQIDTGSKDVFHVID
>d1jlxa2 b.42.3.1 (A:154-299) Agglutinin {Love-lies-bleeding
(Amaranthus caudatus)}
WKSIFQFPKGYVTFKGNNGKYLGVITINQLPCLQFGYDNLNDPKVAHQMFVTSNGTICIKSNYMN
KFWRLSTDDWILVDGNDPRETNEAAALFRSDVHDFNVISLLNMQKTWFIKRFTSGKPGFINCMNA
ATQNVDETAILEIIEL
>d1wba__ b.42.4.1 (-) Winged bean albumin 1 {Goa bean (Psophocarpus
tetragonolobus)}
DDPVYDAEGNKLVNRGKYTIVSFSDGAGIDVVATGNENPEDPLSIVKSTRNIMYATSISSEDKTP
PQPRNILENMRLKINFATDPHKGDVWSVVDFQPDGQQLKLAGRYPNQVKGAFTIQKGSNTPRTYK
LLFCPVGSPCKNIGISTDPEGKKRLVVSYQSDPLVVKFHRH
>d1tie__ b.42.4.1 (-) Erythrina cafra trypsin inhibitor {Erythrina
caffra}
VLLDGNGEVVQNGGTYYLLPQVWAQGGGVQLAKTGEETCPLTVVQSPNELSDGKPIRIESRLRSA
FIPDDDKVRIGFAYAPKCAPSPWWTVVEDEQEGLSVKLSEDESTQFDYPFKFEQVSDQLHSYKLL
YCEGKHEKCASIGINRDQKGYRRLVVTEDYPLTVVLKKDE
>d1eyla_ b.42.4.1 (A:) chymotrypsin inhibitor WCI {Winged bean
(Psophocarpus tetragonolobus)}
EFDDDLVDAEGNLVENGGTYYLLPHIWAHGGGIETAKTGNEPCPLTVVRSPNEVSKGEPIRISSQ
FLSLFIPRGSLVALGFANPPSCAASPWWTVVDSPQGPAVKLSQQKLPEKDILVFKFEKVSHSNIH
VYKLLYCQHDEEDVKCDQYIGIHRDRNGNRRLVVTEENPLELVLLKAKS
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>d1avwb_ b.42.4.1 (B:) Soybean trypsin inhibitor {Soybean (Glycine max)}
DFVLDNEGNPLENGGTYYILSDITAFGGIRAAPTGNERCPLTVVQSRNELDKGIGTIISSPYRIR
FIAEGHPLSLKFDSFAVIMLCVGIPTEWSVVEDLPEGPAVKIGENKDAMDGWFRLERVSEFNNYK
LVFCPQDKCGDIGISIDHDDGTRRLVVSKNKPLVVQFQKLD
>d1avac_ b.42.4.1 (C:) Amylase/subtilisin inhibitor {Barley (Hordeum vulgare), seed}
ADPPPVHDTDGHELRADANYYVLSANRAHGGGLTMAPGHGRHCPLFVSQDPNGQHDGFPVRITPY
GVAPSDKIIRLSTDVRISFRAYTTCLQSTEWHIDSELAAGRRHVITGPVKDPSPSGRENAFRIEK
YSGAEVHEYKLMSCGDWCQDLGVFRDLKGGAWFLGATEPYHVVVFKKAPPA
>d1a8d_2 b.42.4.2 (248-452) Tetanus neurotoxin {Clostridium tetani}
ITFLRDFWGNPLRYDTEYYLIPVASSSKDVQLKNITDYMYLTNAPSYTNGKLNIYYRRLYNGLKF
IIKRYTPNNEIDSFVKSGDFIKLYVSYNNNEHIVGYPKDGNAFNNLDRILRVGYNAPGIPLYKKM
EAVKLRDLKTYSVQLKLYDDKNASLGLVGTHNGQIGNDPNRDILIASNWYFNHLKDKILGCDWYF
VPTDEGWTND
>d3btaa2 b.42.4.2 (A:1079-1295) Botulinum neurotoxin {Clostridium botulinum, serotype A}
NEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVM
TTNIYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSAL
EIPDVGNLSQVVVMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERS
SRTLGCSWEFIPVDDGWGERPL
>d1epwa2 b.42.4.2 (A:1080-1290) Botulinum neurotoxin {Clostridium botulinum, serotype B}
SEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKF
IIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEFYNTIQI
KEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLK
LGCNWQFIPKDEGWTE
>d1dfca1 b.42.5.1 (A:1008-1140) Fascin {Human (Homo sapiens)}
EAVQIQFGLINCGNKYLTAEAFGFKVNASASSLKKKQIWTLEQPPDEAGSAAVCLRSHLGRYLAA
DKDGNVTCEREVPGPDCRFLIVAHDDGRWSLQSEAHRRYFGGTEDRLSCFAQTVSPAEKWSVHIA
MHP
>d1dfca2 b.42.5.1 (A:1141-1259) Fascin {Human (Homo sapiens)}
QVNIYSVTRKRYAHLSARPADEIAVDRDVPWGVDSLITLAFQDQRYSVQTADHRFLRHDGRLVAR
PEPATGYTLEFRSGKVAFRDCEGRYLAPSGPSGTLKAGKATKVGKDELFALEQS
>d1dfca3 b.42.5.1 (A:1260-1382) Fascin {Human (Homo sapiens)}
CAQVVLQAANERNVSTRQGMDLSANQDEETDQETFQLEIDRDTKKCAFRTHTGKYWTLTATGGVQ
STASSKNASCYFDIEWRDRRITLRASNGKFVTSKKNGQLAASVETAGDSELFLMKLIN
>d1dfca4 b.42.5.1 (A:1383-1493) Fascin {Human (Homo sapiens)}
RPIIVFRGEHGFIGCRKVTGTLDANRSSYDVFQLEFNDGAYNIKDSTGKYWTVGSDSAVTSSGDT
PVDFFFEFCDYNKVAIKVGGRYLKGDHAGVLKASAETVDPASLWEY
>d1hcd__ b.42.5.2 (-) Histidine-rich actin-binding protein (hisactophilin) {Dictyostelium discoideum}
MGNRAFKSHHGHFLSAEGEAVKTHHGHHDHHTHFHVENHGGKVALKTHCGKYLSIGDHKQVYLSH
HLHGDHSLFHLEHHGGKVSIKGHHHHYISADHHGHVSTKEHHDHDTTFEEIII
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>d1i8da1 b.43.4.3 (A:1-93) Riboflavin synthase {Escherichia coli}
MFTGIVQGTAKLVSIDEKPNFRTHVVELPDHMLDGLETGASVAHNGCCLTVTEINGNHVSFDLMK
ETLRITNLGDLKVGDWVNVERAAKFSDE
>d1i8da2 b.43.4.3 (A:94-206) Riboflavin synthase {Escherichia coli}
IGGHLMSGHIMTTAEVAKILTSENNRQIWFKVQDSQLMKYILYKGFIGIDGISLTVGEVTPTRFC
VHLIPETLERTTLGKKKLGARVNIEIDPQTQAVVDTVERVLAARENAM
>d1fnc_1 b.43.4.2 (19-154) Ferredoxin reductase (flavodoxin reductase)
N-terminal domain {Spinach (Spinacia oleracea)}
HSKKMEEGITVNKFKPKTPYVGRCLLNTKITGDDAPGETWHMVFSHEGEIPYREGQSVGVIPDGE
DKNGKPHKLRLYSIASSALGDFGDAKSVSLCVKRLIYTNDAGETIKGVCSNFLCDLKPGAEVKLT
GPVGKE
>d1qfza1 b.43.4.2 (A:1-153) Ferredoxin reductase (flavodoxin
reductase) N-terminal domain {Garden pea (Pisum sativum)}
QVTTEAPAKVVKHSKKQDENIVVNKFKPKEPYVGRCLLNTKITGDDAPGETWHMVFSTEGEVPYR
EGQSIGIVPDGIDKNGKPHKLRLYSIASSAIGDFGDSKTVSLCVKRLVYTNDAGEVVKGVCSNFL
CDLKPGSEVKITGPVGKEMLMPK
>d1fb3a1 b.43.4.2 (A:67-207) Ferredoxin reductase (flavodoxin
reductase) N-terminal domain {Paprika (Capsicum annuum)}
ISKKQDEGVVVNKFRPKEPYIGRCLLNTKITGDDAPGETWHMVFSTEGEIPYREGQSIGVIADGV
DANGKPHKLRLYSIASSALGDFGDSKTVSLCVKRLVYTNDKGEEVKGVCSNFLCDLKPGADVKIT
GPVGKEMLMPK
>d1gawa1 b.43.4.2 (A:11-156) Ferredoxin reductase (flavodoxin
reductase) N-terminal domain {Maize (Zea mays), leaf isoform}
PATAKAKKESKKQEEGVVTNLYKPKEPYVGRCLLNTKITGDDAPGETWHMVFSTEGKIPYREGQS
IGVIADGVDKNGKPHKVRLYSIASSAIGDFGDSKTVSLCVKRLIYTNDAGEIVKGVCSNFLCDLQ
PGDNVQITGPVGKEML
>d1jb9a1 b.43.4.2 (A:6-162) Ferredoxin reductase (flavodoxin
reductase) N-terminal domain {Maize (Zea mays), root isoform}
SRSKVSVAPLHLESAKEPPLNTYKPKEPFTATIVSVESLVGPKAPGETCHIVIDHGGNVPYWEGQ
SYGVIPPGENPKKPGAPQNVRLYSIASTRYGDNFDGRTGSLCVRRAVYYDPETGKEDPSKNGVCS
NFLCNSKPGDKIQLTGPSGKIMLLPEE
>d1que_1 b.43.4.2 (1-141) Ferredoxin reductase (flavodoxin reductase)
N-terminal domain {Cyanobacterium (Anabaena sp.), pcc 7119}
TQAKAKHADVPVNLYRPNAPFIGKVISNEPLVKEGGIGIVQHIKFDLTGGNLKYIEGQSIGIIPP
GVDKNGKPEKLRLYSIASTRHGDDVDDKTISLCVRQLEYKHPESGETVYGVCSTYLTHIEPGSEV
KITGPVGKEML
>d1fdr_1 b.43.4.2 (2-100) Ferredoxin reductase (flavodoxin reductase)
N-terminal domain {Escherichia coli}
ADWVTGKVTKVQNWTDALFSLTVHAPVLPFTAGQFTKLGLEIDGERVQRAYSYVNSPDNPDLEFY
LVTVPDGKLSPRLAALKPGDEVQVVSEAAGFFVL
>d1a8p_1 b.43.4.2 (2-100) Ferredoxin reductase (flavodoxin reductase)
N-terminal domain {Azotobacter vinelandii}
SNLNVERVLSVHHWNDTLFSFKTTRNPSLRFENGQFVMIGLEVDGRPLMRAYSIASPNYEEHLEF
FSIKVQNGPLTSRLQHLKEGDELMVSRKPTGTLV
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>d1qfja1 b.43.4.2 (A:1-97) NAD(P)H:flavin oxidoreductase {Escherichia coli}
TTLSCKVTSVEAITDTVYRVRIVPDAAFSFRAGQYLMVVMDERDKRPFSMASTPDEKGFIELHIG
ASEINLYAKAVMDRILKDHQIVVDIPHGEAWL
>d2cnd_1 b.43.4.2 (11-124) Nitrate reductase core domain {Corn (Zea mays)}
GRIHCRLVAKKELSRDVRLFRFSLPSPDQVLGLPIGKHIFVCATIEGKLCMRAYTPTSMVDEIGH
FDLLVKVYFKNEHPKFPNGGLMTQYLDSLPVGSYIDVKGPLGHVEYTGR
>d1ndh_1 b.43.4.2 (3-125) cytochrome b5 reductase {Pig (Sus scrofa), liver}
PAITLENPDIKYPLRLIDKEVVNHDTRRFRFALPSPEHILGLPVGQHIYLSARIDGNLVIRPYTP
VSSDDDKGFVDLVIKVYFKDTHPKFPAGGKMSQYLESMKIGDTIEFRGPNGLLVYQGK
>d1i7pa1 b.43.4.2 (A:29-153) cytochrome b5 reductase {Rat (Rattus norvegicus)}
HHHMITLENPDIKYPLRLIDKEILSHDTRRFRFALPSPQHILGLPIGQHIYLSTRIDGNLVIRPY
TPVSSDDDKGFVDLVVKVYFKETHPKFPAGGKMSQYLENMNIGDTIEFRGPNGLLVYQGK
>d2pia_1 b.43.4.2 (1-103) Phthalate dioxygenase reductase {Pseudomonas cepacia, db01}
TTPQEDGFLRLKIASKEKIARDIWSFELTDPQGAPLPPFEAGANLTVAVPNGSRRTYSLCNDSQE
RNRYVIAVKRDSNGRGGSISFIDDTSEGDAVEVSLPRN
>d1ep3b1 b.43.4.2 (B:2-102) Dihydroorotate dehydrogenase B, PyrK subunit {Lactococcus lactis, isozyme B}
SQLQEMMTVVSQREVAYNIFEMVLKGTLVDEMDLPGQFLHLAVPNGAMLLRRPISISSWDKRAKT
CTILYRIGDETTGTYKLSKLESGAKVDVMGPLGNGF
>d1cqxa2 b.43.4.2 (A:151-261) Flavohemoglobin, central domain {Alcaligenes eutrophus}
WKGWRTFVIREKRPESDVITSFILEPADGGPVVNFEPGQYTSVAIDVPALGLQQIRQYSLSDMPN
GRTYRISVKREGGGPQPPGYVSNLLHDHVNVGDQVKLAAPYGSFHI
>d1ja1a1 b.43.4.1 (A:240-518) NADPH-cytochrome p450 reductase {Rat (Rattus norvegicus)}
SSIRQYELVVHEDMDVAKVYTGEMGRLKSYENQKPPFDAKNPFLAAVTANRKLNQGTERHLMHLE
LDISDSKIRYESGDHVAVYPANDSALVNQIGEILGADLDVIMSLNNLDEESNKKHPFPCPTTYRT
ALTYYLDITNPPRTNVLYELAQYASEPSEQEHLHKMASSSGEGKELYLSWVVEARRHILAILQDY
PSLRPPIDHLCELLPRLQARYYAIASSSKVHPNSVHICAVAVEYEAKSGRVNKGVATSWLRAKEP
AGENGGRALVPMFVRKSQF
>d1ddga1 b.43.4.1 (A:226-446) Sulfite reductase flavoprotein {Escherichia coli}
IHTSPYSKDAPLVASLSVNQKITGRNSEKDVRHIEIDLGDSGLRYQPGDALGVWYQNDPALVKEL
VELLWLKGDEPVTVEGKTLPLNEALQWHFELTVNTANIVENYATLTRSETLLPLVGDKAKLQHYA
ATTPIVDMVRFSPAQLDAEALINLLRPLTPRLYSIASSQAEVENEVHVTVGVVRYDVEGRARAGG
ASSFLADRVEEEGEVRVFIEHNDNFR
>d1f20a1 b.43.4.1 (A:963-1232) Neuronal nitric-oxide synthase FAD/NADP+ domain {Rat (Rattus norvegicus)}
SWKRNKFRLTYVAEAPDLTQGLSNVHKKRVSAARLLSRQNLQSPKSSRSTIFVRLHTNGNQELQY
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QPGDHLGVFPGNHEDLVNALIERLEDAPPANHVVKVEMLEERNTALGVISNWKDESRLPPCTIFQ
AFKYYLDITTPPTPLQLQQFASLATNEKEKQRLLVLSKGLQEYEEWKWGKNPTMVEVLEEFPSIQ
MPATLLLTQLSLLQPRYYSISSSPDMYPDEVHLTVAIVSYHTRDGEGPVHHGVCSSWLNRIQADD
VVPCFVRGAP
>d1fuia1 b.43.2.1 (A:356-591) L-fucose isomerase, C-terminal domain
{Escherichia coli}
AQVFADVRTYWSPEAIERVTGHKLDGLAEHGIIHLINSGSAALDGSCKQRDSEGNPTMKPHWEIS
QQEADACLAATEWCPAIHEYFRGGGYSSRFLTEGGVPFTMTRVNIIKGLGPVLQIAEGWSVELPK
DVHDILNKRTNSTWPTTWFAPRLTGKGPFTDVYSVMANWGANHGVLTIGHVGADFITLASMLRIP
VCMHNVEETKVYRPSAWAAHGMDIEGQDYRACQNYGPLYKR
>d1efca1 b.43.3.1 (A:205-296) Elongation factor Tu (EF-Tu), domain
2 {Escherichia coli}
AIDKPFLLPIEDVFSISGRGTVVTGRVERGIIKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGR
AGENVGVLLRGIKREEIERGQVLAKPG
>d1exma1 b.43.3.1 (A:213-312) Elongation factor Tu (EF-Tu), domain
2 {Thermus thermophilus}
PVRDVDKPFLMPVEDVFTITGRGTVATGRIERGKVKVGDEVEIVGLAPETRKTVVTGVEMHRKTL
QEGIAGDNVGVLLRGVSREEVERGQVLAKPGSITP
>d1d2ea1 b.43.3.1 (A:251-348) Elongation factor Tu (EF-Tu), domain
2 {Cow (Bos taurus), mitochondrial}
TRDLEKPFLLPVESVYSIPGRGTVVTGTLERGILKKGDECEFLGHSKNIRTVVTGIEMFHKSLDR
AEAGDNLGALVRGLKREDLRRGLVMAKPGSIQP
>d1f60a1 b.43.3.1 (A:241-334) Elongation factor eEF-1alpha, domain
2 {Baker's yeast (Saccharomyces cerevisiae)}
DKPLRLPLQDVYKIGGIGTVPVGRVETGVIKPGMVVTFAPAGVTTEVKSVEMHHEQLEQGVPGDN
VGFNVKNVSVKEIRRGNVCGDAKNDPPKG
>d1jnya1 b.43.3.1 (A:228-322) Elongation factor eEF-1alpha, domain
2 {Archaeon Sulfolobus solfataricus}
PVDKPLRIPIQDVYSISGVGTVPVGRVESGVLKVGDKIVFMPAGKVGEVRSIETHHTKMDKAEPG
DNIGFNVRGVEKKDIKRGDVVGHPNNPPTV
>d1dar_1 b.43.3.1 (283-400) Elongation factor G (EF-G), domain II
{Thermus thermophilus}
PLDIPPIKGTTPEGEVVEIHPDPNGPLAALAFKIMADPYVGRLTFIRVYSGTLTSGSYVYNTTKG
RKERVARLLRMHANHREEVEELKAGDLGAVVGLKETITGDTLVGEDAPRVILE
>d1g7sa1 b.43.3.1 (A:228-328) Initiation factor IF2/eIF5b, domains
2 and 4 {Archaeon Methanobacterium thermoautotrophicum}
EDSPARGTILEVKEETGLGMTIDAVIYDGILRKDDTIAMMTSKDVISTRIRSLLKPRPLEEMRES
RKKFQKVDEVVAAAGIKIVAPGIDDVMAGSPLRVVT
>d1g7sa2 b.43.3.1 (A:460-587) Initiation factor IF2/eIF5b, domains
2 and 4 {Archaeon Methanobacterium thermoautotrophicum}
IIKPASIRLIPKLVFRQSKPAIGGVEVLTGVIRQGYPLMNDDGETVGTVESMQDKGENLKSASRG
QKVAMAIKDAVYGKTIHEGDTLYVDIPENHYHILKEQLSGDLTDEELDLMDKIAEIKRKKNPD
>d1d1na_ b.43.3.1 (A:) Initiation factor IF2/eIF5b, domains 2 and 4
{Bacillus stearothermophilus}
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YEEKVIGQAEVRQTFKVSKVGTIAGCYVTDGKITRDSKVRLIRQGIVVYEGEIDSLKRYKDDVRE
VAQGYECGLTIKNFNDIKEGDVIEAYVMQEVARA
>d1jj2b_ b.43.3.2 (B:) Ribosomal protein L3 {Archaeon Haloarcula marismortui}
PQPSRPRKGSLGFGPRKRSTSETPRFNSWPSDDGQPGVQGFAGYKAGMTHVVLVNDEPNSPREGM
EETVPVTVIETPPMRAVALRAYEDTPYGQRPLTEVWTDEFHSELDRTLDVPEDHDPDAAEEQIRD
AHEAGDLGDLRLITHTVPDAVPSVPKKKPDVMETRVGGGSVSDRLDHALDIVEDGGEHAMNDIFR
AGEYADVAGVTKGKGTQGPVKRWGVQKRKGKHARQGWRRRIGNLGPWNPSRVRSTVPQQGQTGYH
QRTELNKRLIDIGEGDEPTVDGGFVNYGEVDGPYTLVKGSVPGPDKRLVRFRPAVRPNDQPRLDP
EVRYVSNESNQG
>d1efca2 b.44.1.1 (A:297-393) Elongation factor Tu (EF-Tu) {Escherichia coli}
TIKPHTKFESEVYILSKDEGGRHTPFFKGYRPQFYFRTTDVTGTIELPEGVEMVMPGDNIKMVVT
LIHPIAMDDGLRFAIREGGRTVGAGVVAKVLS
>d1exma2 b.44.1.1 (A:313-405) Elongation factor Tu (EF-Tu) {Thermus thermophilus}
HTKFEASVYVLKKEEGGRHTGFFSGYRPQFYFRTTDVTGVVQLPPGVEMVMPGDNVTFTVELIKP
VALEEGLRFAIREGGRTVGAGVVTKILE
>d1d2ea2 b.44.1.1 (A:349-451) Elongation factor Tu (EF-Tu) {Cow (Bos taurus), mitochondrial}
HQKVEAQVYILTKEEGGRHKPFVSHFMPVMFSLTWDMACRIILPPGKELAMPGEDLKLTLILRQP
MILEKGQRFTLRDGNRTIGTGLVTDTPAMTEEDKNIKW
>d1f60a2 b.44.1.1 (A:335-441) Elongation factor eEF-1alpha, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
CASFNATVIVLNHPGQISAGYSPVLDCHTAHIACRFDELLEKNDRRSGKKLEDHPKFLKSGDAAL
VKFVPSKPMCVEAFSEYPPLGRFAVRDMRQTVAVGVIKSVDK
>d1jnya2 b.44.1.1 (A:323-429) Elongation factor eEF-1alpha, C-terminal domain {Archaeon Sulfolobus solfataricus}
ADEFTARIIVVWHPTALANGYTPVLHVHTASVACRVSELVSKLDPRTGQEAEKNPQFLKQGDVAI
VKFKPIKPLCVEKYNEFPPLGRFAMRDMGKTVGVGIIVDVKP
>d1flma_ b.45.1.1 (A:) FMN-binding protein {Desulfovibrio vulgaris, strain Miyazaki F}
MLPGTFFEVLKNEGVVAIATQGEDGPHLVNTWNSYLKVLDGNRIVVPVGGMHKTEANVARDERVL
MTLGSRKVAGRNGPGTGFLIRGSAAFRTDGPEFEAIARFKWARAALVITVVSAEQTL
>d1ci0a_ b.45.1.1 (A:) Pyridoxine 5'-phoshate oxidase (PNP oxidase) {Baker's yeast (Saccharomyces cerevisiae)}
FTLNEKQLTDDPIDLFTKWFNEAKEDPRETLPEAITFSSAELPSGRVSSRILLFKELDHRGFTIY
SNWGTSRKAHDIATNPNAAIVFFWKDLQRQVRVEGITEHVNRETSERYFKTRPRGSKIGAWASRQ
SDVIKNREELDELTQKNTERFKDAEDIPCPDYWGGLRIVPLEIEFWQGRPSRLHDRFVYRRKTEN
DPWKVVRLAP
>d1dnla_ b.45.1.1 (A:) Pyridoxine 5'-phoshate oxidase (PNP oxidase) {Escherichia coli}
GGLRRRDLPADPLTLFERWLSQACEAKLADPTAMVVATVDEHGQPYQRIVLLKHYDEKGMVFYTN
LGSRKAHQIENNPRVSLLFPWHTLERQVMVIGKAERLSTLEVMKYFHSRPRDSQIGAWVSKQSSR

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ISARGILESKFLELKQKFQQGEVPLPSFWGGFRVSLEQIEFWQGGEHRLHDRFLYQRENDAWKID
RLAP
>d1ejea_ b.45.1.2 (A:) FMN-binding protein MTH152 {Archaeon
Methanobacterium thermoautotrophicum}
GSQAAHMMSMDFEDFPVESAHRILTPRPTVMVTTVDEEGNINAAPFSFTMPVSIDPPVVAFASAP
DHHTARNIESTHEFVINITPADIIERMWVTARDIPAGENELEAAGLAWTSSRRVKPPRIVEAPGH
LECELLRMFEVGDHNLITGSVVSASVRSGAVKEGLLDVESVKPVLHVGGNKFVVGDHVRHVE
>d1i0ra_ b.45.1.2 (A:) Ferric reductase {Archaeon Archaeoglobus
fulgidus}
MDVEAFYKISYGLYIVTSESNGRKCGQIANTVFQLTSKPVQIAVCLNKENDTHNAVKESGAFGVS
VLELETPMEFIGRFGFRKSSEFEKFDGVEYKTGKTGVPLVTQHAVAVIEAKVVKECDVGTHTLFV
GEAVDAEVLKDAEVLTYADYHLMKKGKTPRT
>d1k28d1 b.106.1.1 (D:4-200) Baseplate structural protein gp27
{Bacteriophage T4}
LQRPGYPNLSVKLFDSYDAWSNNRFVELAATITTLTMRDSLYGRNEGMLQFYDSKNIHTKMDGNE
IIQISVANANDINNVKTRIYGCKHFSVSVDSKGDNIIAIELGTIHSIENLKFGRPFFPDAGESIK
EMLGVIYQDRTLLTPAINAINAYVPDIPWTSTFENYLSYVREVALAVGSDKFVFVWQDIMGVNMM
DY
>d1k28d2 b.106.1.1 (D:201-376) Baseplate structural protein gp27
{Bacteriophage T4}
DMMINQEPYPMIVGEPSLIGQFIQELKYPLAYDFVWLTKSNPHKRDPMKNATIYAHSFLDSSIPM
ITTGKGENSIVVSRSGAYSEMTYRNGYEEAIRLQTMAQYDGYAKCSTIGNFNLTPGVKIIFNDSK
NQFKTEFYVDEVIHELSNNNSVTHLYMFTNATKLETIDPVKVKNEF
>d1fmta1 b.46.1.1 (A:207-314) Methionyl-tRNAfmet formyltransferase,
C-terminal domain {Escherichia coli}
LSKEEARIDWSLSAAQLERCIRAFNPWPMSWLEIEGQPVKVWKASVIDTATNAAPGTILEANKQG
IQVATGDGILNLLSLQPAGKKAMSAQDLLNSRREWFVPGNRLV
>d1ewna_ b.46.1.2 (A:) 3-methyladenine DNA glycosylase (AAG, ANPG,
MPG) {Human (Homo sapiens)}
HLTRLGLEFFDQPAVPLARAFLGQVLVRRLPNGTELRGRIVETQAYLGPEDEAAHSRGGRQTPRN
RGMFMKPGTLYVYIIYGMYFCMNISSQGDGACVLLRALEPLEGLETMRQLRSTLRKGTASRVLKD
RELCSGPSKLCQALAINKSFDQRDLAQDEAVWLERGPLEPSEPAVVAAARVGVGHAGEWARKPLR
FYVRGSPWVSVVDRVAEQD
>d1arb__ b.47.1.1 (-) Achromobacter protease {Achromobacter lyticus,
strain m497-1}
GVSGSCNIDVVCPEGDGRRDIIRAVGAYSKSGTLACTGSLVNNTANDRKMYFLTAHHCGMGTAST
AASIVVYWNYQNSTCRAPNTPASGANGDGSMSQTQSGSTVKATYATSDFTLLELNNAANPAFNLF
WAGWDRRDQNYPGAIAIHHPNVAEKRISNSTSPTSFVAWGGGAGTTHLNVQWQPSGGVTEPGSSG
SPIYSPEKRVLGQLHGGPSSCSATGTNRSDQYGRVFTSWTGGGAAASRLSDWLDPASTGAQFIDG
LDS
>d1qq4a_ b.47.1.1 (A:) alpha-Lytic protease {Lysobacter enzymogenes,
495}
ANIVGGIEYSINNASLCSVGFSVTRGATKGFVTAGHCGTVNATARIGGAVVGTFAARVFPGNDRA
WVSLTSAQTLLPRVANGSSFVTVRGSTEAAVGAAVCHSGRTTGYQCGTITAKNVTANYAEGAVRG
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LTQSNACMGRGDSGGSWITSAGQAQGVMSGGNVQSNGNNCGIPASQRSSLFERLQPILSQYGLSL
VTG
>d2sga__ b.47.1.1 (-) Protease A {Streptomyces griseus, strain k1}
IAGGEAITTGGSRCSLGFNVSVNGVAHALTAGHCTNISASWSIGTRTGTSFPNNDYGIIRHSNPA
AADGRVYLYNGSYQDITTAGNAFVGQAVQRSGSTTGLRSGSVTGLNATVNYGSSGIVYGMIQTNV
CAQPGDSGGSLFAGSTALGLTSGGSGNCRTGGTTFYQPVTEALSAYGATVL
>d1hpga_ b.47.1.1 (A:) Glutamic acid-specific protease {Streptomyces
griseus}
VLGGGAIYGGGSRCSAAFNVTKGGARYFVTAGHCTNISANWSASSGGSVVGVREGTSFPTNDYGI
VRYTDGSSPAGTVDLYNGSTQDISSAANAVVGQAIKKSGSTTKVTSGTVTAVNVTVNYGDGPVYN
MVRTTACSAGGDSGGAHFAGSVALGIHSGSSGCSGTAGSAIHQPVTEALSAYGVTVY
>d1sgt__ b.47.1.1 (-) Trypsin {Streptomyces griseus, strain k1}
VVGGTRAAQGEFPFMVRLSMGCGGALYAQDIVLTAAHCVSGSGNNTSITATGGVVDLQSGAAVKV
RSTKVLQAPGYNGTGKDWALIKLAQPINQPTLKIATTTAYNQGTFTVAGWGANREGGSQQRYLLK
ANVPFVSDAACRSAYGNELVANEEICAGYPDTGGVDTCQGDSGGPMFRKDNADEWIQVGIVSWGY
GCARPGYPGVYTEVSTFASAIASAARTL
>d2sfa__ b.47.1.1 (-) Serine proteinase {Streptomyces fradiae}
IAGGEAIYAAGGGRCSLGFNVRSSSGATYALTAGHCTEIASTWYTNSGQTSLLGTRAGTSFPGND
YGLIRHSNASAADGRVYLYNGSYRDITGAGNAYVGQTVQRSGSTTGLHSGRVTGLNATVNYGGGD
IVSGLIQTNVCAEPGDSGGALFAGSTALGLTSGGSGNCRTGGTTFFQPVTEALSAYGVSIL
>d1sgpe_ b.47.1.1 (E:) Protease B {Streptomyces griseus, strain k1}
ISGGDAIYSSTGRCSLGFNVRSGSTYYFLTAGHCTDGATTWWANSARTTVLGTTSGSSFPNNDYG
IVRYTNTTIPKDGTVGGQDITSAANATVGMAVTRRGSTTGTHSGSVTALNATVNYGGGDVVYGMI
RTNVCAEPGDSGGPLYSGTRAIGLTSGGSGNCSSGGTTFFQPVTEALVAYGVSVY
>d1agja_ b.47.1.1 (A:) Epidermolytic (exfoliative) toxin A
{Staphylococcus aureus}
EVSAEEIKKHEEKWNKYYGVNAFNLPKELFSKVDEKDRQKYPYNTIGNVFVKGQTSATGVLIGKN
TVLTNRHIAKFANGDPSKVSFRPSINTDDNGNTETPYGEYEVKEILQEPFGAGVDLALIRLKPDQ
NGVSLGDKISPAKIGTSNDLKDGDKLELIGYPFDHKVNQMHRSEIELTTLSRGLRYYGFTVPGNS
GSGIFNSNGELVGIHSSKVSHLDREHQINYGVGIGNYVKRIINEKNE
>d1qtfa_ b.47.1.1 (A:) Exfoliative toxin B {Staphylococcus aureus}
KEYSAEEIRKLKQKFEVPPTDKELYTHITDNARSPYNSVGTVFVKGSTLATGVLIGKNTIVTNYH
VAREAAKNPSNIIFTPAQNRDAEKNEFPTPYGKFEAEEIKESPYGQGLDLAIIKLKPNEKGESAG
DLIQPANIPDHIDIAKGDKYSLLGYPYNYSAYSLYQSQIEMFNDSQYFGYTEVGNSGSGIFNLKG
ELIGIHSGKGGQHNLPIGVFFNRKISSLYSVDNTFGDTLGNDLKKRAKLDK
>d1ezxc_ b.47.1.2 (C:) Trypsin(ogen) {Cow (Bos taurus)}
CGGSLINSQWVVSAAHCYKSGIQVRLGEDNINVVEGNEQFISASKSIVHPSYNSNTLNNDIMLIK
LKSAASLNSRVASISLPTSCASAGTQCLISGWGNTKSSGTSYPDVLKCLKAPILSDSSCKSAYPG
QITSNMFCAGYLEGGKDSCQGDSGGPVVCSGKLQGIVSWGSGCAQKNKPGVYTKVCNYVSWIKQT
IASN
>d1hj9a_ b.47.1.2 (A:) Trypsin(ogen) {Cow (Bos taurus)}
IVGGYTCGANTVPYQVSLNSGYHFCGGSLINSQWVVSAAHCYKSGIQVRLGEDNINVVEGNEQFI
SASKSIVHPSYNSNTLNNDIMLIKLKSAASLNSRVASISLPTSCASAGTQCLISGWGNTKSSGTS
YPDVLKCLKAPILSDSSCKSAYPGQITSNMFCAGYLEGGKDSCQGDSGGPVVCSGKLQGIVSWGS
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GCAQKNKPGVYTKVCNYVSWIKQTIASN
>d1mcta_ b.47.1.2 (A:) Trypsin(ogen) {Pig (Sus scrofa)}
IVGGYTCAANSIPYQVSLNSGSHFCGGSLINSQWVVSAAHCYKSRIQVRLGEHNIDVLEGNEQFI
NAAKIITHPNFNGNTLDNDIMLIKLSSPATLNSRVATVSLPRSCAAAGTECLISGWGNTKSSGSS
YPSLLQCLKAPVLSNSSCKSSYPGQITGNMICVGFLQGGKDSCQGDSGGPVVCNGQLQGIVSWGY
GCAQKNKPGVYTKVCNYVNWIQQTIAAN
>d1f7za_ b.47.1.2 (A:) Trypsin(ogen) {Rat (Rattus norvegicus)}
IVGGYTCQENSVPYQVSLNSGYHFCGGSLINDQWVVSAAHCYKSRIQVRLGEHNINVLEGNEQFV
NAAKIIKHPNFDRKTLNNDIMLIKLSSPVKLNARVATVALPSSCAPAGTQCLISGWGNTLSSGVN
EPDLLQCLDAPLLPQADCEASYPGKITDNMVCVGFLEGGKDSCQGDSGGPVVCNGELQGIVSWGY
GCALPDNPGVYTKVCNYVDWIQDTIAAN
>d1trna_ b.47.1.2 (A:) Trypsin(ogen) {Human (Homo sapiens)}
IVGGYNCEENSVPYQVSLNSGYHFCGGSLINEQWVVSAGHCYKSRIQVRLGEHNIEVLEGNEQFI
NAAKIIRHPQYDRKTLNNDIMLIKLSSRAVINARVSTISLPTAPPATGTKCLISGWGNTASSGAD
YPDELQCLDAPVLSQAKCEASYPGKITSNMFCVGFLEGGKDSCQGDSGGPVVCNGQLQGVVSWGD
GCAQKNKPGVYTKVYNYVKWIKNTIAANS
>d1h4wa_ b.47.1.2 (A:) Trypsin(ogen) {Human (Homo sapiens), trypsin
IV (brain isoform)}
IVGGYTCEENSLPYQVSLNSGSHFCGGSLISEQWVVSAAHCYKTRIQVRLGEHNIKVLEGNEQFI
NAVKIIRHPKYNRDTLDNDIMLIKLSSPAVINARVSTISLPTAPPAAGTECLISGWGNTLSFGAD
YPDELKCLDAPVLTQAECKASYPGKITNSMFCVGFLEGGKDSCQRDSGGPVVCNGQLQGVVSWGH
GCAWKNRPGVYTKVYNYVDWIKDTIAANS
>d1a0ja_ b.47.1.2 (A:) Trypsin(ogen) {North atlantic salmon (Salmo
salar)}
IVGGYECRKNSASYQASLQSGYHFCGGSLISSTWVVSAAHCYKSRIQVRLGEHNIAVNEGTEQFI
DSVKVIMHPSYNSRNLDNDIMLIKLSKPASLNSYVSTVALPSSCASSGTRCLVSGWGNLSGSSSN
YPDTLRCLDLPILSSSSCNSAYPGQITSNMFCAGFMEGGKDSCQGDSGGPVVCNGQLQGVVSWGY
GCAQRNKPGVYTKVCNYRSWISSTMSSN
>d1hj8a_ b.47.1.2 (A:) Trypsin(ogen) {North atlantic salmon (Salmo
salar)}
IVGGYECKAYSQPHQVSLNSGYHFCGGSLVNENWVVSAAHCYKSRVEVRLGEHNIKVTEGSEQFI
SSSRVIRHPNYSSYNIDNDIMLIKLSKPATLNTYVQPVALPTSCAPAGTMCTVSGWGNTMSSTAD
SNKLQCLNIPILSYSDCNNSYPGMITNAMFCAGYLEGGKDSCQGDSGGPVVCNGELQGVVSWGYG
CAEPGNPGVYAKVCIFNDWLTSTMASY
>d1gdna_ b.47.1.2 (A:) Trypsin(ogen) {Mold (Fusarium oxysporum)}
IVGGTSASAGDFPFIVSISRNGGPWCGGSLLNANTVLTAAHCVSGYAQSGFQIRAGSLSRTSGGI
TSSLSSVRVHPSYSGNNNDLAILKLSTSIPSGGNIGYARLAASGSDPVAGSSATVAGWGATSEGG
SSTPVNLLKVTVPIVSRATCRAQYGTSAITNQMFCAGVSSGGKDSCQGDSGGPIVDSSNTLIGAV
SWGNGCARPNYSGVYASVGALRSFIDTYA
>d1pytd_ b.47.1.2 (D:) (alpha,gamma)-chymotrypsin(ogen) {Cow (Bos
taurus)}
CGAPIFQPNLSARVVGGEDAIPHSWPWQISLQYLRDNTWRHTCGGTLITPNHVLTAAHCISNTLT
YRVALGKNNLEVEDEAGSLYVGVDTIFVHEKWNSFLVRNDIALIKLAETVELGDTIQVACLPSEG
SLLPQDYPCFVTGWGRLYTNGPIAAELQQGLQPVVDYATCSQRDWWGTTVKETMVCAGGDGVISA
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CNGDSGGPLNCQADGQWDVRGIVSFGSGLSCNTFKKPTVFTRVSAYIDWINQKLQL
>g1gg6.1 b.47.1.2 (A:,B:,C:) (alpha,gamma)-chymotrypsin(ogen) {Cow
(Bos taurus)}
CGVPAIQPVLXIVNGEEAVPGSWPWQVSLQDKTGFHFCGGSLINENWVVTAAHCGVTTSDVVVAG
EFDQGSSSEKIQKLKIAKVFKNSKYNSLTINNDITLLKLSTAASFSQTVSAVCLPSASDDFAAGT
TCVTTGWGLTRYXANTPDRLQQASLPLLSNTNCKKYWGTKIKDAMICAGASGVSSCMGDSGGPLV
CKKNGAWTLVGIVSWGSSTCSTSTPGVYARVTALVNWVQQTLAAN
>d1eq9a_ b.47.1.2 (A:) (alpha,gamma)-chymotrypsin(ogen) {Red fire ant
(Solenopsis invicta)}
IVGGKDAPVGKYPYQVSLRLSGSHRCGASILDNNNVLTAAHCVDGLSNLNRLKVHVGTNYLSESG
DVYDVEDAVVNKNYDDFLLRNDVALVHLTNPIKFNDLVQPIKLSTNDEDLESNPCTLTGWGSTRL
GGNTPNALQEIELIVHPQKQCERDQWRVIDSHICTLTKRGEGACHGDSGGPLVANGAQIGIVSFG
SPCALGEPDVYTRVSSFVSWINANLKK
>d1npma_ b.47.1.2 (A:) Neuropsin {Mouse (Mus musculus)}
ILEGRECIPHSQPWQAALFQGERLICGGVLVGDRWVLTAAHCKKQKYSVRLGDHSLQSRDQPEQE
IQVAQSIQHPCYNNSNPEDHSHDIMLIRLQNSANLGDKVKPVQLANLCPKVGQKCIISGWGTVTS
PQENFPNTLNCAEVKIYSQNKCERAYPGKITEGMVCAGSSNGADTCQGDSGGPLVCDGMLQGITS
WGSDPCGKPEKPGVYTKICRYTTWIKKTMD
>d1azza_ b.47.1.2 (A:) Crab collagenase {Atlantic sand fiddler crab
(Uca pugilator)}
IVGGVEAVPNSWPHQAALFIDDMYFCGGSLISPEWILTAAHCMDGAGFVDVVLGAHNIREDEATQ
VTIQSTDFTVHENYNSFVISNDIAVIRLPVPVTLTAAIATVGLPSTDVGVGTVVTPTGWGLPSDS
ALGISDVLRQVDVPIMSNADCDAVYGIVTDGNICIDSTGGKGTCNGDSGGPLNYNGLTYGITSFG
AAAGCEAGYPDAFTRVTYFLDWIQTQTGITP
>d2hlca_ b.47.1.2 (A:) HL collagenase {Common cattle grub (Hypoderma
lineatum)}
IINGYEAYTGLFPYQAGLDITLQDQRRVWCGGSLIDNKWILTAAHCVHDAVSVVVYLGSAVQYEG
EAVVNSERIISHSMFNPDTYLNDVALIKIPHVEYTDNIQPIRLPSGEELNNKFENIWATVSGWGQ
SNTDTVILQYTYNLVIDNDRCAQEYPPGIIVESTICGDTSDGKSPCFGDSGGPFVLSDKNLLIGV
VSFVSGAGCESGKPVGFSRVTSYMDWIQQNTGIKF
>g1h8d.1 b.47.1.2 (L:,H:) Thrombin {Human (Homo sapiens)}
EADCGLRPLFEKKSLEDKTERELLESYISXIVEGSDAEIGMSPWQVMLFRKSPQELLCGASLISD
RWVLTAAHCLLYPPWDKNFTENDLLVRIGKHSRTRYERNIEKISMLEKIYIHPRYNWRENLDRDI
ALMKLKKPVAFSDYIHPVCLPDRETAASLLQAGYKGRVTGWGNLKETGQPSVLQVVNLPIVERPV
CKDSTRIRITDNMFCAGYKPDEGKRGDACEGDSGGPFVMKSPFNNRWYQMGIVSWGEGCDRDGKY
GFYTHVFRLKKWIQKVIDQFGCSSVLIVVC
>g1jou.1 b.47.1.2 (A:,B:) Thrombin {Human (Homo sapiens)}
SEYQTFFNPRTFGSGEADCGLRPLFEKKSLEDKTERELLESYIDGXIVEGSDAEIGMSPWQVMLF
RKSPQELLCGASLISDRWVLTAAHCLLYPPWDKNFTENDLLVRIGKHSRTRYERNIEKISMLEKI
YIHPRYNWRENLDRDIALMKLKKPVAFSDYIHPVCLPDRETAASLLQAGYKGRVTGWGNLKETWT
ANVGKGQPSVLQVVNLPIVERPVCKDSTRIRITDNMFCAGYKPDEGKRGDACEGDAGGPFVMKSP
FNNRWYQMGIVSWGEGCDRDGKYGFYTHVFRLKKWIQKVIDQFGE
>g1vr1.1 b.47.1.2 (L:,H:) Thrombin {Human (Homo sapiens)}
ADCGLRPLFEKKSLEDKTERELLESYIXIVEGSDAEIGMSPWQVMLFAKHRRSPGERFLCGASLI
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SDRWVLTAAHCLLYPPWDKNFTENDLLVRIGKHSRTRYERNIEKISMLEKIYIHPRYNWRENLDR
DIALMKLKKPVAFSDYIHPVCLPDRETAASLLQAGYKGRVTGWGNLKETWTANVGKGQPSVLQVV
NLPIVERPVCKDSTRIRITDNMFCAYYKPDEGKRGDACEGDSGGPFVMKSPFNNRWYQMGIVSWG
EGCDRDGKYGFYTHVFRLKKWIQKVID
>g2hnt.1 b.47.1.2 (L:,C:,E:,F:) Thrombin {Human (Homo sapiens)}
ADCGLRPLFEKKSLEDKTERELLESYIDXIVEGSDAEIGMSPWQVMLFRKSPQELLCGASLISDR
WVLTAAHCLLYPPWDKNFTENDLLVRIGKHSXEKISMLEKIYIHPRYNWRENLDRDIALMKLKKP
VAFSDYIHPVCLPDRETAASLLQAGYKGRVTGWGXPSVLQVVNLPIVERPVCKDSTRIRITDNMF
CAGYKPDEGKRGDACEGDSGGPFVMKSPFNNRWYQMGIVSWGEGCDRDGKYGFYTHVFRLKKWIQ
KVIDQ
>g1etr.1 b.47.1.2 (L:,H:) Thrombin {Cow (Bos taurus)}
TFGAGEADCGLRPLFEKKQVQDQTEKELFESYIEGRXIVEGQDAEVGLSPWQVMLFRKSPQELLC
GASLISDRWVLTAAHCLLYPPWDKNFTVDDLLVRIGKHSRTRYERKVEKISMLDKIYIHPRYNWK
ENLDRDIALLKLKRPIELSDYIHPVCLPDKQTAAKLLHAGFKGRVTGWGNRRETWTTSVAEVQPS
VLQVVNLPLVERPVCKASTRIRITDNMFCAGYKPGEGKRGDACEGDSGGPFVMKSPYNNRWYQMG
IVSWGEGCDRDGKYGFYTHVFRLKKWIQKVIDRLGS
>d1fona_ b.47.1.2 (A:) Procarboxypeptidase A-S6 subunit III (zymogen
E) {Cow (Bos taurus)}
SWSWQVSLQYEKDGAFHHTCGGSLIAPDWVVTAGHCISTSRTYQVVLGEYDRSVLEGSEQVIPIN
AGDLFVHPLWNSNCVACGNDIALVKLSRSAQLGDKVQLANLPPAGDILPNEAPCYISGWGRLYTG
GPLPDKLQQALLPTVDYEHCSQWDWWGITVKKTMVCAGGDTRSGCNGDSGGPLNCPAADGSWQVH
GVTSFVSAFGCNTIKKPTVFTRVSAFIDWIDETIASN
>d1pytc_ b.47.1.2 (C:) Procarboxypeptidase A-S6 subunit III (zymogen
E) {Cow (Bos taurus)}
SRPSSRVVNGEDAVPYSWSWQVSLQYEKDGAFHHTCGGSLIAPDWVVTAGHCISTSRTYQVVLGE
YDRSVLQGSEQVIPINAGDLFVHPLWNSNCVACGNDIALVKLSRSAQLGDKVQLANLPPAGDILP
NEAPCYISGWGRLYTGGPLPDKLQEALLPVVDYEHCSQYDWWGITVKKTMVCAGGDTRSGCDGDS
GGPLNCPAADGSWQVHGVTSFVSAFGCNTIKKPTVFTRVSAFIDWINETIASN
>d1ppfe_ b.47.1.2 (E:) Elastase {Human (Homo sapiens)}
IVGGRRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNLSRREP
TRQVFAVQRIFENGYDPVNLLNDIVILQLNGSATINANVQVAQLPAQGRRLGNGVQCLAMGWGLL
GRNRGIASVLQELNVTVVTSLCRRSNVCTLVRGRQAGVCFGDSGSPLVCNGLIHGIASFVRGGCA
SGLYPDAFAPVAQFVNWIDSIIQ
>d1brup_ b.47.1.2 (P:) Elastase {Pig (Sus scrofa)}
VVGGEDARPNSWPWQVSLQYDSSGQWRHTCGGTLVDQSWVLTAAHCISSSRTYRVVLGRHSLSTN
EPGSLAVKVSKLVVHQDWNSNQLSNGNDIALLKLASPVSLTDKIQLGCLPAAGTILPNNYVCYVT
GWGRLQTNGASPDILQQGQLLVVDYATCSKPGWWGSTVKTNMICAGGDGIISSCNGDSGGPLNCQ
GANGQWQVHGIVSFGSSLGCNYYHKPSVFTRVSNYIDWINSVIANN
>d1qnja_ b.47.1.2 (A:) Elastase {Pig (Sus scrofa)}
VVGGTEAQRNSWPSQISLQYRSGSSWAHTCGGTLIRQNWVMTAAHCVDRELTFRVVVGEHNLNQN
DGTEQYVGVQKIVVHPYWNTDDVAAGYDIALLRLAQSVTLNSYVQLGVLPRAGTILANNSPCYIT
GWGLTRTNGQLAQTLQQAYLPTVDYAICSSSSYWGSTVKNSMVCAGGDGVRSGCQGDSGGPLHCL
VNGQYAVHGVTSFVSRLGCNVTRKPTVFTRVSAYISWINNVIASN
>d1elt__ b.47.1.2 (-) Elastase {Salmon (Salmo salar)}
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VVGGRVAQPNSWPWQISLQYKSGSSYYHTCGGSLIRQGWVMTAAHCVDSARTWRVVLGEHNLNTN
EGKEQIMTVNSVFIHSGWNSDDVAGGYDIALLRLNTQASLNSAVQLAALPPSNQILPNNNPCYIT
GWGKTSTGGPLSDSLKQAWLPSVDHATCSSSGWWGSTVKTTMVCAGGGANSGCNGDSGGPLNCQV
NGSYYVHGVTSFVSSSGCNASKKPTVFTRVSAYISWMNGIM
>d1ekbb_ b.47.1.2 (B:) Enteropeptidase (enterokinase light chain)
{Cow (Bos taurus)}
IVGGSDSREGAWPWVVALYFDDQQVCGASLVSRDWLVSAAHCVYGRNMEPSKWKAVLGLHMASNL
TSPQIETRLIDQIVINPHYNKRRKNNDIAMMHLEMKVNYTDYIQPICLPEENQVFPPGRICSIAG
WGALIYQGSTADVLQEADVPLLSNEKCQQQMPEYNITENMVCAGYEAGGVDSCQGDSGGPLMCQE
NNRWLLAGVTSFGYQCALPNRPGVYARVPRFTEWIQSFLH
>d1a7s__ b.47.1.2 (-) Heparin binding protein, HBP {Human (Homo
sapiens)}
IVGGRKARPRQFPFLASIQNQGRHFCGGALIHARFVMTAASCFPGVSTVVLGAYDLRRRERQSRQ
TFSISSMSENGYDPQQNLNDLMLLQLDREANLTSSVTILPLPLQNATVEAGTRCQVAGWGSQRSG
GRLSRFPRFVNVTVTPEDQCRPNNVCTGVLTRRGGICNGDGGTPLVCEGLAHGVASFSLGPCGRG
PDFFTRVALFRDWIDGVLNNPGPGPA
>d1a0la_ b.47.1.2 (A:) beta-Tryptase {Human (Homo sapiens)}
IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAHCVGPDVKDLAALRVQLREQHL
YYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFPPGMPCWVTGW
GDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDMLCAGNTRRDSCQGDSG
GPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHYVPKK
>d1cgha_ b.47.1.2 (A:) Cathepsin G {Human (Homo sapiens)}
IIGGRESRPHSRPYMAYLQIQSPAGQSRCGGFLVREDFVLTAAHCWGSNINVTLGAHNIQRRENT
QQHITARRAIRHPQYNQRTIQNDIMLLQLSRRVRRNRNVNPVALPRAQEGLRPGTLCTVAGWGRV
SMRRGTDTLREVQLRVQRDRQCLRIFGSYDPRRQICVGDRRERKAAFKGDSGGPLLCNNVAHGIV
SYGKSSGVPPEVFTRVSSFLPWIRTTMRS
>d1danh_ b.47.1.2 (H:) Coagulation factor VIIa {Human (Homo sapiens)}
IVGGKVCPKGECPWQVLLLVNGAQLCGGTLINTIWVVSAAHCFDKIKNWRNLIAVLGEHDLSEHD
GDEQSRRVAQVIIPSTYVPGTTNHDIALLRLHQPVVLTDHVVPLCLPERTFSERTLAFVRFSLVS
GWGQLLDRGATALELMVLNVPRLMTQDCLQQSRKVGDSPNITEYMFCAGYSDGSKDSCKGDSGGP
HATHYRGTWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQKLMRSEPRPGVLLRAPFP
>d3rp2a_ b.47.1.2 (A:) Chymase (Proteinase II) {Rat (Rattus rattus)}
IIGGVESIPHSRPYMAHLDIVTEKGLRVICGGFLISRQFVLTAAHCKGREITVILGAHDVRKRES
TQQKIKVEKQIIHESYNSVPNLHDIMLLKLEKKVELTPAVNVVPLPSPSDFIHPGAMCWAAGWGK
TGVRDPTSYTLREVELRIMDEKACVDYRYYEYKFQVCVGSPTTLRAAFMGDSGGPLLCAGVAHGI
VSYGHPDAKPPAIFTRVSTYVPWINAVIN
>d1klt__ b.47.1.2 (-) Chymase (Proteinase II) {Human (Homo sapiens)}
IIGGTESKPHSRPYMAYLEIVTSNGPSKFCGGFLIRRNFVLTAAHCAGRSITVTLGAHNITEEED
TWQKLEVIKQFRHPKYNTSTLHHDIMLLKLKEKASLTLAVGTLPFPSQFNFVPPGRMCRVAGWGR
TGVLKPGSDTLQEVKLRLMDPQACSHFRDFDHNLQLCVGNPRKTKSAFKGDSGGPLLCAGVAQGI
VSYGRSDAKPPAVFTRISHYRPWINQILQAN
>g2pka.1 b.47.1.2 (A:,B:) Kallikrein A {Pig (Sus scrofa)}
IIGGRECEKNSHPWQVAIYHYSSFQCGGVLVNPKWVLTAAHCKNDNYEVWLGRHNLFENENTAQF
FGVTADFPHPGFNLSXADGKDYSHDLMLLRLQSPAKITDAVKVLELPTQEPELGSTCEASGWGSI
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EPGPDDFEFPDEIQCVQLTLLQNTFCADAHPDKVTESMLCAGYLPGGKDTCMGDSGGPLICNGMW
QGITSWGHTPCGSANKPSIYTKLIFYLDWIDDTITENP
>d1ton__ b.47.1.2 (-) Tonin {Rat (Rattus rattus)}
IVGGYKCEKNSQPWQVAVINEYLCGGVLIDPSWVITAAHCYSNNYQVLLGRNNLFKDEPFAQRRL
VRQSFRHPDYIPLIVTNDTEQPVHDHSNDLMLLHLSEPADITGGVKVIDLPTKEPKVGSTCLASG
WGSTNPSEMVVSHDLQCVNIHLLSNEKCIETYKDNVTDVMLCAGEMEGGKDTCAGDSGGPLICDG
VLQGITSGGATPCAKPKTPAIYAKLIKFTSWIKKVMKENP
>d1sgfa_ b.47.1.2 (A:) 7S NGF protease subunits {Mouse (Mus musculus)}
NSQPWHVAVYRFNKYQCGGVLLDRNWVLTAAHCYNDKYQVWLGKNNFLEDEPSDQHRLVSKAIPH
PDFNMSLLNEHTPQPEDDYSNDLMLLRLSKPADITDVVKPITLPTEEPKLGSTCLASGWGSTTPI
KYPDDLQCVNLKLLPNEDCDKAHEMKVTDAMLCAGEMDGGSYTCEHDSGGPLICDGILQGITSWG
PEPCGEPTEPSVYTKLIKFSSWIRETMANNP
>d1sgfg_ b.47.1.2 (G:) 7S NGF protease subunits {Mouse (Mus musculus)}
IVGGFKCEKNSQPWHVAVYRYTQYLCGGVLLDPNWVLTAAHCYDDNYKVWLGKNNLFKDEPSAQH
RFVSKAIPHPGFNMSLMRFLEYDYSNDLMLLRLSKPADITDTVKPITLPTEEPKLGSTCLASGWG
SITPTKFQFTDDLYCVNLKLLPNEDCAKAHIEKVTDAMLCAGEMDGGKDTCKGDSGGPLICDGVL
QGITSWGHTPCGEPDMPGVYTKLNKFTSWIKDTMAKNP
>d1dlea_ b.47.1.2 (A:) Factor B {Human (Homo sapiens)}
ADPDESQSLSLCGMVWEHRKGTDYHKQPWQAKISVIRPSKGHESCMGAVVSEYFVLTAAHCFTVD
DKEHSIKVSVGGEKRDLEIEVVLFHPNYNINGKKEAGIPEFYDYDVALIKLKNKLKYGQTIRPIC
LPCTEGTTRALRLPPTTTCQQQKEELLPAQDIKALFVSEEEKKLTRKEVYIKNGDKKGSCERDAQ
YAPGYDKVKDISEVVTPRFLCTGGVSPYADPNTCRGDSGGPLIVHKRSRFIQVGVISWGVVDVCK
NQKRQKQVPAHARDFHINLFQVLPWLKEKLQDEDLGFL
>d1bio__ b.47.1.2 (-) Factor D {Human (Homo sapiens)}
ILGGREAEAHARPYMASVQLNGAHLCGGVLVAEQWVLSAAHCLEDAADGKVQVLLGAHSLSQPEP
SKRLYDVLRAVPHPDSQPDTIDHDLLLLQLSEKATLGPAVRPLPWQRVDRDVAPGTLCDVAGWGI
VNHAGRRPDSLQHVLLPVLDRATCNRRTHHDGAITERLMCAESNRRDSCKGDSGGPLVCGGVLEG
VVTSGSRVCGNRKKPGIYTRVASYAAWIDSVLA
>g1rtf.1 b.47.1.2 (A:,B:) Two-chain tissue plasminogen activator (TC)-T-PA {Human (Homo sapiens)}
TCGLRQYSXIKGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPH
HLTVILGRTYRVVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCL
PPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDT
RSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNMR
P
>d1a5ia_ b.47.1.2 (A:) Single chain tissue plasminogen activator {Vampire bat (Desmodus rotundus)}
TCGLRKYKEPQLHSTGGLFTDITSHPWQAAIFAQNRRSSGERFLCGGILISSCWVLTAAHCFQES
YLPDQLKVVLGRTYRVKPGEEEQTFKVKKYIVHKEFDDDTYNNDIALLQLKSDSPQCAQESDSVR
AICLPEANLQLPDWTECELSGYGKHKSSSPFYSEQLKEGHVRLYPSSRCAPKFLFNKTVTNNMLC
AGDTRSGEIYPNVHDACQGDSGGPLVCMNDNHMTLLGIISWGVGCGEKDVPGVYTKVTNYLGWIR
DNMHL
>d1bqya_ b.47.1.2 (A:) Plasminogen activator from snake venom, TSV-PA {Chinese green tree viper (Trimeresurus stejnejeri)}

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VFGGDECNINEHRSLVVLFNSNGFLCGGTLINQDWVVTAAHCDSNNFQLLFGVHSKKILNEDEQT
RDPKEKFFCPNRKKDDEVDKDIMLIKLDSSVSNSEHIAPLSLPSSPPSVGSVCRIMGWGKTIPTK
EIYPDVPHCANINILDHAVCRTAYSWRQVANTTLCAGILQGGRDTCHFDSGGPLICNGIFQGIVS
WGGHPCGQPGEPGVYTKVFDYLDWIKSIIAGNKDATCPP
>d1ao5a_ b.47.1.2 (A:) Kallikrein-13 {Mouse (Mus musculus)}
VVGGFNCEKNSQPWQVAVYYQKEHICGGVLLDRNWVLTAAHCYVDQYEVWLGKNKLFQEEPSAQH
RLVSKSFPHPGFNMSLLMLQTIPPGADFSDDLMLLRLSKPADITDVVKPIALPTKEPKPGSKCLA
SGWGSITPTRWQKPDDLQCVFITLLPNENCAKVYLQKVTDVMLCAGEMGGGKDTCRDDSGGPLIC
DGILQGTTSYGPVPCGKPGVPAIYTNLIKFNSWIKDTMMKNA
>d1pfxc_ b.47.1.2 (C:) Coagulation factor IXa, protease domain {Pig
(Sus scrofa)}
IVGGENAKPGQFPWQVLLNGKIDAFCGGSIINEKWVVTAAHCIEPGVKITVVAGEYNTEETEPTE
QRRNVIRAIPHHSYNATVNKYSHDIALLELDEPLTLNSYVTPICIADKEYTNIFLKFGSGYVSGW
GRVFNRGRSATILQYLKVPLVDRATCLRSTKFTIYSNMFCAGFHEGGKDSCQGDSGGPHVTEVEG
TSFLTGIISWGEECAVKGKYGIYTKVSRYVNWIKEKTKLT
>d1rfna_ b.47.1.2 (A:) Coagulation factor IXa, protease domain {Human
(Homo sapiens)}
VVGGEDAKPGQFPWQVVLNGKVDAFCGGSIVNEKWIVTAAHCVETGVKITVVAGEHNIEETEHTE
QKRNVIRIIPHHNYNAAINKYNHDIALLELDEPLVLNSYVTPICIADKEYTNIFLKFGSGYVSGW
GRVFHKGRSALVLQYLRVPLVDRATCLRSTKFTIYNNMFCAGFHEGGRDSCQGDSGGPHVTEVEG
TSFLTGIISWGEECAMKGKYGIYTKVSRYVNWIKEKTKLT
>d1fjsa_ b.47.1.2 (A:) Coagulation factor Xa (Chrismas factor),
protease domain {Human (Homo sapiens)}
IVGGQECKDGECPWQALLINEENEGFCGGTILSEFYILTAAHCLYQAKRFKVRVGDRNTEQEEGG
EAVHEVEVVIKHNRFTKETYDFDIAVLRLKTPITFRMNVAPACLPERDWAESTLMTQKTGIVSGF
GRTHEKGRQSTRLKMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKD
TYFVTGIVSWGEGCARKGKYGIYTKVTAFLKWIDRSMKT
>d1kigh_ b.47.1.2 (H:) Coagulation factor Xa (Chrismas factor),
protease domain {Cow (Bos taurus)}
IVGGRDCAEGECPWQALLVNEENEGFCGGTILNEFYVLTAAHCLHQAKRFTVRVGDRNTEQEEGN
EMAHEVEMTVKHSRFVKETYDFDIAVLRLKTPIRFRRNVAPACLPEKDWAEATLMTQKTGIVSGF
GRTHEKGRLSSTLKMLEVPYVDRSTCKLSSSFTITPNMFCAGYDTQPEDACQGDSGGPHVTRFKD
TYFVTGIVSWGEGCARKGKFGVYTKVSNFLKWIDKIMKARAGAAGS
>d1fxya_ b.47.1.2 (A:) Coagulation factor Xa-trypsin chimera
{Synthetic, based on Homo sapiens sequence}
IVGGYNCKDGEVPWQALLINEENEGFCGGTILSEFYILTAAHCLYQAKRFKVRVGDRNTEQEEGG
EAVHEVEVVIKHNRFTKETYDFDIAVLRLKTPITFRMNVAPASLPTAPPATGTKCLISGWGNTAS
SGADYPDELQCLDAPVLSQAKCEASYPGKITSNMFCVGFLEGGKDSCQGDSGGPVVCNGQLQGVV
SWGDGCAQKNKPGVYTKVYNYVKWIKNTIAANS
>d1elva1 b.47.1.2 (A:410-668) Complement C1S protease, catalytic
domain {Human (Homo sapiens)}
CGVPREPFEEKQRIIGGSDADIKNFPWQVFFDNPWAGGALINEYWVLTAAHVVEGNREPTMYVGS
TSVQTSRLAKSKMLTPEHVFIHPGWKLLAVPEGRTNFDNDIALVRLKDPVKMGPTVSPICLPGTS
SDYNLMDGDLGLISGWGRTEKRDRAVRLKAARLPVAPLRKCKEVKVEKPTADAEAYVFTPNMICA
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GGEKGMDSCKGDSGGAFAVQDPNDKTKFYAAGLVSWGPQCGTYGLYTRVKNYVDWIMKTMQENS
>d1autc_ b.47.1.2 (C:) Activated protein c (autoprothrombin IIa)
{Human (Homo sapiens)}
LIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKW
ELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTG
WGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPM
VASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRD
>d1fuja_ b.47.1.2 (A:) Myeloblastin, PR3 {Human (Homo sapiens)}
IVGGHEAQPHSRPYMASLQMRGNPGSHFCGGTLIHPSFVLTAAHCLRDIPQRLVNVVLGAHNVRT
QEPTQQHFSVAQVFLNNYDAENKLNDILLIQLSSPANLSASVATVQLPQQDQPVPHGTQCLAMGW
GRVGAHDPPAQVLQELNVTVVTFFCRPHNICTFVPRRKAGICFGDSGGPLICDGIIQGIDSFVIW
GCATRLFPDFFTRVALYVDWIRSTLR
>g1c5y.1 b.47.1.2 (A:,B:) Urokinase-type plasminogen activator (LMW
U-PA), catalytic domain {Human (Homo sapiens)}
LKFQCGQKTXIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLMSPCWVISATHCFIDYPKKE
DYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTI
CLPSMYNDPQFGTSCEITGFGKEASTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAA
DPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEE
>d1ddja_ b.47.1.2 (A:) Plasmin(ogen), catalytic domain {Human (Homo
sapiens)}
SFDCGKPQVEPKKCPGRVVGGCVAHPHSWPWQVSLRTRFGMHFCGGTLISPEWVLTAAHCLEKSP
RPSSYKVILGAHQEVNLEPHVQEIEVSRLFLEPTRKDIALLKLSSPAVITDKVIPACLPSPNYVV
ADRTECFITGWGETQGTFGAGLLKEAQLPVIENKVCNRYEFLNGRVQSTELCAGHLAGGTDSCQG
DAGGPLVCFEKDKYILQGVTSWGLGCARPNKPGVYVRVSRFVTWIEGVMRNN
>d1fi8a_ b.47.1.2 (A:) Granzyme B {Rat (Rattus norvegicus)}
IIGGHEAKPHSRPYMAYLQIMDEYSGSKKCGGFLIREDFVLTAAHCSGSKIQVTLGAHNIKEQEK
MQQIIPVVKIIPHPAYNSKTISNDIMLLKLKSKAKRSSAVKPLNLPRRNVKVKPGDVCYVAGWGK
LGPMGKYSDTLQEVELTVQEDQKCESYLKNYFDKANEICAGDPKIKRASFRGDSGGPLVCKKVAA
GIVSYGQNDGSTPRAFTKVSTFLSWIKKTMKK
>d1iaua_ b.47.1.2 (A:) Granzyme B {Human (Homo sapiens)}
IIGGHEAKPHSRPYMAYLMIWDQKSLKRCGGFLIRDDFVLTAAHCWGSSINVTLGAHNIKEQEPT
QQFIPVKRPIPHPAYNPKNFSNDIMLLQLERKAKRTRAVQPLRLPSNKAQVKPGQTCSVAGWGQT
APLGKHSHTLQEVKMTVQEDRKCESDLRHYYDSTIELCVGDPEIKKTSFKGDSGGPLVCNKVAQG
IVSYGRNNGMPPRACTKVSSFVHWIKKTMKR
>d1eufa_ b.47.1.2 (A:) Duodenase {Cow (Bos taurus)}
IIGGHEAKPHSRPYMAFLLFKTSGKSHICGGFLVREDFVLTAAHCLGSSINVTLGAHNIMERERT
QQVIPVRRPIPHPDYNDETLANDIMLLKLTRKADITDKVSPINLPRSLAEVKPGMMCSVAGWGRL
GVNMPSTDKLQEVDLEVQSEEKCIARFKNYIPFTQICAGDPSKRKNSFSGDSGGPLVCNGVAQGI
VSYGRNDGTTPDVYTRISSFLSWIHSTMR
>g1fiw.1 b.47.1.2 (L:,A:) Beta-acrosin {Sheep (Ovis aries)}
TTCDGPCGVRFRQNXIIGGQDAAHGAWPWMVSLQIFTYHNNRRYHVCGGSLLNSQWLLTAAHCFR
IKKKVTDWRLIFGAKEVEWGTNKPVKPPLQERYVEKIIIHEKYSASSEANDIALMKITPPVTCGH
FIGPGCLPQFRAGPPRVPQTCWVAGWGFLQENARRTSPMLQEARVDLIDLGLCNSTRWYNGRIRS
TNVCAGYPEGKIDTCQGDSGGPLMCKDSAENSYVVVGITSWGVGCARAKRPGVYTSTWSYLNWIA
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SKIGSTAVHMIQLPT
>g1fiz.1 b.47.1.2 (L:,A:) Beta-acrosin {Pig (Sus scrofa)}
ATCDGPCGLRFRQXVVGGMSAEPGAWPWMVSLQIFMYHNNRRYHTCGGILLNSHWVLTAAHCFKN
KKKVTDWRLIFGANEVVWGSNKPVKPPLQERFVEEIIIHEKYVSGLEINDIALIKITPPVPCGPF
IGPGCLPQFKAGPPRAPQTCWVTGWGYLKEKGPRTSPTLQEARVALIDLELCNSTRWYNGRIRST
NVCAGYPRGKIDTCQGDSGGPLMCRDRAENTFVVVGITSWGVGCARAKRPGVYTSTWPYLNWIAS
KIGSNALQMVQLGTPPR
>d1eaxa_ b.47.1.2 (A:) Matriptase MTSP1 {Human (Homo sapiens)}
VVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLH
DQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPDASHVFPAGKA
IWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPL
SSVEADGRIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWIKENTGV
>d1svpa_ b.47.1.3 (A:) Viral capsid protein {Sindbis virus}
ALKLEADRLFDVKNEDGDVIGHALAMEGKVMKPLHVKGTIDHPVLSKLKFTKSSAYDMEFAQLPV
NMRSEAFTYTSEHPEGFYNWHHGAVQYSGGRFTIPRGVGGRGDAGRPIMDNSGRVVAIVLGGADE
GTRTALSVVTWNSKGKTIKTTPEGTEEWSA
>d1vcpa_ b.47.1.3 (A:) Viral capsid protein {Semliki forest virus}
CIFEVKHEGKVTGYACLVGDKVMKPAHVKGVIDNADLAKLAFKKSSKYDLECAQIPVHMRSDASK
YTHEKPEGHYNWHHGAVQYSGGRFTIPTGAGKPGDSGRPIFDNKGRVVAIVLGGANEGSRTALSV
VTWNKDMVTRVTPEGSEEW
>d1a1qa_ b.47.1.3 (A:) NS3 protease {Human hepatitis C virus (HCV),
different isolates}
PITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAGSKTLAG
PKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRP
VSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMRSPVF
>d1cu1a1 b.47.1.3 (A:705-720,A:3-186) NS3 protease {Human hepatitis
C virus (HCV), different isolates}
GSVVIVGRIILSGSGSXITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNG
VCWTVYHGAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIP
VRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR
SPVFTD
>d1dxwa_ b.47.1.3 (A:) NS3 protease {Human hepatitis C virus (HCV),
different isolates}
TGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAGSKTLAGPKGPITQMYTNVDQDLVGWQ
APPGARSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAV
GIFRAAVCTRGVAKAVDFVPVESMETTMRASKKKK
>g1a1r.1 b.47.1.3 (A:,C:) NS3 protease {Human hepatitis C virus (HCV),
different isolates}
VEGEVQIVSTATQTFLATCINGVCWTVYHGAGTRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS
LTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISYLKGSSGGPLLCPTGHAVGLFRAAV
CTRGVAKAVDFIPVENLETTMRXGSVVIVGRIVLSGKPA
>g1a1r.2 b.47.1.3 (B:,D:) NS3 protease {Human hepatitis C virus (HCV),
different isolates}
PITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTATQTFLATCINGVCWTVYHGAGTRTIAS
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PKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRP
ISYLKGSSGGPLLCPTGHAVGLFRAAVCTRGVAKAVDFIPVENLETTMRXKGSVVIVGRIVLSGK
PAIIPK
>g1dy9.1 b.47.1.3 (A:,C:) NS3 protease {Human hepatitis C virus (HCV), different isolates}
APITAYSQQTRGLLGCIITSLTGRDKNQVDGEVQVLSTATQSFLATCVNGVCWTVYHGAGSKTLA
GPKGPITQMYTNVDQDLVGWPAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPR
PVSYLKGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFIPVESMXGSVVIVGRIILS
>g1ns3.1 b.47.1.3 (A:,C:) NS3 protease {Human hepatitis C virus (HCV), different isolates}
ITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAGSKTLAGP
KGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPV
SYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMRXKGSVVIVGRIILS
>d1befa_ b.47.1.3 (A:) NS3 protease {Dengue virus serotype 2}
WDVPSPPPVGKAELEDGAYRIKQKGILGYSQIGAGVYKEGTFHTMWHVTRGAVLMHKGKRIEPSW
ADVKKDLVSCGGGWKLEGEWKEGEEVQVLALEPGKNPRAVQTKPGLFKTNAGTIGAVSLDFSPGT
SGSPIIDKKGKVVGIYGNGVVTRSGAYVSAIAQTEKSIEDNPEIEDD
>d1cqqa_ b.47.1.4 (A:) 3C cysteine protease (picornain 3C) {Human rhinovirus type 2}
GPEEEFGMSLIKHNSCVITTENGKFTGLGVYDRFVVVPTHADPGKEIQVDGITTKVIDSYDLYNK
NGIKLEITVLKLDRNEKFRDIRRYIPNNEDDYPNCNLALLANQPEPTIINVGDVVSYGNILLSGN
QTARMLKYSYPTKSGYCGGVLYKIGQVLGIHVGGNGRDGFSAMLLRSYFT
>d1hava_ b.47.1.4 (A:) 3C cysteine protease (picornain 3C) {Human hepatitis A virus}
STLEIAGLVRKNLVQFGVGEKNGSVRWVMNALGVKDDWLLVPSHAYKFEKDYEMMEFYFNRGGTY
YSISAGNVVIQSLDVGFQDVVLMKVPTIPKFRDITQHFIKKGDVPRALNRLATLVTTVNGTPMLI
SEGPLKMEEKATYVHKKNDGTTVDLTVDQAWRGKGEGLPGMCGGALVSSNQSIQNAILGIHVAGG
NSILVAKLVTQEMFQNIDKKI
>d2hrva_ b.47.1.4 (A:) 2A cysteine proteinase {Human rhinovirus 2}
GPSDMYVHVGNLIYRNLHLFNSEMHESILVSYSSDLIIYRTNTVGDDYIPSCDCTQATYYCKHKN
RYFPITVTSHDWYEIQESEYYPKHIQYNLLIGEGPCEPGDCGGKLLCKHGVIGIVTAGGDNHVAF
IDLRHFHCA
>d1bco_1 b.48.1.1 (481-560) mu transposase, C-terminal domain {Bacteriophage mu}
TEEQKRMLLLPAEAVNVSRKGEFTLKVGGSLKGAKNVYYNMALMNAGVKKVVVRFDPQQLHSTVY
CYTLDGRFICEAECL
>d1e79a2 b.49.1.1 (A:19-94) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Cow (Bos taurus)}
ADTSVDLEETGRVLSIGDGIARVHGLRNVQAEEMVEFSSGLKGMSLNLEPDNVGVVVFGNDKLIK
EGDIVKRTGAI
>d1e79d2 b.49.1.1 (D:9-81) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Cow (Bos taurus)}
TTGRIVAVIGAVVDVQFDEGLPPILNALEVQGRETRLVLEVAQHLGESTVRTIAMDGTEGLVRGQ
KVLDSGAP

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>d1maba2 b.49.1.1 (A:10-94) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Rat (Rattus norvegicus)}
SSILEERILGADTSVDLEETGRVLSIGDGIARVHGLRNVQAEEMVEFSSGLKGMSLNLEPDNVGV
VVFGNDKLIKEGDIVKRTGAI
>d1mabb2 b.49.1.1 (B:1-81) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Rat (Rattus norvegicus)}
SAAPKAGTATGQIVAVIGAVVDVQFDEGLPPILNALEVQGRESRLVLEVAQHLGESTVRTIAMDG
TEGLVRGQKVLDSGAP
>d1skyb2 b.49.1.1 (B:21-95) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Bacillus sp., strain ps3}
SQIQVSDVGTVIQVGDGIARAHGLDNVMSGEAVEFANAVMGMALNLEENNVGIVILGPYTGIKEG
DEVRRTGRIM
>d1skye2 b.49.1.1 (E:1-82) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Bacillus sp., strain ps3}
MTRGRVIQVMGPVVDVKFENGHLPAIYNALKIQHKARNENEVDIDLTLEVALHLGDDTVRTIAMA
STDGLIRGMEVIDTGAP
>d1fx0a2 b.49.1.1 (A:25-96) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Spinach (Spinacia oleracea), chloroplast}
KVVNTGTVLQVGDGIARIHGLDEVMAGELVEFEEGTIGIALNLESNNVGVVLMGDGLMIQEGSSV
KATGRIA
>d1fx0b2 b.49.1.1 (B:19-97) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Spinach (Spinacia oleracea), chloroplast}
NLGRIAQIIGPVLNVAFPPGKMPNIYNALIVKGRDTAGQPMNVTCEVQQLLGNNRVRAVAMSATD
GLTRGMEVIDTGAP
>d1bd0a1 b.49.2.1 (A:2-11,A:245-382) Alanine racemase {Bacillus stearothermophilus}
NDFHRDTWAEXFSLHSRLVHVKKLQPGEKVSYGATYTAQTEEWIGTIPIGYADGWLRRLQHFHVL
VDGQKAPIVGRICMDQCMIRLPGPLPVGTKVTLIGRQGDEVISIDDVARHLETINYEVPCTISYR
VPRIFFRHKRIMEVRNAIG
>d1d7ka1 b.49.2.1 (A:7-43,A:284-427) Eukaryotic ornithine decarboxylase {Human (Homo sapiens)}
EEFDCHFLDEGFTAKDILDQKINEVSSSDDKDAFYVAXFTLAVNIIAKKIVLKEQTGSDDEDESS
EQTFMYYVNDGVYGSFNCILYDHAHVKPLLQKRPKPDERYYSSSIWGPTCDGLDRIVERCDLPEM
HVGDWMLFENMGAYTVAAASTFNGFQRPTIYYVMSGPAWQLMQQFQNPDFPP
>d7odca1 b.49.2.1 (A:2-43,A:284-418) Eukaryotic ornithine decarboxylase {Mouse (Mus musculus)}
SSFTKDEFDCHILDEGFTAKDILDQKINEVSSSDDKDAFYVAXFTLAVNIIAKKTVWKEQPGSDD
EDESNEQTFMYYVNDGVYGSFNCILYDHAHVKALLQKRPKPDEKYYSSSIWGPTCDGLDRIVERC
NLPEMHVGDWMLFENMGAYTVAAASTFNGFQRPNIYYVMSRPMWQLMK
>d1f3ta1 b.49.2.1 (A:14-43,A:284-422) Eukaryotic ornithine decarboxylase {Trypanosoma brucei}
RFLEGFNTRDALCKKISMNTCDEGDPFFVAXFTLAVNVIAKKVTPGVQTDVGAHAESNAQSFMYY
VNDGVYGSFNCILYDHAVVRPLPQREPIPNEKLYPSSVWGPTCDGLDQIVERYYLPEMQVGEWLL
FEDMGAYTVVGTSSFNGFQSPTIYYVVSGLPDHVVRELKS
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>d2toda1 b.49.2.1 (A:37-43,A:284-410) Eukaryotic ornithine
decarboxylase {Trypanosoma brucei}
GDPFFVAXFTLAVNVIAKKVTPGVQTDVGAHAESNAQSFMYYVNDGVYGSFNCILYDHAVVRPLP
QREPIPNEKLYPSSVWGPTCDGLDQIVERYYLPEMQVGEWLLFEDMGAYTVVGTSSFNGFQSPTI
YYVVS
>d1b6la_ b.50.1.1 (A:) Human immunodeficiency virus type 1 protease
{Human immunodeficiency virus type 1}
PQITLWKRPLVTIRIGGQLKEALLDTGADDTVIEEMNLPGKWKPKMIGGIGGFIKVRQYDQIPVE
IXGHKAIGTVLVGPTPVNIIGRNLLTQIGXTLNF
>d1bdqa_ b.50.1.1 (A:) Human immunodeficiency virus type 1 protease
{Human immunodeficiency virus type 1}
PQITLWQRPLVTIKIGGQLKEALLDTGADDSIVAGIELPGRWKPKMVGGIGGFIKVRQYDQILIE
ICGHKAIGTVLVGPTPINIIGRNLLTQIGCTLNF
>d1c6ya_ b.50.1.1 (A:) Human immunodeficiency virus type 1 protease
{Human immunodeficiency virus type 1}
PQITLWQRPVVTIKIGGQLMEALIDTGADDTVLEEMDLPGRWKPKIIGGIGGFVKVRQYDQIPIE
ICGHKVIGTVLVGPTPTNIIGRNLLTQIGCTLNF
>d1dazc_ b.50.1.1 (C:) Human immunodeficiency virus type 1 protease
{Human immunodeficiency virus type 1}
PQITLWKRPLVTIKIGGQLKEALLDTGADDTVIEEMSLPGRWKPIMIGGIGGFIKVRQYDQIIIE
IAGHKAIGTVLVGPTPVNIIGRNLLTQIGATLNF
>d1difa_ b.50.1.1 (A:) Human immunodeficiency virus type 1 protease
{Human immunodeficiency virus type 1}
PQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKPKMIGGIGGFIKVRQYDQILIE
ICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNF
>d1hvc__ b.50.1.1 (-) Human immunodeficiency virus type 1 protease
{Human immunodeficiency virus type 1}
PQITLWQRPLVTIRIGGQLKEALLDTGADDTVLEEMNLPGKWKPKMIGGIGGFIKVRQYDQILIE
ICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNFGGSSGPQITLWQRPLVTIKIGGQLKEALLDT
GADDTVLEEMSLPGRWKPKMIGGIGGFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLT
QIGCTLNF
>d1idaa_ b.50.1.1 (A:) Human immunodeficiency virus type 2 (HIV-2)
protease {Human immunodeficiency virus type 2}
PQFSLWKRPVVTAYIEGQPVEVLLDTGADDSIVAGIELGNNYSPKIVGGIGGFINTKEYKNVEIE
VLNKKVRATIMTGDTPINIFGRNILTALGMSLNL
>d1az5__ b.50.1.1 (-) Simian immunodeficiency virus (SIV) protease
{Simian immunodeficiency virus, different strains}
PQFHLWKRPVVTAHIEGQPVEVLLDTGADDSIVTGIELGPHYTPKIVGGIGGFINTKEYKNVEVE
VLGKRIKGTIMTGDTPINIFGRNLLTALGMSLNF
>d1k6va_ b.50.1.1 (A:) Simian immunodeficiency virus (SIV) protease
{Simian immunodeficiency virus, different strains}
PQITLWKRPLVTIRIGGQLKEALLDTGADDTVLEEMNLPGRWKPKMIGGIGGFIKVRQYDQIPIE
ICGHKAIGTVLVGPTPTNVIGRNLLTQIGCTLNF
>d1siva_ b.50.1.1 (A:) Simian immunodeficiency virus (SIV) protease
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{Simian immunodeficiency virus, different strains}
PQFSLWRRPVVTAHIEGQPVEVLLDTGADDSIVTGIELGPHYTPKIVGGIGGFINTKEYKNVKIE
VLGKRIKGTIMTGDTPINIFGRNLLTALGMSLNL
>d4fiv__ b.50.1.1 (-) Feline immunodeficiency virus (FIV) protease
{Feline immunodeficiency virus}
VGTTTTLEKRPEILIFVNGYPIKFLLDTGADITILNRRDFQVKNSIENGRQNMIGVGGGKRGTNY
INVHLEIRDENYKTQCIFGNVCVLEDNSLIQPLLGRDNMIKFNIRLVM
>d1baia_ b.50.1.1 (A:) Rous sarcoma virus protease {Rous sarcoma virus,
strain pr-C}
LAMTMEHKDRPLVRVILTNTGSHPVKQRSVYITALLDTGADDTVISEEDWPTDWPVMEAANPQIH
GIGGGIPVRKSRDMIELGVINRDGSLERPLLLFPLVAMTPVNILGRDCLQGLGLRLTNL
>d2rspa_ b.50.1.1 (A:) Rous sarcoma virus protease {Rous sarcoma virus,
strain pr-C}
LAMTMEHKDRPLVRVILTNTGSHPVKQRSVYITALLDSGADITIISEEDWPTDWPVMEAANPQIH
GIGGGIPMRKSRDMIELGVINRDGSLERPLLLFPAVAMVRGSILGRDCLQGLGLRLTNL
>d1fmb__ b.50.1.1 (-) EIAV protease {Equine infectious anemia virus}
VTYNLEKRPTTIVLINDTPLNVLLDTGADTSVLTTAHYNRLKYRGRKYQGTGIGGVGGNVETFST
PVTIKKKGRHIKTRMLVADIPVTILGRDILQDLGAKLVL
>d2er7e_ b.50.1.2 (E:) Endothiapepsin {Chestnut blight fungus
(Endothia parasitica)}
STGSATTTPIDSLDDAYITPVQIGTPAQTLNLDFDTGSSDLWVFSSETTASEVDGQTIYTPSKST
TAKLLSGATWSISYGDGSSSSGDVYTDTVSVGGLTVTGQAVESAKKVSSSFTEDSTIDGLLGLAF
STLNTVSPTQQKTFFDNAKASLDSPVFTADLGYHAPGTYNFGFIDTTAYTGSITYTAVSTKQGFW
EWTSTGYAVGSGTFKSTSIDGIADTGTTLLYLPATVVSAYWAQVSGAKSSSSVGGYVFPCSATLP
SFTFGVGSARIVIPGDYIDFGPISTGSSSCFGGIQSSAGIGINIFGDVALKAAFVVFNGATTPTL
GFASK
>d1bxoa_ b.50.1.2 (A:) Acid protease {Fungus (Penicillium
janthinellum), penicillopepsin}
AASGVATNTPTANDEEYITPVTIGGTTLNLNFDTGSADLWVFSTELPASQQSGHSVYNPSATGKE
LSGYTWSISYGDGSSASGNVFTDSVTVGGVTAHGQAVQAAQQISAQFQQDTNNDGLLGLAFSSIN
TVQPQSQTTFFDTVKSSLAQPLFAVALKHQQPGVYDFGFIDSSKYTGSLTYTGVDNSQGFWSFNV
DSYTAGSQSGDGFSGIADTGTTLLLLDDSVVSQYYSQVSGAQQDSNAGGYVFDCSTNLPDFSVSI
SGYTATVPGSLINYGPSGDGSTCLGGIQSNSGIGFSIFGDIFLKSQYVVFDSDGPQLGFAPQA
>d1ibqa_ b.50.1.2 (A:) Acid protease {Fungus (Aspergillus phoenicis),
aspergillopepsin}
SKGSAVTTPQNNDEEYLTPVTVGKSTLHLDFDTGSADLWVFSDELPSSEQTGHDLYTPSSSATKL
SGYSWDISYGDGSSASGDVYRDTVTVGGVTTNKQAVEAASKISSEFVQDTANDGLLGLAFSSINT
VQPKAQTTFFDTVKSQLDSPLFAVQLKHDAPGVYDFGYIDDSKYTGSITYTDADSSQGYWGFSTD
GYSIGDGSSSSSGFSAIADTGTTLILLDDEIVSAYYEQVSGAQESYEAGGYVFSCSTDLPDFTVV
IGDYKAVVPGKYINYAPVSTGSSTCYGGIQSNSGLGLSILGDVFLKSQYVVFNSEGPKLGFAAQA
>d2apr__ b.50.1.2 (-) Acid protease {Bread mold (Rhizopus chinensis)}
AGVGTVPMTDYGNDIEYYGQVTIGTPGKKFNLDFDTGSSDLWIASTLCTNCGSGQTKYDPNQSST
YQADGRTWSISYGDGSSASGILAKDNVNLGGLLIKGQTIELAKREAASFASGPNDGLLGLGFDTI
TTVRGVKTPMDNLISQGLISRPIFGVYLGKAKNGGGGEYIFGGYDSTKFKGSLTTVPIDNSRGWW
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GITVDRATVGTSTVASSFDGILDTGTTLLILPNNIAASVARAYGASDNGDGTYTISCDTSAFKPL
VFSINGASFQVSPDSLVFEEFQGQCIAGFGYGNWGFAIIGDTFLKNNYVVFNQGVPEVQIAPVAE
>d2asi__ b.50.1.2 (-) Acid protease {Rhizomucor miehei}
GSVDTPGYYDFDLEEYAIPVSIGTPGQDFLLLFDTGSSDTWVPHKGCTKSEGCVGSRFFDPSASS
TFKATNYNLNITYGTGANGLYFEDSIAIGDITVTKQILAYVDNVRGPTAEQSPNADIFLDGLFGA
AYPDNTAMEAEYGSTYNTVHVNLYKQGLISSPLFSVYMNTNSGTGEVVFGGVNNTLLGGDIAYTD
VMSRYGGYYFWDAPVTGITVDGSAAVRFSRPQAFTIDTGTNFFIMPSSAASKIVKAALPDATETQ
QGWVVPCASYQNSKSTISIVMQKSGSSSDTIEISVPVSKMLLPVDQSNETCMFIILPDGGNQYIV
GNLFLRFFVNVYDFGNNRIGFAPLASAYENE
>d1eaga_ b.50.1.2 (A:) Acid protease {Yeast (Candida albicans)}
QAVPVTLHNEQVTYAADITVGSNNQKLNVIVDTGSSDLWVPDVNVDCQVTYSDQTADFCKQKGTY
DPSGSSASQDLNTPFKIGYGDGSSSQGTLYKDTVGFGGVSIKNQVLADVDSTSIDQGILGVGYKT
NEAGGSYDNVPVTLKKQGVIAKNAYSLYLNSPDAATGQIIFGGVDNAKYSGSLIALPVTSDRELR
ISLGSVEVSGKTINTDNVDVLLDSGTTITYLQQDLADQIIKAFNGKLTQDSNGNSFYEVDCNLSG
DVVFNFSKNAKISVPASEFAASLQGDDGQPYDKCQLLFDVNDANILGDNFLRSAYIVYDLDDNEI
SLAQVKYTSASSISALT
>d1j71a_ b.50.1.2 (A:) Acid protease {Yeast (Candida tropicalis)}
SDVPTTLINEGPSYAADIVVGSNQQKQTVVIDTGSSDLWVVDTDAECQVTYSGQTNNFCKQEGTF
DPSSSSSAQNLNQDFSIEYGDLTSSQGSFYKDTVGFGGISIKNQQFADVTTTSVDQGIMGIGFTA
DEAGYNLYDNVPVTLKKQGIINKNAYSLYLNSEDASTGKIIFGGVDNAKYTGTLTALPVTSSVEL
RVHLGSINFDGTSVSTNADVVLDSGTTITYFSQSTADKFARIVGATWDSRNEIYRLPSCDLSGDA
VFNFDQGVKITVPLSELILKDSDSSICYFGISRNDANILGDNFLRRAYIVYDLDDKTISLAQVKY
TSSSDISAL
>d1dpja_ b.50.1.2 (A:) Acid protease {Baker's yeast (Saccharomyces cerevisiae), proteinase A}
GGHDVPLTNYLNAQYYTDITLGTPPQNFKVILDTGSSNLWVPSNECGSLACFLHSKYDHEASSSY
KANGTEFAIQYGTGSLEGYISQDTLSIGDLTIPKQDFAEATSEPGLTFAFGKFDGILGLGYDTIS
VDKVVPPFYNAIQQDLLDEKRFAFYLGDTSKDTENGGEATFGGIDESKFKGDITWLPVRRKAYWE
VKFEGIGLGDEYAELESHGAAIDTGTSLITLPSGLAEMINAEIGAKKGWTGQYTLDCNTRDNLPD
LIFNFNGYNFTIGPYDYTLEVSGSCISAITPMDFPEPVGPLAIVGDAFLRKYYSIYDLGNNAVGL
AKAI
>g1b5f.1 b.50.1.2 (A:,B:) Plant acid proteinase, phytepsin {Cynara carduncculus}
GSAVVALTNDRDTSYFGEIGIGTPPQKFTVIFDTGSSVLWVPSSKCINSKACRAHSMYESSDSST
YKENGTFGAIIYGTGSITGFFSQDSVTIGDLVVKEQDFIEATDEADNVFLHRLFDGILGLSFQTI
SVPVWYNMLNQGLVKERRFSFWLNRNVDEEEGGELVFGGLDPNHFRGDHTYVPVTYQYYWQFGIG
DVLIGDKSTGFCAPGCQAFADSGTSLLSGPTAIVTQINHAIGANXEELQVDCNTLSSMPNVSFTI
GGKKFGLTPEQYILKVGKGEATQCISGFTAMDATLLGPLWILGDVFMRPYHTVFDYGNLLVGFAE
AA
>d1qdma2 b.50.1.2 (A:2-247,A:248-338) Plant acid proteinase, phytepsin {Barley (Hordeum vulgare)}
EEEGDIVALKNYMNAQYFGEIGVGTPPQKFTVIFDTGSSNLWVPSAKCYFSIACYLHSRYKAGAS
STYKKNGKPAAIQYGTGSIAGYFSEDSVTVGDLVVKDQEFIEATKEPGITFLVAKFDGILGLGFK
EISVGKAVPVWYKMIEQGLVSDPVFSFWLNRHVDEGEGGEIIFGGMDPKHYVGEHTYVPVTQKGY
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WQFDMGDVLVGGKSTGFCAGGCAAIADSGTSLLAGPTAIITEINEKIGAAGXSPMGESAVDCGSL
GSMPDIEFTIGGKKFALKPEEYILKVGEGAAAQCISGFTAMDIPPPRGPLWILGDVFMGPYHTVF
DYGKLRIGFAKAA
>d3psg__ b.50.1.2 (-) Pepsin(ogen) {Pig (Sus scrofa)}
LVKVPLVRKKSLRQNLIKDGKLKDFLKTHKHNPASKYFPEAAALIGDEPLENYLDTEYFGTIGIG
TPAQDFTVIFDTGSSNLWVPSVYCSSLACSDHNQFNPDDSSTFEATSQELSITYGTGSMTGILGY
DTVQVGGISDTNQIFGLSETEPGSFLYYAPFDGILGLAYPSISASGATPVFDNLWDQGLVSQDLF
SVYLSSNDDSGSVVLLGGIDSSYYTGSLNWVPVSVEGYWQITLDSITMDGETIACSGGCQAIVDT
GTSLLTGPTSAIANIQSDIGASENSDGEMVISCSSIDSLPDIVFTIDGVQYPLSPSAYILQDDDS
CTSGFEGMDVPTSSGELWILGDVFIRQYYTVFDRANNKVGLAPVA
>d4pep__ b.50.1.2 (-) Pepsin(ogen) {Pig (Sus scrofa)}
IGDEPLENYLDTEYFGTIGIGTPAQDFTVIFDTGSSNLWVPSVYCSSLACSDHNQFNPDDSSTFE
ATSQELSITYGTGSMTGILGYDTVQVGGISDTNQIFGLSETEPGSFLYYAPFDGILGLAYPSISA
SGATPVFDNLWDQGLVSQDLFSVYLSSNDDSGSVVLLGGIDSSYYTGSLNWVPVSVEGYWQITLD
SITMDGETIACSGGCQAIVDTGTSLLTGPTSAIANIQSDIGASENSDGEMVISCSSIDSLPDIVF
TIDGVQYPLSPSAYILQDDDSCTSGFEGMDVPTSSGELWILGDVFIRQYYTVFDRANNKVGLAPV
A
>d1psoe_ b.50.1.2 (E:) Pepsin(ogen) {Human (Homo sapiens), 3A}
VDEQPLENYLDMEYFGTIGIGTPAQDFTVVFDTGSSNLWVPSVYCSSLACTNHNRFNPEDSSTYQ
STSETVSITYGTGSMTGILGYDTVQVGGISDTNQIFGLSETEPGSFLYYAPFDGILGLAYPSISS
SGATPVFDNIWNQGLVSQDLFSVYLSADDQSGSVVIFGGIDSSYYTGSLNWVPVTVEGYWQITVD
SITMNGEAIACAEGCQAIVDTGTSLLTGPTSPIANIQSDIGASENSDGDMVVSCSAISSLPDIVF
TINGVQYPVPPSAYILQSEGSCISGFQGMNLPTESGELWILGDVFIRQYFTVFDRANNQVGLAPV
A
>g1htr.1 b.50.1.2 (P:,B:) Pepsin(ogen) {Human (Homo sapiens),
progastricsin (pepsinogen C)}
AVVKVPLKKFKSIRETMKEKGLLGEFLRTHKYDPAWKYRFGDLXSVTYEPMAYMDAAYFGEISIG
TPPQNFLVLFDTGSSNLWVPSVYCQSQACTSHSRFNPSESSTYSTNGQTFSLQYGSGSLTGFFGY
DTLTVQSIQVPNQEFGLSENEPGTNFVYAQFDGIMGLAYPALSVDEATTAMQGMVQEGALTSPVF
SVYLSNQQGSSGGAVVFGGVDSSLYTGQIYWAPVTQELYWQIGIEEFLIGGQASGWCSEGCQAIV
DTGTSLLTVPQQYMSALLQATGAQEDEYGQFLVNCNSIQNLPSLTFIINGVEFPLPPSSYILSNN
GYCTVGVEPTYLSSQNGQPLWILGDVFLRSYYSVYDLGNNRVGFATAA
>d1am5__ b.50.1.2 (-) Pepsin(ogen) {Atlantic cod (Gadus morhua)}
RVTEQMKNEADTEYYGVISIGTPPESFKVIFDTGSSNLWVSSSHCSAQACSNHNKFKPRQSSTYV
ETGKTVDLTYGTGGMRGILGQDTVSVGGGSDPNQELGESQTEPGPFQAAAPFDGILGLAYPSIAA
AGAVPVFDNMGSQSLVEKDLFSFYLSGGGANGSEVMLGGVDNSHYTGSIHWIPVTAEKYWQVALD
GITVNGQTAACEGCQAIVDTGTSKIVAPVSALANIMKDIGASENQGEMMGNCASVQSLPDITFTI
NGVKQPLPPSAYIEGDQAFCTSGLGSSGVPSNTSELWIFGDVFLRNYYTIYDRTNNKVGFAPAA
>d1mpp__ b.50.1.2 (-) Pepsin {Mucor pusillus}
GSVDTPGLYDFDLEEYAIPVSIGTPGQDFYLLFDTGSSDTWVPHKGCDNSEGCVGKRFFDPSSSS
TFKETDYNLNITYGTGGANGIYFRDSITVGGATVKQQTLAYVDNVSGPTAEQSPDSELFLDGIFG
AAYPDNTAMEAEYGDTYNTVHVNLYKQGLISSPVFSVYMNTNDGGGQVVFGGVNNTLLGGDIQYT
DVLKSRGGYFFWDAPVTGVKIDGSDAVSFDGAQAFTIDTGTNFFIAPSSFAEKVVKAALPDATES
QQGYTVPCSKYQDSKTTFSLVLQKSGSSSDTIDVSVPISKMLLPVDKSGETCMFIVLPDGGNQFI
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VGNLFLRFFVNVYDFGKNRIGFAPLASGYEND
>g1lyb.1 b.50.1.2 (A:,B:) Cathepsin D {Human (Homo sapiens)}
GPIPEVLKNYMDAQYYGEIGIGTPPQCFTVVFDTGSSNLWVPSIHCKLLDIACWIHHKYNSDKSS
TYVKNGTSFDIHYGSGSLSGYLSQDTVSVPCQXGGVKVERQVFGEATKQPGITFIAAKFDGILGM
AYPRISVNNVLPVFDNLMQQKLVDQNIFSFYLSRDPDAQPGGELMLGGTDSKYYKGSLSYLNVTR
KAYWQVHLDQVEVASGLTLCKEGCEAIVDTGTSLMVGPVDEVRELQKAIGAVPLIQGEYMIPCEK
VSTLPAITLKLGGKGYKLSPEDYTLKVSQAGKTLCLSGFMGMDIPPPSGPLWILGDVFIGRYYTV
FDRDNNRVGFAEAA
>d3cms__ b.50.1.2 (-) Chymosin (synonim: renin) {Cow (Bos taurus)}
GEVASVPLTNYLDSQYFGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSST
FQNLGKPLSIHYGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDFFTYAEFDGILGMAYPSL
ASEYSIPVFDNMMNRHLVAQDLFSVYMDRNGQESMLTLGAIDPSYYTGSLHWVPVTVQQYWQFTV
DSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYMPTVV
FEINGKMYPLTPSAYTSQDQGFCTSGFQSENHSQKWILGDVFIREYYSVFDRANNLVGLAKAI
>d1hrna_ b.50.1.2 (A:) Chymosin (synonim: renin) {Human (Homo sapiens)}
GNTTSSVILTNYMDTQYYGEIGIGTPPQTFKVVFDTGSSNVWVPSSKCSRLYTACVYHKLFDASD
SSSYKHNGTELTLRYSTGTVSGFLSQDIITVGGITVTQMFGEVTEMPALPFMLAEFDGVVGMGFI
EQAIGRVTPIFDNIISQGVLKEDVFSFYYNRDSENSQSLGGQIVLGGSDPQHYEGNFHYINLIKT
GVWQIQMKGVSVGSSTLLCEDGCLALVDTGASYISGSTSSIEKLMEALGAKKRLFDYVVKCNEGP
TLPDISFHLGGKEYTLTSADYVFQESYSSKKLCTLAIHAMDIPPPTGPTWALGATFIRKFYTEFD
RRNNRIGFALAR
>d1smra_ b.50.1.2 (A:) Chymosin (synonim: renin) {Mouse (Mus musculus)}
TDLISPVVLTNYLNSQYYGEIGIGTPPQTFKVIFDTGSANLWVPSTKCSRLYLACGIHSLYESSD
SSSYMENGDDFTIHYGSGRVKGFLSQDSVTVGGITVTQTFGEVTQLPLIPFMLAQFDGVLGMGFP
AQAVGGVTPVFDHILSQGVLKEKVFSVYYNRGPHLLGGEVVLGGSDPQHYQGDFHYVSLSKTDSW
QITMKGVSVGSSTLLCEEGCEVVVDTGSSFISAPTSSLKLIMQALGAKEKRLHEYVVSCSQVPTL
PDISFNLGGRAYTLSSTDYVLQYPNRRDKLCTVALHAMDIPPPTGPVWVLGATFIRKFYTEFDRH
NNRIGFALAR
>d1fkna_ b.50.1.2 (A:) beta-secretase (memapsin) {Human (Homo sapiens)}
RRGSFVEMVDNLRGKSGQGYYVEMTVGSPPQTLNILVDTGSSNFAVGAAPHPFLHRYYQRQLSST
YRDLRKGVYVPYTQGKWEGELGTDLVSIPHGPNVTVRANIAAITESDKFFINGSNWEGILGLAYA
EIARPDDSLEPFFDSLVKQTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSLW
YTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRLPKKVFEAAVKSIKAASST
EKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSFRITILPQQYLRPVEDVATSQDDC
YKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGY
N
>d1pfza_ b.50.1.2 (A:) Plasmepsin ii (a hemoglobin-degrading enzyme) {Plasmodium falciparum}
HLTIGFKVENAHDRILKTIKTHKLKNYIKESVNFLNSGLTKTNYLGSSNDNIELVDFQNIMFYGD
AEVGDNQQPFTFILDTGSANLWVPSVKCTTAGCLTKHLYDSSKSRTYEKDGTKVEMNYVSGTVSG
FFSKDLVTVGNLSLPYKFIEVIDTNGFEPTYTASTFDGILGLGWKDLSIGSVDPIVVELKNQNKI
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ENALFTFYLPVHDKHTGFLTIGGIEERFYEGPLTYEKLNHDLYWQITLDAHVGNIMLEKANCIVD
SGTSAITVPTDFLNKMLQNLDVIKVPFLPFYVTLCNNSKLPTFEFTSENGKYTLEPEYYLQHIED
VGPGLCMLNIIGLDFPVPTFILGDPFMRKYFTVFDYDNHSVGIALAKKNL
>d1smea_ b.50.1.2 (A:) Plasmepsin ii (a hemoglobin-degrading enzyme) {Plasmodium falciparum}
SSNDNIELVDFQNIMFYGDAEVGDNQQPFTFILDTGSANLWVPSVKCTTAGCLTKHLYDSSKSRT
YEKDGTKVEMNYVSGTVSGFFSKDLVTVGNLSLPYKFIEVIDTNGFEPTYTASTFDGILGLGWKD
LSIGSVDPIVVELKNQNKIENALFTFYLPVHDKHTGFLTIGGIEERFYEGPLTYEKLNHDLYWQI
TLDAHVGNIMLEKANCIVDSGTSAITVPTDFLNKMLQNLDVIKVPFLPFYVTLCNNSKLPTFEFT
SENGKYTLEPEYYLQHIEDVGPGLCMLNIIGLDFPVPTFILGDPFMRKYFTVFDYDNHSVGIALA
KKNL
>d1qs8a_ b.50.1.2 (A:) Plasmepsin ii (a hemoglobin-degrading enzyme) {Plasmodium vivax}
SENDVIELDDVANIMFYGEGEVGDNHQKFMLIFDTGSANLWVPSKKCNSSGCSIKNLYDSSKSKS
YEKDGTKVDITYGSGTVKGFFSKDLVTLGHLSMPYKFIEVIDTDDLEPIYSSVEFDGILGLGWKD
LSIGSIDPIVVELKNQNKIDNALFTFYLPVHDVHAGYLTIGGIEEKFYEGNITYEKLNHDLYWQI
DLDVHFGKQTMEKANVIVDSGTTTITAPSEFLNKFFANLNVIKVPFLPFYVTTCDNKEMPTLEFK
SANNTYTLEPEYYMNPILEVDDTLCMITMLPVDIDSNTFILGDPFMRKYFTVFDYDKESVGFAIA
KN
>d1ile_2 b.51.1.1 (198-386) Isoleucyl-tRNA synthetase (IleRS) {Thermus thermophilus}
KEIQDPSVYVRFPLKEPKKLGLEKASLLIWTTTPWTLPGNVAAAVHPEYTYAAFQVGDEALILEE
GLGRKLLGEGTQVLKTFPGKALEGLPYTPPYPQALEKGYFVVLADYVSQEDGTGIVHQAPAFGAE
DLETARVYGLPLLKTVDEEGKLLVEPFKGLYFREANRAILRDLRGRGLLFKEESYLHSY
>d1ffya2 b.51.1.1 (A:201-394) Isoleucyl-tRNA synthetase (IleRS) {Staphylococcus aureus}
HDKRSASIYVAFNVKDDKGVVDADAKFIIWTTTPWTIPSNVAITVHPELKYGQYNVNGEKYIIAE
ALSDAVAEALDWDKASIKLEKEYTGKELEWVVAQHPFLDRESLVINGDHVTTDAGTGCVHTAPGH
GEDDYIVGQQYELPVISPIDDKGVFTEEGGQFEGMFYDKANKAVTDLLTEKGALLKLDFITHSY
>d1gaxa2 b.51.1.1 (A:190-342) Valyl-tRNA synthetase (ValRS) {Thermus thermophilus}
TEPTPGKLYTLRYEVEGGGFIEIATVRPETVFADQAIAVHPEDERYRHLLGKRARIPLTEVWIPI
LADPAVEKDFGTGALKVTPAHDPLDYEIGERHGLKPVSVINLEGRMEGERVPEALRGLDRFEARR
KAVELFREAGHLVKEEDYTIALA
>d1gmua1 b.107.1.1 (A:1-70) Urease metallochaperone UreE, N-terminal domain {Klebsiella aerogenes}
MLYLTQRLEIPAAATASVTLPIDVRVKSRVKVTLNDGRDAGLLLPRGLLLRGGDVLSNEEGTEFV
QVIAA
>d1eara1 b.107.1.1 (A:1-74) Urease metallochaperone UreE, N-terminal domain {Bacillus pasteurii}
MVITKIVGHIDDLSHQIKKVDWLEVEWEDLNKRILRKETENGTDIAIKLENSGTLRYGDVLYESD
DTLIAIRTK
>d2eng__ b.52.1.1 (-) Endoglucanase V {Humicola insolens}
ADGRSTRYWDCCKPSCGWAKKAPVNQPVFSCNANFQRITDFDAKSGCEPGGVAYSCADQTPWAVN
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DDFALGFAATSIAGSNEAGWCCACYELTFTSGPVAGKKMVVQSTSTGGDLGSNHFDLNIPGGGVG
IFDGCTPQFGGLPGQRYGGISSRNECDRFPDALKPGCYWRFDWFKNADNPSFSFRQVQCPAELVA
RTGCRRNDDGNFPAV
>d1bw3__ b.52.1.2 (-) Barwin {Barley (Hordeum vulgare)}
EQANDVRATYHYYRPAQNNWDLGAPAVSAYCATWDASKPLSWRSKYGWTAFCGPAGPRGQAACGK
CLRVTNPATGAQITARIVDQCANGGLDLDWDTVFTKIDTNGIGYQQGHLNVNYQFVDCRD
>g1aw8.1 b.52.2.1 (A:,B:) Pyruvoyl dependent aspartate decarboxylase, ADC {Escherichia coli}
MIRTMLQGKLHRVKVTHADLHYEGXSCAIDQDFLDAAGILENEAIDIWNVTNGKRFSTYAIAAER
GSRIISVNGAAAHCASVGDIVIIASFVTMPDEEARTWRPNVAYFEGDNEMK
>d1eu1a1 b.52.2.2 (A:626-780) Dimethylsulfoxide reductase (DMSO reductase) {Rhodobacter sphaeroides}
ERLGGAGAKYPLHVVASHPKSRLHSQLNGTSLRDLYAVAGHEPCLINPADAAARGIADGDVLRVF
NDRGQILVGAKVSDAVMPGAIQIYEGGWYDPLDPSEEGTLDKYGDVNVLSLDVGTSKLAQGNCGQ
TILADVEKYAGAPVTVTVFDTPKGA
>d1dmr_1 b.52.2.2 (626-781) Dimethylsulfoxide reductase (DMSO reductase) {Rhodobacter capsulatus}
ERLDGPGAKYPLHIAASHPFNRLHSQLNGTVLREGYAVQGHEPCLMHPDDAAARGIADGDVVRVH
NDRGQILTGVKVTDAVMKGVIQIYEGGWYDPSDVTEPGTLDKYGDVNVLSADIGTSKLAQGNCGQ
TVLAEVEKYTGPAVTLTGFVAPKAAE
>d1aa6_1 b.52.2.2 (565-715) Formate dehydrogenase H {Escherichia coli}
PIDKLTDEYPMVLSTVREVGHYSCRSMTGNCAALAALADEPGYAQINTEDAKRLGIEDEALVWVH
SRKGKIITRAQVSDRPNKGAIYMTYQWWIGACNELVTENLSPITKTPEYKYCAVRVEPIADQRAA
EQYVIDEYNKLKTRLREAALA
>d1tmo_1 b.52.2.2 (632-798) Trimethylamine N-oxide reductase {Shewanella massilia}
ERSHGGPGSDKHPIWLQSCHPDKRLHSQMCESREYRETYAVNGREPVYISPVDAKARGIKDGDIV
RVFNDRGQLLAGAVVSDNFPKGIVRIHEGAWYGPVGKDGSTEGGAEVGALCSYGDPNTLTLDIGT
SKLAQACSAYTCLVEFEKYQGKVPKVSSFDGPIEVEI
>d1g8ka1 b.52.2.2 (A:683-825) Arsenite oxidase large subunit {Alcaligenes faecalis}
LPATVQQQKDKYRFWLNNGRNNEVWQTAYHDQYNSLMQERYPMAYIEMNPDDCKQLDVTGGDIVE
VYNDFGSTFAMVYPVAEIKRGQTFMLFGYVNGIQGDVTTDWTDRDIIPYYKGTWGDIRKVGSMSE
FKRTVSFKSRRFG
>d2napa1 b.52.2.2 (A:601-723) Dissimilatory nitrate reductase (NAP) {Desulfovibrio desulfuricans}
AAEEPDAEYPLYLTSMRVIDHWHTATMTGKVPELQKANPIAFVEINEEDAARTGIKHGDSVIVET
RRDAMELPARVSDVCRPGLIAVPFFDPKKLVNKLFLDATDPVSREPEYKICAARVRKA
>d1qcsa1 b.52.2.3 (A:0-85) N-terminal domain of NSF-N, NSF-Nn {Hamster (Cricetulus griseus)}
NMAGRSMQAARCPTDELSLSNCAVVSEKDYQSGQHVIVRTSPNHKYIFTLRTHPSVVPGSVAFSL
PQRKWAGLSIGQEIEVALYSF
>d1cr5a1 b.52.2.3 (A:26-107) N-terminal domain of NSF-N, NSF-Nn
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{Baker's yeast (Saccharomyces cerevisiae), sec18p}
TRHLKVSNCPNNSYALANVAAVSPNDFPNNIYIIIDNLFVFTTRHSNDIPPGTIGFNGNQRTWGG
WSLNQDVQAKAFDLFKY
>d1cz4a1 b.52.2.3 (A:1-91) N-terminal domain of VAT-N, VAT-Nn
{Archaeon Thermoplasma acidophilum}
MESNNGIILRVAEANSTDPGMSRVRLDESSRRLLDAEIGDVVEIEKVRKTVGRVYRARPEDENKG
IVRIDSVMRNNCGASIGDKVKVRKVR
>d1e32a1 b.52.2.3 (A:21-106) Membrane fusion atpase p97 N-terminal
domain , P97-Nn {Mouse (Mus musculus)}
NRPNRLIVDEAINEDNSVVSLSQPKMDELQLFRGDTVLLKGKKRREAVCIVLSDDTCSDEKIRMN
RVVRNNLRVRLGDVISIQPCP
>d1dfup_ b.53.1.1 (P:) Ribosomal protein L25 {Escherichia coli}
MFTINAEVRKEQGKGASRRLRAANKFPAIIYGGKEAPLAIELDHDKVMNMQAKAEFYSEVLTIVV
DGKEIKVKAQDVQRHPYKPKLQHIDFVRA
>d1feua_ b.53.1.1 (A:) Ribosomal protein TL5 (general stress protein
CTC) {Thermus thermophilus}
MEYRLKAYYREGEKPSALRRAGKLPGLMYNRHLNRKVYVDLVEFDKVFRQASIHHVIVLELPDGQ
SLPTLVRQVNLDKRRRRPEHVDFFVLSDEPVEMYVPLRFVGTPAGVRAGGVLQEIHRDILVKVSP
RNIPEFIEVDVSGLEIGDSLHASDLKLPPGVELAVSPEETIAAVVPPEDVEKLAE
>d1gtra1 b.53.1.2 (A:339-547) Gln-tRNA synthetase (GlnRS), C-terminal
(anticodon-binding) domain {Escherichia coli}
APRAMAVIDPVKLVIENYQGEGEMVTMPNHPNKPEMGSRQVPFSGEIWIDRADFREEANKQYKRL
VLGKEVRLRNAYVIKAERVEKDAEGNITTIFCTYDADTLSKDPADGRKVKGVIHWVSAAHALPVE
IRLYDRLFSVPNPGAADDFLSVINPESLVIKQGFAEPSLKDAVAGKAFQFEREGYFCLDSRHSTA
EKPVFNRTVGLRDT
>d1h9db_ b.54.1.1 (B:) Core binding factor beta, CBF {Human (Homo
sapiens)}
PRVVPDQRSKFENEEFFRKLSRECEIKYTGFRDRPHEERQARFQNACRDGRSEIAFVATGTNLSL
QFFPASWQGEQRQTPSREYVDLEREAGKVYLKAPMILNGVCVIWKGWIDLQRLDGMGCLEFDEER
AQQE
>d1mai__ b.55.1.1 (-) Phospholipase C delta-1 {Rat (Rattus
norvegicus)}
GLQDDPDLQALLKGSQLLKVKSSSWRRERFYKLQEDCKTIWQESRKVMRSPESQLFSIEDIQEVR
MGHRTEGLEKFARDIPEDRCFSIVFKDQRNTLDLIAPSPADAQHWVQGLRKIIH
>d1btn__ b.55.1.1 (-) beta-spectrin {Mouse (Mus musculus), brain}
MEGFLNRKHEWEAHNKKASSRSWHNVYCVINNQEMGFYKDAKSAASGIPYHSEVPVSLKEAICEV
ALDYKKKKHVFKLRLSDGNEYLFQAKDDEEMNTWIQAISSA
>d1dro__ b.55.1.1 (-) beta-spectrin {Fruit fly (Drosophila
melanogaster)}
GSGTGAGEGHEGYVTRKHEWDSTTKKASNRSWDKVYMAAKAGRISFYKDQKGYKSNPELTFRGEP
SYDLQNAAIEIASDYTKKKHVLRVKLANGALFLLQAHDDTEMSQWVTSLKAQSDSTA
>d1dyna_ b.55.1.1 (A:) Dynamin {Human (Homo sapiens)}
ILVIRKGWLTINNIGIMKGGSKEYWFVLTAENLSWYKDDEEKEKKYMLSVDNLKLRDVEKGFMSS
KHIFALFNTEQRNVYKDYRQLELACETQEEVDSWKASFLRAGVYPERV

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>d1btka_ b.55.1.1 (A:) Bruton's tyrosine kinase {Human (Homo sapiens)}
AAVILESIFLKRSQQKKKTSPLNFKKCLFLLTVHKLSYYEYDFERGRRGSKKGSIDVEKITCVET
VVPEKNPPPERQIPRRGEESSEMEQISIIERFPYPFQVVYDEGPLYVFSPTEELRKRWIHQLKNV
IRYNSDLVQKYHPCFWIDGQYLCCSQTAKNAMGCQILEN
>d1pls__ b.55.1.1 (-) Pleckstrin, N-terminal domain {Human (Homo
sapiens)}
MEPKRIREGYLVKKGSVFNTWKPMWVVLLEDGIEFYKKKSDNSPKGMIPLKGSTLTSPCQDFGKR
MFVFKITTTKQQDHFFQAAFLEERDAWVRDINKAIKCIEGLEHHHHHH
>d1dbha2 b.55.1.1 (A:418-550) Son of sevenless-1 (sos-1) {Human (Homo
sapiens)}
AIKKMNEIQKNIDGWEGKDIGQCCNEFIMEGTLTRVGAKHERHIFLFDGLMICCKSNHGQPRLPG
ASNAEYRLKEKFFMRKVQINDKDDTNEYKHAFEIILKDENSVIFSAKSAEEKNNWMAALISLQYR
STL
>d1foea2 b.55.1.1 (A:1240-1401) GEF of TIAM1 (T-Lymphoma invasion and
metastasis indusing protein 1) {Mouse (Mus musculus)}
EFGAVFDQLIAEQTGEKKEVADLSMGDLLLHTSVIWLNPPASLGKWKKEPELAAFVFKTAVVLVY
KDGSKQKKKLVGSHRLSIYEEWDPFRFRHMIPTEALQVRALPSADAEANAVCEIVHVKSESEGRP
ERVFHLCCSSPESRKDFLKSVHSILRDKHRRQ
>d1bak__ b.55.1.1 (-) G-protein coupled receptor kinase 2
(beta-adrenergic receptor kinase 1) {Human (Homo sapiens)}
GSHMGKDCIMHGYMSKMGNPFLTQWQRRYFYLFPNRLEWRGEGEAPQSLLTMEEIQSVEETQIKE
RKCLLLKIRGGKQFILQCDSDPELVQWKKELRDAYREAQQLVQRVPKMKNKPRS
>d1faoa_ b.55.1.1 (A:) Dual adaptor of phosphotyrosine and
3-phosphoinositides DAPP1/PHISH {Human (Homo sapiens)}
PSLGTKEGYLTKQGGLVKTWKTRWFTLHRNELKYFKDQMSPEPIRILDLTECSAVQFDYSQERVN
CFCLVFPFRTFYLCAKTGVEADEWIKILRWKLSQI
>d1fgya_ b.55.1.1 (A:) Grp1 {Mouse (Mus musculus)}
TFFNPDREGWLLKLGGRVKTWKRRWFILTDNCLYYFEYTTDKEPRGIIPLENLSIREVLDPRKPN
CFELYNPSHKGQVIKACKTEADGRVVEGNHVVYRISAPSPEEKEEWMKSIKASISRDPFYDM
>d1fhoa_ b.55.1.1 (A:) UNC-89 {Nematode (Caenorhabditis elegans)}
MGDTGKLGRIIRHDAFQVWEGDEPPKLRYVFLFRNKIMFTEQDASTSPPSYTHYSSIRLDKYNIR
QHTTDEDTIVLQPQEPGLPSFRIKPKDFETSEYVRKAWLRDIAEEQEKYAAERD
>d1aqca_ b.55.1.2 (A:) X11 {Human (Homo sapiens)}
MEDLIDGIIFAANYLGSTQLLSDKTPSKNVRMMQAQEAVSRIKMAQKLAKSRKKAPEGESQPMTE
VDLFILTQRIKVLNADTQETMMDHPLRTISYIADIGNIVVLMARRRIPRSNSQENVEASHPSQDG
KRQYKMICHVFESEDAQLIAQSIGQAFSVAYQEFLR
>d1qqga1 b.55.1.2 (A:12-114) Insulin receptor substrate 1, IRS-1
{Human (Homo sapiens)}
DVRKVGYLRKPKSMHKRFFVLRAASEAGGPARLEYYENEKKWRHKSSAPKRSIPLESCFNINKRA
DSKNKHLVALYTRDEHFAIAADSEAEQDSWYQALLQLH
>d1qqga2 b.55.1.2 (A:159-262) Insulin receptor substrate 1, IRS-1
{Human (Homo sapiens)}
AFKEVWQVILKPKGLGQTKNLIGIYRLCLTSKTISFVKLNSEAAAVVLQLMNIRRCGHSENFFFI
EVGRSAVTGPGEFWMQVDDSVVAQNMHETILEAMRAMSD
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>d1shca_ b.55.1.2 (A:) Shc adaptor protein {Human (Homo sapiens)}
GSHMGQLGGEEWTRHGSFVNKPTRGWLHPNDKVMGPGVSYLVRYMGCVEVLQSMRALDFNTRTQV
TREAISLVCEAVPGAKGATRRRKPCSRPLSSILGRSNLKFAGMPITLTVSTSSLNLMAADCKQII
ANHHMQSISFASGGDPDTAEYVAYVAKDPVNQRACHILECPEGLAQDVISTIGQAFELRFKQYLR
>d1ddma_ b.55.1.2 (A:) Numb {Fruit fly (Drosophila melanogaster)}
HQWQADEEAVRSATCSFSVKYLGCVEVFESRGMQVCEEALKVLRQSRRRPVRGLLHVSGDGLRVV
DDETKGLIVDQTIEKVSFCAPDRNHERGFSYICRDGTTRRWMCHGFLACKDSGERLSHAVGCAFA
VCLER
>d1rrpb_ b.55.1.3 (B:) Nuclear pore complex protein Nup358 {Human (Homo
sapiens)}
HFEPVVPLPDKIEVKTGEEDEEEFFCNRAKLFRFDVESKEWKERGIGNVKILRHKTSGKIRLLMR
REQVLKICANHYISPDMKLTPNAGSDRSFVWHALDYADELPKPEQLAIRFKTPEEAALFKCKFEE
AQSI
>d1k5db_ b.55.1.3 (B:) Ran-binding protein 1, Ranbp1 {Human (Homo
sapiens)}
NHDPQFEPIVSLPEQEIKTLEEDEEELFKMRAKLFRFASENDLPEWKERGTGDVKLLKHKEKGAI
RLLMRRDKTLKICANHYITPMMELKPNAGSDRAWVWNTHADFADECPKPELLAIRFLNAENAQKF
KTKFEECRKEIEEREK
>d1evha_ b.55.1.4 (A:) Enabled {Mouse (Mus musculus)}
SEQSICQARAAVMVYDDANKKWVPAGGSTGFSRVHIYHHTGNNTFRVVGRKIQDHQVVINCAIPK
GLKYNQATQTFHQWRDARQVYGLNFGSKEDANVFASAMMHALEVLN
>d1qc6a_ b.55.1.4 (A:) Ena/vasp-like protein {Mouse (Mus musculus)}
MSEQSICQARASVMVYDDTSKKWVPIKPGQQGFSRINIYHNTASSTFRVVGVKLQDQQVVINYSI
VKGLKYNQATPTFHQWRDARQVYGLNFASKEEATTFSNAMLFALNIMN
>d1egxa_ b.55.1.4 (A:) Vasodilator-stimulated phosphoprotein (VASP)
{Human (Homo sapiens)}
MSETVICSSRATVMLYDDGNKRWLPAGTGPQAFSRVQIYHNPTANSFRVVGRKMQPDQQVVINCA
IVRGVKYNQATPNFHQWRDARQVWGLNFGSKEDAAQFAAGMASALEALEG
>d1ddwa_ b.55.1.4 (A:) Homer {Rat (Rattus norvegicus)}
MGEQPIFSTRAHVFQIDPNTKKNWVPTSKHAVTVSYFYDSTRNVYRIISLDGSKAIINSTITPNM
TFTKTSQKFGQWADSRANTVYGLGFSSEHHLSKFAEKFQEFKEAAR
>d1i7aa_ b.55.1.4 (A:) Homer {Mouse (Mus musculus), 2b/vesl 2}
EQPIFTTRAHVFQIDPSTKKNWVPASKQAVTVSYFYDVTRNSYRIISVDGAKVIINSTITPNMTF
TKTSQKFGQWADSRANTVFGLGFSSELQLTKFAEKFQEVREAAR
>d1e5wa2 b.55.1.5 (A:199-346) Moesin {Human (Homo sapiens)}
EMYGVNYFSIKNKKGSELWLGVDALGLNIYEQNDRLTPKIGFPWSEIRNISFNDKKFVIKPIDKK
APDFVFYAPRLRINKRILALCMGNHELYMRRRKPDTIEVQQMKAQAREEKHQKQMERAMLENEKK
KREMAEKEKEKIEREKEE
>d1ef1a2 b.55.1.5 (A:199-297) Moesin {Human (Homo sapiens)}
EMYGVNYFSIKNKKGSELWLGVDALGLNIYEQNDRLTPKIGFPWSEIRNISFNDKKFVIKPIDKK
APDFVFYAPRLRINKRILALCMGNHELYMRRRKP
>d1gc7a2 b.55.1.5 (A:199-297) Radixin {Mouse (Mus musculus)}
EMYGVNYFEIKNKKGTELWLGVDALGLNIYEHDDKLTPKIGFPWSEIRNISFNDKKFVIKPIDKK
APDFVFYAPRLRINKRILALCMGNHELYMRRRKP
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>d1gg3a2 b.55.1.5 (A:188-279) Erythroid membrane protein 4.1R {Human (Homo sapiens)}
GVDLHKAKDLEGVDIILGVCSSGLLVYKDKLRINRFPWPKVLKISYKRSSFFIKIRPGEQEQYES
TIGFKLPSYRAAKKLWKVCVEHHTFFR
>d1h4ra2 b.55.1.5 (A:215-313) Merlin {Human (Homo sapiens)}
EMYGVNYFAIRNKKGTELLLGVDALGLHIYDPENRLTPKISFPWNEIRNISYSDKEFTIKPLDKK
IDVFKFNSSKLRVNKLILQLCIGNHDLFMRRRKA
>d1ytfc1 b.56.1.1 (C:) Transcription factor IIA (TFIIA), N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
ENLMLCLYDKVTRTKARWKCSLKDGVVTINRNDYTFQKAQVEAEWV
>d1ytfd2 b.56.1.1 (D:55-119) Transcription factor IIA (TFIIA), N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
NTQSKLTVKGNLDTYGFCDDVWTFIVKNCQVTVEDSHRDASQNGSGDSQSVISVDKLRIVACNSK
>d1iega_ b.57.1.1 (A:) Human cytomegalovirus protease {Human cytomegalovirus}
QAVAPVYVGGFLARYDQSPDEAELLLPRDVVEHWLHAQGQGQPSLSVALPLNINHDDTAVVGHVA
AMQSVRDGLFCLGCVTSPRFLEIVRRASEKSELVSRGPVSPLQPDKVVEFLSGSYAGLSLASRRC
DDVEQATSLSGSETTPFKAVALCSVGRRRGTLAVYGRDPEWVTQRFPDLTAADRDGLRAQWQRCG
STAVDASGDPFRSDSYGLLGNSVDALYIRERLPKLRYDKQLVGVTERESYVKA
>d1jq6a_ b.57.1.1 (A:) Human cytomegalovirus protease {Human cytomegalovirus}
VAPVYVGGFLARYDQSPDEAELLLPRDVVEHWLHAQGQGQPSLSVALPLNINHDDTAVVGHVAAM
QSVRDGLFCLGCVTSPRFLEIVRRASEKSELVSRGPVSPLQPDKVVEFLSGSYAGLSLSSRRCDD
VEQATSLSGSETTPFKHVALCSVGRRRGTLAVYGRDPEWVTQRFPDLTAADRDGLRAQWQRCGST
AVDASGDPFRSDSYGLLGNYVDALY
>d1at3a_ b.57.1.1 (A:) HSV-2 protease {Herpes simplex virus type 2}
RAVPIYVAGFLALYDSGDPGELALDPDTVRAALPPENPLPINVDHRARCEVGRVLAVVNDPRGPF
FVGLIACVQLERVLETAASAAIFERRGPALSREERLLYLITNYLPSVSLSTKRRGDEVPPDRTLF
AHVALCAIGRRLGTIVTYDTSLDAAIAPFRHLDPATREGVRREAAEAELALAGRTWAPGVEALTH
TLLSTAVNNMMLRDRWSLVAERRRQAGIAGHTYLQA
>d1fl1a_ b.57.1.1 (A:) KSHV protease {Kaposi's sarcoma-associated herpes virus}
AQGLYVGGFVDVVSCPKLEQELYLDPDQVTDYLPVTEPLPITIEHLPETEVGWTLGLFQVSHGIF
CTGAITSPAFLELASRLADTSHVARAPVKNLPKEPLLEILHTWLPGLSLSSIHPRELSQTPSGPV
FQHVSLCALGRRRGTVAVYGHDAEWVVSRFSSVSKSERAHILQHVSSCRLEDLSTPNFVSPLETL
MAKAIDAGFIRDRLDLLKTDRGVASILSPVYLKA
>d1vzv__ b.57.1.1 (-) VZV protease {Varicella-Zoster virus}
EALYVAGYLALYSKDEGELNITPEIVRSALPPTSKIPINIDHRKDCVVGEVIAIIEDIRGPFFLG
IVRCPQLHAVLFEAAHSNFFGNRDSVLSPLERALYLVTNYLPSVSLSSKRLFTHVALCVVGRRVG
TVVNYDCTPESSIEPFRVLSMESKARLLSLVKDYAGLNKVWKVSEDKLAKVLLSTAVNNMLLRDR
WDVVAKRRREAGIMGH
>d1a49a1 b.58.1.1 (A:116-217) Pyruvate kinase (PK) {Rabbit (Oryctolagus cuniculus)}
PEIRTGLIKGSGTAEVELKKGATLKITLDNAYMEKCDENILWLDYKNICKVVDVGSKVYVDDGLI

SLQVKQKGPDFLVTEVENGGFLGSKKGVNLPGAAVDL
>d1pkm_1 b.58.1.1 (116-217) Pyruvate kinase (PK) {Cat (Felis domestica)}
PEIRTGLIKGSGTAEVELKKGATLKITLDNAYMEKCDENVLWLDYKNICKVVEVGSKVYVDDGLI
SLLVKEKGADFLVTEVENGGSLGSKKGVNLPGAAVDL
>d1pkla1 b.58.1.1 (A:88-186) Pyruvate kinase (PK) {Leishmania mexicana}
EIRTGQFVGGDAVMERGATCYVTTDPAFADKGTKDKFYIDYQNLSKVVRPGNYIYIDDGILILQV
QSHEDEQTLECTVTNSHTISDRRGVNLPGCDVDL
>d1a3wa1 b.58.1.1 (A:88-188) Pyruvate kinase (PK) {Baker's yeast (Saccharomyces cerevisiae)}
PEIRTGTTTNDVDYPIPPNHEMIFTTDDKYAKACDDKIMYVDYKNITKVISAGRIIYVDDGVLSF
QVLEVVDDKTLKVKALNAGKICSHKGVNLPGTDVDL
>d1e0ta1 b.58.1.1 (A:70-167) Pyruvate kinase (PK) {Escherichia coli}
PEIRTMKLEGGNDVSLKAGQTFTFTTDKSVIGNSEMVAVTYEGFTTDLSVGNTVLVDDGLIGMEV
TAIEGNKVICKVLNNGDLGENKGVNLPGVSIAL
>d1g8fa1 b.58.1.2 (A:2-168) ATP sulfurylase N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
PAPHGGILQDLIARDALKKNELLSEAQSSDILVWNLTPRQLCDIELILNGGFSPLTGFLNENDYS
SVVTDSRLADGTLWTIPITLDVDEAFANQIKPDTRIALFQDDEIPIAILTVQDVYKPNKTIEAER
VFRGDPEHPAISYLFNVAGDYYVGGSLEAIQLPQHYD
>d1i2da1 b.58.1.2 (A:2-170) ATP sulfurylase N-terminal domain {Fungus (Penicillium chrysogenum)}
ANAPHGGVLKDLLARDAPRQAELAAEAESLPAVTLTERQLCDLELIMNGGFSPLEGFMNQADYDR
VCEDNRLADGNVFSMPITLDASQEVIDEKKLQAGSRITLRDFRDDRNLAILTIDDIYRPDKTKEA
KLVFGGDPEHPAIVYLNNTVKEFYIGGKIEAVNKLNHYD
>d1jhda1 b.58.1.2 (A:1-173) ATP sulfurylase N-terminal domain {unnamed symbiont of Riftia pachyptila}
MIKPVGSDELKPLFVYDPEEHHKLSHEAESLPSVVISSQAAGNAVMMGAGYFSPLQGFMNVADAM
GAAEKMTLSDGSFFPVPVLCLLENTDAIGDAKRIALRDPNVEGNPVLAVMDIEAIEEVSDEQMAV
MTDKVYRTTDMDHIGVKTFNSQGRVAVSGPIQVLNFSYFQADF
>d1ik9a1 b.59.1.1 (A:1-117) XRCC4, N-terminal domain {Human (Homo sapiens)}
MERKISRIHLVSEPSITHFLQVSWEKTLESGFVITLTDGHSAWTGTVSESEISQEADDMAMEKGK
YVGELRKALLSGAGPADVYTFNFSKESAYFFFEKNLKDVSFRLGSFNLEKVE
>d1hbq__ b.60.1.1 (-) Retinol binding protein {Cow (Bos taurus)}
ERDCRVSSFRVKENFDKARFAGTWYAMAKKDPEGLFLQDNIVAEFSVDENGQMSATAKGRVRLLN
NWDVCADMVGTFTDTEDPAKFKMKYWGVASFLQKGNDDHWIIDTDYETFAVQYSCRLLNLDGTCA
DSYSFVFARDPSGFSPEVQKIVRQRQEELCLARQYRLIPHNGYCNGK
>d1aqb__ b.60.1.1 (-) Retinol binding protein {Pig (Sus scrofa domestica)}
ERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIVAEFSVDENGHMSATAKGRVRLLN
NWDVCADMVGTFTDTEDPAKFKMKYWGVASFLQKGNDDHWIIDTDYDTYAVQYSCRLQNLDGTCA
DSYSFVFARDPHGFSPEVQKIVRQRQEELCLARQYRIITHNGYCD

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>d1rbp__ b.60.1.1 (-) Retinol binding protein {Human (Homo sapiens)}
ERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIVAEFSVDETGQMSATAKGRVRLLN
NWDVCADMVGTFTDTEDPAKFKMKYWGVASFLQKGNDDHWIVDTDYDTYAVQYSCRLLNLDGTCA
DSYSFVFSRDPNGLPPEAQKIVRQRQEELCLARQYRLIVHNGYCD
>d1iiua_ b.60.1.1 (A:) Retinol binding protein {Chicken (Gallus gallus), plasma isoform}
MDCRVSSFKVKENFDKNRYSGTWYAMAKKDPEGLFLQDNVVAQFTVDENGQMSATAKGRVRLFNN
WDVCADMIGSFTDTEDPAKFKMKYWGVASFLQKGNDDHWVVDTDYDTYALHYSCRELNEDGTCAD
SYSFVFSRDPKGLPPEAQKIVRQRQIDLCLDRKYRVIVHNGFCS
>d1hn2a_ b.60.1.1 (A:) Odorant-binding protein {Cow (Bos taurus)}
AQEEEAEQNLSELSGPWRTVYIGSTNPEKIQENGPFRTYFRELVFDDEKGTVDFYFSVKRDGKWK
NVHVKATKQDDGTYVADYEGQNVFKIVSLSRTHLVAHNINVDKHGQTTELTELFVKLNVEDEDLE
KFWKLTEDKGIDKKNVVNFLENENHPHPE
>d1dzka_ b.60.1.1 (A:) Odorant-binding protein {Pig (Sus scrofa)}
FELSGKWITSYIGSSDLEKIGENAPFQVFMRSIEFDDKESKVYLNFFSKENGICEEFSLIGTKQE
GNTYDVNYAGNNKFVVSYASETALIISNINVDEEGDKTIMTGLLGKGTDIEDQDLEKFKEVTREN
GIPEENIVNIIERDDCPA
>d1bj7__ b.60.1.1 (-) Lipocalin allergen {Cow (Bos taurus), bos d 2}
IDPSKIPGEWRIIYAAADNKDKIVEGGPLRNYYRRIECINDCESLSITFYLKDQGTCLLLTEVAK
RQEGYVYVLEFYGTNTLEVIHVSENMLVTYVENYDGERITKMTEGLAKGTSFTPEELEKYQQLNS
ERGVPNENIENLIKTDNCPP
>d1ew3a_ b.60.1.1 (A:) Lipocalin allergen {Horse (Equus caballus), equ c 1}
VAIRNFDISKISGEWYSIFLASDVKEKIEENGSMRVFVDVIRALDNSSLYAEYQTKVNGECTEFP
MVFDKTEEDGVYSLNYDGYNVFRISEFENDEHIILYLVNFDKDRPFQLFEFYAREPDVSPEIKEE
FVKIVQKRGIVKENIIDLTKIDRCFQLRG
>d1e5pa_ b.60.1.1 (A:) Aphrodisin, a sex pheromone {Golden hamster (Mesocricetus auratus)}
FAELQGKWYTIVIAADNLEKIEEGGPLRFYFRHIDCYKNCSEMEITFYVITNNQCSKTTVIGYLK
GNGTYETQFEGNNIFQPLYITSDKIFFTNKNMDRAGQETNMIVVAGKGNALTPEENEILVQFAHE
KKIPVENILNILATDTCPE
>d1beba_ b.60.1.1 (A:) beta-Lactoglobulin {Cow (Bos taurus)}
QTMKGLDIQKVAGTWYSLAMAASDISLLDAQSAPLRVYVEELKPTPEGDLEILLQKWENGECAQK
KIIAEKTKIPAVFKIDALNENKVLVLDTDYKKYLLFCMENSAEPEQSLVCQCLVRTPEVDDEALE
KFDKALKALPMHIRLSFNPTQLEEQC
>d1exsa_ b.60.1.1 (A:) beta-Lactoglobulin {Pig (Sus scrofa)}
VEVTPIMTELDTQKVAGTWHTVAMAVSDVSLLDAKSSPLKAYVEGLKPTPEGDLEILLQKRENDK
CAQEVLLAKKTDIPAVFKINALDENQLFLLDTDYDSHLLLCMENSASPEHSLVCQSLARTLEVDD
QIREKFEDALKTLSVPMRILPAQLEEQCRV
>d1epba_ b.60.1.1 (A:) Retinoic acid-binding protein {Rat (Rattus norvegicus), albino}
VKDFDISKFLGFWYEIAFASKMGTPGLAHKEEKMGAMVVELKENLLALTTTYYSEDHCVLEKVTA
TEGDGPAKFQVTRLSGKKEVVVEATDYLTYAIIDITSLVAGAVHRTMKLYSRSLDDNGEALYNFR
KITSDHGFSETDLYILKHDLTCVKVLQSAA
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>d1jv4a_ b.60.1.1 (A:) Major urinary protein/alpha-2u-globulin {Mouse (Mus musculus)}
EEASSTGRNFNVEKINGEWHTIILASDKREKIEDNGNFRLFLEQIHVLEKSLVLKFHTVRDEECS
ELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLINEKDGETFQLMGLYGREPDLSSDI
KERFAQLCEEHGILRENIIDLSNANRC
>d2a2ua_ b.60.1.1 (A:) Major urinary protein/alpha-2u-globulin {Rat (Rattus norvegicus)}
EEASSTRGNLDVAKLNGDWFSIVVASNKREKIEENGSMRVFMQHIDVLENSLGFKFRIKENGECR
ELYLVAYKTPEDGEYFVEYDGGNTFTILKTDYDRYVMFHLINFKNGETFQLMVLYGRTKDLSSDI
KEKFAKLCEAHGITRDNIIDLTKTDRCL
>d1qqsa_ b.60.1.1 (A:) Neutrophil gelatinase-associated lipocalin (NGAL) {Human (Homo sapiens)}
TSDLIPAPPLSKVPLQQNFQDNQFQGKWYVVGLAGNAILREDKDPQKMYATIYEEKEDASYNVTS
VLFRKKKCDYAIRTFVPGCQPGEFTLGNIKSYPGLTSYLVRVVSTNYNQHAMVFFKKVSQNREYF
KITLYGRTKELTSELKNNFIRFSKSLGLPENHIVFPVPIDQCID
>d1bbpa_ b.60.1.1 (A:) Bilin-binding protein {Cabbage butterfly (Pieris brassicae)}
NVYHDGACPEVKPVDNFDWSNYHGKWWEVAKYPNSVEKYGKCGWAEYTPEGKSVKVSNYHVIHGK
EYFIEGTAYPVGDSKIGKIYHKLTYGGVTKENVFNVLSTDNKNYIIGYYCKYDEDKKGHQDFVWV
LSRSKVLTGEAKTAVENYLIGSPVVDSQKLVYSDFSEAACKVN
>d1i4ua_ b.60.1.1 (A:) Alpha-crustacyanin {European lobster (Homarus gammarus)}
DKIPDFVVPGKCASVDRNKLWAEQTPNRNSYAGVWYQFALTNNPYQLIEKCVRNEYSFDGKQFVI
ESTGIAYDGNLLKRNGKLYPNPFGEPHLSIDYENSFAAPLVILETDYSNYACLYSCIDYNFGYHS
DFSFIFSRSANLADQYVKKCEAAFKNINVDTTRFVKTVQGSSCPYDTQKTL
>d1qfta_ b.60.1.1 (A:) Histamine binding protein {Brown ear tick (Rhipicephalus appendiculatus)}
NQPDWADEAANGAHQDAWKSLKADVENVYYMVKATYKNDPVWGNDFTCVGVMANDVNEDEKSIQA
EFLFMNNADTNMQFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAYSDDNCDVIYVPGTDGN
EEGYELWTTDYDNIPANCLNKFNEYAVGRETRDVFTSACLEIAAA
>d1np1a_ b.60.1.1 (A:) Nitrophorin 1 {Rhodnius prolixus}
KCTKNALAQTGFNKDKYFNGDVWYVTDYLDLEPDDVPKRYCAALAAGTASGKLKEALYHYDPKTQ
DTFYDVSELQEESPGKYTANFKKVEKNGNVKVDVTSGNYYTFTVMYADDSSALIHTCLHKGNKDL
GDLYAVLNRNKDTNAGDKVKGAVTAASLKFSDFISTKDNKCEYDNVSLKSLLTK
>d1euoa_ b.60.1.1 (A:) Nitrophorin 2 (prolixin-s) {Rhodnius prolixus}
MDCSTNISPKQGLDKAKYFSGKWYVTHFLDKDPQVTDQYCSSFTPRESDGTVKEALYHYNANKKT
SFYNIGEGKLESSGLQYTAKYKTVDKKKAVLKEADEKNSYTLTVLEADDSSALVHICLREGSKDL
GDLYTVLTHQKDAEPSAKVKSAVTQAGLQLSQFVGTKDLGCQYDDQFTSL
>d1koia_ b.60.1.1 (A:) Nitrophorin 4 {Rhodnius prolixus}
ACTKNAIAQTGFNKDKYFNGDVWYVTDYLDLEPDDVPKRYCAALAAGTASGKLKEALYHYDPKTQ
DTFYDVSELQVESLGKYTANFKKVDKNGNVKVAVTAGNYYTFTVMYADDSSALIHTCLHKGNKDL
GDLYAVLNRNKDAAAGDKVKSAVSAATLEFSKFISTKENNCAYDNDSLKSLLTK
>d1hms__ b.60.1.2 (-) Muscle fatty acid binding protein (m-fabp) {Human (Homo sapiens)}
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VDAFLGTWKLVDSKNFDDYMKSLGVGFATRQVASMTKPTTIIEKNGDILTLKTHSTFKNTEISFK
LGVEFDETTADDRKVKSIVTLDGGKLVHLQKWDGQETTLVRELIDGKLILTLTHGTAVCTRTYEK
E
>d1bwya_ b.60.1.2 (A:) Muscle fatty acid binding protein (m-fabp) {Cow
(Bos taurus)}
VDAFVGTWKLVDSKNFDDYMKSLGVGFATRQVGNMTKPTTIIEVNGDTVIIKTQSTFKNTEISFK
LGVEFDETTADDRKVKSIVTLDGGKLVHVQKWNGQETSLVREMVDGKLILTLTHGTAVCTRTYEK
QA
>d1a57__ b.60.1.2 (-) Intestinal fatty acid binding protein {Rat
(Rattus norvegicus)}
AFDGTWKVDRNENYSGAHDNLKLTITQEGNKFTVKESSNFRNIDVVFELGVDFAYSLADGTELTG
TWTMEGNKLVGKFKRVDNGKELIAVREISGNELIQTYTYEGVEAKRIFKKE
>d1ifc__ b.60.1.2 (-) Intestinal fatty acid binding protein {Rat
(Rattus norvegicus)}
AFDGTWKVDRNENYEKFMEKMGINVVKRKLGAHDNLKLTITQEGNKFTVKESSNFRNIDVVFELG
VDFAYSLADGTELTGTWTMEGNKLVGKFKRVDNGKELIAVREISGNELIQTYTYEGVEAKRIFKK
E
>d3ifba_ b.60.1.2 (A:) Intestinal fatty acid binding protein {Human
(Homo sapiens)}
AFDSTWKVDRSENYDKFMEKMGVNIVKRKLAAHDNLKLTITQEGNKFTVKESSAFRNIEVVFELG
VTFNYNLADGTELRGTWSLEGNKLIGKFKRTDNGNELNTVREIIGDELVQTYVYEGVEAKRIFKK
D
>d1fdqa_ b.60.1.2 (A:) Brain fatty acid binding protein {Human (Homo
sapiens)}
VEAFCATWKLTNSQNFDEYMKALGVGFATRQVGNVTKPTVIISQEGDKVVIRTLSTFKNTEISFQ
LGEEFDETTADDRNCKSVVSLDGDKLVHIQKWDGKETNFVREIKDGKMVMTLTFGDVVAVRHYEK
A
>d1b56__ b.60.1.2 (-) Epidermal fatty acid binding protein {Human (Homo
sapiens)}
TVQQLEGRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTLKTTQFSC
TLGEKFEETTADGRKTQTVCNFTDGALVQHQEWDGKESTITRKLKDGKLVVECVMNNVTCTRIYE
KVE
>d1lid__ b.60.1.2 (-) Adipocyte lipid-binding protein, ALBP {Mouse
(Mus musculus)}
CDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDLVTIRSESTFKNTEISFK
LGVEFDEITADDRKVKSIITLDGGALVQVQKWDGKSTTIKRKRDGDKLVVECVMKGVTSTRVYER
A
>d1mdc__ b.60.1.2 (-) Fatty acid-binding protein {Tobacco hornworm
(Manduca sexta)}
SYLGKVYSLVKQENFDGFLKSAGLSDDKIQALVSDKPTQKMEANGDSYSNTSTGGGGAKTVSFKS
GVEFDDVIGAGDSVKSMYTVDGNVVTHVVKGDAGVATFKKEYNGDDLVVTITSSNWDGVARRYYK
A
>d1ftpa_ b.60.1.2 (A:) Fatty acid-binding protein {Desert locust
(Schistocerca gregaria)}
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VKEFAGIKYKLDSQTNFEEYMKAIGVGAIERKAGLALSPVIELEILDGDKFKLTSKTAIKNTEFT
FKLGEEFDEETLDGRKVKSTITQDGPNKLVHEQKGDHPTIIIREFSKEQCVITIKLGDLVATRIY
KAQ
>d1cbs__ b.60.1.2 (-) Cellular retinoic-acid-binding protein (CRABP)
{Human (Homo sapiens), CRABP-II}
PNFSGNWKIIRSENFEELLKVLGVNVMLRKIAVAAASKPAVEIKQEGDTFYIKTSTTVRTTEINF
KVGEEFEEQTVDGRPCKSLVKWESENKMVCEQKLLKGEGPKTSWTRELTNDGELILTMTADDVVC
TRVYVRE
>d1cbia_ b.60.1.2 (A:) Cellular retinoic-acid-binding protein (CRABP)
{Cow and mouse (Bos taurus) and (Mus musculus), CRABP-I, identical
sequences}
PNFAGTWKMRSSENFDELLKALGVNAMLRKVAVAAASKPHVEIRQDGDQFYIKTSTTVRTTEINF
KVGEGFEEETVDGRKCRSLPTWENENKIHCTQTLLEGDGPKTYWTRELANDELILTFGADDVVCT
RIYVRE
>d1crb__ b.60.1.2 (-) Cellular retinol-binding protein II (CRBP) {Rat
(Rattus norvegicus)}
PVDFNGYWKMLSNENFEEYLRALDVNVALRKIANLLKPDKEIVQDGDHMIIRTLSTFRNYIMDFQ
VGKEFEEDLTGIDDRKCMTTVSWDGDKLQCVQKGEKEGRGWTQWIEGDELHLEMRAEGVTCKQVF
KKVH
>d1opaa_ b.60.1.2 (A:) Cellular retinol-binding protein II (CRBP) {Rat
(Rattus norvegicus)}
TKDQNGTWEMESNENFEGYMKALDIDFATRKIAVRLTQTKIIVQDGDNFKTKTNSTFRNYDLDFT
VGVEFDEHTKGLDGRNVKTLVTWEGNTLVCVQKGEKENRGWKQWVEGDKLYLELTCGDQVCRQVF
KKK
>d1ggla_ b.60.1.2 (A:) Cellular retinol-binding protein III {Human
(Homo sapiens)}
PPNLTGYYRFVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRNYTVQFD
VGVEFEEDLRSVDGRKCQTIVTWEEEHLVCVQKGEVPNRGWRHWLEGEMLYLELTARDAVCEQVF
RKVH
>d1lfo__ b.60.1.2 (-) Liver fatty acid binding protein {Rat (Rattus
norvegicus)}
MNFSGKYQVQSQENFEPFMKAMGLPEDLIQKGKDIKGVSEIVHEGKKVKLTITYGSKVIHNEFTL
GEECELETMTGEKVKAVVKMEGDNKMVTTFKGIKSVTEFNGDTITNTMTLGDIVYKRVSKRI
>d1pmpa_ b.60.1.2 (A:) P2 myelin protein {Cow (Bos taurus), caudal
spinal root myelin}
SNKFLGTWKLVSSENFDEYMKALGVGLATRKLGNLAKPRVIISKKGDIITIRTESPFKNTEISFK
LGQEFEETTADNRKTKSTVTLARGSLNQVQKWNGNETTIKRKLVDGKMVVECKMKDVVCTRIYEK
V
>d1eal__ b.60.1.2 (-) Ileal lipid binding protein {Pig (Sus scrofa)}
AFTGKYEIESEKNYDEFMKRLALPSDAIDKARNLKIISEVKQDGQNFTWSQQYPGGHSITNTFTI
GKECDIETIGGKKFKATVQMEGGKVVVNSPNYHHTAEIVDGKLVEVSTVGGVSYERVSKKLA
>d1avgi_ b.60.1.3 (I:) Thrombin inhibitor {Triatomine bug (Triatoma
pallidipennis)}
AEGDDCSIEKAMGDFKPEEFFNGTWYLAHGPGVTSPAVCQKFTTSGSKGFTQIVEIGYNKFESNV
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KFQCNQVDNKNGEQYSFKCKSSDNTEFEADFTFISVSYDNFALVCRSITFTSQPKEDRYLVFERT
KSDTDPDAKEIC
>d1swga_ b.61.1.1 (A:) Streptavidin {Streptomyces avidinii}
SRYVLTGRYDSAPATDGSGTALGWTVAWKNNYRNAHSATTWSGQYVGGAEARINTQWLLTSGTTE
ANAWKSTLVGHDTFTKVKPSAASGGGSAEAGITGTWYNQLGSTFIVTAGADGALTGTYESA
>d1swua_ b.61.1.1 (A:) Streptavidin {Streptomyces avidinii}
GITGTWYNQLGSTFIVTAGADGALTGTFESAVGNAESRYVLTGRYDSAPATDGSGTALGWTVAWK
NNYRNAHSATTWSGQYVGGAEARINTQWLLTSGTTEANAWKSTLVGHDTFTKVKP
>d1ij8a_ b.61.1.1 (A:) Avidin {Chicken (Gallus gallus)}
KCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYTTAVTATSNEIKESPLHGTENTINKRTQPTFGFT
VNWKFSESTTVFTGQCFIDRNGKEVLKTMWLLRSSVNDIGDDWKATRVGINIFTRL
>d1smpi_ b.61.2.1 (I:) Metalloprotease inhibitor {Erwinia
chrysanthemi}
SSLRLPSAAELSGQWVLSGAEQHCDIRLNTDVLDGTTWKLAGDTACLQKLLPEAPVGWRPTPDGL
TLTQADGSAVAFFSRNRDRYEHKLVDGSVRTLKKK
>d1jiwi_ b.61.2.1 (I:) Metalloprotease inhibitor {Pseudomonas
aeruginosa, aprin}
SSLILLSASDLAGQWTLQQDEAPAICHLELRDSEVAEASGYDLGGDTACLTRWLPSEPRAWRPTP
AGIALLERGGLTLMLLGRQGEGDYRVQKGDGGQLVLRRAT
>d1ei5a1 b.61.3.1 (A:336-417) D-aminopeptidase, middle and C-terminal
domains {Ochrobactrum anthropi}
EVSRVEADSAWFGSWLDDETGLVLSLEDAGHGRMKARFGTSPEMMDVVSANEARSAVTTIRRDGE
TIELVRASENLRLSMKR
>d1ei5a2 b.61.3.1 (A:418-520) D-aminopeptidase, middle and C-terminal
domains {Ochrobactrum anthropi}
VKGEAKHDIIGRYHSDELDADLLLVSEGGAIYGAFEGFLGKSDMYPLYSVGSDVWLLPVQRSMDA
PSPGEWKLVFRRDDKGEITGLSVGCWLARGVEYRRVQP
>d1jjua5 b.61.4.1 (A:166-273) Quinohemoprotein amine dehydrogenase
A chain, domain 3 {Paracoccus denitrificans}
PDAYADDASGAYVLAGRQPGRGDYTGRLVLKKAGEDYEVTMTLDFADGSRSFSGTGRILGAGEWR
ATLSDGTVTIRQIFALQDGRFSGRWHDADSDVIGGRLAAVKAD
>d1jmxa5 b.61.4.1 (A:163-281) Quinohemoprotein amine dehydrogenase
A chain, domain 3 {Pseudomonas putida}
ESAAWAEWQKARPKADALPGQWAFSGHMLAKGDVRGVMSVTPDQGDTFKVEVKGAYADGTPFNGS
GSAILYNGYEWRGNVKVGDANLRQVFAALDGEMKGRMFEAEHDERGLDFTAVKE
>d2cpl__ b.62.1.1 (-) Cyclophilin (eukaryotic) {Human (Homo sapiens),
variant A}
VNPTVFFDIAVDGEPLGRVSFELFADKVPKTAENFRALSTGEKGFGYKGSCFHRIIPGFMCQGGD
FTRHNGTGGKSIYGEKFEDENFILKHTGPGILSMANAGPNTNGSQFFICTAKTEWLDGKHVVFGK
VKEGMNIVEAMERFGSRNGKTSKKITIADCGQLE
>d1cyna_ b.62.1.1 (A:) Cyclophilin (eukaryotic) {Human (Homo sapiens),
variant B}
GPKVTVKVYFDLRIGDEDVGRVIFGLFGKTVPKTVDNFVALATGEKGFGYKNSKFHRVIKDFMIQ
GGDFTRGDGTGGKSIYGERFPDENFKLKHYGPGWVSMANAGKDTNGSQFFITTVKTAWLDGKHVV
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FGKVLEGMEVVRKVESTKTDSRDKPLKDVIIADCGKIEVEKPFAIAKE
>d1qoia_ b.62.1.1 (A:) Cyclophilin (eukaryotic) {Human (Homo sapiens),
U4/U6 snRNP-specific cyclophilin snucyp-20}
NSSPVNPVVFFDVSIGGQEVGRMKIELFADVVPKTAENFRQFCTGEFRKDGVPIGYKGSTFHRVI
KDFMIQGGDFVNGDGTGVASIYRGPFADENFKLRHSAPGLLSMANSGPSTNGCQFFITCSKCDWL
DGKHVVFGKIIDGLLVMRKIENVPTGPNNKPKLPVVISQCGEM
>d2rmca_ b.62.1.1 (A:) Cyclophilin (eukaryotic) {Mouse (Mus musculus),
variant C}
KRGPSVTDKVFFDVRIGDKDVGRIVIGLFGNVVPKTVENFVALATGEKGYGYKGSIFHRVIKDFM
IQGGDFTARDGTGGMSIYGETFPDENFKLKHYGIGWVSMANAGPDTNGSQFFITLTKPTWLDGKH
VVFGKVLDGMTVVHSIELQATDGHDRPLTDCTIVNSGKIDVKTPFVVEVPDW
>d1a33__ b.62.1.1 (-) Cyclophilin (eukaryotic) {Nematode (Brugia
malayi)}
KDRRRVFLDVTIDGNLAGRIVMELYNDIAPRTCNNFLMLCTGMAGTGKISGKPLHYKGSTFHRVI
KNFMIQGGDFTKGDGTGGESIYGGMFDDEEFVMKHDEPFVVSMANKGPNTNGSQFFITTTPAPHL
NNIHVVFGKVVSGQEVVTKIEYLKTNSKNRPLADVVILNCGELV
>d1dywa_ b.62.1.1 (A:) Cyclophilin (eukaryotic) {Caenorhabditis
elegans, isoform 3}
MSRSKVFFDITIGGKASGRIVMELYDDVVPKTAGNFRALCTGENGIGKSGKPLHFKGSKFHRIIP
NFMIQGGDFTRGNGTGGESIYGEKFPDENFKEKHTGPGVLSMANAGPNTNGSQFFLCTVKTEWLD
GKHVVFGRVVEGLDVVKAVESNGSQSGKPVKDCMIADCGQLK
>d1qnga_ b.62.1.1 (A:) Cyclophilin (eukaryotic) {Plasmodium
falciparum}
SKRSKVFFDISIDNSNAGRIIFELFSDITPRTCENFRALCTGEKIGSRGKNLHYKNSIFHRIIPQ
FMCQGGDITNGNGSGGESIYGRSFTDENFNMKHDQPGLLSMANAGPNTNSSQFFITLVPCPWLDG
KHVVFGKVIEGMNVVREMEKEGAKSGYVKRSVVITDCGEL
>d1ihga2 b.62.1.1 (A:2-196) Cyclophilin 40 isomerase domain {Cow (Bos
taurus)}
SHPSPQAKPSNPSNPRVFFDVDIGGERVGRIVLELFADIVPKTAENFRALCTGEKGIGPTTGKPL
HFKGCPFHRIIKKFMIQGGDFSNQNGTGGESIYGEKFEDENFHYKHDKEGLLSMANAGSNTNGSQ
FFITTVPTPHLDGKHVVFGQVIKGMGVAKILENVEVKGEKPAKLCVIAECGELKEGDDWGIFPKD
>d1clh__ b.62.1.1 (-) Bacterial cyclophilin {Escherichia coli}
AKGDPHVLLTTSAGNIELELDKQKAPVSVQNFVDYVNSGFYNNTTFHRVIPGFMIQGGGFTEQMQ
QKKPNPPIKNEADNGLRNTRGTIAMARTADKDSATSQFFINVADNAFLDHGQRDFGYAVFGKVVK
GMDVADKISQVPTHDVGPYQNVPSKPVVILSAKVLP
>d1lopa_ b.62.1.1 (A:) Bacterial cyclophilin {Escherichia coli}
MVTFHTNHGDIVIKTFDDKAPETVKNFLDYCREGFYNNTIFHRVINGFMIQGGGFEPGMKQKATK
EPIKNEANNGLKNTRGTLAMARTQAPHSATAQFFINVVDNDFLNFSGESLQGWGYCVFAEVVDGM
DEVDKIKGVATGRSGMHQDVPKEDVIIESVTVSE
>d1jsg__ b.63.1.1 (-) p14-TCL1 {Human (Homo sapiens)}
CPTLGEAVTDHPDRLWAWEKFVYLDEKQHAWLPLTIEIKDRLQLRVLLRREDVVLGRPMTPTQIG
PSLLPIMWQLYPDGRYRSSDSSFWRLVYHIKIDGVEDMLLELLPDD
>d1jnpa_ b.63.1.1 (A:) p14-TCL1 {Mouse (Mus musculus)}
RAETPAHPNRLWIWEKHVYLDEFRRSWLPVVIKSNEKFQVILRQEDVTLGEAMSPSQLVPYELPL
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MWQLYPKDRYRSADSMYWQILYHIKFRDVEDMLLEL
>d1a1x__ b.63.1.1 (-) p13-MTCP1 {Human (Homo sapiens)}
AGEDVGAPPDHLWVHQEGIYRDEYQRTWVAVVEEETSFLRARVQQIQVPLGDAARPSHLLTSQLP
LMWQLYPEERYMDNNSRLWQIQHHLMVRGVQELLLKLLPDD
>d1ijaa_ b.100.1.1 (A:) Sortase {Staphylococcus aureus}
MQAKPQIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENESLDDQNISIAGHTFI
DRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRDVKPTDVGVLDEQKGKDKQLTLITCDDYN
EKTGVWEKRKIFVATEVK
>d1c39a_ b.64.1.1 (A:) Cation-dependent mannose 6-phosphate receptor, extracytoplasmic domain {Cow (Bos taurus)}
EKTCDLVGEKGKESEKELALLKRLTPLFQKSFESTVGQSPDMYSYVFRVCREAGQHSSGAGLVQI
QKSNGKETVVGRFNETQIFQGSNWIMLIYKGGDEYDNHCGREQRRAVVMISCNRHTLADNFNPVS
EERGKVQDCFYLFEMDSSLACS
>d1e6fa_ b.64.1.1 (A:) Cation-independent mannose-6-phosphate receptor (MIR-receptor) {Human (Homo sapiens)}
DDCQVTNPSTGHLFDLSSLSGRAGFTAAYSEKGLVYMSICGENENCPPGVGACFGQTRISVGKAN
KRLRYVDQVLQLVYKDGSPCPSKSGLSYKSVISFVCRPEAGPTNRPMLISLDKQTCTLFFSWHTP
LACE
>d1f3ua_ b.65.1.1 (A:) TFIIF beta subunit, Rap30 {Human (Homo sapiens)}
AERGELDLTGAKQNTGVWLVKVPKYLSQQWAKASGRGEVGKLRIAKTQGRTEVSFTLNEDLANIH
DIGGKPASVSAPREHPFVLQSVGGQTLTVFTESSSDKLSLEGIVVQRAECRPA
>d1f3ub_ b.65.1.1 (B:) TFIIF alpha subunit, Rap74 {Human (Homo sapiens)}
GPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFATWNQARLERDLSNKKIYQEEEMPESGAGS
EFNRKLREEARRKKYGIVLKEFRPEDQPWLLRVNGKSGRKFKGIKKGGVTENTSYYIFTQCPDGA
FEAFPVHNWYNFTPLARHR
>d1f3ud_ b.65.1.1 (D:) TFIIF alpha subunit, Rap74 {Human (Homo sapiens)}
SSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFATWNQARLERDLSNKKIYQEEEMPESGAGSEF
NRKLREEARRKKYGIVLKEFRPEDQPWLLRVNGKSGRKFKGIKKGGVTENTSYYIFTQCPDGAFE
AFPVHNWYNFTPLARHRTLTAEEAEEEWERRN
>d1hxn__ b.66.1.1 (-) Hemopexin {Rabbit (Oryctolagus cuniculus)}
ESTRCDPDLVLSAMVSDNHGATYVFSGSHYWRLDTNRDGWHSWPIAHQWPQGPSTVDAAFSWEDK
LYLIQDTKVYVFLTKGGYTLVNGYPKRLEKELGSPPVISLEAVDAAFVCPGSSRLHIMAGRRLWW
LDLKSGAQATWTELPWPHEKVDGALCMEKPLGPNSCSTSGPNLYLIHGPNLYCYRHVDKLNAAKN
LPQPQRVSRLLGCTH
>d1qhua1 b.66.1.1 (A:24-215) Hemopexin {Rabbit (Oryctolagus cuniculus)}
IEQCSDGWSFDATTLDDNGTMLFFKDEFVWKSHRGIRELISERWKNFIGPVDAAFRHGHTSVYLI
KGDKVWVYTSEKNEKVYPKSLQDEFPGIPFPLDAAVECHRGECQDEGILFFQGNRKWFWDLTTGT
KKERSWPAVGNCTSALRWLGRYYCFQGNQFLRFNPVSGEVPPGYPLDVRDYFLSCPGRGHRS
>d1gen__ b.66.1.1 (-) Gelatinase A (MMP-2), C-terminal domain {Human (Homo sapiens)}
LGPVTPEICKQDIVFDGIAQIRGEIFFFKDRFIWRTVTPRDKPMGPLLVATFWPELPEKIDAVYE

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APQEEKAVFFAGNEYWIYSASTLERGYPKPLTSLGLPPDVQRVDAAFNWSKNKKTYIFAGDKFWR
YNEVKKKMDPGFPKLIADAWNAIPDNLDAVVDLQGGGHSYFFKGAYYLKLENQSLKSVKFGSIKS
DWLGC
>d1fbl_1 b.66.1.1 (272-466) Collagenase, C-terminal domain {Pig (Sus
scrofa)}
PQTPQVCDSKLTFDAITTLRGELMFFKDRFYMRTNSFYPEVELNFISVFWPQVPNGLQAAYEIAD
RDEVRFFKGNKYWAVRGQDVLYGYPKDIHRSFGFPSTVKNIDAAVFEEDTGKTYFFVAHECWRYD
EYKQSMDTGYPKMIAEEFPGIGNKVDAVFQKDGFLYFFHGTRQYQFDFKTKRILTLQKANSWFNC
>d1pex__ b.66.1.1 (-) Collagenase-3 (MMP-13), C-terminal domain
{Human (Homo sapiens)}
TPDKCDPSLSLDAITSLRGETMIFKDRFFWRLHPQQVDAELFLTKSFWPELPNRIDAAYEHPSHD
LIFIFRGRKFWALNGYDILEGYPKKISELGLPKEVKKISAAVHFEDTGKTLLFSGNQVWRYDDTN
HIMDKDYPRLIEEDFPGIGDKVDAVYEKNGYIYFFNGPIQFEYSIWSNRIVRVMPANSILWC
>d1tl2a_ b.67.1.1 (A:) Tachylectin-2 {Japanese horseshoe crab
(Tachypleus tridentatus)}
GGESMLRGVYQDKFYQGTYPQNKNDNWLARATLIGKGGWSNFKFLFLSPGGELYGVLNDKIYKGT
PPTHDNDNWMGRAKKIGNGGWNQFQFLFFDPNGYLYAVSKDKLYKASPPQSDTDNWIARATEVGS
GGWSGFKFLFFHPNGYLYAVHGQQFYKALPPVSNQDNWLARATKIGQGGWDTFKFLFFSSVGTLF
GVQGGKFYEDYPPSYAYDNWLARAKLIGNGGWDDFRFLFF
>d3sil__ b.68.1.1 (-) Salmonella sialidase {Salmonella typhimurium,
strain lt2}
EKSVVFKAEGEHFTDQKGNTIVGSGSGGTTKYFRIPAMCTTSKGTIVVFADARHNTASDQSFIDT
AAARSTDGGKTWNKKIAIYNDRVNSKLSRVMDPTCIVANIQGRETILVMVGKWNNNDKTWGAYRD
KAPDTDWDLVLYKSTDDGVTFSKVETNIHDIVTKNGTISAMLGGVGSGLQLNDGKLVFPVQMVRT
KNITTVLNTSFIYSTDGITWSLPSGYCEGFGSENNIIEFNASLVNNIRNSGLRRSFETKDFGKTW
TEFPPMDKKVDNRNHGVQGSTITIPSGNKLVAAHSSAQNKNNDYTRSDISLYAHNLYSGEVKLID
DFYPKVGNASGAGYSCLSYRKNVDKETLYVVYEANGSIEFQDLSRHLPVIKSYN
>d1f8ea_ b.68.1.1 (A:) Influenza neuraminidase {Influenza A virus,
different strains}
RDFNNLTKGLCTINSWHIYGKDNAVRIGEDSDVLVTREPYVSCDPDECRFYALSQGTTIRGKHSN
GTIHDRSQYRALISWPLSSPPTVYNSRVECIGWSSTSCHDGKTRMSICISGPNNNASAVIWYNRR
PVTEINTWARNILRTQESECVCHNGVCPVVFTDGSATGPAETRIYYFKEGKILKWEPLAGTAKHI
EECSCYGERAEITCTCRDNWQGSNRPVIRIDPVAMTHTSQYICSPVLTDNPRPNDPTVGKCNDPY
PGNNNNGVKGFSYLDGVNTWLGRTISIASRSGYEMLKVPNALTDDKSKPTQGQTIVLNTDWSGYS
GSFMDYWAEGECYRACFYVELIRGRPKEDKVWWTSNSIVSMCSSTEFLGQWDWPDGAKIEYFL
>d2bat__ b.68.1.1 (-) Influenza neuraminidase {Influenza A virus,
different strains}
VEYRNWSKPQCQITGFAPFSKDNSIRLSAGGDIWVTREPYVSCDPVKCYQFALGQGTTLDNKHSN
DTVHDRIPHRTLLMNELGVPFHLGTRQVCIAWSSSSCHDGKAWLHVCITGDDKNATASFIYDGRL
VDSIGSWSQNILRTQESECVCINGTCTVVMTDGSASGRADTRILFIEEGKIVHISPLAGSAQHVE
ECSCYPRYPGVRCICRDNWKGSNRPVVDINMEDYSIDSSYVCSGLVGDTPRNDDRSSNSNCRNPN
NERGTQGVKGWAFDNGNDLWMGRTISKDLRSGYETFKVIGGWSTPNSKSQINRQVIVDSDNRSGY
SGIFSVEGKSCINRCFYVELIRGRKQETRVWWTSNSIVVFCGTSGTYGTGSWPDGANINFMPI
>d1inv__ b.68.1.1 (-) Influenza neuraminidase {Influenza B virus,
```

```
different strains}
EPEWTYPRLSCQGSTFQKALLISPHRFGEIKGNSAPLIIREPFVACGPKECRHFALTHYAAQPGG
YYNGTRKDRNKLRHLVSVKLGKIPTVENSIFHMAAWSGSACHDGREWTYIGVDGPDNDALVKIKY
GEAYTDTYHSYAHNILRTQESACNCIGGDCYLMITDGSASGISKCRFLKIREGRIIKEILPTGRV
EHTEECTCGFASNKTIECACRDNSYTAKRPFVKLNVETDTAEIRLMCTKTYLDTPRPDDGSIAGP
CESNGDKWLGGIKGGFVHQRMASKIGRWYSRTMSKTNRMGMELYVRYDGDPWTDSDALTLSGVMV
SIEEPGWYSFGFEIKDKKCDVPCIGIEMVHDGGKDTWHSAATAIYCLMGSGQLLWDTVTGVDMAL
>d1nsca_ b.68.1.1 (A:) Influenza neuraminidase {Influenza B virus,
different strains}
EPEWTYPRLSCQGSTFQKALLISPHRFGEARGNSAPLIIREPFIACGPKECKHFALTHYAAQPGG
YYNGTREDRNKLRHLISVKLGKIPTVENSIFHMAAWSGSACHDGREWTYIGVDGPDSNALIKIKY
GEAYTDTYHSYANNILRTQESACNCIGGDCYLMITDGSASGISKCRFLKIREGRIIKEIFPTGRV
EHTEECTCGFASNKTIECACRDNSYTAKRPFVKLNVETDTAEIRLMCTETYLDTPRPDDGSITGP
CESNGDKGRGGIKGGFVHQRMASKIGRWYSRTMSKTERMGMELYVRYDGDPWTDSDALAHSGVMV
SMKEPGWYSFGFEIKDKKCDVPCIGIEMVHDGGKKTWHSAATAIYCLMGSGQLLWDTVTGVDMAL
>d1e8ua_ b.68.1.1 (A:) Paramyxovirus hemagglutinin-neuraminidase
head domain {Newcastle disease virus}
GAPIHDPDFIGGIGKELIVDNASDVTSFYPSAFQEHLNFIPAPTTGSGCTRIPSFDMSATHYCYT
HNVILSGCRDHSHSHQYLALGVLRTTATGRIFFSTLRSISLDDTQNRKSCSVSATPLGCDMLCSK
VTETEEEDYNSAVPTLMAHGRLGFDGQYHEKDLDVTTLFEDWVANYPGVGGGSFIDGRVWFSVYG
GLKPNSPSDTVQEGKYVIYKRYNDTCPDEQDYQIRMAKSSYKPGRFGGKRIQQAILSIKVSTSLG
EDPVLTVPPNTVTLMGAEGRILTVGTSHFLYQRGSSYFSPALLYPMTVSNKTATLHSPYTFNAFT
RPGSIPCQASARCPNSCVTGVYTDPYPLIFYRNHTLRGVFGTMLDSEQARLNPASAVFDSTSRSR
ITRVSSSSTKAAYTTSTCFKVVKTNKTYCLSIAEISNTLFGEFRIVPLLVEILKND
>d1eur__ b.68.1.1 (-) Micromonospora sialidase, N-terminal domain
{Micromonospora viridifaciens}
GEPLYTEQDLAVNGREGFPNYRIPALTVTPDGDLLASYDGRPTGIDAPGPNSILQRRSTDGGRTW
GEQQVVSAGQTTAPIKGFSDPSYLVDRETGTIFNFHVYSQRQGFAGSRPGTDPADPNVLHANVAT
STDGGLTWSHRTITADITPDPGWRSRFAASGEGIQLRYGPHAGRLIQQYTIINAAGAFQAVSVYS
DDHGRTWRAGEAVGVGMDENKTVELSDGRVLLNSRDSARSGYRKVAVSTDGGHSYGPVTIDRDLP
DPTNNASIIRAFPDAPAGSARAKVLLFSNAASQTSRSQGTIRMSCDDGQTWPVSKVFQPGSMSYS
TLTALPDGTYGLLYEPGTGIRYANFNLAWLGGICAP
>d2sli_2 b.68.1.1 (277-759) Leech intramolecular trans-sialidase,
C-terminal domain {North american leech (Macrobdella decora)}
GENIFYAGDVTESNYFRIPSLLTLSTGTVISAADARYGGTHDSKSKINIAFAKSTDGGNTWSEPT
LPLKFDDYIAKNIDWPRDSVGKNVQIQGSASYIDPVLLEDKLTKRIFLFADLMPAGIGSSNASVG
SGFKEVNGKKYLKLRWHKDAGRAYDYTIREKGVIYNDATNQPTEFRVDGEYNLYQHDTNLTCKQY
DYNFSGNNLIESKTDVDVNMNIFYKNSVFKAFPTNYLAMRYSDDEGASWSDLDIVSSFKPEVSKF
LVVGPGIGKQISTGENAGRLLVPLYSKSSAELGFMYSDDHGDNWTYVEADNLTGGATAEAQIVEM
PDGSLKTYLRTGSNCIAEVTSIDGGETWSDRVPLQGISTTSYGTQLSVINYSQPIDGKPAIILSS
PNATNGRKNGKIWIGLVNDTGNTGIDKYSVEWKYSYAVDTPQMGYSYSCLAELPDGQVGLLYEKY
DSWSRNELHLKDILKFEKYSISELTGQA
>d1kit_3 b.68.1.1 (217-346,544-781) Vibrio cholerae sialidase {Vibrio
cholerae}
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VIFRGPDRIPSIVASSVTPGVVTAFAEKRVGGGDPGALSNTNDIITRTSRDGGITWDTELNLTEQ
INVSDEFDFSDPRPIYDPSSNTVLVSYARWPTDAAQNGDRIKPWMPNGIFYSVYDVASGNWQAPI
XVNPGPGHGITLTRQQNISGSQNGRLIYPAIVLDRFFLNVMSIYSDDGGSNWQTGSTLPIPFRWK
SSSILETLEPSEADMVELQNGDLLLTARLDFNQIVNGVNYSPRQQFLSKDGGITWSLLEANNANV
FSNISTGTVDASITRFEQSDGSHFLLFTNPQGNPAGTNGRQNLGLWFSFDEGVTWKGPIQLVNGA
SAYSDIYQLDSENAIVIVETDNSNMRILRMPITLLKQKLTLSQN
>d1crua_ b.68.2.1 (A:) Soluble quinoprotein glucose dehydrogenase {Acinetobacter calcoaceticus}
DVPLTPSQFAKAKSENFDKKVILSNLNKPHALLWGPDNQIWLTERATGKILRVNPESGSVKTVFQ
VPEIVNDADGQNGLLGFAFHPDFKNNPYIYISGTFKNPKSTDKELPNQTIIRRYTYNKSTDTLEK
PVDLLAGLPSSKDHQSGRLVIGPDQKIYYTIGDQGRNQLAYLFLPNQAQHTPTQQELNGKDYHTY
MGKVLRLNLDGSIPKDNPSFNGVVSHIYTLGHRNPQGLAFTPNGKLLQSEQGPNSDDEINLIVKG
GNYGWPNVAGYKDDSGYAYANYSAAANKSIKDLAQNGVKVAAGVPVTKESEWTGKNFVPPLKTLY
TVQDTYNYNDPTCGEMTYICWPTVAPSSAYVYKGGKKAITGWENTLLVPSLKRGVIFRIKLDPTY
STTYDDAVPMFKSNNRYRDVIASPDGNVLYVLTDTAGNVQKDDGSVTNTLENPGSLIKFT
>d1h6la_ b.68.3.1 (A:) Thermostable phytase (3-phytase) {Bacillus amyloliquefaciens}
KLSDPYHFTVNAAAETEPVDTAGDAADDPAIWLDPKNPQNSKLITTNKKSGLAVYSLEGKMLHSY
HTGKLNNVDIRYDFPLNGKKVDIAAASNRSEGKNTIEIYAIDGKNGTLQSITDPNRPIASAIDEV
YGFSLYHSQKTGKYYAMVTGKEGEFEQYELNADKNGYISGKKVRAFKMNSQTEGMAADDEYGSLY
IAEEDEAIWKFSAEPDGGSNGTVIDRADGRHLTPDIEGLTIYYAADGKGYLLASSQGNSSYAIYE
RQGQNKYVADFQITDGPETDGTSDTDGIDVLGFGLGPEYPFGLFVAQNGENIDHGQKANQNFKMV
PWERIADKIGFHPQVNKQVDPRKMTDRS
>d1crza1 b.68.4.1 (A:141-409) TolB, C-terminal domain {Escherichia coli}
AFRTRIAYVVQTNGGQFPYELRVSDYDGYNQFVVHRSPQPLMSPAWSPDGSKLAYVTFESGRSAL
VIQTLANGAVRQVASFPRHNGAPAFSPDGSKLAFALSKTGSLNLYVMDLASGQIRQVTDGRSNNT
EPTWFPDSQNLAFTSDQAGRPQVYKVNINGGAPQRITWEGSQNQDADVSSDGKFMVMVSSNGGQQ
HIAKQDLATGGVQVLSSTFLDETPSLAPNGTMVIYSSSQGMGSVLNLVSTDGRFKARLPATDGQV
KFPAWSPYL
>d1ijqa1 b.68.5.1 (A:377-642) Low density lipoprotein (LDL) reseptor YWTD domain {Human (Homo sapiens)}
IAYLFFTNRHEVRKMTLDRSEYTSLIPNLRNVVALDTEVASNRIYWSDLSQRMICSTQLDRAHGV
SSYDTVISRDIQAPDGLAVDWIHSNIYWTDSVLGTVSVADTKGVKRKTLFRENGSKPRAIVVDPV
HGFMYWTDWGTPAKIKKGGLNGVDIYSLVTENIQWPNGITLDLLSGRLYWVDSKLHSISSIDVNG
GNRKTILEDEKRLAHPFSLAVFEDKVFWTDIINEAIFSANRLTGSDVNLLAENLLSPEDMVLFHN
LTQPRG
>d1e1aa_ b.68.6.1 (A:) Diisopropylfluorophosphatase (phosphotriesterase, DFP) {Squid (Loligo vulgaris)}
IPVIEPLFTKVTEDIPGAEGPVFDKNGDFYIVAPEVEVNGKPAGEILRIDLKTGKKTVICKPEVN
GYGGIPAGCQCDRDANQLFVADMRLGLLVVQTDGTFEEIAKKDSEGRRMQGCNDCAFDYEGNLWI
TAPAGEVAPADYTRSMQEKFGSIYCFTTDGQMIQVDTAFQFPNGIAVRHMNDGRPYQLIVAETPT
KKLWSYDIKGPAKIENKKVWGHIPGTHEGGADGMDFDEDNNLLVANWGSSHIEVFGPDGGQPKMR
IRCPFEKPSNLHFKPQTKTIFVTEHENNAVWKFEWQRNGKKQYCETLKFGIF

>d1k32a2 b.68.7.1 (A:39-319) Tricorn protease N-terminal domain {Archaeon Thermoplasma acidophilum}
MPNLLLNPDIHGDRIIFVCCDDLWEHDLKSGSTRKIVSNLGVINNARFFPDGRKIAIRVMRGSSL
NTADLYFYNGENGEIKRITYFSGKSTGRRMFTDVAGFDPDGNLIISTDAMQPFSSMTCLYRVEND
GINFVPLNLGPATHILFADGRRVIGRNTFELPHWKGYRGGTRGKIWIEVNSGAFKKIVDMSTHVS
SPVIVGHRIYFITDIDGFGQIYSTDLDGKDLRKHTSFTDYYPRHLNTDGRRILFSKGGSIYIFNP
DTEKIEKIEIGDLESPEDRII
>d1k3ia3 b.69.1.1 (A:151-537) Galactose oxidase, central domain {Fungi (Fusarium spp)}
YTAPQPGLGRWGPTIDLPIVPAAAAIEPTSGRVLMWSSYRNDAFGGSPGGITLTSSWDPSTGIVS
DRTVTVTKHDMFCPGISMDGNGQIVVTGGNDAKKTSLYDSSSDSWIPGPDMQVARGYQSSATMSD
GRVFTIGGSWSGGVFEKNGEVYSPSSKTWTSLPNAKVNPMLTADKQGLYRSDNHAWLFGWKKGSV
FQAGPSTAMNWYYTSGSGDVKSAGKRQSNRGVAPDAMCGNAVMYDAVKGKILTFGGSPDYQDSDA
TTNAHIITLGEPGTSPNTVFASNGLYFARTFHTSVVLPDGSTFITGGQRRGIPFEDSTPVFTPEI
YVPEQDTFYKQNPNSIVRVYHSISLLLPDGRVFNGGGGLCGDCTTNHFDAQIFTPNYLYNSN
>d1mdah_ b.69.2.1 (H:) Methylamine dehydrogenase, H-chain {Paracoccus denitrificans}
EKSKVAGSAAAASAAAASDGSSCDHGPGAISRRSHITLPAYFAGTTENWVSCAGCGVTLGHSLGA
FLSLAVAGHSGSDFALASTSFARSAKGKRTDYVEVFDPVTFLPIADIELPDAPRFSVGPRVHIIG
NCASSACLLFFLFGSSAAAGLSVPGASDDQLTKSASCFHIHPGAAATHYLGSCPASLAASDLAAA
PAAAGIVGAQCTGAQNCSSQAAQANYPGMLVWAVASSILQGDIPAAGATMKAAIDGNESGRKADN
FRSAGFQMVAKLKNTDGIMILTVEHSRSCLAAAENTSSVTASVGQTSGPISNGHDSDAIIAAQDG
ASDNYANSAGTEVLDIYDAASDQDQSSVELDKGPESLSVQNEA
>d2bbkh_ b.69.2.1 (H:) Methylamine dehydrogenase, H-chain {Paracoccus denitrificans}
DEPRILEAPAPDARRVYVNDPAHFAAVTQQFVIDGEAGRVIGMIDGGFLPNPVVADDGSFIAHAS
TVFSRIARGERTDYVEVFDPVTLLPTADIELPDAPRFLVGTYPWMTSLTPDGKTLLFYQFSPAPA
VGVVDLEGKAFKRMLDVPDCYHIFPTAPDTFFMHCRDGSLAKVAFGTEGTPEITHTEVFHPEDEF
LINHPAYSQKAGRLVWPTYTGKIHQIDLSSGDAKFLPAVEALTEAERADGWRPGGWQQVAYHRAL
DRIYLLVDQRDEWRHKTASRFVVVLDAKTGERLAKFEMGHEIDSINVSQDEKPLLYALSTGDKTL
YIHDAESGEELRSVNQLGHGPQVITTADMG
>d2madh_ b.69.2.1 (H:) Methylamine dehydrogenase, H-chain {Gram negative methylotrophic bacteria (Thiobacillus versutus)}
SSASAAAAAAAAALAAGAADGPTNDEAPGADGRRSYINLPAHHSAIIQQWVLDAGSGSILGHVNG
GFLPNPVAAHSGSEFALASTSFSRIAKGKRTDYVEVFDPVTFLPIADIELPDAPRFDVGPYSWMN
ANTPNNADLLFFQFAAGPAVGLVVQGGSSDDQLLSSPTCYHIHPGAPSTFYLLCAQGGLAKTDHA
GGAAGAGLVGAMLTAAQNLLTQPAQANKSGRIVWPVYSGKILQADISAAGATNKAPIDALSGGRK
ADTWRPGGWQQVAYLKSSDGIYLLTSEQSAWKLHAAAKEVTSVTGLVGQTSSQISLGHDVDAISV
AQDGGPDLYALSAGTEVLHIYDAGAGDQDQSTVELGSGPQVLSVMNEA
>d1jjub_ b.69.2.2 (B:) Quinohemoprotein amine dehydrogenase B chain {Paracoccus denitrificans}
RDYILAPARPDKLVVIDTEKMAVDKVITIADAGPTPMVPMVAPGGRIAYATVNKSESLVKIDLVT
GETLGRIDLSTPEERVKSLFGAALSPDGKTLAIYESPVRLELTHFEVQPTRVALYDAETLSRRKA
FEAPRQITMLAWARDGSKLYGLGRDLHVMDPEAGTLVEDKPIQSWEAETYAQPDVLAVWNQHESS

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GVMATPFYTARKDIDPADPTAYRTGLLTMDLETGEMAMREVRIMDVFYFSTAVNPAKTRAFGAYN
VLESFDLEKNASIKRVPLPHSYYSVNVSTDGSTVWLGGALGDLAAYDAETLEKKGQVDLPGNASM
SLASVRLFTRDE
>d1jmxb_ b.69.2.2 (B:) Quinohemoprotein amine dehydrogenase B chain
{Pseudomonas putida}
GPALKAGHEYMIVTNYPNNLHVVDVASDTVYKSCVMPDKFGPGTAMMAPDNRTAYVLNNHYGDIY
GIDLDTCKNTFHANLSSVPGEVGRSMYSFAISPDGKEVYATVNPTQRLNDHYVVKPPRLEVFSTA
DGLEAKPVRTFPMPRQVYLMRAADDGSLYVAGPDIYKMDVKTGKYTVALPLRNWNRKGYSAPDVL
YFWPHQSPRHEFSMLYTIARFKDDKQDPATADLLYGYLSVDLKTGKTHTQEFADLTELYFTGLRS
PKDPNQIYGVLNRLAKYDLKQRKLIKAANLDHTYYCVAFDKKGDKLYLGGTFNDLAVFNPDTLEK
VKNIKLPGGDMSTTTPQVFIR
>d1qnia2 b.69.3.1 (A:10-450) Nitrous oxide reductase, N-terminal
domain {Pseudomonas nautica}
AHVAPGELDEYYGFWSGGHQGEVRVLGVPSMRELMRIPVFNVDSATGWGITNESKEILGGDQQYL
NGDCHHPHISMTDGRYDGKYLFINDKANTRVARIRLDIMKTDKITHIPNVQAIHGLRLQKVPKTN
YVFCNAEFVIPQPNDGTDFSLDNSYTMFTAIDAETMDVAWQVIVDGNLDNTDADYTGKYATSTCY
NSERAVDLAGTMRNDRDWVVVFNVERIAAAVKAGNFKTIGDSKVPVVDGRGESEFTRYIPVPKNP
HGLNTSPDGKYFIANGKLSPTVSVIAIDKLDDLFEDKIELRDTIVAEPELGLGPLHTTFDGRGNA
YTTLFIDSQVCKWNIADAIKHYNGDRVNYIRQKLDVQYQPGHNHASLTESRDADGKWLVVLSKFS
KDRFLPVGPLHPENDQLIDISGEEMKLVHDGPTYAEPHDCILVRRDQIKTK
>d1fwxa2 b.69.3.1 (A:8-451) Nitrous oxide reductase, N-terminal
domain {Paracoccus denitrificans}
ADGSVAPGQLDDYYGFWSSGQSGEMRILGIPSMRELMRVPVFNRCSATGWGQTNESVRIHERTMS
ERTKKFLAANGKRIHDNGDLHHVHMSFTEGKYDGRFLFMNDKANTRVARVRCDVMKCDAILEIPN
AKGIHGLRPQKWPRSNYVFCNGEDETPLVNDGTNMEDVANYVNVFTAVDADKWEVAWQVLVSGNL
DNCDADYEGKWAFSTSYNSEKGMTLPEMTAAEMDHIVVFNIAEIEKAIAAGDYQELNGVKVVDGR
KEASSLFTRYIPIANNPHGCNMAPDKKHLCVAGKLSPTVTVLDVTRFDAVFYENADPRSAVVAEP
ELGLGPLHTAFDGRGNAYTSLFLDSQVVKWNIEDAIRAYAGEKVDPIKDKLDVHYQPGHLKTVMG
ETLDATNDWLVCLSKFSKDRFLNVGPLKPENDQLIDISGDKMVLVHDGPTFAEPHDAIAVHPSIL
SDIK
>d1tbga_ b.69.4.1 (A:) beta1-subunit of the signal-transducing G
protein heterotrimer {Cow (Bos taurus)}
MSELDQLRQEAEQLKNQIRDARKACADATLSQITNNIDPVGRIQMRTRRTLRGHLAKIYAMHWGT
DSRLLVSASQDGKLIIWDSYTTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTRE
GNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIETGQQTTTFTGHTGDVMSLSLAPD
TRLFVSGACDASAKLWDVREGMCRQTFTGHESDINAICFFPNGNAFATGSDDATCRLFDLRADQE
LMTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRAGVLAGHDNRVSCLGVTDDGM
AVATGSWDSFLKIWN
>d1erja_ b.69.4.1 (A:) Tup1, C-therminal domain {Baker's yeast
(Saccharomyces cerevisiae)}
HYLVPYNQRANHSKPIPPFLLDLDSQSVPDALKKQTNDYYILYNPALPREIDVELHKSLDHTSVV
CCVKFSNDGEYLATGCNKTTQVYRVSDGSLVARLSDDSAANKDPENLNTSSSPSSDLYIRSVCFS
PDGKFLATGAEDRLIRIWDIENRKIVMILQGHEQDIYSLDYFPSGDKLVSGSGDRTVRIWDLRTG
QCSLTLSIEDGVTTVAVSPGDGKYIAAGSLDRAVRVWDSETGFLVERLDSENESGTGHKDSVYSV
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VFTRDGQSVVSGSLDRSVKLWNLQNANNKSDSKTPNSGTCEVTYIGHKDFVLSVATTQNDEYILS
GSKDRGVLFWDKKSGNPLLMLQGHRNSVISVAVANGSSLGPEYNVFATGSGDCKARIWKYKKI
>d1k8kc_ b.69.4.1 (C:) Arp2/3 complex 41 kDa subunit ARPC1 {Cow (Bos
taurus)}
AYHSFLVEPISCHAWNKDRTQIAICPNNHEVHIYEKSGNKWVQVHELKEHNGQVTGVDWAPDSNR
IVTCGTDRNAYVWTLKGRTWKPTLVILRINRAARCVRWAPNEKKFAVGSGSRVISICYFEQENDW
WVCKHIKKPIRSTVLSLDWHPNSVLLAAGSCDFKCRIFSAYIKEVEERPAPTPWGSKMPFGELMF
ESSSSCGWVHGVCFSANGSRVAWVSHDSTVCLADADKKMAVATLASETLPLLAVTFITESSLVAA
GHDCFPVLFTYDSAAGKLSFGGRLDVPKQSSQRGLTARERFQNLDKKASSEGSAAAGAGLDSLHK
NSVSQISVLSGGKAKCSQFCTTGMDGGMSIWDVRSLESALKDLKIV
>d1a12a_ b.69.5.1 (A:) Regulator of chromosome condensation RCC1
{Human (Homo sapiens)}
KKVKVSHRSHSTEPGLVLTLGQGDVGQLGLGENVMERKKPALVSIPEDVVQAEAGGMHTVCLSKS
GQVYSFGCNDEGALGRDTSVEGSEMVPGKVELQEKVVQVSAGDSHTAALTDDGRVFLWGSFRDNN
GVIGLLEPMKKSMVPVQVQLDVPVVKVASGNDHLVMLTADGDLYTLGCGEQGQLGRVPELFANRG
GRQGLERLLVPKCVMLKSRGSRGHVRFQDAFCGAYFTFAISHEGHVYGFGLSNYHQLGTPGTESC
FIPQNLTSFKNSTKSWVGFSGGQHHTVCMDSEGKAYSLGRAEYGRLGLGEGAEEKSIPTLISRLP
AVSSVACGASVGYAVTKDGRVFAWGMGTNYQLGTGQDEDAWSPVEMMGKQLENRVVLSVSSGGQH
TVLLVKDKEQS
>d1jtdb_ b.69.5.2 (B:) of beta-lactamase inhibitor protein-II,
BLIP-II {Streptomyces exfoliatus}
VAATSVVAWGGNNDWGEATVPAEAQSGVDAIAGGYFHGLALKGGKVLGWGANLNGQLTMPAATQS
GVDAIAAGNYHSLALKDGEVIAWGGNEDGQTTVPAEARSGVDAIAAGAWASYALKDGKVIAWGDD
SDGQTTVPAEAQSGVTALDGGVYTALAVKNGGVIAWGDNYFGQTTVPAEAQSGVDDVAGGIFHSL
ALKDGKVIAWGDNRYKQTTVPTEALSGVSAIASGEWYSLALKNGKVIAWGSSRTAPSSVQSGVSS
IEAGPNAAYALKG
>d1c9la2 b.69.6.1 (A:3-330) Clathrin heavy-chain terminal domain {Rat
(Rattus norvegicus)}
QILPIRFQEHLQLQNLGINPANIGFSTLTMESDKFICIREKVGEQAQVVIIDMNDPSNPIRRPIS
ADSAIMNPASKVIALKAGKTLQIFNIEMKSKMKAHTMTDDVTFWKWISLNTVALVTDNAVYHWSM
EGESQPVKMFDRHSSLAGCQIINYRTDAKQKWLLLTGISAQQNRVVGAMQLYSVDRKVSQPIEGH
AASFAQFKMEGNAEESTLFCFAVRGQAGGKLHIIEVGTPPTGNQPFPKKAVDVFFPPEAQNDFPV
AMQISEKHDVVFLITKYGYIHLYDLETGTCIYMNRISGETIFVTAPHEATAGIIGVNRKGQVLSV
CVE
>d1jv2a4 b.69.8.1 (A:1-438) Integrin alpha N-terminal domain {Human
(Homo sapiens)}
FNLDVDSPAEYSGPEGSYFGFAVDFFVPSASSRMFLLVGAPKANTTQPGIVEGGQVLKCDWSSTR
RCQPIEFDATGNRDYAKDDPLEFKSHQWFGASVRSKQDKILACAPLYHWRTEMKQEREPVGTCFL
QDGTKTVEYAPCRSQDIDADGQGFCQGGFSIDFTKADRVLLGGPGSFYWQGQLISDQVAEIVSKY
DPNVYSIKYNNQLATRTAQAIFDDSYLGYSVAVGDFNGDGIDDFVSGVPRAARTLGMVYIYDGKN
MSSLYNFTGEQMAAYFGFSVAATDINGDDYADVFIGAPLFMDRGSDGKLQEVGQVSVSLQRASGD
FQTTKLNGFEVFARFGSAIAPLGDLDQDGFNDIAIAAPYGGEDKKGIVYIFNGRSTGLNAVPSQI
LEGQWAARSMPPSFGYSMKGATDIDKNGYPDLIVGAFGVDRAILYRAR
>d1qfma1 b.69.7.1 (A:1-430) Prolyl oligopeptidase, N-terminal domain
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{Pig (Sus scrofa)}
MLSFQYPDVYRDETAIQDYHGHKVCDPYAWLEDPDSEQTKAFVEAQNKITVPFLEQCPIRGLYKE
RMTELYDYPKYSCHFKKGKRYFYFYNTGLQNQRVLYVQDSLEGEARVFLDPNILSDDGTVALRGY
AFSEDGEYFAYGLSASGSDWVTIKFMKVDGAKELPDVLERVKFSCMAWTHDGKGMFYNAYPQQDG
KSDGTETSTNLHQKLYYHVLGTDQSEDILCAEFPDEPKWMGGAELSDDGRYVLLSIREGCDPVNR
LWYCDLQQESNGITGILKWVKLIDNFEGEYDYVTNEGTVFTFKTNRHSPNYRLINIDFTDPEESK
WKVLVPEHEKDVLEWVACVRSNFLVLCYLHDVKNTLQLHDLATGALLKIFPLEVGSVVGYSGQKK
DTEIFYQFTSFLSPGIIYHCDLTKEELEPRVFREVTVKGI
>d1k32a3 b.69.9.1 (A:320-679) Tricorn protease N-terminal domain {Archaeon Thermoplasma acidophilum}
SIPSKFAEDFSPLDGDLIAFVSRGQAFIQDVSGTYVLKVPEPLRIRYVRRGGDTKVAFIHGTREG
DFLGIYDYRTGKAEKFEENLGNVFAMGVDRNGKFAVVANDRFEIMTVDLETGKPTVIERSREAMI
TDFTISDNSRFIAYGFPLKHGETDGYVMQAIHVYDMEGRKIFAATTENSHDYAPAFDADSKNLYY
LSYRSLDPSPDRVVLNFSFEVVSKPFVIPLIPGSPNPTKLVPRSMTSEAGEYDLNDMYKRSSPIN
VDPGDYRMIIPLESSILIYSVPVHGEFAAYYQGAPEKGVLLKYDVKTRKVTEVKNNLTDLRLSAD
RKTVMVRKDDGKIYTFPLEKPEDERTVETDKRPLV
>d1g72a_ b.70.1.1 (A:) Methanol dehydrogenase, heavy chain {Methylophilus methylotrophus, w3a1}
DADLDKQVNTAGAWPIATGGYYSQHNSPLAQINKSNVKNVKAAWSFSTGVLNGHEGAPLVIGDMM
YVHSAFPNNTYALNLNDPGKIVWQHKPKQDASTKAVMCCDVVDRGLAYGAGQIVKKQANGHLLAL
DAKTGKINWEVEVCDPKVGSTLTQAPFVAKDTVLMGCSGAELGVRGAVNAFDLKTGELKWRAFAT
GSDDSVRLAKDFNSANPHYGQFGLGTKTWEGDAWKIGGGTNWGWYAYDPKLNLFYYGSGNPAPWN
ETMRPGDNKWTMTIWGRDLDTGMAKWGYQKTPHDEWDFAGVNQMVLTDQPVNGKMTPLLSHIDRN
GILYTLNRENGNLIVAEKVDPAVNVFKKVDLKTGTPVRDPEFATRMDHKGTNICPSAMGFHNQGV
DSYDPESRTLYAGLNHICMDWEPFMLPYRAGQFFVGATLAMYPGPNGPTKKEMGQIRAFDLTTGK
AKWTKWEKFAAWGGTLYTKGGLVWYATLDGYLKALDNKDGKELWNFKMPSGGIGSPMTYSFKGKQ
YIGSMYGVGGWPGVGLVFDLTDPSAGLGAVGAFRELQNHTQMGGGLMVFSL
>d1h4ia_ b.70.1.1 (A:) Methanol dehydrogenase, heavy chain {Methylobacterium extorquens}
NDKLVELSKSDDNWVMPGKNYDSNNFSDLKQINKGNVKQLRPAWTFSTGLLNGHEGAPLVVDGKM
YIHTSFPNNTFALGLDDPGTILWQDKPKQNPAARAVACCDLVNRGLAYWPGDGKTPALILKTQLD
GNVAALNAETGETVWKVENSDIKVGSTLTIAPYVVKDKVIIGSSGAELGVRGYLTAYDVKTGEQV
WRAYATGPDKDLLLASDFNIKNPHYGQKGLGTGTWEGDAWKIGGGTNWGWYAYDPGTNLIYFGTG
NPAPWNETMRPGDNKWTMTIFGRDADTGEAKFGYQKTPHDEWDYAGVNVMMLSEQKDKDGKARKL
LTHPDRNGIVYTLDRTDGALVSANKLDDTVNVFKSVDLKTGQPVRDPEYGTRMDHLAKDICPSAM
GYHNQGHDSYDPKRELFFMGINHICMDWEPFMLPYRAGQFFVGATLNMYPGPKGDRQNYEGLGQI
KAYNAITGDYKWEKMERFAVWGGTMATAGDLVFYGTLDGYLKARDSDTGDLLWKFKIPSGAIGYP
MTYTHKGTQYVAIYYGVGGWPGVGLVFDLADPTAGLGAVGAFKKLANYTQMGGGVVVFSLDGKGP
YDDPNVGEWK
>d1flga_ b.70.1.1 (A:) Ethanol dehydrogenase {Pseudomonas aeruginosa}
KDVTWEDIANDDKTTGDVLQYGMGTHAQRWSPLKQVNADNVFKLTPAWSYSFGDEKQRGQESQAI
VSDGVIYVTASYSRLFALDAKTGKRLWTYNHRLPDDIRPCCDVVNRGAAIYGDKVFFGTLDASVV
ALNKNTGKVVWKKKFADHGAGYTMTGAPTIVKDGKTGKVLLIHGSSGDEFGVVGRLFARDPDTGE
EIWMRPFVEGHMGRLNGKDSTVTGDVKAPSWPDDRNSPTGKVESWSHGGGAPWQSASFDAETNTI

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IVGAGNPGPWNTWARTAKGGNPHDYDSLYTSGQVGVDPSSGEVKWFYQHTPNDAWDFSGNNELVL
FDYKAKDGKIVKATAHADRNGFFYVVDRSNGKLQNAFPFVDNITWASHIDLKTGRPVEREGQRPP
LPEPGQKHGKAVEVSPPFLGGKNWNPMAYSQDTGLFYVPANHWKEDYWTEEVSYTKGSAYLGMGF
RIKRMYDDHVGSLRAMDPVSGKVVWEHKEHLPLWAGVLATAGNLVFTGTGDGYFKAFDAKSGKEL
WKFQTGSGIVSPPITWEQDGEQYLGVTVGYGGAVPLWGGDMADLTRPVAQGGSFWVFKLPSW
>d1kb0a2 b.70.1.1 (A:1-573) Quinoprotein alcohol dehydrogenase, N-terminal domain {Comamonas testosteroni}
TGPAAQAAAAVQRVDGDFIRANAARTPDWPTIGVDYAETRYSRLDQINAANVKDLGLAWSYNLES
TRGVEATPVVVDGIMYVSASWSVVHAIDTRTGNRIWTYDPQIDRSTGFKGCCDVVNRGVALWKGK
VYVGAWDGRLIALDAATGKEVWHQNTFEGQKGSLTITGAPRVFKGKVIIGNGGAEYGVRGYITAY
DAETGERKWRWFSVPGDPSKPFEDESMKRAARTWDPSGKWWEAGGGGTMWDSMTFDAELNTMYVG
TGNGSPWSHKVRSPKGGDNLYLASIVALDPDTGKYKWHYQETPGDNWDYTSTQPMILADIKIAGK
PRKVILHAPKNGFFFVLDRTNGKFISAKNFVPVNWASGYDKHGKPIGIAAARDGSKPQDAVPGPY
GAHNWHPMSFNPQTGLVYLPAQNVPVNLMDDKKWEFNQAGPGKPQSGTGWNTAKFFNAEPPKSKP
FGRLLAWDPVAQKAAWSVEHVSPWNGGTLTTAGNVVFQGTADGRLVAYHAATGEKLWEAPTGTGV
VAAPSTYMVDGRQYVSVAVGWGGVYGLAARATERQGPGTVYTFVVGGKARMPE
>d1nira2 b.70.2.1 (A:118-543) C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase {Pseudomonas aeruginosa}
EWGMPEMRESWKVLVKPEDRPKKQLNDLDLPNLFSVTLRDAGQIALVDGDSKKIVKVIDTGYAVH
ISRMSASGRYLLVIGRDARIDMIDLWAKEPTKVAEIKIGIEARSVESSKFKGYEDRYTIAGAYWP
PQFAIMDGETLEPKQIVSTRGMTVDTQTYHPEPRVAAIIASHEHPEFIVNVKETGKVLLVNYKDI
DNLTVTSIGAAPFLHDGGWDSSHRYFMTAANNSNKVAVIDSKDRRLSALVDVGKTPHPGRGANFV
HPKYGPVWSTSHLGDGSISLIGTDPKNHPQYAWKKVAELQGQGGGSLFIKTHPKSSHLYVDTTFN
PDARISQSVAVFDLKNLDAKYQVLPIAEWADLGEGAKRVVQPEYNKRGDEVWFSVWNGKNDSSAL
VVVDDKTLKLKAVVKDPRLITPTGKFNVYNTQHDVY
>d1qksa2 b.70.2.1 (A:136-567) C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase {Paracoccus denitrificans}
EFGMKEMRESWKVHVAPEDRPTQQMNDWDLENLFSVTLRDAGQIALIDGSTYEIKTVLDTGYAVH
ISRLSASGRYLFVIGRDGKVNMIDLWMKEPTTVAEIKIGSEARSIETSKMEGWEDKYAIAGAYWP
PQYVIMDGETLEPKKIQSTRGMTYDEQEYHPEPRVAAILASHYRPEFIVNVKETGKILLVDYTDL
NNLKTTEISAERFLHDGGLDGSHRYFITAANARNKLVVIDTKEGKLVAIEDTGGQTPHPGRGANF
VHPTFGPVWATSHMGDDSVALIGTDPEGHPDNAWKILDSFPALGGGSLFIKTHPNSQYLYVDATL
NPEAEISGSVAVFDIKAMTGDGSDPEFKTLPIAEWAGITEGQPRVVQGEFNKDGTEVWFSVWNGK
DQESALVVVDDKTLELKHVIKDERLVTPTGKFNVYNTMTDTY
>d1e43a1 b.71.1.1 (A:394-483) Bacterial alpha-Amylase {Bacillus licheniformis}
YAYGAQHDYFDHHDIVGWTREGDSSVANSGLAALITDGPGGAKRMYVGRQNAGETWHDITGNRSE
PVVINSEGWGEFHVNGGSVSIYVQR
>d1g94a1 b.71.1.1 (A:355-448) Bacterial alpha-Amylase {Pseudoalteromonas haloplanctis (Alteromonas haloplanctis)}
NWAVTNWWDNTNNQISFGRGSSGHMAINKEDSTLTATVQTDMASGQYCNVLKGELSADAKSCSGE
VITVNSDGTINLNIGAWDAMAIHKNAKLN
>d1bag_1 b.71.1.1 (348-425) Bacterial alpha-Amylase {Bacillus subtilis}
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QPEELSNPNGNNQIFMNQRGSHGVVLANAGSSSVSINTATKLPDGRYDNKAGAGSFQVNDGKLTG
TINARSVAVLYPD
>d1hvxa1 b.71.1.1 (A:394-483) Bacterial alpha-Amylase {Bacillus stearothermophilus}
YAYGTQHDYLDHSDIIGWTREGVTEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSD
TVTINSDGWGEFKVNGGSVSVWVPR
>d1gjwa1 b.71.1.1 (A:573-636) Maltosyltransferase {Thermotoga maritima}
GKFENLTTKDLVMYSYEKNGQKIVIAANVGKEPKEITGGRVWNGKWSDEEKVVLKPLEFALVVQ
>d1cgt_3 b.71.1.1 (407-494) Cyclodextrin glycosyltransferase {Bacillus circulans, different strains}
GSTQQRWINNDVYVYERKFGKSVAVVAVNRNLSTSASITGLSTSLPTGSYTDVLGGVLNGNNITS
TNGSINNFTLAAGATAVWQYTTA
>d1kcla3 b.71.1.1 (A:407-495) Cyclodextrin glycosyltransferase {Bacillus circulans, different strains}
GSTQERWINNDVLIYERKFGSNVAVVAVNRNLNAPASISGLVTSLPQGSYNDVLGGLLNGNTLSV
GSGGAASNFTLAAGGTAVWQYTAA
>d1cyg_3 b.71.1.1 (403-491) Cyclodextrin glycosyltransferase {Bacillus stearothermophilus}
GDTEQRWINGDVYVYERQFGKDVVLVAVNRSSSSNYSITGLFTALPAGTYTDQLGGLLDGNTIQV
GSNGSVNAFDLGPGEVGVWAYSAT
>d1qhoa3 b.71.1.1 (A:408-495) Cyclodextrin glycosyltransferase {Bacillus stearothermophilus, maltogenic alpha-amylase}
GTTTQRWINNDVYIYERKFFNDVVLVAINRNTQSSYSISGLQTALPNGSYADYLSGLLGGNGISV
SNGSVASFTLAPGAVSVWQYSTS
>d1pama3 b.71.1.1 (A:407-496) Cyclodextrin glycosyltransferase {Bacillus sp., strain 1011}
GSTHERWINNDVIIYERKFGNNVAVVAINRNMNTPASITGLVTSLPRGSYNDVLGGILNGNTLTV
GAGGAASNFTLAPGGTAVWQYTTDA
>d1ciu_3 b.71.1.1 (407-495) Cyclodextrin glycosyltransferase {Thermoanaerobacterium thermosulfurigenes, EM1}
GTTQQRWINNDVYIYERKFGNNVALVAINRNLSTSYNITGLYTALPAGTYTDVLGGLLNGNSISV
ASDGSVTPFTLSAGEVAVWQYVSS
>d1hx0a1 b.71.1.1 (A:404-496) Animal alpha-amylase {Pig (Sus scrofa)}
QPFANWWDNGSNQVAFGRGNRGFIVFNNDDWQLSSTLQTGLPGGTYCDVISGDKVGNSCTGIKVY
VSSDGTAQFSISNSAEDPFIAIHAESKL
>d1smd_1 b.71.1.1 (404-496) Animal alpha-amylase {Human (Homo sapiens)}
QPFTNWYDNGSNQVAFGRGNRGFIVFNNDDWTFSLTLQTGLPAGTYCDVISGDKINGNCTGIKIY
VSDDGKAHFSISNSAEDPFIAIHAESKL
>d1jae_1 b.71.1.1 (379-471) Animal alpha-amylase {Yellow mealworm (Tenebrio molitor), larva}
GTQVENWWSNDDNQIAFSRGSQGFVAFTNGGDLNQNLNTGLPAGTYCDVISGELSGGSCTGKSVT
VGDNGSADISLGSAEDDGVLAIHVNAKL
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>d2aaa_1 b.71.1.1 (382-476) Fungal alpha-amylase {Aspergillus niger, acid amylase}
YANDAFYTDSNTIAMAKGTSGSQVITVLSNKGSSGSSYTLTLSGSGYTSGTKLIEAYTCTSVTVD
SSGDIPVPMASGLPRVLLPASVVDSSSLCG
>d2taaa1 b.71.1.1 (A:382-478) Fungal alpha-amylase {Aspergillus oryzae, Taka-amylase}
YKNPYIKDDTTIAMRKGTDGSQIVTILSNKGASGDSYTLSLSGASYTAGQQLTEVIGCTTVTVGS
DGNVPVPMAGGLPRVLYPTEKLAGSKICSDSS
>d7taa_1 b.71.1.1 (382-476) Fungal alpha-amylase {Aspergillus oryzae, Taka-amylase}
YKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVG
SDGNVPVPMAGGLPRVLYPTEKLAGSKICS
>d1smaa2 b.71.1.1 (A:506-588) Maltogenic amylase {Thermus sp.}
GDVAFLTADDEVNHLVYAKTDGNETVMIIINRSNEAAEIPMPIDARGKWLVNLLTGERFAAEAET
LCVSLPPYGFVLYAVESW
>d1bvza2 b.71.1.1 (A:503-585) Maltogenic amylase {Thermoactinomyces vulgaris, TVAII}
GNVRSWHADKQANLYAFVRTVQDQHVGVVLNNRGEKQTVLLQVPESGGKTWLDCLTGEEVHGKQG
QLKLTLRPYQGMILWNGR
>d1eh9a2 b.71.1.1 (A:491-557) Glycosyltrehalose trehalohydrolase {Archaeon Sulfolobus solfataricus, km1}
CDRRVNVVNGENWLIIKGREYFSLYVFSKSSIEVKYSGTLLLSSNNSFPQHIEEGKYEFDKGFAL
YK
>d1bf2_2 b.71.1.1 (638-750) Isoamylase {Pseudomonas amyloderamosa}
YSGSQLTWYQPSGAVADSNYWNNTSNYAIAYAINGPSLGDSNSIYVAYNGWSSSVTFTLPAPPSG
TQWYRVTDTCDWNDGASTFVAPGSETLIGGAGTTYGQCGQSLLLLISK
>d1gcya1 b.71.1.1 (A:358-418) G4-amylase (1,4-alpha-D-glucan maltotetrahydrolase) {Pseudomonas stutzeri}
RADSAISFHSGYSGLVATVSGSQQTLVVALNSDLGNPGQVASGSFSEAVNASNGQVRVWRS
>d1avaa1 b.71.1.1 (A:347-403) Plant alpha-amylase {Barley (Hordeum vulgare), seeds, AMY2 isozyme}
HNESKLQIIEADADLYLAEIDGKVIVKLGPRYDVGNLIPGGFKVAAHGNDYAVWEKI
>d1uok_1 b.71.1.1 (480-558) Oligo-1,6-glucosidase {Bacillus cereus}
GSYDLILENNPSIFAYVRTYGVEKLLVIANFTAEECIFELPEDISYSEVELLIHNYDVENGPIEN
ITLRPYEAMVFKLK
>d1g5aa1 b.71.1.1 (A:555-628) Amylosucrase {Neisseria polysaccharea}
RLVTFNTNNKHIIGYIRNNALLAFGNFSEYPQTVTAHTLQAMPFKAHDLIGGKTVSLNQDLTLQP
YQVMWLEIA
>d1f8ab1 b.72.1.1 (B:1-42) Mitotic rotamase PIN1 {Human (Homo sapiens)}
GSHGMADEEKLPPGWEKRMSRSSGRVYYFNHITNASQWERPS
>d1i8hb_ b.72.1.1 (B:) Mitotic rotamase PIN1 {Human (Homo sapiens)}
KLPPGWEKRMSRSSGRVYYFNHITNASQWERPSGNSSSG
>d1pina1 b.72.1.1 (A:6-39) Mitotic rotamase PIN1 {Human (Homo

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sapiens)}
KLPPGWEKRMSRSSGRVYYFNHITNASQWERPSG
>d1e0la_ b.72.1.1 (A:) Formin binding protein FBP28 domain {Domestic mouse (Mus musculus)}
GATAVSEWTEYKTADGKTYYYNNRTLESTWEKPQELK
>d1eg3a3 b.72.1.1 (A:47-84) Dystrophin {Human (Homo sapiens)}
PASQHFLSTSVQGPWERAISPNKVPYYINHETQTTCWD
>d1i5hw_ b.72.1.1 (W:) Ubiquitin ligase NEDD4 WWIII domain {Rat (Rattus norvegicus)}
GSPVDSNDLGPLPPGWEERTHTDGRVFFINHNIKKTQWEDPRMQNVAITG
>d1e0na_ b.72.1.1 (A:) Hypothetical protein Yjq8 (Set2p) {Baker's yeast (Saccharomyces cerevisiae)}
PGWEIIHENGRPLYYNAEQKTKLHYPP
>d1jmqa_ b.72.1.1 (A:) Yap65 ww domain {Human (Homo sapiens)}
FEIPDDVPLPAGWEMAKTSSGQRYFKNHIDQTTTWQDPRKAMLSQM
>d1k9ra_ b.72.1.1 (A:) Yap65 ww domain {Human (Homo sapiens)}
FEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRK
>d1aiw__ b.72.2.1 (-) Cellulose-binding domain of endoglucanase Z {Erwinia chrysanthemi}
MGDCANANVYPNWVSKDWAGGQPTHNEAGQSIVYKGNLYTANWYTASVPGSDSSWTQVGSCN
>d1ed7a_ b.72.2.1 (A:) Chitin-binding domain of chitinase A1 {Bacillus circulans}
AWQVNTAYTAGQLVTYNGKTYKCLQPHTSLAGWEPSNVPALWQLQ
>d1goia1 b.72.2.1 (A:447-498) Chitinase B, C-terminal domain {Serratia marcescens}
NLPIMTAPAYVPGTTYAQGALVSYQGYVWQTKWGYITSAPGSDSAWLKVGRV
>d1dkga1 b.73.1.1 (A:139-197) Head domain of nucleotide exchange factor GrpE {Escherichia coli}
VEVIAETNVPLDPNVHQAIAMVESDDVAPGNVLGIMQKGYTLNGRTIRAAMVTVAKAKA
>d1e44b_ b.101.1.1 (B:) Ribonuclease domain of colicin E3 {Escherichia coli}
GFKDYGHDYHPAPKTENIKGLGDLKPGIPKTPKQNGGGKRKRWTGDKGRKIYEWDSQHGELEGYR
ASDGQHLGSFDPKTGNQLKGPDPKRNIKKYL
>d1hcb__ b.74.1.1 (-) Carbonic anhydrase {Human (Homo sapiens), erythrocytes, isozyme I}
PDWGYDDKNGPEQWSKLYPIANGNNQSPVDIKTSETKHDTSLKPISVSYNPATAKEIINVGHSFH
VNFEDNDNRSVLKGGPFSDSYRLFQFHFHWGSTNEHGSEHTVDGVKYSAELHVAHWNSAKYSSLA
EAASKADGLAVIGVLMKVGEANPKLQKVLDALQAIKTKGKRAPFTNFDPSTLLPSSLDFWTYPGS
LTHPPLYESVTWIICKESISVSSEQLAQFRSLLSNVEGDNAVPMQHNNRPTQPLKGRTVRASF
>d2cba__ b.74.1.1 (-) Carbonic anhydrase {Human (Homo sapiens), erythrocytes, isozyme II}
HHWGYGKHNGPEHWHKDFPIAKGERQSPVDIDTHTAKYDPSLKPLSVSYDQATSLRILNNGHAFN
VEFDDSQDKAVLKGGPLDGTYRLIQFHFHWGSLDGQGSEHTVDKKKYAAELHLVHWNTKYGDFGK
AVQQPDGLAVLGIFLKVGSAKPGLQKVVDVLDSIKTKGKSADFTNFDPRGLLPESLDYWTYPGSL
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TTPPLLECVTWIVLKEPISVSSEQVLKFRKLNFNGEGEPEELMVDNWRPAQPLKNRQIKASFK

>d1flja_ b.74.1.1 (A:) Carbonic anhydrase {Rat (Rattus norvegicus), isozyme III}

AKEWGYASHNGPEHWHELYPIAKGDNQSPIELHTKDIRHDPSLQPWSVSYDPGSAKTILNNGKTC
RVVFDDTFDRSMLRGGPLSGPYRLRQFHLHWGSSDDHGSEHTVDGVKYAAELHLVHWNPKYNTFG
EALKQPDGIAVVGIFLKIGREKGEFQILLDALDKIKTKGKEAPFNHFDPSCLFPACRDYWTYHGS
FTTPPCEECIVWLLLKEPMTVSSDQMAKLRSLFASAENEPPVPLVGNWRPPQPIKGRVVRASFK

>d1znca_ b.74.1.1 (A:) Carbonic anhydrase {Human (Homo sapiens), isozyme IV}

WCYEVQAESSNYPCLVPVKWGGNCQKDRQSPINIVTTKAKVDKKLGRFFFSGYDKKQTWTVQNNG
HSVMMLLENKASISGGGLPAPYQAKQLHLHWSDLPYKGSEHSLDGEHFAMEMHIVHEKEKGTSRN
VKEAQDPEDEIAVLAFLVEAGTQVNEGFQPLVEALSNIPKPEMSTTMAESSLLDLLPKEEKLRHY
FRYLGSLTTPTCDEKVVWTVFREPIQLHREQILAFSQKLYYDKEQTVSMKDNVRPLQQLGQRTVI
KS

>d2znc__ b.74.1.1 (-) Carbonic anhydrase {Mouse (Mus musculus), isozyme IV}

WCYEIQTEDPRSSCLGPEKWPGACKENQQSPINIVTARTKVNPRLTPFILVGYDQKQQWPIKNNQ
HTVEMTLGGGACIIGGDLPARYEAVQLHLHWSNGNDNGSEHSIDGRHFAMEMHIVHKKLTSSKED
SKDKFAVLAFMIEVGDKVNKGFQPLVEALPSISKPHSTSTVRESSLQDMLPPSTKMYTYFRYNGS
LTTPNCDETVIWTVYKQPIKIHKNQFLEFSKNLYYDEDQKLNMKDNVRPLQPLGKRQVFKSHA

>d1dmxa_ b.74.1.1 (A:) Carbonic anhydrase {Mouse (Mus musculus), liver, isozyme V}

GTRQSPINIQWKDSVYDPQLAPLRVSYDAASCRYLWNTGYFFQVEFDDSCEDSGISGGPLGNHYR
LKQFHFHWGATDEWGSEHAVDGHTYPAELHLVHWNSTKYENYKKASVGENGLAVIGVFLKLGAHH
QALQKLVDVLPEVRHKDTQVAMGPFDPSCLMPACRDYWTYPGSLTTPPLAESVTWIVQKTPVEVS
PSQLSMFRTLLFSGRGEEEDVMVNNYRPLQPLRDRKLRSSFR

>d1jd0a_ b.74.1.1 (A:) Carbonic anhydrase {Human (Homo sapiens), isozyme XII}

KWTYFGPDGENSWSKKYPSCGGLLQSPIDLHSDILQYDASLTPLEFQGYNLSANKQFLLTNNGHS
VKLNLPSDMHIQGLQSRYSATQLHLHWGNPNDPHGSEHTVSGQHFAAELHIVHYNSDLYPDASTA
SNKSEGLAVLAVLIEMGSFNPSYDKIFSHLQHVKYKGQEAFVPGFNIEELLPERTAEYYRYRGSL
TTPPCNPTVLWTVFRNPVQISQEQLLALETALYCTHMDDPSPREMINNFRQVQKFDERLVYTSFS

>d1kopa_ b.74.1.1 (A:) Carbonic anhydrase {Neisseria gonorrhoeae}

HTHWGYTGHDSPESWGNLSEEFRLCSTGKNQSPVNITETVSGKLPAIKVNYKPSMVDVENNGHTI
QVNYPEGGNTLTVNGRTYTLKQFHFHVPSENQIKGRTFPMEAHFVHLDENKQPLVLAVLYEAGKT
NGRLSSIWNVMPMTAGKVKLNQPFDASTLLPKRLKYYRFAGSLTTPPCTEGVSWLVLKTYDHIDQ
AQAEKFTRAVGSENNRPVQPLNARVVIE

>d1koqa_ b.74.1.1 (A:) Carbonic anhydrase {Neisseria gonorrhoeae}

THWGYTGHDSPESWGNLSEEFRLCSTGKNQSPVNITETVSGKLPAIKVNYKPSMVDVENNGHTIQ
VNYPEGGNTLTVNGRTYTLKQFHFLTVNGRTYTLKQFHFHVPSENQIKGRTFPMEAHFVHLDENK
QPLVLAVLYEAGKTNGRLSLAVLYEAGKTNGRLSSIWNVMPMTAGKVKLNQPFDASTLLPKRLKY
YRFAGSLTTPPCTEGVSWLVLKTYDHIDQAQAEKFTRAVGSENNRPVQPLNARVVIE

>d4bcl__ b.75.1.1 (-) Bacteriochlorophyll A protein {Prosthecochloris aestuarii, strain 2k}

TTTAHSDYEIILEGGSSSWGQVKGRAKVNVPAAIPLLPTDCNIRIDAKPLDAQKGVVRFTTKIES
VVDSVKNTLNVEVDIANETKDRRIAVGEGSLSVGDFSHSFSFEGSVVNMYYYRSDAVRRNIPNPI
YMQGRQFHDILMKVPLDNNDLVDTWEGFQQSISGGGANFGDWIREFWFIGPAFAAINEGGQRISP
IVVNSSNVEGGEKGPVGVTRWKFSHAGSGVVDSISRWTELFPVEQLNKPASIEGGFRSDSQGIEV
KVDGNLPGVSRDAGGGLRRILNHPLIPLVHHGMVGKFNDFTVDTQLKIVLPKGYKIRYAAPQFRS
QNLEEYRWSGGAYARWVEHVCKGGTGQFEVLYAQ
>d1ksaa_ b.75.1.1 (A:) Bacteriochlorophyll A protein {Green sulfur bacterium (Chlorobium tepidum)}
TTAHSDYEIVLEGGSSSWGKVKARAKVNAPPASPLLPADCDVKLNVKPLDPAKGFVRISAVFESI
VDSTKNKLTIEADIANETKERRISVGEGMVSVGDFSHTFSFEGSVVNLFYYRSDAVRRNVPNPIY
MQGRQFHDILMKVPLDNNDLIDTWEGTVKAIGSTGAFNDWIRDFWFIGPAFTALNEGGQRISRIE
VNGLNTESGPKGPVGVSRWRFSHGGSGMVDSISRWAELFPSDKLNRPAQVEAGFRSDSQGIEVKV
DGEFPGVSVDAGGGLRRILNHPLIPLVHHGMVGKFNNFNVDAQLKVVLPKGYKIRYAAPQYRSQN
LEEYRWSGGAYARWVEHVCKGGVGQFEILYAQ
>d1ospo_ b.76.1.1 (O:) Outer surface protein A {Lyme disease spirochete (Borrelia burgdorferi)}
SLDEKNSVSVDLPGEMKVLVSKEKNKDGKYDLIATVDKLELKGTSDKNNGSGVLEGVKADKCKVK
LTISDDLGQTTLEVFKEDGKTLVSKKVTSKDKSSTEEKFNEKGEVSEKIITRADGTRLEYTGIKS
DGSGKAKEVLKGYVLEGTLTAEKTTLVVKEGTVTLSKNISKSGEVSVELNDTDSSAATKKTAAWN
SGTSTLTITVNSKKTKDLVFTKENTITVQQYDSNGTKLEGSAVEITKLDEIKNALK
>d1vmoa_ b.77.1.1 (A:) Vitelline membrane outer protein-I (VMO-I) {Hen (Gallus gallus)}
RTREYTSVITVPNGGHWGKWGIRQFCHSGYANGFALKVEPSQFGRDDTALNGIRLRCLDGSVIES
LVGKWGTWTSFLVCPTGYLVSFSLRSEKSQGGGDDTAANNIQFRCSDEAVLVGDGLSWGRFGPWS
KRCKICGLQTKVESPQGLRDDTALNNVRFFCCK
>d1dlc_2 b.77.2.1 (290-499) delta-Endotoxin (insectocide), middle domain {Bacillus thuringiensis tenebrionis, CRYIIIA (BT13)}
LYPKEVKTELTRDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGND
SFNYWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGV
TKVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFLMQGS
RGTIPVLTWTHKSVD
>d1ji6a2 b.77.2.1 (A:291-502) delta-Endotoxin (insectocide), middle domain {Bacillus thuringiensis, CRY3bb1}
LYSKGVKTELTRDIFTDPIFSLNTLQEYGPTFLSIENSIRKPHLFDYLQGIEFHTRLQPGYFGKD
SFNYWSGNYVETRPSIGSSKTITSPFYGDKSTEPVQKLSFDGQKVYRTIANTDVAAWPNGKVYLG
VTKVDFSQYDDQKNETSTQTYDSKRNNGHVSAQDSIDQLPPETTDEPLEKAYSHQLNYAECFLMQ
DRRGTIPFFTWTHRSVD
>d1ciy_2 b.77.2.1 (256-461) delta-Endotoxin (insectocide), middle domain {Bacillus thuringiensis, CRYIA (A)}
PIRTVSQLTREIYTNPVLENFDGSFRGMAQRIEQNIRQPHLMDILNSITIYTDVHRGFNYWSGHQ
ITASPVGFSGPEFAFPLFGNAGNAAPPVLVSLTGLGIFRTLSSPLYRRIILGSGPNNQELFVLDG
TEFSFASLTTNLPSTIYRQRGTVDSLDVIPPQDNSVPPRAGFSHRLSHVTMLSQAAGAVYTLRAP
TFSWQHRSAEF
>d1i5pa2 b.77.2.1 (A:264-472) delta-Endotoxin (insectocide), middle

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domain {Bacillus thuringiensis subsp. kurstaki, CRY2AA}
YQSLMVSSGANLYASGSGPQQTQSFTAQNWPFLYSLFQVNSNYILSGISGTRLSITFPNIGGLPG
STTTHSLNSARVNYSGGVSSGLIGATNLNHNFNCSTVLPPLSTPFVRSWLDSGTDRAGVATSTNW
QTESFQTTLSLRCGAFSARGNSNYFPDYFIRNISGVPLVIRNEDLTRPLHYNQIRNIESPSGTPG
GARAYLVSVHNRKN
>g1jac.5 b.77.3.1 (B:,A:) Jacalin {Jackfruit (Artocarpus integrifolia)}
SGKSQTVIVGSWGAKXGKAFDDGAFTGIREINLSYNKETAIGDFQVVYDLNGSPYVGQNHKSFIT
GFTPVKISLDFPSEYIMEVSGYTGNVSGYVVVRSLTFKTNKKTYGPYGVTSGTPFNLPIENGLIV
GFKGSIGYWLDYFSMYLSL
>g1jot.2 b.77.3.1 (B:,A:) Lectin MPA {Osage orange (Maclura pomifera)}
RNGKSQSIIVGPWGDRXGVTFDDGAYTGIREINFEYNSETAIGGLRVTYDLNGMPFVAEDHKSFI
TGFKPVKISLEFPSEYIVEVSGYVGKVEGYTVIRSLTFKTNKQTYGPYGVTNGTPFSLPIENGLI
VGFKGSIGYWLDYFSIYLSL
>d1c3ma_ b.77.3.1 (A:) Heltuba lectin {Jerusalem artishoke (Helianthus tuberosus)}
ASDIAVQAGPWGGNGGKRWLQTAHGGKITSIIIKGGTCIFSIQFVYKDKDNIEYHSGKFGVLGDK
AETITFAEDEDITAISGTFGAYYHMTVVTSLTFQTNKKVYGPFGTVASSSFSLPLTKGKFAGFFG
NSGDVLDSIGGVVVP
>d1jpc__ b.78.1.1 (-) Lectin (agglutinin) {Snowdrop (Galanthus nivalis)}
DNILYSGETLSTGEFLNYGSFVFIMQEDCNLVLYDVDKPIWATNTGGLSRSCFLSMQTDGNLVVY
NPSNKPIWASNTGGQNGNYVCILQKDRNVVIYGTDRWATGTHT
>d1bwua_ b.78.1.1 (A:) Lectin (agglutinin) {Garlic (Allium sativum)}
RNILRNDEGLYGGQSLDVNPYHFIMQEDCNLVLYDHSTSVWASNTGILGKKGCRAVLQSDGNFVV
YDAEGRSLWASHSVRGNGNYVLVLQEDGNVVIYRSDIWSTN
>d1bwud_ b.78.1.1 (D:) Lectin (agglutinin) {Garlic (Allium sativum)}
RNILTNDEGLYGGQSLDVNPYHLIMQEDCNLVLYDHSTAVWSSNTDIPGKKGCKAVLQSDGNFVV
YDAEGASLWASHSVRGNGNYVLVLQEDGNVVIYRSDIWSTNTYR
>d1kj1a_ b.78.1.1 (A:) Lectin (agglutinin) {Garlic (Allium sativum)}
RNLLTNGEGLYAGQSLDVEPYHFIMQEDCNLVLYDHSTSVWASNTGILGKKGCKAVLQSDGNFVV
YDAEGRSLWASHSVRGNGNYVLVLQEDGNVVIYGSDIWSTGTYK
>d1kj1d_ b.78.1.1 (D:) Lectin (agglutinin) {Garlic (Allium sativum)}
RNILMNDEGLYAGQSLDVEPYHLIMQEDCNLVLYDHSTAVWTTNTDIPGKKGCKAVLQSDGNFVV
YDAEGRSLWASHSVRGNGNYVLVLQEDGNVVIYGSDIWSTNTYK
>d1npla_ b.78.1.1 (A:) Lectin (agglutinin) {Daffodil (Narcissus pseudonarcissus)}
DNILYSGETLSPGEFLNNGRYVFIMQEDCNLVLYDVDKPIWATNTGGLDRRCHLSMQSDGNLVVY
SPRNNPIWASNTGGENGNYVCVLQKDRNVVIYGTARWATGTNIH
>d1b2pa_ b.78.1.1 (A:) Lectin (agglutinin) {Bluebell (Scilla campanulata)}
NNIIFSKQPDDNHPQILHATESLEILFGTHVYRFIMQTDCNLVLYDNNNPIWATNTGGLGNGCRA
VLQPDGVLVVITNENVTVWQSPVAGKAGHYVLVLQPDRNVVIYGDALWATQTVR
>d1dlpa1 b.78.1.1 (A:1-115) Fetuin-binding protein Scafet precursor
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{Bluebell (Scilla campanulata)}
NNILFGLSHEGSHPQTLHAAQSLELSSFRFTMQSDCNLVLFDSDVRVWASNTAGATGCRAVLQSD
GLLVILTAQNTIRWSSGTKGSIGNYVLVLQPDRTVTIYGPGLWDSGTSNK
>d1dlpa2 b.78.1.1 (A:116-235) Fetuin-binding protein Scafet precursor
{Bluebell (Scilla campanulata)}
GSVVVANNGNSILYSTQGNDNHPQTLHATQSLQLSPYRLSMETDCNLVLFDRDDRVWSTNTAGKG
TGCRAVLQPNGRMDVLTNQNIAVWTSGNSRSAGRYVFVLQPDRNLAIYGGALWTT
>d1kapp1 b.79.1.1 (P:247-470) Metalloprotease, C-terminal domain
{Pseudomonas aeruginosa, alkaline protease}
GANLTTRTGDTVYGFNSNTERDFYSATSSSSKLVFSVWDAGGNDTLDFSGFSQNQKINLNEKALS
DVGGLKGNVSIAAGVTVENAIGGSGSDLLIGNDVANVLKGGAGNDILYGGLGADQLWGGAGADTF
VYGDIAESSAAAPDTLRDFVSGQDKIDLSGLDAFVNGGLVLQYVDAFAGKAGQAILSYDAASKAG
SLAIDFSGDAHADFAINLIGQATQADIVV
>d1sat_1 b.79.1.1 (247-471) Metalloprotease, C-terminal domain
{Serratia marcescens}
GANLSTRTGDTVYGFNSNTGRDFLSTTSNSQKVIFAAWDAGGNDTFDFSGYTANQRINLNEKSFS
DVGGLKGNVSIAAGVTIENAIGGSGNDVIVGNAANNVLKGGAGNDVLFGGGGADELWGGAGKDIF
VFSAASDSAPGASDWIRDFQKGIDKIDLSFFDKEANSSSFIHFVDHFSGTAGEALLSYNASSNVT
DLSVNIGGHAAPDFLVKIVGQVDVATDFIV
>d1air__ b.80.1.1 (-) Pectate lyase {Erwinia chrysanthemi, type C}
ATDTGGYAATAGGNVTGAVSKTATSMQDIVNIIDAARLDANGKKVKGGAYPLVITYTGNEDSLIN
AAAANICGQWSKDPRGVEIKEFTKGITIIGANGSSANFGIWIKKSSDVVVQNMRIGYLPGGAKDG
DMIRVDDSPNVWVDHNELFAANHECDGTPDNDTTFESAVDIKGASNTVTVSYNYIHGVKKVGLDG
SSSSDTGRNITYHHNYYNDVNARLPLQRGGLVHAYNNLYTNITGSGLNVRQNGQALIENNWFEKA
INPVTSRYDGKNFGTWVLKGNNITKPADFSTYSITWTADTKPYVNADSWTSTGTFPTVAYNYSPV
SAQCVKDKLPGYAGVGKNLATLTSTAC
>d1pcl__ b.80.1.1 (-) Pectate lyase {Erwinia chrysanthemi, type E}
AVETDAATTGWATQNGGTTGGAKAAKAVEVKNISDFKKALNGTDSSAKIIKVTGPIDISGGKAYT
SFDDQKARSQISIPSNTTIIGVGSNGKFTNGSLVIKGVKNVILRNLYIETPVDVAPHYESGDGWN
AEWDAAVIDNSTNVWVDHVTISDGSFTDDKYTTKDGEKYVQHDGALDIKKGSDYVTISYSRFELH
DKTILIGHSDSNGSQDSGKLRVTFHNNVFDRVTERAPRVRFGSIHAYNNVYLGDVKHSVYPYLYS
FGLGTSGSILSESNSFTLSNLKSIDGKNPECSIVKQFNSKVFSDKGSLVNGSTTTKLDTCGLTAY
KPTLPYKYSAQTMTSSLATSINNNAGYGKL
>d1bn8a_ b.80.1.1 (A:) Pectate lyase {Bacillus subtilis}
ADLGHQTLGSNDGWGAYSTGTTGGSKASSSNVYTVSNRNQLVSALGKETNTTPKIIYIKGTIDMN
VDDNLKPLGLNDYKDPEYDLDKYLKAYDPSTWGKKEPSGTQEEARARSQKNQKARVMVDIPANTT
IVGSGTNAKVVGGNFQIKSDNVIIRNIEFQDAYDYFPQWDPTDGSSGNWNSQYDNITINGGTHIW
IDHCTFNDGSRPDSTSPKYYGRKYQHHDGQTDASNGANYITMSYNYYHDHDKSSIFGSSDSKTSD
DGKLKITLHHNRYKNIVQRAPRVRFGQVHVYNNYYEGSTSSSSYPFSYAWGIGKSSKIYAQNNVI
DVPGLSAAKTISVFSGGTALYDSGTLLNGTQINASAANGLSSSVGWTPSLHGSIDASANVKSNVI
NQAGAGKLN
>d1ee6a_ b.80.1.1 (A:) Pectate lyase {Bacillus sp., strain ksmp15}
APTVVHETIRVPAGQTFDGKGQTYVANPNTLGDGSQAENQKPIFRLEAGASLKNVVIGAPAADGV
HCYGDCTITNVIWEDVGEDALTLKSSGTVNISGGAAYKAYDKVFQINAAGTINIRNFRADDIGKL
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VRQNGGTTYKVVMNVENCNISRVKDAILRTDSSTSTGRIVNTRYSNVPTLFKGFKSGNTTASGNT
QY
>d1idk__ b.80.1.2 (-) Pectin lyase {Aspergillus niger, type A}
VGVSGSAEGFAKGVTGGGSATPVYPDTIDELVSYLGDDEARVIVLTKTFDFTDSEGTTTGTGCAP
WGTASACQVAIDQDDWCENYEPDAPSVSVEYYNAGTLGITVTSNKSLIGEGSSGAIKGKGLRIVS
GAENIIIQNIAVTDINPKYVWGGDAITLDDCDLVWIDHVTTARIGRQHYVLGTSADNRVSLTNNY
IDGVSDYSATCDGYHYWAIYLDGDADLVTMKGNYIYHTSGRSPKVQDNTLLHAVNNYWYDISGHA
FEIGEGGYVLAEGNVFQNVDTVLETYEGEAFTVPSSTAGEVCSTYLGRDCVINGFGSSGTFSEDS
TSFLSDFEGKNIASASAYTSVASRVVANAGQGNL
>d1qcxa_ b.80.1.2 (A:) Pectin lyase {Aspergillus niger, type B}
AGVVGAAEGFAHGVTGGGSASPVYPTTTDELVSYLGDNEPRVIILDQTFDFTGTEGTETTTGCAP
WGTASQCQVAINLHSWCDNYQASAPKVSVTYDKAGILPITVNSNKSIVGQGTKGVIKGKGLRVVS
GAKNVIIQNIAVTDINPKYVWGGDAITVDDSDLVWIDHVTTARIGRQHIVLGTSADNRVTISYSL
IDGRSDYSATCNGHHYWGVYLDGSNDMVTLKGNYFYNLSGRMPKVQGNTLLHAVNNLFHNFDGHA
FEIGTGGYVLAEGNVFQDVNVVVETPISGQLFSSPDANTNQQCASVFGRSCQLNAFGNSGSMSGS
DTSIISKFAGKTIAAAHPPGAIAQWTMKNAGQGK
>d1rmg__ b.80.1.3 (-) Rhamnogalacturonase A {Aspergillus aculeatus}
QLSGSVGPLTSASTKGATKTCNILSYGAVADNSTDVGPAITSAWAACKSGGLVYIPSGNYALNTW
VTLTGGSATAIQLDGIIYRTGTASGNMIAVTDTTDFELFSSTSKGAVQGFGYVYHAEGTYGARIL
RLTDVTHFSVHDIILVDAPAFHFTMDTCSDGEVYNMAIRGGNEGGLDGIDVWGSNIWVHDVEVTN
KDECVTVKSPANNILVESIYCNWSGGCAMGSLGADTDVTDIVYRNVYTWSSNQMYMIKSNGGSGT
VSNVLLENFIGHGNAYSLDIDGYWSSMTAVAGDGVQLNNITVKNWKGTEANGATRPPIRVVCSDT
APCTDLTLEDIAIWTESGSSELYLCRSAYGSGYCLKDSSSHTSYTTTSTVTAAPSGYSATTMAAD
LATAFGLTASIPIPTIPTSFYPGLTPYSALAG
>d1bhe__ b.80.1.3 (-) Polygalacturonase {Erwinia carotovora, subsp.
carotovora}
SDSRTVSEPKTPSSCTTLKADSSTATSTIQKALNNCDQGKAVRLSAGSTSVFLSGPLSLPSGVSL
LIDKGVTLRAVNNAKSFENAPSSCGVVDKNGKGCDAFITAVSTTNSGIYGPGTIDGQGGVKLQDK
KVSWWELAADAKVKKLKQNTPRLIQINKSKNFTLYNVSLINSPNFHVVFSDGDGFTAWKTTIKTP
STARNTDGIDPMSSKNITIAYSNIATGDDNVAIKAYKGRAETRNISILHNDFGTGHGMSIGSETM
GVYNVTVDDLKMNGTTNGLRIKSDKSAAGVVNGVRYSNVVMKNVAKPIVIDTVYEKKEGSNVPDW
SDITFKDVTSETKGVVVLNGENAKKPIEVTMKNVKLTSDSTWQIKNVNVKK
>d1ia5a_  b.80.1.3  (A:)  Polygalacturonase  {Fungus  (Aspergillus
aculeatus)}
ATTCTFSGSNGASSASKSKTSCSTIVLSNVAVPSGTTLDLTKLNDGTHVIFSGETTFGYKEWSGP
LISVSGSDLTITGASGHSINGDGSRWWDGEGGNGGKTKPKFFAAHSLTNSVISGLKIVNSPVQVF
SVAGSDYLTLKDITIDNSDGDDNGGHNTDAFDIGTSTYVTISGATVYNQDDCVAVNSGENIYFSG
GYCSGGHGLSIGSVGGRSDNTVKNVTFVDSTIINSDNGVRIKTNIDTTGSVSDVTYKDITLTSIA
KYGIVVQQNYGDTSSTPTTGVPITDFVLDNVHGSVVSSGTNILISCGSGSCSDWTWTDVSVSGGK
TSSKCTNVPSGASC
>d1czfa_ b.80.1.3 (A:) Polygalacturonase {Fungus (Aspergillus niger),
endo-polygalacturonase II}
DSCTFTTAAAAKAGKAKCSTITLNNIEVPAGTTLDLTGLTSGTKVIFEGTTTFQYEEWAGPLISM
SGEHITVTGASGHLINCDGARWWDGKGTSGKKKPKFFYAHGLDSSSITGLNIKNTPLMAFSVQAN
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DITFTDVTINNADGDTQGGHNTDAFDVGNSVGVNIIKPWVHNQDDCLAVNSGENIWFTGGTCIGG
HGLSIGSVGDRSNNVVKNVTIEHSTVSNSENAVRIKTISGATGSVSEITYSNIVMSGISDYGVVI
QQDYEDGKPTGKPTNGVTIQDVKLESVTGSVDSGATEIYLLCGSGSCSDWTWDDVKVTGGKKSTA
CKNFPSVASC
>d1hg8a_ b.80.1.3 (A:) Polygalacturonase {Fusarium moniliforme}
DPCSVTEYSGLATAVSSCKNIVLNGFQVPTGKQLDLSSLQNDSTVTFKGTTTFATTADNDFNPIV
ISGSNITITGASGHVIDGNGQAYWDGKGSNSNSNQKPDHFIVVQKTTGNSKITNLNIQNWPVHCF
DITGSSQLTISGLILDNRAGDKPNAKSGSLPAAHNTDGFDISSSDHVTLDNNHVYNQDDCVAVTS
GTNIVVSNMYCSGGHGLSIGSVGGKSDNVVDGVQFLSSQVVNSQNGCRIKSNSGATGTINNVTYQ
NIALTNISTYGVDVQQDYLNGGPTGKPTNGVKISNIKFIKVTGTVASSAQDWFILCGDGSCSGFT
FSGNAITGGGKTSSCNYPTNTCPS
>d1dbga_ b.80.1.4 (A:) Chondroitinase B {Flavobacterium heparinum}
QVVASNETLYQVVKEVKPGGLVQIADGTYKDVQLIVSNSGKSGLPITIKALNPGKVFFTGDAKVE
LRGEHLILEGIWFKDGNRAIQAWKSHGPGLVAIYGSYNRITACVFDCFDEANSAYITTSLTEDGK
VPQHCRIDHCSFTDKITFDQVINLNNTARAIKDGSVGGPGMYHRVDHCFFSNPQKPGNAGGGIRI
GYYRNDIGRCLVDSNLFMRQDSEAEIITSKSQENVYYGNTYLNCQGTMNFRHGDHQVAINNFYIG
NDQRFGYGGMFVWGSRHVIACNYFELSETIKSRGNAALYLNPGAMASEHALAFDMLIANNAFINV
NGYAIHFNPLDERRKEYCAANRLKFETPHQLMLKGNLFFKDKPYVYPFFKDDYFIAGKNSWTGNV
ALGVEKGIPVNISANRSAYKPVKIKDIQPIEGIALDLNALISKGITGKPLSWDEVRPYWLKEMPG
TYALTARLSADRAAKFKAVIKRNKEH
>d1h80a_ b.80.1.8 (A:) iota-carrageenase {Alteromonas sp., atcc
43554}
VSPKTYKDADFYVAPTQQDVNYDLVDDFGANGNDTSDDSNALQRAINAISRKPNGGTLLIPNGTY
HFLGIQMKSNVHIRVESDVIIKPTWNGDGKNHRLFEVGVNNIVRNFSFQGLGNGFLVDFKDSRDK
NLAVFKLGDVRNYKISNFTIDDNKTIFASILVDVTERNGRLHWSRNGIIERIKQNNALFGYGLIQ
TYGADNILFRNLHSEGGIALRMETDNLLMKNYKQGGIRNIFADNIRCSKGLAAVMFGPHFMKNGD
VQVTNVSSVSCGSAVRSDSGFVELFSPTDEVHTRQSWKQAVESKLGRGCAQTPYARGNGGTRWAA
RVTQKDACLDKAKLEYGIEPGSFGTVKVFDVTARFGYNADLKQDQLDYFSTSNPMCKRVCLPTKE
QWSKQGQIYIGPSLAAVIDTTPETSKYDYDVKTFNVKRINFPVNSHKTIDTNTESSRVCNYYGMS
ECSSSRWER
>d1qjva_ b.80.1.5 (A:) Pectin methylesterase PemA {Erwinia
chrysanthemi}
ATTYNAVVSKSSSDGKTFKTIADAIASAPAGSTPFVILIKNGVYNERLTITRNNLHLKGESRNGA
VIAAATAAGTLKSDGSKWGTAGSSTITISAKDFSAQSLTIRNDFDFPANQAKSDSDSSKIKDTQA
VALYVTKSGDRAYFKDVSLVGYQDTLYVSGGRSFFSDCRISGTVDFIFGDGTALFNNCDLVSRYR
ADVKSGNVSGYLTAPSTNINQKYGLVITNSRVIRESDSVPAKSYGLGRPWHPTTTFSDGRYADPN
AIGQTVFLNTSMDNHIYGWDKMSGKDKNGNTIWFNPEDSRFFEYKSYGAGAAVSKDRRQLTDAQA
AEYTQSKVLGDWTPTLP
>d1qq1a_ b.80.1.6 (A:) P22 tailspike protein {Salmonella phage P22}
YSIEADKKFKYSVKLSDYPTLQDAASAAVDGLLIDRDYNFYGGETVDFGGKVLTIECKAKFIGDG
NLIFTKLGKGSRIAGVFMESTTTPWVIKPWTDDNQWLTDAAAVVATLKQSKTDGYQPTVSDYVKF
PGIETLLPPNAKGQNITSTLEIRECIGVEVHRASGLMAGFLFRGCHFCKMVDANNPSGGKDGIIT
FENLSGDWGKGNYVIGGRTSYGSVSSAQFLRNNGGFERDGGVIGFTSYRAGGSGVKTWQGTVGST
TSRNYNLQFRDSVVIYPVWDGFDLGADTDMNPELDRPGDYPITQYPLHQLPLNHLIDNLLVRGAL
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GVGFGMDGKGMYVSNITVEDCAGSGAYLLTHESVFTNIAIIDTNTKDFQANQIYISGACRVNGLR
LIGIRSTDGQSLTIDAPNSTVSGITGMVDPSRINVANLAEEGLGNIRANSFGYDSAAIKLRIHKL
SKTLDSGALYSHINGGAGSGSAYTQLTAISGSTPDAVSLKVNHKDCRGAEIPFVPDIASDDFIKD
SSCFLPYWENNSTSLKALVKKPNGELVRLTLATL
>d1daba_ b.80.1.7 (A:) Virulence factor P.69 pertactin {Bordetella
pertussis}
DWNNQSIVKTGERQHGIHIQGSDPGGVRTASGTTIKVSGRQAQGILLENPAAELQFRNGSVTSSG
QLSDDGIRRFLGTVTVKAGKLVADHATLANVGDTWDDDGIALYVAGEQAQASIADSTLQGAGGVQ
IERGANVTVQRSAIVDGGLHIGALQSLQPEDLPPSRVVLRDTNVTAVPASGAPAAVSVLGASELT
LDGGHITGGRAAGVAAMQGAVVHLQRATIRRGDALAGGAVPGGAVPGGAVPGGFGPGGFGPVLDG
WYGVDVSGSSVELAQSIVEAPELGAAIRVGRGARVTVPGGSLSAPHGNVIETGGARRFAPQAAPL
SITLQAGAHAQGKALLYRVLPEPVKLTLTGGADAQGDIVATELPSIPGTSIGPLDVALASQARWT
GATRAVDSLSIDNATWVMTDNSNVGALRLASDGSVDFQQPAEAGRFKVLTVNTLAGSGLFRMNVF
ADLGLSDKLVVMQDASGQHRLWVRNSGSEPASANTLLLVQTPLGSAATFTLANKDGKVDIGTYRY
RLAANGNGQWSLVGAKAPP
>d1ezga_ b.80.2.1 (A:) Insect cysteine-rich antifreeze protein
{Yellow mealworm (Tenebrio molitor)}
QCTGGADCTSCTGACTGCGNCPNAVTCTNSQHCVKANTCTGSTDCNTAQTCTNSKDCFEANTCTD
STNCYKATACTNSSGCP
>d1hf2a1 b.80.3.1 (A:100-206) Cell-division inhibitor MinC,
C-terminal domain {Thermotoga maritima}
TGKVIKRNIRSGQTVVHSGDVIVFGNVNKGAEILAGGSVVVFGKAQGNIRAGLNEGGQAVVAALD
LQTSLIQIAGFITHSKGEENVPSIAHVKGNRIVIEPFDKVSF
>d1ea0a1 b.80.4.1 (A:1203-1472) Alpha subunit of glutamate synthase,
C-terminal domain {Azospirillum brasilense}
GRNEVPDTLDARIVADARPLFEEGEKMQLAYNARNTQRAIGTRLSSMVTRKFGMFGLQPGHITIR
LRGTAGQSLGAFAVQGIKLEVMGDANDYVGKGLSGGTIVVRPTTSSPLETNKNTIIGNTVLYGAT
AGKLFAAGQAGERFAVRNSGATVVVEGCGSNGCEYMTGGTAVILGRVGDNFAAGMTGGMAYVYDL
DDSLPLYINDESVIFQRIEVGHYESQLKHLIEEHVTETQSRFAAEILNDWAREVTKFWQVVPKEM
LNRLEVPVHL
>d1kq5a_ b.80.5.1 (A:) C-terminal domain of adenylylcyclase
associated protein {Baker's yeast (Saccharomyces cerevisiae)}
MPPRKELVGNKWFIENYENETESLVIDANKDESIFIGKCSQVLVQIKGKVNAISLSETESCSVVL
DSSISGMDVIKSNKFGIQVNHSLPQISIDKSDGGNIYLSKESLNTEIYTSCSTAINVNLPIGEDD
DYVEFPISEQMKHSFADGKFKSAVFE
>d1lxa__ b.81.1.1 (-) UDP N-acetylglucosamine acyltransferase
{Escherichia coli, gene lpxA}
MIDKSAFVHPTAIVEEGASIGANAHIGPFCIVGPHVEIGEGTVLKSHVVVNGHTKIGRDNEIYQF
ASIGEVNQDLKYAGEPTRVEIGDRNRIRESVTIHRGTVQGGGLTKVGSDNLLMINAHIAHDCTVG
NRCILANNATLAGHVSVDDFAIIGGMTAVHQFCIIGAHVMVGGCSGVAQDVPPYVIAQGNHATPF
GVNIEGLKRRGFSREAITAIRNAYKLIYRSGKTLDEVKPEIAELAETYPEVKAFTDFFARSTRGL
IR
>d3tdt__ b.81.1.2 (-) Tetrahydrodipicolinate-N-succinlytransferase,
THDP-succinlytransferase, DapD {Mycobacterium bovis}
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MQQLQNVIESAFERRADITPANVDTVTREAVNQVIGLLDSGALRVAEKIDGQWVTHQWLKKAVLL
SFRINDNKVMDGAETRYYDKVPMKFADYDEARFQKEGFRVVPPATVRQGAFIARNTVLMPSYVNI
GAYVDEGTMVDTWATVGSCAQIGKNVHLSGGVGIGGVLEPLQANPTIIEDNCFIGARSEVVEGVI
VEEGSVISMGVYLGQSTRIYDRETGEIHYGRVPAGSVVVSGNLPSKDGSYSLYCAVIVKKVDAKT
RGKVGINELLRTID
>d1xat__ b.81.1.3 (-) Xenobiotic acetyltransferase {Pseudomonas aeruginosa}
NYFESPFRGKLLSEQVSNPNIRVGRYSYYSGYYHGHSFDDCARYLMPDRDDVDKLVIGSFCSIGS
GAAFIMAGNQGHRAEWASTFPFHFMHEEPAFAGAVNGYQPAGDTLIGHEVWIGTEAMFMPGVRVG
HGAIIGSRALVTGDVEPYAIVGGNPARTIRKRFSDGDIQNLLEMAWWDWPLADIEAAMPLLCTGD
IPALYQHWKQRQA
>d1kk6a_ b.81.1.3 (A:) Xenobiotic acetyltransferase {Enterococcus faecium, VAT(D)}
MGPNPMKMYPIEGNKSVQFIKPILEKLENVEVGEYSYYDSKNGETFDKQILYHYPILNDKLKIGK
FCSIGPGVTIIMNGANHRMDGSTYPFNLFGNGWEKHMPKLDQLPIKGDTIIGNDVWIGKDVVIMP
GVKIGDGAIVAANSVVVKDIAPYMLAGGNPANEIKQRFDQDTINQLLDIKWWNWPIDIINENIDK
ILDNSIIREVIW
>d1fxja1 b.81.1.4 (A:252-329) N-acetylglucosamine 1-phosphate uridyltransferase GlmU, C-terminal domain {Escherichia coli}
VMLRDPARFDLRGTLTHGRDVEIDTNVIIEGNVTLGHRVKIGTGCVIKNSVIGDDCEISPYTVVE
DANLAAACTIGPF
>d1hv9a1 b.81.1.4 (A:252-452) N-acetylglucosamine 1-phosphate uridyltransferase GlmU, C-terminal domain {Escherichia coli}
VMLRDPARFDLRGTLTHGRDVEIDTNVIIEGNVTLGHRVKIGTGCVIKNSVIGDDCEISPYTVVE
DANLAAACTIGPFARLRPGAELLEGAHVGNFVEMKKARLGKGSKAGHLTYLGDAEIGDNVNIGAG
TITCNYDGANKFKTIIGDDVFVGSDTQLVAPVTVGKGATIAAGTTVTRNVGENALAISRVPQTQK
EGWRRP
>d1hm9a1 b.81.1.4 (A:252-459) N-acetylglucosamine 1-phosphate uridyltransferase GlmU, C-terminal domain {Streptococcus pneumoniae}
VSFVNPEATYIDIDVEIAPEVQIEANVILKGQTKIGAETVLTNGTYVVDSTIGAGAVITNSMIEE
SSVADGVTVGPYAHIRPNSSLGAQVHIGNFVEVKGSSIGENTKAGHLTYIGNCEVGSNVNFGAGT
ITVNYDGKNKYKTVIGDNVFVGSNSTIIAPVELGDNSLVGAGSTITKDVPADAIAIGRGRQINKD
EYATRLPHHPKNQ
>d1qrea_ b.81.1.5 (A:) Carbonic anhydrase {Archaeon Methanosarcina thermophila}
TVDEFSNIRENPVTPWNPEPSAPVIDPTAYIDPQASVIGEVTIGANVMVSPMASIRSDEGMPIFV
GDRSNVQDGVVLHALETINEEGEPIEDNIVEVDGKEYAVYIGNNVSLAHQSQVHGPAAVGDDTFI
GMQAFVFKSKVGNNCVLEPRSAAIGVTIPDGRYIPAGMVVTSQAEADKLPEVTDDYAYSHTNEAV
VYVNVHLAEGYKETS
>d1ewwa_ b.81.2.1 (A:) An insect antifreeze protein {Spruce budworm (Choristoneura fumiferana)}
DGSCTNTNSQLSANSKCEKSTLTNCYVDKSEVYGTTCTGSRFDGVTITTSTSTGSRISGPGCKIS
TCIITGGVPAPSAACKISGCTFSAN
>d1dzra_ b.82.1.1 (A:) dTDP-4-dehydrorhamnose 3,5-epimerase RmlC
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{Salmonella typhimurium}
MMIVIKTAIPDVLILEPKVFGDERGFFFESYNQQTFEELIGRKVTFVQDNHSKSKKNVLRGLHFQ
RGENAQGKLVRCAVGEVFDVAVDIRKESPTFGQWVGVNLSAENKRQLWIPEGFAHGFVTLSEYAE
FLYKATNYYSPSSEGSILWNDEAIGIEWPFSQLPELSAKDAAAPLLDQALLTE
>d1ep0a_ b.82.1.1 (A:) dTDP-4-dehydrorhamnose 3,5-epimerase RmlC
{Archaeon Methanobacterium thermoautotrophicum}
EFRFIKTSLDGAIIIEPEVYTDERGYFMETFNEAIFQENGLEVRFVQDNESMSVRGVLRGLHFQR
EKPQGKLVRVIRGEIFDVAVDLRKNSDTYGEWTGVRLSDENRREFFIPEGFAHGFLALSDECIVN
YKCTELYHPEYDSGIPWDDPDIGIDWPLEMVDDLIISEKDRNWKPLRENPVYL
>d1fi2a_ b.82.1.2 (A:) Germin {Barley (Hordeum vulgare)}
TDPDPLQDFCVADLDGKAVSVNGHTCKPMSEAGDDFLFSSKLTKAGNTSTPNGSAVTELDVAEWP
GTNTLGVSMNRVDFAPGGTNPPHIHPRATEIGMVMKGELLVGILGSLDSGNKLYSRVVRAGETFV
IPRGLMHFQFNVGKTEAYMVVSFNSQNPGIVFVPLTLFGSDPPIPTPVLTKALRVEAGVVELLKS
KFAGGS
>d2phla1 b.82.1.2 (A:11-210) Seed storage 7S protein {French bean
(Phaseolus vulgaris), phaseolin}
DNPFYFNSDNSWNTLFKNQYGHIRVLQRFDQQSKRLQNLEDYRLVEFRSKPETLLLPQQADAELL
LVVRSGSAILVLVKPDDRREYFFLTSDNPIFSDHQKIPAGTIFYLVNPDPKEDLRIIQLAMPVNN
PQIHEFFLSSTEAQQSYLQEFSKHILEASFNSKFEEINRVLFEEEGQQEGVIVNIDSEQIKELSK
HAKSS
>d2phla2 b.82.1.2 (A:220-381) Seed storage 7S protein {French bean
(Phaseolus vulgaris), phaseolin}
NTIGNEFGNLTERTDNSLNVLISSIEMEEGALFVPHYYSKAIVILVVNEGEAHVELVGPKGNKET
LEYESYRAELSKDDVFVIPAAYPVAIKATSNVNFTGFGINANNNNRNLLAGKTDNVISSIGRALD
GKDVLGLTFSGSGDEVMKLINKQSGSYFVDAH
>d1dgwa_ b.82.1.2 (A:) Seed storage 7S protein {Jack bean (Canavalia
ensiformis), canavalin/vinculin}
NNPYLFRSNKFLTLFKNQHGSLRLLQRFNEDTEKLENLRDYRVLEYCSKPNTLLLPHHSDSDLLV
LVLEGQAILVLVNPDGRDTYKLDQGDAIKIQAGTPFYLINPDNNQNLRILKFAITFRRPGTVEDF
FLSSTKRLPSYLSAFSKNFLEASYDSPYDEIEQTLLQEEQEGVIVKMP
>g1dgr.3 b.82.1.2 (M:,N:) Seed storage 7S protein {Jack bean (Canavalia
ensiformis), canavalin/vinculin}
QLRRYAATLSEGDIIVIPSSFPVALKAASDLNMVGIGVNAENNERNFLAGHKENVIRQIPRQVSD
LTFPGSGEEVEELLENQKESYFVDGQPXDKPFNLRSRDPIYSNNYGKLYEITPEKNSQLRDLDIL
LNCLQMNEGALFVPHYNSRATVILVANEGRAEVELVGLE
>g1dgw.1 b.82.1.2 (X:,Y:) Seed storage 7S protein {Jack bean (Canavalia
ensiformis), canavalin/vinculin}
DKPFNLRSRDPIYSNNYGKLYEITPEKNSQLRDLDILLNCLQMNEGALFVPHYNSRATVILVANE
GRAEVELVGLEXQLRRYAATLSEGDIIVIPSSFPVALKAASDLNMVGIGVNAENNERNFLAGHKE
NVIRQIPRQVSDLTFPGSGEEVEELLENQKESYFVDGQP
>d1fxza1 b.82.1.2 (A:10-248) Seed storage 7S protein {Soybean (Glycine
max), proglycinin}
NECQIQKLNALKPDNRIESEGGLIETWNPNNKPFQCAGVALSRCTLNRNALRRPSYTNGPQEIYI
QQGKGIFGMIYPGCPSTFEEPQQPQQRGQSSRPQDRHQKIYNFREGDLIAVPTGVAWWMYNNEDT
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PVVAVSIIDTNSLENQLDQMPRRFYLAGNQEQEFLKYQQEQGGHQSQKGKHQQEEENEGGSILSG
FTLEFLEHAFSVDKQIAKNLQGENEGEDKGAIVTVKGGLSVIKP
>d1fxza2 b.82.1.2 (A:297-470) Seed storage 7S protein {Soybean (Glycine max), proglycinin}
ICTMRLRHNIGQTSSPDIYNPQAGSVTTATSLDFPALSWLRLSAEFGSLRKNAMFVPHYNLNANS
IIYALNGRALIQVVNCNGERVFDGELQEGRVLIVPQNFVVAARSQSDNFEYVSFKTNDTPMIGTL
AGANSLLNALPEEVIQHTFNLKSQQARQIKNNNPFKFLVPPQES
>d1pmi__ b.82.1.3 (-) Phosphomannose isomerase {Yeast (Candida albicans)}
SSEKLFRIQCGYQNYDWGKIGSSSAVAQFVHNSDPSITIDETKPYAELWMGTHPSVPSKAIDLNN
QTLRDLVTAKPQEYLGESIITKFGSSKELPFLFKVLSIEKVLSIQAHPDKKLGAQLHAADPKNYP
DDNHKPEMAIAVTDFEGFCGFKPLDQLAKTLATVPELNEIIGQELVDEFISGIKLPAEVGSQDDV
NNRKLLQKVFGKLMNTDDDVIKQQTAKLLERTDREPQVFKDIDSRLPELIQRLNKQFPNDIGLFC
GCLLLNHVGLNKGEAMFLQAKDPHAYISGDIIECMAASDNVVRAGFTPKFKDVKNLVEMLTYSYE
SVEKQKMPLQEFPRSKGDAVKSVLYDPPIAEFSVLQTIFDKSKGGKQVIEGLNGPSIVIATNGKG
TIQITGDDSTKQKIDTGYVFFVAPGSSIELTADSANQDQDFTTYRAFVEA
>d1eyba_ b.82.1.4 (A:) Homogentisate dioxygenase {Human (Homo sapiens)}
AELKYISGFGNECSSEDPRCPGSLPEGQNNPQVCPYNLYAEQLSGSAFTCPRSTNKRSWLYRILP
SVSHKPFESIDEGHVTHNWDEVDPDPNQLRWKPFEIPKASQKKVDFVSGLHTLCGAGDIKSNNGL
AIHIFLCNTSMENRCFYNSDGDFLIVPQKGNLLIYTEFGKMLVQPNEICVIQRGMRFSIDVFEET
RGYILEVYGVHFELPDLGPIGANGLANPRDFLIPIAWYEDRQVPGGYTVINKYQGKLFAAKQDVS
PFNVVAWHGNYTPYKYNLKNFMVINSVAFDHADPSIFTVLTAKSVRPGVAIADFVIFPPRWGVAD
KTFRPPYYHRNCMSEFMGLIRGHYEAKQGGFLPGGGSLHSTMTPHGPDADCFEKASKVKLAPERI
ADGTMAFMFESSLSLAVTKWGLKASRCLDENYHKCWEPLKSHFTPNSRN
>d1qjea_ b.82.2.1 (A:) Isopenicillin N synthase {Emericella nidulans}
SKANVPKIDVSPLFGDDQAAKMRVAQQIDAASRDTGFFYAVNHGINVQRLSQKTKEFHMSITPEE
KWDLAIRAYNKEHQDQVRAGYYLSIPGKKAVESFCYLNPNFTPDHPRIQAKTPTHEVNVWPDETK
HPGFQDFAEQYYWDVFGLSSALLKGYALALGKEENFFARHFKPDDTLASVVLIRYPYLDPYPEAA
IKTAADGTKLSFEWHEDVSLITVLYQSNVQNLQVETAAGYQDIEADDTGYLINCGSYMAHLTNNY
YKAPIHRVKWVNAERQSLPFFVNLGYDSVIDPFDPREPNGKSDREPLSYGDYLQNGLVSLINKNG
QT
>d1dcs__ b.82.2.1 (-) Deacetoxycephalosporin C synthase {Streptomyces clavuligerus}
MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKRA
VTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFERIWTQYFDRQYTAS
RAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQT
PCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTS
SVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGGNYVNIRRTSKA
>d1gp6a_ b.82.2.1 (A:) Anthocyanidin synthase {Mouse-ear cress (Arabidopsis thaliana)}
VAVERVESLAKSGIISIPKEYIRPKEELESINDVFLEEKKEDGPQVPTIDLKNIESDDEKIRENC
IEELKKASLDWGVMHLINHGIPADLMERVKKAGEEFFSLSVEEKEKYANDQATGKIQGYGSKLAN
NASGQLEWEDYFFHLAYPEEKRDLSIWPKTPSDYIEATSEYAKCLRLLATKVFKALSVGLGLEPD

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RLEKEVGGLEELLLQMKINYYPKCPQPELALGVEAHTDVSALTFILHNMVPGLQLFYEGKWVTAK
CVPDSIVMHIGDTLEILSNGKYKSILHRGLVNKEKVRISWAVFCEPPKDKIVLKPLPEMVSVESP
AKFPPRTFAQHIEHKLFGKEQEEL
>d1ds1a_ b.82.2.2 (A:) Clavaminate synthase {Streptomyces
clavuligerus}
TSVDCTAYGPELRALAARLPRTPRADLYAFLDAAHTAAASLPGALATALDTFNAEGSEDGHLLLR
GLPVEADADLPTTPSSTPAPEDRSLLTMEAMLGLVGRRLGLHTGYRELRSGTVYHDVYPSPGAHH
LSSETSETLLEFHTEMAYHRLQPNYVMLACSRADHERTAATLVASVRKALPLLDERTRARLLDRR
MPCCVDVAFRGGVDDPGAIAQVKPLYGDADDPFLGYDRELLAPEDPADKEAVAALSKALDEVTEA
VYLEPGDLLIVDNFRTTHARTPFSPRWDGKDRWLHRVYIRTDRNGQLSGGERAGDVVAFTPRG
>d1jr7a_ b.82.2.3 (A:) Gab protein (hypothetical protein YgaT)
{Escherichia coli}
GQDYSGFTLTPSAQSPRLLELTFTEQTTKQFLEQVAEWPVQALEYKSFLRFRVAKILDDLCANQL
QPLLLKTLLNRAEGALLINAVGVDDVKQADEMVKLATAVAHLIGRSNFDAMSGQYYARFVVKNVD
NSDSYLRQPHRVMELHNDGTYVEEITDYVLMMKIDEQNMQGGNSLLLHLDDWEHLDNYFRHPLAR
RPMRFAAPPSKNVSKDVFHPVFDVDQQGRPVMRYIDQFVQPKDFEEGVWLSELSDAIETSKGILS
VPVPVGKFLLINNLFWLHGRDRFTPHPDLRRELMRQRGYFAYASNHYQTHQ
>d1e5sa_ b.82.2.4 (A:) Type II Proline 3-hydroxylase (proline oxidase)
{Streptomyces sp.}
MRSHILGKIELDQTRLAPDLAYLAAVPTVEEEYDEFSNGFWKHVPLWNASGDSEDRLYRDLKDAA
AQPTAHVEHVPYLKEIVTTVFDGTHLQMARSRNLKNAIVIPHRDFVELDREVDRYFRTFMVLEDS
PLAFHSNEDTVIHMRPGEIWFLDAATVHSAVNFSEISRQSLCVDFAFDGPFDEKEIFADATLYAP
GSTPDLPERRPFTAEHRRRILSLGQVIERENFRDILFLLSKVHYKYDVHPSETYDWLIEISKQAG
DEKMVVKAEQIRDFAVEARALSERFSLTSW
>d1ft9a2 b.82.3.1 (A:2-133) CO-sensing protein CooA, N-terminal
domain {Rhodospirillum rubrum}
PPRFNIANVLLSPDGETFFRGFRSKIHAKGSLVCTGEGDENGVFVVVDGRLRVYLVGEEREISLF
YLTSGDMFCMHSGCLVEATERTEVRFADIRTFEQKLQTCPSMAWGLIAILGRALTSCMRTIEDLM
FH
>d1hw5a2 b.82.3.2 (A:1-137) Catabolite gene activator protein,
N-terminal domain {Escherichia coli}
VLGKPQTDPTLEWFLSHCHIHKYPSKSTLIHQGEKAETLYYIVKGSVAVLIKDEEGKEMILSYLN
QGDFIGELGLFEEGQERSAWVRAKTACEVAEISYKKFRQLIQVNPDILMRLSAQMARRLQVLAEK
VGNLAFL
>d1rgs_1 b.82.3.2 (113-244) Regulatory subunit of Protein kinase A
{Cow (Bos taurus)}
RKVIPKDYKTMAALAKAIEKNVLFSHLDDNERSDIFDAMFPVSFIAGETVIQQGDEGDNFYVIDQ
GEMDVYVNNEWATSVGEGGSFGELALIYGTPRAATVKAKTNVKLWGIDRDSYRRILMGSTLRKRK
MY
>d1rgs_2 b.82.3.2 (245-376) Regulatory subunit of Protein kinase A
{Cow (Bos taurus)}
EEFLSKVSILESLDKWERLTVADALEPVQFEDGQKIVVQGEPGDEFFIILEGSAAVLQRRSENEE
FVEVGRLGPSDYFGEIALLMNRPRAATVVARGPLKCVKLDRPRFERVLGPCSDILKRNIQQYNSF
VS
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>d1cx4a1 b.82.3.2 (A:130-265) Regulatory subunit of Protein kinase
A {Rat (Rattus norvegicus)}
RIIHPKTDDQRNRLQEACKDILLFKNLDPEQMSQVLDAMFEKLVKEGEHVIDQGDDGDNFYVIDR
GTFDIYVKCDGVGRCVGNYDNRGSFGELALMYNTPRAATITATSPGALWGLDRVTFRRIIVKNNA
KKRKMY
>d1cx4a2 b.82.3.2 (A:266-412) Regulatory subunit of Protein kinase
A {Rat (Rattus norvegicus)}
ESFIESLPFLKSLEVSERLKVVDVIGTKVYNDGEQIIAQGDSADSFFIVESGEVRITMKRKGKSD
IEENGAVEIARCLRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIA
TYEEQLVALFGTNMDIV
>d2arca_ b.82.4.1 (A:) Regulatory protein AraC {Escherichia coli}
DPLLPGYSFNAHLVAGLTPIEANGYLDFFIDRPLGMKGYILNLTIRGQGVVKNQGREFVCRPGDI
LLFPPGEIHHYGRHPEAREWYHQWVYFRPRAYWHEWLNWPSIFANTGFFRPDEAHQPHFSDLFGQ
IINAGQGEGRYSELLAINLLEQLLLRRMEAI
>d1ig3a1 b.82.6.1 (A:179-263) Thiamin pyrophosphokinase,
substrate-binding domain {Mouse (Mus musculus)}
DSLIYLLQPGKHRLHVDTGMEGSWCGLIPVGQPCNQVTTTGLKWNLTNDVLGFGTLVSTSNTYDG
SGLVTVETDHPLLWTMAIKS
>d1ig0a1 b.82.6.1 (A:224-319) Thiamin pyrophosphokinase,
substrate-binding domain {Baker's yeast (Saccharomyces cerevisiae)}
TDLIFLIKKNGTLIEYDPQFRNTCIGNCGLLPIGEATLVKETRGLKWDVKNWPTSVVTGRVSSSN
RFVGDNCCFIDTKDDIILNVEIFVDKLIDFL
>d1wapa_ b.82.5.1 (A:) Trp RNA-binding attenuation protein (TRAP)
{Bacillus subtilis}
DFVVIKAVEDGVNVIGLTRGTDTKFHHSEKLDKGEVIIAQFTEHTSAIKVRGEALIQTAYGEMKS
EKK
>d1c9sa_ b.82.5.1 (A:) Trp RNA-binding attenuation protein (TRAP)
{Bacillus stearothermophilus}
SDFVVIKALEDGVNVIGLTRGADTRFHHSEKLDKGEVLIAQFTEHTSAIKVRGKAYIQTRHGVIE
SEGK
>g1h6w.1 b.108.1.1 (A:,B:) Heat- and protease-stable fragment of the
short fibre {Bacteriophage T4}
TGATLNGRGSTTSMRGVVKLTTTAGSQSGGDASSALAWNADVIHQRGGQTINGTLRINNTLTIAS
GGANITGTVNMTGGYIQGKRVVTQNEIDRTIPVGAIMMWAADSLPSDAWRFCHGGTVSASDCPLY
ASRIGTRYGGSSSNPGLPDMRXSLNYIIKVKE
>d1k28a2 b.108.1.2 (A:362-584) Tail-associated lysozyme gp5,
C-terminal domain {Bacteriophage T4}
DPADPPIPNDSRILFKEPVSSYKGEYPYVHTMETESGHIQEFDDTPGQERYRLVHPTGTYEEVSP
SGRRTRKTVDNLYDITNADGNFLVAGDKKTNVGGSEIYYNMDNRLHQIDGSNTIFVRGDETKTVE
GNGTILVKGNVTIIVEGNADITVKGDATTLVEGNQTNTVNGNLSWKVAGTVDWDVGGDWTEKMAS
MSSISSGQYTIDGSRIDIGSVDHHHHHH
>d1qiua2 b.83.1.1 (A:319-395) Adenovirus {Human adenovirus type 2}
VSIKKSSGLNFDNTAIAINAGKGLEFDTNTSESPDINPIKTKIGSGIDYNENGAMITKLGAGLSF
DNSGAITIGNKN
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>d1kkea2 b.83.1.2 (A:313-455) Reovirus attachment protein sigma 1 {Reovirus}
YRFRQSMWIGIVSYSGSGLNWRVQVNSDIFIVDDYIHICLPAFDGFSIADGGDLSLNFVTGLLPP
LLTGDTEPAFHNDVVTYGAQTVAIGLSSGGAPQYMSKNLWVEQWQDGVLRLRVEGGGSITHSNSK
WPAMTVSYPRSFT
>d1h8ga_ b.109.1.1 (A:) Choline binding domain of autolysin C-LytA {Streptococcus pneumoniae}
TDGNWYWFDNSGEMATGWKKIADKWYYFNEEGAMKTGWVKYKDTWYYLDAKEGAMVSNAFIQSAD
GTGWYYLKPDGTLADRPEFTVEPDGLITVK
>d1hcxa_ b.109.1.1 (A:) Choline binding domain of autolysin C-LytA {Streptococcus pneumoniae}
GSYPKDKFEKINGTWYYFDSSGYMLADRWRKHTDGNWYWFDNSGEMATGWKKIADKWYYFNEEGA
MKTGWVKYKDTWYYLDAKEGAMVSNAFIQSADGTGWYYLKPDGTLADRPEFTVEPDGLITVK
>d1bdo__ b.84.1.1 (-) Biotinyl domain of acetyl-CoA carboxylase {Escherichia coli}
EISGHIVRSPMVGTFYRTPSPDAKAFIEVGQKVNVGDTLCIVEAMKMMNQIEADKSGTVKAILVE
SGQPVEFDEPLVVIE
>d1dd2a_ b.84.1.1 (A:) Biotin carboxyl carrier domain of transcarboxylase (TC 1.3S) {Propionibacterium freudenreichii, subsp. shermanii}
AGAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERD
AVQGGQGLIKIG
>d1htp__ b.84.1.1 (-) Protein H of glycine cleavage system {Pea (Pisum sativum)}
SNVLDGLKYAPSHEWVKHEGSVATIGITDHAQDHLGEVVFVELPEPGVSVTKGKGFGAVESVKAT
SDVNSPISGEVIEVNTGLTGKPGLINSSPYEDGWMIKIKPTSPDELESLLGAKEYTKFCEEEDAA
H
>d1lac__ b.84.1.1 (-) Ipoyl domain of dihydrolipoamide acetyltransferase {Bacillus stearothermophilus}
AFEFKLPDIGEGIHEGEIVKWFVKPGDEVNEDDVLCEVQNDKAVVEIPSPVKGKVLEILVPEGTV
ATVGQTLITLDAPGY
>d1iyu__ b.84.1.1 (-) Ipoyl domain of dihydrolipoamide acetyltransferase {Azotobacter vinelandii}
SEIIRVPDIGGDGEVIELLVKTGDLIEVEQGLVVLESAKASMEVPSPKAGVVKSVSVKLGDKLKE
GDAIIELEPAAGAR
>d1qjoa_ b.84.1.1 (A:) Ipoyl domain of dihydrolipoamide acetyltransferase {Escherichia coli}
MVKEVNVPDIGGDEVEVTEVMVKVGDKVAAEQSLITVEGDKASMEVPAPFAGVVKELKVNVGDKV
KTGSLIMIFEVEGAA
>d1gjxa_ b.84.1.1 (A:) Ipoyl domain of dihydrolipoamide acetyltransferase {Neisseria meningitidis}
ALVELKVPDIGGHENVDIIAVEVNVGDTIAVDDTLITLETDKATMDVPAEVAGVVKEVKVKVGDK
ISEGGLIVVVEAEGTA
>d1fyc__ b.84.1.1 (-) Ipoyl domain of dihydrolipoamide

acetyltransferase {Human (Homo sapiens)}
GSNMSYPPHMQVLLPALSPTMTMGTVQRWEKKVGEKLSEGDLLAEIETDKATIGFEVQEEGYLAK
ILVPEGTRDVPLGTPLCIIVEKEADISAFADYRPTEVTDLK
>d1ghk__ b.84.1.1 (-) Lipoyl domain of the 2-oxoglutarate dehydrogenase complex {Azotobacter vinelandii}
AIDIKAPTFPESIADGTVATWHKKPGEAVKRDELIVDIETDKVVMEVLAEADGVIAEIVKNEGDT
VLSGELLGKLTEGG
>d1pmr__ b.84.1.1 (-) Lipoyl domain of the 2-oxoglutarate dehydrogenase complex {Escherichia coli}
SSVDILVPDLPESVADATVATWHKKPGDAVVRDEVLVEIETDKVVLEVPASADGILDAVLEDEGT
TVTSRQILGRLREGN
>d1k8ma_ b.84.1.1 (A:) Lipoyl domain of the mitochondrial branched-chain alpha-ketoacid dehydrogenase {Human (Homo sapiens)}
MGQVVQFKLSDIGEGIREVTVKEWYVKEGDTVSQFDSICEVQSDKASVTITSRYDGVIKKLYYNL
DDIAYVGKPLVDIETEALKDLE
>d1dv1a1 b.84.2.1 (A:331-446) Biotin carboxylase subunit of acetyl-CoA carboxylase, C-terminal domain {Escherichia coli}
RGHAVECRINAEDPNTFLPSPGKITRFHAPGGFGVRWESHIYAGYTVPPYYDSMIGKLICYGENR
DVAIARMKNALQELIIDGIKTNVDLQIRIMNDENFQHGGTNIHYLEKKLGL
>d1gsoa1 b.84.2.1 (A:328-426) Glycinamide ribonucleotide synthetase (GAR-syn). {Escherichia coli}
ERASLGVVMAAGGYPGDYRTGDVIHGLPLEEVAGGKVFHAGTKLADDEQVVTNGGRVLCVTALGH
TVAEAQKRAYALMTDIHWDDCFCRKDIGWRAIER
>d1b6ra1 b.84.2.1 (A:277-355) N5-carboxyaminoimidazole ribonucleotide synthetase, AIRC, PurK {Escherichia coli}
NNPSVMINLIGSDVNYDWLKLPLVHLHWYDKEVRPGRKVGHLNLTDSDTSRLTATLEALIPLLPP
EYASGVIWAQSKFG
>d1eyza1 b.84.2.1 (A:319-392) Glycinamide ribonucleotide transformylase PurT {Escherichia coli}
GPAASAVILPQLTSQNVTFDNVQNAVGADLQIRLFGKPEIDGSRRLGVALATAESVVDAIERAKH
AAGQVKVQG
>d1hcz_2 b.84.2.2 (168-230) Cytochrome f, small domain {Turnip (Brassica rapa)}
NTVYNATAGGIISKILRKEKGGYEITIVDASNERQVIDIIPRGLELLVSEGESIKLDQPLTSN
>d1e2wa2 b.84.2.2 (A:169-232) Cytochrome f, small domain {Chlamydomonas reinhardtii}
TIYNASAAGKIVAITALSEKKGGFEVSIEKANGEVVVDKIPAGPDLIVKEGQTVQADQPLTNNP
>d1ci3m2 b.84.2.2 (M:170-231) Cytochrome f, small domain {Phormidium laminosum}
AVYNASAAGVITAIAKADDGSAEVKIRTEDGTTIVDKIPAGPELIVSEGEEVAAGAALTNNP
>d1gpr__ b.84.3.1 (-) Glucose permease IIa domain, IIa-glc {Bacillus subtilis}
EPLQNEIGEEVFVSPITGEIHPITDVPDQVFSGKMMGDGFAILPSEGIVVSPVRGKILNVFPTKH
AIGLQSDGGREILIHFGIDTVSLKGEGFTSFVSEGDRVEPGQKLLEVDLDAVKPNVPSLMTPIVF

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TNLAEGETVSIKASGSVNREQEDIVKIE
>d2gpr__ b.84.3.1 (-) Glucose permease IIa domain, IIa-glc {Mycoplasma
capricolum}
MWFFNKNLKVLAPCDGTIITLDEVEDEVFKERMLGDGFAINPKSNDFHAPVSGKLVTAFPTKHAF
GIQTKSGVEILLHIGLDTVSLDGNGFESFVTQDQEVNAGDKLVTVDLKSVAKKVPSIKSPIIFTN
NGGKTLEIVKMGEVKQGDVVAILK
>d1glaf_ b.84.3.1 (F:) Glucose-specific factor III (glsIII)
{Escherichia coli}
GLFDKLKSLVSDDKKDTGTIEIIAPLSGEIVNIEDVPDVVFAEKIVGDGIAIKPTGNKMVAPVDG
TIGKIFETNHAFSIESDSGVELFVHFGIDTVELKGEGFKRIAEEGQRVKVGDTVIEFDLPLLEEK
AKSTLTPVVISNMDEIKELIKLSGSVTVGETPVIRIKK
>d2f3ga_ b.84.3.1 (A:) Glucose-specific factor III (glsIII)
{Escherichia coli}
TIEIIAPLSGEIVNIEDVPDVVFAEKIVGDGIAIKPTGNKMVAPVDGTIGKIFETNHAFSIESDS
GVELFVHFGIDTVELKGEGFKRIAEEGQRVKVGDTVIEFDLPLLEEKAKSTLTPVVISNMDEIKE
LIKLSGSVTVGETPVIRIKK
>d1hg7a_ b.85.1.1 (A:) Type III antifreeze protein {Ocean pout
(Macrozoarces americanus), different isoforms}
MNQASVVANQLIPINTALTLVMMRSEVVTPVGIPAEDIPRLVSMQVNRAVPLGTTLMPDMVKGYA
A
>d1ops__ b.85.1.1 (-) Type III antifreeze protein {Ocean pout
(Macrozoarces americanus), different isoforms}
SQSVVATQLIPMNTALTPAMMEGKVTNPIGIPFAEMSQLVGKQVNTPVAKGQTLMPNMVKTYAA
>d1c8aa2 b.85.1.1 (A:69-134) Type III antifreeze protein {Antarctic
eel pout (Austrolycichthys brachycephalus) and (Lycodichthys
dearborni)}
SPGLKSVVANQLIPINTALTLVMMKAEEVSPKGIPSEEISKLVGMQVNRAVYLDQTLMPDMVKNY
E
>d3rdn__ b.85.1.1 (-) Type III antifreeze protein {Antarctic eel pout
(Austrolycichthys brachycephalus) and (Lycodichthys dearborni)}
NKASVVANQLIPINTALTLIMMKAEVVTPMGIPAEEIPNLVGMQVNRAVPLGTTLMPDMVKNYED
GTTSPGLK
>d1c5ea_ b.85.2.1 (A:) Head decoration protein D (gpD, major capsid
protein D) {Bacteriophage lambda}
SDPAHTATAPGGLSAKAPAMTPLMLDTSSRKLVAWDGTTDGAAVGILAVAADQTSTTLTFYKSGT
FRYEDVLWPEAASDETKKRTAFAGTAISIV
>d1ejrb_ b.85.3.1 (B:) Urease, beta-subunit {Klebsiella aerogenes}
MIPGEYHVKPGQIALNTGRATCRVVVENHGDRPIQVGSHYHFAEVNPALKFDRQQAAGYRLNIPA
GTAVRFEPGQKREVELVAFAGHRAVFGFRGEVMGPL
>d4ubpb_ b.85.3.1 (B:) Urease, beta-subunit {Bacillus pasteurii}
NYIVPGEYRVAEGEIEINAGREKTTIRVSNTGDRPIQVGSHIHFVEVNKELLFDRAEGIGRRLNI
PSGTAARFEPGEEMEVELTELGGNREVFGISDLTNGSVDNKELILQRAKELGYKGVE
>d1e9ya1 b.85.3.1 (A:106-238) Urease, beta-subunit {Helicobacter
pylori}
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LVPGELFLKNEDITINEGKKAVSVKVKNVGDRPVQIGSHFHFFEVNRCLDFDREKTFGKRLDIAA
GTAVRFEPGEEKSVELIDIGGNRRIFGFNALVDRQADNESKKIALHRAKERGFHGAKSDDNYVKT
IKE

>d1g8la1 b.85.6.1 (A:327-409) Molybdenum cofactor biosynthesis protein MoeA, C-terminal domain {Escherichia coli}

LPARQRVRTASRLKKTPGRLDFQRGVLQRNADGELEVTTTGHQGSHIFSSFSLGNCFIVLERDRG
NVEVGEWVEVEPFNALFG

>d1euwa_ b.85.4.1 (A:) Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase) {Escherichia coli}

MMKKIDVKILDPRVGKEFPLPTYATSGSAGLDLRACLNDAVELAPGDTTLVPTGLAIHIADPSLA
AMMLPRSGLGHKHGIVLGNLVGLIDSDYQGQLMISVWNRGQDSFTIQPGERIAQMIFVPVVQAEF
NLVEDF

>d1f7da_ b.85.4.1 (A:) Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase) {Feline immunodeficiency virus}

MIIEGDGILDKRSEDAGYDLLAAKEIHLLPGEVKVIPTGVKLMLPKGYWGLIIGKSSIGSKGLDV
LGGVIDEGYRGEIGVIMINVSRKSITLMERQKIAQLIILPCKHEVLEQGKVVM

>d1f7ra_ b.85.4.1 (A:) Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase) {Feline immunodeficiency virus}

MIIEGDGILDKRSEDAGYDLLAAKEIHLLPGEVKVIPTGVKLMLPKGYWGLIIGKSSIGSKGLDV
LGGVIDEGYRGEIGVIMINVSRKSITLMERQKIAQLIILPCKHEVLEQGKVVMDSERGDNGYGST
GVF

>d1dun__ b.85.4.1 (-) Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase) {Equine infectious anemia virus}

MLAYQGTQIKEKRDEDAGFDLCVPYDIMIPVSDTKIIPTDVKIQVPPNSFGWVTGKSSMAKQGLL
INGGIIDEGYTGEIQVICTNIGKSNIKLIEGQKFAQLIILQHHSNSRQPWDENKI

>d1tul__ b.85.5.1 (-) ACMNPV telokin-like protein {Baculovirus (Autographa californica), nuclear polyhedrosis virus}

GTPDIIVNAQINSEDENVLDFIIEDEYYLKKRGVGAHIIKVASSPQLRLLYKNAYSTVSCGNYGV
LCNLVQNGEYDLNAIMFNCAEIKLNKGQMLFQTKIWR

>d1at0__ b.86.1.1 (-) Hedgehog {Fruit fly (Drosophila melanogaster)}

CFTPESTALLESGVRKPLGELSIGDRVLSMTANGQAVYSEVILFMDRNLEQMQNFVQLHTDGGAV
LTVTPAHLVSVWQPESQKLTFVFADRIEEKNQVLVRDVETGELRPQRVVKVGSVRSKGVVAPLTR
EGTIVVNSVAASCYA

>d1dfaa1 b.86.1.2 (A:1-180,A:416-454) PI-Scei intein {Baker's yeast (Saccharomyces cerevisiae)}

CFAKGTNVLMADGSIECIENIEVGNKVMGKDGRPREVIKLPRGRETMYSVVQKSQHRAHKSDSSR
EVPELLKFTCNATHELVVRTPRSVRRLSRTIKGVEYFEVITFEMGQKKAPDGRIVELVKEVSKSY
PISEGPERANELVESYRKASNKAYFEWTIEARDLSLLGSHVRKATYQTYAXCRGFYFELQELKED
DYYGITLSDDSDHQFLLANQVVVHN

>d1dq3a1 b.86.1.2 (A:1-128,A:415-454) PI-Pfui intein {Archaeon Pyrococcus furiosus}

CIDGKAKIIFENEGEEHLTTMEEMYERYKHLGEFYDEEYNRWGIDVSNVPIYVKSFDPESKRVVK
GKVNVIWKYELGKDVTKYEIITNKGTKILTSPWHPFFVLTPDFKIVEKRADELKEGDILIGGMXG
LEVVRHITTTNEPRTFYDLTVENYQNYLAGENGMIFVHN

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>d1am2__ b.86.1.2 (-) GyrA intein {Mycobacterium xenopi}
ASITGDALVALPEGESVRIADIVPGARPNSDNAIDLKVLDRHGNPVLADRLFHSGEHPVYAVRTV
EGLRVTGTANHPLLCLVDVAGVPTLLWKLIDEIKPGDYAVIQRSAFSVDCAGFARGKPEFAPTTY
TVGVPGLVRFLEAHHRDPDAKAIADELTDGRFYYAKVASVTDAGVQPVYSLRVDTADHAFITNGF
VSHN
>d1umua_ b.87.1.1 (A:) UmuD' {Escherichia coli}
DYVEQRIDLNQLLIQHPSATYFVKASGDSMIDGGISDGDLLIVDSAITASHGDIVIAAVDGEFTV
KKLQLRPTVQLIPMNSAYSPITISSEDTLDVFGVVIHVVK
>d1jhfa2 b.87.1.1 (A:73-198) LexA C-terminal domain {Escherichia
coli}
EEGLPLVGRVAADEPLLAQQHIEGHYQVDPSLFKPNADFLLRVSGMSMKDIGIMDGDLLAVHKTQ
DVRNGQVVVARIDDEVTVKRLKKQGNKVELLPENSEFKPIVVDLRQQSFTIEGLAVGVIRN
>d1f39a_ b.87.1.1 (A:) lambda repressor C-terminal domain
{Bacteriophage lambda virus}
ASASAFWLEVEGNSMTAPTGSKPSFPDGMLILVDPEQAVEPGDFCIARLGGDEFTFKKLIRDSGQ
VFLQPLNPQYPMIPCNESCSVVGKVIASQWPEETFG
>d1b12a_ b.87.1.2 (A:) Type 1 signal peptidase {Escherichia coli}
RSFIYEPFQIPSGSMMPTLLIGDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKL
DYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATS
GFFEVPKNETKENGIRLSERKETLGDVTHRILTVPIAQDQVGMYYQQPGQQLATWIVPPGQYFMM
GDNRDNSADSRYWGFVPEANLVGRATAIWMSFDKQEGEWPTGLRLSRIGGIH
>d1jcha2 b.110.1.1 (A:84-315) Colicin E3 translocation domain
{Escherichia coli}
VAAPVAFGFPALSTPGAGGLAVSISAGALSAAIADIMAALKGPFKFGLWGVALYGVLPSQIAKDD
PNMMSKIVTSLPADDITESPVSSLPLDKATVNVNVRVVDDVKDERQNISVVSGVPMSVPVVDAKP
TERPGVFTASIPGAPVLNISVNNSTPAVQTLSPGVTNNTDKDVRPAFGTQGGNTRDAVIRFPKDS
GHNAVYVSVSDVLSPDQVKQRQDEENRRQQEWDATHP
>d1hxra_ b.88.1.1 (A:) RabGEF Mss4 {Rat (Rattus norvegicus)}
ELVSAEGRNRKAVLCQRCGSRVLQPGTALFSRRQLFLPSMRKKPDLVDGSNPDGDVLEEHWLVND
MFIFENVGFTKDVGNVKFLVCADCEIGPIGWHCLDDKNSFYVALERVSHE
>d1fwqa_ b.88.1.1 (A:) RabGEF Mss4 {Human (Homo sapiens)}
ELVSAEGRNRKAVLCQRCGSRVLQPGTALFSRRQLFLPSMRKKPALSDGSNPDGDLLQEHWLVED
MFIFENVGFTKDVGNIKFLVCADCEIGPIGWHCLDDKNSFYVALERVSHE
>d1h6qa_ b.88.1.2 (A:) Translationally controlled tumor-associated
protein tctp, p23fyp {Fission yeast (Schizosaccharomyces pombe)}
MLLYKDVISGDELVSDAYDLKEVDDIVYEADCQMVTVKQGGDVDIGANPSAEDAEENAEEGTETV
NNLVYSFRLSPTSFDKKSYMSYIKGYMKAIKARLQESNPERVPVFEKNAIGFVKKILANFKDYDF
YIGESMDPDAMVVLMNYREDGITPYMIFFKDGLVSEKF
>d3ezma_ b.89.1.1 (A:) Cyanovirin-N {Cyanobacterium (Nostoc
ellipsosporum)}
LGKFSQTCYNSAIQGSVLTSTCERTNGGYNTSSIDLNSVIENVDGSLKWQPSNFIETCRNTQLAG
SSELAAECKTRAQQFVSTKINLDDHIANIDGTLKYE
>d1fjra_ b.102.1.1 (A:) Methuselah ectodomain {Fruit fly (Drosophila
melanogaster)}
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DILECDYFDTVDISAAQKLQNGSYLFEGLLVPAILTGEYDFRILPDDSKQKVARHIRGCVCKLKP
CVRFCCPHDHIMDNGVCYDNMSDEELAELDPFLNVTLDDGSVSRRHFKNELIVQWDLPMPCDGMF
YLDNREEQDKYTLFENGTFFRHFDRVTLRKREYCLQHLTFADGNATSIRIAPHNCLIV
>d1lkta_ b.90.1.1 (A:) Head-binding domain of phage P22 tailspike
protein {Salmonella bacteriophage P22}
ANVVVSNPRPIFTESRSFKAVANGKIYIGQIDTDPVNPANQIPVYIENEDGSHVQITQPLIINAA
GKIVYNGQLVKIVTVQGHSMAIYDANGSQVDYIANVLKY
>d1qqha_ b.91.1.1 (A:) E2 regulatory, transactivation domain {Human
papillomavirus type 18}
KSKAHKAIELQMALQGLAQSAYKTEDWTLQDTCEELWNTEPTHCFKKGGQTVQVYFDGNKDNCMT
YVAWDSVYYMTDAGTWDKTATCVSHRGLYYVKEGYNTFYIEFKSECEKYGNTGTWEVHFGNNVID
CNDSMCSTSDDTVS
>d1dtoa_ b.91.1.1 (A:) E2 regulatory, transactivation domain {Human
papillomavirus type 16}
HMETLCQRLNVCQDKILTHYENDSTDLRDHIDYWKHMRLECAIYYKAREMGFKHINHQVVPTLAV
SKNKALQAIELQLTLETIYNSQYSNEKWTLQDVSLEVYLTAPTGCIKKHGYTVEVQFDGDICNTM
HYTNWTHIYICEEASVTVVEGQVDYYGLYYVHEGIRTYFVQFKDDAEKYSKNKVWEVHAGGQVIL
CPTSVFS
>d1g8la2 b.103.1.1 (A:7-177) Molybdenum cofactor biosynthesis protein
MoeA, N-terminal and linker domains {Escherichia coli}
LMSLDTALNEMLSRVTPLTAQETLPLVQCFGRILASDVVSPLDVPGFDNSAMDGYAVRLADIASG
QPLPVAGKSFAGQPYHGEWPAGTCIRIMTGAPVPEGCEAVVMQEQTEQMDNGVRFTAEVRSGQNI
RRRGEDISAGAVVFPAGTRLTTAELPVIASLGIAEVPVIRK
>d1k6wa1 b.92.1.2 (A:4-55,A:376-426) Cytosine deaminase {Escherichia
coli}
ALQTIINARLPGEEGLWQIHLQDGKISAIDAQSGVMPITENSLDAEQGLVIPXLIILPAENGFDA
LRRQVPVRYSVRGGKVIASTQPAQTTVYLEQPEAIDYKR
>d1ejrc1 b.92.1.1 (C:1002-1129,C:1423-1475) alpha-Subunit of urease
{Klebsiella aerogenes}
SNISRQAYADMFGPTVGDKVRLADTELWIEVEDDLTTYGEEVKFGGGKVIRDGMGQGQMLAADCV
DLVLTNALIVDHWGIVKADIGVKDGRIFAIGKAGNPDIQPNVTIPIGAATEVIAAEGKIVTAGXS
IEVGKLADLVVWSPAFFGVKPATVIKGGMIAIAPMGDINASIPTPQPVHYRP
>d4ubpc1 b.92.1.1 (C:1-131,C:435-483) alpha-Subunit of urease
{Bacillus pasteurii}
MKINRQQYAESYGPTVGDEVRLADTDLWIEVEKDYTTYGDEVNFGGGKVLREGMGENGTYTRTEN
VLDLLLTNALILDYTGIYKADIGVKDGYIVGIGKGGNPDIMDGVTPNMIVGTATEVIAAEGKIVT
AXLVLWEPKFFGVKADRVIKGGIIAYAQIGDPSASIPTPQPVMGRRMYGTV
>d1e9yb1 b.92.1.1 (B:1-131,B:432-480) alpha-Subunit of urease
{Helicobacter pylori}
MKKISRKEYVSMYGPTTGDKVRLGDTDLIAEVEHDYTIYGEELKFGGGKTLREGMSQSNNPSKEE
LDLIITNALIVDYTGIYKADIGIKDGKIAGIGKGGNKDMQDGVKNNLSVGPATEALAGEGLIVTA
GXADLVLWSPAFFGVKPNMIIKGGFIALSQMGDANASIPTPQPVYYREMFA
>d1aqt_2 b.93.1.1 (2-86) Epsilon subunit of F1F0-ATP synthase
N-terminal domain {Escherichia coli}
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STYHLDVVSAEQQMFSGLVEKIQVTGSEGELGIYPGHAPLLTAIKPGMIRIVKQHGHEEFIYLSG
GILEVQPGNVTVLADTAIRG
>d1e79h2 b.93.1.1 (H:15-100) Epsilon subunit of F1F0-ATP synthase N-terminal domain {Cow (Bos taurus)}
QMSFTFASPTQVFFNSANVRQVDVPTQTGAFGILAAHVPTLQVLRPGLVVVHAEDGTTSKYFVSS
GSVTVNADSSVQLLAEEAVTL
>d1hhna_ b.104.1.1 (A:) Calreticulin {Rat (Rattus norvegicus)}
SKKIKDPDAAKPEDWDERAKIDDPTDSKPEDWDKPEHIPDPDAKKPEDWDEEMDGEWEPPVIQNP
EYKGEWKPRQIDNPDYKGTWIHPEIDNPEYSPDANI
>d1jhna3 b.104.1.1 (A:270-411) Calnexin {Dog (Canis familiaris)}
PVNPSREIEDPEDQKPEDWDERPKIPDPDAVKPDDWNEDAPAKIPDEEATKPDGWLDDEPEYVPD
PDAEKPEDWDEDMDGEWEAPQIANPKCESAPGCGVWQRPMIDNPNYKGKWKPPMIDNPNYQGIWK
PRKIPNPDFFED
>d1tph1_ c.1.1.1 (1:) Triosephosphate isomerase {Chicken (Gallus gallus)}
RKFFVGGNWKMNGDKKSLGELIHTLNGAKLSADTEVVCGAPSIYLDFARQKLDAKIGVAAQNCYK
VPKGAFTGEISPAMIKDIGAAWVILGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKLDE
REAGITEKVVFEQTKAIADNVKDWSKVVLAYEPVWAIGTGKTATPQQAQEVHEKLRGWLKTHVSD
AVAQSTRIIYGGSVTGGNCKELASQHDVDGFLVGGASLKPEFVDIINAKH
>d1htia_ c.1.1.1 (A:) Triosephosphate isomerase {Human (Homo sapiens)}
APSRKFFVGGNWKMNGRKQSLGELIGTLNAAKVPADTEVVCAPPTAYIDFARQKLDPKIAVAAQN
CYKVTNGAFTGEISPGMIKDCGATWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEK
LDEREAGITEKVVFEQTKVIADNVKDWSKVVLAYEPVWAIGTGKTATPQQAQEVHEKLRGWLKSN
VSDAVAQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPEFVDIINAKQ
>d1i45a_ c.1.1.1 (A:) Triosephosphate isomerase {Baker's yeast (Saccharomyces cerevisiae)}
ARTFFVGGNFKLNGSKQSIKEIVERLNTASIPENVEVVICPPATYLDYSVSLVKKPQVTVGAQNA
YLKASGAFTGENSVDQIKDVGAKYVILGHSERRSYFHEDDKFIADKTKFALGQGVGVILCIGETL
EEKKAGKTLDVVERQLNAVLEEVKDFTNVVVAYEPVWAIGTGLAATPEDAQDIHASIRKFLASKL
GDKAASELRILYGGSANGSNAVTFKDKADVDGFLVGGASLKPEFVDIINSRN
>d1ttj__ c.1.1.1 (-) Triosephosphate isomerase {Trypanosoma brucei}
SKPQPIAAANWKCNGSQQSLSELIDLFNSTSINHDVQCVVASTSSHLAMTKERLSHPKFVIAAQN
AGNADALASLKDFGVNWIVLGHSERRAYYGETNEIVADKVAAAVASGFMVIACIGETLQERESGR
TAVVVLTQIAAIAKKLKKADWAKVVIAYEPVWAIGTGKVATPQQAQEAHALIRSWVSSKIGADVA
GELRILYGGSVNGKNARTLYQQRDVNGFLVGGASLKPEFVDIIKATQ
>d5tima_ c.1.1.1 (A:) Triosephosphate isomerase {Trypanosoma brucei}
SKPQPIAAANWKCNGSQQSLSELIDLFNSTSINHDVQCVVASTFVHLAMTKERLSHPKFVIAAQN
AIAKSGAFTGEVSLPILKDFGVNWIVLGHSERRAYYGETNEIVADKVAAAVASGFMVIACIGETL
QERESGRTAVVVLTQIAAIAKKLKKADWAKVVIAYEPVWAIGTGKVATPQQAQEAHALIRSWVSS
KIGADVAGELRILYGGSVNGKNARTLYQQRDVNGFLVGGASLKPEFVDIIKATQ
>d1tcda_ c.1.1.1 (A:) Triosephosphate isomerase {Trypanosoma cruzi}
KPQPIAAANWKCNGSESLLVPLIETLNAATFDHDVQCVVAPTFLHIPMTKARLTNPKFQIAAQNA
ITRSGAFTGEVSLQILKDYGISWVVLGHSERRLYYGETNEIVAEKVAQACAAGFHVIVCVGETNE

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EREAGRTAAVVLTQLAAVAQKLSKEAWSRVVIAYEPVWAIGTGKVATPQQAQEVHELLRRWVRSK
LGTDIAAQLRILYGGSVTAKNARTLYQMRDINGFLVGGASLKPEFVEIIEATK
>d1ydva_ c.1.1.1 (A:) Triosephosphate isomerase {Plasmodium falciparum}
RKYFVAANWKCNGTLESIKSLTNSFNNLDFDPSKLDVVVFPVSVHYDHTRKLLQSKFSTGIQNVS
KFGNGSYTGEVSAEIAKDLNIEYVIIGHFERRKYFHETDEDVREKLQASLKNNLKAVVCFGESLE
QREQNKTIEVITKQVKAFVDLIDNFDNVILVYEPLWAIGTGKTATPEQAQLVHKEIRKIVKDTCG
EKQANQIRILYGGSVNTENCSSLIQQEDIDGFLVGNASLKESFVDIIKSAM
>d1amk__ c.1.1.1 (-) Triosephosphate isomerase {Leishmania mexicana}
SAKPQPIAAANWKCNGTTASIEKLVQVFNEHTISHDVQCVVAPTFVHIPLVQAKLRNPKYVISAE
NAIAKSGAFTGEVSMPILKDIGVHWVILGHSERRTYYGETDEIVAQKVSEACKQGFMVIACIGET
LQQREANQTAKVVLSQTSAIAAKLTKDAWNQVVLAYEPVWAIGTGKVATPEQAQEVHLLLRKWVS
ENIGTDVAAKLRILYGGSVNAANAATLYAKPDINGFLVGGASLKPEFRDIIDATR
>d1trea_ c.1.1.1 (A:) Triosephosphate isomerase {Escherichia coli}
MRHPLVMGNWKLNGSRHMVHELVSNLRKELAGVAGCAVAIAPPEMYIDMAKREAEGSHIMLGAQN
VNLNLSGAFTGETSAAMLKDIGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGET
EAENEAGKTEEVCARQIDAVLKTQGAAAFEGAVIAYEPVWAIGTGKSATPAQAQAVHKFIRDHIA
KVDANIAEQVIIQYGGSVNASNAAELFAQPDIDGALVGGASLKADAFAVIVKAAEAAKQA
>d2btma_ c.1.1.1 (A:) Triosephosphate isomerase {Bacillus stearothermophilus}
RKPIIAGNWKMNGTLAEAVQFVEDVKGHVPPADEVISVVCAPFLFLDRLVQAADGTDLKIGAQTM
HFADQGAYTGEVSPVMLKDLGVTYVILGHSERRQMFAETDETVNKKVLAAFTRGLIPIICCGESL
EEREAGQTNAVVASQVEKALAGLTPEQVKQAVIAYEPIWAIGTGKSSTPEDANSVCGHIRSVVSR
LFGPEAAEAIRIQYGGSVKPDNIRDFLAQQQIDGALVGGASLEPASFLQLVEAGRH
>d1aw1a_ c.1.1.1 (A:) Triosephosphate isomerase {Vibrio marinus}
RHPVVMGNWKLNGSKEMVVDLLNGLNAELEGVTGVDVAVAPPALFVDLAERTLTEAGSAIILGAQ
NTDLNNSGAFTGDMSPAMLKEFGATHIIIGHSERREYHAESDEFVAKKFAFLKENGLTPVLCIGE
SDAQNEAGETMAVCARQLDAVINTQGVEALEGAIIAYEPIWAIGTGKAATAEDAQRIHAQIRAHI
AEKSEAVAKNVVIQYGGSVKPENAAAYFAQPDIDGALVGGAALDAKSFAAIAKAAAEAKA
>d1b9ba_ c.1.1.1 (A:) Triosephosphate isomerase {Thermotoga maritima}
TRKLILAGNWKMHKTISEAKKFVSLLVNELHDVKEFEIVVCPPFTALSEVGEILSGRNIKLGAQN
VFYEDQGAFTGEISPLMLQEIGVEYVIVGHSERRRIFKEDDEFINRKVKAVLEKGMTPILCVGET
LEEREKGLTFCVVEKQVREGFYGLDKEEAKRVVIAYEPVWAIGTGRVATPQQAQEVHAFIRKLLS
EMYDEETAGSIRILYGGSIKPDNFLGLIVQKDIDGGLVGGASLKESFIELARIMRGV
>d1hg3a_ c.1.1.1 (A:) Triosephosphate isomerase {Archaeon Pyrococcus woesei}
AKLKEPIIAINFKTYIEATGKRALEIAKAAEKVYKETGVTIVVAPQLVDLRMIAESVEIPVFAQH
IDPIKPGSHTGHVLPEAVKEAGAVGTLLNHSENRMILADLEAAIRRAEEVGLMTMVCSNNPAVSA
AVAALNPDYVAVEPPELIGTGIPVSKAKPEVITNTVELVKKVNPEVKVLCGAGISTGEDVKKAIE
LGTVGVLLASGVTKAKDPEKAIWDLVSGI
>d1qo2a_ c.1.2.1 (A:) Phosphoribosylformimino-5-aminoimidazole carboxamide ribotite isomerase HisA {Thermotoga maritima}
MLVVPAIDLFRGKVARMIKGRKENTIFYEKDPVELVEKLIEEGFTLIHVVDLSNAIENSGENLPV
LEKLSEFAEHIQIGGGIRSLDYAEKLRKLGYRRQIVSSKVLEDPSFLKSLREIDVEPVFSLDTRG
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GRVAFKGWLAEEEIDPVSLLKRLKEYGLEEIVHTEIEKDGTLQEHDFSLTKKIAIEAEVKVLAAG
GISSENSLKTAQKVHTETNGLLKGVIVGRAFLEGILTVEVMKRYAR
>d1thfd_ c.1.2.1 (D:) Cyclase subunit (or domain) of imidazoleglycerolphosphate synthase HisF {Thermotoga maritima}
MLAKRIIACLDVKDGRVVKGSNFENLRDSGDPVELGKFYSEIGIDELVFLDITASVEKRKTMLEL
VEKVAEQIDIPFTVGGGIHDFETASELILRGADKVSINTAAVENPSLITQIAQTFGSQAVVVAID
AKRVDGEFMVFTYSGKKNTGILLRDWVVEVEKRGAGEILLTSIDRDGTKSGYDTEMIRFVRPLTT
LPIIASGGAGKMEHFLEAFLAGADAALAASVFHFREIDVRELKEYLKKHGVNVRLEGL
>d1jvna1 c.1.2.1 (A:230-552) Cyclase subunit (or domain) of imidazoleglycerolphosphate synthase HisF {Baker's yeast (Saccharomyces cerevisiae), His7}
DYSNYGLTRRIIACLDVRTNDQGDLVVTKGDQYDVREKSDGKGVRNLGKPVQLAQKYYQQGADEV
TFLNITSFRDCPLKDTPMLEVLKQAAKTVFVPLTVGGGIKDIVDVDGTKIPALEVASLYFRSGAD
KVSIGTDAVYAAEKYYELGNRGDGTSPIETISKAYGAQAVVISVDPKRVYVNSQADTKNKVFETE
YPGPNGEKYCWYQCTIKGGRESRDLGVWELTRACEALGAGEILLNCIDKDGSNSGYDLELIEHVK
DAVKIPVIASSGAGVPEHFEEAFLKTRADACLGAGMFHRGEFTVNDVKEYLLEHGLKVRMDEE
>d1h5ya_ c.1.2.1 (A:) Cyclase subunit (or domain) of imidazoleglycerolphosphate synthase HisF {Archaeon Pyrobaculum aerophilum}
HMALRIIPCLDIDGGAKVVVKGVNFQGIREVGDPVEMAVRYEEEGADEIAILDITAAPEGRATFI
DSVKRVAEAVSIPVLVGGGVRSLEDATTLFRAGADKVSVNTAAVRNPQLVALLAREFGSQSTVVA
IDAKWNGEYYEVYVKGGREATGLDAVKWAKEVEELGAGEILLTSIDRDGTGLGYDVELIRRVADS
VRIPVIASGGAGRVEHFYEAAAAGADAVLAASLFHFRVLSIAQVKRYLKERGVEVRI
>d1rpxa_ c.1.2.2 (A:) D-ribulose-5-phosphate 3-epimerase {Potato (Solanum tuberosum)}
SRVDKFSKSDIIVSPSILSANFSKLGEQVKAIEQAGCDWIHVDVMDGRFVPNITIGPLVVDSLRP
ITDLPLDVHLMIVEPDQRVPDFIKAGADIVSVHCEQSSTIHLHRTINQIKSLGAKAGVVLNPGTP
LTAIEYVLDAVDLVLIMSVNPGFGGQSFIESQVKKISDLRKICAERGLNPWIEVDGGVGPKNAYK
VIEAGANALVAGSAVFGAPDYAEAIKGIKTSKRPE
>d1dbta_ c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Bacillus subtilis}
MKNNLPIIALDFASAEETLAFLAPFQQEPLFVKVGMELFYQEGPSIVKQLKERNCELFLDLKLHD
IPTTVNKAMKRLASLGVDLVNVHAAGGKKMMQAALEGLEEGTPAGKKRPSLIAVTQLTSTSEQIM
KDELLIEKSLIDTVVHYSKQAEESGLDGVVCSVHEAKAIYQAVSPSFLTVTPGIRMSEDAANDQV
RVATPAIAREKGSSAIVVGRSITKAEDPVKAYKAVRLEWEGI
>d1eixa_ c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Escherichia coli}
VTNSPVVVALDYHNRDDALAFVDKIDPRDCRLKVGKEMFTLFGPQFVRELQQRGFDIFLDLKFHD
IPNTAAHAVAAAADLGVWMVNVHASGGARMMTAAREALVPFGKDAPLLIAVTVLTSMEASDLVDL
GMTLSPADYAERLAALTQKCGLDGVVCSAQEAVRFKQVFGQEFKLVTPGIRPQGSEAGDQRRIMT
PEQALSAGVDYMVIGRPVTQSVDPAQTLKAINASLQ
>d1dvja_ c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Archaeon Methanobacterium thermoautotrophicum}
MDVMNRLILAMDLMNRDDALRVTGEVREYIDTVKIGYPLVLSEGMDIIAEFRKRFGCRIIADFKV
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ADIPETNEKICRATFKAGADAIIVHGFPGADSVRACLNVAEEMGREVFLLTEMSHPGAEMFIQGA
ADEIARMGVDLGVKNYVGPSTRPERLSRLREIIGQDSFLISPGVGAQGGDPGETLRFADAIIVGR
SIYLADNPAAAAAGIIESIKDLLIPEDPAANKARKEAELAAATA
>d1dvjb_ c.1.2.3 (B:) Orotidine 5'-monophosphate decarboxylase (OMP
decarboxylase) {Archaeon Methanobacterium thermoautotrophicum}
RLILAMDLMNRDDALRVTGEVREYIDTVKIGYPLVLSEGMDIIAEFRKRFGCRIIADFKVADIPE
TNEKICRATFKAGADAIIVHGFPGADSVRACLNVAEEMGREVFLLTEMSHPGAEMFIQGAADEIA
RMGVDLGVKNYVGPSTRPERLSRLREIIGQDSFLISPGVGAQGGDPGETLRFADAIIVGRSIYLA
DNPAAAAAGIIESIKD
>d1dqwa_ c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP
decarboxylase) {Baker's yeast (Saccharomyces cerevisiae)}
MHKATYKERAATHPSPVAAKLFNIMHEKQTNLCASLDVRTTKELLELVEALGPKICLLKTHVDIL
TDFSMEGTVKPLKALSAKYNFLLFEDRKFADIGNTVKLQYSAGVYRIAEWADITNAHGVVGPGIV
SGLKQAAEEVTKEPRGLLMLAELSCKGSLSTGEYTKGTVDIAKSDKDFVIGFIAQRDMGGRDEGY
DWLIMTPGVGLDDKGDALGQQYRTVDDVVSTGSDIIIVGRGLFAKGRDAKVEGERYRKAGWEAYL
RRCGQQD
>d1pii_2 c.1.2.4 (255-452) N-(5'phosphoribosyl)antranilate isomerase,
PRAI {Escherichia coli}
GENKVCGLTRGQDAKAAYDAGAIYGGLIFVATSPRCVNVEQAQEVMAAAPLQYVGVFRNHDIADV
VDKAKVLSLAAVQLHGNEEQLYIDTLREALPAHVAIWKALSVGETLPAREFQHVDKYVLDNGQGG
SGQRFDWSLLNGQSLGNVLLAGGLGADNCVEAAQTGCAGLDFNSAVESQPGIKDARLLASVFQTL
RAY
>d1nsj__ c.1.2.4 (-) N-(5'phosphoribosyl)antranilate isomerase, PRAI
{Thermotoga maritima}
MVRVKICGITNLEDALFSVESGADAVGFVFYPKSKRYISPEDARRISVELPPFVFRVGVFVNEEP
EKILDVASYVQLNAVQLHGEEPIELCRKIAERILVIKAVGVSNERDMERALNYREFPILLDTKTP
EYGGSGKTFDWSLILPYRDRFRYLVLSGGLNPENVRSAIDVVRPFAVDVSSGVEAFPGKKDHDSI
KMFIKNAKGL
>d1pii_1 c.1.2.4 (1-254) Indole-3-glycerophosphate synthase, IPGS
{Escherichia coli}
MQTVLAKIVADKAIWVEARKQQQPLASFQNEVQPSTRHFYDALQGARTAFILECKKASPSKGVIR
DDFDPARIAAIYKHYASAISVLTDEKYFQGSFNFLPIVSQIAPQPILCKDFIIDPYQIYLARYYQ
ADACLLMLSVLDDDQYRQLAAVAHSLEMGVLTEVSNEEEQERAIALGAKVVGINNRDLRDLSIDL
NRTRELAPKLGHNVTVISESGINTYAQVRELSHFANGFLIGSALMAHDDLHAAVRRVLL
>d1a53__ c.1.2.4 (-) Indole-3-glycerophosphate synthase, IPGS
{Archaeon Sulfolobus solfataricus}
PRYLKGWLKDVVQLSLRRPSFRASRQRPIISLNERILEFNKRNITAIIAEYKRKSPSGLDVERDP
IEYSKFMERYAVGLSILTEEKYFNGSYETLRKIASSVSIPILMKDFIVKESQIDDAYNLGADTVL
LIVKILTERELESLLEYARSYGMEPLIEINDENDLDIALRIGARFIGINSRDLETLEINKENQRK
LISMIPSNVVKVAESGISERNEIEELRKLGVNAFLIGSSLMRNPEKIKEFIL
>d1qopa_ c.1.2.4 (A:) Trp synthase alpha-subunit {Salmonella
typhimurium}
MERYENLFAQLNDRREGAFVPFVTLGDPGIEQSLKIIDTLIDAGADALELGVPFSDPLADGPTIQ
NANLRAFAAGVTPAQCFEMLAIIREKHPTIPIGLLMYANLVFNNGIDAFYARCEQVGVDSVLVAD
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VPVEESAPFRQAALRHNIAPIFICPPNADDDLLRQVASYGRGYTYLLSRSGVTGAENRGALPLHH
LIEKLKEYHAAPALQGFGISSPEQVSAAVRAGAAGAISGSAIVKIIEKNLASPKQMLAELRSFVS
AMKAASR
>d1geqa_ c.1.2.4 (A:) Trp synthase alpha-subunit {Archaeon Pyrococcus
furiosus}
MFKDGSLIPYLTAGDPDKQSTLNFLLALDEYAGAIELGIPFSDPIADGKTIQESHYRALKNGFKL
REAFWIVKEFRRHSSTPIVLMTYYNPIYRAGVRNFLAEAKASGVDGILVVDLPVFHAKEFTEIAR
EEGIKTVFLAAPNTPDERLKVIDDMTTGFVYLVSLYGTTGAREEIPKTAYDLLRRAKRICRNKVA
VGFGVSKREHVVSLLKEGANGVVVGSALVKIIGEKGREATEFLKKKVEELLGI
>d2tpsa_ c.1.3.1 (A:) Thiamin phosphate synthase {Bacillus subtilis}
HGIRMTRISREMMKELLSVYFIMGSNNTKADPVTVVQKALKGGATLYQFREKGGDALTGEARIKF
AEKAQAACREAGVPFIVNDDVELALNLKADGIHIGQEDANAKEVRAAIGDMILGVSAHTMSEVKQ
AEEDGADYVGLGPIYPTETKKDTRAVQGVSLIEAVRRQGISIPIVGIGGITIDNAAPVIQAGADG
VSMISAISQAEDPESAARKFREEIQTYKTGR
>d1ho1a_ c.1.24.1 (A:) Pyridoxine 5'-phosphate synthase {Escherichia
coli}
AELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRILRQTLD
TRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDACKRLADAGIQVS
LFIDADEEQIKAAAEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAATFAASLGLKVNAGHGLT
YHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLEARG
>d2dora_ c.1.4.1 (A:) Dihydroorotate dehydrogenase {Lactococcus
lactis, isozyme A}
MLNTTFANAKFANPFMNASGVHCMTIEDLEELKASQAGAYITKSSTLEKREGNPLPRYVDLELGS
INSMGLPNLGFDYYLDYVLKNQKENAQEGPIFFSIAGMSAAENIAMLKKIQESDFSGITELNLSC
PNVPGKPQLAYDFEATEKLLKEVFTFFTKPLGVKLPPYFDLVHFDIMAEILNQFPLTYVNSVNSI
GNGLFIDPEAESVVIKPKDGFGGIGGAYIKPTALANVRAFYTRLKPEIQIIGTGGIETGQDAFEH
LLCGATMLQIGTALHKEGPAIFDRIIKELEEIMNQKGYQSIADFHGKLKSL
>d1ep3a_ c.1.4.1 (A:) Dihydroorotate dehydrogenase {Lactococcus
lactis, isozyme B}
MTENNRLSVKLPGLDLKNPIIPASGCFGFGEEYAKYYDLNKLGSIMVKATTLHPRFGNPTPRVAE
TASGMLNAIGLQNPGLEVIMTEKLPWLNENFPELPIIANVAGSEEADYVAVCAKIGDAANVKAIE
LNISCPNVKHGGQAFGTDPEVAAALVKACKAVSKVPLYVKLSPNVTDIVPIAKAVEAAGADGLTM
INTLMGVRFDLKTRQPILANITGGLSGPAIKPVALKLIHQVAQDVDIPIIGMGGVANAQDVLEMY
MAGASAVAVGTANFADPFVCPKIIDKLPELMDQYRIESLESLIQEVKEGKK
>d1d3ga_ c.1.4.1 (A:) Dihydroorotate dehydrogenase {Human (Homo
sapiens)}
MATGDERFYAEHLMPTLQGLLDPESAHRLAVRFTSLGLLPRARFQDSDMLEVRVLGHKFRNPVGI
AAGFDKHGEAVDGLYKMGFGFVEIGSVTPKPQEGNPRPRVFRLPEDQAVINRYGFNSHGLSVVEH
RLRARQQKQAKLTEDGLPLGVNLGKNKTSVDAAEDYAEGVRVLGPLADYLVVNVSSPNTAGLRSL
QGKAELRRLLTKVLQERDGLRRVHRPAVLVKIAPDLTSQDKEDIASVVKELGIDGLIVTNTTVSR
PAGLQGALRSETGGLSGKPLRDLSTQTIREMYALTQGRVPIIGVGGVSSGQDALEKIRAGASLVQ
LYTALTFWGPPVVGKVKRELEALLKEQGFGGVTDAIGADHRR
>d1oyb__ c.1.4.1 (-) Old yellow enzyme (OYE) {Brewer's yeast
(Saccharomyces carlsbergensis)}
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SFVKDFKPQALGDTNLFKPIKIGNNELLHRAVIPPLTRMRALHPGNIPNRDWAVEYYTQRAQRPG
TMIITEGAFISPQAGGYDNAPGVWSEEQMVEWTKIFNAIHEKKSFVWVQLWVLGWAAFPDNLARD
GLRYDSASDNVFMDAEQEAKAKKANNPQHSLTKDEIKQYIKEYVQAAKNSIAAGADGVEIHSANG
YLLNQFLDPHSNTRTDEYGGSIENRARFTLEVVDALVEAIGHEKVGLRLSPYGVFNSMSGGAETG
IVAQYAYVAGELEKRAKAGKRLAFVHLVEPRVTNPFLTEGEGEYEGGSNDFVYSIWKGPVIRAGN
FALHPEVVREEVKDKRTLIGYGRFFISNPDLVDRLEKGLPLNKYDRDTFYQMSAHGYIDYPTYEE
ALKLGWDKK
>d1icpa_ c.1.4.1 (A:) 12-oxophytodienoate reductase 1 (OYE homolog) {Tomato (Lycopersicon esculentum)}
QVDKIPLMSPCKMGKFELCHRVVLAPLTRQRSYGYIPQPHAILHYSQRSTNGGLLIGEATVISET
GIGYKDVPGIWTKEQVEAWKPIVDAVHAKGGIFFCQIWHVGRVSNKDFQPNGEDPISCTDRGLTP
QIMSNGIDIAHFTRPRRLTTDEIPQIVNEFRVAARNAIEAGFDGVEIHGAHGYLIDQFMKDQVND
RSDKYGGSLENRCRFALEIVEAVANEIGSDRVGIRISPFAHYNEAGDTNPTALGLYMVESLNKYD
LAYCHVVEPRMKTAWEKIECTESLVPMRKAYKGTFIVAGGYDREDGNRALIEDRADLVAYGRLFI
SNPDLPKRFELNAPLNKYNRDTFYTSDPIVGYTDYPFLE
>d1gox__ c.1.4.1 (-) Glycolate oxidase {Spinach (Spinacia oleracea)}
MEITNVNEYEAIAKQKLPKMVYDYYASGAEDQWTLAENRNAFSRILFRPRILIDVTNIDMTTTIL
GFKISMPIMIAPTAMQKMAHPEGEYATARAASAAGTIMTLSSWATSSVEEVASTGPGIRFFQLYV
YKDRNVVAQLVRRAERAGFKAIALTVDTPRLGRREADIKNRFVLPPFLTLKNFEGIDLGKMDKAN
DSGLSSYVAGQIDRSLSWKDVAWLQTITSLPILVKGVITAEDARLAVQHGAAGIIVSNHGARQLD
YVPATIMALEEVVKAAQGRIPVFLDGGVRRGTDVFKALALGAAGVFIGRPVVFSLAAEGEAGVKK
VLQMMRDEFELTMALSGCRSLKEISRSHIAADWD
>d1huva_ c.1.4.1 (A:) Membrane-associated (S)-mandelate dehydrogenase {Pseudomonas putida}
NLFNVEDYRKLAQKRLPKMVYDYLEGGAEDEYGVKHNRDVFQQWRFKPKRLVDVSRRSLQAEVLG
KRQSMPLLIGPTGLNGALWPKGDLALARAATKAGIPFVLSTASNMSIEDLARQCDGDLWFQLYVI
HREIAQGMVLKALHTGYTTLVLTTDVAVNGYRERDLHNRFKIPPFLTLKNFEGIDLGKMDKANLE
MQAALMSRQMDASFNWEALRWLRDLWPHKLLVKGLLSAEDADRCIAEGADGVILSNHGGRQLDCA
ISPMEVLAQSVAKTGKPVLIDSGFRRGSDIVKALALGAEAVLLGRATLYGLAARGETGVDEVLTL
LKADIDRTLAQIGCPDITSLSPDYLQNE
>d1h61a_ c.1.4.1 (A:) Pentaerythritol tetranirate reductase {Enterobacter cloacae}
SAEKLFTPLKVGAVTAPNRVFMAPLTRLRSIEPGDIPTPLMGEYYRQRASAGLIISEATQISAQA
KGYAGAPGLHSPEQIAAWKKITAGVHAEDGRIAVQLWHTGRISHSSIQPGGQAPVSASALNANTR
TSLRDENGNAIRVDTTTPRALELDEIPGIVNDFRQAVANAREAGFDLVELHSAHGYLLHQFLSPS
SNQRTDQYGGSVENRARLVLEVVDAVCNEWSADRIGIRVSPIGTFQNVDNGPNEEADALYLIEEL
AKRGIAYLHMSETDLAGGKPYSEAFRQKVRERFHGVIIGAGAYTAEKAEDLIGKGLIDAVAFGRD
YIANPDLVARLQKKAELNPQRPESFYGGGAEGYTDYPSL
>d1djna1 c.1.4.1 (A:1-340) Trimethylamine dehydrogenase, N-terminal domain {Methylophilus methylotrophus, w3a1}
ARDPKHDILFEPIQIGPKTLRNRFYQVPHCIGAGSDKPGFQSAHRSVKAEGGWAALNTEYCSINP
ESDDTHRLSARIWDEGDVRNLKAMTDEVHKYGALAGVELWYGGAHAPNMESRATPRGPSQYASEF
ETLSYCKEMDLSDIAQVQQFYVDAAKRSRDAGFDIVYVYGAHSYLPLQFLNPYYNKRTDKYGGSL
ENRARFWLETLEKVKHAVGSDCAIATRFGVDTVYGPGQIEAEVDGQKFVEMADSLVDMWDITIGD
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IAEWGEDAGPSRFYQQGHTIPWVKLVKQVSKKPVLGVGRYTDPEKMIEIVTKGYADIIGCARPSI
ADPFLPQKVEQGRYD
>d1ltda1 c.1.4.1 (A:98-511) Flavocytochrome b2, C-terminal domain
{Baker's yeast (Saccharomyces cerevisiae)}
APGETKEDIARKEQLKSLLPPLDNIINLYDFEYLASQTLTKQAWAYYSSGANDEVTHRENHNAYH
RIFFKPKILVDVRKVDISTDMLGSHVDVPFYVSATALCKLGNPLEGEKDVARGCGQGVTKVPQMI
STLASCSPEEIIEAAPSDKQIQWYQLYVNSDRKITDDLVKNVEKLGVKALFVTVDAPSLGQREKD
MKLKFSNTKAGPKAMKKTNVEESQGASRALSKFIDPSLTWKDIEELKKKTKLPIVIKGVQRTEDV
IKAAEIGVSGVVLSNHGGRQLDFSRAPIEVLAETMPILEQRNLKDKLEVFVDGGVRRGTDVLKAL
CLGAKGVGLGRPFLYANSCYGRNGVEKAIEILRDEIEMSMRLLGVTSIAELKPDLLDLSTLKART
VGVPNDVLYNEVYEGPTLTEFEDA
>d1h7wa2 c.1.4.1 (A:533-844) Dihydropyrimidine dehydrogenase, domain
4 {Pig (Sus scrofa)}
ISVEMAGLKFINPFGLASAAPTTSSSMIRRAFEAGWGFALTKTFSLDKDIVTNVSPRIVRGTTSG
PMYGPGQSSFLNIELISEKTAAYWCQSVTELKADFPDNIVIASIMCSYNKNDWMELSRKAEASGA
DALELNLSCPHGMGERGMGLACGQDPELVRNICRWVRQAVQIPFFAKLTPNVTDIVSIARAAKEG
GADGVTATNTVSGLMGLKADGTPWPAVGAGKRTTYGGVSGTAIRPIALRAVTTIARALPGFPILA
TGGIDSAESGLQFLHSGASVLQVCSAVQNQDFTVIQDYCTGLKALLYLKSIE
>d1ea0a2 c.1.4.1 (A:423-1193) Alpha subunit of glutamate synthase,
central and FMN domains {Azospirillum brasilense}
TTHLDELVKTASLKGEPSDMDKAELRRRQQAFGLTMEDMELILHPMVEDGKEAIGSMGDDSPIAV
LSDKYRGLHHFFRQNFSQVTNPPIDSLRERRVMSLKTRLGNLGNILDEDETQTRLLQLESPVLTT
AEFRAMRDYMGDTAAEIDATFPVDGGPEALRDALRRIRQETEDAVRGGATHVILTDEAMGPARAA
IPAILATGAVHTHLIRSNLRTFTSLNVRTAEGLDTHYFAVLIGVGATTVNAYLAQEAIAERHRRG
LFGSMPLEKGMANYKKAIDDGLLKIMSKMGISVISSYRGGGNFEAIGLSRALVAEHFPAMVSRIS
GIGLNGIQKKVLEQHATAYNEEVVALPVGGFYRFRKSGDRHGWEGGVIHTLQQAVTNDSYTTFKK
YSEQVNKRPPMQLRDLLELRSTKAPVPVDEVESITAIRKRFITPGMSMGALSPEAHGTLNVAMNR
IGAKSDSGEGGEDPARFRPDKNGDNWNSAIKQVASGRFGVTAEYLNQCRELEIKVAQGAKPGEGG
QLPGFKVTEMIARLRHSTPGVMLISPPPHHDIYSIEDLAQLIYDLKQINPDAKVTVKLVSRSGIG
TIAAGVAKANADIILISGNSGGTGASPQTSIKFAGLPWEMGLSEVHQVLTLNRLRHRVRLRTDGG
LKTGRDIVIAAMLGAEEFGIGTASLIAMGCIMVRQCHSNTCPVGVCVQDDKLRQKFVGTPEKVVN
LFTFLAEEVREILAGLGFRSLNEVIGRTDLLHQVSRGAEHLDDLDLNPRLAQVDPG
>d1eepa_ c.1.5.1 (A:) Inosine monophosphate dehydrogenase (IMPDH)
{Lyme disease spirochete (Borrelia burgdorferi)}
NKITKEALTFDDVSLIPRKSSVLPSEVSLKTQLTKNISLNIPFLSSAMDTVTESQMAIAIAKEGG
IGIIHKNMSIEAQRKEIEKVKTYKFQKTINTNGDTNEQKPEIFTAKQHLEKSDAYKNAEHKEDFP
NACKDLNNKLRVGAAVSIDIDTIERVEELVKAHVDILVIDSAHGHSTRIIELIKKIKTKYPNLDL
IAGNIVTKEAALDLISVGADCLKVGIGPGSICTTRIVAGVGVPQITAICDVYEACNNTNICIIAD
GGIRFSGDVVKAIAAGADSVMIGNLFAGTKESPSEEIIYNGKKFKSYVGMGSISAMKRGSKSRYF
QLENNEPKKLVPEGIEGMVPYSGKLKDILTQLKGGLMSGMGYLGAATISDLKINSKFVKISHS
>d1zfja1 c.1.5.1 (A:2-94,A:221-492) Inosine monophosphate
dehydrogenase (IMPDH) {Streptococcus pyogenes}
SNWDTKFLKKGYTFDDVLLIPAESHVLPNEVDLKTKLADNLTLNIPIITAAMDTVTGSKMAIAIA
RAGGLGVIHKNMSITEQAEEVRKVKRSEXGRLLVAAAVGVTSDTFERAEALFEAGADAIVIDTAH
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GHSAGVLRKIAEIRAHFPNRTLIAGNIATAEGARALYDAGVDVVKVGIGPGSICTTRVVAGVGVP
QVTAIYDAAAVAREYGKTIIADGGIKYSGDIVKALAAGGNAVMLGSMFAGTDEAPGETEIYQGRK
YKTYRGMGSIAAMKKGSSDRYFQGSVNEANKLVPEGIEGRVAYKGAASDIVFQMLGGIRSGMGYV
GAGDIQELHENAQFVEMSGAGLIESHPHDVQITNEAPNYSV
>d1ak5_1 c.1.5.1 (2-101,222-483) Inosine monophosphate dehydrogenase
(IMPDH) {Tritrichomonas foetus}
AKYYNEPCHTFNEYLLIPGLSTVDCIPSNVNLSTPLVKFQKGQQSEINLKIPLVSAIMQSVSGEK
MAIALAREGGISFIFGSQSIESQAAMVHAVKNFKAXHNELVDSQKRYLVGAGINTRDFRERVPAL
VEAGADVLCIDSSDGFSEWQKITIGWIREKYGDKVKVGAGNIVDGEGFRYLADAGADFIKIGIGG
GSICITREQKGIGRGQATAVIDVVAERNKYFEETGIYIPVCSDGGIVYDYHMTLALAMGADFIML
GRYFARFEESPTRKVTINGSVMKEYWGEGSSRARNWQRYDLGGKQKLSFEEGVDSYVPYAGKLKD
NVEASLNKVKSTMCNCGALTIPQLQSKAKITLVSSVSI
>d1jr1a1 c.1.5.1 (A:17-112,A:233-514) Inosine monophosphate
dehydrogenase (IMPDH) {Chinese hamster (Cricetulus griseus)}
GLTAQQLFNCGDGLTYNDFLILPGYIDFTADQVDLTSALTKKITLKTPLVSSPMDTVTEAGMAIA
MALTGGIGFIHHNCTPEFQANEVRKVKKYEQXYPLASKDAKKQLLCGAAIGTHEDDKYRLDLLAL
AGVDVVVLDSSQGNSIFQINMIKYMKEKYPNLQVIGGNVVTAAQAKNLIDAGVDALRVGMGCGSI
CITQEVLACGRPQATAVYKVSEYARRFGVPVIADGGIQNVGHIAKALALGASTVMMGSLLAATTE
APGEYFFSDGIRLKKYRGMGSLDAMDKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVPYL
IAGIQHSCQDIGAKSLTQVRAMMYSGELKFEKRTSSAQVEGGVHSLHSYEKRLF
>d1bd0a2 c.1.6.1 (A:12-244) Alanine racemase {Bacillus
stearothermophilus}
VDLDAIYDNVENLRRLLPDDTHIMAVVKANAYGHGDVQVARTALEAGASRLAVAFLDEALALREK
GIEAPILVLGASRPADAALAAQQRIALTVFRSDWLEEASALYSGPFPIHFHLKMDTGMGRLGVKD
EEETKRIVALIERHPHFVLEGLYTHFATADEVNTDYFSYQYTRFLHMLEWLPSRPPLVHCANSAA
SLRFPDRTFNMVRFGIAMYGLAPSPGIKPLLPYPLKEA
>d1d7ka2 c.1.6.1 (A:44-283) Eukaryotic ornithine decarboxylase {Human
(Homo sapiens)}
DLGDILKKHLRWLKALPRVTPFYAVKCNDSKAIVKTLAATGTGFDCASKTEIQLVQSLGVPPERI
IYANPCKQVSQIKYAANNGVQMMTFDSEVELMKVARAHPKAKLVLRIATDDSKAVCRLSVKFGAT
LRTSRLLLERAKELNIDVVGVSFHVGSGCTDPETFVQAISDARCVFDMGAEVGFSMYLLDIGGGF
PGSEDVKLKFEEITGVINPALDKYFPSDSGVRIIAEPGRYYVASA
>d7odca2 c.1.6.1 (A:44-283) Eukaryotic ornithine decarboxylase {Mouse
(Mus musculus)}
DLGDILKKHLRWLKALPRVTPFYAVKCNDSRAIVSTLAAIGTGFDCASKTEIQLVQGLGVPAERV
IYANPCKQVSQIKYAASNGVQMMTFDSEIELMKVARAHPKAKLVLRIATDDSKAVCRLSVKFGAT
LKTSRLLLERAKELNIDVIGVSFHVGSGCTDPDTFVQAVSDARCVFDMATEVGFSMHLLDIGGGF
PGSEDTKLKFEEITSVINPALDKYFPSDSGVRIIAEPGRYYVASA
>d2toda2 c.1.6.1 (A:44-283) Eukaryotic ornithine decarboxylase
{Trypanosoma brucei}
DLGDIVRKHETWKKCLPRVTPFYAVACNDDWRVLGTLAALGTGFDCASNTEIQRVRGIGVPPEKI
IYANPCKQISHIRYARDSGVDVMTFDCVDELEKVAKTHPKAKMVLRISTDDSLARCRLSVKFGAK
VEDCRFILEQAKKLNIDVTGVSFHVGSGSTDASTFAQAISDSRFVFDMGTELGFNMHILDIGGGF
PGTRDAPLKFEEIAGVINNALEKHFPPDLKLTIVAEPGRYYVASA
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>d1ct5a_ c.1.6.2 (A:) "Hypothetical" protein ybl036c {Baker's yeast (Saccharomyces cerevisiae)}
TGITYDEDRKTQLIAQYESVREVVNAEAKNVHVNENASKILLLVVSKLKPASDIQILYDHGVREF
GENYVQELIEKAKLLPDDIKWHFIGGLQTNKCKDLAKVPNLYSVETIDSLKKAKKLNESRAKFQP
DCNPILCNVQINTSHEDQKSGLNNEAEIFEVIDFFLSEECKYIKLNGLMTIGSWNVSHEDSKENR
DFATLVEWKKKIDAKFGTSLKLSMGMSADFREAIRQGTAEVRIGTDIFG
>d1frb__ c.1.7.1 (-) FR-1 (fibroblast growth factor-induced) protein {Mouse (Mus musculus)}
ATFVELSTKAKMPIVGLGTWKSPPNQVKEAVKAAIDAGYRHIDCAYAYCNENEVGEAIQEKIKEK
AVQREDLFIVSKLWPTCFEKKLLKEAFQKTLTDLKLDYLDLYLIHWPQGLQPGKELFPKDDQGRI
LTSKTTFLEAWEGMEELVDQGLVKALGVSNFNHFQIERLLNKPGLKHKPVTNQVECHPYLTQEKL
IQYCHSKGISVTAYSPLGSPDRPSAKPEDPSLLEDPKIKEIAAKHEKTSAQVLIRFHIQRNVVVI
PKSVTPSRIQENIQVFDFQLSDEEMATILSFNRNWRACLLPETVNMEEYPYDAEY
>d1exba_ c.1.7.1 (A:) Voltage-dependent K+ channel beta subunit {Rat (Rattus norvegicus)}
LQFYRNLGKSGLRVSCLGLGTWVTFGGQITDEMAEHLMTLAYDNGINLFDTAEVYAAGKAEVVLG
NIIKKKGWRRSSLVITTKIFWGGKAETERGLSRKHIIEGLKASLERLQLEYVDVVFANRPDPNTP
MEETVRAMTHVINQGMAMYWGTSRWSSMEIMEAYSVARQFNLIPPICEQAEYHMFQREKVEVQLP
ELFHKIGVGAMTWSPLACGIVSGKYDSGIPPYSRASLKGYQWLKDKILSEEGRRQQAKLKELQAI
AERLGCTLPQLAIAWCLRNEGVSSVLLGASNAEQLMENIGAIQVLPKLSSSIVHEIDSILGNKPY
S
>d1ads__ c.1.7.1 (-) Aldose reductase (aldehyde reductase) {Human (Homo sapiens)}
ASRLLLNNGAKMPILGLGTWKSPPGQVTEAVKVAIDVGYRHIDCAHVYQNENEVGVAIQEKLREQ
VVKREELFIVSKLWCTYHEKGLVKGACQKTLSDLKLDYLDLYLIHWPTGFKPGKEFFPLDESGNV
VPSDTNILDTWAAMEELVDEGLVKAIGISNFNHLQVEMILNKPGLKYKPAVNQIECHPYLTQEKL
IQYCQSKGIVVTAYSPLGSPDRPWAKPEDPSLLEDPRIKAIAAKHNKTTAQVLIRFPMQRNLVVI
PKSVTPERIAENFKVFDFELSSQDMTTLLSYNRNWRVCALLSCTSHKDYPFHEEF
>d2alr__ c.1.7.1 (-) Aldose reductase (aldehyde reductase) {Human (Homo sapiens)}
AASCVLLHTGQKMPLIGLGTWKSEPGQVKAAVKYALSVGYRHIDCAAIYGNEPEIGEALKEDVGP
GKAVPREELFVTSKLWNTKHHPEDVEPALRKTLADLQLEYLDLYLMHWPYAFERGDNPFPKNADG
TICYDSTHYKETWKALEALVAKGLVQALGLSNFNSRQIDDILSVASVRPAVLQVECHPYLAQNEL
IAHCQARGLEVTAYSPLGSSDRAWRDPDEPVLLEEPVVLALAEKYGRSPAQILLRWQVQRKVICI
PKSITPSRILQNIKVFDFTFSPEEMKQLNALNKNWRYIVPMLTVDGKRVPRDAGHPLYPFNDPY
>d1ah4__ c.1.7.1 (-) Aldose reductase (aldehyde reductase) {Pig (Sus scrofa)}
ASHLVLYTGAKMPILGLGTWKSPPGKVTEAVKVAIDLGYRHIDCAHVYQNENEVGLGLQEKLQGQ
VVKREDLFIVSKLWCTDHEKNLVKGACQTTLRDLKLDYLDLYLIHWPTGFKPGKDPFPLDGDGNV
VPDESDFVETWEAMEELVDEGLVKAIGVSNFNHLQVEKILNKPGLKYKPAVNQIEVHPYLTQEKL
IEYCKSKGIVVTAYSPLGSPDRPWAKPEDPSLLEDPRIKAIAAKYNKTTAQVLIRFPMQRNLIVI
PKSVTPERIAENFQVFDFELSPEDMNTLLSYNRNWRVCALMSCASHKDYPFHEEY
>d1hqta_ c.1.7.1 (A:) Aldose reductase (aldehyde reductase) {Pig (Sus scrofa)}
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AASCVLLHTGQKMPLIGLGTWKSEPGQVKAAIKYALTVGYRHIDCAAIFGNELEIGEALQETVGP
GKAVPREELFVTSKLWNTKHHPEDVEPALRKTLADLQLEYLDLYLMHWPYAFERGDNPFPKNADG
TIRYDATHYKDTWKALEALVAKGLVRALGLSNFSSRQIDDVLSVASVRPAVLQVECHPYLAQNEL
IAHCQARGLEVTAYSPLGSSDRAWRDPNEPVLLEEPVVQALAEKYNRSPAQILLRWQVQRKVICI
PKSVTPSRIPQNIQVFDFTFSPEEMKQLDALNKNLRFIVPMLTVDGKRVPRDAGHPLYPFNDPY
>d1afsa_ c.1.7.1 (A:) 3-alpha-hydroxysteroid dehydrogenase {Rat
(Rattus norvegicus)}
MDSISLRVALNDGNFIPVLGFGTTVPEKVAKDEVIKATKIAIDNGFRHFDSAYLYEVEEEVGQAI
RSKIEDGTVKREDIFYTSKLWSTFHRPELVRTCLEKTLKSTQLDYVDLYIIHFPMALQPGDIFFP
RDEHGKLLFETVDICDTWEAMEKCKDAGLAKSIGVSNFNCRQLERILNKPGLKYKPVCNQVECHL
YLNQSKMLDYCKSKDIILVSYCTLGSSRDKTWVDQKSPVLLDDPVLCAIAKKYKQTPALVALRYQ
LQRGVVPLIRSFNAKRIKELTQVFEFQLASEDMKALDGLNRNFRYNNAKYFDDHPNHPF
>d1ihia_ c.1.7.1 (A:) 3-alpha-hydroxysteroid dehydrogenase {Human
(Homo sapiens), type III}
SKYQCVKLNDGHFMPVLGFGTYAPAEVPKSKALEAVKLAIEAGFHHIDSAHVYNNEEQVGLAIRS
KIADGSVKREDIFYTSKLWSNSHRPELVRPALERSLKNLQLDYVDLYLIHFPVSVKPGEEVIPKD
ENGKILFDTVDLCATWEAMEKCKDAGLAKSIGVSNFNHRLLEMILNKPGLKYKPVCNQVECHPYF
NQRKLLDFCKSKDIVLVAYSALGSHREEPWVDPNSPVLLEDPVLCALAKKHKRTPALIALRYQLQ
RGVVVLAKSYNEQRIRQNVQVFEFQLTSEEMKAIDGLNRNVRYLTLDIFAGPPNYPFSDE
>d1c9wa_ c.1.7.1 (A:) CHO reductase {Chinese hampster (Cricetulus
griseus)}
STFVELSTKAKMPIVGLGTWQSPPGQVKEAVKVAIDAGYRHIDCAYAYYNEHEVGEAIQEKIKEK
AVRREDLFIVSKLWPTCFERKLLKEAFQKTLTDLKLDYLDLYLIHWPQGLQPGKELFPKDDQGNV
LTSKITFLDAWEVMEELVDEGLVKALGVSNFNHFQIERILNKPGLKHKPVTNQVECHPYLTQEKL
IEYCHSKGITVTAYSPLGSPNRPWAKPEDPSLLEDPKIKEIAAKHKKTSAQVLIRFHIQRNVVVI
PKSVTPARIHENFQVFDFQLSDQEMATILGFNRNWRACLLPETVNMEEYPYDAEY
>d1hw6a_ c.1.7.1 (A:) 2,5-diketo-D-gluconic acid reductase A
{Corynebacterium sp.}
TVPSIVLNDGNSIPQLGYGVFKVPPADTQRAVEEALEVGYRHIDTAAIYGNEEGVGAAIAASGIA
RDDLFITTKLWNDRHDGDEPAAAIAESLAKLALDQVDLYLVHWPTPAADNYVHAWEKMIELRAAG
LTRSIGVSNHLVPHLERIVAATGVVPAVNQIELHPAYQQREITDWAAAHDVKIESWGPLGQGKYD
LFGAEPVTAAAAAHGKTPAQAVLRWHLQKGFVVFPKSVRRERLEENLDVFDFDLTDTEIAAIDAM
DP
>d1bli_2 c.1.8.1 (3-393) Bacterial alpha-amylase {Bacillus
licheniformis}
LNGTLMQYFEWYMPNDGQHWKRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYDLYDLGEF
HQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEVDPADRNRVISGE
HLIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYKFQGKAWDWEVSNEFGNYDYLM
YADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAVKHIKFSFLRDWVNHVREKTGKEMFTVAEY
WSYDLGALENYLNKTNFNHSVFDVPLHYQFHAASTQGGGYDMRKLLNGTVVSKHPLKSVTFVDNH
DTQPGQSLESTVQTWFKPLAYAFILTRESGYPQVFYGDMYGTKGDSQREIPALKHKIEPILKARK
Q
>d1e43a2 c.1.8.1 (A:1-393) Bacterial alpha-amylase {Bacillus
amyloliquefaciens/Bacillus licheniformis chimera}
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VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLYDLGEF
QQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNPANRNQETSEE
YQIKAWTDFRFPGRGNTYSDFKWHWYHFDGADWDESRKISRIFKFRGEGKAWDWEVSSENGNYDY
LMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSFLRDWVQAVRQATGKEMFTVA
EYWQNNAGKLENYLNKTSFNQSVFDVPLHFNLQAASSQGGGYDMRKLLNGTVVSKHPLKSVTFVD
NHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQVFYGDMYGTKGDSQREIPALKHKIEPILKA
RKQ
>d1g94a2 c.1.8.1 (A:1-354) Bacterial alpha-amylase
{Pseudoalteromonas haloplanctis (Alteromonas haloplanctis)}
TPTTFVHLFEWNWQDVAQECEQYLGPKGYAAVQVSPPNEHITGSQWWTRYQPVSYELQSRGGNRA
QFIDMVNRCSAAGVDIYVDTLINHMAAGSGTGTAGNSFGNKSFPIYSPQDFHESCTINNSDYGND
RYRVQNCELVGLADLDTASNYVQNTIAAYINDLQAIGVKGFRFDASKHVAASDIQSLMAKVNGSP
VVFQEVIDQGGEAVGASEYLSTGLVTEFKYSTELGNTFRNGSLAWLSNFGEGWGFMPSSSAVVFV
DNHDNQRGHGGAGNVITFEDGRLYDLANVFMLAYPYGYPKVMSSYDFHGDTDAGGPNVPVHNNGN
LECFASNWKCEHRWSYIAGGVDFRNNTAD
>d1bag_2 c.1.8.1 (1-347) Bacterial alpha-amylase {Bacillus subtilis}
LTAPSIKSGTILHAWNWSFNTLKHNMKDIHDAGYTAIQTSPINQVKEGNQGDKSMSNWYWLYQPT
SYQIGNRYLGTEQEFKEMCAAAEEYGIKVIVDAVINHTTFDYAAISNEVKSIPNWTHGNTQIKNW
SDRWDVTQNSLLGLYDWNTQNTQVQSYLKRFLERALNDGADGFRFDAAKHIELPDDGSYGSQFWP
NITNTSAEFQYGQILQDSASRDAAYANYMDVTASNYGHSIRSALKNRNLGVSNISHYASDVSADK
LVTWVESHDTYANDDEESTWMSDDDIRLGWAVIASRSGSTPLFFSRPEGGGNGVRFPGKSQIGDR
GSALFEDQAITAVNRFHNVMAG
>d1hvxa2 c.1.8.1 (A:1-393) Bacterial alpha-amylase {Bacillus
stearothermophilus}
AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVYDLYDL
GEFNQKGAVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVEVNPSDRNQEI
SGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRGIGKAWDWEVDTENGN
YDYLMYADLDMDHPEVVTELKSWGKWYVNTTNIDGFRLDAVKHIKFSFFPDWLSYVRSQTGKPLF
TVGEYWSYDINKLHNYIMKTNGTMSLFDAPLHNKFYTASKSGGTFDMRTLMTNTLMKDQPTLAVT
FVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEGYPCVFYGDYYGIPQYNIPSLKSKIDPLLIA
RRD
>d1gjwa2 c.1.8.1 (A:1-572) Maltosyltransferase {Thermotoga maritima}
MLLREINRYCKEKATGKRIYAVPKLWIPGFFKKFDEKSGRCFVDPYELGAEITDWILNQSREWDY
SQPLSFLKGEKTPDWIKRSVVYGSLPRTTAAYNHKGSGYYEENDVLGFREAGTFFKMMLLLPFVK
SLGADAIYLLPVSRMSDLFKKGDAPSPYSVKNPMELDERYHDPLLEPFKVDEEFKAFVEACHILG
IRVILDFIPRTAARDSDLIREHPDWFYWIKVEELADYTPPRAEELPFKVPDEDELEIIYNKENVK
RHLKKFTLPPNLIDPQKWEKIKREEGNILELIVKEFGIITPPGFSDLINDPQPTWDDVTFLRLYL
DHPEASKRFLDPNQPPYVLYDVIKASKFPGKEPNRELWEYLAGVIPHYQKKYGIDGARLDMGHAL
PKELLDLIIKNVKEYDPAFVMIAEELDMEKDKASKEAGYDVILGSSWYFAGRVEEIGKLPDIAEE
LVLPFLASVETPDTPRIATRKYASKMKKLAPFVTYFLPNSIPYVNTGQEIGEKQPMNLGLDTDPN
LRKVLSPTDEFFGKLAFFDHYVLHWDSPDRGVLNFIKKLIKVRHEFLDFVLN
>d1cgt_4 c.1.8.1 (1-406) Cyclodextrin glycosyltransferase {Bacillus
circulans, different strains}
DPDTAVTNKQSFSTDVIYQVFTDRFLDGNPSNNPTGAAYDATCSNLKLYCGGDWQGLINKINDNY
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FSDLGVTALWISQPVENIFATINYSGVTNTAYHGYWARDFKKTNPYFGTMADFQNLITTAHAKGI
KIVIDFAPNHTSPAMETDTSFAENGRLYDNGTLVGGYTNDTNGYFHHNGGSDFSSLENGIYKNLY
DLADFNHNNATIDKYFKDAIKLWLDMGVDGIRVDAVKHMPLGWQKSWMSSIYAHKPVFTFGEWFL
GSAASDADNTDFANKSGMSLLDFRFNSAVRNVFRDNTSNMYALDSMINSTATDYNQVNDQVTFID
NHDMDRFKTSAVNNRRLEQALAFTLTSRGVPAIYYGTEQYLTGNGDPDNRAKMPSFSKSTTAFNV
ISKLAPLRKSNPAIAY
>d1kcla4 c.1.8.1 (A:1-406) Cyclodextrin glycosyltransferase {Bacillus circulans, different strains}
APDTSVSNKQNFSTDVIYQIFTDRFSDGNPANNPTGAAFDGTCTNLRLYCGGDWQGIINKINDGY
LTGMGVTAIWISQPVENIYSIINYSGVNNTAYHGYWARDFKKTNPAYGTIADFQNLIAAAHAKNI
KVIIDFAPNHTSPASSDQPSFAENGRLYDNGTLLGGYTNDTQNLFHHNLGTDFSTTENGIYKNLY
DLADLNHNNSTVDVYLKDAIKMWLDLGIDGIRMDAVKHMPFGWQKSFMAAVNNYKPVFTFGEWFL
GVNEVSPENHKFANESGMSLLDFRFAQKVRQVFRDNTDNMYGLKAMLEGSAADYAQVDDQVTFID
NHDMERFHASNANRRKLEQALAFTLTSRGVPAIYYGTEQYMSGGTDPDNRARIPSFSTSTTAYQV
IQKLAPLRKCNPAIAY
>d1cyg_4 c.1.8.1 (1-402) Cyclodextrin glycosyltransferase {Bacillus stearothermophilus}
AGNLNKVNFTSDVVYQIVVDRFVDGNTSNNPSGALFSSGCTNLRKYCGGDWQGIINKINDGYLTD
MGVTAIWISQPVENVFSVMNDASGSASYHGYWARDFKKPNPFFGTLSDFQRLVDAAHAKGIKVII
DFAPNHTSPASETNPSYMENGRLYDNGTLLGGYTNDANMYFHHNGGTTFSSLEDGIYRNLFDLAD
LNHQNPVIDRYLKDAVKMWIDMGIDGIRMDAVKHMPFGWQKSLMDEIDNYRPVFTFGEWFLSENE
VDANNHYFANESGMSLLDFRFGQKLRQVLRNNSDNWYGFNQMIQDTASAYDEVLDQVTFIDNHDM
DRFMIDGGDPRKVDMALAVLLTSRGVPNIYYGTEQYMTGNGDPNNRKMMSSFNKNTRAYQVIQKL
SSLRRNNPALAY
>d1qhoa4 c.1.8.1 (A:1-407) Cyclodextrin glycosyltransferase {Bacillus stearothermophilus, maltogenic alpha-amylase}
SSSASVKGDVIYQIIIDRFYDGDTTNNNPAKSYGLYDPTKSKWKMYWGGDLEGVRQKLPYLKQLG
VTTIWLSPVLDNLDTLAGTDNTGYHGYWTRDFKQIEEHFGNWTTFDTLVNDAHQNGIKVIVDFVP
NHSTPFKANDSTFAEGGALYNNGTYMGNYFDDATKGYFHHNGDISNWDDRYEAQWKNFTDPAGFS
LADLSQENGTIAQYLTDAAVQLVAHGADGLRIDAVKHFNSGFSKSLADKLYQKKDIFLVGEWYGD
DPGTANHLEKVRYANNSGVNVLDFDLNTVIRNVFGTFTQTMYDLNNMVNQTGNEYKYKENLITFI
DNHDMSRFLSVNSNKANLHQALAFILTSRGTPSIYYGTEQYMAGGNDPYNRGMMPAFDTTTTAFK
EVSTLAGLRRNNAAIQY
>d1pama4 c.1.8.1 (A:1-406) Cyclodextrin glycosyltransferase {Alkalophilic bacillus sp., strain 1011}
APDTSVSNKQNFSTDVIYQIFTDRFSDGNPANNPTGAAFDGSCTNLRLYCGGDWQGIINKINDGY
LTGMGITAIWISQPVENIYSVINYSGVNNTAYHGYWARDFKKTNPAYGTMQDFKNLIDTAHAHNI
KVIIDFAPNHTSPASSDDPSFAENGRLYDNGNLLGGYTNDTQNLFHHYGGTDFSTIENGIYKNLY
DLADLNHNNSSVDVYLKDAIKMWLDLGVDGIRVDAVKHMPFGWQKSFMATINNYKPVFTFGEWFL
GVNEISPEYHQFANESGMSLLDFRFAQKARQVFRDNTDNMYGLKAMLEGSEVDYAQVNDQVTFID
NHDMERFHTSNGDRRKLEQALAFTLTSRGVPAIYYGSEQYMSGGNDPDNRARLPSFSTTTTAYQV
IQKLAPLRKSNPAIAY
>d1ciu_4 c.1.8.1 (1-406) Cyclodextrin glycosyltransferase {Thermoanaerobacterium thermosulfurigenes, EM1}

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ASDTAVSNVVNYSTDVIYQIVTDRFVDGNTSNNPTGDLYDPTHTSLKKYFGGDWQGIINKINDGY
LTGMGVTAIWISQPVENIYAVLPDSTFGGSTSYHGYWARDFKRTNPYFGSFTDFQNLINTAHAHN
IKVIIDFAPNHTSPASETDPTYAENGRLYDNGTLLGGYTNDTNGYFHHYGGTDFSSYEDGIYRNL
FDLADLNQQNSTIDSYLKSAIKVWLDMGIDGIRLDAVKHMPFGWQKNFMDSILSYRPVFTFGEWF
LGTNEIDVNNTYFANESGMSLLDFRFSQKVRQVFRDNTDTMYGLDSMIQSTASDYNFINDMVTFI
DNHDMDRFYNGGSTRPVEQALAFTLTSRGVPAIYYGTEQYMTGNGDPYNRAMMTSFNTSTTAYNV
IKKLAPLRKSNPAIAY
>d1hx0a2 c.1.8.1 (A:1-403) Animal alpha-amylase {Pig (Sus scrofa)}
EYAPQTQSGRTSIVHLFEWRWVDIALECERYLGPKGFGGVQVSPPNENIVVTNPSRPWWERYQPV
SYKLCTRSGNENEFRDMVTRCNNVGVRIYVDAVINHMCGSGAAAGTGTTCGSYCNPGNREFPAVP
YSAWDFNDGKCKTASGGIESYNDPYQVRDCQLVGLLDLALEKDYVRSMIADYLNKLIDIGVAGFR
IDASKHMWPGDIKAVLDKLHNLNTNWFPAGSRPFIFQEVIDLGGEAIKSSEYFGNGRVTEFKYGA
KLGTVVRKWSGEKMSYLKNWGEGWGFMPSDRALVFVDNHDNQRGHGAGGSSILTFWDARLYKIAV
GFMLAHPYGFTRVMSSYRWARNFVNGEDVNDWIGPPNNNGVIKEVTINADTTCGNDWVCEHRWRE
IRNMVWFRNVVDG
>d1smd_2 c.1.8.1 (1-403) Animal alpha-amylase {Human (Homo sapiens)}
EYSSNTQQGRTSIVHLFEWRWVDIALECERYLAPKGFGGVQVSPPNENVAIHNPFRPWWERYQPV
SYKLCTRSGNEDEFRNMVTRCNNVGVRIYVDAVINHMCGNAVSAGTSSTCGSYFNPGSRDFPAVP
YSGWDFNDGKCKTGSGDIENYNDATQVRDCRLSGLLDLALGKDYVRSKIAEYMNHLIDIGVAGFR
IDASKHMWPGDIKAILDKLHNLNSNWFPEGSKPFIYQEVIDLGGEPIKSSDYFGNGRVTEFKYGA
KLGTVIRKWNGEKMSYLKNWGEGWGFMPSDRALVFVDNHDNQRGHGAGGASILTFWDARLYKMAV
GFMLAHPYGFTRVMSSYRWPRYFENGKDVNDWVGPPNDNGVTKEVTINPDTTCGNDWVCEHRWRQ
IRNMVNFRNVVDG
>d1jae_2 c.1.8.1 (1-378) Animal alpha-amylase {Yellow mealworm
(Tenebrio molitor), larva}
EKDANFASGRNSIVHLFEWKWNDIADECERFLQPQGFGGVQISPPNEYLVADGRPWWERYQPVSY
IINTRSGDESAFTDMTRRCNDAGVRIYVDAVINHMTGMNGVGTSGSSADHDGMNYPAVPYGSGDF
HSPCEVNNYQDADNVRNCELVGLRDLNQGSDYVRGVLIDYMNHMIDLGVAGFRVDAAKHMSPGDL
SVIFSGLKNLNTDYGFADGARPFIYQEVIDLGGEAISKNEYTGFGCVLEFQFGVSLGNAFQGGNQ
LKNLANWGPEWGLLEGLDAVVFVDNHDNQRTGGSQILTYKNPKPYKMAIAFMLAHPYGTTRIMSS
FDFTDNDQGPPQDGSGNLISPGINDDNTCSNGYVCEHRWRQVYGMVGFRNAVE
>d2aaa_2 c.1.8.1 (1-381) Fungal alpha-amylases {Aspergillus niger,
acid amylase}
LSAASWRTQSIYFLLTDRFGRTDNSTTATCNTGNEIYCGGSWQGIIDHLDYIEGMGFTAIWISPI
TEQLPQDTADGEAYHGYWQQKIYDVNSNFGTADNLKSLSDALHARGMYLMVDVVPDHMGYAGNGN
DVDYSVFDPFDSSSYFHPYCLITDWDNLTMVEDCWEGDTIVSLPDLDTTETAVRTIWYDWVADLV
SNYSVDGLRIDSVLEVQPDFFPGYNKASGVYCVGEIDNGNPASDCPYQKVLDGVLNYPIYWQLLY
AFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHDNPRFAKYTSDYSQAKNVLSYIFLSDGIP
IVYAGEEQHYAGGKVPYNREATWLSGYDTSAELYTWIATTNAIRKLAIAADSAYIT
>d7taa_2 c.1.8.1 (1-381) Fungal alpha-amylases {Aspergillus oryzae,
Taka-amylase}
ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAIWITPV
TAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVANHMGYDGAGS
SVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLV
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SNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLN
AFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIP
IIYAGQEQHYAGGNDPANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVT
>d1smaa3 c.1.8.1 (A:124-505) Maltogenic amylase, central domain
{Thermus sp.}
DLFQAPDWVKDTVWYQIFPERFANGNPAISPKGARPWGSEDPTPTSFFGGDLQGIIDHLDYLADL
GITGIYLTPIFRAPSNHKYDTADYFEIDPHFGDKETLKTLVKRCHEKGIRVMLDAVFNHCGYEFA
PFQDVLKNGAASRYKDWFHIREFPLQTEPRPNYDTFAFVPHMPKLNTAHPEVKRYLLDVATYWIR
EFDIDGWRLDVANEIDHQFWREFRQAVKALKPDVYILGEIWHDAMPWLRGDQFDAVMNYPLADAA
LRFFAKEDMSASEFADRLMHVLHSYPKQVNEAAFNLLGSHDTPRLLTVCGGDVRKVKLLFLFQLT
FTGSPCIYYGDEIGMTGGNDPECRKCMVWDPEKQNKELYEHVKQLIALRKQYRALRR
>d1bvza3 c.1.8.1 (A:121-502) Maltogenic amylase, central domain
{Thermoactinomyces vulgaris, TVAII}
VFTTPEWAKEAVIYQIFPERFANGDPSNDPPGTEQWAKDARPRHDSFYGGDLKGVIDRLPYLEEL
GVTALYFTPIFASPSHHKYDTADYLAIDPQFGDLPTFRRLVDEAHRRGIKIILDAVFNHAGDQFF
AFRDVLQKGEQSRYKDWFFIEDFPVSKTSRTNYETFAVQVPAMPKLRTENPEVKEYLFDVARFWM
EQGIDGWRLDVANEVDHAFWREFRRLVKSLNPDALIVGEIWHDASGWLMGDQFDSVMNYLFRESV
IRFFATGEIHAERFDAELTRARMLYPEQAAQGLWNLLDSHDTERFLTSCGGNEAKFRLAVLFQMT
YLGTPLIYYGDEIGMAGATDPDCRRPMIWEEKEQNRGLFEFYKELIRLRHRLASLTR
>d1eh9a3 c.1.8.1 (A:91-490) Glycosyltrehalose trehalohydrolase,
central domain {Archaeon Sulfolobus solfataricus, km1}
FNNETFLKKEDLIIYEIHVGTFTPEGTFEGVIRKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGV
YLYAVQNSYGGPEGFRKLVDEAHKKGLGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTFN
FDDAESDEVRKFILENVEYWIKEYNVDGFRLDAVHAIIDTSPKHILEEIADVVHKYNRIVIAESD
LNDPRVVNPKEKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLDDIVKSYKDVFVYDGKYS
NFRRKTHGEPVGELDGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLSPYIPMIFM
GEEYGEENPFYFFSDFSDSKLIQGVREGRKKENGQDTDPQDESTFNASKLSWKIDEEIFSFYKIL
IKMRKELSIA
>d1bf2_3 c.1.8.1 (163-637) Isoamylase, central domain {Pseudomonas
amyloderamosa}
PSTQSTGTKPTRAQKDDVIYEVHVRGFTEQDTSIPAQYRGTYYGAGLKASYLASLGVTAVEFLPV
QETQNDANDVVPNSDANQNYWGYMTENYFSPDRRYAYNKAAGGPTAEFQAMVQAFHNAGIKVYMD
VVYNHTAEGGTWTSSDPTTATIYSWRGLDNATYYELTSGNQYFYDNTGIGANFNTYNTVAQNLIV
DSLAYWANTMGVDGFRFDLASVLGNSCLNGAYTASAPNCPNGGYNFDAADSNVAINRILREFTVR
PAAGGSGLDLFAEPWAIGGNSYQLGGFPQGWSEWNGLFRDSLRQAQNELGSMTIYVTQDANDFSG
SSNLFQSSGRSPWNSINFIDVHDGMTLKDVYSCNGANNSQAWPYGPSDGGTSTNYSWDQGMSAGT
GAAVDQRRAARTGMAFEMLSAGTPLMQGGDEYLRTLQCNNNAYNLDSSANWLTYSWTTDQSNFYT
FAQRLIAFRKAHPALRPSSW
>d1gcya2 c.1.8.1 (A:1-357) G4-amylase (1,4-alpha-D-glucan
maltotetrahydrolase) {Pseudomonas stutzeri}
DQAGKSPNAVRYHGGDEIILQGFHWNVVREAPNDWYNILRQQAATIAADGFSAIWMPVPWRDFSS
WSDGSKSGGGEGYFWHDFNKNGRYGSDAQLRQAASALGGAGVKVLYDVVPNHMNRGYPDKEINLP
AGQGFWRNDCADPGNYPNDCDDGDRFIGGDADLNTGHPQVYGMFRDEFTNLRSQYGAGGFRFDFV
RGYAPERVNSWMTDSADNSFCVGELWKGPSEYPNWDWRNTASWQQIIKDWSDRAKCPVFDFALKE
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RMQNGSIADWKHGLNGNPDPRWREVAVTFVDNHDTGYSPGQNGGQHHWALQDGLIRQAYAYILTS
PGTPVVYWDHMYDWGYGDFIRQLIQVRRAAGV
>d1avaa2 c.1.8.1 (A:1-346) Plant alpha-amylase {Barley (Hordeum
vulgare), seeds, AMY2 isozyme}
QVLFQGFNWESWKHNGGWYNFLMGKVDDIAAAGITHVWLPPASQSVAEQGYMPGRLYDLDASKYG
NKAQLKSLIGALHGKGVKAIADIVINHRTAEHKDGRGIYCIFEGGTPDARLDWGPHMICRDDRPY
ADGTGNPDTGADFGAAPDIDHLNLRVQKELVEWLNWLKADIGFDGWRFDFAKGYSADVAKIYIDR
SEPSFAVAEIWTSLAYGGDGKPNLNQDQHRQELVNWVDKVGGKGPATTFDFTTKGILNVAVEGEL
WRLRGTDGKAPGMIGWWPAKAVTFVDNHDTGSTQHMWPFPSDRVMQGYAYILTHPGTPCIFYDHF
FDWGLKEEIDRLVSVRTRHGI
>d1uok_2 c.1.8.1 (1-479) Oligo-1,6, glucosidase {Bacillus cereus}
MEKQWWKESVVYQIYPRSFMDSNGDGIGDLRGIISKLDYLKELGIDVIWLSPVYESPNDDNGYDI
SDYCKIMNEFGTMEDWDELLHEMHERNMKLMMDLVVNHTSDEHNWFIESRKSKDNKYRDYYIWRP
GKEGKEPNNWGAAFSGSAWQYDEMTDEYYLHLFSKKQPDLNWDNEKVRQDVYEMMKFWLEKGIDG
FRMDVINFISKEEGLPTVETEEEGYVSGHKHFMNGPNIHKYLHEMNEEVLSHYDIMTVGEMPGVT
TEEAKLYTGEERKELQMVFQFEHMDLDSGEGGKWDVKPCSLLTLKENLTKWQKALEHTGWNSLYW
NNHDQPRVVSRFGNDGMYRIESAKMLATVLHMMKGTPYIYQGEEIGMTNVRFESIDEYRDIETLN
MYKEKVMERGEDIEKVMQSIYIKGRDNARTPMQWDDQNHAGFTTGEPWITVNPNYKEINVKQAIQ
NKDSIFYYYKKLIELRKNNEIVVY
>d1g5aa2 c.1.8.1 (A:1-554) Amylosucrase {Neisseria polysaccharea}
SPNSQYLKTRILDIYTPEQRAGIEKSEDWRQFSRRMDTHFPKLMNELDSVYGNNEALLPMLEMLL
AQAWQSYSQRNSSLKDIDIARENNPDWILSNKQVGGVCYVDLFAGDLKGLKDKIPYFQELGLTYL
HLMPLFKCPEGKSDGGYAVSSYRDVNPALGTIGDLREVIAALHEAGISAVVDFIFNHTSNEHEWA
QRCAAGDPLFDNFYYIFPDRRMPDQYDRTLREIFPDQHPGGFSQLEDGRWVWTTFNSFQWDLNYS
NPWVFRAMAGEMLFLANLGVDILRMDAVAFIWKQMGTSCENLPQAHALIRAFNAVMRIAAPAVFF
KSEAIVHPDQVVQYIGQDECQIGYNPLQMALLWNTLATREVNLLHQALTYRHNLPEHTAWVNYVR
SHDDIGWTFADEDAAYLGISGYDHRQFLNRFFVNRFDGSFARGVPFQYNPSTGDCRVSGTAAALV
GLAQDDPHAVDRIKLLYSIALSTGGLPLIYLGDEVGTLNDDDWSQDSNKSDDSRWAHRPRYNEAL
YAQRNDPSTAAGQIYQDLRHMIAVRQSNPRFDGG
>d1eswa_ c.1.8.1 (A:) Amylomaltase MalQ {Thermus aquaticus}
MELPRAFGLLLHPTSLPGPYGVGVLGREARDFLRFLKEAGGRYWQVLPLGPTGYGDSPYQSFSAF
AGNPYLIDLRPLAERGYVRLEDPGFPQGRVDYGLLYAWKWPALKEAFRGFKEKASPEEREAFAAF
REREAWWLEDYALFMALKGAHGGLPWNRWPLPLRKREEKALREAKSALAEEVAFHAFTQWLFFRQ
WGALKAEAEALGIRIIGDMPIFVAEDSAEVWAHPEWFHLDEEGRPTVVAGVPPDYFSETGQRWGN
PLYRWDVLEREGFSFWIRRLEKALELFHLVRIDHFRGFEAYWEIPASCPTAVEGRWVKAPGEKLF
QKIQEVFGEVPVLAEDLGVITPEVEALRDRFGLPGMKVLQFAFDDGMENPFLPHNYPAHGRVVVY
TGTHDNDTTLGWYRTATPHEKAFMARYLADWGITFREEEEVPWALMHLGMKSVARLAVYPVQDVL
ALGSEARMNYPGRPSGNWAWRLLPGELSPEHGARLRAMAEATERL
>d1byb__ c.1.8.2 (-) beta-Amylase {Soybean (Glycine max)}
SNMLLNYVPVYVMLPLGVVNVDNVFEDPDGLKEQLLQLRAAGVDGVMVDVWWGIIELKGPKQYDW
RAYRSLFQLVQECGLTLQAIMSFHQCGGNVGDIVNIPIPQWVLDIGESNHDIFYTNRSGTRNKEY
LTVGVDNEPIFHGRTAIEIYSDYMKSFRENMSDFLESGLIIDIEVGLGPAGELRYPSYPQSQGWE
FPRIGEFQCYDKYLKADFKAAVARAGHPEWELPDDAGKYNDVPESTGFFKSNGTYVTEKGKFFLT
WYSNKLLNHGDQILDEANKAFLGCKVKLAIKVSGIHWWYKVENHAAELTAGYYNLNDRDGYRPIA
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RMLSRHHAILNFTCLEMRDSEQPSDAKSGPQELVQQVLSGGWREDIRVAGENALPRYDATAYNQI
ILNAKPQGVNNNGPPKLSMFGVTYLRLSDDLLQKSNFNIFKKFVLKMHADQDYCANPQKYNHAIT
PLKPSAPKIPIEVLLEATKPTLPFPWLPETDMKVDG
>d1b1ya_ c.1.8.2 (A:) beta-Amylase {Barley (Hordeum vulgare)}
MKGNYVQVYVMLPLDAVSVNNRFEKGDELRAQLRKLVEAGVDGVMVDVWWGLVEGKGPKAYDWSA
YKQLFELVQKAGLKLQAIMSFHQCGGNVGDAVNIPIPQWVRDVGTRDPDIFYTDGHGTRNIEYLT
LGVDNQPLFHGRSAVQMYADYMTSFRENMKDFLDAGVIVDIEVGLGPAGELRYPSYPQSHGWSFP
GIGEFICYDKYLQADFKAAAAAVGHPEWEFPNDAGQYNDTPERTQFFRDNGTYLSEKGRFFLAWY
SNNLIKHGDRILDEANKVFLGYKVQLAIKIAGVHWWYKVPSHAAELTAGYYNLHDRDGYRTIARM
LKRHRASINFTCAEMRDSEQPPDAMSAPEELVQQVLSAGWREGLNVSCENALPRYDPTAYNTILR
NARPHGINQSGPPEHKLFGFTYLRLSNQLVEGQNYVNFKTFVDRMHANLPRDPYVDPMAPLPRSG
PEISIEMILQAAQPKIQPFPFQEHTDLPVGPTGGMGGQAEGPTCG
>d1fa2a_ c.1.8.2 (A:) beta-Amylase {Sweet potato (Ipomoea batatas)}
APIPGVMPIGNYVSLYVMLPLGVVNADNVFPDKEKVEDELKQVKAGGCDGVMVDVWWGIIEAKGP
KQYDWSAYRELFQLVKKCGLKIQAIMSFHQCGGNVGDAVFIPIPQWILQIGDKNPDIFYTNRAGN
RNQEYLSLGVDNQRLFQGRTALEMYRDFMESFRDNMADFLKAGDIVDIEVGCGAAGELRYPSYPE
TQGWVFPGIGEFQCYDKYMVADWKEAVKQAGNADWEMPGKGAGTYNDTPDKTEFFRPNGTYKTDM
GKFFLTWYSNKLIIHGDQVLEEANKVFVGLRVNIAAKVSGIHWWYNHVSHAAELTAGFYNVAGRD
GYRPIARMLARHHATLNFTCLEMRDSEQPAEAKSAPQELVQQVLSSGWKEYIDVAGENALPRYDA
TAYNQMLLKLRPNGVNLNGPPKLKMSGLTYLRLSDDLLQTDNFELFKKFVKKMHADLDPSPNAIS
PAVLERSNSAITIDELMEATKGSRPFPWYDVTDMPVDGSNPFD
>d1b9za2 c.1.8.2 (A:1-417) Bacterial beta-amylase, catalytic domain
{Bacillus cereus}
AVNGKGMNPDYKAYLMAPLKKIPEVTNWETFENDLRWAKQNGFYAITVDFWWGDMEKNGDQQFDF
SYAQRFAQSVKNAGMKMIPIISTHQCGGNVGDDCNVPIPSWVWNQKSDDSLYFKSETGTVNKETL
NPLASDVIRKEYGELYTAFAAAMKPYKDVIAKIYLSGGPAGELRYPSYTTSDGTGYPSRGKFQAY
TEFAKSKFRLWVLNKYGSLNEVNKAWGTKLISELAILPPSDGEQFLMNGYLSMYGKDYLEWYQGI
LENHTKLIGELAHNAFDTTFQVPIGAKIAGVHWQYNNPTIPHGAEKPAGYNDYSHLLDAFKSAKL
DVTFTCLEMTDKGSYPEYSMPKTLVQNIATLANEKGIVLNGENALSIGNEEEYKRVAEMAFNYNF
AGFTLLRYQDVMYNNSLMGKFKDLLGV
>d1xyza_ c.1.8.3 (A:) Xylanase {Clostridium thermocellum, XynZ}
NALRDYAEARGIKIGTCVNYPFYNNSDPTYNSILQREFSMVVCENEMKFDALQPRQNVFDFSKGD
QLLAFAERNGMQMRGHTLIWHNQNPSWLTNGNWNRDSLLAVMKNHITTVMTHYKGKIVEWDVANE
CMDDSGNGLRSSIWRNVIGQDYLDYAFRYAREADPDALLFYNDYNIEDLGPKSNAVFNMIKSMKE
RGVPIDGVGFQCHFINGMSPEYLASIDQNIKRYAEIGVIVSFTEIDIRIPQSENPATAFQVQANN
YKELMKICLANPNCNTFVMWGFTDKYTWIPGTFPGYGNPLIYDSNYNPKPAYNAIKEALM
>d1hiza_ c.1.8.3 (A:) Xylanase {Bacillus stearothermophilus, Xt6}
SYAKKPHISALNAPQLDQRYKNEFTIGAAVEPYQLQNEKDVQMLKRHFNSIVAENVMKPISIQPE
EGKFNFEQADRIVKFAKANGMDIRFHTLVWHSQVPQWFFLDKEGKPMVNETDPVKREQNKQLLLK
RLETHIKTIVERYKDDIKYWDVVNEVVGDDGKLRNSPWYQIAGIDYIKVAFQAARKYGGDNIKLY
MNDYNTEVEPKRTALYNLVKQLKEEGVPIDGIGHQSHIQIGWPSEAEIEKTINMFAALGLDNQIT
ELDVSMYGWPPRAYPTYDAIPKQKFLDQAARYDRLFKLYEKLSDKISNVTFWGIADNHTWLDSRA
DVYYDANGNVVVDPNAPYAKVEKGKGKDAPFVFGPDYKVKPAYWAIIDHK
>d1bg4__ c.1.8.3 (-) Xylanase {Penicillium simplicissimum}
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EASVSIDAKFKAHGKKYLGTIGDQYTLTKNTKNPAIIKADFGQLTPENSMKWDATEPNRGQFTFS
GSDYLVNFAQSNGKLIRGHTLVWHSQLPGWVSSITDKNTLISVLKNHITTVMTRYKGKIYAWDVL
NEIFNEDGSLRNSVFYNVIGEDYVRIAFETARSVDPNAKLYINDYNLDSAGYSKVNGMVSHVKKW
LAAGIPIDGIGSQTHLGAGAGSAVAGALNALASAGTKEIAITELDIAGASSTDYVNVVNACLNQA
KCVGITVWGVADPDSWRSSSSPLLFDGNYNPKAAYNAIANAL
>d1edg__ c.1.8.3 (-) Endoglucanase CelA {Clostridium cellulolyticum}
MYDASLIPNLQIPQKNIPNNDGMNFVKGLRLGWNLGNTFDAFNGTNITNELDYETSWSGIKTTKQ
MIDAIKQKGFNTVRIPVSWHPHVSGSDYKISDVWMNRVQEVVNYCIDNKMYVILNTHHDVDKVKG
YFPSSQYMASSKKYITSVWAQIAARFANYDEHLIFEGMNEPRLVGHANEWWPELTNSDVVDSINC
INQLNQDFVNTVRATGGKNASRYLMCPGYVASPDGATNDYFRMPNDISGNNNKIIVSVHAYCPWN
FAGLAMADGGTNAWNINDSKDQSEVTWFMDNIYNKYTSRGIPVIIGECGAVDKNNLKTRVEYMSY
YVAQAKARGILCILWDNNNFSGTGELFGFFDRRSCQFKFPEIIDGMVKYAFGLIN
>d1ceo__ c.1.8.3 (-) Endoglucanase CelC {Clostridium thermocellum}
MVSFKAGINLGGWISQYQVFSKEHFDTFITEKDIETIAEAGFDHVRLPFDYPIIESDDNVGEYKE
DGLSYIDRCLEWCKKYNLGLVLDMHHAPGYRFQDFKTSTLFEDPNQQKRFVDIWRFLAKRYINER
EHIAFELLNQVVEPDSTRWNKLMLECIKAIREIDSTMWLYIGGNNYNSPDELKNLADIDDDYIVY
NFHFYNPFFFTHQKAHWSESAMAYNRTVKYPGQYEGIEEFVKNNPKYSFMMELNNLKLNKELLRK
DLKPAIEFREKKKCKLYCGEFGVIAIADLESRIKWHEDYISLLEEYDIGGAVWNYKKMDFEIYNE
DRKPVSQELVNILAR
>d1cz1a_ c.1.8.3 (A:) Exo-beta-(1,3)-glucanase {Yeast (Candida
albicans)}
AWDYDNNVIRGVNLGGWFVLEPYMTPSLFEPFQNGNDQSGVPVDEYHWTQTLGKEAALRILQKHW
STWITEQDFKQISNLGLNFVRIPIGYWAFQLLDNDPYVQGQVQYLEKALGWARKNNIRVWIDLHG
APGSQNGFDNSGLRDSYNFQNGDNTQVTLNVLNTIFKKYGGNEYSDVVIGIELLNEPLGPVLNMD
KLKQFFLDGYNSLRQTGSVTPVIIHDAFQVFGYWNNFLTVAEGQWNVVVDHHHYQVFSGGELSRN
INDHISVACNWGWDAKKESHWNVAGEWSAALTDCAKWLNGVNRGARYEGAYDNAPYIGSCQPLLD
ISQWSDEHKTDTRRYIEAQLDAFEYTGGWVFWSWKTENAPEWSFQTLTYNGLFPQPVTDRQFPNQ
CGFH
>d1ecea_ c.1.8.3 (A:) Endocellulase E1 {Acidothermus cellulolyticus}
AGGGYWHTSGREILDANNVPVRIAGINWFGFETCNYVVHGLWSRDYRSMLDQIKSLGYNTIRLPY
SDDILKPGTMPNSINFYQMNQDLQGLTSLQVMDKIVAYAGQIGLRIILDRHRPDCSGQSALWYTS
SVSEATWISDLQALAQRYKGNPTVVGFDLHNEPHDPACWGCGDPSIDWRLAAERAGNAVLSVNPN
LLIFVEGVQSYNGDSYWWGGNLQGAGQYPVVLNVPNRLVYSAHDYATSVYPQTWFSDPTFPNNMP
GIWNKNWGYLFNQNIAPVWLGEFGTTLQSTTDQTWLKTLVQYLRPTAQYGADSFQWTFWSWNPDS
GDTGGILKDDWQTVDTVKDGYLAPIKSSIFDPV
>d7a3ha_ c.1.8.3 (A:) Endoglucanase Cel5a {Bacillus agaradhaerens}
SVVEEHGQLSISNGELVNERGEQVQLKGMSSHGLQWYGQFVNYESMKWLRDDWGINVFRAAMYTS
SGGYIDDPSVKEKVKEAVEAAIDLDIYVIIDWHILSDNDPNIYKEEAKDFFDEMSELYGDYPNVI
YEIANEPNGSDVTWGNQIKPYAEEVIPIIRNNDPNNIIIVGTGTWSQDVHHAADNQLADPNVMYA
FHFYAGTHGQNLRDQVDYALDQGAAIFVSEWGTSAATGDGGVFLDEAQVWIDFMDERNLSWANWS
LTHKDESSAALMPGANPTGGWTEAELSPSGTFVREKIRES
>d1egza_ c.1.8.3 (A:) Endoglucanase Cel5a {Erwinia chrysanthemi}
SVEPLSVNGNKIYAGEKAKSFAGNSLFWSNNGWGGEKFYTADTVASLKKDWKSSIVRAAMGVQES
GGYLQDPAGNKAKVERVVDAAIANDMYAIIGWHSHSAENNRSEAIRFFQEMARKYGNKPNVIYEI
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YNEPLQVSWSNTIKPYAEAVISAIRAIDPDNLIIVGTPSWSQNVDEASRDPINAKNIAYTLHFYA
GTHGESLRNKARQALNNGIALFVTEWGTVNADGNGGVNQTETDAWVTFMRDNNISNANWALNDKN
EGASTYYPDSKNLTESGKKVKSIIQSWPYKA
>d1g0ca_ c.1.8.3 (A:) Alkaline cellulase K catalytic domain {Bacillus
sp.}
PAGMQAVKSPSEAGALQLVELNGQLTLAGEDGTPVQLRGMSTHGLQWFGEIVNENAFVALSNDWG
SNMIRLAMYIGENGYATNPEVKDLVYEGIELAFEHDMYVIVDWHVHAPGDPRADVYSGAYDFFEE
IADHYKDHPKNHYIIWELANEPSPNNNGGPGLTNDEKGWEAVKEYAEPIVEMLREKGDNMILVGN
PNWSQRPDLSADNPIDAENIMYSVHFYTGSHGASHIGYPEGTPSSERSNVMANVRYALDNGVAVF
ATEWGTSQANGDGGPYFDEADVWLNFLNKHNISWANWSLTNKNEISGAFTPFELGRTDATDLDPG
ANQVWAPEELSLSGEYVRARIKGIEYTPIDRTK
>d1bqca_ c.1.8.3 (A:) Beta-mannanase {Thermomonospora fusca}
ATGLHVKNGRLYEANGQEFIIRGVSHPHNWYPQHTQAFADIKSHGANTVRVVLSNGVRWSKNGPS
DVANVISLCKQNRLICMLEVHDTTGYGEQSGASTLDQAVDYWIELKSVLQGEEDYVLINIGNEPY
GNDSATVAAWATDTSAAIQRLRAAGFEHTLVVDAPNWGQDWTNTMRNNADQVYASDPTGNTVFSI
HMYGVYSQASTITSYLEHFVNAGLPLIIGEFGHDHSDGNPDEDTIMAEAERLKLGYIGWSWSGNG
GGVEYLDMVYNFDGDNLSPWGERIFYGPNGIASTAKEAVIFG
>d1qnra_ c.1.8.3 (A:) Beta-mannanase {Trichoderma reesei}
ASSFVTISGTQFNIDGKVGYFAGTNCYWCSFLTNHADVDSTFSHISSSGLKVVRVWGFNDVNTQP
SPGQIWFQKLSATGSTINTGADGLQTLDYVVQSAEQHNLKLIIPFVNNWSDYGGINAYVNAFGGN
ATTWYTNTAAQTQYRKYVQAVVSRYANSTAIFAWELGNEPRCNGCSTDVIVQWATSVSQYVKSLD
SNHLVTLGDEGLGLSTGDGAYPYTYGEGTDFAKNVQIKSLDFGTFHLYPDSWGTNYTWGNGWIQT
HAAACLAAGKPCVFEEYGAQQNPCTNEAPWQTTSLTTRGMGGDMFWQWGDTFANGAQSNSDPYTV
WYNSSNWQCLVKNHVDAIN
>d1j9ya_ c.1.8.3 (A:) Mannanase 26A {Pseudomonas fluorescens, subsp.
cellulosa}
PVTVKLVDSQATMETRSLFAFMQEQRRHSIMFGHQHETTQGLTITRTDGTQSDTFNAVGDFAAVY
GWDTLSIVAPKAEGDIVAQVKKAYARGGIITVSSHFDNPKTDTQKGVWPVGTSWDQTPAVVDSLP
GGAYNPVLNGYLDQVAEWANNLKDEQGRLIPVIFRLYHENTGSWFWWGDKQSTPEQYKQLFRYSV
EYLRDVKGVRNFLYAYSPNNFWDVTEANYLERYPGDEWVDVLGFDTYGPVADNADWFRNVVANAA
LVARMAEARGKIPVISEIGIRAPDIEAGLYDNQWYRKLISGLKADPDAREIAFLLVWRNAPQGVP
GPNGTQVPHYWVPANRPENINNGTLEDFQAFYADEFTAFNRDIEQVYQRPT
>d1ghsa_ c.1.8.3 (A:) Plant beta-glucanases {Barley (Hordeum vulgare),
1,3-beta-glucanase}
IGVCYGVIGNNLPSRSDVVQLYRSKGINGMRIYFADGQALSALRNSGIGLILDIGNDQLANIAAS
TSNAASWVQNNVRPYYPAVNIKYIAAGNEVQGGATQSILPAMRNLNAALSAAGLGAIKVSTSIRF
DEVANSFPPSAGVFKNAYMTDVARLLASTGAPLLANVYPYFAYRDNPGSISLNYATFQPGTTVRD
QNNGLTYTSLFDAMVDAVYAALEKAGAPAVKVVVSESGWPSAGGFAASAGNARTYNQGLINHVGG
GTPKKREALETYIFAMFNENQKTGDATERSFGLFNPDKSPAYNIQF
>d1aq0a_ c.1.8.3 (A:) Plant beta-glucanases {Barley (Hordeum vulgare),
1,3-1,4-beta-glucanase}
IGVCYGMSANNLPAASTVVSMFKSNGIKSMRLYAPNQAALQAVGGTGINVVVGAPNDVLSNLAAS
PAAAASWVKSNIQAYPKVSFRYVCVGNEVAGGATRNLVPAMKNVHGALVAAGLGHIKVTTSVSQA
ILGVFSPPSAGSFTGEAAAFMGPVVQFLARTNAPLMANIYPYLAWAYNPSAMDMGYALFNASGTV
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VRDGAYGYQNLFDTTVDAFYTAMGKHGGSSVKLVVSESGWPSGGGTAATPANARFYNQHLINHVG
RGTPRHPGAIETYIFAMFNENQKDSGVEQNWGLFYPNMQHVYPINF
>d1jz8a5 c.1.8.3 (A:334-625) beta-Galactosidase, domain 3 {Escherichia coli}
EVRIENGLLLLNGKPLLIRGVNRHEHHPLHGQVMDEQTMVQDILLMKQNNFNAVRCSHYPNHPLW
YTLCDRYGLYVVDEANIETHGMVPMNRLTDDPRWLPAMSERVTRMVQRDRNHPSVIIWSLGNESG
HGANHDALYRWIKSVDPSRPVQYEGGGADTTATDIICPMYARVDEDQPFPAVPKWSIKKWLSLPG
ETRPLILCQYAHAMGNSLGGFAKYWQAFRQYPRLQGGFVWDWVDQSLIKYDENGNPWSAYGGDFG
DTPNDRQFCMNGLVFADRTPHPALTEAKHQQQ
>d1bhga3 c.1.8.3 (A:329-632) beta-Glucuronidase, domain 3 {Human (Homo sapiens)}
VAVTKSQFLINGKPFYFHGVNKHEDADIRGKGFDWPLLVKDFNLLRWLGANAFRTSHYPYAEEVM
QMCDRYGIVVIDECPGVGLALPQFFNNVSLHHHMQVMEEVVRRDKNHPAVVMWSVANEPASHLES
AGYYLKMVIAHTKSLDPSRPVTFVSNSNYAADKGAPYVDVICLNSYYSWYHDYGHLELIQLQLAT
QFENWYKKYQKPIIQSEYGAETIAGFHQDPPLMFTEEYQKSLLEQYHLGLDQKRRKYVVGELIWN
FADFMTEQSPTRVLGNKKGIFTRQRQPKSAAFLLRERYWKIANE
>d1e0wa_ c.1.8.3 (A:) Xylanase A, catalytic core {Streptomyces lividans}
AESTLGAAAAQSGRYFGTAIASGRLSDSTYTSIAGREFNMVTAENEMKIDATEPQRGQFNFSSAD
RVYNWAVQNGKQVRGHTLAWHSQQPGWMQSLSGSALRQAMIDHINGVMAHYKGKIVQWDVVNEAF
ADGSSGARRDSNLQRSGNDWIEVAFRTARAADPSAKLCYNDYNVENWTWAKTQAMYNMVRDFKQR
GVPIDCVGFQSHFNSGSPYNSNFRTTLQNFAALGVDVAITELDIQGAPASTYANVTNDCLAVSRC
LGITVWGVRDSDSWRSEQTPLLFNNDGSKKAAYTAVLDALNG
>d1clxa_ c.1.8.3 (A:) Xylanase A, catalytic core {Pseudomonas fluorescens}
GLASLADFPIGVAVAASGGNADIFTSSARQNIVRAEFNQITAENIMKMSYMYSGSNFSFTNSDRL
VSWAAQNGQTVHGHALVWHPSYQLPNWASDSNANFRQDFARHIDTVAAHFAGQVKSWDVVNEALF
DSADDPDGRGSANGYRQSVFYRQFGGPEYIDEAFRRARAADPTAELYYNDFNTEENGAKTTALVN
LVQRLLNNGVPIDGVGFQMHVMNDYPSIANIRQAMQKIVALSPTLKIKITELDVRLNNPYDGNSS
NDYTNRNDCAVSCAGLDRQKARYKEIVQAYLEVVPPGRRGGITVWGIADPDSWLYTHQNLPDWPL
LFNDNLQPKPAYQGVVEALS
>d1fxma_ c.1.8.3 (A:) Xylanase A, catalytic core {Thermoascus aurantiacus}
QAAQSVDQLIKARGKVYFGVATDQNRLTTGKNAAIIQADFGQVTPENSMKWDATEPSQGNFNFAG
ADYLVNWAQQNGKLIRGHTLVWHSQLPSWVSSITDKNTLTNVMKNHITTLMTRYKGKIRAWDVVN
EAFNEDGSLRQTVFLNVIGEDYIPIAFQTARAADPNAKLYINDYNLDSASYPKTQAIVNRVKQWR
AAGVPIDGIGSQTHLSAGQGAGVLQALPLLASAGTPEVAITELDVAGASPTDYVNVVNACLNVQS
CVGITVWGVADPDSWRASTTPLLFDGNFNPKPAYNAIVQDLQ
>d1tux__ c.1.8.3 (-) Xylanase A, catalytic core {Thermoascus aurantiacus}
AAAQSVDQLIDARGKVYFGVATDQNRLTTGKNAAIIQADFGQVTPENSMKWDATEPSQGNFNFAG
ADYLVNWAQQNGKLIRGHTLVWHSQLPSWVVSITDKNTLTNVMKNHITTIMTRYIGKIRAWDVVN
EAFNEDGSLRQTVFNNVIGEDYIPIAFRTARAADPNAKLYINDYNLDSASKPKTSAIVKRVKKWR
AAGVPIDGIGSQTHLSAGQGASIDAALPNLASAGTPEVAITELDIAGATSTDYVDVVNACLDVDS
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CIGITVWGVADPDSWRASTTPLLFDGNFNPKPAYNAIVQLL
>d1xyfa2 c.1.8.3 (A:1-303) Xylanase A, catalytic core {Streptomyces
olivaceoviridis}
AESTLGAAAAQSGRYFGTAIASGKLGDSAYTTIASREFNMVTAENEMKIDATEPQRGQFNFSAGD
RVYNWAVQNGKQVRGHTLAWHSQQPGWMQSLSGSTLRQAMIDHINGVMGHYKGKIAQWDVVNEAF
SDDGSGGRRDSNLQRTGNDWIEVAFRTARAADPAAKLCYNDYNIENWTWAKTQGVYNMVRDFKQR
GVPIDCVGFQSHFNSGSPYNSNFRTTLQNFAALGVDVAITELDIQGASSSTYAAVTNDCLAVSRC
LGITVWGVRDTDSWRSGDTPLLFNGDGSKKAAYTAVLNALNGG
>d1fh9a_ c.1.8.3 (A:) Xylanase A, catalytic core {Cellulomonas fimi}
ATTLKEAADGAGRDFGFALDPNRLSEAQYKAIADSEFNLVVAENAMKWDATEPSQNSFSFGAGDR
VASYAADTGKELYGHTLVWHSQLPDWAKNLNGSAFESAMVNHVTKVADHFEGKVASWDVVNEAFA
DGGGRRQDSAFQQKLGNGYIETAFRAARAADPTAKLCINDYNVEGINAKSNSLYDLVKDFKARGV
PLDCVGFQSHLIVGQVPGDFRQNLQRFADLGVDVRITELDIRMRTPSDATKLATQAADYKKVVQA
CMQVTRCQGVTVWGITDKYSWVPDVFPGEGAALVWDASYAKKPAYAAVMEAF
>d1e4mm_ c.1.8.4 (M:) Plant beta-glucosidase (myrosinase) {White
mustard (Sinapis alba)}
EITCQENLPFTCGNTDALNSSSFSSDFIFGVASSAYQIEGTIGRGLNIWDGFTHRYPNKSGPDHG
NGDTTCDSFSYWQKDIDVLDELNATGYRFSIAWSRIIPRGKRSRGVNEKGIDYYHGLISGLIKKG
ITPFVTLFHWDLPQTLQDEYEGFLDPQIIDDFKDYADLCFEEFGDSVKYWLTINQLYSVPTRGYG
SALDAPGRCSPTVDPSCYAGNSSTEPYIVAHHQLLAHAKVVDLYRKNYTHQGGKIGPTMITRWFL
PYNDTDRHSIAATERMKEFFLGWFMGPLTNGTYPQIMIDTVGERLPSFSPEESNLVKGSYDFLGL
NYYFTQYAQPSPNPVNSTNHTAMMDAGAKLTYINASGHYIGPLFEKDKADSTDNIYYYPKGIYSV
MDYFKNKYYNPLIYVTENGISTPGDENRNQSMLDYTRIDYLCSHLCFLNKVIKEKDVNVKGYLAW
ALGDNYEFNKGFTVRFGLSYIDWNNVTDRDLKKSGQWYQSFISP
>d1cbg__ c.1.8.4 (-) Plant beta-glucosidase (myrosinase) {Creeping
white clover (Trifolium repens)}
FKPLPISFDDFSDLNRSCFAPGFVFGTASSAFQYEGAAFEDGKGPSIWDTFTHKYPEKIKDRTNG
DVAIDEYHRYKEDIGIMKDMNLDAYRFSISWPRVLPKGKLSGGVNREGINYYNNLINEVLANGMQ
PYVTLFHWDVPQALEDEYRGFLGRNIVDDFRDYAELCFKEFGDRVKHWITLNEPWGVSMNAYAYG
TFAPGRCSDWLKLNCTGGDSGREPYLAAHYQLLAHAAAARLYKTKYQASQNGIIGITLVSHWFEP
ASKEKADVDAAKRGLDFMLGWFMHPLTKGRYPESMRYLVRKRLPKFSTEESKELTGSFDFLGLNY
YSSYYAAKAPRIPNARPAIQTDSLINATFEHNGKPLGPMAASSWLCIYPQGIRKLLLYVKNHYNN
PVIYITENGRNEFNDPTLSLQESLLDTPRIDYYYRHLYYVLTAIGDGVNVKGYFAWSLFDNMEWD
SGYTVRFGLVFVDFKNNLKRHPKLSAHWFKSFLKK
>d1e55a_ c.1.8.4 (A:) Plant beta-glucosidase (myrosinase) {Maize (Zea
mays), zmglu1}
VQMLSPSEIPQRDWFPSDFTFGAATSAYQIEGAWNEDGKGESNWDHFCHNHPERILDGSNSDIGA
NSYHMYKTDVRLLKEMGMDAYRFSISWPRILPKGTKEGGINPDGIKYYRNLINLLLENGIEPYVT
IFHWDVPQALEEKYGGFLDKSHKSIVEDYTYFAKVCFDNFGDKVKNWLTFNDPQTFTSFSYGTGV
FAPGRCSPGLDCAYPTGNSLVEPYTAGHNILLAHAEAVDLYNKHYKRDDTRIGLAFDVMGRVPYG
TSFLDKQAEERSWDINLGWFLEPVVRGDYPFSMRSLARERLPFFKDEQKEKLAGSYNMLGLNYYT
SRFSKNIDISPNYSPVLNTDDAYASQEVNGPDGKPIGPPMGNPWIYMYPEGLKDLLMIMKNKYGN
PPIYITENGIGDVDTKETPLPMEAALNDYKRLDYIQRHIATLKESIDLGSNVQGYFAWSLLDNFE
WFAGFTERYGIVYVDRNNNCTRYMKESAKWLKEFNTA
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>d1pbga_ c.1.8.4 (A:) 6-phospho-beta-D-galactosidase, PGAL {Lactococcus lactis}
MTKTLPKDFIFGGATAAYQAEGATHTDGKGPVAWDKYLEDNYWYTAEPASDFYHKYPVDLELAEE
YGVNGIRISIAWSRIFPTGYGEVNEKGVEFYHKLFAECHKRHVEPFVTLHHFDTPEALHSNGDFL
NRENIEHFIDYAAFCFEEFPEVNYWTTFNEIGPIGDGQYLVGKFPPGIKYDLAKVFQSHHNMMVS
HARAVKLYKDKGYKGEIGVVHALPTKYPYDPENPADVRAAELEDIIHNKFILDATYLGHYSDKTM
EGVNHILAENGGELDLRDEDFQALDAAKDLNDFLGINYYMSDWMQAFDGETEIIHNGKGEKGSSK
YQIKGVGRRVAPDYVPRTDWDWIIYPEGLYDQIMRVKNDYPNYKKIYITENGLGYKDEFVDNTVY
DDGRIDYVKQHLEVLSDAIADGANVKGYFIWSLMDVFSWSNGYEKRYGLFYVDFDTQERYPKKSA
HWYKKLAETQVIE
>d1e4ia_ c.1.8.4 (A:) Beta-glucosidase A {Bacillus polymyxa}
TIFQFPQDFMWGTATAAYQIEGAYQEDGRGLSIWDTFAHTPGKVFNGDNGNVACDSYHRYEEDIR
LMKELGIRTYRFSVSWPRIFPNGDGEVNQKGLDYYHRVVDLLNDNGIEPFCTLYHWDLPQALQDA
GGWGNRRTIQAFVQFAETMFREFHGKIQHWLTFNEPWCIAFLSNMLGVHAPGLTNLQTAIDVGHH
LLVAHGLSVRRFRELGTSGQIGIAPNVSWAVPYSTSEEDKAACARTISLHSDWFLQPIYQGSYPQ
FLVDWFAEQGATVPIQDGDMDIIGEPIDMIGINYYSMSVNRFNPEAGFLQSEEINMGLPVTDIGW
PVESRGLYEVLHYLQKYGNIDIYITENGACINDEVVNGKVQDDRRISYMQQHLVQVHRTIHDGLH
VKGYMAWSLLDNFEWAEGYNMRFGMIHVDFRTQVRTPKQSYYWYRNVVSNNWLETRR
>d1qoxa_ c.1.8.4 (A:) Beta-glucosidase A {Bacillus circulans, subsp. alkalophilus}
SIHMFPSDFKWGVATAAYQIEGAYNEDGRGMSIWDTFAHTPGKVKNGDNGNVACDSYHRVEEDVQ
LLKDLGVKVYRFSISWPRVLPQGTGEVNRAGLDYYHRLVDELLANGIEPFCTLYHWDLPQALQDQ
GGWGSRITIDAFAEYAELMFKELGGKIKQWITFNEPWCMAFLSNYLGVHAPGNKDLQLAIDVSHH
LLVAHGRAVTLFRELGISGEIGIAPNTSWAVPYRRTKEDMEACLRVNGWSGDWYLDPIYFGEYPK
FMLDWYENLGYKPPIVDGDMELIHQPIDFIGINYYTSSMNRYNPGEAGGMLSSEAISMGAPKTDI
GWEIYAEGLYDLLRYTADKYGNPTLYITENGACYNDGLSLDGRIHDQRRIDYLAMHLIQASRAIE
DGINLKGYMEWSLMDNFEWAEGYGMRFGLVHVDYDTLVRTPKDSFYWYKGVISRGWLDL
>d1gowa_ c.1.8.4 (A:) beta-Glycosidase {Archaeon Sulfolobus solfataricus}
MYSFPNSFRFGWSQAGFQSEMGTPGSEDPNTDWYKWVHDPENMAAGLVSGDLPENGPGYWGNYKT
FHDNAQKMGLKIARLNSEWSRQFPNPLPRPQNFDESKQDVTEVEINENELKRLDEYANKDALNHY
REIFKDLKSRGLYFIQNMYHWPLPLWLHDPIRVRRGDFTGPSGWLSTRTVYEFARFSAYTAWKFD
DLVDEYSTMNEPNVVGGLGYVGVKSGFPPGYLSFELSRRAMYNIIQAHARAYDGIKSVSKKPVGI
IYANSSFQPLTDKDMEAVEMAENDNRWWFFDAIIRGEITRGNEKIVRDDLKGRLDWIGVNYYTRT
VVKRTEKGYVSLGGYGHGCERNSVSLAGLPTSDFGWEFFPEGLYDVLTKYWNRYHLYMYVTENGI
ADDADYQRPYYLVSHVYQVHRAINSGADVRGYLHWSLADNYEWASGFSMRFGLLKVDYNTKRLYW
RPSALVYREIATNGAITDEIEHLNSVPPVKPLRH
>d1qvba_ c.1.8.4 (A:) beta-Glycosidase {Archaeon Thermosphaera aggregans}
MKFPKDFMIGYSSSPFQFEAGIPGSEDPNSDWWVWVHDPENTAAGLVSGDFPENGPGYWNLNQND
HDLAEKLGVNTIRVGVEWSRIFPKPTFNVKVPVERDENGSIVHVDVDDKAVERLDELANKEAVNH
YVEMYKDWVERGRKLILNLYHWPLPLWLHNPIMVRRMGPDRAPSGWLNEESVVEFAKYAAYIAWK
MGELPVMWSTMNEPNVVYEQGYMFVKGGFPPGYLSLEAADKARRNMIQAHARAYDNIKRFSKKPV
GLIYAFQWFELLEGPAEVFDKFKSSKLYYFTDIVSKGSSIINVEYRRDLANRLDWLGVNYYSRLV
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YKIVDDKPIILHGYGFLCTPGGISPAENPCSDFGWEVYPEGLYLLLKELYNRYGVDLIVTENGVS
DSRDALRPAYLVSHVYSVWKAANEGIPVKGYLHWSLTDNYEWAQGFRQKFGLVMVDFKTKKRYLR
PSALVFREIATHNGIPDELQHLTLIQ
>d2hvm__ c.1.8.5 (-) Hevamine A (chitinase/lysozyme) {Para rubber tree (Hevea brasiliensis)}
GGIAIYWGQNGNEGTLTQTCSTRKYSYVNIAFLNKFGNGQTPQINLAGHCNPAAGGCTIVSNGIR
SCQIQGIKVMLSLGGGIGSYTLASQADAKNVADYLWNNFLGGKSSSRPLGDAVLDGIDFDIEHGS
TLYWDDLARYLSAYSKQGKKVYLTAAPQCPFPDRYLGTALNTGLFDYVWVQFYNNPPCQYSSGNI
NNIINSWNRWTTSINAGKIFLGLPAAPEAAGSGYVPPDVLISRILPEIKKSPKYGGVMLWSKFYD
DKNGYSSSILDSV
>d1nar__ c.1.8.5 (-) Seed storage protein {Vicia narbonensis, Narbonin}
PKPIFREYIGVKPNSTTLHDFPTEIINTETLEFHYILGFAIESYYESGKGTGTFEESWDVELFGP
EKVKNLKRRHPEVKVVISIGGRGVNTPFDPAEENVWVSNAKESLKLIIQKYSDDSGNLIDGIDIH
YEHIRSDEPFATLMGQLITELKKDDDLNINVVSIAPSENNSSHYQKLYNAKKDYINWVDYQFSNQ
QKPVSTDDAFVEIFKSLEKDYHPHKVLPGFSTDPLDTKHNKITRDIFIGGCTRLVQTFSLPGVFF
WNANDSVIPKRDGDKPFIVELTLQQLLAA
>d1cnv__ c.1.8.5 (-) Seed storage protein {Jack bean (Canavalia ensiformis), Concanavalin B}
DISSTEIAVYWGQREDGLLRDTCKTNNYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFL
ESQIKECQRMGVKVFLALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVALDGIHFDI
QKPVDELNWDNLLEELYQIKDVYQSTFLLSAAPGCLSPDEYLDNAIQTRHFDYIFVRFYNDRSCQ
YSTGNIQRIRNAWLSWTKSVYPRDKNLFLELPASQATAPGGGYIPPSALIGQVLPYLPDLQTRYA
GIALWNRQADKETGYSTNIIRYL
>d2ebn__ c.1.8.5 (-) Endo-beta-N-acetylglucosaminidase {Flavobacterium meningosepticum, endoglycosidase F1}
TTKANIKLFSFTEVNDTNPLNNLNFTLKNSGKPLVDMVVLFSANINYDAANDKVFVSNNPNVQHL
LTNRAKYLKPLQDKGIKVILSILGNHDRSGIANLSTARAKAFAQELKNTCDLYNLDGVFFDDEYS
AYQTPPPSGFVTPSNNAAARLAYETKQAMPNKLVTVYVYSRTSSFPTAVDGVNAGSYVDYAIHDY
GGSYDLATNYPGLAKSGMVMSSQEFNQGRYATAQALRNIVTKGYGGHMIFAMDPNRSNFTSGQLP
ALKLIAKELYGDELVYSNTPYSKDW
>d1eoka_ c.1.8.5 (A:) Endo-beta-N-acetylglucosaminidase {Flavobacterium meningosepticum, endoglycosidase F3}
NGVCIAYYITDGRNPTFKLKDIPDKVDMVILFGLKYWSLQDTTKLPGGTGMMGSFKSYKDLDTQI
RSLQSRGIKVLQNIDDDVSWQSSKPGGFASAAAYGDAIKSIVIDKWKLDGISLDIEHSGAKPNPI
PTFPGYAATGYNGWYSGSMAATPAFLNVISELTKYFGTTAPNNKQLQIASGIDVYAWNKIMENFR
NNFNYIQLQSYGANVSRTQLMMNYATGTNKIPASKMVFGAYAEGGTNQANDVEVAKWTPTQGAKG
GMMIYTYNSNVSYANAVRDAVK
>d1edt__ c.1.8.5 (-) Endo-beta-N-acetylglucosaminidase {Streptomyces plicatus, endoglycosidase H}
KQGPTSVAYVEVNNNSMLNVGKYTLADGGGNAFDVAVIFAANINYDTGTKTAYLHFNENVQRVLD
NAVTQIRPLQQQGIKVLLSVLGNHQGAGFANFPSQQAASAFAKQLSDAVAKYGLDGVDFDDEYAE
YGNNGTAQPNDSSFVHLVTALRANMPDKIISLYNIGPAASRLSYGGVDVSDKFDYAWNPYYGTWQ
VPGIALPKAQLSPAAVEIGRTSRSTVADLARRTVDEGYGVYLTYNLDGGDRTADVSAFTRELYGS
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EAVRT
>d1edqa2 c.1.8.5 (A:133-443,A:517-563) Chitinase A, catalytic domain {Serratia marcescens}
TDGSHLAPLKEPLLEKNKPYKQNSGKVVGSYFVEWGVYGRNFTVDKIPAQNLTHLLYGFIPICGG
NGINDSLKEIEGSFQALQRSCQGREDFKVSIHDPFAALQKAQKGVTAWDDPYKGNFGQLMALKQA
HPDLKILPSIGGWTLSDPFFFMGDKVKRDRFVGSVKEFLQTWKFFDGVDIDWEFPGGKGANPNLG
SPQDGETYVLLMKELRAMLDQLSVETGRKYELTSAISAGKDKIDKVAYNVAQNSMDHIFLMSYDF
YGAFDLKNLGHQTALNAPAWKPDTAYTTVNGVNALLAQGVKPGKIVVGTAMXDARSVQAKGKYVL
DKQLGGLFSWEIDADNGDILNSMNASLGNSAGVQ
>d1goia2 c.1.8.5 (A:3-291,A:380-446) Chitinase B, catalytic domain {Serratia marcescens}
TRKAVIGYYFIPTNQINNYTETDTSVVPFPVSNITPAKAKQLTHINFSFLDINSNLECAWDPATN
DAKARDVVNRLTALKAHNPSLRIMFSIGGWYYSNDLGVSHANYVNAVKTPASRAKFAQSCVRIMK
DYGFDGVNIDWEYPQAAEVDGFIAALQEIRTLLNQQTITDGRQALPYQLTIAGAGGAFFLSRYYS
KLAQIVAPLDYINLMTYDLAGPWEKVTNHQAALFGDAAGPTFYNALREANLGWSWEELTRAFPSP
FSLTVDAAVQQHLMMEGVPSAKIVMGVPFXDDAESFKYKAKYIKQQQLGGVMFWHLGQDNRNGDL
LAALDRYFNAADYDDSQLDMGTGLRYTGVGPG
>d1d2ka1 c.1.8.5 (A:36-292,A:355-427) Chitinase 1 {Fungus (Coccidioides immitis)}
GGFRSVVYFVNWAIYGRGHNPQDLKADQFTHILYAFANIRPSGEVYLSDTWADTDKHYPGDKWDE
PGNNVYGCIKQMYLLKKNNRNLKTLLSIGGWTYSPNFKTPASTEEGRKKFADTSLKLMKDLGFDG
IDIDWEYPEDEKQANDFVLLLKACREALDAYSAKHPNGKKFLLTIASPAGPQNYNKLKLAEMDKY
LDFWNLMAYDFSGSWDKVSGHMSNVFPSTTKPESTPFSSDKAVKDYIKAGVPANKIVLGMPLXDT
VKIAGKKAEYITKNGMGGGMWWESSSDKTGNESLVGTVVNGLGGTGKLEQRENELSYPESVYDNL
KNGMPS
>d1e9la1 c.1.8.5 (A:22-266,A:337-393) Chitinase-like lectin ym1, saccharide binding domain {Mouse (Mus musculus)}
YQLMCYYTSWAKDRPIEGSFKPGNIDPCLCTHLIYAFAGMQNNEITYTHEQDLRDYEALNGLKDK
NTELKTLLAIGGWKFGPAPFSAMVSTPQNRQIFIQSVIRFLRQYNFDGLNLDWQYPGSRGSPPKD
KHLFSVLVKEMRKAFEEESVEKDIPRLLLTSTGAGIIDVIKSGYKIPELSQSLDYIQVMTYDLHD
PKDGYTGENSPLYKSPYDIGKSADLNVDSIISYWKDHGAASEKLIVGFPAXDNVRSFKLKAQWLK
DNNLGGAVVWPLDMDDFSGSFCHQRHFPLTSTLKGDLNIHSAS
>d1jfxa_ c.1.8.8 (A:) Streptomyces lysozyme {Streptomyces coelicolor, "mueller" dsm3030}
DTSGVQGIDVSHWQGSINWSSVKSAGMSFAYIKATEGTNYKDDRFSANYTNAYNAGIIRGAYHFA
RPNASSGTAQADYFASNGGGWSRDNRTLPGVLDIEHNPSGAMCYGLSTTQMRTWINDFHARYKAR
TTRDVVIYTTASWWNTCTGSWNGMAAKSPFWVAHWGVSAPTVPSGFPTWTFWQYSATGRVGGVSG
DVDRNKFNGSAARLLALANNTA
>d1qba_3 c.1.8.6 (338-780) Bacterial chitobiase (beta-N-acetylhexosaminidase) {Serratia marcescens}
FPYRGIFLDVARNFHKKDAVLRLLDQMAAYKLNKFHFHLSDDEGWRIEIPGLPELTEVGGQRCHD
LSETTCLLPQYGQGPDVYGGFFSRQDYIDIIKYAQARQIEVIPEIDMPAHARAAVVSMEARYKKL
HAAGKEQEANEFRLVDPTDTSNTTSVQFFNRQSYLNPCLDSSQRFVDKVIGEIAQMHKEAGQPIK
TWHFGGDEAKNIRLGAGYTDKAKPEPGKGIIDQGNEDKPWAKSQVCQTMIKEGKVADMEHLPSYF

GQEVSKLVKAHGIDRMQAWQDGLKDAESSKAFATSRVGVNFWDTLYWGGFDSVNDWANKGYEVVV
SNPDYVYMDFPYEVNPDERGYYWGTRFSDERKVFSFAPDNMPQNAETSVDRDGNHFNAKSDKPWP
GAYGLSAQLWSETQRTDPQMEYMIFPRALSVAERSWHRAGWEQDYRAGREYKG
>d1jaka1 c.1.8.6 (A:151-506) beta-N-acetylhexosaminidase {Streptomyces plicatus}
YAWRSAMLDVSRHFFGVDEVKRYIDRVARYKYNKLHLHLSDDQGWRIAIDSWPRLATYGGSTEVG
GGPGGYYTKAEYKEIVRYAASRHLEVVPEIDMPGHTNAALASYAELNCDGVAPPLYTGTKVGFSS
LCVDKDVTYDFVDDVIGELAALTPGRYLHIGGDEAHSTPKADFVAFMKRVQPIVAKYGKTVVGWH
QLAGAEPVEGALVQYWGLDRTGDAEKAEVAEAARNGTGLILSPADRTYLDMKYTKDTPLGLSWAG
YVEVQRSYDWDPAGYLPGAPADAVRGVEAPLWTETLSDPDQLDYMAFPRLPGVAELGWSPASTHD
WDTYKVRLAAQAPYWEAAGIDFYRSPQVPWT
>d1iexa1 c.1.8.7 (A:1-388) Beta-D-glucan exohydrolase, N-terminal domain {Barley (Hordeum vulgare)}
DYVLYKDATKPVEDRVADLLGRMTLAEKIGQMTQIERLVATPDVLRDNFIGSLLSGGGSVPRKGA
TAKEWQDMVDGFQKACMSTRLGIPMIYGIDAVHGQNNVYGATIFPHNVGLGATRDPYLVKRIGEA
TALEVRATGIQYAFAPCIAVCRDPRWGRCYESYSEDRRIVQSMTELIPGLQGDVPKDFTSGMPFV
AGKNKVAACAKHFVGDGGTVDGINENNTIINREGLMNIHMPAYKNAMDKGVSTVMISYSSWNGVK
MHANQDLVTGYLKDTLKFKGFVISDWEGIDRITTPAGSDYSYSVKASILAGLDMIMVPNKYQQFI
SILTGHVNGGVIPMSRIDDAVTRILRVKFTMGLFENPYADPAMAEQLGKQEHRDLAREAARKS
>d1fcqa_ c.1.8.9 (A:) Bee venom hyaluronidase {Honeybee (Apis mellifera)}
EFNVYWNVPTFMCHKYGLRFEEVSEKYGILQNWMDKFRGEEIAILYDPGMFPALLKDPNGNVVAR
NGGVPQLGNLTKHLQVFRDHLINQIPDKSFPGVGVIDFESWRPIFRQNWASLQPYKKLSVEVVRR
EHPFWDDQRVEQEAKRRFEKYGQLFMEETLKAAKRMRPAANWGYYAYPYCYNLTPNQPSAQCEAT
TMQENDKMSWLFESEDVLLPSVYLRWNLTSGERVGLVGGRVKEALRIARQMTTSRKKVLPYYWYK
YQDRRDTDLSRADLEATLRKITDLGADGFIIWGSSDDINTKAKCLQFREYLNNELGPAVKR
>d1a4ma_ c.1.9.1 (A:) Adenosine deaminase (ADA) {Mouse (Mus musculus)}
TPAFNKPKVELHVHLDGAIKPETILYFGKKRGIALPADTVEELRNIIGMDKPLSLPGFLAKFDYY
MPVIAGCREAIKRIAYEFVEMKAKEGVVYVEVRYSPHLLANSKVDPMPWNQTEGDVTPDDVVDLV
NQGLQEGEQAFGIKVRSILCCMRHQPSWSLEVLELCKKYNQKTVVAMDLAGDETIEGSSLFPGHV
EAYEGAVKNGIHRTVHAGEVGSPEVVREAVDILKTERVGHGYHTIEDEALYNRLLKENMHFEVCP
WSSYLTGAWDPKTTHAVVRFKNDKANYSLNTDDPLIFKSTLDTDYQMTKKDMGFTEEEFKRLNIN
AAKSSFLPEEEKKELLERLYREYQ
>d1j79a_ c.1.9.4 (A:) Dihydroorotase {Escherichia coli}
SQVLKIRRPDDWHLHLRDGDMLKTVVPYTSEIYGRAIVMPNLAPPVTTVEAAVAYRQRILDAVPA
PHDFTPLMTCYLTDSLDPNELERGFNEGVFTAAKLYPANATTNSSHGVTSVDAIMPVLERMEKIG
MPLLVHGEVTHADIDIFDREARFIESVMEPLRQRLTALKVVFEHITTKDAADYVRDGNERLAATI
TPQHLMFNRNHMLVGGVRPHLYCLPILKRNIHQQALRELVASGFQRVFLGTDSAPHARHRKESSC
GCAGCFNAPTALGSYATVFEEMNALQHFEAFCSVNGPQFYGLPVNDTFIELVREEQQVAESIALT
DDTLVPFLAGETVRWSVK
>d1k6wa2 c.1.9.5 (A:56-375) Cytosine deaminase catalytic domain {Escherichia coli}
PFVEPHIHLDTTQTAGQPNWNQSGTLFEGIERWAERKALLTHDDVKQRAWQTLKWQIANGIQHVR
THVDVSDATLTALKAMLEVKQEVAPWIDLQIVAFPQEGILSYPNGEALLEEALRLGADVVGAIPH

FEFTREYGVESLHKTFALAQKYDRLIDVHCDEIDDEQSRFVETVAALAHHEGMGARVTASHTTAM
HSYNGAYTSRLFRLLKMSGINFVANPLVNIHLQGRFDTYPKRRGITRVKEMLESGINVCFGHDDV
FDPWYPLGTANMLQVLHMGLHVCQLMGYGQINDGLNLITHHSARTLNLQDYGIAAGNSAN
>d1ejrc2 c.1.9.2 (C:1130-1422,C:1476-1567) alpha-subunit of urease, catalytic domain {Klebsiella aerogenes}
GIDTHIHWICPQQAEEALVSGVTTMVGGGTGPAAGTHATTCTPGPWYISRMLQAADSLPVNIGLL
GKGNVSQPDALREQVAAGVIGLKIHEAWGATPAAIDCALTVADEMDIQVALHSDTLNESGFVEDT
LAAIGGRTIHTFHTEGAGGGHAPDIITACAHPNILPSSTNPTLPYTLNTIDEHLDMLMVCHHLDP
DIAEDVAFAESRIRRETIAAEDVLHDLGAFSLTSSDSQAMGRVGEVILRTWQVAHRMKVQRGALA
EETGDNDNFRVKRYIAKYTINPALTHGIAHEVGXMFGALGSARHHCRLTFLSQAAAANGVAERLN
LRSAIAVVKGCRTVQKADMVHNSLQPNITVDAQTYEVRVDGELITSEPADVLPMAQRYFLF
>d4ubpc2 c.1.9.2 (C:132-434,C:484-570) alpha-subunit of urease, catalytic domain {Bacillus pasteurii}
GGIDTHVHFINPDQVDVALANGITTLFGGGTGPAEGSKATTVTPGPWNIEKMLKSTEGLPINVGI
LGKGHGSSIAPIMEQIDAGAAGLKIHEDWGATPASIDRSLTVADEADVQVAIHSDTLNEAGFLED
TLRAINGRVIHSFHVEGAGGGHAPDIMAMAGHPNVLPSSTNPTRPFTVNTIDEHLDMLMVCHHLK
QNIPEDVAFADSRIRPETIAAEDILHDLGIISMMSTDALAMGRAGEMVLRTWQTADKMKKQRGPL
AEEKNGSDNFRLKRYVSKYTINPAIAQGIAHEVGSIEEGKFADXGDLIHDTNITFMSKSSIQQGV
PAKLGLKRRIGTVKNCRNIGKKDMKWNDVTTDIDINPETYEVKVDGEVLTCEPVKELPMAQRYFL
F
>d1e9yb2 c.1.9.2 (B:132-431,B:481-569) alpha-subunit of urease, catalytic domain {Helicobacter pylori}
GIDTHIHFISPQQIPTAFASGVTTMIGGGTGPADGTNATTITPGRRNLKWMLRAAEEYSMNLGFL
AKGNASNDASLADQIEAGAIGFKIHEDWGTTPSAINHALDVADKYDVQVAIHTDTLNEAGCVEDT
MAAIAGRTMHTFHTEGAGGGHAPDIIKVAGEHNILPASTNPTIPFTVNTEAEHMDMLMVCHHLDK
SIKEDVQFADSRIRPQTIAAEDTLHDMGAFSITSSDSQAMGRVGEVITRTWQTADKNKKEFGRLK
EEKGDNDNFRIKRYLSKYTINPAIAHGISEYVGSVEVGKVXHHGKAKYDANITFVSQAAYDKGIK
EELGLERQVLPVKNCRNVTKKDMQFNNTTAHIEVNPETYHVFVDGKEVTSKPANKVSLAQLFSIF
>d1i0da_ c.1.9.3 (A:) Phosphotriesterase {Pseudomonas diminuta}
DRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRRARAAGVRTIV
DVSTFDIGRDVSLLAEVSRAADVHIVAATGLWFDPPLSMRLRSVEELTQFFLREIQYGIEDTGIR
AGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDGEQQAAIFESEGLSPSRVCIG
HSDDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASASALLGIRSWQTRALLIKALIDQGYMK
QILVSNDWLFGFSSYVTNIMDVMDRVNPDGMAFIPLRVIPFLREKGVPQETLAGITVTNPARFLS
PTLRAS
>d1bf6a_ c.1.9.3 (A:) Phosphotriesterase homology protein {Escherichia coli}
SFDPTGYTLAHEHLHIDLSGFKNNVDCRLDQYAFICQEMNDLMTRGVRNVIEMTNRYMGRNAQFM
LDVMRETGINVVACTGYYQDAFFPEHVATRSVQELAQEMVDEIEQGIDGTELKAGIIAEIGTSEG
KITPLEEKVFIAAALAHNQTGRPISTHTSFSTMGLEQLALLQAHGVDLSRVTVGHCDLKDNLDNI
LKMIDLGAYVQFDTIGKNSYYPDEKRIAMLHALRDRGLLNRVMLSMDITRRSHLKANGGYGYDYL
LTTFIPQLRQSGFSQADVDVMLRENPSQFFQ
>d1jcla_ c.1.10.1 (A:) Deoxyribose-phosphate aldolase DeoC {Escherichia coli}

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HMTDLKASSLRALKLMDLTTLNDDDTDEKVIALCHQAKTPVGNTAAICIYPRFIPIARKTLKEQG
TPEIRIATVTNFPHGNDDIDIALAETRAAIAYGADEVDVVFPYRALMAGNEQVGFDLVKACKEAC
AAANVLLKVIIETGELKDEALIRKASEISIKAGADFIKTSTGKVAVNATPESARIMMEVIRDMGV
EKTVGFKPAGGVRTAEDAQKYLAIADELFGADWADARHYRFGASSLLASLLKALGHG
>d1nal1_ c.1.10.1 (1:) N-acetylneuraminate lyase {Escherichia coli}
NLRGVMAALLTPFDQQQALDKASLRRLVQFNIQQGIDGLYVGGSTGEAFVQSLSEREQVLEIVAE
EGKGKIKLIAHVGCVTTAESQQLAASAKRYGFDAVSAVTPFYYPFSFEEHCDHYRAIIDSADGLP
MVVYNIPALSGVKLTLDQINTLVTLPGVGALKQTSGDLYQMEQIRREHPDLVLYNGYDEIFASGL
LAGADGGIGSTYNIMGWRYQGIVKALKEGDIQTAQKLQTECNKVIDLLIKTGVFRGLKTVLHYMD
VVSVPLCRKPFGPVDEKYQPELKALAQQLMQ
>d1f74a_ c.1.10.1 (A:) N-acetylneuraminate lyase {Haemophilus influenzae}
MRDLKGIFSALLVSFNEDGTINEKGLRQIIRHNIDKMKVDGLYVGGSTGENFMLSTEEKKEIFRI
AKDEAKDQIALIAQVGSVNLKEAVELGKYATELGYDCLSAVTPFYYKFSFPEIKHYYDTIIAETG
SNMIVYSIPFLTGVNMGIEQFGELYKNPKVLGVKFTAGDFYLLERLKKAYPNHLIWAGFDEMMLP
AASLGVDGAIGSTFNVNGVRARQIFELTKAGKLKEALEIQHVTNDLIEGILANGLYLTIKELLKL
EGVDAGYCREPMTSKATAEQVAKAKDLKAKFLS
>d1dhpa_ c.1.10.1 (A:) Dihydrodipicolinate synthase {Escherichia coli}
MFTGSIVAIVTPMDEKGNVCRASLKKLIDYHVASGTSAIVSVGTTGESATLNHDEHADVVMMTLD
LADGRIPVIAGTGANATAEAISLTQRFNDSGIVGCLTVTPYYNRPSQEGLYQHFKAIAEHTDLPQ
ILYNVPSRTGCDLLPETVGRLAKVKNIIGIKEATGNLTRVNQIKELVSDDFVLLSGDDASALDFM
QLGGHGVISVTANVAARDMAQMCKLAAEGHFAEARVINQRLMPLHNKLFVEPNPIPVKWACKELG
LVATDTLRLPMTPITDSGRETVRAALKHAGLL
>d1qo5b_ c.1.10.1 (B:) Fructose-1,6-bisphosphate aldolase {Human (Homo sapiens), liver isozyme}
AHRFPALTQEQKKELSEIAQSIVANGKGILAADESVGTMGNRLQRIKVENTEENRRQFREILFSV
DSSINQSIGGVILFHETLYQKDSQGKLFRNILKEKGIVVGIKLDQGGAPLAGTNKETTIQGLDGL
SERCAQYKKDGVDFGKWRAVLRIADQCPSSLAIQENANALARYASICQQNGLVPIVEPEVIPDGD
HDLEHCQYVTEKVLAAVYKALNDHHVYLEGTLLKPNMVTAGHACTKKYTPEQVAMATVTALHRTV
PAAVPGICFLSGGMSEEDATLNLNAINLCPLPKPWKLSFSYGRALQASALAAWGGKAANKEATQE
AFMKRAMANCQAAKGQYVHTGSS
>d1adoa_ c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Rabbit (Oryctolagus cuniculus), muscle isozyme}
PHSHPALTPEQKKELSDIAHRIVAPGKGILAADESTGSIAKRLQSIGTENTEENRRFYRQLLLTA
DDRVNPCIGGVILFHETLYQKADDGRPFPQVIKSKGGVVGIKVDKGVVPLAGTNGETTTQGLDGL
SERCAQYKKDGADFAKWRCVLKIGEHTPSALAIMENANVLARYASICQQNGIVPIVEPEILPDGD
HDLKRCQYVTEKVLAAVYKALSDHHIYLEGTLLKPNMVTPGHACTQKYSHEEIAMATVTALRRTV
PPAVTGVTFLSGGQSEEEASINLNAINKCPLLKPWALTFSYGRALQASALKAWGGKKENLKAAQE
EYVKRALANSLACQGKYTSSGQAGAAASESLFISNHAY
>d1fdja_ c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Rabbit (Oryctolagus cuniculus), liver isozyme}
AHRFPALTPEQKKELSDIAQRIVANGKGILAADESVGTMGNRLQRIKVENSEENRRQFREILFTV
DNSINQSIGGVILFHETLYQKDSQGKLFRNILKEKGIVVGIKLDQGGAPLAGTNKETTIQGLDGL
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SERCAQYKKDGVDFGKWRAVLRIADQCPSSLAIQENANTLARYASICQQNGLVPIVEPEVIPDGD
HDLEHCQYVTEKVLAAVYKALNDHHVYLEGTLLKPNMVTAGHACTKKYTPEQVAMATVTALHRTV
PAAVPGICFLSGGMSEEDATLNLNAINLCPLPKPWKLSFSYGRALQASALAAWGGKAENKKATQE
AFMKRAVVNCQAAKGQYVHTGSSGAASTQSLFTASYTY
>d1fbaa_ c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Drosophila melanogaster}
TTYFNYPSKELQDELREIAQKIVAPGKGILAADESGPTMGKRLQDIGVENTEDNRRAYRQLLFST
DPKLAENISGVILFHETLYQKADDGTPFAEILKKKGIILGIKVDKGVVPLFGSEDEVTTQGLDDL
AARCAQYKKDGCDFAKWRCVLKIGKNTPSYQSILENANVLARYASICQSQRIVPIVEPEVLPDGD
HDLDRAQKVTETVLAAVYKALSDHHVYLEGTLLKPNMVTAGQSAKKNTPEEIALATVQALRRTVP
AAVTGVTFLSGGQSEEEATVNLSAINNVPLIRPWALTFSYGRALQASVLRAWAGKKENIAAGQNE
LLKRAKANGDAAQGKYVAGSAGAGSGSLFVANHAY
>d1a5ca_ c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Plasmodium falciparum}
LPADVAEELATTAQKLVQAGKGILAADESTQTIKKRFDNIKLENTIENRASYRDLLFGTKGLGKF
ISGAILFEETLFQKNEAGVPMVNLLHNENIIPGIKVDKGLVNIPCTDEEKSTQGLDGLAERCKEY
YKAGARFAKWRTVLVIDTAKGKPTDLSIHETAWGLARYASICQQNRLVPIVEPEILADGPHSIEV
CAVVTQKVLSCVFKALQENGVLLEGALLKPNMVTAGYECTAKTTTQDVGFLTVRTLRRTVPPALP
GVVFLSGGQSEEEASVNLNSINALGPHPWALTFSYGRALQASVLNTWQGKKENVAKAREVLLQRA
EANSLATYGKYKGGAGG
>d1epxa_ c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Trypanosome (Leishmania mexicana)}
MSRVTVLQSQLPAYNRLKTPYESELIATVKKLTTPGKGLLAADESIGSCTKRFQPIGLSNTEEHR
RQYRALMLEAEGFEQYISGVILHDETVGQKASNGQTFPEYLTARGVVPGIKTDMGLCPLLEGAEG
EQMTEGLDGYVKRASAYYKKGCRFCKWRNVYKIQNGTVSESAVRFNAETLARYAILSQMSGLVPI
VEPEVMIDGKHDIDTCQRVSEHVWREVVAALQRHGVIWEGCLLKPNMVVPGAESGKTAAPEQVAH
YTVMTLARTMPAMLPGVMFLSGGLSEVQASEYLNAINNSPLPRPYFLSFSYARALQSSALKAWGG
KESGLAAGRRAFLHRARMNSMAQLGKYKRSDD
>d1f2ja_ c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Trypanosome (Trypanosoma brucei)}
SKRVEVLLTQLPAYNRLKTPYEAELIETAKKMTAPGKGLLAADESTGSCSKRFAGIGLSNTAEHR
RQYRALMLECEGFEQYISGVILHDETVYQKAKTGETFPQYLRRRGVVPGIKTDCGLEPLVEGAKG
EQMTAGLDGYIKRAKKYYAMGCRFCKWRNVYKIQNGTVSEAVVRFNAETLARYAILSQLCGLVPI
VEPEVMIDGTHDIETCQRVSQHVWSEVVSALHRHGVVWEGCLLKPNMVVPGAESGLKGHAEQVAE
YTVKTLARVIPPALPGVTFLSGGLSEVMASEYLNAMNNCPLPRPWKLTFSYARALQSSAIKRWGG
KESGVEAGRRAFMHRAKMNSLAQLGKYNRADD
>d1euaa_ c.1.10.1 (A:) KDPG aldolase {Escherichia coli}
MKNWKTSAESILTTGPVVPVIVVKKLEHAVPMAKALVAGGVRVLEVTLRTECAVDAIRAIAKEVP
EAIVGAGTVLNPQQLAEVTEAGAQFAISPGLTEPLLKAATEGTIPLIPGISTVSELMLGMDYGLK
EFKFFPAEANGGVKALQAIAGPFSQVRFCPTGGISPANYRDYLALKSVLCIGGSWLVPADALEAG
DYDRITKLAREAVEGAKL
>d1qfea_ c.1.10.1 (A:) Type I 3-dehydroquinate dehydratase {Salmonella typhi}
MKTVTVKNLIIGEGMPKIIVSLMGRDINSVKAEALAYREATFDILEWRVDHFMDIASTQSVLTAA

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RVIRDAMPDIPLLFTFRSAKEGGEQTITTQHYLTLNRAAIDSGLVDMIDLELFTGDADVKATVDY
AHAHNVYVVMSNHDFHQTPSAEEMVSRLRKMQALGADIPKIAVMPQSKHDVLTLLTATLEMQQHY
ADRPVITMSMAKEGVISRLAGEVFGSAATFGAVKQASAPGQIAVNDLRSVLMILHNA
>d1i2oa_ c.1.10.1 (A:) Transaldolase {Escherichia coli}
TDKLTSLRQYTTVVADTGDIAAMKLYQPQDATTNPSLILNAAQIPEYRKLIDDAVAWAKQQSNDR
AQQIVDATDKLAVNIGLEILKLVPGRISTAVDARLSYDTEASIAKAKRLIKLYNDAGISNDRILI
KLASTWQGIRAAEQLEKEGINCNLTLLFSFAQARACAEAGVFLISPFVGRILDWYKANTDKKEYA
PAEDPGVVSVSEIYQYYKEHGYETVVMGASFRNIGEILELAGCDRLTIAPALLKELAESEGAIER
KLSYTGEVKARPARITESEFLWQHNQDPMAVDKLAEGIRKFAIDQEKLEKMIGDLL
>d1f05a_ c.1.10.1 (A:) Transaldolase {Human (Homo sapiens)}
MESALDQLKQFTTVVADTGDFHAIDEYKPQDATTNPSLILAAAQMPAYQELVEEAIAYGRKLGGS
QEDQIKNAIDKLFVLFGAEILKKIPGRVSTEVDARLSFDKDAMVARARRLIELYKEAGISKDRIL
IKLSSTWEGIQAGKELEEQHGIHCNMTLLFSFAQAVACAEAGVTLISPFVGRILDWHVANTDKKS
YEPLEDPGVKSVTKIYNYYKKFSYKTIVMGASFRNTGEIKALAGCDFLTISPKLLGELLQDNAKL
VPVLSAKAAQASDLEKIHLDEKSFRWLHNEDQMAVEKLSDGIRKFAADAVKLERMLTERMFN
>d1dosa_ c.1.10.2 (A:) Fructose-bisphosphate aldolase {Escherichia
coli}
SKIFDFVKPGVITGDDVQKVFQVAKENNFALPAVNCVGTDSINAVLETAAKVKAPVIVQFSNGGA
SFIAGKGVKSDVPQGAAILGAISGAHHVHQMAEHYGVPVILHTDHCAKKLLPWIDGLLDAGEKHF
AATGKPLFSSHMIDLSEESLQENIEICSKYLERMSKIGMTLEIELGCTGGEEDGVDNSHMDASAL
YTQPEDVDYAYTELSKISPRFTIAASFGNVHGVYKAGNVVLTPTILRDSQEYVSKKHNLPHNSLN
FVFHGGSGSTAQEIKDSVSYGVVKMNIDTDTQWATWEGVLNYYKANEAYLQGQLGNPKGEDQPNK
KYYDPRVWLRAGQTSMIARLEKAFQELNAIDVL
>d1h7na_ c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD
(porphobilinogen synthase) {Baker's yeast (Saccharomyces
cerevisiae)}
MHTAEFLETEPTEISSVLAGGYNHPLLRQWQSERQLTKNMLIFPLFISDNPDDFTEIDSLPNINR
IGVNRLKDYLKPLVAKGLRSVILFGVPLIPGTKDPVGTAADDPAGPVIQGIKFIREYFPELYIIC
DVCLCEYTSHGHCGVLYDDGTINRERSVSRLAAVAVNYAKAGAHCVAPSDMIDGRIRDIKRGLIN
ANLAHKTFVLSYAAKFSGNLYGPFRDAACSAPSNGDRKCYQLPPAGRGLARRALERDMSEGADGI
IVKPSTFYLDIMRDASEICKDLPICAYHVSGEYAMLHAAAEKGVVDLKTIAFESHQGFLRAGARL
IITYLAPEFLDWLDE
>d1e51a_ c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD
(porphobilinogen synthase) {Human (Homo sapiens)}
MQPQSVLHSGYFHPLLRAWQTATTTLNASNLIYPIFVTDVPDDIQPITSLPGVARYGVKRLEEML
RPLVEEGLRCVLIFGVPSRVPKDERGSAADSEESPAIEAIHLLRKTFPNLLVACDVCLCPYTSHG
HCGLLSENGAFRAEESRQRLAEVALAYAKAGCQVVAPSDMMDGRVEAIKEALMAHGLGNRVSVMS
YSAKFASCFYGPFRDAAKSSPAFGDRRCYQLPPGARGLALRAVDRDVREGADMLMVKPGMPYLDI
VREVKDKHPDLPLAVYHVSGEFAMLWHGAQAGAFDLKAAVLEAMTAFRRAGADIIITYYTPQLLQ
WLK
>d1b4ka_ c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD
(porphobilinogen synthase) {Pseudomonas aeruginosa}
YPYTRLRRNRRDDFSRRLVRENVLTVDDLILPVFVLDGVNQRESIPSMPGVERLSIDQLLIEAEE
WVALGIPALALFPVTPVEKKSLDAAEAYNPEGIAQRATRALRERFPELGIITDVALDPFTTHGQD
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GILDDDGYVLNDVSIDVLVRQALSHAEAGAQVVAPSDMMDGRIGAIREALESAGHTNVRIMAYSA
KYASAYYGPFRDAVGSASNLGKGNKATYQMDPANSDEALHEVAADLAEGADMVMVKPGMPYLDIV
RRVKDEFRAPTFVYQVSGEYAMHMGAIQNGWLAESVILESLTAFKRAGADGILTYFAKQAAEQLR
R
>d1b4ea_ c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD
(porphobilinogen synthase) {Escherichia coli}
TDLSQRPRRLRKSPALRAMFEETTLSLNDLVLPIFVEEEIDDYKAVEAMPGVMRIPEKHLAREIE
RIANAGIRSVMTFGISHHTDETGSDAWREDGLVARMSRICKQTVPEMIVMSDTCFCEYTSHGHCG
VLKEHGVDNDATLENLGKQAVVAAAAGADFIAPSAAMDGQVQAIRQALDAAGFKDTAIMSYSTKF
ASSFYGPFREAAGSALKGDRKSYQMNPMNRREAIRESLLDEAQGADCLMVKPAGAYLDIVRELRE
RTELPIGAYQVSGEYAMIKFAALAGAIDEEKVVLESLGSIKRAGADLIFSYFALDLAEKKILR
>d1gg1a_ c.1.10.4 (A:) 3-deoxy-D-arabino-heptulosonate-7-phosphate
synthase (DAHP synthase, AroG) {Escherichia coli}
DLRIKEIKELLPPVALLEKFPATENAANTVAHARKAIHKILKGNDDRLLVVIGPCSIHDPVAAKE
YATRLLALREELKDELEIVMRVYFEKPRTTVGWKGLINDPHMDNSFQINDGLRIARKLLLDINDS
GLPAAGEFLDMITPQYLADLMSWGAIGARTTESQVHRELASGLSCPVGFKNGTDGTIKVAIDAIN
AAGAPHCFLSVTKWGHSAIVNTSGNGDCHIILRGGKEPNYSAKHVAEVKEGLNKAGLPAQVMIDF
SHANSSKQFKKQMDVCADVCQQIAGGEKAIIGVMVESHLVEGNQSLESGEPLAYGKSITDACIGW
EDTDALLRQLANAVKARR
>d1d9ea_ c.1.10.4 (A:) 3-deoxy-D-manno-octulosonate 8-phosphate
synthase (KDO8P synthase) {Escherichia coli}
MKQKVVSIGDINVANDLPFVLFGGMNVLESRDLAMRICEHYVTVTQKLGIPYVFKASFDKANRSS
IHSYRGPGLEEGMKIFQELKQTFGVKIITDVHEPSQAQPVADVVDVIQLPAFLARQTDLVEAMAK
TGAVINVKKPQFVSPGQMGNIVDKFKEGGNEKVILCDRGANFGYDNLVVDMLGFSIMKKVSGNSP
VIFDVTHALQCRDPFGAASGGRRAQVAELARAGMAVGLAGLFIEAHPDPEHAKCDGPSALPLAKL
EPFLKQMKAIDDLVKGFEELDTSK
>d1jcxa_ c.1.10.4 (A:) 3-deoxy-D-manno-octulosonate 8-phosphate
synthase (KDO8P synthase) {Aquifex aeolicus}
EKFLVIAGPCAIESEELLLKVGEEIKRLSEKFKEVEFVFKSSFDKANRSSIHSFRGHGLEYGVKA
LRKVKEEFGLKITTDIHESWQAEPVAEVADIIQIPAFLCRQTDLLLAAAKTGRAVNVKKGQFLAP
WDTKNVVEKLKFGGAKEIYLTERGTTFGYNNLVVDFRSLPIMKQWAKVIYDATHSVQLPGGLGDK
SGGMREFIFPLIRAAVAVGCDGVFMETHPEPEKALSDASTQLPLSQLEGIIEAILEIREVASKYY
ETI
>d1onea1 c.1.11.1 (A:142-436) Enolase {Baker's yeast (Saccharomyces
cerevisiae)}
SPYVLPVPFLNVLNGGSHAGGALALQEFMIAPTGAKTFAEALRIGSEVYHNLKSLTKKRYGASAG
NVGDEGGVAPNIQTAEEALDLIVDAIKAAGHDGKVKIGLDCASSEFFKDGKYDLDFKNPNSDKSK
WLTGPQLADLYHSLMKRYPIVSIEDPFAEDDWEAWSHFFKTAGIQIVADDLTVTNPKRIATAIEK
KAADALLLKVNQIGTLSESIKAAQDSFAAGWGVMVSHRSGETEDTFIADLVVGLRTGQIKTGAPA
RSERLAKLNQLLRIEEELGDNAVFAGENFHHGDKL
>d1pdz_1 c.1.11.1 (140-433) Enolase {Lobster (Homarus vulgaris)}
DEVILPVPAFNVINGGSHAGNKLAMQEFMILPTGATSFTEAMRMGTEVYHHLKAVIKARFGLDAT
AVGDEGGFAPNILNNKDALDLIQEAIKKAGYTGKIEIGMDVAASEFYKQNNIYDLDFKTANNDGS
QKISGDQLRDMYMEFCKDFPIVSIEDPFDQDDWETWSKMTSGTTIQIVGDDLTVTNPKRITTAVE
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KKACKCLLLKVNQIGSVTESIDAHLLAKKNGWGTMVSHRSGETEDCFIADLVVGLCTGQIKTGAP
CRSERLAKYNQILRIEEELGSGAKFAGKNFRAPS
>d1e9ia1 c.1.11.1 (A:140-430) Enolase {Escherichia coli}
PGKYSMPVPMMNIINGGEHADNNVDIQEFMIQPVGAKTVKEAIRMGSEVFHHLAKVLKAKGMNTA
VGDEGGYAPNLGSNAEALAVIAEAVKAAGYELGKDITLAMDCAASEFYKDGKYVLAGEGNKAFTS
EEFTHFLEELTKQYPIVSIEDGLDESDWDGFAYQTKVLGDKIQLVGDDLFVTNTKILKEGIEKGI
ANSILIKFNQIGSLTETLAAIKMAKDAGYTAVISHRSGETEDATIADLAVGTAAGQIKTGSMSRS
DRVAKYNQLIRIEEALGEKAPYNGRKEIKGQ
>d1bqg_1 c.1.11.2 (144-422) D-glucarate dehydratase {Pseudomonas
putida}
EGQQRDAVEMLGYLFYVGDRNKTDLGYRSEHEADNEWFRLRNKEALTPESVVALAEAAYDRYGFK
DFKLKGGVLRGEDEIAAVTALSERFPDARITLDPNGAWSLKEAVALCRDQHHVLAYAEDPCGAEN
GYSGREVMAEFRRSTGLRTATNMIATDWRQMGHAIQLQSVDIPLADPHFWTMQGSVRVAQMCNEW
GLTWGSHSNNHFDISLAMFTHVAAAAPGNITAIDTHWIWQDGQRLTKEPLQIKGGLVEVPKKPGL
GVELDWDALMKAHEVYKSM
>d1ec7a1 c.1.11.2 (A:138-446) D-glucarate dehydratase {Escherichia
coli}
DGQQRSEVEMLGYLFFVGNRKATPLPYQSQPDDSCDWYRLRHEEAMTPDAVVRLAEAAYEKYGFN
DFKLKGGVLAGEEEAESIVALAQRFPQARITLDPNGAWSLNEAIKIGKYLKGSLAYAEDPCGAEQ
GFSGREVMAEFRRATGLPTATNMIATDWRQMGHTLSLQSVDIPLADPHFWTMQGSVRVAQMCHEF
GLTWGSHSNNHFDISLAMFTHVAAAAPGKITAIDTHWIWQEGNQRLTKEPFEIKGGLVQVPEKPG
LGVEIDMDQVMKAHELYQKHGLGARDDAMGMQYLIPGWTFDNKRPCMVR
>d1fhua1 c.1.11.2 (A:100-320) O-succinylbenzoate synthase
{Escherichia coli}
QAANYRAAPLCNGDPDDLILKLADMPGEKVAKVKVGLYEAVRDGMVVNLLLEAIPDLHLRLDANR
AWTPLKGQQFAKYVNPDYRDRIAFLEEPCKTRDDSRAFARETGIAIAWDESLREPDFAFVAEEGV
RAVVIKPTLTGSLEKVREQVQAAHALGLTAVISSSIESSLGLTQLARIAAWLTPDTIPGLDTLDL
MQAQQVRRWPGSTLPVVEVDALERLL
>d1muca1 c.1.11.2 (A:131-372) Muconate-lactonizing enzyme
{Pseudomonas putida}
RVRDSLEVAWTLASGDTARDIAEARHMLEIRRHRVFKLKIGANPVEQDLKHVVTIKRELGDSASV
RVDVNQYWDESQAIRACQVLGDNGIDLIEQPISRINRGGQVRLNQRTPAPIMADESIESVEDAFS
LAADGAASIFALKIAKNGGPRAVLRTAQIAEAAGIGLYGGTMLEGSIGTLASAHAFLTLRQLTWG
TELFGPLLLTEEIVNEPPQYRDFQLHIPRTPGLGLTLDEQRLARFAR
>d2mnr_1 c.1.11.2 (133-359) Mandelate racemase {Pseudomonas putida}
PVQAYDSHSLDGVKLATERAVTAAELGFRAVKTKIGYPALDQDLAVVRSIRQAVGDDFGIMVDYN
QSLDVPAAIKRSQALQQEGVTWIEEPTLQHDYEGHQRIQSKLNVPVQMGENWLGPEEMFKALSIG
ACRLAMPDAMKIGGVTGWIRASALAQQFGIPMSSHLFQEISAHLLAATPTAHWLERLDLAGSVIE
PTLTFEGGNAVIPDLPGVGIIWREKEIGKYLV
>d2chr_1 c.1.11.2 (127-370) Chlormuconate cycloisomerase
{Alcaligenes eutrophus}
PLRSAIPIAWTLASGDTKRDLDSAVEMIERRRHNRFKVKLGFRSPQDDLIHMEALSNSLGSKAYL
RVDVNQAWDEQVASVYIPELEALGVELIEQPVGRENTQALRRLSDNNRVAIMADESLSTLASAFD
LARDRSVDVFSLKLCNMGGVSATQKIAAVAEASGIASYGGTMLDSTIGTSVALQLYSTVPSLPFG
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CELIGPFVLADTLSHEPLEIRDYELQVPTGVGHGMTLDEDKVRQYARVS
>d1jpdx1 c.1.11.2 (X:114-321) L-Ala-D/L-Glu epimerase {Escherichia coli}
TLPETVITAQTVVIGTPDQMANSASTLWQAGAKLLKVKLDNHLISERMVAIRTAVPDATLIVDAN
ESWRAEGLAARCQLLADLGVAMLEQPLPAQDDAALENFIHPLPICADESCHTRSNLKALKGRYEM
VNIKLDKTGGLTEALALATEARAQGFSLMLGCMLCTSRAISAALPLVPQVSFADLDGPTWLAVDV
EPALQFTTGELHL
>d1jpma1 c.1.11.2 (A:126-359) L-Ala-D/L-Glu epimerase {Bacillus subtilis}
YRDTLETDYTVSVNSPEEMAADAENYLKQGFQTLKIKVGKDDIATDIARIQEIRKRVGSAVKLRL
DANQGWRPKEAVTAIRKMEDAGLGIELVEQPVHKDDLAGLKKVTDATDTPIMADESVFTPRQAFE
VLQTRSADLINIKLMKAGGISGAEKINAMAEACGVECMVGSMIETKLGITAAAHFAASKRNITRF
DFDAPLMLKTDVFNGGITYSGSTISMPGKPGLGIIGAAL
>d1kcza1 c.1.11.2 (A:161-413) beta-Methylaspartase {Clostridium tetanomorphum}
GAEINAVPVFAQSGDDRYDNVDKMIIKEADVLPHALINNVEEKLGLKGEKLLEYVKWLRDRIIKL
RVREDYAPIFHIDVYGTIGAAFDVDIKAMADYIQTLAEAAKPFHLRIEGPMDVEDRQKQMEAMRD
LRAELDGRGVDAELVADEWCNTVEDVKFFTDNKAGHMVQIKTPDLGGVNNIADAIMYCKANGMGA
YCGGTCNETNRSAEVTTNIGMACGARQVLAKPGMGVDEGMMIVKNEMNRVLALVGRRK
>d1kkoa1 c.1.11.2 (A:161-411) beta-Methylaspartase {Citrobacter amalonaticus}
PCVPEAIPLFGQSGDDRYIAVDKMILKGVDVLPHALINNVEEKLGFKGEKLREYVRWLSDRILSL
RSSPRYHPTLHIDVYGTIGLIFDMDPVRCAEYIASLEKEAQGLPLYIEGPVDAGNKPDQIRMLTA
ITKELTRLGSGVKIVADEWCNTYQDIVDFTDAGSCHMVQIKTPDLGGIHNIVDAVLYCNKHGMEA
YQGGTCNETEISARTCVHVALAARPMRMLIKPGMGFDEGLNIVFNEMNRTIALLQT
>d1a49a2 c.1.12.1 (A:12-115,A:218-395) Pyruvate kinase, N-terminal domain {Rabbit (Oryctolagus cuniculus)}
IQTQQLHAAMADTFLEHMCRLDIDSAPITARNTGIICTIGPASRSVETLKEMIKSGMNVARMNFS
HGTHEYHAETIKNVRTATESFASDPILYRPVAVALDTKGXPAVSEKDIQDLKFGVEQDVDMVFAS
FIRKAADVHEVRKILGEKGKNIKIISKIENHEGVRRFDEILEASDGIMVARGDLGIEIPAEKVFL
AQKMIIGRCNRAGKPVICATQMLESMIKKPRPTRAEGSDVANAVLDGADCIMLSGETAKGDYPLE
AVRMQHLIAREAEAAMFHRKLFE
>d1pkla2 c.1.12.1 (A:1-87,A:187-357) Pyruvate kinase, N-terminal domain {Leishmania mexicana}
SQLAHNLTLSIFDPVANYRAARIICTIGPSTQSVEALKGLIQSGMSVARMNFSHGSHEYHQTTIN
NVRQAAAELGVNIAIALDTKGPXPAVSAKDRVDLQFGVEQGVDMIFASFIRSAEQVGDVRKALGP
KGRDIMIICKIENHQGVQNIDSIIEESDGIMVARGDLGVEIPAEKVVVAQKILISKCNVAGKPVI
CATQMLESMTYNPRPTRAEVSDVANAVFNGADCVMLSGETAKGKYPNEVVQYMARICLEAQSAL
>d1a3wa2 c.1.12.1 (A:2-87,A:189-366) Pyruvate kinase, N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
SRLERLTSLNVVAGSDLRRTSIIGTIGPKTNNPETLVALRKAGLNIVRMNFSHGSYEYHKSVIDN
ARKSEELYPGRPLAIALDTKGXPALSEKDKEDLRFGVKNGVHMVFASFIRTANDVLTIREVLGEQ
GKDVKIIVKIENQQGVNNFDEILKVTDGVMVARGDLGIEIPAPEVLAVQKKLIAKSNLAGKPVIC
ATQMLESMTYNPRPTRAEVSDVGNAILDGADCVMLSGETAKGNYPINAVTTMAETAVIAEQAIAY
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LPNYD
>d1e0ta2 c.1.12.1 (A:1-69,A:168-344) Pyruvate kinase, N-terminal
domain {Escherichia coli}
MKKTKIVCTIGPKTESEEMLAKMLDAGMNVMRLNFSHGDYAEHGQRIQNLRNVMSKTGKTAAILL
DTKGXPALAEKDKQDLIFGCEQGVDFVAASFIRKRSDVIEIREHLKAHGGENIHIISKIENQEGL
NNFDEILEASDGIMVARGDLGVEIPVEEVIFAQKMMIEKCIRARKVVITATMMLDSMIKNPRPTD
AEAGDVANAILDGTDAVMLSGESAKGKYPLEAVSIMATICERTDRVMNSRLE
>d1kbla1 c.1.12.2 (A:510-873) Pyruvate phosphate dikinase, C-terminal
domain {Clostridium symbiosum}
IETQEASVSGSFERIMVWADKFRTLKVRTNADTPEDTLNAVKLGAEGIGLCRTEHMFFEADRIMK
IRKMILSDSVEAREEALNELIPFQKGDFKAMYKALEGRPMTVRYLDPPLHEFVPHTEEEQAELAK
NMGLTLAEVKAKVDELHEFNPMMGHRGCRLAVTYPEIAKMQTRAVMEAAIEVKEETGIDIVPEIM
IPLVGEKKELKFVKDVVVEVAEQVKKEKGSDMQYHIGTMIEIPRAALTADAIAEEAEFFSFGTND
LTQMTFGFSRDDAGKFLDSYYKAKIYESDPFARLDQTGVGQLVEMAVKKGRQTRPGLKCGICGEH
GGDPSSVEFCHKVGLNYVSCSPFRVPIARLAAAQAALNN
>d1fiy__ c.1.12.3 (-) Phosphoenolpyruvate carboxylase {Escherichia
coli}
QYSALRSNVSMLGKVLGETIKDALGEHILERVETIRKLSKSSRAGNDANRQELLTTLQNLSNDEL
LPVARAFSQFLNLANTAEQYHSISPKGEAASNPEVIARTLRKLKNQPELSEDTIKKAVESLSLEL
VLTAHPTEITRRTLIHKMVEVNACLKQLDNKDIADYEHNQLMRRLRQLIAQSWHTDEIRKLRPSP
VDEAKWGFAVVENSLWQGVPNYLRELNEQLEENLGYKLPVEFVPVRFTSWMGGDRDGNPNVTADI
TRHVLLLSRWKATDLFLKDIQVLVSELSMVEATPELLALVGEEGAAEPYRYLMKNLRSRLMATQA
WLEARLKGEELPKPEGLLTQNEELWEPLYACYQSLQACGMGIIANGDLLDTLRRVKCFGVPLVRI
DIRQESTRHTEALGELTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWQPSAETREVLDTC
QVIAEAPQGSIAAYVISMAKTPSDVLAVHLLLKEAGIGFAMPVAPLFETLDDLNNANDVMTQLLN
IDWYRGLIQGKQMVMIGYSDSAKDAGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRG
GAPAHAALLSQPPGSLKGGLRVTEQGEMIRFKYGLPEITVSSLSLYTGAILEANLLPPPEPKESW
RRIMDELSVISCDVYRGYVRENKDFVPYFRSATPEQELGKLPLGSRPAKRRPTGGVESLRAIPWI
FAWTQNRLMLPAWLGAGTALQKVVEDGKQSELEAMCRDWPFFSTRLGMLEMVFAKADLWLAEYYD
QRLVDKALWPLGKELRNLQEEDIKVVLAIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAELLH
RSRQAEKEGQEPDPRVEQALMVTIAGIAAGMRNTG
>d1pyma_ c.1.12.4 (A:) Phosphoenolpyruvate mutase {Blue mussel
(Mytilus edulis)}
VKKTTQLKQMLNSKDLEFIMEAHNGLSARIVQEAGFKGIWGSGLSVSAQLGVRDSNEASWTQVVE
VLEFMSDASDVPILLDADTGYGNFNNARRLVRKLEDRGVAGACLEDKLFPKTNSLHDGRAQPLAD
IEEFALKIKACKDSQTDPDFCIVARVEAFIAGWGLDEALKRAEAYRNAGADAILMHSKKADPSDI
EAFMKAWNNQGPVVIVPTKYYKTPTDHFRDMGVSMVIWANHNLRASVSAIQQTTKQIYDDQSLVN
VEDKIVSVKEIFRLQRDDELVQAEDKYLPKN
>d1dxea_ c.1.12.5 (A:) 2-dehydro-3-deoxy-galactarate aldolase
{Escherichia coli}
DVFPNKFKAALAAKQVQIGCWSALSNPISTEVLGLAGFDWLVLDGEHAPNDISTFIPQLMALKGS
ASAPVVRVPTNEPVIIKRLLDIGFYNFLIPFVETKEEAELAVASTRYPPEGIRGVSVSHRANMFG
TVADYFAQSNKNITILVQIESQQGVDNVDAIAATEGVDGIFVGPSDLAAALGHLGNASHPDVQKA
IQHIFNRASAHGKPSGILAPVEADARRYLEWGATFVAVGSDLGVFRSATQKLADTFKK
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>d1dqua_ c.1.12.6 (A:) Isocitrate lyase {Aspergillus nidulans}
SYIEEEDQRYWDEVAAVKNWWKDSRWRYTKRPFTAEQIVAKRGNLKIEYPSNVQAKKLWGILERN
FKNKEASFTYGCLDPTMVTQMAKYLDTVYVSGWQSSSTASSTDEPSPDLADYPMNTVPNKVNHLW
MAQLFHDRKQREERMTTPKDQRHKVANVDYLRPIIADADTGHGGLTAVMKLTKLFVERGAAGIHI
EDQAPGTKKCGHMAGKVLVPISEHINRLVAIRAQADIMGTDLLAIARTDSEAATLITSTIDHRDH
PFIIGSTNPDIQPLNDLMVMAEQAGKNGAELQAIEDEWLAKAGLKLFNDAVVDAINNSPLPNKKA
AIEKYLTQSKGKSNLEARAIAKEIAGTDIYFDWEAPRTREGYYRYQGGTQCAINRAVAYAPFADL
IWMESKLPDYKQAKEFADGVHAVWPEQKLAYNLSPSFNWKKAMPRDEQETYIKRLGALGYAWQFI
TLAGLHTTALISDTFAKAYAKQGMRAYGELVQEPEMANGVDVVTHQKWSGANYVDNMLKMITGG
>d1f8ma_ c.1.12.6 (A:) Isocitrate lyase {Mycobacterium tuberculosis}
ASVVGTPKSAEQIQQEWDTNPRWKDVTRTYSAEDVVALQGSVVEEHTLARRGAEVLWEQLHDLEW
VNALGALTGNMAVQQVRAGLKAIYLSGWQVAGDANLSGHTYPDQSLYPANSVPQVVRRINNALQR
ADQIAKIEGDTSVENWLAPIVADGEAGFGGALNVYELQKALIAAGVAGSHWEDQLASEKKCGHLG
GKVLIPTQQHIRTLTSARLAADVADVPTVVIARTDAEAATLITSDVDERDQPFITGERTREGFYR
TKNGIEPCIARAKAYAPFADLIWMETGTPDLEAARQFSEAVKAEYPDQMLAYNCSPSFNWKKHLD
DATIAKFQKELAAMGFKFQFITLAGFHALNYSMFDLAYGYAQNQMSAYVELQEREFAAEERGYTA
TKHQREVGAGYFDRIATTVDPNSSTTALTGSTEEGQF
>d1igwa_ c.1.12.6 (A:) Isocitrate lyase {Escherichia coli}
KTRTQQIEELQKEWTQPRWEGITRPYSAEDVVKLRGSVNPECTLAQLGAAKMWRLLHGESKKGYI
NSLGALTGGQALQQAKAGIEAVYLSGWQVAADANLAASMYPDQSLYPANSVPAVVERINNTFRRA
DQIQWSAGIEPGDPRYVDYFLPIVADAEAGFGGVLNAFELMKAMIEAGAAAVHFEDQLASVKKCG
HMGGKVLVPTQEAIQKLVAARLCADVTGVPTLLVARTDADAADLITSDCDPYDSEFITGERTSEG
FFRTHAGIEQAISRGLAYAPYADLVWCETSTPDLELARRFAQAIHAKYPGKLLAYNCSPSFNWQK
NLDDKTIASFQQQLSDMGYKFQFITLAGIHSMWFNMFDLANAYAQGEGMKHYVEKVQQPEFAAAK
DGYTFVSHQQEVGTGYFDKVTTIIQG
>d1d8ca_ c.1.13.1 (A:) Malate synthase G {Escherichia coli}
QTITQSRLRIDANFKRFVDEEVLPGTGLDAAAFWRNFDEIVHDLAPENRQLLAERDRIQAALDEW
HRSNPGPVKDKAAYKSFLRELGYLVPQPERVTVETTGIDSEITSQAGPQLVVPAMNARYALNAAN
ARWGSLYDALYGSDIIPQEGAMVSGYDPQRGEQVIAWVRRFLDESLPLENGSYQDVVAFKVVDKQ
LRIQLKNGKETTLRTPAQFVGYRGDAAAPTCILLKNNGLHIELQIDANGRIGKDDPAHINDVIVE
AAISTILDCEDSVAAVDAEDKILLYRNLLGLMQGTLQEKMEKNGRQIVRKLNDDRHYTAADGSEI
SLHGRSLLFIRNVGHLMTIPVIWDSEGNEIPEGILDGVMTGAIALYDLKVQKNSRTGSVYIVKPK
MHGPQEVAFANKLFTRIETMLGMAPNTLKMGIMDEERRTSLNLRSCIAQARNRVAFINTGFLDRT
GDEMHSVMEAGPMLRKNQMKSTPWIKAYERNNVLSGLFCGLRGKAQIGKGMWAMPDLMADMYSQK
GDQLRAGANTAWVPSPTAATLHALHYHQTNVQSVQANIAQTEFNAEFEPLLDDLLTIPVAENANW
SAQEIQQELDNNVQGILGYVVRWVEQGIGCSKVPDIHNVALMEDRATLRISSQHIANWLRHGILT
KEQVQASLENMAKVVDQQNAGDPAYRPMAGNFANSCAFKAASDLIFLGVKQPNGYTEPLLHAWRL
REKES
>d3rubl1 c.1.14.1 (L:148-467) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Tobacco (Nicotiana tabacum), variant turkish samsun}
FQGPPHGIQVERDKLNKYGRPLLGCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFM
RWRDRFLFCAEALYKAQAETGEIKGHYLNATAGTCEEMIKRAVFARELGVPIVMHDYLTGGFTAN
TSLAHYCRDNGLLLHIHRAMHAVIDRQKNHGIHFRVLAKALRMSGGDHIHSGTVVGKLEGERDIT
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LGFVDLLRDDFVEQDRSRGIYFTQDWVSLPGVLPVASGGIHVWHMPALTEIFGDDSVLQFGGMTL
GHPWGNAPGAVANRVALEACVKARNEGRDLAQEGNEIIREACKWSPELAAACEVWKEIVF
>d1bura1 c.1.14.1 (A:148-475) Ribulose 1,5-bisphosphate
carboxylase-oxygenase {Spinach (Spinacia oleracea)}
FQGPPHGIQVERDKLNKYGRPLLGCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFM
RWRDRFLFCAEALYKAQAETGEIKGHYLNATAGTCEDMMKRAVFARELGVPIVMHDYLTGGFTAN
TTLSHYCRDNGLLLHIHRAMHAVIDRQKNHGMHFRVLAKALRLSGGDHIHSGTVVGKLEGERDIT
LGFVDLLRDDYTEKDRSRGIYFTQSWVSTPGVLPVASGGIHVWHMPALTEIFGDDSVLQFGGGTL
GHPWGNAPGAVANRVALEACVQARNEGRDLAREGNTIIREATKWSPELAAACEVWKEIKFEFPAM
DTV
>d1bwva1 c.1.14.1 (A:150-478) Ribulose 1,5-bisphosphate
carboxylase-oxygenase {Galdieria partita}
GPATGVILERERLDKFGRPLLGCTTKPKLGLSGKNYGRVVYEALKGGLDFVKDDENINSQPFMRW
RERYLFTMEAVNKASAATGEVKGHYLNVTAATMEEMYARANFAKELGSVIIMIDLVIGYTAIQTM
AKWARDNDMILHLHRAGNSTYSRQKNHGMNFRVICKWMRMAGVDHIHAGTVVGKLEGDPIITRGF
YKTLLLPKLERNLQEGLFFDMEWASLRKVMPVASGGIHAGQMHQLIHYLGEDVVLQFGGGTIGHP
DGIQAGATANRVALEAMILARNENRDYLTEGPEILREAAKTCGALRTALDLWKDITFNYTSTDTS
DFV
>d1gk8a1 c.1.14.1 (A:150-475) Ribulose 1,5-bisphosphate
carboxylase-oxygenase {Chlamydomonas reinhardtii}
GPPHGIQVERDKLNKYGRGLLGCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMRW
RDRFLFVAEAIYKAQAETGEVKGHYLNATAGTCEEMMKRAVCAKELGVPIIMHDYLTGGFTANTS
LAIYCRDNGLLLHIHRAMHAVIDRQRNHGIHFRVLAKALRMSGGDHLHSGTVVGKLEGEREVTLG
FVDLMRDDYVEKDRSRGIYFTQDWCSMPGVMPVASGGIHVWHMPALVEIFGDDACLQFGGGTLGH
PWGNAPGAAANRVALEACTQARNEGRDLAREGGDVIRSACKWSPELAAACEVWKEIKFEFDTIDK
L
>d1bxna1 c.1.14.1 (A:151-467) Ribulose 1,5-bisphosphate
carboxylase-oxygenase {Alcaligenes eutrophus}
FAGPSTGIIVERERLDKFGRPLLGATTKPKLGLSGRNYGRVVYEGLKGGLDFMKDDENINSQPFM
HWRDRFLFVMDAVNKASAATGEVKGSYLNVTAGTMEEMYRRAEFAKSLGSVIIMVDLIVGWTCIQ
SMSNWCRQNDMILHLHRAGHGTYTRQKNHGVSFRVIAKWLRLAGVDHMHTGTAVGKLEGDPLTVQ
GYYNVCRDAYTQTDLTRGLFFDQDWASLRKVMPVASGGIHAGQMHQLIHLFGDDVVLQFGGGTIG
HPQGIQAGATANRVALEAMVLARNEGRDILNEGPEILRDAARWCGPLRAALDTWGDI
>d1rbla1 c.1.14.1 (A:148-475) Ribulose 1,5-bisphosphate
carboxylase-oxygenase {Synechococcus sp., strain pcc 6301}
FQGPPHGIQVERDLLNKYGRPMLGCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENINSQPFQ
RWRDRFLFVADAIHKSQAETGEIKGHYLNVTAPTCEEMMKRAEFAKELGMPIIMHDFLTAGFTAN
TTLAKWCRDNGVLLHIHRAMHAVIDRQRNHGIHFRVLAKCLRLSGGDHLHSGTVVGKLEGDKAST
LGFVDLMREDHIEADRSRGVFFTQDWASMPGVLPVASGGIHVWHMPALVEIFGDDSVLQFGGGTL
GHPWGNAPGATANRVALEACVQARNEGRDLYREGGDILREAGKWSPELAAALDLWKEIKFEFETM
DKL
>d5ruba1 c.1.14.1 (A:138-457) Ribulose 1,5-bisphosphate
carboxylase-oxygenase {Rhodospirillum rubrum}
GPSVNISALWKVLGRPEVDGGLVVGTIIKPKLGLRPKPFAEACHAFWLGGDFIKNDEPQGNQPFA
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PLRDTIALVADAMRRAQDETGEAKLFSANITADDPFEIIARGEYVLETFGENASHVALLVDGYVA
GAAAITTARRRFPDNFLHYHRAGHGAVTSPQSKRGYTAFVHCKMARLQGASGIHTGTMGFGKMEG
ESSDRAIAYMLTQDEAQGPFYRQSWGGMKACTPIISGGMNALRMPGFFENLGNANVILTAGGGAF
GHIDGPVAGARSLRQAWQAWRDGVPVLDYAREHKELARAFESFPGDADQIYPGWRKALGV
>d1geha1    c.1.14.1    (A:137-443)    Ribulose    1,5-bisphosphate
carboxylase-oxygenase {Archaeon Thermococcus kodakaraensis}
DGPAFGIEGVRKMLEIKDRPIYGVVPKPKVGYSPEEFEKLAYDLLSNGADYMKDDENLTSPWYNR
FEERAEIMAKIIDKVENETGEKKTWFANITADLLEMEQRLEVLADLGLKHAMVDVVITGWGALRY
IRDLAADYGLAIHGHRAMHAAFTRNPYHGISMFVLAKLYRLIGIDQLHVGTAGAGKLEGGKWDVI
QNARILRESHYKPDENDVFHLEQKFYSIKAAFPTSSGGLHPGNIQPVIEALGTDIVLQLGGGTLG
HPDGPAAGARAVRQAIDAIMQGIPLDEYAKTHKELARALEKWGHVTP
>d1qtwa_ c.1.15.1 (A:) Endonuclease IV {Escherichia coli}
MKYIGAHVSAAGGLANAAIRAAEIDATAFALFTKNQRQWRAAPLTTQTIDEFKAACEKYHYTSAQ
ILPHDSYLINLGHPVTEALEKSRDAFIDEMQRCEQLGLSLLNFHPGSHLMQISEEDCLARIAESI
NIALDKTQGVTAVIENTAGQGSNLGFKFEHLAAIIDGVEDKSRVGVCIDTCHAFAAGYDLRTPAE
CEKTFADFARTVGFKYLRGMHLNDAKSTFGSRVDRHHSLGEGNIGHDAFRWIMQDDRFDGIPLIL
ETINPDIWAEEIAWLKAQQTEKAVA
>d1d8wa_ c.1.15.2 (A:) L-rhamnose isomerase {Escherichia coli}
TQLEQAWELAKQRFAAVGIDVEEALRQLDRLPVSMHCWQGDDVSGFENPEGSLTGGIQATGNYPG
KARNASELRADLEQAMRLIPGPKRLNLHAIYLESDTPVSRDQIKPEHFKNWVEWAKANQLGLDFN
PSCFSHPLSADGFTLSHADDSIRQFWIDHCKASRRVSAYFGEQLGTPSVMNIWIPDGMKDITVDR
LAPRQRLLAALDEVISEKLNPAHHIDAVESKLFGIGAESYTVGSNEFYMGYATSRQTALCLDAGH
FHPTEVISDKISAAMLYVPQLLLHVSRPVRWDSDHVVLLDDETQAIASEIVRHDLFDRVHIGLDF
FDASINRIAAWVIGTRNMKKALLRALLEPTAELRKLEAPGDYTARLALLEEQKSLPWQAVWEMYC
QRHDTPAGSEWLESVRAYEKEILSRR
>d1dxia_ c.1.15.3 (A:) D-xylose isomerase {Streptomyces murinus}
MSFQPTPEDRFTFGLWTVGWQGRDPFGDATRPALDPVETVQRLAELGAYGVTFHDDDLIPFGSSD
TERESHIKRFRQALDATGMTVPMATTNLFTHPVFKDGGFTANDRDVRRYALRKTIGNIDLAAELG
AKTYVAWGGREGAESGGAKDVRDALDRMKEAFDLLGEYVTAQGYDLRFAIEPKPNEPRGDILLPT
VGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGKLFHIDLNGQSGIKYDQDLRF
GAGDLRAAFWLVDLLETAGYEGPRHFDFKPPRTEDFDGVWASAAGCMRNYLILKDRAAAFRADPE
VQEALRAARLDQLAQPTAADGLDALLADRAAFEDFDVDAAAARGMAFEHLDQLAMDHLLGARG
>d2gyia_    c.1.15.3    (A:)    D-xylose    isomerase    {Streptomyces
olivochromogenes}
YQPTPEDRFTFGLWTVGWQGRDPFGDATRPALDPVETVQRLAELGAHGVTFHDDDLIPFGSSDTE
RESHIKRFRQALDATGMTVPMATTNLFTHPVFKDGGFTANDRDVRRYALRKTIRNIDLAVELGAK
TYVAWGGREGAESGAAKDVRVALDRMKEAFDLLGEYVTSQGYDTRFAIEPKPNEPRGDILLPTVG
HALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGKLFHIDLNGQSGIKYDQDLRFGA
GDLRAAFWLVDLLESAGYEGPRHFDFKPPRTEDIDGVWASAAGCMRNYLILKERAAAFRADPEVQ
EALRASRLDELAQPTAADGVQELLADRTAFEDFDVDAAAARGMAFERLDQLAMDHLLGAR
>d1xis__ c.1.15.3 (-) D-xylose isomerase {Streptomyces rubiginosus}
NYQPTPEDRFTFGLWTVGWQGRDPFGDATRRALDPVESVRRLAELGAHGVTFHDDDLIPFGSSDS
EREEHVKRFRQALDDTGMKVPMATTNLFTHPVFKDGGFTANDRDVRRYALRKTIRNIDLAVELGA
ETYVAWGGREGAESGGAKDVRDALDRMKEAFDLLGEYVTSQGYDIRFAIEPKPNEPRGDILLPTV
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GHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGKLFHIDLNGQNGIKYDQDLRFG
AGDLRAAFWLVDLLESAGYSGPRHFDFKPPRTEDFDGVWASAAGCMRNYLILKERAAAFRADPEV
QEALRASRLDELARPTAADGLQALLDDRSAFEEFDVDAAAARGMAFERLDQLAMDHLLGARG
>d1qt1a_ c.1.15.3 (A:) D-xylose isomerase {Streptomyces diastaticus, M1033}
SYQPTPEDKFTFGLWTVGWQGRDPFGDATRGALDPAESVRRLAELGAHGVTFHDDDLIPFGATDS
ERAEHIKRFRQGLDETGMKVPMATTNLFTHPVFKDGGFTANDRDVRRYALRKTIRNIDLAVELGA
QTYVAWGGREGAESGAAKDVRVALDRMKEAFDLLGEYVTSQGYDTPFAIEPKPNEPRGDILLPTI
GHALAFIDGLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGKLFHIDLNGQSGIKYDQDLRFG
PGDLRAAFWLVDLLESAGYEGPRHFDFKPPRTEDFDGVWASAAGCMRNYLILKERAAAFRADPEV
QEALRAARLDELAQPTAGDGLQALLPDRSAFEDFDPDAAAARGMAFERLDQLAMDHLLGARG
>d4xiaa_ c.1.15.3 (A:) D-xylose isomerase {Arthrobacter, strain b3728}
VQPTPADHFTFGLWTVGWTGADPFGVATRANLDPVEAVHKLAELGAYGITFHDNDLIPFDATAAE
REKILGDFNQALADTGLKVPMVTTNLFSHPVFKDGGFTSNDRSIRRFALAKVLHNIDLAAEMGAE
TFVMWGGREGSEYDGSKDLAAALDRMREGVDTAAGYIKDKGYNLRIALEPKPNEPRGDIFLPTVG
HGLAFIEQLEHGDIVGLNPETGHEQMAGLNFTHGIAQALWAEKLFHIDLNGQRGIKYDQDLVFGH
GDLTSAFFTVDLLENGFPNGGPKYTGPRHFDYKPSRTDGYDGVWDSAKANMSMYLLLKERALAFR
ADPEVQEAMKTSGVFELGETTLNAGESAADLMNDSASFAGFDAEAAAERNFAFIRLNQLAIEHLL
GSR
>d1xima_ c.1.15.3 (A:) D-xylose isomerase {Actinoplanes missouriensis}
VQATREDKFSFGLWTVGWQARDAFGDATRTALDPVEAVHKLAEIGAYGITFHDDDLVPFGSDAQT
RDGIIAGFKKALDETGLIVPMVTTNLFTHPVFKDGGFTSNDRSVRRYAIRKVLRQMDLGAELGAK
TLVLWGGREGAEYDSAKDVSAALDRYREALNLLAQYSEDRGYGLRFAIEPKPNEPRGDILLPTAG
HAIAFVQELERPELFGINPETGHEQMSNLNFTQGIAQALWHKKLFHIDLNGQHGPKFDQDLVFGH
GDLLNAFSLVDLLENGPDGAPAYDGPRHFDYKPSRTEDYDGVWESAKANIRMYLLLKERAKAFRA
DPEVQEALAASKVAELKTPTLNPGEGYAELLADRSAFEDYDADAVGAKGFGFVKLNQLAIEHLLG
AR
>d1a0ca_ c.1.15.3 (A:) D-xylose isomerase {Clostridium thermosulfurogenes, also known as Thermoanaerobacter thermosulfurigenes}
NKYFENVSKIKYEGPKSNNPYSFKFYNPEEVIDGKTMEEHLRFSIAYWHTFTADGTDQFGKATMQ
RPWNHYTDPMDIAKARVEAAFEFFDKINAPYFCFHDRDIAPEGDTLRETNKNLDTIVAMIKDYLK
TSKTKVLWGTANLFSNPRFVHGASTSCNADVFAYSAAQVKKALEITKELGGENYVFWGGREGYET
LLNTDMEFELDNFARFLHMAVDYAKEIGFEGQFLIEPKPKEPTKHQYDFDVANVLAFLRKYDLDK
YFKVNIEANHATLAFHDFQHELRYARINGVLGSIDANTGDMLLGWDTDQFPTDIRMTTLAMYEVI
KMGGFDKGGLNFDAKVRRASFEPEDLFLGHIAGMDAFAKGFKVAYKLVKDRVFDKFIEERYASYK
DGIGADIVSGKADFRSLEKYALERSQIVNKSGRQELLESILNQYLFA
>d1a0da_ c.1.15.3 (A:) D-xylose isomerase {Bacillus stearothermophilus}
PYFDNISTIAYEGPASKNPLAFKFYNPEEKVGDKTMEEHLRFSVAYWHTFTGDGSDPFGAGNMIR
PWNKYSGMDLAKARVEAAFEFFEKLNIPFFCFHDVDIAPEGETLKETYKNLDIIVDMIEEYMKTS
KTKLLWNTANLFTHPRFVHGAATSCNADVFAYAAAKVKKGLEIAKRLGAENYVFWGGREGYETLL
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NTDMKLELDNLARFLHMAVDYAKEIGFDGQFLIEPKPKEPTKHQYDFDVATALAFLQTYGLKDYF
KFNIEANHATLAGHTFEHELRVARIHGMLGSVDANQGDMLLGWDTDEFPTDLYSTTLAMYEILKN
GGLGRGGLNFDAKVRRGSFEPEDLFYAHIAGMDSFAVGLKVAHRLIEDRVFDEFIEERYKSYTEG
IGREIVEGTADFHKLEAHALQLGEIQNQSGRQERLKTLLNQYLLEVC
>d1a0ea_ c.1.15.3 (A:) D-xylose isomerase {Thermotoga neapolitana}
AEFFPEIPKVQFEGKESTNPLAFKFYDPEEIIDGKPLKDHLKFSVAFWHTFVNEGRDPFGDPTAD
RPWNRYTDPMDKAFARVDALFEFCEKLNIEYFCFHDRDIAPEGKTLRETNKILDKVVERIKERMK
DSNVKLLWGTANLFSHPRYMHGAATTCSADVFAYAAAQVKKALEITKELGGEGYVFWGGREGYET
LLNTDLGFELENLARFLRMAVDYAKRIGFTGQFLIEPKPKEPTKHQYDFDVATAYAFLKSHGLDE
YFKFNIEANHATLAGHTFQHELRMARILGKLGSIDANQGDLLLGWDTDQFPTNVYDTTLAMYEVI
KAGGFTKGGLNFDAKVRRASYKVEDLFIGHIAGMDTFALGFKVAYKLVKDGVLDKFIEEKYRSFR
EGIGRDIVEGKVDFEKLEEYIIDKETIELPSGKQEYLESLINSYIVKTILELR
>d1bxca_ c.1.15.3 (A:) D-xylose isomerase {Thermus aquaticus, subsp.
Caldophilus}
MYEPKPEHRFTFGLWTVGNVGRDPFGDAVRERLDPVYVGHKLAELGVHGVNLHDEDLIPRGTPPQ
ERDQIVRRFKRALDETGLKVPMVTGNLFSDPGFKDGGFTSRDPWVRAYAFRKSLETMDLGAELGA
EIYVVWPGREGAEVEATGKARKVWDWVREPLNFMAAYAEDQGYGYRFALEPKPNEPRGDIYFATV
GSMLALIHTLERPERFGLNPEFAHETMAGLNFVHAVAQALDAGKLLHIDLNGQRMNRFDQDLRFG
SENLKAAFLLVDLLESSGYQGPRHFDAHALRTEDEEGVWAFARGCMRTYLILKERAEAFREDPEV
KELLAAYYQEDPAALPLMDPYSHEKAEALKRAELPLEAKRHRGYALERLDQLAVEYLLGVRG
>d1bxba_ c.1.15.3 (A:) D-xylose isomerase {Thermus aquaticus, subsp.
Thermophilus}
MYEPKPEHRFTFGLWTVGNVGRDPFGDAVRERLDPVYVVHKLAELGAYGVNLHDEDLIPRGTPPQ
ERDQIVRRFKKALDETGLKVPMVTANLFSDPAFKDGAFTSPDPWVRAYALRKSLETMDLGAELGA
EIYVVWPGREGAEVEATGKARKVWDWVREALNFMAAYAEDQGYGYRFALEPKPNEPRGDIYFATV
GSMLAFIHTLDRPERFGLNPEFAHETMAGLNFVHAVAQALDAGKLFHIDLNDQRMSRFDQDLRFG
SENLKAAFFLVDLLESSGYQGPRHFDAHALRTEDEEGVWAFARGCMRTYLILKERAEAFREDPEV
KELLAAYYQEDPAALALLGPYSREKAEALKRAELPLEAKRRRGYALERLDQLAVEYLLGVRG
>d1luca_ c.1.16.1 (A:) Bacterial luciferase (alkanal monooxygenase)
{Vibrio harveyi}
MKFGNFLLTYQPPELSQTEVMKRLVNLGKASEGCGFDTVWLLEHHFTEFGLLGNPYVAAAHLLGA
TETLNVGTAAIVLPTAHPVRQAEDVNLLDQMSKGRFRFGICRGLYDKDFRVFGTDMDNSRALMDC
WYDLMKEGFNEGYIAADNEHIKFPKIQLNPSAYTQGGAPVYVVAESASTTEWAAERGLPMILSWI
INTHEKKAQLDLYNEVATEHGYDVTKIDHCLSYITSVDHDSNRAKDICRNFLGHWYDSYVNATKI
FDDSDQTKGYDFNKGQWRDFVLKGHKDTNRRIDYSYEINPVGTPEECIAIIQQDIDATGIDNICC
GFEANGSEEEIIASMKLFQSDVMPYLKEKQ
>d1lucb_ c.1.16.1 (B:) Bacterial luciferase (alkanal monooxygenase)
{Vibrio harveyi}
MKFGLFFLNFMNSKRSSDQVIEEMLDTAHYVDQLKFDTLAVYENHFSNNGVVGAPLTVAGFLLGM
TKNAKVASLNHVITTHHPVRVAEEACLLDQMSEGRFAFGFSDCEKSADMRFFNRPTDSQFQLFSE
CHKIINDAFTTGYCHPNNDFYSFPKISVNPHAFTEGGPAQFVNATSKEVVEWAAKLGLPLVFRWD
DSNAQRKEYAGLYHEVAQAHGVDVSQVRHKLTLLVNQNVDGEAARAEARVYLEEFVRESYSNTDF
EQKMGELLSENAIGTYEESTQAARVAIECCGAADLLMSFESMEDKAQQRAVIDVVNANIV
>d1nfp__ c.1.16.2 (-) Non-fluorescent flavoprotein (luxF, FP390)
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{Photobacterium leiognathi}
MTKWNYGVFFLNFYHVGQQEPSLTMSNALETLRIIDEDTSIYDVVAFSEHHIDKSYNDETKLAPF
VSLGKQIHVLATSPETVVKAAKYGMPLLFKWDDSQQKRIELLNHYQAAAAKFNVDIANVRHRLML
FVNVNDNPTQAKAELSIYLEDYLSYTQAETSIDEIINSNAAGNFDTCLHHVAEMAQGLNNKVDFL
FCFESMKDQENKKSLMINFDKRVINYRKEHNLN
>d1fvpa_ c.1.16.2 (A:) Non-fluorescent flavoprotein (luxF, FP390)
{Photobacterium phosphoreum}
MNKWNYGVFFVNFYNKGQQEPSKTMNNALETLRIIDEDTSIYDVINIDDHYLVKKDSEDKKLAPF
ITLGEKLYVLATSENTVDIAAKYALPLVFKWDDINEERLKLLSFYNASASKYNKNIDLVRHQLML
HVNVNEAETVAKEELKLYIENYVACTQPSNFNGSIDSIIQSNVTGSYKDCLSYVANLAGKFDNTV
DFLLCFESMQDQNKKKSVMIDLNNQVIKFRQDNNLI
>d1ezwa_ c.1.16.3 (A:) Coenzyme F420 dependent
tetrahydromethanopterin reductase {Archaeon Methanopyrus kandleri}
AEVSFGIELLPDDKPTKIAHLIKVAEDNGFEYAWICDHYNNYSYMGVLTLAAVITSKIKLGPGIT
NPYTRHPLITASNIATLDWISGGRAIIGMGPGDKATFDKMGLPFPCKIPIWNPEAEDEVGPATAI
REVKEVIYQYLEGGPVEYEGKYVKTGTADVKARSIQGSDIPFYMGAQGPIMLKTAGEIANGVLVN
ASNPKDFEVAVPKIEEGAKEAGRSLDEIDVAAYTCFSIDKDEDKAIEATKIVVAFIVMGSPDVVL
ERHGIDTEKAEQIAEAIGKGDFGTAIGLVDEDMIEAFSIAGDPDTVVDKIEELLKAGVTQVVVGS
PIGPDKEKAIELVGQEVIPHFK
>d1f07a_ c.1.16.3 (A:) Coenzyme F420 dependent
tetrahydromethanopterin reductase {Archaeon Methanobacterium
thermoautotrophicum}
MKFGIEFVPNEPIEKIVKLVKLAEDVGFEYAWITDHYNNKNVYETLALIAEGTETIKLGPGVTNP
YVRSPAITASAIATLDELSNGRATLGIGPGDKATFDALGIEWVKPVSTIRDAIAMMRTLLAGEKT
ESGAQLMGVKAVQEKIPIYMGAQGPMMLKTAGEISDGALINASNPKDFEAAVPLIKEGAEAAGKS
IADIDVAAYTCCSIDEDAAAAANAAKIVVAFIAAGSPPPVFERHGLPADTGKKFGELLGKGDFGG
AIGAVDDALMEAFSVVGTPDEFIPKIEALGEMGVTQYVAGSPIGPDKEKSIKLLGEVIASF
>d1qapa1 c.1.17.1 (A:130-296) Quinolinic acid
phosphoribosyltransferase, C-terminal domain {Salmonella
typhimurium}
VASEVRRYVGLLAGTQTQLLDTRKTLPGLRTALKYAVLCGGGANHRLGLTDAFLIKENHIIASGS
VRQAVEKAFWLHPDVPVEVEVENLDELDDALKAGADIIMLDNFNTDQMREAVKRVNGQARLEVSG
NVTAETLREFAETGVDFISVGALTKHVRALDLSMRFC
>d1qpoa1 c.1.17.1 (A:117-285) Quinolinic acid
phosphoribosyltransferase, C-terminal domain {Mycobacterium
tuberculosis}
IATATAAWVDAVRGTKAKIRDTRKTLPGLRALQKYAVRTGGGVNHRLGLGDAALIKDNHVAAAGS
VVDALRAVRNAAPDLPCEVEVDSLEQLDAVLPEKPELILLDNFAVWQTQTAVQRRDSRAPTVMLE
SSGGLSLQTAATYAETGVDYLAVGALTHSVRVLDIGLDM
>d1qasa3 c.1.18.1 (A:299-625) Phospholipase C isozyme D1 (PLC-D1) {Rat
(Rattus norvegicus)}
DQPLSHYLVSSSHNTYLLEDQLTGPSSTEAYIRALCKGCRCLELDCWDGPNQEPIIYHGYTFTSK
ILFCDVLRAIRDYAFKASPYPVILSLENHCSLEQQRVMARHLRAILGPILLDQPLDGVTTSLPSP
EQLKGKILLKGKKLGGLLPAGGENGSEATDVSDEVEAAEMEDEAVRSQVQHKPKEDKLKLVPELS
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DMIIYCKSVHFGGFSSPGTSGQAFYEMASFSESRALRLLQESGNGFVRHNVSCLSRIYPAGWRTD
SSNYSPVEMWNGGCQIVALNFQTPGPEMDVYLGCFQDNGGCGYVLKPAFLRDPNTTFNSRALTQG
PW
>d2ptd__ c.1.18.2 (-) Phosphatidylinositol-specific phospholipase C
{Bacillus cereus}
ASSVNELENWSKWMQPIPDSIPLARISIPGTHDSGTFKLQNPIKQVWGMTQEYDFRYQMDHGARI
FDIRGRLTDDNTIVLHHGPLYLYVTLHEFINEAKQFLKDNPSETIIMSLKKEYEDMKGAEDSFSS
TFEKKYFVDPIFLKTEGNIKLGDARGKIVLLKRYSGSNEPGGYNNFYWPDNETFTTTVNQNANVT
VQEKYKVSYDEKVKSIKDTMDETMNNSEDLNHLYINFTSLSSGGTAWNSPYYYASYINPEIANYI
KQKNPARVGWVIQDYINEKWSPLLYQEVIRANKSLI
>d2plc__ c.1.18.2 (-) Phosphatidylinositol-specific phospholipase C
{Listeria monocytogenes}
VTTKQWMSALPDTTNLAALSIPGTHDTMSYNGDITWTLTKPLAQTQTMSLYQQLEAGIRYIDIRA
KDNLNIYHGPIFLNASLSGVLETITQFLKKNPKETIIMRLKDEQNSNDSFDYRIQPLINIYKDYF
YTTPRTDTSNKIPTLKDVRGKILLLSENHTKKPLVINSRKFGMQFGAPNQVIQDDYNGPSVKTKF
KEIVQTAYQASKADNKLFLNHISATSLTFTPRQYAAALNNKVEQFVLNLTSEKVRGLGILIMDFP
EKQTIKNIIKNNKF
>d7reqa1 c.1.19.1 (A:4-560) Methylmalonyl-CoA mutase, alpha and beta
subunits {Propionibacterium freudenreichii, subsp. shermanii}
LPRFDSVDLGNAPVPADAARRFEELAAKAGTGEAWETAEQIPVGTLFNEDVYKDMDWLDTYAGIP
PFVHGPYATMYAFRPWTIRQYAGFSTAKESNAFYRRNLAAGQKGLSVAFDLPTHRGYDSDNPRVA
GDVGMAGVAIDSIYDMRELFAGIPLDQMSVSMTMNGAVLPILALYVVTAEEQGVKPEQLAGTIQN
DILKEFMVRNTYIYPPQPSMRIISEIFAYTSANMPKWNSISISGYHMQEAGATADIEMAYTLADG
VDYIRAGESVGLNVDQFAPRLSFFWGIGMNFFMEVAKLRAARMLWAKLVHQFGPKNPKSMSLRTH
SQTSGWSLTAQDVYNNVVRTCIEAMAATQGHTQSLHTNSLDEAIALPTDFSARIARNTQLFLQQE
SGTTRVIDPWSGSAYVEELTWDLARKAWGHIQEVEKVGGMAKAIEKGIPKMRIEEAAARTQARID
SGRQPLIGVNKYRLEHEPPLDVLKVDNSTVLAEQKAKLVKLRAERDPEKVKAALDKITWAAGNPD
DKDPDRNLLKLCIDAGRAMATVGEMSDALEKVFGRYT
>d7reqb1 c.1.19.1 (B:16-475) Methylmalonyl-CoA mutase, alpha and beta
subunits {Propionibacterium freudenreichii, subsp. shermanii}
LTPTTLSLAGDFPKATEEQWEREVEKVLNRGRPPEKQLTFAECLKRLTVHTVDGIDIVPMYRPKD
APKKLGYPGVAPFTRGTTVRNGDMDAWDVRALHEDPDEKFTRKAILEGLERGVTSLLLRVDPDAI
APEHLDEVLSDVLLEMTKVEVFSRYDQGAAAEALVSVYERSDKPAKDLALNLGLDPIGFAALQGT
EPDLTVLGDWVRRLAKFSPDSRAVTIDANIYHNAGAGDVAELAWALATGAEYVRALVEQGFTATE
AFDTINFRVTATHDQFLTIARLRALREAWARIGEVFGVDEDKRGARQNAITSWRELTREDPYVNI
LRGSIATFSASVGGAESITTLPFTQALGLPEDDFPLRIARNTGIVLAEEVNIGRVNDPAGGSYYV
ESLTRSLADAAWKEFQEVEKLGGMSKAVMTEHVTKVLDACNAERAKRLANRKQPITAVSEFPMIG
ARSIE
>d1ccwb_ c.1.19.2 (B:) Glutamate mutase, large subunit {Clostridium
cochlearium}
MELKNKKWTDEEFHKQREEVLQQWPTGKEVDLQEAVDYLKKIPAEKNFAEKLVLAKKKGITMAQP
RAGVALLDEHIELLRYLQDEGGADFLPSTIDAYTRQNRYDECENGIKESEKAGRSLLNGFPGVNF
GVKGCRKVLEAVNLPLQARHGTPDSRLLAEIIHAGGWTSNEGGGISYNVPYAKNVTIEKSLLDWQ
YCDRLVGFYEEQGVHINREPFGPLTGTLVPPSMSNAVGITEALLAAEQGVKNITVGYGECGNMIQ
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DIAALRCLEEQTNEYLKAYGYNDVFVTTVFHQWMGGFPQDESKAFGVIVTATTIAALAGATKVIV
KTPHEAIGIPTKEANAAGIKATKMALNMLEGQRMPMSKELETEMAVIKAETKCILDKMFELGKGD
LAIGTVKAFETGVMDIPFGPSKYNAGKMMPVRDNLGCVRYLEFGNVPFTEEIKNYNRERLQERAK
FEGRDVSFQMVIDDIFAVGKGRLIGRPE
>d1eexa_ c.1.19.3 (A:) Diol dehydratase, alpha subunit {Klebsiella oxytoca}
MRSKRFEALAKRPVNQDGFVKEWIEEGFIAMESPNDPKPSIKIVNGAVTELDGKPVSDFDLIDHF
IARYGINLNRAEEVMAMDSVKLANMLCDPNVKRSEIVPLTTAMTPAKIVEVVSHMNVVEMMMAMQ
KMRARRTPSQQAHVTNVKDNPVQIAADAAEGAWRGFDEQETTVAVARYAPFNAIALLVGSQVGRP
GVLTQCSLEEATELKLGMLGHTCYAETISVYGTEPVFTDGDDTPWSKGFLASSYASRGLKMRFTS
GSGSEVQMGYAEGKSMLYLEARCIYITKAAGVQGLQNGSVSCIGVPSAVPSGIRAVLAENLICSS
LDLECASSNDQTFTHSDMRRTARLLMQFLPGTDFISSGYSAVPNYDNMFAGSNEDAEDFDDYNVI
QRDLKVDGGLRPVREEDVIAIRNKAARALQAVFAGMGLPPITDEEVEAATYAHGSKDMPERNIVE
DIKFAQEIINKNRNGLEVVKALAQGGFTDVAQDMLNIQKAKLTGDYLHTSAIIVGDGQVLSAVND
VNDYAGPATGYRLQGERWEEIKNIPGALDPN
>d1f3ea_ c.1.20.1 (A:) tRNA-guanine transglycosylase {Zymomonas mobilis}
RPRFSFSIAAREGKARTGTIEMKRGVIRTPAFMPVGTAATVKALKPETVRATGADIILGNTYHLM
LRPGAERIAKLGGLHSFMGWDRPILTDSGGYQVMSLSSLTKQSEEGVTFKSHLDGSRHMLSPERS
IEIQHLLGSDIVMAFDECTPYPATPSRAASSMERSMRWAKRSRDAFDSRKEQAENAALFGIQQGS
VFENLRQQSADALAEIGFDGYAVGGLAVGEGQDEMFRVLDFSVPMLPDDKPHYLMGVGKPDDIVG
AVERGIDMFDCVLPTRSGRNGQAFTWDGPINIRNARFSEDLKPLDSECHCAVCQKWSRAYIHHLI
RAGEILGAMLMTEHNIAFYQQLMQKIRDSISEGRFSQFAQDFRARYF
>d1aj2__ c.1.21.1 (-) Dihydropteroate synthetase {Escherichia coli}
MKLFAQGTSLDLSHPHVMGILNVTPDSFSDGGTHNSLIDAVKHANLMINAGATIIDVGGESTRPG
AAEVSVEEELQRVIPVVEAIAQRFEVWISVDTSKPEVIRESAKVGAHIINDIRSLSEPGALEAAA
ETGLPVCLMHMQGNPKTMQEAPKYDDVFAEVNRYFIEQIARCEQAGIAKEKLLLDPGFGFGKNLS
HNYSLLARLAEFHHFNLPLLVGMSRKSMIGQLLNVGPSERLSGSLACAVIAAMQGAHIIRVHDVK
ETVEAMRVVEATLSAKENKRYE
>d1ad1a_ c.1.21.1 (A:) Dihydropteroate synthetase {Staphylococcus aureus}
TKTKIMGILNVTPDSFSDGGKFNNVESAVTRVKAMMDEGADIIDVGGVSTRPGHEMITVEEELNR
VLPVVEAIVGFDVKISVDTFRSEVAEACLKLGVDIINDQWAGLYDHRMFQVVAKYDAEIVLMHNG
NGNRDEPVVEEMLTSLLAQAHQAKIAGIPSNKIWLDPGIGFAKTRNEEAEVMARLDELVATEYPV
LLATSRKRFTKEMMGYDTTPVERDEVTAATTAYGIMKGVRAVRVHNVELNAKLAKGIDFLKENEN
ARHN
>d1eyea_ c.1.21.1 (A:) Dihydropteroate synthetase {Mycobacterium tuberculosis}
PVQVMGVLNVTDDSFSDGGCYLDLDDAVKHGLAMAAAGAGIVDVGGESSRPGATRVDPAVETSRV
IPVVKELAAQGITVSIDTMRADVARAALQNGAQMVNDVSGGRADPAMGPLLAEADVPWVLMHWRA
VSADTPHVPVRYGNVVAEVRADLLASVADAVAAGVDPARLVLDPGLGFAKTAQHNWAILHALPEL
VATGIPVLVGASRKRFLGALLAGPDGVMRPTDGRDTATAVISALAALHGAWGVRVHDVRASVDAI
KVVEAWMGAE
>d1f6ya_ c.1.21.2 (A:) Methyltetrahydrofolate: corrinoid/iron-sulfur
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protein methyltransferase MetR {Moorella thermoacetica}
MLIIGERINGMFGDIKRAIQERDPAPVQEWARRQEEGGARALDLNVGPAVQDKVSAMEWLVEVTQ
EVSNLTLCLDSTNIKAIEAGLKKCKNRAMINSTNAEREKVEKLFPLAVEHGAALIGLTMNKTGIP
KDSDTRLAFAMELVAAADEFGLPMEDLYIDPLILPANVAQDHAPEVLKTLQQIKMLADPAPKTVL
GLSNVSQNCQNRPLINRTFLAMAMACGLMSAIADACDEALIETAATAEILLNQTVYCDSFVKMFK
TR
>d1uroa_ c.1.22.1 (A:) Uroporphyrinogen decarboxylase, UROD {Human
(Homo sapiens)}
GFPELKNDTFLRAAWGEETDYTPVWCMRQAGRYLPEFRETRAAQDFFSTCRSPEACCELTLQPLR
RFPLDAAIIFSDILVVPQALGMEVTMVPGKGPSFPEPLREEQDLERLRDPEVVASELGYVFQAIT
LTRQRLAGRVPLIGFAGAPWTLMTYMVEGGGSSTMAQAKRWLYQRPQASHQLLRILTDALVPYLV
GQVVAGAQALQLFESHAGHLGPQLFNKFALPYIRDVAKQVKARLREAGLAPVPMIIFAKDGHFAL
EELAQAGYEVVGLDWTVAPKKARECVGKTVTLQGNLDPCALYASEEEIGQLVKQMLDDFGPHRYI
ANLGHGLYPDMDPEHVGAFVDAVHKHSRLLRQ
>d1j93a_ c.1.22.1 (A:) Uroporphyrinogen decarboxylase, UROD {Tobacco
(Nicotiana tabacum), UROD-III}
TQPLLLDAVRGKEVERPPVWLMRQAGRYMKSYQLLCEKYPLFRDRSENVDLVVEISLQPWKVFRP
DGVILFSDILTPLSGMNIPFDIIKGKGPVIFDPLRTAADVEKVREFIPEKSVPYVGEALTILRKE
VNNQAAVLGFVGAPFTLASYVVEGGSSKNFTKIKRLAFAEPKVLHALLQKFATSMAKYIRYQADS
GAQAVQIFDSWATELSPVDFEEFSLPYLKQIVDSVKLTHPNLPLILYASGSGGLLERLPLTGVDV
VSLDWTVDMADGRRRLGPNVAIQGNVDPGVLFGSKEFITNRINDTVKKAGKGKHILNLGHGIKVG
TPEENFAHFFEIAKGLRY
>d1b5ta_   c.1.23.1   (A:)   Methylenetetrahydrofolate   reductase
{Escherichia coli}
GQINVSFEFFPPRTSEMEQTLWNSIDRLSSLKPKFVSVTYGANSGERDRTHSIIKGIKDRTGLEA
APHLTCIDATPDELRTIARDYWNNGIRHIVALRGDLPPGSGKPEMYASDLVTLLKEVADFDISVA
AYPEVHPEAKSAQADLLNLKRKVDAGANRAITQFFFDVESYLRFRDRCVSAGIDVEIIPGILPVS
NFKQAKKFADMTNVRIPAWMAQMFDGLDDDAETRKLVGANIAMDMVKILSREGVKDFHFYTLNRA
EMSYAICHTLGVRPA
>d1heta2 c.2.1.1 (A:175-324) Alcohol dehydrogenase {Horse (Equus
caballus)}
GFSTGYGSAVKVAKVTQGSTCAVFGLGGVGLSVIMGCKAAGAARIIGVDINKDKFAKAKEVGATE
CVNPQDYKKPIQEVLTEMSNGGVDFSFEVIGRLDTMVTALSCCQEAYGVSVIVGVPPDSQNLSMN
PMLLLSGRTWKGAIFGGFKS
>d1d1ta2 c.2.1.1 (A:175-324) Alcohol dehydrogenase {Human (Homo
sapiens), different isozymes}
GFSTGYGAAVKTGKVKPGSTCVVFGLGGVGLSVIMGCKSAGASRIIGIDLNKDKFEKAMAVGATE
CISPKDSTKPISEVLSEMTGNNVGYTFEVIGHLETMIDALASCHMNYGTSVVVGVPPSAKMLTYD
PMLLFTGRTWKGCVFGGLKS
>d1ht0a2 c.2.1.1 (A:175-324) Alcohol dehydrogenase {Human (Homo
sapiens), different isozymes}
GFSTGYGSAVKVAKVTPGSTCAVFGLGGVGLSVVMGCKAAGAARIIAVDINKDKFAKAKELGATE
CINPQDYKKPIQEVLKEMTDGGVDFSFEVIGQLDTMMASLLCCHEACGTSVIVGVPPDSQNLSIN
PMLLLTGRTWKGAIFGGFKS
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>d1teha2 c.2.1.1 (A:175-324) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}
GISTGYGAAVNTAKLEPGSVCAVFGLGGVGLAVIMGCKVAGASRIIGVDINKDKFARAKEFGATE
CINPQDFSKPIQEVLIEMTDGGVDYSFECIGNVKVMRAALEACHKGWGVSVVVGVAASGEEIATR
PFQLVTGRTWKGTAFGGWKS
>d1e3ia2 c.2.1.1 (A:175-324) Alcohol dehydrogenase {Mouse (Mus musculus), class II}
LIGCGFSSGYGAAINTAKVTPGSTCAVFGLGCVGLSAIIGCKIAGASRIIAIDINGEKFPKAKAL
GATDCLNPRELDKPVQDVITELTAGGVDYSLDCAGTAQTLKAAVDCTVLGWGSCTVVGAKVDEMT
IPTVDVILGRSINGTFFGGW
>d1cdoa2 c.2.1.1 (A:176-324) Alcohol dehydrogenase {Cod (Gadus callarias)}
GVSTGFGAAVNTAKVEPGSTCAVFGLGAVGLAAVMGCHSAGAKRIIAVDLNPDKFEKAKVFGATD
FVNPNDHSEPISQVLSKMTNGGVDFSLECVGNVGVMRNALESCLKGWGVSVLVGWTDLHDVATRP
IQLIAGRTWKGSMFGGFKG
>d1keva2 c.2.1.1 (A:151-314) Bacterial secondary alcohol dehydrogenase {Clostridium beijerinckii}
MMTTGFHGAELADIQMGSSVVVIGIGAVGLMGIAGAKLRGAGRIIGVGSRPICVEAAKFYGATDI
LNYKNGHIVDQVMKLTNGKGVDRVIMAGGGSETLSQAVSMVKPGGIISNINYHGSGDALLIPRVE
WGCGMAHKTIKGGLCPGGRLRAEMLRDMVVYNRV
>d1ykfa2 c.2.1.1 (A:151-314) Bacterial secondary alcohol dehydrogenase {Thermoanaerobacter brockii}
MMTTGFHGAELADIELGATVAVLGIGPVGLMAVAGAKLRGAGRIIAVGSRPVCVDAAKYYGATDI
VNYKDGPIESQIMNLTEGKGVDAAIIAGGNADIMATAVKIVKPGGTIANVNYFGEGEVLPVPRLE
WGCGMAHKTIKGGLCPGGRLRMERLIDLVFYKRV
>d1e3ja2 c.2.1.1 (A:151-313) Ketose reductase (sorbitol dehydrogenase) {Silverleaf whitefly (Bemisia argentifolii)}
LEPLSVGVHACRRAGVQLGTTVLVIGAGPIGLVSVLAAKAYGAFVVCTARSPRRLEVAKNCGADV
TLVVDPAKEEESSIIERIRSAIGDLPNVTIDCSGNEKCITIGINITRTGGTLMLVGMGSQMVTVP
LVNACAREIDIKSVFRYCNDYPIALEMVASGRC
>d1qora2 c.2.1.1 (A:136-265) Quinone oxidoreductase {Escherichia coli}
YEIKPDEQFLFHAAAGGVGLIACQWAKALGAKLIGTVGTAQKAQSALKAGAWQVINYREEDLVER
LKEITGGKKVRVVYDSVGRDTWERSLDCLQRRGLMVSFGNSSGAVTGVNLGILNQKGSLYVTRPS
>d1udc__ c.2.1.2 (-) Uridine diphosphogalactose-4-epimerase (UDP-galactose 4-epimerase) {Escherichia coli}
MRVLVTGGSGYIGSHTCVQLLQNGHDVIILDNLCNSKRSVLPVIERLGGKHPTFVEGDIRNEALM
TEILHDHAIDTVIHFAGLKAVGESVQKPLEYYDNNVNGTLRLISAMRAANVKNFIFSSSATVYGD
QPKIPYVESFPTGTPQSPYGKSKLMVEQILTDLQKAQPDWSIALLRYFNPVGAHPSGDMGEDPQG
IPNNLMPYIAQVAVGRRDSLAIFGNDYPTEDGTGVRDYIHVMDLADGHVVAMEKLANKPGVHIYN
LGAGVGNSVLDVVNAFSKACGKPVNYHFAPRREGDLPAYWADASKADRELNWRVTRTLDEMAQDT
WHWQSRHPQGYPD
>d1ek6a_ c.2.1.2 (A:) Uridine diphosphogalactose-4-epimerase (UDP-galactose 4-epimerase) {Human (Homo sapiens)}
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MAEKVLVTGGAGYIGSHTVLELLEAGYLPVVIDNFHNAFRGGGSLPESLRRVQELTGRSVEFEEM
DILDQGALQRLFKKYSFMAVIHFAGLKAVGESVQKPLDYYRVNLTGTIQLLEIMKAHGVKNLVFS
SSATVYGNPQYLPLDEAHPTGGCTNPYGKSKFFIEEMIRDLCQADKTWNAVLLRYFNPTGAHASG
CIGEDPQGIPNNLMPYVSQVAIGRREALNVFGNDYDTEDGTGVRDYIHVVDLAKGHIAALRKLKE
QCGCRIYNLGTGTGYSVLQMVQAMEKASGKKIPYKVVARREGDVAACYANPSLAQEELGWTAALG
LDRMCEDLWRWQKQNPSGFGT
>d1bxka_ c.2.1.2 (A:) dTDP-glucose 4,6-dehydratase (RmlB)
{Escherichia coli}
MRKILITGGAGFIGSALVRYIINETSDAVVVVDKLTYAGNLMSLAPVAQSERFAFEKVDICDRAE
LARVFTEHQPDCVMHLAAESHVDRSIDGPAAFIETNIVGTYTLLEAARAYWNALTEDKKSAFRFH
HISTDEVYGDLHSTDDFFTETTPYAPSSPYSASKASSDHLVRAWLRTYGLPTLITNCSNNYGPYH
FPEKLIPLMILNALAGKSLPVYGNGQQIRDWLYVEDHARALYCVATTGKVGETYNIGGHNERKNL
DVVETICELLEELAPNKPHGVAHYRDLITFVADRPGHDLRYAIDASKIARELGCVPQETFESGMR
KTVQWYLANESWWKQVQDGSYQGER
>d1kepa_ c.2.1.2 (A:) dTDP-glucose 4,6-dehydratase (RmlB)
{Streptococcus suis, serotype 2}
QFKNIIVTGGAGFIGSNFVHYVYNNHPDVHVTVLDKLTYAGNKANLEAILGDRVELVVGDIADAE
LVDKLAAKADAIVHYAAESHNDNSLNDPSPFIHTNFIGTYTLLEAARKYDIRFHHVSTDEVYGDL
PLREDLPGHGEGPGEKFTAETNYNPSSPYSSTKAASDLIVKAWVRSFGVKATISNCSNNYGPYQH
IEKFIPRQITNILAGIKPKLYGEGKNVRDWIHTNDHSTGVWAILTKGRMGETYLIGADGEKNNKE
VLELILEKMGQPKDAYDHVTDRAGHDLRYAIDASKLRDELGWTPQFTDFSEGLEETIQWYTDNQD
WWKAEKEAVEANYAKTQEVIK
>d1kewa_ c.2.1.2 (A:) dTDP-glucose 4,6-dehydratase (RmlB)
{Streptococcus suis, serotype 2}
MKILITGGAGFIGSAVVRHIIKNTQDTVVNIDKLTYAGNLESLSDISESNRYNFEHADICDSAEI
TRIFEQYQPDAVMHLAAESHVDRSITGPAAFIETNIVGTYALLEVARKYWSALGEDKKNNFRFHH
ISTDEVYGDLPHPDEVENSVTLPLFTETTAYAPSSPYSASKASSDHLVRAWRRTYGLPTIVTNCS
NNYGPYHFPEKLIPLVILNALEGKPLPIYGKGDQIRDWLYVEDHARALHMVVTEGKAGETYNIGG
HNEKKNLDVVFTICDLLDEIVPKATSYREQITYVADRPGHDRRYAIDAGKISRELGWKPLETFES
GIRKTVEWYLANTQWVNNVKSGAYQSWIEQNYEGRQ
>d1e6ua_ c.2.1.2 (A:) GDP-4-keto-6-deoxy-d-mannose
epimerase/reductase (GDP-fucose synthetase) {Escherichia coli}
AKQRVFIAGHRGMVGSAIRRQLEQRGDVELVLRTRDELNLLDSRAVHDFFASERIDQVYLAAAKV
GGIVANNTYPADFIYQNMMIESNIIHAAHQNDVNKLLFLGSSCIYPKLAKQPMAESELLQGTLEP
TNEPYAIAKIAGIKLCESYNRQYGRDYRSVMPTNLYGPHDNFHPSNSHVIPALLRRFHEATAQKA
PDVVVWGSGTPMREFLHVDDMAAASIHVMELAHEVWLENTQPMLSHINVGTGVDCTIRELAQTIA
KVVGYKGRVVFDASKPDGTPRKLLDVTRLHQLGWYHEISLEAGLASTYQWFLENQ
>d1db3a_ c.2.1.2 (A:) GDP-mannose 4,6-dehydratase {Escherichia coli}
SKVALITGVTGQDGSYLAEFLLEKGYEVHGIKRRASSFNTERVDHIYQDPHTCNPKFHLHYGDLS
DTSNLTRILREVQPDEVYNLGAMSHVAVSFESPEYTADVDAMGTLRLLEAIRFLGLEKKTRFYQA
STSELYGLVQEIPQKETTPFYPRSPYAVAKLYAYWITVNYRESYGMYACNGILFNHESPRRGETF
VTRKITRAIANIAQGLESCLYLGNMDSLRDWGHAKDYVKMQWMMLQQEQPEDFVIATGVQYSVRQ
FVEMAAAQLGIKLRFEGTGVEEKGIVVSVTGHDAPGVKPGDVIIAVDPRYFRPAEVETLLGDPTK
AHEKLGWKPEITLREMVSEMVANDLEAAKKHS
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>d1eq2a_ c.2.1.2 (A:) ADP-L-glycero-D-mannoheptose 6-epimerase {Escherichia coli}
MIIVTGGAGFIGSNIVKALNDKGITDILVVDNLKDGTKFVNLVDLNIADYMDKEDFLIQIMAGEE
FGDVEAIFHEGACSSTTEWDGKYMMDNNYQYSKELLHYCLEREIPFLYASSAATYGGRTSDFIES
REYEKPLNVYGYSKFLFDEYVRQILPEANSQIVGFRYFNVYGPREGHKGSMASVAFHLNTQLNNG
ESPKLFEGSENFKRDFVYVGDVADVNLWFLENGVSGIFNLGTGRAESFQAVADATLAYHKKGQIE
YIPFPDKLKGRYQAFTQADLTNLRAAGYDKPFKTVAEGVTEYMAWLN
>d1qrra_ c.2.1.2 (A:) Sulfolipid biosynthesis protein SQD1 {Thale cress (Arabidopsis thaliana)}
KRVMVIGGDGYCGWATALHLSKKNYEVCIVDNLVRRLFDHQLGLESLTPIASIHDRISRWKALTG
KSIELYVGDICDFEFLAESFKSFEPDSVVHFGEQRSAPYSMIDRSRAVYTQHNNVIGTLNVLFAI
KEFGEECHLVKLGTMGEYGTPNIDIEEGYITITHNGRTDTLPYPKQASSFYHLSKVHDSHNIAFT
CKAWGIRATDLNQGVVYGVKTDETEMHEELRNRLDYDAVFGTALNRFCVQAAVGHPLTVYGKGGQ
TRGYLDIRDTVQCVEIAIANPAKAGEFRVFNQFTEQFSVNELASLVTKAGSKLGLDVKKMTVPNP
RVEAEEHYYNAKHTKLMELGLEPHYLSDSLLDSLLNFAVQFKDRVDTKQIMPSVSWKKIGVKTKS
>d1k6xa_ c.2.1.2 (A:) Negative transcriptional regulator NmrA {Aspergillus nidulans}
QQKKTIAVVNATGRQAASLIRVAAAVGHHVRAQVHSLKGLIAEELQAIPNVTLFQGPLLNNVPLM
DTLFEGAHLAFINTTSQAGDEIAIGKDLADAAKRAGTIQHYIYSSMPDHSLYGPWPAVPMWAPKF
TVENYVRQLGLPSTFVYAGIYNNNFTSLPYPLFQMELMPDGTFEWHAPFDPDIPLPWLDAEHDVG
PALLQIFKDGPQKWNGHRIALTFETLSPVQVCAAFSRALNRRVTYVQVPKVEIKVNIPVGYREQL
EAIEVVFGEHKAPYFPLPEFSRPAAGSPKGLGPANGKGAGAGMMQGPGGVISQRVTDEARKLWSG
WRDMEEYAREVFPIEEEANGLDWML
>d1cyda_ c.2.1.2 (A:) Carbonyl reductase {Mouse (Mus musculus)}
LNFSGLRALVTGAGKGIGRDTVKALHASGAKVVAVTRTNSDLVSLAKECPGIEPVCVDLGDWDAT
EKALGGIGPVDLLVNNAALVIMQPFLEVTKEAFDRSFSVNLRSVFQVSQMVARDMINRGVPGSIV
NVSSMVAHVTFPNLITYSSTKGAMTMLTKAMAMELGPHKIRVNSVNPTVVLTDMGKKVSADPEFA
RKLKERHPLRKFAEVEDVVNSILFLLSDRSASTSGGGILVDAGYLAS
>d1oaa__ c.2.1.2 (-) Sepiapterin reductase {Mouse (Mus musculus)}
ADGLGCAVCVLTGASRGFGRALAPQLARLLSPGSVMLVSARSESMLRQLKEELGAQQPDLKVVLA
AADLGTEAGVQRLLSAVRELPRPEGLQRLLLINNAATLGDVSKGFLNVNDLAEVNNYWALNLTSM
LCLTSGTLNAFQDSPGLSKTVVNISSLCALQPYKGWGLYCAGKAARDMLYQVLAAEEPSVRVLSY
APGPLDNDMQQLARETSKDPELRSKLQKLKSDGALVDCGTSAQKLLGLLQKDTFQSGAHVDFYD
>d1hdr__ c.2.1.2 (-) Dihydropteridin reductase (pteridine reductase) {Human (Homo sapiens)}
EARRVLVYGGRGALGSRCVQAFRARNWWVASVDVVENEEASASIIVKMTDSFTEQADQVTAEVGK
LLGEEKVDAILCVAGGWAGGNAKSKSLFKNCDLMWKQSIWTSTISSHLATKHLKEGGLLTLAGAK
AALDGTPGMIGYGMAKGAVHQLCQSLAGKNSGMPPGAAAIAVLPVTLDTPMNRKSMPEADFSSWT
PLEFLVETFHDWITGKNRPSSGSLIQVVTTEGRTELTPAYF
>d1e7wa_ c.2.1.2 (A:) Dihydropteridin reductase (pteridine reductase) {Leishmania major}
TVPVALVTGAAKRLGRSIAEGLHAEGYAVCLHYHRSAAEANALSATLNARRPNSAITVQADLSNV
ATAPVSGADGSAPVTLFTRCAELVAACYTHWGRCDVLVNNASSFYPTPLLRNDEDGHEPCVGDRE
AMETATADLFGSNAIAPYFLIKAFAHRVAGTPAKHRGTNYSIINMVDAMTNQPLLGYTIYTMAKG
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ALEGLTRSAALELAPLQIRVNGVGPGLSVLVDDMPPAVWEGHRSKVPLYQRDSSAAEVSDVVIFL
CSSKAKYITGTCVKVDGGYSLTRA
>d1fds__ c.2.1.2 (-) Human estrogenic 17beta-hydroxysteroid
dehydrogenase {Human (Homo sapiens)}
ARTVVLITGCSSGIGLHLAVRLASDPSQSFKVYATLRDLKTQGRLWEAARALACPPGSLETLQLD
VRDSKSVAAARERVTEGRVDVLVCNAGLGLLGPLEALGEDAVASVLDVNVVGTVRMLQAFLPDMK
RRGSGRVLVTGSVGGLMGLPFNDVYCASKFALEGLCESLAVLLLPFGVHLSLIECGPVHTAFMEK
VLGSPEEVLDRTDIHTFHRFYQYLAHSKQVFREAAQNPEEVAEVFLTALRAPKPTLRYFTTERFL
PLLRMRLDDPSGSNYVTAMHREVFGDV
>d1fmca_ c.2.1.2 (A:) 7-alpha-hydroxysteroid dehydrogenase
{Escherichia coli}
MFNSDNLRLDGKCAIITGAGAGIGKEIAITFATAGASVVVSDINADAANHVVDEIQQLGGQAFAC
RCDITSEQELSALADFAISKLGKVDILVNNAGGGGPKPFDMPMADFRRAYELNVFSFFHLSQLVA
PEMEKNGGGVILTITSMAAENKNINMTSYASSKAAASHLVRNMAFDLGEKNIRVNGIAPGAILTD
ALKSVITPEIEQKMLQHTPIRRLGQPQDIANAALFLCSPAASWVSGQILTVSGGGVQELN
>d1hdca_ c.2.1.2 (A:) 3-alpha,20-beta-hydroxysteroid dehydrogenase
{Streptomyces hydrogenans}
NDLSGKTVIITGGARGLGAEAARQAVAAGARVVLADVLDEEGAATARELGDAARYQHLDVTIEED
WQRVVAYAREEFGSVDGLVNNAGISTGMFLETESVERFRKVVEINLTGVFIGMKTVIPAMKDAGG
GSIVNISSAAGLMGLALTSSYGASKWGVRGLSKLAAVELGTDRIRVNSVHPGMTYTPMTAETGIR
QGEGNYPNTPMGRVGEPGEIAGAVVKLLSDTSSYVTGAELAVDGGWTTGPTVKYVMGQ
>d1fjha_ c.2.1.2 (A:) 3-alpha-hydroxysteroid dehydrogenase
{Comamonas testosteroni}
MSIIVISGCATGIGAATRKVLEAAGHQIVGIDIRDAEVIADLSTAEGRKQAIADVLAKCSKGMDG
LVLCAGLGPQTKVLGNVVSVNYFGATELMDAFLPALKKGHQPAAVVISSVASAHLAFDKNPLALA
LEAGEEAKARAIVEHAGEQGGNLAYAGSKNALTVAVRKRAAAWGEAGVRLNTIAPGATETPLLQA
GLQDPRYGESIAKFVPPMGRRAEPSEMASVIAFLMSPAASYVHGAQIVIDGGIDAVMRPTQF
>d1bdb__ c.2.1.2 (-) Cis-biphenyl-2,3-dihydrodiol-2,3-dehydrogenase
{Pseudomonas sp., lb400}
MKLKGEAVLITGGASGLGRALVDRFVAEGAKVAVLDKSAERLAELETDHGDNVLGIVGDVRSLED
QKQAASRCVARFGKIDTLIPNAGIWDYSTALVDLPEESLDAAFDEVFHINVKGYIHAVKACLPAL
VASRGNVIFTISNAGFYPNGGGPLYTAAKHAIVGLVRELAFELAPYVRVNGVGSGGINSDLRGPS
SLGMGSKAISTVPLADMLKSVLPIGRMPEVEEYTGAYVFFATRGDAAPATGALLNYDGGLGVRGF
FSGAGGNDLLEQLNIH
>d1b16a_ c.2.1.2 (A:) Drosophila alcohol dehydrogenase {Fruit fly
(Drosophila lebanonensis)}
MDLTNKNVIFVAALGGIGLDTSRELVKRNLKNFVILDRVENPTALAELKAINPKVNITFHTYDVT
VPVAESKKLLKKIFDQLKTVDILINGAGILDDHQIERTIAINFTGLVNTTTAILDFWDKRKGGPG
GIIANICSVTGFNAIHQVPVYSASKAAVVSFTNSLAKLAPITGVTAYSINPGITRTPLVHTFNSW
LDVEPRVAELLLSHPTQTSEQCGQNFVKAIEANKNGAIWKLDLGTLEAIEWTKHWDSHI
>d1gcoa_ c.2.1.2 (A:) Glucose dehydrogenase {Bacillus megaterium}
MYKDLEGKVVVITGSSTGLGKSMAIRFATEKAKVVVNYRSKEDEANSVLEEIKKVGGEAIAVKGD
VTVESDVINLVQSAIKEFGKLDVMINNAGLENPVSSHEMSLSDWNKVIDTNLTGAFLGSREAIKY
FVENDIKGTVINMSSVHEKIPWPLFVHYAASKGGMKLMTETLALEYAPKGIRVNNIGPGAINTPI
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NAEKFADPEQRADVESMIPMGYIGEPEEIAAVAAWLASSEASYVTGITLFADGGMTQYPSFQAGR
G
>d1gega_ c.2.1.2 (A:) meso-2,3-butanediol dehydrogenase {Klebsiella pneumoniae}
KKVALVTGAGQGIGKAIALRLVKDGFAVAIADYNDATAKAVASEINQAGGHAVAVKVDVSDRDQV
FAAVEQARKTLGGFDVIVNNAGVAPSTPIESITPEIVDKVYNINVKGVIWGIQAAVEAFKKEGHG
GKIINACSQAGHVGNPELAVYSSSKFAVRGLTQTAARDLAPLGITVNGYCPGIVKTPMWAEIDRQ
VSEAAGKPLGYGTAEFAKRITLGRLSEPEDVAACVSYLASPDSDYMTGQSLLIDGGMVFN
>d1h5qa_ c.2.1.2 (A:) Mannitol dehydrogenase {Mushroom (Agaricus bisporus)}
PGFTISFVNKTIIVTGGNRGIGLAFTRAVAAAGANVAVIYRSAADAVEVTEKVGKEFGVKTKAYQ
CDVSNTDIVTKTIQQIDADLGPISGLIANAGVSVVKPATELTHEDFAFVYDVNVFGVFNTCRAVA
KLWLQKQQKGSIVVTSSMSSQIINQSSLNGSLTQVFYNSSKAACSNLVKGLAAEWASAGIRVNAL
SPGYVNTDQTAHMDKKIRDHQASNIPLNRFAQPEEMTGQAILLLSDHATYMTGGEYFIDGGQLIW
>d1edoa_ c.2.1.2 (A:) beta-keto acyl carrier protein reductase {Oil seed rape (Brassica napus)}
SPVVVVTGASRGIGKAIALSLGKAGCKVLVNYARSAKAAEEVSKQIEAYGGQAITFGGDVSKEAD
VEAMMKTAIDAWGTIDVVVNNAGITRDTLLIRMKKSQWDEVIDLNLTGVFLCTQAATKIMMKKRK
GRIINIASVVGLIGNIGQANYAAAKAGVIGFSKTAAREGASRNINVNVVCPGFIASDMTAKLGED
MEKKILGTIPLGRTGQPENVAGLVEFLALSPAASYITGQAFTIDGGIAI
>d1i01a_ c.2.1.2 (A:) beta-keto acyl carrier protein reductase {Escherichia coli}
MNFEGKIALVTGASRGIGRAIAETLAARGAKVIGTATSENGAQAISDYLGANGKGLMLNVTDPAS
IESVLEKIRAEFGEVDILVNNAGITRDNLLMRMKDEEWNDIIETNLSSVFRLSKAVMRAMMKKRH
GRIITIGSVVGTMGNGGQANYAAAKAGLIGFSKSLAREVASRGITVNVVAPGFIETDMTRALSDD
QRAGILAQVPAGRLGGAQEIANAVAFLASDEAAYITGETLHVNGGM
>d1eno__ c.2.1.2 (-) Enoyl-ACP reductase {Oil seed rape (Brassica napus)}
LPIDLRGKRAFIAGIADDNGYGWAVAKSLAAAGAEILVGTWVPALNIFETSLRRGKFDQSRVLPD
GSLMEIKKVYPLDAVFDNPEDVPEDVKANKRYAGSSNWTVQEAAECVRQDFGSIDILVHSLANGP
EVSKPLLETSRKGYLAAISASSYSFVSLLSHFLPIMNPGGASISLTYIASERIIPGYGGGMSSAK
AALESDTRVLAFEAGRKQNIRVNTISAGPLGSRAAKAIGFIDTMIEYSYNNAPIQKTLTADEVGN
AAAFLVSPLASAITGATIYVDNGLNSMGVALDSPVFK
>d1eny__ c.2.1.2 (-) Enoyl-ACP reductase {Mycobacterium tuberculosis, TB, gene InhA}
AGLLDGKRILVSGIITDSSIAFHIARVAQEQGAQLVLTGFDRLRLIQRITDRLPAKAPLLELDVQ
NEEHLASLAGRVTEAIGAGNKLDGVVHSIGFMPQTGMGINPFFDAPYADVSKGIHISAYSYASMA
KALLPIMNPGGSIVGMDFDPSRAMPAYNWMTVAKSALESVNRFVAREAGKYGVRSNLVAAGPIRT
LAMSAIVGGALGEEAGAQIQLLEEGWDQRAPIGWNMKDATPVAKTVCALLSDWLPATTGDIIYAD
GGAHTQLL
>d1qg6a_ c.2.1.2 (A:) Enoyl-ACP reductase {Escherichia coli}
GFLSGKRILVTGVASKLSIAYGIAQAMHREGAELAFTYQNDKLKGRVEEFAAQLGSDIVLQCDVA
EDASIDTMFAELGKVWPKFDGFVHSIGFAPGDQLDGDYVNAVTREGFKIAHDISSYSFVAMAKAC
RSMLNPGSALLTLSYLGAERAIPNYNVMGLAKASLEANVRYMANAMGPEGVRVNAISAGPIRTLA
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ASGIKDFRKMLAHCEAVTPIRRTVTIEDVGNSAAFLCSDLSAGISGEVVHVDGGFSIAAMNE
>d1ae1a_ c.2.1.2 (A:) Tropinone reductase {Jimsonweed (Datura
stramonium), I}
RWSLKGTTALVTGGSKGIGYAIVEELAGLGARVYTCSRNEKELDECLEIWREKGLNVEGSVCDLL
SRTERDKLMQTVAHVFDGKLNILVNNAGVVIHKEAKDFTEKDYNIIMGTNFEAAYHLSQIAYPLL
KASQNGNVIFLSSIAGFSALPSVSLYSASKGAINQMTKSLACEWAKDNIRVNSVAPGVILTPLVE
TAIKKNPHQKEEIDNFIVKTPMGRAGKPQEVSALIAFLCFPAASYITGQIIWADGGFTANGGF
>d2ae2a_ c.2.1.2 (A:) Tropinone reductase {Jimsonweed (Datura
stramonium), II}
AGRWNLEGCTALVTGGSRGIGYGIVEELASLGASVYTCSRNQKELNDCLTQWRSKGFKVEASVCD
LSSRSERQELMNTVANHFHGKLNILVNNAGIVIYKEAKDYTVEDYSLIMSINFEAAYHLSVLAHP
FLKASERGNVVFISSVSGALAVPYEAVYGATKGAMDQLTRCLAFEWAKDNIRVNGVGPGVIATSL
VEMTIQDPEQKENLNKLIDRCALRRMGEPKELAAMVAFLCFPAASYVTGQIIYVDGGLMANCGF
>d1g0oa_ c.2.1.2 (A:) 1,3,8-trihydroxynaphtalene reductase (THNR,
naphtol reductase) {Rice blast fungus (Magnaporthe grisea)}
KYDAIPGPLGPQSASLEGKVALVTGAGRGIGREMAMELGRRGCKVIVNYANSTESAEEVVAAIKK
NGSDAACVKANVGVVEDIVRMFEEAVKIFGKLDIVCSNSGVVSFGHVKDVTPEEFDRVFTINTRG
QFFVAREAYKHLEIGGRLILMGSITGQAKAVPKHAVYSGSKGAIETFARCMAIDMADKKITVNVV
APGGIKTDMYHAVCREYIPNGENLSNEEVDEYAAVQWSPLRRVGLPIDIARVVCFLASNDGGWVT
GKVIGIDGGACM
>d1ja9a_ c.2.1.2 (A:) 1,3,6,8-tetrahydroxynaphthalene reductase
{Rice blast fungus (Magnaporthe grisea)}
SKPLAGKVALTTGAGRGIGRGIAIELGRRGASVVVNYGSSSKAAEEVVAELKKLGAQGVAIQADI
SKPSEVVALFDKAVSHFGGLDFVMSNSGMEVWCDELEVTQELFDKVFNLNTRGQFFVAQQGLKHC
RRGGRIILTSSIAAVMTGIPNHALYAGSKAAVEGFCRAFAVDCGAKGVTVNCIAPGGVKTDMFDE
NSWHYAPGGYKGMPQEKIDEGLANMNPLKRIGYPADIGRAVSALCQEESEWINGQVIKLTGGGI
>d1hdoa_ c.2.1.2 (A:) Biliverdin IX beta reductase {Human (Homo
sapiens)}
MAVKKIAIFGATGQTGLTTLAQAVQAGYEVTVLVRDSSRLPSEGPRPAHVVVGDVLQAADVDKTV
AGQDAVIVLLGTRNDLSPTTVMSEGARNIVAAMKAHGVDKVVACTSAFLLWDPTKVPPRLQAVTD
DHIRMHKVLRESGLKYVAVMPPHIGDQPLTGAYTVTLDGRGPSRVISKHDLGHFMLRCLTTDEYD
GHSTYPSHQY
>d1e6wa_ c.2.1.2 (A:) 3-hydroxyacyl-CoA dehydrogenase {Rat (Rattus
norvegicus)}
SVKGLVAVITGGASGLGLSTAKRLVGQGATAVLLDVPNSEGETEAKKLGGNCIFAPANVTSEKEV
QAALTLAKEKFGRIDVAVNCAGIAVAIKTYHEKKNQVHTLEDFQRVINVNLIGTFNVIRLVAGVM
GQNEPDQGGQRGVIINTASVAAFEGQVGQAAYSASKGGIVGMTLPIARDLAPIGIRVVTIAPGLF
ATPLLTTLPDKVRNFLASQVPFPSRLGDPAEYAHLVQMVIENPFLNGEVIRLDGAIRMQP
>d1hu4a_ c.2.1.2 (A:) Carbonyl reductase/20beta-hydroxysteroid
dehydrogenase {Pig (Sus scrofa)}
SSNTRVALVTGANKGIGFAIVRDLCRQFAGDVVLTARDVARGQAAVKQLQAEGLSPRFHQLDIID
LQSIRALCDFLRKEYGGLDVLVNNAAIAFQLDNPTPFHIQAELTMKTNFMGTRNVCTELLPLIKP
QGRVVNVSSTEGVRALNECSPELQQKFKSETITEEELVGLMNKFVEDTKNGVHRKEGWSDSTYGV
TKIGVSVLSRIYARKLREQRAGDKILLNACCPGWVRTDMGGPKAPKSPEVGAETPVYLALLPSDA
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EGPHGQFVTDKKVVEWGVPPESYPWVNA
>d1gado1  c.2.1.3  (O:0-148,O:313-330)  Glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) {Escherichia coli}
TIKVGINGFGRIGRIVFRAAQKRSDIEIVAINDLLDADYMAYMLKYDSTHGRFDGTVEVKDGHLI
VNGKKIRVTAERDPANLKWDEVGVDVVAEATGLFLTDETARKHITAGAKKVVMTGPSKDNTPMFV
KGANFDKYAGQDIVSNASXNETGYSNKVLDLIAHISK
>d1gd1o1  c.2.1.3  (O:0-148,O:313-333)  Glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) {Bacillus stearothermophilus, nca 1503}
AVKVGINGFGRIGRNVFRAALKNPDIEVVAVNDLTDANTLAHLLKYDSVHGRLDAEVSVNGNNLV
VNGKEIIVKAERDPENLAWGEIGVDIVVESTGRFTKREDAAKHLEAGAKKVIISAPAKNEDITIV
MGVNQDKYDPKAHHVISNASXNETGYSHRVVDLAAYIASKGL
>d1cero1  c.2.1.3  (O:1-148,O:313-333)  Glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) {Thermus aquaticus}
MKVGINGFGRIGRQVFRILHSRGVEVALINDLTDNKTLAHLLKYDSIYHRFPGEVAYDDQYLYVD
GKAIRATAVKDPKEIPWAEAGVGVVIESTGVFTDADKAKAHLEGGAKKVIITAPAKGEDITIVMG
VNHEAYDPSRHHIISNASXNEWGYANRVADLVELVLRKGV
>d1hdgo1  c.2.1.3  (O:1-148,O:313-331)  Glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) {Thermotoga maritima}
ARVAINGFGRIGRLVYRIIYERKNPDIEVVAINDLTDTKTLAHLLKYDSVHKKFPGKVEYTENSL
IVDGKEIKVFAEPDPSKLPWKDLGVDFVIESTGVFRNREKAELHLQAGAKKVIITAPAKGEDITV
VIGCNEDQLKPEHTIISCASXNEYGYSNRVVDTLELLLKM
>d1b7go1  c.2.1.3  (O:1-138,O:301-340)  Glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) {Archaeon Sulfolobus solfataricus}
MVNVAVNGYGTIGKRVADAIIKQPDMKLVGVAKTSPNYEAFIAHRRGIRIYVPQQSIKKFEESGI
PVAGTVEDLIKTSDIVVDTTPNGVGAQYKPIYLQLQRNAIFQGGEKAEVADISFSALCNYNEALG
KKYIRVVSXESIVVPENIDAIRASMKLMSAEDSMRITNESLGILKGYLI
>d1cf2o1  c.2.1.3  (O:1-138,O:304-336)  Glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) {Archaeon Methanothermus fervidus}
MKAVAINGYGTVGKRVADAIAQQDDMKVIGVSKTRPDFEARMALKKGYDLYVAIPERVKLFEKAG
IEVAGTVDDMLDEADIVIDCTPEGIGAKNLKMYKEKGIKAIFQGGEKHEDIGLSFNSLSNYEESY
GKDYTRVVXIVPENVDAVRAILEMEEDKYKSINKTNKAMNIL
>d1ggaa1  c.2.1.3  (A:1-164,A:334-358)  Glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) {Trypanosoma brucei brucei, glycosome}
TIKVGINGFGRIGRMVFQALCDDGLLGNEIDVVAVVDMNTDARYFAYQMKYDSVHGKFKHSVSTT
KSKPSVAKDDTLVVNGHRILCVKAQRNPADLPWGKLGVEYVIESTGLFTVKSAAEGHLRGGARKV
VISAPASGGAKTFVMGVNHNNYNPREQHVVSNASXNEWGYSHRVVDLVRHMAARDRAAKL
>d1i32a1  c.2.1.3  (A:1-165,A:335-358)  Glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) {Leishmania mexicana}
APIKVGINGFGRIGRMVFQAICDQGLIGTEIDVVAVVDMSTNAEYFAYQMKHDTVHGRPKYTVEA
VKSSPSVETADVLVVNGHRIKCVKAQRNPADLPWGKLGVDYVIESTGLFTDKLKAEGHIKGGAKK
VVISAPASGGAKTIVMGVNQHEYSPASHHVVSNASXNEWAYSHRVVDLVRYMAAKDAASS
>d1dssg1  c.2.1.3  (G:1-148,G:313-334)  Glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) {Lobster (Palinurus versicolor)}
SKIGINGFGRIGRLVLRAALEMGAQVVAVNDPFIALEYMVYMFKYDSTHGMFKGEVKAEDGALVV
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DGKKITVFNEMKPENIPWSKAGAEYIVESTGVFTTIEKASAHFKGGAKKVIISAPSADAPMFVCG
VNLEKYSKDMKVVSNASXNEFGYSQRVIDLIKHMQKVDSA
>d3gpdg1 c.2.1.3 (G:1-150,G:315-334) Glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) {Human (Homo sapiens)}
GKVKVGVDGFGRIGRLVTRAAFNSGKVDIVAINDPFIDLHYMVYMFQYDSTHGKFHGTVKAEDGK
LVIDGKAITIFQERDPENIKWGDAGTAYVVESTGVFTTMEKAGAHLKGGAKRIVISAPSADAPMF
VMGVNHFKYANSLKIISNASXNEFGYSERVVDLMAHMASKE
>d1jn0a1 c.2.1.3 (A:0-148,A:313-333) Glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) {Spinach (Spinacia oleracea)}
KLKVAINGFGRIGRNFLRCWHGKDSPLDVVVINDTGGVKQASHLLKYDSILGTFDADVKTAGDSA
ISVGKVIKVVSDRNPVNLPWGDMGIDLVIEGTGVFVDRDGAGKHLQAGAKKVLITAPGKGDIPTY
VVGVNEEGYTHADTIISNASXNEWGYSQRVVDLADIVANKWQ
>d1gl3a1 c.2.1.3 (A:1-133,A:355-367) Aspartate beta-semialdehyde
dehydrogenase {Escherichia coli}
MKNVGFIGWRGMVGSVLMQRMVEERDFDAIRPVFFSTSQLGQAAPSFGGTTGTLQDAFDLEALKA
LDIIVTCQGGDYTNEIYPKLRESGWQGYWIDAASSLRMKDDAIIILDPVNQDVITDGLNNGIRTF
VGGXAAEPLRRMLRQLA
>d1ebfa1 c.2.1.3 (A:2-150,A:341-359) Homoserine dehydrogenase
{Baker's yeast (Saccharomyces cerevisiae)}
STKVVNVAVIGAGVVGSAFLDQLLAMKSTITYNLVLLAEAERSLISKDFSPLNVGSDWKAALAAS
TTKTLPLDDLIAHLKTSPKPVILVDNTSSAYIAGFYTKFVENGISIATPNKKAFSSDLATWKALF
SNKPTNGFVYHEATVGAGLXAAVTAAGVLGDVIKIAQRL
>d1e5qa1 c.2.1.3 (A:2-124,A:392-450) Saccharopine reductase {Rice
blast fungus (Magnaporthe grisea)}
ATKSVLMLGSGFVTRPTLDVLTDSGIKVTVACRTLESAKKLSAGVQHSTPISLDVNDDAALDAEV
AKHDLVISLIPYTFHATVIKSAIRQKKHVVTTSYVSPAMMELDQAAKDAGITVMNEIGXYSAMAK
LVGVPCAVAVKFVLDGTISDRGVLAPMNSKINDPLMKELKEKYGIECKEKVVA
>d1f06a1 c.2.1.3 (A:1-118,A:269-320) Diaminopimelic acid
dehydrogenase (DAPDH) {Corynebacterium glutamicum}
MTNIRVAIVGYGNLGRSVEKLIAKQPDMDLVGIFSRRATLDTKTPVFDVADVDKHADDVDVLFLC
MGSATDIPEQAPKFAQFACTVDTYDNHRDIPRHRQVMNEAATAAGNVALVSTGXRNPDFTASSQI
AFGRAAHRMKQQGQSGAFTVLEVAPYLLSPENLDDLIARDV
>d1dih_1 c.2.1.3 (2-130,241-273) Dihydrodipicolinate reductase
{Escherichia coli}
HDANIRVAIAGAGGRMGRQLIQAALALEGVQLGAALEREGSSLLGSDAGELAGAGKTGVTVQSSL
DAVKDDFDVFIDFTRPEGTLNHLAFCRQHGKGMVIGTTGFDEAGKQAIRDAAADIAIVFAANFSX
MTFANGAVRSALWLSGKESGLFDMRDVLDLNNL
>d1k5ha2 c.2.1.3 (A:1-125,A:275-300) 1-deoxy-D-xylulose-5-phosphate
reductoisomerase {Escherichia coli}
MKQLTILGSTGSIGCSTLDVVRHNPEHFRVVALVAGKNVTRMVEQCLEFSPRYAVMDDEASAKLL
KTMLQQQGSRTEVLSGQQAACDMAALEDVDQVMAAIVGAAGLLPTLAAIRAGKTILLANKXDMRT
PIAHTMAWPNRVNSGVKPLDFC
>d1gcua1 c.2.1.3 (A:1-128,A:247-292) Biliverdin reductase {Rat
(Rattus norvegicus)}
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MDAEPKRKFGVVVVGVGRAGSVRLRDLKDPRSAAFLNLIGFVSRRELGSLDEVRQISLEDALRSQ
EIDVAYICSESSSHEDYIRQFLQAGKHVLVEYPMTLSFAAAQELWELAAQKGRVLHEEHVELLXK
NIFLKDQDIFVQKLLDQVSAEDLAAEKKRIMHCLGLASDIQKLCH
>d1evja1     c.2.1.3     (A:30-160,A:323-381)     Glucose-fructose
oxidoreductase, N-terminal domain {Zymomonas mobilis}
RRFGYAIVGLGKYALNQILPGFAGCQHSRIEALVDGNAEKAKIVAAEYGVDPRKIYDYSNFDKIA
KDPKIDAVYIILPNSLHAEFAIRAFKAGKHVMCEKPMATSVADCQRMIDAAKAANKKLMIGYRCH
YXNQFSAQLDHLAEAVINNKPVRSPGEEGMQDVRLIQAIYEAARTGRPVNTDWGYVRQGGY
>d1h6da1     c.2.1.3     (A:51-212,A:375-433)     Glucose-fructose
oxidoreductase, N-terminal domain {Zymomonas mobilis}
QAATLPAGASQVPTTPAGRPMPYAIRPMPEDRRFGYAIVGLGKYALNQILPGFAGCQHSRIEALV
SGNAEKAKIVAAEYGVDPRKIYDYSNFDKIAKDPKIDAVYIILPNSLHAEFAIRAFKAGKHVMCE
KPMATSVADCQRMIDAAKAANKKLMIGYRCHYXNQFSAQLDHLAEAVINNKPVRSPGEEGMQDVR
LIQAIYEAARTGRPVNTDWGYVRQGGY
>d1dpga1   c.2.1.3   (A:1-181,A:413-426)   Glucose   6-phosphate
dehydrogenase, N-terminal domain {Leuconostoc mesenteroides}
VSEIKTLVTFFGGTGDLAKRKLYPSVFNLYKKGYLQKHFAIVGTARQALNDDEFKQLVRDCIKDF
TDDQAQAEAFIEHFSYRAHDVTDAASYAVLKEAIEEAADKFDIDGNRIFYMSVAPRFFGTIAKYL
KSEGLLADTGYNRLMIEKPFGTSYDTAAELQNDLENAFDDNQLFRIDHYLGXEPYERMIHDTMNG
D
>d1qkia1   c.2.1.3   (A:12-199,A:435-449)   Glucose   6-phosphate
dehydrogenase, N-terminal domain {Human (Homo sapiens)}
VCGILREELFQGDAFHQSDTHIFIIMGASGDLAKKKIYPTIWWLFRDGLLPENTFIVGYARSRLT
VADIRKQSEPFFKATPEEKLKLEDFFARNSYVAGQYDDAASYQRLNSHMNALHLGSQANRLFYLA
LPPTVYEAVTKNIHESCMSQIGWNRIIVEKPFGRDLQSSDRLSNHISSLFREDQIYRIXDAYERL
ILDVFCGSQ
>d2naca1 c.2.1.4 (A:148-335) Formate dehydrogenase {Pseudomonas sp.,
strain 101}
ISVAEHVVMMILSLVRNYLPSHEWARKGGWNIADCVSHAYDLEAMHVGTVAAGRIGLAVLRRLAP
FDVHLHYTDRHRLPESVEKELNLTWHATREDMYPVCDVVTLNCPLHPETEHMINDETLKLFKRGA
YIVNTARGKLCDRDAVARALESGRLAGYAGDVWFPQPAPKDHPWRTMPYNGMTPHISG
>d1qp8a1 c.2.1.4 (A:83-263) Putative formate dehydrogenase {Archaeon
Pyrobaculum aerophilum}
ADAVAEFALALLLAPYKRIIQYGEKMKRGDYGRDVEIPLIQGEKVAVLGLGEIGTRVGKILAALG
AQVRGFSRTPKEGPWRFTNSLEEALREARAAVCALPLNKHTRGLVKYQHLALMAEDAVFVNVGRA
EVLDRDGVLRILKERPQFIFASDVWWGRNDFAKDAEFFSLPNVVATPWVAG
>d1dxy_1  c.2.1.4  (101-299)  D-2-hydroxyisocaproate  dehydrogenase
{Lactobacillus casei}
SPAAIAEFALTDTLYLLRNMGKVQAQLQAGDYEKAGTFIGKELGQQTVGVMGTGHIGQVAIKLFK
GFGAKVIAYDPYPMKGDHPDFDYVSLEDLFKQSDVIDLHVPGIEQNTHIINEAAFNLMKPGAIVI
NTARPNLIDTQAMLSNLKSGKLAGVGIDTYEYETEDLLNLAKHGSFKDPLWDELLGMPNVVLSPH
IAYY
>d1gdha1    c.2.1.4    (A:101-291)    D-glycerate    dehydrogenase
{Hyphomicrobium methylovorum}
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VTVATAEIAMLLLLGSARRAGEGEKMIRTRSWPGWEPLELVGEKLDNKTLGIYGFGSIGQALAKR
AQGFDMDIDYFDTHRASSSDEASYQATFHDSLDSLLSVSQFFSLNAPSTPETRYFFNKATIKSLP
QGAIVVNTARGDLVDNELVVAALEAGRLAYAGFDVFAGEPNINEGYYDLPNTFLFPHIGSA
>d1psda1 c.2.1.4 (A:108-295) Phosphoglycerate dehydrogenase {Escherichia coli}
NTRSVAELVIGELLLLLRGVPEANAKAHRGVWNKLAAGSFEARGKKLGIIGYGHIGTQLGILAES
LGMYVYFYDIENKLPLGNATQVQHLSDLLNMSDVVSLHVPENPSTKNMMGAKEISLMKPGSLLIN
ASRGTVVDIPALCDALASKHLAGAAIDVFPTEPATNSDPFTSPLCEFDNVLLTPHIGG
>d2dlda1 c.2.1.4 (A:104-300) D-lactate dehydrogenase {Lactobacillus helveticus}
PNAIAEHAAIQAARVLRQDKRMDEKMAKRDLRWAPTIGREVRDQVVGVVGTGHIGQVFMRIMEGF
GAKVIAYDIFKNPELEKKGYYVDSLDDLYKQADVISLHVPDVPANVHMINDKSIAEMKDGVVIVN
CSRGRLVDTDAVIRGLDSGKIFGFVMDTYEDEVGVFNKDWEGKEFPDKRLADLIDRPNVLVTPHT
AF
>d1pjca1 c.2.1.4 (A:136-303) L-alanine dehydrogenase {Phormidium lapideum}
AGRLSVQFGARFLERQQGGRGVLLGGVPGVKPGKVVILGGGVVGTEAAKMAVGLGAQVQIFDINV
ERLSYLETLFGSRVELLYSNSAEIETAVAEADLLIGAVLVPGRRAPILVPASLVEQMRTGSVIVD
VAVDQGGCVETLHPTSHTQPTYEVFGVVHYGVPNMPGA
>d1f8ga1 c.2.1.4 (A:144-326) Nicotinamide nucleotide transhydrogenase dI component {Rhodospirillum rubrum}
AGYRAVIDGAYEFARAFPMMMTAAGTVPPARVLVFGVGVAGLQAIATAKRLGAVVMATDVRAATK
EQVESLGGKFITVDDEAMKTAETAGGYAKEMGEEFRKKQAEAVLKELVKTDIAITTALIPGKPAP
VLITEEMVTKMKPGSVIIDLAVEAGGNCPLSEPGKIVVKHGVKIVGHTNVPSR
>d1b3ra1 c.2.1.4 (A:190-352) S-adenosylhomocystein hydrolase {Rat (Rattus norvegicus)}
NLYGCRESLIDGIKRATDVMIAGKVAVVAGYGDVGKGCAQALRGFGARVIITEIDPINALQAAME
GYEVTTMDEACKEGNIFVTTTGCVDIILGRHFEQMKDDAIVCNIGHFDVEIDVKWLNENAVEKVN
IKPQVDRYLLKNGHRIILLAEGRLVNLGCAMGH
>d1gpja2 c.2.1.10 (A:144-302) Glutamyl tRNA-reductase middle domain {Archaeon Methanopyrus kandleri}
SEGAVSIGSAAVELAERELGSLHDKTVLVVGAGEMGKTVAKSLVDRGVRAVLVANRTYERAVELA
RDLGGEAVRFDELVDHLARSDVVVSATAAPHPVIHVDDVREALRKRDRRSPILIIDIANPRDVEE
GVENIEDVEVRTIDDLRVIARENLERRRK
>d1mlda1 c.2.1.5 (A:1-144) Malate dehydrogenase {Pig (Sus scrofa)}
AKVAVLGASGGIGQPLSLLLKNSPLVSRLTLYDIAHTPGVAADLSHIETRATVKGYLGPEQLPDC
LKGCDVVVIPAGVPRKPGMTRDDLFNTNATIVATLTAACAQHCPDAMICIISNPVNSTIPITAEV
FKKHGVYNPNKIFG
>d5mdha1 c.2.1.5 (A:1-154) Malate dehydrogenase {Pig (Sus scrofa)}
SEPIRVLVTGAAGQIAYSLLYSIGNGSVFGKDQPIILVLLDITPMMGVLDGVLMELQDCALPLLK
DVIATDKEEIAFKDLDVAILVGSMPRRDGMERKDLLKANVKIFKCQGAALDKYAKKSVKVIVVGN
PANTNCLTASKSAPSIPKENFSCL
>d7mdha1 c.2.1.5 (A:23-197) Malate dehydrogenase {Sorghum (Sorghum vulgare), chloroplast}
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DCFGVFCTTYDLKAEDKTKSWKKLVNIAVSGAAGMISNHLLFKLASGEVFGQDQPIALKLLGSER
SFQALEGVAMELEDSLYPLLREVSIGIDPYEVFEDVDWALLIGAKPRGPGMERAALLDINGQIFA
DQGKALNAVASKNVKVLVVGNPCNTNALICLKNAPDIPAKNFHAL
>d1civa1 c.2.1.5 (A:12-193) Malate dehydrogenase {Flaveria bidentis, chloroplast}
LPAKQKPECFGVFCLTYDLKAEEETKSWKKIINVAVSGAAGMISNHLLFKLASGEVFGPDQPISL
KLLGSERSFAALEGVAMELEDSLYPLLRQVSIGIDPYEIFQDAEWALLIGAKPRGPGMERADLLD
INGQIFAEQGKALNAVASPNVKVMVVGNPCNTNALICLKNAPNIPPKNFHAL
>d2cmd_1 c.2.1.5 (1-145) Malate dehydrogenase {Escherichia coli}
MKVAVLGAAGGIGQALALLLKTQLPSGSELSLYDIAPVTPGVAVDLSHIPTAVKIKGFSGEDATP
ALEGADVVLISAGVRRKPGMDRSDLFNVNAGIVKNLVQQVAKTCPKACIGIITNPVNTTVAIAAE
VLKKAGVYDKNKLFG
>d1bdma1 c.2.1.5 (A:0-154) Malate dehydrogenase {Thermus flavus}
MKAPVRVAVTGAAGQIGYSLLFRIAAGEMLGKDQPVILQLLEIPQAMKALEGVVMELEDCAFPLL
AGLEATDDPDVAFKDADYALLVGAAPRKAGMERRDLLQVNGKIFTEQGRALAEVAKKDVKVLVVG
NPANTNALIAYKNAPGLNPRNFTAM
>d2hlpa1 c.2.1.5 (A:22-162) Malate dehydrogenase {Archaeon Haloarcula marismortui}
TKVSVVGAAGTVGAAAAGYNIALRDIADEVVFVDIPDKEDDTVGQAADTNHGIAYDSNTRVRQGGY
EDTAGSDVVVITAGIPRQPGQTRIDLAGDNAPIMEDIQSSLDEHNDDYISLTTSNPVDLLNRHLY
EAGDRSREQVIG
>d1b8pa1 c.2.1.5 (A:3-158) Malate dehydrogenase {Aquaspirillum arcticum}
KTPMRVAVTGAAGQICYSLLFRIANGDMLGKDQPVILQLLEIPNEKAQKALQGVMMEIDDCAFPL
LAGMTAHADPMTAFKDADVALLVGARPRGPGMERKDLLEANAQIFTVQGKAIDAVASRNIKVLVV
GNPANTNAYIAMKSAPSLPAKNFTAM
>d1guya1 c.2.1.5 (A:1-143) Malate dehydrogenase {Chloroflexus aurantiacus}
MRKKISIIGAGFVGSTTAHWLAAKELGDIVLLDIVEGVPQGKALDLYEASPIEGFDVRVTGTNNY
ADTANSDVIVVTSGAPRKPGMSREDLIKVNADITRACISQAAPLSPNAVIIMVNNPLDAMTYLAA
EVSGFPKERVIGQ
>d1gv0a1 c.2.1.5 (A:1-142) Malate dehydrogenase {Chlorobium tepidum}
MKITVIGAGNVGATTAFRLAEKQLARELVLLDVVEGIPQGKALDMYESGPVGLFDTKVTGSNDYA
DTANSDIVVITAGLPRKPGMTREDLLSMNAGIVREVTGRIMEHSKNPIIVVVSNPLDIMTHVAWQ
KSGLPKERVIGM
>d1guza1 c.2.1.5 (A:1-142) Malate dehydrogenase {Chlorobium vibrioforme}
MKITVIGAGNVGATTAFRLAEKQLARELVLLDVVEGIPQGKALDMYESGPVGLFDTKVTGSNDYA
DTANSDIVIITAGLPRKPGMTREDLLMKNAGIVKEVTDNIMKHSKNPIIIVVSNPLDIMTHVAWV
RSGLPKERVIGM
>d1hyha1 c.2.1.5 (A:21-166) L-2-hydroxyisocapronate dehydrogenase, L-HICDH {Lactobacillus confusus}
ARKIGIIGLGNVGAAVAHGLIAQGVADDYVFIDANEAKVKADQIDFQDAMANLEAHGNIVINDWA
ALADADVVISTLGNIKLQQDNPTGDRFAELKFTSSMVQSVGTNLKESGFHGVLVVISNPVDVITA
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LFQHVTGFPAHKVIGT
>d5ldh_1 c.2.1.5 (1-162) Lactate dehydrogenase {Pig (Sus scrofa)}
ATLKEKLIAPVAQQETTIPDNKITVVGVGQVGMACAISILGKSLTDELALVDVLEDKLKGEMMDL
QHGSLFLQTPKIVANKDYSVTANSKIVVVTAGVRQQEGESRLNLVQRNVNVFKFIIPQIVKYSPN
CIIIVVSNPVDILTYVAWKLSGLPKHRVIG
>d9ldta1 c.2.1.5 (A:1-162) Lactate dehydrogenase {Pig (Sus scrofa)}
ATLKDQLIHNLLKEEHVPHNKITVVGVGAVGMACAISILMKELADEIALVDVMEDKLKGEMMDLQ
HGSLFLRTPKIVSGKDYNVTANSRLVVITAGARQQEGESRLNLVQRNVNIFKFIIPNIVKYSPNC
KLLVVSNPVDILTYVAWKISGFPKNRVIG
>d1i0za1 c.2.1.5 (A:1-160) Lactate dehydrogenase {Human (Homo sapiens), heart isoform (H chain)}
ATLKEKLIAPVAEEEATVPNNKITVVGVGQVGMACAISILGKSLADELALVDVLEDKLKGEMMDL
QHGSLFLQTPKIVADKDYSVTANSKIVVVTAGVRQQEGESRLNLVQRNVNVFKFIIPQIVKYSPD
CIIIVVSNPVDILTYVTWKLSGLPKHRVIG
>d1i10a1 c.2.1.5 (A:1-159) Lactate dehydrogenase {Human (Homo sapiens), muscle isoform (M chain)}
ATLKDQLIYNLLKEEQTPQNKITVVGVGAVGMACAISILMKDLADELALVDVIEDKLKGEMMDLQ
HGSLFLRTPKIVSGKDYNVTANSKLVIITAGARQQEGESRLNLVQRNVNIFKFIIPNVVKYSPNC
KLLIVSNPVDILTYVAWKISGFPKNRVIG
>d2ldx_1 c.2.1.5 (1-159) Lactate dehydrogenase {Mouse (Mus musculus)}
STVKEQLIQNLVPEDKLSRCKITVVGVGDVGMACAISILLKGLADELALVDADTDKLRGEALDLQ
HGSLFLSTPKIVFGKDYNVSANSKLVIITAGARMVSGQTRLDLLQRNVAIMKAIVPGVIQNSPDC
KIIVVTNPVDILTYVVWKISGFPVGRVIG
>d1ldm_1 c.2.1.5 (1-160) Lactate dehydrogenase {Dogfish (Squalus acanthias)}
ATLKDKLIGHLATSQEPRSYNKITVVGVGAVGMACAISILMKDLADEVALVDVMEDKLKGEMMDL
QHGSLFLHTAKIVSGKDYSVSAGSKLVVITAGARQQEGESRLNLVQRNVNIFKFIIPNIVKHSPD
CIILVVSNPVDVLTYVAWKLSGLPMHRIIG
>d1ceqa1 c.2.1.5 (A:19-163) Lactate dehydrogenase {Malaria parasite (Plasmodium falciparum)}
PKAKIVLVGSGMIGGVMATLIVQKNLGDVVLFDIVKNMPHGKALDTSHTNVMAYSNCKVSGSNTY
DDLAGSDVVIVTAGFTKAPGKSDKEWNRDDLLPLNNKIMIEIGGHIKKNCPNAFIIVVTNPVDVM
VQLLHQHSGVPKNKIIGL
>d1ldna1 c.2.1.5 (A:15-162) Lactate dehydrogenase {Bacillus stearothermophilus}
MKNNGGARVVVIGAGFVGASYVFALMNQGIADEIVLIDANESKAIGDAMDFNHGKVFAPKPVDIW
HGDYDDCRDADLVVICAGANQKPGETRLDLVDKNIAIFRSIVESVMASGFQGLFLVATNPVDILT
YATWKFSGLPHERVIGSG
>d1llc_1 c.2.1.5 (13-164) Lactate dehydrogenase {Lactobacillus casei}
ASITDKDHQKVILVGDGAVGSSYAFAMVLQGIAQEIGIVDIFKDKTKGDAIDLSNALPFTSPKKI
YSAEYSDAKDADLVVITAGAPKQPGETRLDLVNKNLKILKSIVDPIVDSGFNLIFLVAANPVDIL
TYATWKLSGFPKNRVVGSG
>d1ez4a1 c.2.1.5 (A:16-162) Lactate dehydrogenase {Lactobacillus pentosus}
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SMPNHQKVVLVGDGAVGSSYAFAMAQQGIAEEFVIVDVVKDRTKGDALDLEDAQAFTAPKKIYSG
EYSDCKDADLVVITAGAPQKPGESRLDLVNKNLNILSSIVKPVVDSGFDGIFLVAANPVDILTYA
TWKFSGFPKERVIGSG
>d1llda1 c.2.1.5 (A:7-149) Lactate dehydrogenase {Bifidobacterium longum, strain am101-2}
PTKLAVIGAGAVGSTLAFAAAQRGIAREIVLEDIAKERVEAEVLDMQHGSSFYPTVSIDGSDDPE
ICRDADMVVITAGPRQKPGQSRLELVGATVNILKAIMPNLVKVAPNAIYMLITNPVDIATHVAQK
LTGLPENQIFGSG
>d1a5z_1 c.2.1.5 (22-163) Lactate dehydrogenase {Thermotoga maritima}
MKIGIVGLGRVGSSTAFALLMKGFAREMVLIDVDKKRAEGDALDLIHGTPFTRRANIYAGDYADL
KGSDVVIVAAGVPQKPGETRLQLLGRNARVMKEIARNVSKYAPDSIVIVVTNPVDVLTYFFLKES
GMDPRKVFGS
>d1hyea1 c.2.1.5 (A:1-145) MJ0490, lactate/malate dehydrogenase {Archaeon Methanococcus jannaschii}
MKVTIIGASGRVGSATALLLAKEPFMKDLVLIGREHSINKLEGLREDIYDALAGTRSDANIYVES
DENLRIIDESDVVIITSGVPRKEGMSRMDLAKTNAKIVGKYAKKIAEICDTKIFVITNPVDVMTY
KALVDSKFERNQVFG
>d1qmga2 c.2.1.6 (A:82-307) Acetohydroxy acid isomeroreductase, ketoacid reductoisomerase (KARI) {Spinach (Spinacia oleracea)}
SATTFDFDSSVFKKEKVTLSGHDEYIVRGGRNLFPLLPDAFKGIKQIGVIGWGSQAPAQAQNLKD
SLTEAKSDVVVKIGLRKGSNSFAEARAAGFSEENGTLGDMWETISGSDLVLLLISDSAQADNYEK
VFSHMKPNSILGLSHGFLLGHLQSLGQDFPKNISVIAVCPKGMGPSVRRLYVQGKEVNGAGINSS
FAVHQDVDGRATDVALGWSIALGSPFTFATT
>d2pgd_2 c.2.1.6 (1-176) 6-phosphogluconate dehydrogenase {Sheep (Ovis orientalis aries)}
AQADIALIGLAVMGQNLILNMNDHGFVVCAFNRTVSKVDDFLANEAKGTKVLGAHSLEEMVSKLK
KPRRIILLVKAGQAVDNFIEKLVPLLDIGDIIIDGGNSEYRDTMRRCRDLKDKGILFVGSGVSGG
EDGARYGPSLMPGGNKEAWPHIKAIFQGIAAKVGTGEPCCDWVGDD
>d1pgja2 c.2.1.6 (A:1-178) 6-phosphogluconate dehydrogenase {Trypanosoma brucei}
SMDVGVVGLGVMGANLALNIAEKGFKVAVFNRTYSKSEEFMKANASAPFAGNLKAFETMEAFAAS
LKKPRKALILVQAGAATDSTIEQLKKVFEKGDILVDTGNAHFKDQGRRAQQLEAAGLRFLGMGIS
GGEEGARKGPAFFPGGTLSVWEEIRPIVEAAAAKADDGRPCVTMNGSG
>d1f0ya2 c.2.1.6 (A:12-203) Short chain L-3-hydroxyacyl CoA dehydrogenase {Human (Homo sapiens)}
KIIVKHVTVIGGGLMGAGIAQVAAATGHTVVLVDQTEDILAKSKKGIEESLRKVAKKKFAENPKA
GDEFVEKTLSTIATSTDAASVVHSTDLVVEAIVENLKVKNELFKRLDKFAAEHTIFASNTSSLQI
TSIANATTRQDRFAGLHFFNPVPVMKLVEVIKTPMTSQKTFESLVDFSKALGKHPVSCKDTP
>d1dlja2 c.2.1.6 (A:1-196) UDP-glucose dehydrogenase (UDPGDH) {Streptococcus pyogenes}
MKIAVAGSGYVGLSLGVLLSLQNEVTIVDILPSKVDKINNGLSPIQDEYIEYYLKSKQLSIKATL
DSKAAYKEAELVIIATPTNYNSRINYFDTQHVETVIKEVLSVNSHATLIIKSTIPIGFITEMRQK
FQTDRIIFSPEFLRESKALYDNLYPSRIIVSCEENDSPKVKADAEKFALLLKSAAKKNNVPVLIM
G

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>d1bg6_2 c.2.1.6 (4-187) N-(1-D-carboxylethyl)-L-norvaline dehydrogenase {Arthrobacter, strain 1c}
SKTYAVLGLGNGGHAFAAYLALKGQSVLAWDIDAQRIKEIQDRGAIIAEGPGLAGTAHPDLLTSD
IGLAVKDADVILIVVPAIHHASIAANIASYISEGQLIILNPGATGGALEFRKILRENGAPEVTIG
ETSSMLFTCRSERPGQVTVNAIKGAMDFACLPAAKAGWALEQIGSVLPQYVAVE
>d1evya2 c.2.1.6 (A:9-188) Glycerol-3- phosphate dehydrogenase {Trypanosome (Leishmania mexicana)}
KDELLYLNKAVVFGSGAFGTALAMVLSKKCREVCVWHMNEEEVRLVNEKRENVLFLKGVQLASNI
TFTSDVEKAYNGAEIILFVIPTQFLRGFFEKSGGNLIAYAKEKQVPVLVCTKGIERSTLKFPAEI
IGEFLPSPLLSVLAGPSFAIEVATGVFTCVSIASADINVARRLQRIMSTG
>d1ks9a2 c.2.1.6 (A:1-167) Ketopantoate reductase PanE {Escherichia coli}
MKITVLGCGALGQLWLTALCKQGHEVQGWLRVPQPYCSVNLVETDGSIFNESLTANDPDFLATSD
LLLVTLKAWQVSDAVKSLASTLPVTTPILLIHNGMGTIEELQNIQQPLLMGTTTHAARRDGNVII
HVANGITHIGPARQQDGDYSYLADILQTVLPDVAWHN
>d1jaya_ c.2.1.6 (A:) Coenzyme F420H2:NADP+ oxidoreductase (FNO) {Archaeon Archaeoglobus fulgidus}
MRVALLGGTGNLGKGLALRLATLGHEIVVGSRREEKAEAKAAEYRRIAGDASITGMKNEDAAEAC
DIAVLTIPWEHAIDTARDLKNILREKIVVSPLVPVSRGAKGFTYSSERSAAEIVAEVLESEKVVS
ALHTIPAARFANLDEKFDWDVPVCGDDDESKKVVMSLISEIDGLRPLDAGPLSNSRLVESLTPLI
LNIMRFNGMGELGIKFL
>d1bgva1 c.2.1.7 (A:195-449) Glutamate dehydrogenase {Clostridium symbiosum}
KARSFGGSLVRPEATGYGSVYYVEAVMKHENDTLVGKTVALAGFGNVAWGAAKKLAELGAKAVTL
SGPDGYIYDPEGITTEEKINYMLEMRASGRNKVQDYADKFGVQFFPGEKPWGQKVDIIMPCATQN
DVDLEQAKKIVANNVKYYIEVANMPTTNEALRFLMQQPNMVVAPSKAVNAGGVLVSGFEMSQNSE
RLSWTAEEVDSKLHQVMTDIHDGSAAAAERYGLGYNLVAGANIVGFQKIADAMMAQGIAW
>d1gtma1 c.2.1.7 (A:181-419) Glutamate dehydrogenase {Archaeon Pyrococcus furiosus}
GGSLGRIEATARGASYTIREAAKVLGWDTLKGKTIAIQGYGNAGYYLAKIMSEDFGMKVVAVSDS
KGGIYNPDGLNADEVLKWKNEHGSVKDFPGATNITNEELLELEVDVLAPAAIEEVITKKNADNIK
AKIVAEVANGPVTPEADEILFEKGILQIPDFLCNAGGVTVSYFEWVQNITGYYWTIEEVRERLDK
KMTKAFYDVYNIAKEKNIHMRDAAYVVAVQRVYQAMLDRGWVKH
>d1euza1 c.2.1.7 (A:181-419) Glutamate dehydrogenase {Archaeon Thermococcus profundus}
IGGSLGRGTATAQGAIFTIREAAKALGIDLKGKKIAVQGYGNAGYYTAKLAKEQLGMTVVAVSDS
RGGIYNPDGLDPDEVLKWKREHGSVKDFPGATNITNEELLELEVDVLAPAAIEEVITEKNADNIK
AKIVAEVANGPVTPEADDILREKGILQIPDFLCNAGGVTVSYFEWVQNINGYYWTEEEVREKLDK
KMTKAFWEVYNTHKDKNIHMRDAAYVVAVSRVYQAMKDRGWVKK
>d1bvua1 c.2.1.7 (A:181-418) Glutamate dehydrogenase {Archaeon Thermococcus litoralis}
GGIVARMDATARGASYTVREAAKALGMDLKGKTIAIQGYGNAGYYMAKIMSEEYGMKVVAVSDTK
GGIYNPDGLNADEVLAWKKKTGSVKDFPGATNITNEELLELEVDVLAPSAIEEVITKKNADNIKA
KIVAELANGPTTPEADEILYEKGILIIPDFLCNAGGVTVSYFEWVQNITGDYWTVEETRAKLDKK
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MTKAFWDVYNTHKEKNINMRDAAYVVAVSRVYQAMKDRGWIKK
>d1b26a1 c.2.1.7 (A:179-412) Glutamate dehydrogenase {Thermotoga maritima}
GGSKGREEATGRGVKVCAGLAMDVLGIDPKKATVAVQGFGNVGQFAALLISQELGSKVVAVSDSR
GGIYNPEGFDVEELIRYKKEHGTVVTYPKGERITNEELLELDVDILVPAALEGAIHAGNAERIKA
KAVVEGANGPTTPEADEILSRRGILVVPDILANAGGVTVSYFEWVQDLQSFFWDLDQVRNALEKM
MKGAFNDVMKVKEKYNVDMRTAAYILAIDRVAYATKKRG
>d1hwxa1 c.2.1.7 (A:209-501) Glutamate dehydrogenase {Cow (Bos taurus)}
HGRISATGRGVFHGIENFIENASYMSILGMTPGFGDKTFAVQGFGNVGLHSMRYLHRFGAKCVAV
GESDGSIWNPDGIDPKELEDFKLQHGTILGFPKAKIYEGSILEVDCDILIPAASEKQLTKSNAPR
VKAKIIAEGANGPTTPQADKIFLERNIMVIPDLYLNAGGVTVSYFQILKNLNHVSYGRLTFKYER
DSNYHLLMSVQESLERKFGKHGGTIPIVPTAEFQDRISGASEKDIVHSGLAYTMERSARQIMRTA
MKYNLGLDLRTAAYVNAIEKVFRVYNEAGVTFT
>d1leha1 c.2.1.7 (A:135-364) Leucine dehydrogenase {Bacillus sphaericus}
GISPAFGSSGNPSPVTAYGVYRGMKAAAKEAFGSDSLEGLAVSVQGLGNVAKALCKKLNTEGAKL
VVTDVNKAAVSAAVAEEGADAVAPNAIYGVTCDIFAPCALGAVLNDFTIPQLKAKVIAGSADNQL
KDPRHGKYLHELGIVYAPDYVINAGGVINVADELYGYNRTRAMKRVDGIYDSIEKIFAISKRDGV
PSYVAADRMAEERIAKVAKARSQFLQDQRNILNGR
>d1c1da1 c.2.1.7 (A:149-349) Phenylalanine dehydrogenase {Rhodococcus sp., M4}
SAFTTAVGVFEAMKATVAHRGLGSLDGLTVLVQGLGAVGGSLASLAAEAGAQLLVADTDTERVAH
AVALGHTAVALEDVLSTPCDVFAPCAMGGVITTEVARTLDCSVVAGAANNVIADEAASDILHARG
ILYAPDFVANAGGAIHLVGREVLGWSESVVHERAVAIGDTLNQVFEISDNDGVTPDEAARTLAGR
RAREAS
>d1a4ia1 c.2.1.7 (A:127-296) Methylenetetrahydrofolate dehydrogenase/cyclohydrolase {Human (Homo sapiens)}
LTSINAGRLARGDLNDCFIPCTPKGCLELIKETGVPIAGRHAVVVGRSKIVGAPMHDLLLWNNAT
VTTCHSKTAHLDEEVNKGDILVVATGQPEMVKGEWIKPGAIVIDCGINYVPDDKKPNGRKVVGDV
AYDEAKERASFITPVPGGVGPMTVAMLMQSTVESAKRFLE
>d1b0aa1 c.2.1.7 (A:123-288) Methylenetetrahydrofolate dehydrogenase/cyclohydrolase {Escherichia coli}
FHPYNVGRLCQRAPRLRPCTPRGIVTLLERYNIDTFGLNAVVIGASNIVGRPMSMELLLAGCTTT
VTHRFTKNLRHHVENADLLIVAVGKPGFIPGDWIKEGAIVIDVGINRLENGKVVGDVVFEDAAKR
ASYITPVPGGVGPMTVATLIENTLQACVEYHDPQDE
>d1edza1 c.2.1.7 (A:149-319) Methylenetetrahydrofolate dehydrogenase/cyclohydrolase {Baker's yeast (Saccharomyces cerevisiae)}
PCTPLAIVKILEFLKIYNNLLPEGNRLYGKKCIVINRSEIVGRPLAALLANDGATVYSVDVNNIQ
KFTRGESLKLNKHHVEDLGEYSEDLLKKCSLDSDVVITGVPSENYKFPTEYIKEGAVCINFACTK
NFSDDVKEKASLYVPMTGKVTIAMLLRNMLRLVRNVELSKE
>d1do8a1 c.2.1.7 (A:280-573) Mitochondrial NAD(P)-dependenent malic enzyme {Human (Homo sapiens)}
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IQGTAAVALAGLLAAQKVISKPISEHKILFLGAGEAALGIANLIVMSMVENGLSEQEAQKKIWMF
DKYGLLVKGRKAKIDSYQEPFTHSAPESIPDTFEDAVNILKPSTIIGVAGAGRLFTPDVIRAMAS
INERPVIFALSNPTAQAECTAEEAYTLTEGRCLFASGSPFGPVKLTDGRVFTPGQGNNVYIFPGV
ALAVILCNTRHISDSVFLEAAKALTSQLTDEELAQGRLYPPLANIQEVSINIAIKVTEYLYANKM
AFRYPEPEDKAKYVKERTWRSEYDSLLPDVYEWP
>d1id1a_ c.2.1.9 (A:) Rck domain from putative potassium channel Kch
{Escherichia coli}
HRKDHFIVCGHSILAINTILQLNQRGQNVTVISNLPEDDIKQLEQRLGDNADVIPGDSNDSSVLK
KAGIDRCRAILALSDNDADNAFVVLSAKDMSSDVKTVLAVSDSKNLNKIKMVHPDIILSPQLFGS
EILARVLNGEEINNDMLVSMLLN
>d1jkja1 c.2.1.8 (A:1-121) Succinyl-CoA synthetase, alpha-chain,
N-terminal (CoA-binding) domain {Escherichia coli}
SILIDKNTKVICQGFTGSQGTFHSEQAIAYGTKMVGGVTPGKGGTTHLGLPVFNTVREAVAATGA
TASVIYVPAPFCKDSILEAIDAGIKLIITITEGIPTLDMLTVKVKLDEAGVRMIGP
>d1euca1 c.2.1.8 (A:1-130) Succinyl-CoA synthetase, alpha-chain,
N-terminal (CoA-binding) domain {Pig (Sus scrofa)}
CSYTASRKHLYVDKNTKVICQGFTGKQGTFHSQQALEYGTNLVGGTTPGKGGKTHLGLPVFNTVK
EAKEQTGATASVIYVPPPFAAAAINEAIDAEVPLVVCITEGIPQQDMVRVKHRLLRQGKTRLIGP
>d1djna2 c.3.1.1 (A:490-645) Trimethylamine dehydrogenase,
C-terminal domain {Methylophilus methylotrophus, w3a1}
RWNTDGTNCLTHDPIPGADASLPDQLTPEQVMDGKKKIGKRVVILNADTYFMAPSLAEKLATAGH
EVTIVSGVHLANYMHFTLEYPNMMRRLHELHVEELGDHFCSRIEPGRMEIYNIWGDGSKRTYRGP
GVSPRDANTSHRWIEFDSLVLVTGRH
>d1cjca1 c.3.1.1 (A:107-331) Adrenodoxin reductase of mitochondrial
p450 systems {Cow (Bos taurus)}
HQALDIPGEELPGVFSARAFVGWYNGLPENRELAPDLSCDTAVILGQGNVALDVARILLTPPDHL
EKTDITEAALGALRQSRVKTVWIVGRRGPLQVAFTIKELREMIQLPGTRPMLDPADFLGLQDRIK
EAARPRKRLMELLLRTATEKPGVEEAARRASASRAWGLRFFRSPQQVLPSPDGRRAAGIRLAVTR
LEGIGEATRAVPTGDVEDLPCGLVLSSIGY
>d1h7wa3 c.3.1.1 (A:288-440) Dihydropyrimidine dehydrogenase, domain
3 {Pig (Sus scrofa)}
PKTDDIFQGLTQDQGFYTSKDFLPLVAKSSKAGMCACHSPLPSIRGAVIVLGAGDTAFDCATSAL
RCGARRVFLVFRKGFVNIRAVPEEVELAKEEKCEFLPFLSPRKVIVKGGRIVAVQFVRTEQDETG
KWNEDEDQIVHLKADVVISAFGS
>d1coy_1 c.3.1.2 (4-318,451-506) Cholesterol oxidase {Brevibacterium
sterolicum}
RTLADGDRVPALVIGSGYGGAVAALRLTQAGIPTQIVEMGRSWDTPGSDGKIFCGMLNPDKRSMW
LADKTDQPVSNFMGFGINKSIDRYVGVLDSERFSGIKVYQGRGVGGGSLVNGGMAVTPKRNYFEE
ILPSVDSNEMYNKYFPRANTGLGVNNIDQAWFESTEWYKFARTGRKTAQRSGFTTAFVPNVYDFE
YMKKEAAGQVTKSGLGGEVIYGNNAGKKSLDKTYLAQAAATGKLTITTLHRVTKVAPATGSGYSV
TMEQIDEQGNVVATKVVTADRVFFAAGSVGTSKLLVSMKAQGHLPNLSSQVGEGWXGVLLNKATD
NFGRLPEYPGLYVVDGSLVPGNVGVNPFVTITALAERNMDKIISSDI
>d1ijha1 c.3.1.2 (A:9-318,A:451-506) Cholesterol oxidase
{Streptomyces sp.}
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GYVPAVVIGTGYGAAVSALRLGEAGVQTLMLEMGQLWNQPGPDGNIFCGMLNPDKRSSWFKNRTE
APLGSFLWLDVVNRNIDPYAGVLDRVNYDQMSVYVGRGVGGGSLVNGGMAVEPKRSYFEEILPRV
DSSEMYDRYFPRANSMLRVNHIDTKWFEDTEWYKFARVSREQAGKAGLGTVFVPNVYDFGYMQRE
AAGEVPKSALATEVIYGNNHGKQSLDKTYLAAALGTGKVTIQTLHQVKTIRQTKDGGYALTVEQK
DTDGKLLATKEISCRYLFLGAGSLGSTELLVRARDTGTLPNLNSEVGAGWXGCVLGKATDDYGRV
AGYKNLYVTDGSLIPGSVGVLPFVTITALAERNVERIIKQDV
>d1k0ia1 c.3.1.2 (A:1-173,A:276-394) p-Hydroxybenzoate hydroxylase,
PHBH {Pseudomonas aeruginosa}
MKTQVAIIGAGPSGLLLGQLLHKAGIDNVILERQTPDYVLGRIRAGVLEQGMVDLLREAGVDRRM
ARDGLVHEGVEIAFAGQRRRIDLKRLSGGKTVTVYGQTEVTRDLMEAREACGATTVYQAAEVRLH
DLQGERPYVTFERDGERLRLDCDYIAGCDGFHGISRQSIPAERXMQHGRLFLAGDAAHIVPPTGA
KGLNLAASDVSTLYRLLLKAYREGRGELLERYSAICLRRIWKAERFSWWMTSVLHRFPDTDAFSQ
RIQQTELEYYLGSEAGLATIAENYVGLPYEEIE
>d1el8a1 c.3.1.2 (A:1-217,A:322-385) Sarcosine oxidase {Bacillus sp.,
strain b0618}
STHFDVIVVGAGSMGMAAGYQLAKQGVKTLLVDAFDPPHTNGSHHGDTRIIRHAYGEGREYVPLA
LRSQELWYELEKETHHKIFTKTGVLVFGPKGESAFVAETMEAAKEHSLTVDLLEGDEINKRWPGI
TVPENYNAIFEPNSGVLFSENCIRAYRELAEARGAKVLTHTRVEDFDISPDSVKIETANGSYTAD
KLIVSMGAWNSKLLSKLNLDIPXDEHFIIDLHPEHSNVVIAAGFSGHGFKFSSGVGEVLSQLALT
GKTEHDISIFSINRPALKESLQ
>d1foha5 c.3.1.2 (A:1-240,A:342-461) Phenol hydroxylase {Soil-living
yeast (Trichosporon cutaneum)}
TKYSESYCDVLIVGAGPAGLMAARVLSEYVRQKPDLKVRIIDKRSTKVYNGQADGLQCRTLESLK
NLGLADKILSEANDMSTIALYNPDENGHIRRTDRIPDTLPGISRYHQVVLHQGRIERHILDSIAE
ISDTRIKVERPLIPEKMEIDSSKAEDPEAYPVTMTLRYMSDHESTPLQFGHKTENSLFHSNLQTQ
EEEDANYRLPEGKEAGEIETVHCKYVIGCDGGHSWVRRTLGFEMIXVTEKFSKDERVFIAGDACH
THSPKAGQGMNTSMMDTYNLGWKLGLVLTGRAKRDILKTYEEERHAFAQALIDFDHQFSRLFSGR
PAKDVADEMGVSMDVFKEAFVKGNEFASGTAINYDE
>d1cf3a1 c.3.1.2 (A:3-324,A:521-583) Glucose oxidase {Aspergillus
niger}
GIEASLLTDPKDVSGRTVDYIIAGGGLTGLTTAARLTENPNISVLVIESGSYESDRGPIIEDLNA
YGDIFGSSVDHAYETVELATNNQTALIRSGNGLGGSTLVNGGTWTRPHKAQVDSWETVFGNEGWN
WDNVAAYSLQAERARAPNAKQIAAGHYFNASCHGVNGTVHAGPRDTGDDYSPIVKALMSAVEDRG
VPTKKDFGCGDPHGVSMFPNTLHEDQVRSDAAREWLLPNYQRPNLQVLTGQYVGKVLLSQNGTTP
RAVGVEFGTHKGNTHNVYAKHEVLLAAGSAVSPTILEYSGIGMKSILEPLGIDTVVDLPVGLXCS
MMPKEMGGVVDNAARVYGVQGLRVIDGSIPPTQMSSHVMTVFYAMALKISDAILEDYASMQ
>d1gpea1 c.3.1.2 (A:1-328,A:525-587) Glucose oxidase {Penicillium
amagasakiense}
YLPAQQIDVQSSLLSDPSKVAGKTYDYIIAGGGLTGLTVAAKLTENPKIKVLVIEKGFYESNDGA
IIEDPNAYGQIFGTTVDQNYLTVPLINNRTNNIKAGKGLGGSTLINGDSWTRPDKVQIDSWEKVF
GMEGWNWDNMFEYMKKAEAARTPTAAQLAAGHSFNATCHGTNGTVQSGARDNGQPWSPIMKALMN
TVSALGVPVQQDFLCGHPRGVSMIMNNLDENQVRVDAARAWLLPNYQRSNLEILTGQMVGKVLFK
QTASGPQAVGVNFGTNKAVNFDVFAKHEVLLAAGSAISPLILEYSGIGLKSVLDQANVTQLLDLP
VGIXCSMMSRELGGVVDATAKVYGTQGLRVIDGSIPPTQVSSHVMTIFYGMALKVADAILDDYAK
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SA
>d1b5qa1 c.3.1.2 (A:5-293,A:406-463) Polyamine oxidase {Maize (Zea mays)}
PRVIVVGAGMSGISAAKRLSEAGITDLLILEATDHIGGRMHKTNFAGINVELGANWVEGVNGGKM
NPIWPIVNSTLKLRNFRSDFDYLAQNVYKEDGGVYDEDYVQKRIELADSVEEMGEKLSATLHASG
RDDMSILAMQRLNEHQPNGPATPVDMVVDYYKFDYEFAEPPRVTSLQNTVPLATFSDFGDDVYFV
ADQRGYEAVVYYLAGQYLKTDDKSGKIVDPRLQLNKVVREIKYSPGGVTVKTEDNSVYSADYVMV
SASLGVLQSDLIQFKPKLPTWKVRAIYQFXWPVGVNRYEYDQLRAPVGRVYFTGEHTSEHYNGYV
HGAYLSGIDSAEILINCAQKKMC
>d1f8ra1 c.3.1.2 (A:4-319,A:433-486) L-amino acid oxidase {Malayan pit viper (Calloselasma rhodostoma)}
RNPLAECFQENDYEEFLEIARNGLKATSNPKHVVIVGAGMAGLSAAYVLAGAGHQVTVLEASERP
GGRVRTYRNEEAGWYANLGPMRLPEKHRIVREYIRKFDLRLNEFSQENDNAWYFIKNIRKKVGEV
KKDPGLLKYPVKPSEAGKSAGQLYEESLGKVVEELKRTNCSYILNKYDTYSTKEYLIKEGDLSPG
AVDMIGDLLNEDSGYYVSFIESLKHDDIFAYEKRFDEIVDGMDKLPTAMYRDIQDKVHFNAQVIK
IQQNDQKVTVVYETLSKETPSVTADYVIVCTTSRAVRLIKFNPPLLPKKAHALRSVXFTPYQFQH
FSDPLTASQGRIYFAGEYTAQAHGWIDSTIKSGLRAARDVNLASEN
>d1gosa1 c.3.1.2 (A:4-289,A:402-500) Monoamine oxidase B {Human (Homo sapiens)}
KCDVVVVGGGISGMAAAKLLHDSGLNVVVLEARDRVGGRTYTLRNQKVKYVDLGGSYVGPTQNRI
LRLAKELGLETYKVNEVERLIHHVKGKSYPFRGPFPPVWNPITYLDHNNFWRTMDDMGREIPSDA
PWKAPLAEEWDNMTMKELLDKLCWTESAKQLATLFVNLCVTAETHEVSALWFLWYVKQCGGTTRI
ISTTNGGQERKFVGGSGQVSERIMDLLGDRVKLERPVIYIDQTRENVLVETLNHEMYEAKYVISA
IPPTLGMKIHFNPPLPMMRNQMITRVXFPPGILTQYGRVLRQPVDRIYFAGTETATHWSGYMEGA
VEAGERAAREILHAMGKIPEDEIWQSEPESVDVPAQPITTTFLERHLPSVPGLLRLIGLTT
>d1d5ta1 c.3.1.3 (A:-2-291,A:389-431) Guanine nucleotide dissosiation inhibitor, GDI {Cow (Bos taurus)}
HHMDEEYDVIVLGTGLTECILSGIMSVNGKKVLHMDRNPYYGGESSSITPLEELYKRFQLLEGPP
ETMGRGRDWNVDLIPKFLMANGQLVKMLLYTEVTRYLDFKVVEGSFVYKGGKIYKVPSTETEALA
SNLMGMFEKRRFRKFLVFVANFDENDPKTFEGVDPQNTSMRDVYRKFDLGQDVIDFTGHALALYR
TDDYLDQPCLETINRIKLYSESLARYGKSPYLYPLYGLGELPQGFARLSAIYGGTYMLNKPVDDI
IMENGKVVGVKSEGEVARCKQLICDPSYVPDRVXPIDDGSESQVFCSCSYDATTHFETTCNDIKD
IYKRMAGSAFDF
>d1chua2 c.3.1.4 (A:2-237,A:354-422) L-aspartate oxidase {Escherichia coli}
NTLPEHSCDVLIIGSGAAGLSLALRLADQHQVIVLSKGPVTEGSTFYAQGGIAAVFDETDSIDSH
VEDTLIAGAGICDRHAVEFVASNARSCVQWLIDQGVLFDTHIQPNGEESYHLTREGGHSHRRILH
AADATGREVETTLVSKALNHPNIRVLERTNAVDLIVSDKIGLPGTRRVVGAWVWNRNKETVETCH
AKAVVLATGGASKVYQYTTNPDISSGDGIAMAWRAGCRVANXCGGVMVDDHGRTDVEGLYAIGEV
SYTGLHGANRMASNSLLECLVYGWSAAEDITRRMPYAHDISTLPPW
>d1fuma2 c.3.1.4 (A:1-225,A:358-442) Fumarate reductase flavoprotein subunit {Escherichia coli}
QTFQADLAIVGAGGAGLRAAIAAAQANPNAKIALISKVYPMRSHTVAAEGGSAAVAQDHDSFEYH
FHDTVAGGDWLCEQDVVDYFVHHCPTEMTQLELWGCPWSRRPDGSVNVRRFGGMKIERTWFAADK
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TGFHMLHTLFQTSLQFPQIQRFDEHFVLDILVDDGHVRGLVAMNMMEGTLVQIRANAVVMATGGA
GRVYRYNTNGGIVTGDGMGMALSHGVPLRDXMGGIETDQNCETRIKGLFAVGECSSVGLHGANRL
GSNSLAELVVFGRLAGEQATERAATAGNGNEAAIEAQAAGVEQRLKDLVNQ
>d1qlaa2 c.3.1.4 (A:1-250,A:372-457) Fumarate reductase flavoprotein subunit {Wolinella succinogenes}
MKVQYCDSLVIGGGLAGLRAAVATQQKGLSTIVLSLIPVKRSHSAAAQGGMQASLGNSKMSDGDN
EDLHFMDTVKGSDWGCDQKVARMFVNTAPKAIRELAAWGVPWTRIHKGDRMAIINAQKTTITEED
FRHGLIHSRDFGGTKKWRTCYTADATGHTMLFAVANECLKLGVSIQDRKEAIALIHQDGKCYGAV
VRDLVTGDIIAYVAKGTLIATGGYGRIYKNTTNAVVCEGTGTAIALETGIAQLGNXMGGIRTDYR
GEAKLKGLFSAGEAACWDMHGFNRLGGNSVSEAVVAGMIVGEYFAEHCANTQVDLETKTLEKFVK
GQEAYMKSLVES
>d1e39a2 c.3.1.4 (A:103-359,A:506-568) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella frigidimarina}
PTIAELAKDKSERQAALASAPHDTVDVVVVGSGGAGFSAAISATDSGAKVILIEKEPVIGGNAKL
AAGGMNAAWTDQQKAKKITDSPELMFEDTMKGGQNINDPALVKVLSSHSKDSVDWMTAMGADLTD
VGMMGGASVNRAHRPTGGAGVGAHVVQVLYDNAVKRNIDLRMNTRGIEVLKDDKGTVKGILVKGM
YKGYYWVKADAVILATGGFAKNNERVAKLDPSLKGFISTNQPGAVGDGLDVAENAGGALKDMXTM
GGVMIDTKAEVMNAKKQVIPGLYGAGEVTGGVHGANRLGGNAISDIITFGRLAGEEAAKYS
>d1qo8a2 c.3.1.4 (A:103-359,A:506-565) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella frigidimarina}
DGWDQDKIQKAIAAGPSETTQVLVVGAGSAGFNASLAAKKAGANVILVDKAPFSGGNSMISAGGM
NAVGTKQQTAHGVEDKVEWFIEDAMKGGRQQNDIKLVTILAEQSADGVQWLESLGANLDDLKRSG
GARVDRTHRPHGGKSSGPEIIDTLRKAAKEQGIDTRLNSRVVKLVVNDDHSVVGAVVHGKHTGYY
MIGAKSVVLATGGYGMNKEMIAYYRPTMKDMTSSNNITATGDGVLMAKEIGASMTDIDWVQAXAI
NTTASVLDLQSKPIDGLFAAGEVTGGVHGYNRLGGNAIADTVVFGRIAGDNAAKHALD
>d1d4ca2 c.3.1.4 (A:103-359,A:506-570) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella putrefaciens}
KFVPVDADKAAQDKAIAAGVKETTDVVIIGSGGAGLAAAVSARDAGAKVILLEKEPIPGGNTKLA
AGGMNAAETKPQAKLGIEDKKQIMIDDTMKGGRNINDPELVKVLANNSSDSIDWLTSMGADMTDV
GRMGGASVNRSHRPTGGAGVGAHVAQVLWDNAVKRGTDIRLNSRVVRILEDASGKVTGVLVKGEY
TGYYVIKADAVVIAAGGFAKNNERVSKYDPKLKGFKATNHPGATGDGLDVALQAGAATRDLEXMG
GLVIDTKAEVKSEKTGKPITGLYAAGEVTGGVHGANRLGGNAISDIVTYGRIAGASAAKFAKD
>d1jnra2 c.3.1.4 (A:2-256,A:402-502) Adenylylsulfate reductase A subunit {Archaeon Archaeoglobus fulgidus}
VYYPKKYELYKADEVPTEVVETDILIIGGGFSGCGAAYEAAYWAKLGGLKVTLVEKAAVERSGAV
AQGLSAINTYIDLTGRSERQNTLEDYVRYVTLDMMGLAREDLVADYARHVDGTVHLFEKWGLPIW
KTPDGKYVREGQWQIMIHGESYKPIIAEAAKMAVGEENIYERVFIFELLKDNNDPNAVAGAVGFS
VREPKFYVFKAKAVILATGGATLLFRPRSTGEAAGRTWYAIFDTGSGYYMGLKAGAMLTQXAGFW
VCGPEDLMPEEYAKLFPLKYNRMTTVKGLFAIGDCAGANPHKFSSGSFTEGRIAAKAAVRFILEQ
KPNPEIDDAVVEELKKKAYAPMERFMQYKDLS
>d3grs_1 c.3.1.5 (18-165,291-363) Glutathione reductase {Human (Homo sapiens)}
VASYDYLVIGGGSGGLASARRAAELGARAAVVESHKLGGTCVNVGCVPKKVMWNTAVHSEFMHDH
ADYGFPSCEGKFNWRVIKEKRDAYVSRLNAIYQNNLTKSHIEIIRGHAAFTSDPKPTIEVSGKKY

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TAPHILIATGGMPSTPHEXRVPNTKDLSLNKLGIQTDDKGHIIVDEFQNTNVKGIYAVGDVCGKA
LLTPVAIAAGRKLAHRLFEYKEDSKLD
>d3grs_2 c.3.1.5 (166-290) Glutathione reductase {Human (Homo sapiens)}
SQIPGASLGITSDGFFQLEELPGRSVIVGAGYIAVEMAGILSALGSKTSLMIRHDKVLRSFDSMI
STNCTEELENAGVEVLKFSQVKEVKKTLSGLEVSMVTAVPGRLPVMTMIPDVDCLLWAIG
>d1gera2 c.3.1.5 (A:147-262) Glutathione reductase {Escherichia coli}
DIPGVEYGIDSDGFFALPALPERVAVVGAGYIAVELAGVINGLGAKTHLFVRKHAPLRSFDPMIS
ETLVEVMNAEGPQLHTNAIPKAVVKNTDGSLTLELEDGRSETVDCLIWAIG
>d1gesa1 c.3.1.5 (A:3-146,A:263-335) Glutathione reductase {Escherichia coli}
KHYDYIAIGGGSGGIASINRAAMYGQKCALIEAKELGGTCVNVGCVPKKVMWHAAQIREAIHMYG
PDYGFDTTINKFNWETLIASRTAYIDRIHTSYENVLGKNNVDVIKGFARFVDAKTLEVNGETITA
DHILIATGGRPSHPXREPANDNINLEAAGVKTNEKGYIVVDKYQNTNIEGIYAVGDNTGAVELTP
VAVAAGRRLSERLFNNKPDEHLD
>d1gesa2 c.3.1.5 (A:147-262) Glutathione reductase {Escherichia coli}
DIPGVEYGIDSDGFFALPALPERVAVVGAGYIGVELGGVINGLGAKTHLFEMFDAPLPSFDPMIS
ETLVEVMNAEGPQLHTNAIPKAVVKNTDGSLTLELEDGRSETVDCLIWAIG
>d1feca1 c.3.1.5 (A:1-169,A:287-357) Trypanothione reductase {Crithidia fasciculata}
SRAYDLVVIGAGSGGLEAGWNAASLHKKRVAVIDLQKHHGPPHYAALGGTCVNVGCVPKKLMVTG
ANYMDTIRESAGFGWELDRESVRPNWKALIAAKNKAVSGINDSYEGMFADTEGLTFHQGFGALQD
NHTVLVRESADPNSAVLETLDTEYILLATGSWPQHLGIEXVPRSQTLQLEKAGVEVAKNGAIKVD
AYSKTNVDNIYAIGDVTDRVMLTPVAINEGAAFVDTVFANKPRATD
>d1feca2 c.3.1.5 (A:170-286) Trypanothione reductase {Crithidia fasciculata}
GDDLCITSNEAFYLDEAPKRALCVGGGYISIEFAGIFNAYKARGGQVDLAYRGDMILRGFDSELR
KQLTEQLRANGINVRTHENPAKVTKNADGTRHVVFESGAEADYDVVMLAIGR
>d1aoga1 c.3.1.5 (A:3-169,A:287-357) Trypanothione reductase {Trypanosoma cruzi}
SKIFDLVVIGAGSGGLEAAWNAATLYKKRVAVIDVQMVHGPPFFSALGGTCVNVGCVPKKLMVTG
AQYMEHLRESAGFGWEFDRTTLRAEWKNLIAVKDEAVLNINKSYDEMFRDTEGLEFFLGWGSLES
KNVVNVRESADPASAVKERLETEHILLASGSWPHMPNXGRSPRTKDLQLQNAGVMIKNGGVQVDE
YSRTNVSNIYAIGDVTNRVMLTPVAINEAAALVDTVFGTTPRKT
>d1aoga2 c.3.1.5 (A:170-286) Trypanothione reductase {Trypanosoma cruzi}
IPGIEHCISSNEAFYLPEPPRRVLTVGGGFISVEFAGIFNAYKPKDGQVTLCYRGEMILRGFDHT
LREELTKQLTANGIQILTKENPAKVELNADGSKSVTFESGKKMDFDLVMMAI
>d1h6va1 c.3.1.5 (A:10-170,A:293-366) Mammalian thioredoxin reductase {Rat (Rattus norvegicus)}
SYDFDLIIIGGGSGGLAAAKEAAKFDKKVMVLDFVTPTPLGTNWGLGGTCVNVGCIPKKLMHQAA
LLGQALKDSRNYGWKLEDTVKHDWEKMTESVQNHIGSLNWGYRVALREKKVVYENAYGKFIGPHK
IMATNNKGKEKVYSAERFLIATGERPRYLGIXRDSCTRTIGLETVGVKINEKTGKIPVTDEEQTN
VPYIYAIGDILEGKLELTPVAIQAGRLLAQRLYGGSTVKCD
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>d1h6va2 c.3.1.5 (A:171-292) Mammalian thioredoxin reductase {Rat
(Rattus norvegicus)}
PGDKEYCISSDDLFSLPYCPGKTLVVGASYVALECAGFLAGIGLDVTVMVRSILLRGFDQDMANK
IGEHMEEHGIKFIRQFVPTKIEQIEAGTPGRLKVTAKSTNSEETIEDEFNTVLLAVG
>d1trb_1 c.3.1.5 (1-118,245-316) Thioredoxin reductase {Escherichia
coli}
GTTKHSKLLILGSGPAGYTAAVYAARANLQPVLITGMEKGGQLTTTTEVENWPGDPNDLTGPLLM
ERMHEHATKFETEIIFDHINKVDLQNRPFRLNGDNGEYTCDALIIATGASARYXHSPNTAIFEGQ
LELENGYIKVQSGIHGNATQTSIPGVFAAGDVMDHIYRQAITSAGTGCMAALDAERYLDGL
>d1trb_2 c.3.1.5 (119-244) Thioredoxin reductase {Escherichia coli}
LGLPSEEAFKGRGVSACATSDGFFYRNQKVAVIGGGNTAVEEALYLSNIASEVHLIHRRDGFRAE
KILIKRLMDKVENGNIILHTNRTLEEVTGDQMGVTGVRLRDTQNSDNIESLDVAGLFVAIG
>d1vdc_1 c.3.1.5 (1-117,244-316) Thioredoxin reductase {Mouse-ear
cress (Arabidopsis thaliana)}
LETHNTRLCIVGSGPAAHTAAIYAARAELKPLLFEGWMANDIAPGGQLTTTTDVENFPGFPEGIL
GVELTDKFRKQSERFGTTIFTETVTKVDFSSKPFKLFTDSKAILADAVILAIGAVAKXGHEPATK
FLDGGVELDSDGYVVTKPGTTQTSVPGVFAAGDVQDKKYRQAITAAGTGCMAALDAEHYLQEI
>d1vdc_2 c.3.1.5 (118-243) Thioredoxin reductase {Mouse-ear cress
(Arabidopsis thaliana)}
RLSFVGSGEVLGGFWNRGISACAVCDGAAPIFRNKPLAVIGGGDSAMEEANFLTKYGSKVYIIHR
RDAFRASKIMQQRALSNPKIDVIWNSSVVEAYGDGERDVLGGLKVKNVVTGDVSDLKVSGLFFAI
>d1hyua1 c.3.1.5 (A:199-325,A:452-521) Alkyl hydroperoxide reductase
subunit F (AhpF), C-terminal domains {Salmonella typhimurium}
AEKRAAEALNKRDAYDVLIVGSGPAGAAAAVYSARKGIRTGLMGERFGGQVLDTVDIENYISVPK
TEGQKLAGALKAHVSDYDVDVIDSQSASKLVPAATEGGLHQIETASGAVLKARSIIIATGAKXLP
NTHWLEGALERNRMGEIIIDAKCETSVKGVFAAGDCTTVPYKQIIIATGEGAKASLSAFDYLIRT
KIA
>d1fl2a1 c.3.1.5 (A:212-325,A:452-521) Alkyl hydroperoxide reductase
subunit F (AhpF), C-terminal domains {Escherichia coli}
AYDVLIVGSGPAGAAAAIYSARKGIRTGLMGERFGGQILDTVDIENYISVPKTEGQKLAGALKVH
VDEYDVDVIDSQSASKLIPAAVEGGLHQIETASGAVLKARSIIVATGAKXLPNTNWLEGAVERNR
MGEIIIDAKCETNVKGVFAAGDCTTVPYKQIIIATGEGAKASLSAFDYLIRTKTA
>d1fl2a2 c.3.1.5 (A:326-451) Alkyl hydroperoxide reductase subunit
F (AhpF), C-terminal domains {Escherichia coli}
WRNMNVPGEDQYRTKGVTYCPHCDGPLFKGKRVAVIGGGNSGVEAAIDLAGIVEHVTLLEFAPEM
KADQVLQDKLRSLKNVDIILNAQTTEVKGDGSKVVGLEYRDRVSGDIHNIELAGIFVQIGL
>d1nhp_1 c.3.1.5 (1-119,243-321) NADH peroxidase {Enterococcus
faecalis}
MKVIVLGSSHGGYEAVEELLNLHPDAEIQWYEKGDFISFLSAGMQLYLEGKVKDVNSVRYMTGEK
MESRGVNVFSNTEITAIQPKEHQVTVKDLVSGEERVENYDKLIISPGAVPFELDXGVRPNTAWLK
GTLELHPNGLIKTDEYMRTSEPDVFAVGDATLIKYNPADTEVNIALATNARKQGRFAVKNLEEPV
KPFP
>d1nhp_2 c.3.1.5 (120-242) NADH peroxidase {Enterococcus faecalis}
IPGKDLDNIYLMRGRQWAIKLKQKTVDPEVNNVVVIGSGYIGIEAAEAFAKAGKKVTVIDILDRP
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LGVYLDKEFTDVLTEEMEANNITIATGETVERYEGDGRVQKVVTDKNAYDADLVVVAV
>d1d7ya1 c.3.1.5 (A:5-115,A:237-308) NADH-dependent ferredoxin
reductase, BphA4 {Pseudomonas sp., KKS102}
ALKAPVVVLGAGLASVSFVAELRQAGYQGLITVVGDEAERPYDRPPLSKDFMAHGDAEKIRLDCK
RAPEVEWLLGVTAQSFDPQAHTVALSDGRTLPYGTLVLATGAAPRAXVLANDALARAAGLACDDG
IFVDAYGRTTCPDVYALGDVTRQRNPLSGRFERIETWSNAQNQGIAVARHLVDP
>d1d7ya2 c.3.1.5 (A:116-236) NADH-dependent ferredoxin reductase,
BphA4 {Pseudomonas sp., KKS102}
LPTLQGATMPVHTLRTLEDARRIQAGLRPQSRLLIVGGGVIGLELAATARTAGVHVSLVETQPRL
MSRAAPATLADFVARYHAAQGVDLRFERSVTGSVDGVVLLDDGTRIAADMVVVGIG
>d1lvl_1 c.3.1.5 (1-150,266-335) Dihydrolipoamide dehydrogenase
{Pseudomonas putida}
QQTIQTTLLIIGGGPGGYVAAIRAGQLGIPTVLVEGQALGGTCLNIGCIPSKALIHVAEQFHQAS
RFTEPSPLGISVASPRLDIGQSVAWKDGIVDRLTTGVAALLKKHGVKVVHGWAKVLDGKQVEVDG
QRIQCEHLLLATGSSSVELPXRRPRTKGFNLECLDLKMNGAAIAIDERCQTSMHNVWAIGDVAGE
PMLAHRAMAQGEMVAEIIAGKARRFE
>d1lvl_2 c.3.1.5 (151-265) Dihydrolipoamide dehydrogenase
{Pseudomonas putida}
MLPLGGPVISSTEALAPKALPQHLVVVGGGYIGLELGIAYRKLGAQVSVVEARERILPTYDSELT
APVAESLKKLGIALHLGHSVEGYENGCLLANDGKGGQLRLEADRVLVAVG
>d1lpfa1 c.3.1.5 (A:1-158,A:278-348) Dihydrolipoamide dehydrogenase
{Pseudomonas fluorescens}
SQKFDVVVIGAGPGGYVAAIRAAQLGLKTACIEKYIGKEGKVALGGTCLNVGCIPSKALLDSSYK
YHEAKEAFKVHGIEAKGVTIDVPAMVARKANIVKNLTGGIATLFKANGVTSFEGHGKLLANKQVE
VTGLDGKTQVLEAENVIIASGSRPVEIPXRRPVTTDLLAADSGVTLDERGFIYVDDHCKTSVPGV
FAIGDVVRGAMLAHKASEEGVMVAERIAGHKAQMN
>d1lpfa2 c.3.1.5 (A:159-277) Dihydrolipoamide dehydrogenase
{Pseudomonas fluorescens}
PAPLSDDIIVDSTGALEFQAVPKKLGVIGAGVIGLELGSVWARLGAEVTVLEALDKFLPAADEQI
AKEALKVLTKQGLNIRLGARVTASEVKKKQVTVTFTDANGEQKETFDKLIVAVG
>d3lada1 c.3.1.5 (A:1-158,A:278-348) Dihydrolipoamide dehydrogenase
{Azotobacter vinelandii}
SQKFDVIVIGAGPGGYVAAIKSAQLGLKTALIEKYKGKEGKTALGGTCLNVGCIPSKALLDSSYK
FHEAHESFKLHGISTGEVAIDVPTMIARKDQIVRNLTGGVASLIKANGVTLFEGHGKLLAGKKVE
VTAADGSSQVLDTENVILASGSKPVEIPXRRPVTTDLLAADSGVTLDERGFIYVDDYCATSVPGV
YAIGDVVRGAMLAHKASEEGVVVAERIAGHKAQMN
>d3lada2 c.3.1.5 (A:159-277) Dihydrolipoamide dehydrogenase
{Azotobacter vinelandii}
PAPVDQDVIVDSTGALDFQNVPGKLGVIGAGVIGLELGSVWARLGAEVTVLEAMDKFLPAVDEQV
AKEAQKILTKQGLKILLGARVTGTEVKNKQVTVKFVDAEGEKSQAFDKLIVAVG
>d1ebda1 c.3.1.5 (A:7-154,A:272-346) Dihydrolipoamide dehydrogenase
{Bacillus stearothermophilus}
AIETETLVVGAGPGGYVAAIRAAQLGQKVTIVEKGNLGGVCLNVGCIPSKALISASHRYEQAKHS
EEMGIKAENVTIDFAKVQEWKASVVKKLTGGVEGLLKGNKVEIVKGEAYFVDANTVRVVNGDSAQ
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TYTFKNAIIATGSRPIELXVGRRPNTDELGLEQIGIKMTNRGLIEVDQQCRTSVPNIFAIGDIVP
GPALAHKASYEGKVAAEAIAGHPSAVDYV
>d1ebda2   c.3.1.5   (A:155-271)   Dihydrolipoamide   dehydrogenase
{Bacillus stearothermophilus}
PNFKFSNRILDSTGALNLGEVPKSLVVIGGGYIGIELGTAYANFGTKVTILEGAGEILSGFEKQM
AAIIKKRLKKKGVEVVTNALAKGAEEREDGVTVTYEANGETKTIDADYVLVT
>d1ojt_1 c.3.1.5 (117-275,401-470) Dihydrolipoamide dehydrogenase
{Neisseria meningitidis}
GSADAEYDVVVLGGGPGGYSAAFAAADEGLKVAIVERYKTLGGVCLNVGCIPSKALLHNAAVIDE
VRHLAANGIKYPEPELDIDMLRAYKDGVVSRLTGGLAGMAKSRKVDVIQGDGQFLDPHHLEVSLT
AGDAYEQAAPTGEKKIVAFKNCIIAAGSRXAPNGKLISAEKAGVAVTDRGFIEVDKQMRTNVPHI
YAIGDIVGQPMLAHKAVHEGHVAAENCAGHKAYFD
>d1ojt_2 c.3.1.5 (276-400) Dihydrolipoamide dehydrogenase {Neisseria
meningitidis}
VTKLPFIPEDPRIIDSSGALALKEVPGKLLIIGGGIIGLEMGTVYSTLGSRLDVVEMMDGLMQGA
DRDLVKVWQKQNEYRFDNIMVNTKTVAVEPKEDGVYVTFEGANAPKEPQRYDAVLVAAGR
>d1jeha1 c.3.1.5 (A:1-160,A:283-355) Dihydrolipoamide dehydrogenase
{Baker's yeast (Saccharomyces cerevisiae)}
TINKSHDVVIIGGGPAGYVAAIKAAQLGFNTACVEKRGKLGGTCLNVGCIPSKALLNNSHLFHQM
HTEAQKRGIDVNGDIKINVANFQKAKDDAVKQLTGGIELLFKKNKVTYYKGNGSFEDETKIRVTP
VDGLEGTVKEDHILDVKNIIVATGSEVTPFXVGRRPYIAGLGAEKIGLEVDKRGRLVIDDQFNSK
FPHIKVVGDVTFGPMLAHKAEEEGIAAVEMLKTGHGHVN
>d1jeha2 c.3.1.5 (A:161-282) Dihydrolipoamide dehydrogenase {Baker's
yeast (Saccharomyces cerevisiae)}
PGIEIDEEKIVSSTGALSLKEIPKRLTIIGGGIIGLEMGSVYSRLGSKVTVVEFQPQIGASMDGE
VAKATQKFLKKQGLDFKLSTKVISAKRNDDKNVVEIVVEDTKTNKQENLEAEVLLVA
>d1dxla1 c.3.1.5 (A:4-152,A:276-347) Dihydrolipoamide dehydrogenase
{Garden pea (Pisum sativum)}
SDENDVVIIGGGPGGYVAAIKAAQLGFKTTCIEKRGALGGTCLNVGCIPSKALLHSSHMYHEAKH
SFANHGVKVSNVEIDLAAMMGQKDKAVSNLTRGIEGLFKKNKVTYVKGYGKFVSPSEISVDTIEG
ENTVVKGKHIIIATGSDVKXGRTPFTSGLNLDKIGVETDKLGRILVNERFSTNVSGVYAIGDVIP
GPMLAHKAEEDGVACVEYLAGKVGHVD
>d1dxla2 c.3.1.5 (A:153-275) Dihydrolipoamide dehydrogenase {Garden
pea (Pisum sativum)}
SLPGVTIDEKKIVSSTGALALSEIPKKLVVIGAGYIGLEMGSVWGRIGSEVTVVEFASEIVPTMD
AEIRKQFQRSLEKQGMKFKLKTKVVGVDTSGDGVKLTVEPSAGGEQTIIEADVVLVSA
>d1fcda1  c.3.1.5  (A:1-114,A:256-327)  Flavocytochrome  c  sulfide
dehydrogenase,  FCSD,  flavin-binding  subunit  {Purple  phototrophic
bacterium (Chromatium vinosum)}
AGRKVVVVGGGTGGATAAKYIKLADPSIEVTLIEPNTDYYTCYLSNEVIGGDRKLESIKHGYDGL
RAHGIQVVHDSATGIDPDKKLVKTAGGAEFGYDRCVVAPGIELIYDKIEXQRAGKIAQIAGLTND
AGWCPVDIKTFESSIHKGIHVIGDASIANPMPKSGYSANSQGKVAAAAVVVLLKGEE
>d1fcda2 c.3.1.5 (A:115-255) Flavocytochrome c sulfide dehydrogenase,
FCSD,   flavin-binding   subunit   {Purple   phototrophic   bacterium
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(Chromatium vinosum)}
GYSEEAAAKLPHAWKAGEQTAILRKQLEDMADGGTVVIAPPAAPFRCPPGPYERASQVAYYLKAH
KPMSKVIILDSSQTFSKQSQFSKGWERLYGFGTENAMIEWHPGPDSAVVKVDGGEMMVETAFGDE
FKADVINLIPP
>d1djna3 c.4.1.1 (A:341-489,A:646-729) Trimethylamine dehydrogenase, middle domain {Methylophilus methylotrophus, w3a1}
DIRVCIGCNVCISRWEIGGPPMICTQNATAGEEYRRGWHPEKFRQTKNKDSVLIVGAGPSGSEAA
RVLMESGYTVHLTDTAEKIGGHLNQVAALPGLGEWSYHRDYRETQITKLLKKNKESQLALGQKPM
TADDVLQYGADKVIIATGAXSECTLWNELKARESEWAENDIKGIYLIGDAEAPRLIADATFTGHR
VAREIEEANPQIAIPYKRETIAWGTPHMPGGNFKIEYKV
>d1cjca2 c.4.1.1 (A:6-106,A:332-460) Adrenodoxin reductase of mitochondrial p450 systems {Cow (Bos taurus)}
TPQICVVGSGPAGFYTAQHLLKHHSRAHVDIYEKQLVPFGLVRFGVAPDHPEVKNVINTFTQTAR
SDRCAFYGNVEVGRDVTVQELQDAYHAVVLSYGAEDXKSRPIDPSVPFDPKLGVVPNMEGRVVDV
PGLYCSGWVKRGPTGVITTTMTDSFLTGQILLQDLKAGHLPSGPRPGSAFIKALLDSRGVWPVSF
SDWEKLDAEEVSRGQASGKPREKLLDPQEMLRLLGH
>d1h7wa4 c.4.1.1 (A:184-287,A:441-532) Dihydropyrimidine dehydrogenase, domain 2 {Pig (Sus scrofa)}
EAYSAKIALLGAGPASISCASFLARLGYSDITIFEKQEYVGGLSTSEIPQFRLPYDVVNFEIELM
KDLGVKIICGKSLSENEITLNTLKEEGYKAAFIGIGLPEXVLRDPKVKEALSPIKFNRWDLPEVD
PETMQTSEPWVFAGGDIVGMANTTVESVNDGKQASWYIHKYIQAQYGASVSAKPELPLFYTPVDL
VD
>d1an9a1 c.4.1.2 (A:1-194,A:288-340) D-amino acid oxidase, N-terminal domain {Pig (Sus scrofa)}
MRVVVIGAGVIGLSTALCIHERYHSVLQPLDVKVYADRFTPFTTTDVAAGLWQPYTSEPSNPQEA
NWNQQTFNYLLSHIGSPNAANMGLTPVSGYNLFREAVPDPYWKDMVLGFRKLTPRELDMFPDYRY
GWFNTSLILEGRKYLQWLTERLTERGVKFFLRKVESFEEVARGGADVIINCTGVWAGVLQPDPLX
QVRLEREQLRFGSSNTEVIHNYGHGGYGLTIHWGCALEVAKLFGKVLEERNLL
>d1c0pa1 c.4.1.2 (A:999-1193,A:1289-1361) D-amino acid oxidase, N-terminal domain {Yeast (Rhodotorula gracilis)}
LMMHSQKRVVVLGSGVIGLSSALILARKGYSVHILARDLPEDVSSQTFASPWAGANWTPFMTLTD
GPRQAKWEESTFKKWVELVPTGHAMWLKGTRRFAQNEDGLLGHWYKDITPNYRPLPSSECPPGAI
GVTYDTLSVHAPKYCQYLARELQKLGATFERRTVTSLEQAFDGADLVVNATGLGAKSIAGIDDQA
XRGGPRVEAERIVLPLDRTKSPLSLGRGSARAAKEKEVTLVHAYGFSSAGYQQSWGAAEDVAQLV
DEAFQRYHG
>d1i8ta1 c.4.1.3 (A:1-244,A:314-367) UDP-galactopyranose mutase, N-terminal domain {Escherichia coli}
MYDYIIVGSGLFGAVCANELKKLNKKVLVIEKRNHIGGNAYTEDCEGIQIHKYGAHIFHTNDKYI
WDYVNDLVEFNRFTNSPLAIYKDKLFNLPFNMNTFHQMWGVKDPQEAQNIINAQKKKYGDKVPEN
LEEQAISLVGEDLYQALIKGYTEKQWGRSAKELPAFIIKRIPVRFTFDNNYFSDRYQGIPVGGYT
KLIEKMLEGVDVKLGIDFLKDKDSLASKAHRIIYTGPIDQYFDYRFGALXNDNKNMELFKKYREL
ASREDKVIFGGRLAEYKYYDMHQVISAALYQVKNIMSTD
>d2uaga1 c.5.1.1 (A:1-93) UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase MurD, N-terminal

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domain {Escherichia coli}
ADYQGKNVVIIGLGLTGLSCVDFFLARGVTPRVMDTRMTPPGLDKLPEAVERHTGSLNDEWLMAA
DLIVASPGIALAHPSLSAAADAGIEIVG
>d1tml__ c.6.1.1 (-) Cellulase E2 {Thermomonospora fusca, strain yx}
NDSPFYVNPNMSSAEWVRNNPNDPRTPVIRDRIASVPQGTWFAHHNPGQITGQVDALMSAAQAAG
KIPILVVYNAPGRDCGNHSSGGAPSHSAYRSWIDEFAAGLKNRPAYIIVEPDLISLMSSCMQHVQ
QEVLETMAYAGKALKAGSSQARIYFDAGHSAWHSPAQMASWLQQADISNSAHGIATNTSNYRWTA
DEVAYAKAVLSAIGNPSLRAVIDTSRNGNGPAGNEWCDPSGRAIGTPSTTNTGDPMIDAFLWIKL
PGEADGCIAGAGQFVPQAAYEMAIAA
>d1qjwa_ c.6.1.1 (A:) Cellobiohydrolase II (Cel6) {Trichoderma reesei,
Cel6a}
ATYSGNPFVGVTPWANAYYASEVSSLAIPSLTGAMATAAAAVAKVPSFMWLDTLDKTPLMEQTLA
DIRTANKNGGNYAGQFVVFDLPDRDCAALASNGEYSIADGGVAKYKNYIDTIRQIVVEYSDIRTL
LVIEPDSLANLVTNLGTPKCANAQSAYLECINYAVTQLNLPNVAMYLDAGHAGWLGWPANQDPAA
QLFANVYKNASSPRALRGLATNVANYNGWNITSPPSYTQGNAVYNEKLYIHAIGPLLANHGWSNA
FFITDQGRSGKQPTGQQQWGDWCNVIGTGFGIRPSANTGDSLLDSFVWVKPGGECDGTSDSSAPR
FDSHCALPDALQPAPQAGAWFQAYFVQLLTNANPSFL
>d2bvwa_ c.6.1.1 (A:) Cellobiohydrolase II (Cel6) {Humicola insolens,
Cel6a}
NGNPFEGVQLWANNYYRSEVHTLAIPQITDPALRAAASAVAEVPSFQWLDRNVTVDTLLVQTLSE
IREANQAGANPQYAAQIVVYDLPDRDCAAAASNGEWAIANNGVNNYKAYINRIREILISFSDVRT
ILVIEPDSLANMVTNMNVPKCSGAASTYRELTIYALKQLDLPHVAMYMDAGHAGWLGWPANIQPA
AELFAKIYEDAGKPRAVRGLATNVANYNAWSVSSPPPYTSPNPNYDEKHYIEAFRPLLEARGFPA
QFIVDQGRSGKQPTGQKEWGHWCNAIGTGFGMRPTANTGHQYVDAFVWVKPGGECDGTSDTTAAR
YDYHCGLEDALKPAPEAGQWFNEYFIQLLRNANPPF
>d1dysa_ c.6.1.1 (A:) Cellobiohydrolase II (Cel6) {Humicola insolens,
Cel6b}
GNPFSGRTLLVNSDYSSKLDQTRQAFLSRGDQTNAAKVKYVQEKVGTFYWISNIFLLRDIDVAIQ
NARAAKARGENPIVGLVLYNLPDRDCSAGESSGELKLSQNGLNRYKNEYVNPFAQKLKAASDVQF
AVILEPDAIGNMVTGTSAFCRNARGPQQEAIGYAISQLQASHIHLYLDVANGGWLGWADKLEPTA
QEVATILQKAGNNAKIRGFSSNVSNYNPYSTSNPPPYTSGSPSPDESRYATNIANAMRQRGLPTQ
FIIDQSRVALSGARSEWGQWCNVNPAGFGQPFTTNTNNPNVDAIVWVKPGGESDGQCGMGGAPAA
GMWFDAYAQMLTQNAHDEIA
>d1cm5a_ c.7.1.1 (A:) Pyruvate formate-lyase, PFL {Escherichia coli}
SELNEKLATAWEGFTKGDWQNEVNVRDFIQKNYTPYEGDESFLAGATEATTTLWDKVMEGVKLEN
RTHAPVDFDTAVASTITSHDAGYINKQLEKIVGLQTEAPLKRALIPFGGIKMIEGSCKAYNRELD
PMIKKIFTEYRKTHNQGVFDVYTPDILRCRKSGVLTGLPDAYGRGRIIGDYRRVALYGIDYLMKD
KLAQFTSLQADLENGVNLEQTIRLREEIAEQHRALGQMKEMAAKYGYDISGPATNAQEAIQWTYF
GYLAAVKSQNGAAMSFGRTSTFLDVYIERDLKAGKITEQEAQEMVDHLVMKLRMVRFLRTPEYDE
LFSGDPIWATESIGGMGLDGRTLVTKNSFRFLNTLYTMGPSPEPNMTILWSEKLPLNFKKFAAKV
SIDTSSLQYENDDLMRPDFNNDDYAIAAAVSPMIVGKQMQFFGARANLAKTMLYAINGGVDEKLK
MQVGPKSEPIKGDVLNYDEVMERMDHFMDWLAKQYITALNIIHYMHDKYSYEASLMALHDRDVIR
TMACGIAGLSVAADSLSAIKYAKVKPIRDEDGLAIDFEIEGEYPQFGNNDPRVDDLAVDLVERFM
KKIQKLHTYRDAIPTQSVLTITSNVVYGKKTGNTPDGRRAGAPFGPGANPMHGRDQKGAVASLTS
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VAKLPFAYAKDGISYTFSIVPNALGKDDEVRKTNLAGLMDGYFHHEASIEGGQHLNVNVMNREML
LDAMENPEKYPQLTIRVSGYAVRFNSLTKEQQQDVITRTFTQSM
>d1qhma_ c.7.1.1 (A:) Pyruvate formate-lyase, PFL {Escherichia coli}
NEKLATAWEGFTKGDWQNEVNVRDFIQKNYTPYEGDESFLAGATEATTTLWDKVMEGVKLENRTH
APVDFDTAVASTITSHDAGYINKQLEKIVGLQTEAPLKRALIPFGGIKMIEGSCKAYNRELDPMI
KKIFTEYRKTHNQGVFDVYTPDILRCRKSGVLTGLPDAYGRGRIIGDYRRVALYGIDYLMKDKLA
QFTSLQADLENGVNLEQTIRLREEIAEQHRALGQMKEMAAKYGYDISGPATNAQEAIQWTYFGYL
AAVKSQNGAAMSFGRTSTFLDVYIERDLKAGKITEQEAQEMVDHLVMKLRMVRFLRTPEYDELFS
GDPIWATESIGGMGLDGRTLVTKNSFRFLNTLYTMGPSPEPNMTILWSEKLPLNFKKFAAKVSID
TSSLQYENDDLMRPDFNNDDYAIACCVSPMIVGKQMQFFGARANLAKTMLYAINGGVDEKLKMQV
GPKSEPIKGDVLNYDEVMERMDHFMDWLAKQYITALNIIHYMHDKYSYEASLMALHDRDVIRTMA
CGIAGLSVAADSLSAIKYAKVKPIRDEDGLAIDFEIEGEYPQFGNNDPRVDDLAVDLVERFMKKI
QKLHTYRDAIPTQSVLTITSNVVYGKK
>d1rlr_2 c.7.1.2 (222-748) R1 subunit of ribonucleotide reductase,
C-terminal domain {Escherichia coli}
FSSCVLIECGDSLDSINATSSAIVKYVSQRAGIGINAGRIRALGSPIRGGEAFHTGCIPFYKHFQ
TAVKSCSQGGVRGGAATLFYPMWHLEVESLLVLKNNRGVEGNRVRHMDYGVQINKLMYTRLLKGE
DITLFSPSDVPGLYDAFFADQEEFERLYTKYEKDDSIRKQRVKAVELFSLMMQERASTGRIYIQN
VDHCNTHSPFDPAIAPVRQSNLCLEIALPTKPLNDVNDENGEIALCTLSAFNLGAINNLDELDEL
AILAVRALDALLDYQDYPIPAAKRGAMGRRTLGIGVINFAYYLAKHGKRYSDGSANNLTHKTFEA
IQYYLLKASNELAKEQGACPWFNETTYAKGILPIDTYKKDLDTIANEPLHYDWEALRESIKTHGL
RNSTLSALMPSETSSQISNATNGIEPPRGYVSIKASKDGILRQVVPDYEHLHDAYELLWEMPGND
GYLQLVGIMQKFIDQSISANTNYDPSRFPSGKVPMQQLLKDLLTAYKFGVKTLYYQNTRDDIDDL
SNFQL
>d1b8ba_ c.7.1.3 (A:) Class III anaerobic ribonucleotide triphosphate
reductase NRDD subunit {Bacteriophage T4}
SRVFPTQRDLMAGIVSKHIAKNMVPSFIMKAHESGIIHVHDIDYSPALPFTNCCLVDLKGMLENG
FKLGNAQIETPKSIGVATAIMAQITAQVASHQYGGTTFANVDKVLSPYVKRTYAKHIEDAEKWQI
ADALNYAQSKTEKDVYDAFQAYEYEVNTLFSSNGQTPFVTLTFGTGTDWTERMIQKAILKNRIKG
LGRDGITPIFPKLVMFVEEGVNLYKDDPNYDIKQLALECASKRMYPDIISAKNNKAITGSSVPVS
PMGCRSFLSVWKDSTGNEILDGRNNLGVVTLNLPRIALDSYIGTQFNEQKFVELFNERMDLCFEA
LMCRISSLKGVKATVAPILYQEGAFGVRLKPDDDIIELFKNGRSSVSLGYIGIHELNILVGRDIG
REILTKMNAHLKQWTERTGFAFSLYSTPAENLCYRFCKLDTEKYGSVKDVTDKGWYTNSFHVSVE
ENITPFEKISREAPYHFIATGGHISYVELPDMKNNLKGLEAVWDYAAQHLDYFGVNMPVDKCFTC
GSTHEMTPTENGFVCSICGETDPKKMNTIRRTCAYLGNPNERG
>d1kbla2 c.8.1.1 (A:377-509) Pyruvate phosphate dikinase, central
domain {Clostridium symbiosum}
LHPTFNPAALKAGEVIGSALPASPGAAAGKVYFTADEAKAAHEKGERVILVRLETSPEDIEGMHA
AEGILTVRGGMTSHAAVVARGMGTCCVSGCGEIKINEEAKTFELGGHTFAEGDYISLDGSTGKIY
KGD
>d1zyma2 c.8.1.2 (A:3-21,A:145-249) N-terminal domain of enzyme I of
the PEP:sugar phosphotransferase system {Escherichia coli}
SGILASPGIAFGKALLLKEXKIIDLSAIQDEVILVAADLTPSETAQLNLKKVLGFITDAGGRTSH
TSIMARSLELPAIVGTGSVTSQVKNDDYLILDAVNNQVYVNPTNEVIDKMRAVQEQVASE
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>d1aco_1 c.8.2.1 (529-754) Aconitase, C-terminal domain {Cow (Bos taurus)}
VDVSPTSQRLQLLEPFDKWDGKDLEDLQILIKVKGKCTTDHISAAGPWLKFRGHLDNISNNLLIG
AINSENRKANSVRNAVTQEFGPVPDTARYYKQHGIRWVVIGDENYGEGSSREHSALEPRFLGGRA
IITKSFARIHETNLKKQGLLPLTFADPADYNKIHPVDKLTIQGLKDFAPGKPLTCIIKHPNGTQE
TILLNHTFNETQIEWFRAGSALNRMKELQQK
>d1a9xb1 c.8.3.1 (B:1502-1652) Carbamoyl phosphate synthetase, small subunit N-terminal domain {Escherichia coli}
IKSALLVLEDGTQFHGRAIGATGSAVGEVVFNTSMTGYQEILTDPSYSRQIVTLTYPHIGNVGTN
DADEESSQVHAQGLVIRDLPLIASNFRNTEDLSSYLKRHNIVAIADIDTRKLTRLLREKGAQNGC
IIAGDNPDAALALEKARAFPG
>d1de4c2 c.8.4.1 (C:190-382) Transferrin receptor ectodomain, apical domain {Human (Homo sapiens)}
IQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKKDFEDLYTPVNGSI
VIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHAHLGTGDPYTPGFPSFNHT
QFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDSTCRMVTSESKNVKLTVSNVLK
>d1dk7a_ c.8.5.1 (A:) GroEL {Escherichia coli}
EGMQFDRGYLSPYFINKPETGAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLLIIAEDVE
GEALATLVVNTMRGIVKVAAVKAPGFGDRRKAMLQDIATLTGGTVISEEIGMELEKATLEDLGQA
KRVVINKDTTTIIDGV
>d1kid__ c.8.5.1 (-) GroEL {Escherichia coli}
GLVPRGSEGMQFDRGYLSPYFINKPETGAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLL
IIAEDVEGEALATLVVNTMRGIVKVAAVKAPGFGDRRKAMLQDIATLTGGTVISEEIGMELEKAT
LEDLGQAKRVVINKDTTTIIDGVGEEAAIQGRVAQIRQQIEEATSDYDREKLQERVAKLAGGV
>d1oela2 c.8.5.1 (A:191-366) GroEL {Escherichia coli}
EGMQFDRGYLSPYFINKPETGAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLLIIAEDVE
GEALATAVVNTIRGIVKVAAVKAPGFGDRRKAMLQDIATLTGGTVISEEIGMELEKATLEDLGQA
KRVVINKDTTTIIDGVGEEAAIQGRVAQIRQQIEEATSDYDREKLQ
>d1ioka2 c.8.5.1 (A:191-366) GroEL {Paracoccus denitrificans}
EGMQFDRGYLSPYFVTNADKMIAELEDAYILLHEKKLSSLQPMVPLLESVIQSQKPLLIVAEDVE
GEALATLVVNKLRGGLKIAAVKAPGFGDRRKAMLQDIAILTGGQVISEDLGMKLENVTIDMLGRA
KKVSINKDNTTIVDGAGEKAEIEARVSQIRQQIEETTSDYDREKLQ
>d1srva_ c.8.5.1 (A:) GroEL {Thermus thermophilus}
GYQFDKGYISPYFVTNPETMEAVLEDAFILIVEKKVSNVRELLPILEQVAQTGKPLLIIAEDVEG
EALATLVVNKLRGTLSVAAVKAPGFGDRRKEMLKDIAAVTGGTVISEELGFKLENATLSMLGRAE
RVRITKDETTIVGGK
>d1a6db2 c.8.5.2 (B:216-367) Thermosome {Archaeon Thermoplasma acidophilum}
GIIVDKEKVHPGMPDVVKDAKIALLDAPLEIKKPEFDTNLRIEDPSMIQKFLAQEENMLREMVDK
IKSVGANVVITQKGIDDMAQHYLSRAGIYAVRRVKKSDMDKLAKATGASIVSTIDEISSSDLGTA
ERVEQVKVGEDYMTFVTGCKNP
>d1ass__ c.8.5.2 (-) Thermosome {Archaeon Thermoplasma acidophilum}
MSGIVIDKEKVHSKMPDVVKNAKIALIDSALEIKKTEIEAKVQISDPSKIQDFLNQETNTFKQMV
EKIKKSGANVVLCQKGIDDVAQHYLAKEGIYAVRRVKKSDMEKLAKATGAKIVTDLDDLTPSVLG
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EAETVEERKIGDDRMTFVMGCK
>d1ay7b_ c.9.1.1 (B:) Barstar (barnase inhibitor) {Bacillus
amyloliquefaciens}
KKAVINGEQIRSISDLHQTLKKELALPEYYGENLDALWDCLTGWVEYPLVLEWRQFEQSKQLTEN
GAESVLQVFREAKAEGCDITIILS
>d1jj2x_ c.9.2.1 (X:) Ribosomal protein L32e {Archaeon Haloarcula
marismortui}
TELQARGLTEKTPDLSDEDARLLTQRHRVGKPQFNRQDHHKKKRVSTSWRKPRGQLSKQRRGIKG
KGDTVEAGFRSPTAVRGKHPSGFEEVRVHNVDDLEGVDGDTEAVRIASKVGARKRERIEEEAEDA
GIRVLNPTYVEV
>d1e8ca1 c.98.1.1 (A:3-87) UDP-N-acetylmuramyl tripeptide synthetase
MurE {Escherichia coli}
RNLRDLLAPWVPDAPSRALREMTLDSRVAAAGDLFVAVVGHQADGRRYIPQAIAQGVAAIIAEAK
DEATDGEIREMHGVPVIYLS
>d1gg4a3 c.98.1.1 (A:1-81) UDP-murNac-tripeptide
D-alanyl-D-alanine-adding enzyme MurF {Escherichia coli}
MISVTLSQLTDILNGELQGADITLDAVTTDTRKLTPGCLFVALKGERFDAHDFADQAKAGGAGAL
LVSRPLDIDLPQLIVK
>d2bnh__ c.10.1.1 (-) Ribonuclease inhibitor {Pig (Sus scrofa)}
MNLDIHCEQLSDARWTELLPLLQQYEVVRLDDCGLTEEHCKDIGSALRANPSLTELCLRTNELGD
AGVHLVLQGLQSPTCKIQKLSLQNCSLTEAGCGVLPSTLRSLPTLRELHLSDNPLGDAGLRLLCE
GLLDPQCHLEKLQLEYCRLTAASCEPLASVLRATRALKELTVSNNDIGEAGARVLGQGLADSACQ
LETLRLENCGLTPANCKDLCGIVASQASLRELDLGSNGLGDAGIAELCPGLLSPASRLKTLWLWE
CDITASGCRDLCRVLQAKETLKELSLAGNKLGDEGARLLCESLLQPGCQLESLWVKSCSLTAACC
QHVSLMLTQNKHLLELQLSSNKLGDSGIQELCQALSQPGTTLRVLCLGDCEVTNSGCSSLASLLL
ANRSLRELDLSNNCVGDPGVLQLLGSLEQPGCALEQLVLYDTYWTEEVEDRLQALEGSKPGLRVI
S
>d1a4ya_ c.10.1.1 (A:) Ribonuclease inhibitor {Human (Homo sapiens)}
SLDIQSLDIQCEELSDARWAELLPLLQQCQVVRLDDCGLTEARCKDISSALRVNPALAELNLRSN
ELGDVGVHCVLQGLQTPSCKIQKLSLQNCCLTGAGCGVLSSTLRTLPTLQELHLSDNLLGDAGLQ
LLCEGLLDPQCRLEKLQLEYCSLSAASCEPLASVLRAKPDFKELTVSNNDINEAGVRVLCQGLKD
SPCQLEALKLESCGVTSDNCRDLCGIVASKASLRELALGSNKLGDVGMAELCPGLLHPSSRLRTL
WIWECGITAKGCGDLCRVLRAKESLKELSLAGNELGDEGARLLCETLLEPGCQLESLWVKSCSFT
AACCSHFSSVLAQNRFLLELQISNNRLEDAGVRELCQGLGQPGSVLRVLWLADCDVSDSSCSSLA
ATLLANHSLRELDLSNNCLGDAGILQLVESVRQPGCLLEQLVLYDIYWSEEMEDRLQALEKDKPS
LRVIS
>d1yrga_ c.10.1.2 (A:) Rna1p (RanGAP1), N-terminal domain {Fission
yeast (Schizosaccharomyces pombe)}
ARFSIEGKSLKLDAITTEDEKSVFAVLLEDDSVKEIVLSGNTIGTEAARWLSENIASKKDLEIAE
FSDIFTGRVKDEIPEALRLLLQALLKCPKLHTVRLSDNAFGPTAQEPLIDFLSKHTPLEHLYLHN
NGLGPQAGAKIARALQELAVNKKAKNAPPLRSIICGRNRLENGSMKEWAKTFQSHRLLHTVKMVQ
NGIRPEGIEHLLLEGLAYCQELKVLDLQDNTFTHLGSSALAIALKSWPNLRELGLNDCLLSARGA
AAVVDAFSKLENIGLQTLRLQYNEIELDAVRTLKTVIDEKMPDLLFLELNGNRFSEEDDVVDEIR
EVFSTRGRGELDELDDME
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>d1fqva2 c.10.1.3 (A:146-431) Cyclin A/CDK2-associated p19, Skp2
{Human (Homo sapiens)}
ESLWQTLDLTGKNLHPDVTGRLLSQGVIAFRCPRSFMDQPLAEHFSPFRVQHMDLSNSVIEVSTL
HGILSQCSKLQNLSLEGLRLSDPIVNTLAKNSNLVRLNLSGCSGFSEFALQTLLSSCSRLDELNL
SWCFDFTEKHVQVAVAHVSETITQLNLSGYRKNLQKSDLSTLVRRCPNLVHLDLSDSVMLKNDCF
QEFFQLNYLQHLSLSRCYDIIPETLLELGEIPTLKTLQVFGIVPDGTLQLLKEALPHLQINCSHF
TTIARPTIGNKKNQEIWGIKCRLTLQ
>d1fs2a2 c.10.1.3 (A:146-401) Cyclin A/CDK2-associated p19, Skp2
{Human (Homo sapiens)}
ESLWQTLDEFRVQHMDLSNSVIEVSTLHGILSQCSKLQNLSLEGLRLSDPIVNTLAKNSNLVRLN
LSGCSGFSEFALQTLLSSCSRLDELNLSWCFDFTEKHVQVAVAHVSETITQLNLSGYRKNLQKSD
LSTLVRRCPNLVHLDLSDSVMLKNDCFQEFFQLNYLQHLSLSRCYDIIPETLLELGEIPTLKTLQ
VFGIVPDGTLQLLKEALPHLQIN
>d1h6ta2 c.10.2.1 (A:31-240) Internalin B {Listeria monocytogenes}
GPLGSETITVPTPIKQIFSDDAFAETIKDNLKKKSVTDAVTQNELNSIDQIIANNSDIKSVQGIQ
YLPNVTKLFLNGNKLTDIKPLANLKNLGWLFLDENKVKDLSSLKDLKKLKSLSLEHNGISDINGL
VHLPQLESLYLGNNKITDITVLSRLTKLDTLSLEDNQISDIVPLAGLTKLQNLYLSKNHISDLRA
LAGLKNLDVLELFSQ
>d1h6ua2 c.10.2.1 (A:36-262) Internalin H {Listeria monocytogenes}
GSITQPTAINVIFPDPALANAIKIAAGKSNVTDTVTQADLDGITTLSAFGTGVTTIEGVQYLNNL
IGLELKDNQITDLAPLKNLTKITELELSGNPLKNVSAIAGLQSIKTLDLTSTQITDVTPLAGLSN
LQVLYLDLNQITNISPLAGLTNLQYLSIGNAQVSDLTPLANLSKLTTLKADDNKISDISPLASLP
NLIEVHLKNNQISDVSPLANTSNLFIVTLTNQ
>d1jl5a_ c.10.2.6 (A:) Leucine rich effector protein YopM {Yersinia
pestis}
KSKTEYYNAWSEWERNAPPGNGEQREMAVSRLRDCLDRQAHELELNNLGLSSLPELPPHLESLVA
SCNSLTELPELPQSLKSLLVDNNNLKALSDLPPLLEYLGVSNNQLEKLPELQNSSFLKIIDVDNN
SLKKLPDLPPSLEFIAAGNNQLEELPELQNLPFLTAIYADNNSLKKLPDLPLSLESIVAGNNILE
ELPELQNLPFLTTIYADNNLLKTLPDLPPSLEALNVRDNYLTDLPELPQSLTFLDVSENIFSGLS
ELPPNLYYLNASSNEIRSLCDLPPSLEELNVSNNKLIELPALPPRLERLIASFNHLAEVPELPQN
LKQLHVEYNPLREFPDIPESVEDLRMNS
>d1dcea3 c.10.2.2 (A:444-567) Rab geranylgeranyltransferase
alpha-subunit, C-terminal domain {Rat (Rattus norvegicus)}
RVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRALPPALAALRCLEVLQASDNALENVDGVANLP
RLQELLLCNNRLQQSAAIQPLVSCPRLVLLNLQGNSLCQEEGIQERLAEMLPSVSSILT
>d1koha1 c.10.2.3 (A:201-362) mRNA export factor tap {Human (Homo
sapiens)}
LNELKPEQVEQLKLIMSKRYDGSQQALDLKGLRSDPDLVAQNIDVVLNRRSSMAATLRIIEENIP
ELLSLNLSNNRLYRLDDMSSIVQKAPNLKILNLSGNELKSERELDKIKGLKLEELWLDGNSLSDT
FRDQSTYISAIRERFPKLLRLDGHELPPPIAF
>d1a9na_ c.10.2.4 (A:) Splicesomal U2A' protein {Human (Homo sapiens)}
VKLTAELIEQAAQYTNAVRDRELDLRGYKIPVIENLGATLDQFDAIDFSDNEIRKLDGFPLLRRL
KTLLVNNNRICRIGEGLDQALPDLTELILTNNSLVELGDLDPLASLKSLTYLCILRNPVTNKKHY
RLYVIYKVPQVRVLDFQKVKLKERQEAEKMFK
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>d1igra1 c.10.2.5 (A:1-149) L1 and L2 domains of the type 1 insulin-like
growth factor receptor {Human (Homo sapiens)}
EICGPGIDIRNDYQQLKRLENCTVIEGYLHILLISKAEDYRSYRFPKLTVITEYLLLFRVAGLES
LGDLFPNLTVIRGWKLFYNYALVIFEMTNLKDIGLYNLRNITRGAIRIEKNADLCYLSTVDWSLI
LDAVSNNYIVGNKPPKECG
>d1igra2 c.10.2.5 (A:300-478) L1 and L2 domains of the type 1
insulin-like growth factor receptor {Human (Homo sapiens)}
KVCEEEKKTKTIDSVTSAQMLQGCTIFKGNLLINIRRGNNIASELENFMGLIEVVTGYVKIRHSH
ALVSLSFLKNLRLILGEEQLEGNYSFYVLDNQNLQQLWDWDHRNLTIKAGKMYFAFNPKLCVSEI
YRMEEVTGTKGRQSKGDINTRNNGERASCESDVDDDDKEQKLISEEDLN
>d1ds9a_ c.11.1.1 (A:) Outer arm dynein light chain 1 {Green algae
(Chlamydomonas reinhardtii)}
MAKATTIKDAIRIFEERKSVVATEAEKVELHGMIPPIEKMDATLSTLKACKHLALSTNNIEKISS
LSGMENLRILSLGRNLIKKIENLDAVADTLEELWISYNQIASLSGIEKLVNLRVLYMSNNKITNW
GEIDKLAALDKLEDLLLAGNPLYNDYKENNATSEYRIEVVKRLPNLKKLDGMPVDVDEREQANVA
RGG
>d1jj2k_ c.12.1.1 (K:) Ribosomal protein L15 (L15p) {Archaeon
Haloarcula marismortui}
TSKKKRQRGSRTHGGGSHKNRRGAGHRGGRGDAGRDKHEFHNHEPLGKSGFKRPQKVQEEAATID
VREIDENVTLLAADDVAEVEDGGFRVDVRDVVEEADDADYVKVLGAGQVRHELTLIADDFSEGAR
EKVEGAGGSVELTDLGEERQ
>d1jj2n_ c.12.1.1 (N:) Ribosomal protein L18e {Archaeon Haloarcula
marismortui}
SKTNPRLSSLIADLKSAARSSGGAVWGDVAERLEKPRRTHAEVNLGRIERYAQEDETVVVPGKVL
GSGVLQKDVTVAAVDFSGTAETKIDQVGEAVSLEQAIENNPEGSHVRVIR
>d1aua_2 c.13.1.1 (97-299) C-terminal domain of phosphatidylinositol
transfer protein sec14p {Baker's yeast (Saccharomyces cerevisiae)}
YDEKPLIAKFYPQYYHKTDKDGRPVYFEELGAVNLHEMNKVTSEERMLKNLVWEYESVVQYRLPA
CSRAAGHLVETSCTIMDLKGISISSAYSVMSYVREASYISQNYYPERMGKFYIINAPFGFSTAFR
LFKPFLDPVTVSKIFILGSSYQKELLKQIPAENLPVKFGGKSEVDESKGGLYLSDIGPWRDPKYI
GPEGEAPE
>d1h4xa_ c.13.2.1 (A:) Anti-sigma factor antagonist SpoIIaa {Bacillus
sphaericus}
AFQLEMVTRETVVIRLFGELDHHAVEQIRAKISTAIFQGAVTTIIWNFERLSFMDSSGVGLVLGR
MRELEAVAGRTILLNPSPTMRKVFQFSGLGPWMMDATEEEAIDRVR
>d1auz__ c.13.2.1 (-) Anti-sigma factor antagonist SpoIIaa {Bacillus
subtilis}
SLGIDMNVKESVLCIRLTGELDHHTAETLKQKVTQSLEKDDIRHIVLNLEDLSFMDSSGLGVILG
RYKQIKQIGGEMVVCAISPAVKRLFDMSGLFKIIRFEQSEQQALLTLGVAS
>d1tyfa_ c.14.1.1 (A:) Clp protease, ClpP subunit {Escherichia coli}
SRGERSFDIYSRLLKERVIFLTGQVEDHMANLIVAQMLFLEAENPEKDIYLYINSPGGVITAGMS
IYDTMQFIKPDVSTICMGQAASMGAFLLTAGAKGKRFCLPNSRVMIHQPLGGYQGQATDIEIHAR
EILKVKGRMNELMALHTGQSLEQIERDTERDRFLSAPEAVEYGLVDSILTHRN
>d1fc6a4 c.14.1.2 (A:78-156,A:249-463) Photosystem II D1 C-terminal
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processing protease {Algae (Scenedesmus obliquus)}
VTSEQLLFLEAWRAVDRAYVDKSFNGQSWFKLRETYLKKEPMDRRAQTYDAIRKMLAVLDDPFTR
FLEPSRLAALRRGTXKVTINPVTFTTCSNVAAAALPPGAAKQQLGYVRLATFNSNTTAAAQQAFT
ELSKQGVAGLVLDIRNNGGGLFPAGVNVARMLVDRGDLVLIADSQGIRDIYSADGNSIDSATPLV
VLVNRGTASASEVLAGALKDSKRGLIAGERTFGKGLIQTVVDLSDGSGVAVTVARYQTPAGVDIN
KIGVSPDVQLDPEVLPTDLEGVCRVLGSDAAPRLF
>d1k32a4 c.14.1.2 (A:680-762,A:854-1061) Tricorn protease {Archaeon Thermoplasma acidophilum}
SSIHEEFLQMYDEAWKLARDNYWNEAVAKEISERIYEKYRNLVPLCKTRYDLSNVIVEMQGEYRT
SHSYEMGGTFTDKDPFRSXDDRFIRYRSWVEANRRYVHERSKGTIGYIHIPDMGMMGLNEFYRLF
INESSYQGLIVDVRFNGGGFVSQLIIEKLMNKRIGYDNPRRGTLSPYPTNSVRGKIIAITNEYAG
SDGDIFSFSFKKLGLGKLIGTRTWGGVVGITPKRRLIDGTVLTQPEFAFWFRDAGFGVENYGVDP
DVEIEYAPHDYLSGKDPQIDYAIDALIEELRN
>d1j7xa_ c.14.1.2 (A:) Interphotoreceptor retinoid-binding protein IRBP {African clawed frog (Xenopus laevis)}
DPSVTHVLHQLCDILANNYAFSERIPTLLQHLPNLDYSTVISEEDIAAKLNYELQSLTEDPRLVL
KSKTDTLVMPGDSIQAENIPEDEAMLQALVNTVFKVSILPGNIGYLRFDQFADVSVIAKLAPFIV
NTVWEPITITENLIIDLRYNVGGSSTAVPLLLSYFLDPETKIHLFTLHNRQQNSTDEVYSHPKVL
GKPYGSKKGVYVLTSHQTATAAEEFAYLMQSLSRATIIGEITSGNLMHSKVFPFGDTQLSVTVPI
INFIDSNGDYWLGGGVVPDAIVLADEALDKAKEIIAFHPPLA
>d1nzya_ c.14.1.3 (A:) 4-Chlorobenzoyl-CoA dehalogenase {Pseudomonas sp., strain CBS-3}
MYEAIGHRVEDGVAEITIKLPRHRNALSVKAMQEVTDALNRAEEDDSVGAVMITGAEDAFCAGFY
LREIPLDKGVAGVRDHFRIAALWWHQMIHKIIRVKRPVLAAINGVAAGGGLGISLASDMAICADS
AKFVCAWHTIGIGNDTATSYSLARIVGMRRAMELMLTNRTLYPEEAKDWGLVSRVYPKDEFREVA
WKVARELAAAPTHLQVMAKERFHAGWMQPVEECTEFEIQNVIASVTHPHFMPCLTRFLDGHRADR
PQVELPAGV
>d1ey3a_ c.14.1.3 (A:) Enoyl-CoA hydratase (crotonase) {Rat (Rattus norvegicus)}
FQYIITEKKGKNSSVGLIQLNRPKALNALCNGLIEELNQALETFEEDPAVGAIVLTGGEKAFAAG
ADIKEMQNRTFQDCYSGKFLSHWDHITRIKKPVIAAVNGYALGGGCELAMMCDIIYAGEKAQFGQ
PEILLGTIPGAGGTQRLTRAVGKSLAMEMVLTGDRISAQDAKQAGLVSKIFPVETLVEEAIQCAE
KIANNSKIIVAMAKESVNAAFEMTLTEGNKLEKKLFYSTFATDDRREGMSAFVEKRKANFKDH
>d1dcia_ c.14.1.3 (A:) Dienoyl-CoA isomerase (delta3-delta2-enoyl-CoA isomerase) {Rat (Rattus norvegicus)}
AYESIQVTSAQKHVLHVQLNRPEKRNAMNRAFWRELVECFQKISKDSDCRAVVVSGAGKMFTSGI
DLMDMASDILQPPGDDVARIAWYLRDLISRYQKTFTVIEKCPKPVIAAIHGGCIGGGVDLISACD
IRYCTQDAFFQVKEVDVGLAADVGTLQRLPKVIGNRSLVNELTFTARKMMADEALDSGLVSRVFP
DKDVMLNAAFALAADISSKSPVAVQGSKINLIYSRDHSVDESLDYMATWNMSMLQTQDIIKSVQA
AMEKKDSKSITFSKL
>d1hnua_ c.14.1.3 (A:) Dienoyl-CoA isomerase (delta3-delta2-enoyl-CoA isomerase) {Baker's yeast (Saccharomyces cerevisiae)}
NEKISYRIEGPFFIIHLINPDNLNALEGEDYIYLGELLELADRNRDVYFTIIQSSGRFFSSGADF
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KGIAKAQGDDTNKYPSETSKWVSNFVARNVYVTDAFIKHSKVLICCLNGPAIGLSAALVALCDIV
YSINDKVYLLYPFANLGLITEGGTTVSLPLKFGTNTTYECLMFNKPFKYDIMCENGFISKNFNMP
SSNAEAFNAKVLEELREKVKGLYLPSCLGMKKLLKSNHIDAFNKANSVEVNESLKYWVDGEPLKR
FRQ
>d1hzda_ c.14.1.3 (A:) AUH protein {Human (Homo sapiens)}
EDELRVRHLEEENRGIVVLGINRAYGKNSLSKNLIKMLSKAVDALKSDKKVRTIIIRSEVPGIFC
AGADLKERAKMSSSEVGPFVSKIRAVINDIANLPVPTIAAIDGLALGGGLELALACDIRVAASSA
KMGLVETKLAIIPGGGGTQRLPRAIGMSLAKELIFSARVLDGKEAKAVGLISHVLEQNQEGDAAY
RKALDLAREFLPQGPVAMRVAKLAINQGMEVDLVTGLAIEEACYAQTIPTKDRLEGLLAFKEKRP
PRYKGE
>d1ef8a_ c.14.1.3 (A:) Methylmalonyl CoA decarboxylase {Escherichia
coli}
MSYQYVNVVTINKVAVIEFNYGRKLNALSKVFIDDLMQALSDLNRPEIRCIILRAPSGSKVFSAG
HDIHELPSGGRDPLSYDDPLRQITRMIQKFPKPIISMVEGSVWGGAFEMIMSSDLIIAASTSTFS
MTPVNLGVPYNLVGIHNLTRDAGFHIVKELIFTASPITAQRALAVGILNHVVEVEELEDFTLQMA
HHISEKAPLAIAVIKEELRVLGEAHTMNSDEFERIQGMRRAVYDSEDYQEGMNAFLEKRKPNFVG
H
>d1jnxx1 c.15.1.3 (X:1649-1757) Breast cancer associated protein,
BRCA1 {Human (Homo sapiens)}
RMSMVVSGLTPEEFMLVYKFARKHHITLTNLITEETTHVVMKTDAEFVCERTLKYFLGIAGGKWV
VSYFWVTQSIKERKMLNEHDFEVRGDVVNGRNHQGPKRARESQD
>d1jnxx2 c.15.1.3 (X:1758-1859) Breast cancer associated protein,
BRCA1 {Human (Homo sapiens)}
RKIFRGLEICCYGPFTNMPTDQLEWMVQLCGASVVKELSSFTLGTGVHPIVVVQPDAWTEDNGFH
AIGQMCEAPVVTREWVLDSVALYQCQELDTYLIPQIP
>d1cdza_ c.15.1.1 (A:) DNA-repair protein XRCC1 {Human (Homo sapiens)}
ELPDFFQGKHFFLYGEFPGDERRKLIRYVTAFNGELEDYMSDRVQFVITAQEWDPSFEEALMDNP
SLAFVRPRWIYSCNEKQKLLPHQLYGVVPQA
>d1in1a_ c.15.1.2 (A:) DNA ligase III alpha {Human (Homo sapiens)}
GSADETLCQTKVLLDIFTGVRLYLPPSTPDFSRLRRYFVAFDGDLVQEFDMTSATHVLGSRDKNP
AAQQVSPEWIWACIRKRRLVAPC
>d1dgtb3 c.15.1.2 (B:2582-2660) NAD+-dependent DNA ligase, domain 4
{Thermus filiformis}
EEVSDLLSGLTFVLTGELSRPREEVKALLGRLGAKVTDSVSRKTSYLVVGENPGSKLEKARALGV
AVLTEEEFWRFLKE
>d1rvv1_ c.16.1.1 (1:) Lumazine synthase {Bacillus subtilis}
MNIIQGNLVGTGLKIGIVVGRFNDFITSKLLSGAEDALLRHGVDTNDIDVAWVPGAFEIPFAAKK
MAETKKYDAIITLGTVIRGATTHYDYVCNEAAKGIAQAANTTGVPVIFGIVTTENIEQAIERAGT
KAGNKGVDCAVSAIEMANLNRSFE
>d1di0a_ c.16.1.1 (A:) Lumazine synthase {Brucella abortus}
TSFKIAFIQARWHADIVDEARKSFVAELAAKTGGSVEVEIFDVPGAYEIPLHAKTLARTGRYAAI
VGAAFVIDGGIYDHDFVATAVINGMMQVQLETEVPVLSVVLTPHHFHESKEHHDFFHAHFKVKGV
EAAHAALQIVSERSRIAA
>d1hqka_ c.16.1.1 (A:) Lumazine synthase {Aquifex aeolicus}
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MQIYEGKLTAEGLRFGIVASRFNHALVDRLVEGAIDCIVRHGGREEDITLVRVPGSWEIPVAAGE
LARKEDIDAVIAIGVLIRGATPHFDYIASEVSKGLANLSLELRKPITFGVITADTLEQAIERAGT
KHGNKGWEAALSAIEMANLFKSLR
>d1c41a_ c.16.1.1 (A:) Lumazine synthase {Rice blast fungus
(Magnaporthe grisea)}
GPTPQQHDGSALRIGIVHARWNETIIEPLLAGTKAKLLACGVKESNIVVQSVPGSWELPIAVQRL
YSASQLQTPSSGPSLSAGDLLGSSTTDLTALPTTTASSTGPFDALIAIGVLIKGETMHFEYIADS
VSHGLMRVQLDTGVPVIFGVLTVLTDDQAKARAGVIEGSHNHGEDWGLAAVEMGVRRRDWAAGKT
>d1c2ya_ c.16.1.1 (A:) Lumazine synthase {Spinach (Spinacia
oleracea)}
MNELEGYVTKAQSFRFAIVVARFNEFVTRRLMEGALDTFKKYSVNEDIDVVWVPGAYELGVTAQA
LGKSGKYHAIVCLGAVVKGDTSHYDAVVNSASSGVLSAGLNSGVPCVFGVLTCDNMDQAINRAGG
KAGNKGAESALTAIEMASLFEHHLK
>d1ejba_ c.16.1.1 (A:) Lumazine synthase {Baker's yeast
(Saccharomyces cerevisiae)}
AVKGLGKPDQVYDGSKIRVGIIHARWNRVIIDALVKGAIERMASLGVEENNIIIETVPGSYELPW
GTKRFVDRQAKLGKPLDVVIPIGVLIKGSTMHFEYISDSTTHALMNLQEKVDMPVIFGLLTCMTE
EQALARAGIDEAHSMHNHGEDWGAAAVEMAVKFGKNAF
>d1cp3a_ c.17.1.1 (A:) Apopain (caspase-3, cpp32) {Human (Homo
sapiens)}
NSYKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVEL
MRDVSKEDHSKRSSFVCVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACR
GTELDCGIETDSGVDDDMACHKIPVDADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADK
LEFMHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH
>g1ibc.1 c.17.1.1 (A:,B:) Interleukin-1beta converting enzyme (a
cysteine protease) {Human (Homo sapiens)}
GNVKLCSLEEAQRIWKQKSAEIYPIMDKSSRTRLALIICNEEFDSIPRRTGAEVDITGMTMLLQN
LGYSVDVKKNLTASDMTTELEAFAHRPEHKTSDSTFLVFMSHGIREGICGKKHSEQVPDILQLNA
IFNMLNTKNCPSLKDKPKVIIIQACRGDSPGVVWFKDXAIKKAHIEKDFIAFCSSTPDNVSWRHP
TMGSVFIGRLIEHMQEYACSCDVEEIFRKVRFSFEQPAGRAQMPTTERVTLTRCFYLFPGH
>d1f1ja_ c.17.1.1 (A:) Caspase-7 {Human (Homo sapiens)}
YQYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDL
LKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRSKTLLEKPKLFFIQACR
GTELDDGIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEH
GKDLEIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYFS
>g1qtn.1 c.17.1.1 (A:,B:) Caspase-8 {Human (Homo sapiens)}
DKVYQMKSKPRGYCLIINNHNFAKAREKVPKLHSIRDRNGTHLDAGALTTTFEELHFEIKPHDDC
TVEQIYEILKIYQLMDHSNMDCFICCILSHGDKGIIYGTDGQEAPIYELTSQFTGLKCPSLAGKP
KVFFIQACQGDNYQKGIPVETDXTRYIPDEADFLLGMATVNNCVSYRNPAEGTWYIQSLCQSLRE
RCPRGDDILTILTEVNYEVSNKDDKKNMGKQMPQPTFTLRKKLVFPSD
>d1jxqa_ c.17.1.1 (A:) Caspase-9 {Human (Homo sapiens)}
MGALESLRGNADLAYILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRRRFSSLHFMVEV
KGDLTAKKMVLALLELARQDHGALDCCVVVILSHGCQASHLQFPGAVYGTDGCPVSVEKIVNIFN
GTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDESPGSNPEPDATPFQEGLRTFDQLDAIS
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SLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYK
QMPGCFNFLRKKLFFKTS
>d1cvra2 c.17.1.2 (A:1-350) Gingipain R (RgpB), N-terminal domain
{Porphyromonas gingivalis}
YTPVEEKENGRMIVIVAKKYEGDIKDFVDWKNQRGLRTEVKVAEDIASPVTANAIQQFVKQEYEK
EGNDLTYVLLVGDHKDIPAKITPGIKSDQVYGQIVGNDHYNEVFIGRFSCESKEDLKTQIDRTIH
YERNITTEDKWLGQALCIASAEGGPSADNGESDIQHENVIANLLTQYGYTKIIKCYDPGVTPKNI
IDAFNGGISLVNYTGHGSETAWGTSHFGTTHVKQLTNSNQLPFIFDVACVNGDFLFSMPCFAEAL
MRAQKDGKPTGTVAIIASTIDQYWAPPMRGQDEMNEILCEKHPNNIKRTFGGVTMNGMFAMVEKY
KKDGENMLDTWTVFGDPSLLVRTLV
>d1akz__ c.18.1.1 (-) Uracil-DNA glycosylase {Human (Homo sapiens)}
MEFFGESWKKHLSGEFGKPYFIKLMGFVAEERKHYTVYPPPHQVFTWTQMCDIKDVKVVILGQDP
YHGPNQAHGLCFSVQRPVPPPPSLENIYKELSTDIEDFVHPGHGDLSGWAKQGVLLLNAVLTVRA
HQANSHKERGWEQFTDAVVSWLNQNSNGLVFLLWGSYAQKKGSAIDRKRHHVLQTAHPSPLSVYR
GFFGCRHFSKTNELLQKSGKKPIDWKEL
>d1laue_ c.18.1.1 (E:) Uracil-DNA glycosylase {Herpes simplex virus
type 1}
LDWTTFRRVFLIDDAWRPLMEPELANPLTAHLLAEYNRRCQTEEVLPPREDVFSWTRYCTPDEVR
VVIIGQDPYHHPGQAHGLAFSVRANVPPPPSLRNVLAAVKNCYPEARMSGHGCLEKWARDGVLLL
NTTLTVKRGAAASHSRIGWDRFVGGVIRRLAARRPGLVFMLWGTHAQNAIRPDPRVHCVLKFSHP
SPLSKVPFGTCQHFLVANRYLETRSISPIDWSV
>d3euga_ c.18.1.1 (A:) Uracil-DNA glycosylase {Escherichia coli}
LTWHDVLAEEKQQPHFLNTLQTVASERQSGVTIYPPQKDVFNAFRFTELGDVKVVILGQDPYHGP
GQAHGLAFSVRPGIAIPPSLLNMYKELENTIPGFTRPNHGYLESWARQGVLLLNTVLTVRAGQAH
SHASLGWETFTDKVISLINQHREGVVFLLWGSHAQKKGAIIDKQRHHVLKAPHPSPLSAHRGFFG
CNHFVLANQWLEQHGETPIDWMPVLPAESE
>d1muga_ c.18.1.2 (A:) G:T/U mismatch-specific DNA glycosylase
{Escherichia coli}
MVEDILAPGLRVVFCGINPGLSSAGTGFPFAHPANRFWKVIYQAGFTDRQLKPQEAQHLLDYRCG
VTKLVDRPTVQANEVSKQELHAGGRKLIEKIEDYQPQALAILGKQAYEQGFSQRGAQWGKQTLTI
GSTQIWVLPNPSGLSRVSLEKLVEAYRELDQALVV
>d1mla_1 c.19.1.1 (3-127,198-307) Catalytic domain of malonyl-CoA ACP
transacylase {Escherichia coli}
QFAFVFPGQGSQTVGMLADMAASYPIVEETFAEASAALGYDLWALTQQGPAEELNKTWQTQPALL
TASVALYRVWQQQGGKAPAMMAGHSLGEYSALVCAGVIDFADAVRLVEMRGKFMQEAVPEXVPSH
CALMKPAADKLAVELAKITFNAPTVPVVNNVDVKCETNGDAIRDALVRQLYNPVQWTKSVEYMAA
QGVEHLYEVGPGKVLTGLTKRIVDTLTASALNEPSAMAAAL
>d1g7sa3 c.20.1.1 (A:329-459) Initiation factor IF2/eIF5b, domain 3
{Archaeon Methanobacterium thermoautotrophicum}
DPEKVREEILSEIEDIKIDTDEAGVVVKADTLGSLEAVVKILRDMYVPIKVADIGDVSRRDVVNA
GIALQEDRVYGAIIAFNVKVIPSAAQELKNSDIKLFQGNVIYRLMEEYEEWVRGIEEEKKKKWME
A
>d1jj2i_ c.21.1.1 (I:) Ribosomal protein L13 {Archaeon Haloarcula
marismortui}
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AEFDADVIVDARDCIMGRVASQVAEQALDGETVAVVNAERAVITGREEQIVEKYEKRVDIGNDNG
YFYPKRPDGIFKRTIRGMLPHKKQRGREAFESVRVYLGNPYDEDGEVLDGTSLDRLSNIKFVTLG
EISETLGANKTW
>d1dmga_ c.22.1.1 (A:) Ribosomal protein L4 {Thermotoga maritima}
AQVDLLNVKGEKVGTLEISDFVFNIDPNYDVMWRYVDMQLSNRRAGTASTKTRGEVSGGGRKPWP
QKHTGRARHGSIRSPIWRHGGVVHGPKPRDWSKKLNKKMKKLALRSALSVKYRENKLLVLDDLKL
ERPKTKSLKEILQNLQLSDKKTLIVLPWKEEGYMNVKLSGRNLPDVKVIIADNPNNSKNGEKAVR
IDGLNVFDMLKYDYLVLTRDMVSKIEEVLG
>d1jj2c_ c.22.1.1 (C:) Ribosomal protein L4 {Archaeon Haloarcula
marismortui}
MQATIYDLDGNTDGEVDLPDVFETPVRSDLIGKAVRAAQANRKQDYGSDEYAGLRTPAESFGSGR
GQAHVPKLDGRARRVPQAVKGRSAHPPKTEKDRSLDLNDKERQLAVRSALAATADADLVADRGHE
FDRDEVPVVVSDDFEDLVKTQEVVSLLEALDVHADIDRADETKIKAGQGSARGRKYRRPASILFV
TSDEPSTAARNLAGADVATASEVNTEDLAPGGAPGRLTVFTESALAEVAER
>d1hey__ c.23.1.1 (-) CheY protein {Escherichia coli}
DKELKFLVVGNGGTGKSTVRNLLKELGFNNVEDAEDGVDALNKLQAGGYGFVISDWNMPNMDGLE
LLKTIRADGAMSALPVLMVTAEAKKENIIAAAQAGASGYVVKPFTAATLEEKLNKIFEKLGM
>d1jbea_ c.23.1.1 (A:) CheY protein {Escherichia coli}
ADKELKFLVVDDFSTMRRIVRNLLKELGFNNVEEAEDGVDALNKLQAGGYGFVISDWNMPNMDGL
ELLKTIRADGAMSALPVLMVTAEAKKENIIAAAQAGASGYVVKPFTAATLEEKLNKIFEKLGM
>d1tmy__ c.23.1.1 (-) CheY protein {Thermotoga maritima}
GKRVLIVDDAAFMRMMLKDIITKAGYEVAGEATNGREAVEKYKELKPDIVTMDITMPEMNGIDAI
KEIMKIDPNAKIIVCSAMGQQAMVIEAIKAGAKDFIVKPFQPSRVVEALNKVS
>d1a04a2 c.23.1.1 (A:5-142) Nitrate/nitrite response regulator (NARL),
receiver domain {Escherichia coli}
EPATILLIDDHPMLRTGVKQLISMAPDITVVGEASNGEQGIELAESLDPDLILLDLNMPGMNGLE
TLDKLREKSLSGRIVVFSVSNHEEDVVTALKRGADGYLLKDMEPEDLLKALHQAAAGEMVLSEAL
TPVLAASL
>d1ntr__ c.23.1.1 (-) NTRC receiver domain {Salmonella typhimurium}
MQRGIVWVVDDDSSIRWVLERALAGAGLTCTTFENGNEVLAALASKTPDVLLSDIRMPGMDGLAL
LKQIKQRHPMLPVIIMTAHSDLDAAVSAYQQGAFDYLPKPFDIDEAVALVERAISHYQE
>d1dbwa_ c.23.1.1 (A:) Transcriptional regulatory protein FixJ,
receiver domain {Rhizobium meliloti}
MQDYTVHIVDDEEPVRKSLAFMLTMNGFAVKMHQSAEAFLAFAPDVRNGVLVTDLRMPDMSGVEL
LRNLGDLKINIPSIVITGHGDVPMAVEAMKAGAVDFIEKPFEDTVIIEAIERASEHLV
>d1qkka_ c.23.1.1 (A:) Transcriptional regulatory protein DctD,
receiver domain {Sinorhizobium meliloti}
PSVFLIDDDRDLRKAMQQTLELAGFTVSSFASATEALAGLSADFAGIVISDIRMPGMDGLALFRK
ILALDPDLPMILVTGHGDIPMAVQAIQDGAYDFIAKPFAADRLVQSARRAEEKRRLVMENRSLRR
AAEAASEGL
>d1dz3a_ c.23.1.1 (A:) Sporulation response regulator Spo0A {Bacillus
stearothermophilus}
SIKVCIADDNRELVSLLDEYISSQPDMEVIGTAYNGQDCLQMLEEKRPDILLLDIIMPHLDGLAV
LERIRAGFEHQPNVIMLTAFGQEDVTKKAVELGASYFILKPFDMENLAHHIRQVYGKT
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>d1nat__ c.23.1.1 (-) Sporulation response regulator Spo0F {Bacillus subtilis}
NEKILIVDDQYGIRILLNEVFNKEGYQTFQAANGLQALDIVTKERPDLVLLDMKIPGMDGIEILK
RMKVIDENIRVIIMTAYGELDMIQESKELGALTHFAKPFDIDEIRDAVKKYLPL
>d1a2oa1 c.23.1.1 (A:1-140) Methylesterase CheB, N-terminal domain {Salmonella typhimurium}
MSKIRVLSVDDSALMRQIMTEIINSHSDMEMVATAPDPLVARDLIKKFNPDVLTLDVEMPRMDGL
DFLEKLMRLRPMPVVMVSSLTGKGSEVTLRALELGAIDFVTKPQLGIREGMLAYSEMIAEKVRTA
ARARIAAHKP
>d1kgsa2 c.23.1.1 (A:2-123) PhoB receiver domain {Thermotoga maritima}
NVRVLVVEDERDLADLITEALKKEMFTVDVCYDGEEGMYMALNEPFDVVILDIMLPVHDGWEILK
SMRESGVNTPVLMLTALSDVEYRVKGLNMGADDYLPKPFDLRELIARVRALIRRKSE
>d1b00a_ c.23.1.1 (A:) PhoB receiver domain {Escherichia coli}
ARRILVVEDEAPIREMVCFVLEQNGFQPVEAEDYDSAVNQLNEPWPDLILLDWMLPGGSGIQFIK
HLKRESMTRDIPVVMLTARGEEEDRVRGLETGADDYITKPFSPKELVARIKAVMRRI
>d1dcfa_ c.23.1.2 (A:) Receiver domain of the ethylene receptor {Thale cress (Arabidopsis thaliana)}
HMSNFTGLKVLVMDENGVSRMVTKGLLVHLGCEVTTVSSNEECLRVVSHEHKVVFMDVCMPGVEN
YQIALRIHEKFTKQRHQRPLLVALSGNTDKSTKEKCMSFGLDGVLLKPVSLDNIRDVLSDLLEPR
VLYE
>d1qo0d_ c.23.1.3 (D:) Negative regulator of the amidase operon AmiR {Pseudomonas aeruginosa}
SANSLLGSLRELQVLVLNPPGEVSDALVLQLIRIGCSVRQCWPPPEAFDVPVDVVFTSIFQNRHH
DEIAALLAAGTPRTTLVALVEYESPAVLSQIIELECHGVITQPLDAHRVLPVLVSARRISEEMAK
LKQKTEQLQDRIAGQARINQAKVLLMQRHGWDEREAHQHLSREAMKRREPILKIAQELL
>d1fyva_ c.23.2.1 (A:) Toll-like receptor 1, TLR1 {Human (Homo sapiens)}
NIPLEELQRNLQFHAFISYSGHDSFWVKNELLPNLEKEGMQICLHERNFVPGKSIVENIITCIEK
SYKSIFVLSPNFVQSEWCHYELYFAHHNLFHEGSNSLILILLEPIPQYSIPSSYHKLKSLMARRT
YLEWPKEKSKRGLFWANLRAAINIKLTEQAK
>d1fywa_ c.23.2.1 (A:) Toll-like receptor 2, TLR2 {Human (Homo sapiens)}
SRNICYDAFVSYSERDAYWVENLMVQELENFNPPFKLCLHKRDFIPGKWIIDNIIDSIEKSHKTV
FVLSENFVKSEWCKYELDFSHFRLFDENNDAAILILLEPIEKKAIPQRFCKLRKIMNTKTYLEWP
MDEAQREGFWVNLRAAIKS
>d1eiwa_ c.23.3.1 (A:) Hypothetical protein MTH538 {Archaeon Methanobacterium thermoautotrophicum}
VTAEIRLYITEGEVEDYRVFLERLEQSGLEWRPATPEDADAVIVLAGLWGTRRDEILGAVDLARK
SSKPIITVRPYGLENVPPELEAVSSEVVGWNPHCIRDALEDALDVI
>d1jkja2 c.23.4.1 (A:122-287) Succinyl-CoA synthetase, alpha-chain, C-terminal domain {Escherichia coli}
NCPGVITPGECKIGIQPGHIHKPGKVGIVSRSGTLTYEAVKQTTDYGFGQSTCVGIGGDPIPGSN
FIDILEMFEKDPQTEAIVMIGEIGGSAEEEAAAYIKEHVTKPVVGYIAGVTAPKGKRMGHAGAII
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AGGKGTADEKFAALEAAGVKTVRSLADIGEALKTVL
>d1euca2 c.23.4.1 (A:131-306) Succinyl-CoA synthetase, alpha-chain,
C-terminal domain {Pig (Sus scrofa)}
NCPGVINPGECKIGIMPGHIHKKGRIGIVSRSGTLTYEAVHQTTQVGLGQSLCVGIGGDPFNGTD
FTDCLEIFLNDPATEGIILIGEIGGNAEENAAEFLKQHNSGPKSKPVVSFIAGLTAPPGRRMGHA
GAIIAGGKGGAKEKITALQSAGVVVSMSPAQLGTTIYKEFEKRKML
>d1jkjb1 c.23.4.1 (B:239-388) Succinyl-CoA synthetase, beta-chain,
C-terminal domain {Escherichia coli}
DPREAQAAQWELNYVALDGNIGCMVNGAGLAMGTMDIVKLHGGEPANFLDVGGGATKERVTEAFK
IILSDDKVKAVLVNIFGGIVRCDLIADGIIGAVAEVGVNVPVVVRLEGNNAELGAKKLADSGLNI
IAAKGLTDAAQQVVAAVEGK
>d1eucb1 c.23.4.1 (B:246-393) Succinyl-CoA synthetase, beta-chain,
C-terminal domain {Pig (Sus scrofa)}
EPIENEAAKYDLKYIGLDGNIACFVNGAGLAMATCDIIFLNGGKPANFLDLGGGVKESQVYQAFK
LLTADPKVEAILVNIFGGIVNCAIIANGITKACRELELKVPLVVRLEGTNVHEAQNILTNSGLPI
TSAVDLEDAAKKAVASVT
>d2fcr__ c.23.5.1 (-) Flavodoxin {Chondrus crispus}
KIGIFFSTSTGNTTEVADFIGKTLGAKADAPIDVDDVTDPQALKDYDLLFLGAPTWNTGADTERS
GTSWDEFLYDKLPEVDMKDLPVAIFGLGDAEGYPDNFCDAIEEIHDCFAKQGAKPVGFSNPDDYD
YEESKSVRDGKFLGLPLDMVNDQIPMEKRVAGWVEAVVSETGV
>d1f4pa_ c.23.5.1 (A:) Flavodoxin {Desulfovibrio vulgaris}
PKALIVYGSTTGNTEYTAETIARELADAGYEVDSRDAASVEAGGLFEGFDLVLLGCSTWGDDSIE
LQDDFIPLFDSLEETGAQGRKVACFGCGDSSWEYFCGAVDAIEEKLKNLGAEIVQDGLRIDGDPR
AARDDIVGWAHDVRGAI
>d1rcf__ c.23.5.1 (-) Flavodoxin {Anabaena, pcc 7119 and 7120}
SKKIGLFYGTQTGKTESVAEIIRDEFGNDVVTLHDVSQAEVTDLNDYQYLIIGCPTWNIGELQSD
WEGLYSELDDVDFNGKLVAYFGTGDQIGYADNFQDAIGILEEKISQRGGKTVGYWSTDGYDFNDS
KALRNGKFVGLALDEDNQSDLTDDRIKSWVAQLKSEFGL
>d1ag9a_ c.23.5.1 (A:) Flavodoxin {Escherichia coli}
AITGIFFGSDTGNTENIAKMIQKQLGKDVADVHDIAKSSKEDLEAYDILLLGIPTWYYGEAQCDW
DDFFPTLEEIDFNGKLVALFGCGDQEDYAEYFCDALGTIRDIIEPRGATIVGHWPTAGYHFEASK
GLADDDHFVGLAIDEDRQPELTAERVEKWVKQISEELHLDEILNA
>d1czna_ c.23.5.1 (A:) Flavodoxin {Anacystis nidulans and
Synechococcus, pcc 7942}
AKIGLFYGTQTGVTQTIAESIQQEFGGESIVDLNDIANADASDLNAYDYLIIGCPTWNVGELQSD
WEGIYDDLDSVNFQGKKVAYFGAGDQVGYSDNFQDAMGILEEKISSLGSQTVGYWPIEGYDFNES
KAVRNNQFVGLAIDEDNQPDLTKNRIKTWVSQLKSEFGL
>d5nul__ c.23.5.1 (-) Flavodoxin {Clostridium beijerinckii}
MKIVYWSGTGNTEKMAELIAKGIIESGKDVNTINVSDVNIDELLNEDILILGCSAMTDEVLEESE
FEPFIEEISTKISGKKVALFGSYGWGDGKWMRDFEERMNGYGCVVVETPLIVQNEPDEAEQDCIE
FGKKIANI
>d1fuea_ c.23.5.1 (A:) Flavodoxin {Helicobacter pylori}
GKIGIFFGTDSGNAEAIAEKISKAIGNAEVVDVAKASKEQFNGFTKVILVAPTAGAGDLQTDWED
FLGTLEASDFANKTIGLVGLGDQDTYSETFAEGIFHIYEKAKAGKVVGQTSTDGYHFAASKAVEG
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GKFVGLVIDEDNQDDLTDERIAKWVEQVRGSFA
>d1bvyf_ c.23.5.1 (F:) FMN-binding domain of the cytochrome P450bm-3 {Bacillus megaterium}
NTPLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNGHPPDN
AKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADRGEADASDD
FEGTYEEWREHMWSDVAAYFNL
>d1e5da1 c.23.5.1 (A:251-402) Rubredoxin oxygen:oxidoreductase (ROO), C-terminal domain {Desulfovibrio gigas}
PTNKVVIFYDSMWHSTEKMARVLAESFRDEGCTVKLMWCKACHHSQIMSEISDAGAVIVGSPTHN
NGILPYVAGTLQYIKGLRPQNKIGGAFGSFGWSGESTKVLAEWLTGMGFDMPATPVKVKNVPTHA
DYEQLKTMAQTIARALKAKLAA
>d1ja1a2 c.23.5.2 (A:63-239) NADPH-cytochrome p450 reductase, N-terminal domain {Rat (Rattus norvegicus)}
PVKESSFVEKMKKTGRNIIVFYGSQTGTAEEFANRLSKDAHRYGMRGMSADPEEYDLADLSSLPE
IDKSLVVFCMATYGEGDPTDNAQDFYDWLQETDVDLTGVKFAVFGLGNKTYEHFNAMGKYVDQRL
EQLGAQRIFELGLGDDDGNLEEDFITWREQFWPAVCEFFGVEATGEE
>d1b1ca_ c.23.5.2 (A:) NADPH-cytochrome p450 reductase, N-terminal domain {Human (Homo sapiens)}
SSFVEKMKKTGRNIIVFYGSQTGTAEEFANRLSKDAHRYGMRGMSADPEEYDLADLSSLPEIDNA
LVVFCMATYGEGDPTDNAQDFYDWLQETDVDLSGVKFAVFGLGNKTYEHFNAMGKYVDKRLEQLG
AQRIFELGLGDDDGNLEEDFITWREQFWPAVCEHFGV
>d1dxqa_ c.23.5.3 (A:) NAD(P)H:quinone reductase {Mouse (Mus musculus)}
AARRALIVLAHSEKTSFNYAMKEAAVEALKKRGWEVLESDLYAMNFNPIISRNDITGELKDSKNF
QYPSESSLAYKEGRLSPDIVAEHKKLEAADLVIFQFPLQWFGVPAILKGWFERVLVAGFAYTYAA
MYDNGPFQNKKTLLSITTGGSGSMYSLQGVHGDMNVILWPIQSGILRFCGFQVLEPQLVYSIGHT
PPDARMQILEGWKKRLETVWEETPLYFAPSSLFDLNFQAGFLLMKEVQEEQKKNKFGLSVGHHLG
KSIPADNQIKARK
>d1qrda_ c.23.5.3 (A:) NAD(P)H:quinone reductase {Rat (Rattus rattus)}
AVRRALIVLAHAERTSFNYAMKEAAVEALKKKGWEVVESDLYAMNFNPLISRNDITGEPKDSENF
QYPVESSLAYKEGRLSPDIVAEQKKLEAADLVIFQFPLYWFGVPAILKGWFERVLVAGFAYTYAT
MYDKGPFQNKKTLLSITTGGSGSMYSLQGVHGDMNVILWPIQSGILRFCGFQVLEPQLVYSIGHT
PPDARVQVLEGWKKRLETVWEESPLYFAPSSLFDLNFQAGFLLKKEVQEEQKKNKFGLSVGHHLG
KSIPADNQIKARK
>d1d4aa_ c.23.5.3 (A:) NAD(P)H:quinone reductase {Human (Homo sapiens)}
VGRRALIVLAHSERTSFNYAMKEAAAAALKKKGWEVVESDLYAMNFNPIISRKDITGKLKDPANF
QYPAESVLAYKEGHLSPDIVAEQKKLEAADLVIFQFPLQWFGVPAILKGWFERVFIGEFAYTYAA
MYDKGPFRSKKAVLSITTGGSGSMYSLQGIHGDMNVILWPIQSGILHFCGFQVLEPQLTYSIGHT
PADARIQILEGWKKRLENIWDETPLYFAPSSLFDLNFQAGFLMKKEVQDEEKNKKFGLSVGHHLG
KSIPTDNQIKARK
>d1qr2a_ c.23.5.3 (A:) Quinone reductase type 2 (menadione reductase) {Human (Homo sapiens)}
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AGKKVLIVYAHQEPKSFNGSLKNVAVDELSRQGCTVTVSDLYAMNFEPRATDKDITGTLSNPEVF
NYGVETHEAYKQRSLASDITDEQKKVREADLVIFQFPLYWFSVPAILKGWMDRVLCQGFAFDIPG
FYDSGLLQGKLALLSVTTGGTAEMYTKTGVNGDSRYFLWPLQHGTLHFCGFKVLAPQISFAPEIA
SEEERKGMVAAWSQRLQTIWKEEPIPCTAHWHFGQ
>d1bmta2 c.23.6.1 (A:741-896) Methionine synthase, C-terminal domain {Escherichia coli}
EQGKTNGKMVIATVKGDVHDIGKNIVGVVLQCNNYEIVDLGVMVPAEKILRTAKEVNADLIGLSG
LITPSLDEMVNVAKEMERQGFTIPLLIGGATTSKAHTAVKIEQNYSGPTVYVQNASRTVGVVAAL
LSDTQRDDFVARTRKEYETVRIQHGR
>d1fmfa_ c.23.6.1 (A:) Glutamate mutase, small subunit {Clostridium tetanomorphum}
MEKKTIVLGVIGSDCHAVGNKILDHSFTNAGFNVVNIGVLSSQEDFINAAIETKADLICVSSLYG
QGEIDCKGLREKCDEAGLKGIKLFVGGNIVVGKQNWPDVEQRFKAMGFDRVYPPGTSPETTIADM
KEVLGVE
>d1ccwa_ c.23.6.1 (A:) Glutamate mutase, small subunit {Clostridium cochlearium}
MEKKTIVLGVIGSDCHAVGNKILDHAFTNAGFNVVNIGVLSPQELFIKAAIETKADAILVSSLYG
QGEIDCKGLRQKCDEAGLEGILLYVGGNIVVGKQHWPDVEKRFKDMGYDRVYAPGTPPEVGIADL
KKDLNIE
>d7reqa2 c.23.6.1 (A:561-728) Methylmalonyl-CoA mutase C-terminal domains of alpha and beta subunits {Propionibacterium freudenreichii, subsp. shermanii}
AQIRTISGVYSKEVKNTPEVEEARELVEEFEQAEGRRPRILLAKMGQDGHDRGQKVIATAYADLG
FDVDVGPLFQTPEETARQAVEADVHVVGVSSLAGGHLTLVPALRKELDKLGRPDILITVGGVIPE
QDFDELRKDGAVEIYTPGTVIPESAISLVKKLRASLDA
>d7reqb2 c.23.6.1 (B:476-638) Methylmalonyl-CoA mutase C-terminal domains of alpha and beta subunits {Propionibacterium freudenreichii, subsp. shermanii}
TKPFPAAPARKGLAWHRDSEVFEQLMDRSTSVSERPKVFLACLGTRRDFGGREGFSSPVWHIAGI
DTPQVEGGTTAEIVEAFKKSGAQVADLCSSAKVYAQQGLEVAKALKAAGAKALYLSGAFKEFGDD
AAEAEKLIDGRLFMGMDVVDTLSSTLDILGVAK
>d1c4ka1 c.23.7.1 (A:1-107) Ornithine decarboxylase N-terminal "wing" domain {Lactobacillus sp., strain 30a}
SSSLKIASTQEARQYFDTDRVVVDAVGSDFTDVGAVIAMDYETDVIDAADATKFGIPVFAVTKDA
QAISADELKKIFHIIDLENKFDATVNAREIETAVNNYEDSIL
>d1qcza_ c.23.8.1 (A:) N5-carboxyaminoimidazole ribonucleotide (N5-CAIR) mutase PurE {Escherichia coli}
PARVAIVMGSKSDWATMQFAAEIFEILNVPHHVEVVSAHRTPDKLFSFAESAEENGYQVIIAGAG
GAAHLPGMIAAKTLVPVLGVPVQSAALSGVDSLYSIVQMPRGIPVGTLAIGKAGAANAALLAAQI
LATHDKELHQRLNDWRKAQTDEVLENPDPRGAA
>d1cex__ c.23.9.1 (-) Cutinase {Fungus (Fusarium solani), subsp. pisi}
RTTRDDLINGNSASCADVIFIYARGSTETGNLGTLGPSIASNLESAFGKDGVWIQGVGGAYRATL
GDNALPRGTSSAAIREMLGLFQQANTKCPDATLIAGGYSQGAALAAASIEDLDSAIRDKIAGTVL
FGYTKNLQNRGRIPNYPADRTKVFCNTGDLVCTGSLIVAAPHLAYGPDARGPAPEFLIEKVRAVR
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GS
>d1g66a_ c.23.9.1 (A:) Acetylxylan esterase {Penicillium
purpurogenum}
SCPAIHVFGARETTASPGYGSSSTVVNGVLSAYPGSTAEAINYPACGGQSSCGGASYSSSVAQGI
AAVASAVNSFNSQCPSTKIVLVGYSQGGEIMDVALCGGGDPNQGYTNTAVQLSSSAVNMVKAAIF
MGDPMFRAGLSYEVGTCAAGGFDQRPAGFSCPSAAKIKSYCDASDPYCCNGSNAATHQGYGSEYG
SQALAFVKSKLG
>d1qoza_ c.23.9.1 (A:) Acetylxylan esterase {Trichoderma reesei}
ECPAIHVFGARETTVSQGYGSSATVVNLVIQAHPGTTSEAIVYPACGGQASCGGISYANSVVNGT
NAAAAAINNFHNSCPDTQLVLVGYSQGAQIFDNALCGGGDPGEGITNTAVPLTAGAVSAVKAAIF
MGDPRNIHGLPYNVGTCTTQGFDARPAGFVCPSASKIKSYCDAADPYCCTGNDPNVHQGYGQEYG
QQALAFINSQLS
>d1esc__ c.23.10.1 (-) Esterase {Streptomyces scabies}
DPVPTVFFGDSYTANFGIAPVTNQDSERGWCFQAKENYPAVATRSLADKGITLDVQADVSCGGAL
IHHFWEKQELPFGAGELPPQQDALKQDTQLTVGSLGGNTLGFNRILKQCSDELRKPSLLPGDPVD
GDEPAAKCGEFFGTGDGKQWLDDQFERVGAELEELLDRIGYFAPDAKRVLVGYPRLVPEDTTKCL
TAAPGQTQLPFADIPQDALPVLDQIQKRLNDAMKKAAADGGADFVDLYAGTGANTACDGADRGIG
GLLEDSQLELLGTKIPWYAHPNDKGRDIQAKQVADKIEEILN
>d1flca2 c.23.10.2 (A:1-150,A:307-427) Esterase domain of
haemagglutinin-esterase-fusion glycoprotein HEF1 {Influenza C virus}
EKIKICLQKQVNSSFSLHNGFGGNLYATEEKRMFELVKPKAGASVLNQSTWIGFGDSRTDKSNSA
FPRSADVSAKTADKFRFLSGGSLMLSMFGPPGKVDYLYQGCGKHKVFYEGVNWSPHAAINCYRKN
WTDIKLNFQKNIYELASQSHXEKGPVTAVQSIWGKGRESDYAVDQACLSTPGCMLIQKQKPYIGE
ADDHHGDQEMRELLSGLDYEARCISQSGWVNETSPFTEKYLLPPKFGRCPLAAKEESIPKIPDGL
LIPTSGTDTTVT
>d1es9a_ c.23.10.3 (A:) Platelet-activating factor acetylhydrolase
{Cow (Bos taurus)}
ENPASKPTPVQDVQGDGKWMSLHHRFVADSKDKEPEVVFIGDSLVQLMHQCEIWRELFSPLHALN
FGIGGDSTQHVLWRLENGELEHIRPKIVVVWVGTNNHGHTAEQVTGGIKAIVQLVNERQPQARVV
VLGLLPRGQHPNPLREKNRRVNELVRAALAGHPRAHFLDADPGFVHSDGTISHHDMYDYLHLSRL
GYTPVCRALHSLLLRLL
>d1fxwf_ c.23.10.3 (F:) Platelet-activating factor acetylhydrolase
{Cow (Bos taurus)}
SNPAAIPHAAEDIQGDDRWMSQHNRFVLDCKDKEPDVLFVGDSMVQLMQQYEIWRELFSPLHALN
FGIGGDTTRHVLWRLKNGELENIKPKVIVVWVGTNNHENTAEEVAGGIEAIVQLINTRQPQAKII
VLGLLPRGEKPNPLRQKNAKVNQLLKVSLPKLANVQLLDTDGGFVHSDGAISCHDMFDFLHLTGG
GYAKICKPLHELIMQLL
>d1k7ca_ c.23.10.4 (A:) Rhamnogalacturonan acetylesterase {Fungus
(Aspergillus aculeatus)}
TTVYLAGDSTMAKNGGGSGTNGWGEYLASYLSATVVNDAVAGRSARSYTREGRFENIADVVTAGD
YVIVEFGHNDGGSLSTDNGRTDCSGTGAEVCYSVYDGVNETILTFPAYLENAAKLFTAKGAKVIL
SSQTPNNPWETGTFVNSPTRFVEYAELAAEVAGVEYVDHWSYVDSIYETLGNATVNSYFPIDHTH
TSPAGAEVVAEAFLKAVVCTGTSLKSVLTTTSFEGTCL
>d1iexa2 c.23.11.1 (A:389-603) Beta-D-glucan exohydrolase,
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C-terminal domain {Barley (Hordeum vulgare)}
LVLLKNGKTSTDAPLLPLPKKAPKILVAGSHADNLGYQCGGWTIEWQGDTGRTTVGTTILEAVKA
AVDPSTVVVFAENPDAEFVKSGGFSYAIVAVGEHPYTETKGDNLNLTIPEPGLSTVQAVCGGVRC
ATVLISGRPVVVQPLLAASDALVAAWLPGSEGQGVTDALFGDFGFTGRLPRTWFKSVDQLPMNVG
DAHYDPLFRLGYGLTTNATK
>d2naca2 c.23.12.1 (A:1-147,A:336-374) Formate dehydrogenase
{Pseudomonas sp., strain 101}
AKVLCVLYDDPVDGYPKTYARDDLPKIDHYPGGQTLPTPKAIDFTPGQLLGSVSGELGLRKYLES
NGHTLVVTSDKDGPDSVFERELVDADVVISQPFWPAYLTPERIAKAKNLKLALTAGIGSDHVDLQ
SAIDRNVTVAEVTYCNSXTTLTAQARYAAGTREILECFFEGRPIRDEYLIVQGGALA
>d1qp8a2 c.23.12.1 (A:1-82,A:264-302) Putative formate dehydrogenase
{Archaeon Pyrobaculum aerophilum}
MELYVNFELPPEAEEELRKYFKIVRGGDLGNVEAALVSRITAEELAKMPRLKFIQVVTAGLDHLP
WESIPPHVTVAGNAGSNXGYGNERVWRQMVMEAVRNLITYATGGRPRNIAKREDYIG
>d1dxy_2 c.23.12.1 (1-100,300-330) D-2-hydroxyisocaproate
dehydrogenase {Lactobacillus casei}
MKIIAYGARVDEIQYFKQWAKDTGNTLEYHTEFLDENTVEWAKGFDGINSLQTTPYAAGVFEKMH
AYGIKFLTIRNVGTDNIDMTAMKQYGIRLSNVPAYXTETAVHNMVYFSLQHLVDFLTKGETSTEV
TG
>d1gdha2 c.23.12.1 (A:2-100,A:292-321) D-glycerate dehydrogenase
{Hyphomicrobium methylovorum}
KKKILITWPLPEAAMARARESYDVIAHGDDPKITIDEMIETAKSVDALLITLNEKCRKEVIDRIP
ENIKCISTYSIGFDHIDLDACKARGIKVGNAPHGXATQAREDMAHQANDLIDALFGGADMSYALA
>d1psda2 c.23.12.1 (A:7-107,A:296-326) Phosphoglycerate
dehydrogenase {Escherichia coli}
EKDKIKFLLVEGVHQKALESLRAAGYTNIEFHKGALDDEQLKESIRDAHFIGLRSRTHLTEDVIN
AAEKLVAIGCFCIGTNQVDLDAAAKRGIPVFNAPFSXSTQEAQENIGLEVAGKLIKYSDNGSTLS
AVN
>d2dlda2 c.23.12.1 (A:1-103,A:301-337) D-lactate dehydrogenase
{Lactobacillus helveticus}
MTKVFAYAIRKDEEPFLNEWKEAHKDIDVDYTDKLLTPETAKLAKGADGVVVYQQLDYTADTLQA
LADAGVTKMSLRNVGVDNIDMDKAKELGFQITNVPVYSXYTTHAVRNMVVKAFNNNLKLINGEKP
DSPVALNKNKF
>d1pjca2 c.23.12.2 (A:1-135,A:304-361) L-alanine dehydrogenase
{Phormidium lapideum}
MEIGVPKEIKNQEFRVGLSPSSVRTLVEAGHTVFIETQAGIGAGFADQDYVQAGAQVVPSAKDAW
SREMVVKVKEPLPAEYDLMQKDQLLFTYLHLAAARELTEQLMRVGLTAIAYETVELPNRSLPLLT
PMSIIXVPWTATQALNNSTLPYVVKLANQGLKALETDDALAKGLNVQAHRLVHPAVQQVFPDLA
>d1f8ga2 c.23.12.2 (A:1-143,A:327-384) Nicotinamide nucleotide
transhydrogenase dI component {Rhodospirillum rubrum}
MKIAIPKERRPGEDRVAISPEVVKKLVGLGFEVIVEQGAGVGASITDDALTAAGATIASTAAQAL
SQADVVWKVQRPMTAEEGTDEVALIKEGAVLMCHLGALTNRPVVEALTKRKITAYAMELMPRISR
AQSMDILSSQSNLXVAADASPLFAKNLLNFLTPHVDKDTKTLVMKLEDETVSGTCVTRDGAIVHP
ALTGQGA
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>d1a7aa2 c.23.12.3 (A:2-189,A:353-432) S-adenosylhomocystein hydrolase {Human (Homo sapiens)}
SDKLPYKVADIGLAAWGRKALDIAENEMPGLMRMRERYSASKPLKGARIAGCLHMTVETAVLIET
LVTLGAEVQWSSCNIFSTQNHAAAAIAKAGIPVYAWKGETDEEYLWCIEQTLYFKDGPLNMILDD
GGDLTNLIHTKYPQLLPGIRGISEETTTGVHNLYKMMANGILKVPAINVNDSVTKSKFXHPSFVM
SNSFTNQVMAQIELWTHPDKYPVGVHFLPKKLDEAVAEAHLGKLNVKLTKLTEKQAQYLGMSCDG
PFKPDHYRY
>d1b3ra2 c.23.12.3 (A:4-189,A:353-431) S-adenosylhomocystein hydrolase {Rat (Rattus norvegicus)}
LPYKVADIGLAAWGRKALDIAENEMPGLMRMREMYSASKPLKGARIAGCLHMTVETAVLIETLVA
LGAEVRWSSCNIFSTQDHAAAAIAKAGIPVFAWKGETDEEYLWCIEQTLHFKDGPLNMILDDGGD
LTNLIHTKHPQLLSGIRGISEETTTGVHNLYKMMANGILKVPAINVNDSVTKSKFDXPSFVMSNS
FTNQVMAQIELWTHPDKYPVGVHFLPKKLDEAVAEAHLGKLNVKLTKLTEKQAQYLGMPINGPFK
PDHYRY
>d2dhqa_ c.23.13.1 (A:) Type II 3-dehydroquinate dehydratase {Mycobacterium tuberculosis}
LIVNVINGPNLGRLGRREPAVYGGTTHDELVALIEREAAELGLKAVVRQSDSEAQLLDWIHQAAD
AAEPVILNAGGLTHTSVALRDACAELSAPLIEVHISNVHAREEFRRHSYLSPIATGVIVGLGIQG
YLLALRYLAEH
>d1d0ia_ c.23.13.1 (A:) Type II 3-dehydroquinate dehydratase {Streptomyces coelicolor}
PRSLANAPIMILNGPNLNLLGQRQPEIYGSDTLADVEALCVKAAAAHGGTVDFRQSNHEGELVDW
IHEARLNHCGIVINPAAYSHTSVAILDALNTCDGLPVVEVHISNIHQREPFRHHSYVSQRADGVV
AGCGVQGYVFGVERIAALAG
>d1f8ya_ c.23.14.1 (A:) Nucleoside 2-deoxyribosyltransferase {Lactobacillus leichmannii}
PKKTIYFGAGWFTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVDEHPEYLHDKVWAT
ATYNNDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVLLVIPDEDYGKPINLMSWGVSD
NVIKMSQLKDFNFNKPRFDFYEGAVY
>d1fjgb_ c.23.15.1 (B:) Ribosomal protein S2 {Thermus thermophilus}
VKELLEAGVHFGHERKRWNPKFARYIYAERNGIHIIDLQKTMEELERTFRFIEDLAMRGGTILFV
GTKKQAQDIVRMEAERAGMPYVNQRWLGGMLTNFKTISQRVHRLEELEALFASPEIEERPKKEQV
RLKHELERLQKYLSGFRLLKRLPDAIFVVDPTKEAIAVREARKLFIPVIALADTDSDPDLVDYII
PGNDDAIRSIQLILSRAVDLIIQARGGVVEPSPSYALVQEAE
>d1f2va_ c.23.17.1 (A:) Precorrin-8x methylmutase {Pseudomonas denitrificans}
PEYDYIRDGNAIYERSFAIIRAEADLSRFSEEEADLAVRMVHACGSVEATRQFVFSPDFVSSARA
ALKAGAPILCDAEMVAHGVTRARLPAGNEVICTLRDPRTPALAAEIGNTRSAAALKLWSERLAGS
VVAIGNAPTALFFLLEMLRDGAPKPAAILGMPVGFVGAAESKDALAENSYGVPFAIVRGRLGGSA
MTAAALNSLARPGL
>d1gpma2 c.23.16.1 (A:3-207) GMP synthetase {Escherichia coli}
ENIHKHRILILDFGSQYTQLVARRVRELGVYCELWAWDVTEAQIRDFNPSGIILSGGPESTTEEN
SPRAPQYVFEAGVPVFGVCYGMQTMAMQLGGHVEASNEREFGYAQVEVVNDSALVRGIEDALTAD
GKPLLDVWMSHGDKVTAIPSDFITVASTESCPFAIMANEEKRFYGVQFHPEVTHTRQGMRMLERF
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VRDICQCEAL
>d1a9xb2 c.23.16.1 (B:1653-1880) Carbamoyl phosphate synthetase,
small subunit C-terminal domain {Escherichia coli}
LNGMDLAKEVTTAEAYSWTQGSWTLTGGLPQAKKEDELPFHVVAYDFGAKRNILRMLVDRGCRLT
IVPAQTSAEDVLKMNPDGIFLSNGPGDPAPCDYAITAIQKFLETDIPVFGICLGHQLLALASGAK
TVKMKFGHHGGNHPVKDVEKNVVMITAQNHGFAVDEATLPANLRVTHKSLFDGTLQGIHRTDKPA
FSFQGNPEASPGPHDAAPLFDHFIELIEQYRKT
>d1qdlb_ c.23.16.1 (B:) Anthranilate synthase GAT subunit, TrpG
{Archaeon Sulfolobus solfataricus}
MDLTLIIDNYDSFVYNIAQIVGELGSYPIVIRNDEISIKGIERIDPDRLIISPGPGTPEKREDIG
VSLDVIKYLGKRTPILGVCLGHQAIGYAFGAKIRRARKVFHGKISNIILVNNSPLSLYYGIAKEF
KATRYHSLVVDEVHRPLIVDAISAEDNEIMAIHHEEYPIYGVQFHPESVGTSLGYKILYNFLNRV
>d1i1qb_ c.23.16.1 (B:) Anthranilate synthase GAT subunit, TrpG
{Salmonella typhimurium}
ADILLLDNIDSFTWNLADQLRTNGHNVVIYRNHIPAQTLIDRLATMKNPVLMLSPGPGVPSEAGC
MPELLTRLRGKLPIIGICLGHQAIVEAYGGYVGQAGEILHGKATSIEHDGQAMFAGLANPLPVAR
YHSLVGSNVPAGLTINAHFNGMVMAVRHDADRVCGFQFHPESILTTQGARLLEQTLAWAQQK
>d1i7qb_ c.23.16.1 (B:) Anthranilate synthase GAT subunit, TrpG
{Serratia marcescens}
ADILLLDNVDSFTYNLVDQLRASGHQVVIYRNQIGAEVIIERLQHMEQPVLMLSPGPGTPSEAGC
MPELLQRLRGQLPIIGICLGHQAIVEAYGGQVGQAGEILHGKASAIAHDGEGMFAGMANPLPVAR
YHSLVGSNIPADLTVNARFGEMVMAVRDDRRRVCGFQFHPESILTTHGARLLEQTLAWALAK
>d1k9vf_ c.23.16.1 (F:) GAT subunit (or domain) of
imidazoleglycerolphosphate synthase HisF {Thermotoga maritima}
MRIGIISVGPGNIMNLYRGVKRASENFEDVSIELVESPRNDLYDLLFIPGVGHFGEGMRRLREND
LIDFVRKHVEDERYVVGVCLGMQLLFEESEEAPGVKGLSLIEGNVVKLRSRRLPHMGWNEVIFKD
TFPNGYYYFVHTYRAVCEEEHVLGTTEYDGEIFPSAVRKGRILGFQFHPEKSSKIGRKLLEKVIE
CSLSR
>d1jvna2 c.23.16.1 (A:-3-229) GAT subunit (or domain) of
imidazoleglycerolphosphate synthase HisF {Baker's yeast
(Saccharomyces cerevisiae), His7}
GSHMPVVHVIDVESGNLQSLTNAIEHLGYEVQLVKSPKDFNISGTSRLILPGVGNYGHFVDNLFN
RGFEKPIREYIESGKPIMGICVGLQALFAGSVESPKSTGLNYIDFKLSRFDDSEKPVPEIGWNSC
IPSENLFFGLDPYKRYYFVHSFAAILNSEKKKNLENDGWKIAKAKYGSEEFIAAVNKNNIFATQF
HPEKSGKAGLNVIENFLKQQSPPIPNYSAEEKELLMN
>d1g2ia_ c.23.16.2 (A:) Intracellular protease {Archaeon Pyrococcus
horikoshii}
MKVLFLTANEFEDVELIYPYHRLKEEGHEVYIASFERGTITGKHGYSVKVDLTFDKVNPEEFDAL
VLPGGRAPERVRLNEKAVSIARKMFSEGKPVASICHGPQILISAGVLRGRKGTSYPGIKDDMINA
GVEWVDAEVVVDGNWVSSRVPADLYAWMREFVKLLK
>d1cf9a1 c.23.16.3 (A:598-753) Catalase, C-terminal domain
{Escherichia coli, HPII}
VKGRVVAILLNDEVRSADLLAILKALKAKGVHAKLLYSRMGEVTADDGTVLPIAATFAGAPSLTV
DAVIVPCGNIADIADNGDANYYLMEAYKHLKPIALAGDARKFKATIKIADQGEEGIVEADSADGS
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FMDELLTLMAAHRVWSRIPKIDKIPA
>d1fyea_ c.23.16.4 (A:) Aspartyl dipeptidase PepE {Salmonella typhimurium}
MELLLLSNSTLPGKAWLEHALPLIANQLNGRRSAVFIPFAGVTQTWDEYTDKTAEVLAPLGVNVT
GIHRVADPLAAIEKAEIIIVGGGNTFQLLKESRERGLLAPMADRVKRGALYIGWSAGANLACPTI
RTTNDMPIVDPNGFDALDLFPLQINPHFTNALPEGHKGETREQRIRELLVVAPELTVIGLPEGNW
IQVSNGQAVLGGPNTTWVFKAGEEAVALEAGHRF
>d1a9xa2 c.24.1.1 (A:936-1073) Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain {Escherichia coli}
NSTMKKHGRALLSVREGDKERVVDLAAKLLKQGFELDATHGTAIVLGEAGINPRLVNKVHEGRPH
IQDRIKNGEYTYIINTTSGRRAIEDSRVIRRSALQYKVHYDTTLNGGFATAMALNADATEKVISV
QEMHAQIK
>d1b93a_ c.24.1.2 (A:) Methylglyoxal synthase, MgsA {Escherichia coli}
MELTTRTLPARKHIALVAHDHCKQMLMSWVERHQPLLEQHVLYATGTTGNLISRATGMNVNAMLS
GPMGGDQQVGALISEGKIDVLIFFWDPLNAVPHDPDVKALLRLATVWNIPVATNVATADFIIQSP
HFNDAVDILIPDYQRYLA
>d1g8ma1 c.24.1.3 (A:4-200) IMP cyclohydrolase domain of bifunctional purine biosynthesis enzyme ATIC {Chicken (Gallus gallus)}
RQQLALLSVSEKAGLVEFARSLNALGLGLIASGGTATALRDAGLPVRDVSDLTGFPEMLGGRVKT
LHPAVHAGILARNIPEDNADMNKQDFSLVRVVVCNLYPFVKTVSSPGVTVPEAVEKIDIGGVALL
RAAAKNHARVTVVCDPADYSSVAKEMAASKDKDTSVETRRHLALKAFTHTAQYDAAISDYFRKEY
SK
>d1fnc_2 c.25.1.1 (155-314) Ferredoxin reductase (flavodoxin reductase) {Spinach (Spinacia oleracea)}
MLMPKDPNATIIMLGTGTGIAPFRSFLWKMFFEKHDDYKFNGLAWLFLGVPTSSSLLYKEEFEKM
KEKAPDNFRLDFAVSREQTNEKGEKMYIQTRMAQYAVELWEMLKKDNTYVYMCGLKGMEKGIDDI
MVSLAAAEGIDWIEYKRQLKKAEQWNVEVY
>d1qfza2 c.25.1.1 (A:154-308) Ferredoxin reductase (flavodoxin reductase) {Garden pea (Pisum sativum)}
DPNATVIMLGTGTGIAPFRSFLWKMFFEKHEDYQFNGLAWLFLGVPTSSSLLYKEEFEKMKEKAP
ENFRLDFAVSREQVNDKGEKMYIQTRMAQYAEELWELLKKDNTFVYMCGLKGMEKGIDDIMVSLA
AKDGIDWIEYKRTLKKAEQWNVEVS
>d1fb3a2 c.25.1.1 (A:208-362) Ferredoxin reductase (flavodoxin reductase) {Paprika (Capsicum annuum)}
DPNATVIMLGTGTGIAPFRSFLWKMFFEKHDDYKFNGLAWLFLGVPTSSSLLYKEEFEKMKEKAP
ENFRLDFAVSREQTNEKGEKMYIQTRMAQYAEELWTLLKKDNTFVYMCGLKGMEQGIDDIMSSLA
AKEGIDWADYKKQLKKAEQWNVEVY
>d1gawa2 c.25.1.1 (A:157-314) Ferredoxin reductase (flavodoxin reductase) {Maize (Zea mays), leaf isoform}
MPKDPNATIIMLATGTGIAPFRSFLWKMFFEKHDDYKFNGLGWLFLGVPTSSSLLYKEEFGKMKE
RAPENFRVDYAVSREQTNAAGERMYIQTRMAEYKEELWELLKKDNTYVYMCGLKGMEKGIDDIMV
SLAEKDGIDWFDYKKQLKRGDQWNVEVY
>d1jb9a2 c.25.1.1 (A:163-316) Ferredoxin reductase (flavodoxin
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reductase) {Maize (Zea mays), root isoform}
DPNATHIMIATGTGVAPFRGYLRRMFMEDVPNYRFGGLAWLFLGVANSDSLLYDEEFTSYLKQYP
DNFRYDKALSREQKNRSGGKMYVQDKIEEYSDEIFKLLDGGAHIYFCGLKGMMPGIQDTLKKVAE
RRGESWDQKLAQLKKNKQWHVEVY
>d1que_2 c.25.1.1 (142-303) Ferredoxin reductase (flavodoxin reductase) {Cyanobacterium (Anabaena sp.), pcc 7119}
LPDDPEANVIMLATGTGIAPMRTYLWRMFKDAERAANPEYQFKGFSWLVFGVPTTPNILYKEELE
EIQQKYPDNFRLTYAISREQKNPQGGRMYIQDRVAEHADQLWQLIKNQKTHTYICGLRGMEEGID
AALSAAAAKEGVTWSDYQKDLKKAGRWHVETY
>d1fdr_2 c.25.1.1 (101-248) Ferredoxin reductase (flavodoxin reductase) {Escherichia coli}
DEVPHCETLWMLATGTAIGPYLSILRLGKDLDRFKNLVLVHAARYAADLSYLPLMQELEKRYEGK
LRIQTVVSRETAAGSLTGRIPALIESGELESTIGLPMNKETSHVMLCGNPQMVRDTQQLLKETRQ
MTKHLRRRPGHMTAEHYW
>d1a8p_2 c.25.1.1 (101-258) Ferredoxin reductase (flavodoxin reductase) {Azotobacter vinelandii}
TSDLLPGKHLYMLSTGTGLAPFMSLIQDPEVYERFEKVVLIHGVRQVNELAYQQFITEHLPQSEY
FGEAVKEKLIYYPTVTRESFHNQGRLTDLMRSGKLFEDIGLPPINPQDDRAMICGSPSMLDESCE
VLDGFGLKISPRMGEPGDYLIERAFVEK
>d1qfja2 c.25.1.1 (A:98-232) NAD(P)H:flavin oxidoreductase {Escherichia coli}
RDDEERPMILIAGGTGFSYARSILLTALARNPNRDITIYWGGREEQHLYDLCELEALSLKHPGLQ
VVPVVEQPEAGWRGRTGTVLTAVLQDHGTLAEHDIYIAGRFEMAKIARDLFCSERNAREDRLFGD
AFAFI
>d2cnd_2 c.25.1.1 (125-270) Nitrate reductase {Corn (Zea mays)}
GSFVINGKQRNARRLAMICGGSGITPMYQIIQAVLRDQPEDHTEMHLVYANRTEDDILLRDELDR
WAAEYPDRLKVWYVIDQVKRPEEGWKYSVGFVTEAVLREHVPEGGDDTLALACGPPPMIQFAISP
NLEKMKYDMANSFVVF
>d1ndh_2 c.25.1.1 (126-272) cytochrome b5 reductase {Pig (Sus scrofa), liver}
GKFAIRPDKKSSPVIKTVKSVGMIAGGTGITPMLQVIRAIMKDPDDHTVCHLLFANQTEKDILLR
PELEELRNEHSARFKLWYTVDRAPEAWDYSQGFVNEEMIRDHLPPPEEEPLVLMCGPPPMIQYAC
LPNLERVGHPKERCFAF
>d1i7pa2 c.25.1.1 (A:154-300) cytochrome b5 reductase {Rat (Rattus norvegicus)}
GKFAIRADKKSNPVVRTVKSVGMIAGGTGITPMLQVIRAVLKDPNDHTVCYLLFANQSEKDILLR
PELEELRNEHSSRFKLWYTVDKAPDAWDYSQGFVNEEMIRDHLPPPGEETLILMCGPPPMIQFAC
LPNLERVGHPKERCFTF
>d2pia_2 c.25.1.2 (104-223) Phthalate dioxygenase reductase {Pseudomonas cepacia, db01}
EFPLDKRAKSFILVAGGIGITPMLSMARQLRAEGLRSFRLYYLTRDPEGTAFFDELTSDEWRSDV
KIHHDHGDPTKAFDFWSVFEKSKPAQHVYCCGPQALMDTVRDMTGHWPSGTVHFE
>d1ep3b2 c.25.1.3 (B:103-262) Dihydroorotate dehydrogenase B, PyrK subunit {Lactococcus lactis, isozyme B}

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PVAEVTSTDKILIIGGGIGVPPLYELAKQLEKTGCQMTILLGFASENVKILENEFSNLKNVTLKI
ATDDGSYGTKGHVGMLMNEIDFEVDALYTCGAPAMLKAVAKKYDQLERLYISMESRMACGIGACY
ACVEHDKEDESHALKVCEDGPVFLGKQLSL
>d1ja1a3 c.25.1.4 (A:519-678) NADPH-cytochrome p450 reductase {Rat
(Rattus norvegicus)}
RLPFKSTTPVIMVGPGTGIAPFMGFIQERAWLREQGKEVGETLLYYGCRRSDEDYLYREELARFH
KDGALTQLNVAFSREQAHKVYVQHLLKRDREHLWKLIHEGGAHIYVAGDARNMAKDVQNTFYDIV
AEFGPMEHTQAVDYVKKLMTKGRYSLNVWS
>d1ddga2 c.25.1.4 (A:447-599) Sulfite reductase flavoprotein
{Escherichia coli}
LPANPETPVIMIGPGTGIAPFRAFMQQRAADEAPGKNWLFFGNPHFTEDFLYQVEWQRYVKEGVL
TRIDLAWSRDQKEKVYVQDKLREQGAELWRWINDGAHIYVCGDANRMAKDVEQALLEVIAEFGGM
DTEAADEFLSELRVERRYQRDVY
>d1f20a2 c.25.1.4 (A:1233-1397) Neuronal nitric-oxide synthase
FAD/NADP+ domain {Rat (Rattus norvegicus)}
SFHLPRNPQVPCILVGPGTGIAPFRSFWQQRQFDIQHKGMNPCPMVLVFGCRQSKIDHIYREETL
QAKNKGVFRELYTAYSREPDRPKKYVQDVLQEQLAESVYRALKEQGGHIYVCGDVTMAADVLKAI
QRIMTQQGKLSEEDAGVFISRLRDDNRYHEDIFGV
>d1cqxa3 c.25.1.5 (A:262-403) Flavohemoglobin, C-terminal domain
{Alcaligenes eutrophus}
DVDAKTPIVLISGGVGLTPMVSMLKVALQAPPRQVVFVHGARNSAVHAMRDRLREAAKTYENLDL
FVFYDQPLPEDVQGRDYDYPGLVDVKQIEKSILLPDADYYICGPIPFMRMQHDALKNLGIHEARI
HYEVFGPDLFAE
>d4ts1a_ c.26.1.1 (A:) Tyrosyl-tRNA synthetase (TyrRS) {Bacillus
stearothermophilus, nca 1503}
MDLLAELQWRGLVNQTTDEDGLRKLLNEERVTLYCGFDPTADSLHIGHLATILTMRRFQQAGHRP
IALVGGATGLIGDPSGKKSERTLNAKETVEAWSARIKEQLGRFLDFEADGNPAKIKNNYDWIGPL
DVITFLRDVGKHFSVNYMMAKESVQSRIETGISFTEFSYMMLQAYDFLRLYETEGCRLQIGGSDQ
WGNITAGLELIRKTKGEARAFGLTIPLVTKADGTKFGKTESGTIWLDKEKTSPYEFYQFWINTDD
RDVIRYLKYFTFLSKEEIEALEQELREAPEKRAAQKTLAEEVTKLVHGEEALRQAIRYA
>d1jila_ c.26.1.1 (A:) Tyrosyl-tRNA synthetase (TyrRS)
{Staphylococcus aureus}
TNVLIEDLKWRGLIYQQTDEQGIEDLLNKEQVTLYCGADPTADSLHIGHLLPFLTLRRFQEHGHR
PIVLIGGGTGMIGDPSGKSEERVLQTEEQVDKNIEGISKQMHNIFEFGTDHGAVLVNNRDWLGQI
SLISFLRDYGKHVGVNYMLGKDSIQSRLEHGISYTEFTYTILQAIDFGHLNRELNCKIQVGGSDQ
WGNITSGIELMRRMYGQTDAYGLTIPLVTKSDGKKFGKSESGAVWLDAEKTSPYEFYQFWINQSD
EDVIKFLKYFTFLGKEEIDRLEQSKNEAPHLREAQKTLAEEVTKFIHGEDALNDAIRISQALF
>d1i6la_ c.26.1.1 (A:) Tryptophanyl-tRNA synthetase (TrpRS) {Bacillus
stearothermophilus}
MKTIFSGIQPSGVITIGNYIGALRQFVELQHEYNCYFCIVDQHAITVWQDPHELRQNIRRLAALY
LAVGIDPTQATLFIQSEVPAHAQAAWMLQCIVYIGELERMTQFKEKSAGKEAVSAGLLTYPPLMA
ADILLYNTDIVPVGEDQKQHIELTRDLAERFNKRYGELFTIPEARIPKVGARIMSLVDPTKKMSK
SDPNPKAYITLLDDAKTIEKKIKSAVTDSEGTIRYDKEAKPGISNLLNIYSTLSGQSIEELERQY
EGKGYGVFKADLAQVVIETLRPIQERYHHWMESEELDRVLDEGAEKANRVASEMVRKMEQAMGLG
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R
>d1gtra2 c.26.1.1 (A:8-338) Glutaminyl-tRNA synthetase (GlnRS) {Escherichia coli}
TNFIRQIIDEDLASGKHTTVHTRFPPEPNGYLHIGHAKSICLNFGIAQDYKGQCNLRFDDTNPVK
EDIEYVESIKNDVEWLGFHWSGNVRYSSDYFDQLHAYAIELINKGLAYVDELTPEQIREYRGTLT
QPGKNSPYRDRSVEENLALFEKMRAGGFEEGKACLRAKIDMASPFIVMRDPVLYRIKFAEHHQTG
NKWCIYPMYDFTHCISDALEGITHSLCTLEFQDNRRLYDWVLDNITIPVHPRQYEFSRLNLEYTV
MSKRKLNLLVTDKHVEGWDDPRMPTISGLRRRGYTAASIREFCKRIGVTKQDNTIEMASLESCIR
EDLNEN
>d1gln_2 c.26.1.1 (1-305) Glutamyl-tRNA synthetase (GluRS) {Thermus thermophilus}
MVVTRIAPSPTGDPHVGTAYIALFNYAWARRNGGRFIVRIEDTDRARYVPGAEERILAALKWLGL
SYDEGPDVAAPTGPYRQSERLPLYQKYAEELLKRGWAYRAFETPEELEQIRKEKGGYDGRARNIP
PEEAEERARRGEPHVIRLKVPRPGTTEVKDELRGVVVYDNQEIPDVVLLKSDGYPTYHLANVVDD
HLMGVTDVIRAEEWLVSTPIHVLLYRAFGWEAPRFYHMPLLRNPDKTKISKRKSHTSLDWYKAEG
FLPEALRNYLCLMGFSMPDGREIFTLEEFIQAFTWERVSLGGPVF
>d1a8h_2 c.26.1.1 (1-348) Methionyl-tRNA synthetase (MetRS) {Thermus thermophilus}
MEKVFYVTTPIYYVNAEPHLGHAYTTVVADFLARWHRLDGYRTFFLTGTDEHGETVYRAAQAAGE
DPKAFVDRVSGRFKRAWDLLGIAYDDFIRTTEERHKKVVQLVLKKVYEAGDIYYGEYEGLYCVSC
ERFYTEKELVEGLCPIHGRPVERRKEGNYFFRMEKYRPWLQEYIQENPDLIRPEGYRNEVLAMLA
EPIGDLSISRPKSRVPWGIPLPWDENHVTYVWFDALLNYVSALDYPEGEAYRTFWPHAWHLIGKD
ILKPHAVFWPTMLKAAGIPMYRHLNVGGFLLGPDGRKMSKTLGNVVDPFALLEKYGRDALRYYLL
REIPYGQDTPVSEEALRTRYEAD
>d1f4la2 c.26.1.1 (A:4-140,A:176-388) Methionyl-tRNA synthetase (MetRS) {Escherichia coli}
AKKILVTCALPYANGSIHLGHMLEHIQADVWVRYQRMRGHEVNFICADDAHGTPIMLKAQQLGIT
PEQMIGEMSQEHQTDFAGFNISYDNYHSTHSEENRQLSELIYSRLKENGFIKNRTISQLYDPEKG
MFLPDRFXVVSGATPVMRDSEHFFFDLPSFSEMLQAWTRSGALQEQVANKMQEWFESGLQQWDIS
RDAPYFGFEIPNAPGKYFYVWLDAPIGYMGSFKNLCDKRGDSVSFDEYWKKDSTAELYHFIGKDI
VYFHSLFWPAMLEGSNFRKPSNLFVHGYVTVNGAKMSKSRGTFIKASTWLNHFDADSLRYYYTAK
LSSRIDDIDLNLEDFVQRVNADIVNK
>d1ile_3 c.26.1.1 (1-197,387-641) Isoleucyl-tRNA synthetase (IleRS) {Thermus thermophilus}
MFKEVGEPNFPKLEEEVLAFWKREKIFQKSVENRKGGPRYTVYEGPPTANGLPHVGHAQARSYKD
LFPRYKTMRGYYAPRRAGWDTHGLPVELEVEKKLGLKSKREIEAYGIERFNQACRESVFTYEKEW
EAFTERIAYWVDLEDAYATLEPTYIESIWWSLKNLFDRGLLYRDHKVVPYCPRCGTPLSSHEVAL
GYXPHCWRCSTPLMYYATESWFIKNTLFKDELIRNNQEIHWVPPHIKEGRYGEWLKNLVDWALSR
NRYWGTPLPIWVCQACGKEEAIGSFQELKARATKPLPEPFDPHRPYVDQVELACACGGTMRRVPY
VIDVWYDSGAMPFASLHYPFEHEEVFRESFPADFIAEGIDQTRGWFNSLHQLGVMLFGSIAFKNV
ICHGLILDEKGQKMSKSKGNVVDPWDIIRKFGADALRWYIYVSAPPEADRRFGPNLVRETVRD
>d1ffya3 c.26.1.1 (A:1-200,A:395-644) Isoleucyl-tRNA synthetase (IleRS) {Staphylococcus aureus}
MDYEKTLLMPKTDFPMRGGLPNKEPQIQEKWDAEDQYHKALEKNKGNETFILHDGPPYANGNLHM
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GHALNKILKDFIVRYKTMQGFYAPYVPGWDTHGLPIEQALTKKGVDRKKMSTAEFREKCKEFALE
QIELQKKDFRRLGVRGDFNDPYITLKPEYEAAQIRIFGEMADKGLIYKGKKPVYWSPSSESSLAE
AEIEYXPHDWRTKKPVIFRATPQWFASISKVRQDILDAIENTNFKVNWGKTRIYNMVRDRGEWVI
SRQRVWGVPLPVFYAENGEIIMTKETVNHVADLFAEHGSNIWFEREAKDLLPEGFTHPGSPNGTF
TKETDIMDVWFDSGSSHRGVLETRPELSFPADMYLEGSDQYRGWFNSSITTSVATRGVSPYKFLL
SHGFVMDGEGKKMSKSLGNVIVPDQVVKQKGADIARLWVSSTDYLADVRISDEILKQTSDD
>d1gaxa3 c.26.1.1 (A:1-189,A:343-578) Valyl-tRNA synthetase (ValRS) {Thermus thermophilus}
MDLPKAYDPKSVEPKWAEKWAKNPFVANPKSGKPPFVIFMPPPNVTGSLHMGHALDNSLQDALIR
YKRMRGFEAVWLPGTDHAGIATQVVVERLLLKEGKTRHDLGREKFLERVWQWKEESGGTILKQLK
RLGASADWSREAFTMDEKRSRAVRYAFSRYYHEGLAYRAPRLVNWCPRCETTLSDLEVEXTCSRC
GTPIEYAIFPQWWLRMRPLAEEVLKGLRRGDIAFVPERWKKVNMDWLENVKDWNISRQLWWGHQI
PAWYCEDCQAVNVPRPERYLEDPTSCEACGSPRLKRDEDVFDTWFSSALWPLSTLGWPEETEDLK
AFYPGDVLVTGYDILFLWVSRMEVSGYHFMGERPFKTVLLHGLVLDEKGQKMSKSKGNVIDPLEM
VERYGADALRFALIYLATGGQDIRLDLRWLEMARNF
>d1f7ua2 c.26.1.1 (A:136-483) Arginyl-tRNA synthetase (ArgRS) {Baker's yeast (Saccharomyces cerevisiae)}
SCKLVENKKVIIEFSSPNIAKPFHAGHLRSTIIGGFLANLYEKLGWEVIRMNYLGDWGKQFGLLA
VGFERYGNEEALVKDPIHHLFDVYVRINKDIEEEGDSIPLEQSTNGKAREYFKRMEDGDEEALKI
WKRFREFSIEKYIDTYARLNIKYDVYSGESQVSKESMLKAIDLFKEKGLTHEDKGAVLIDLTKFN
KKLGKAIVQKSDGTTLYLTRDVGAAMDRYEKYHFDKMIYVIASQQDLHAAQFFEILKQMGFEWAK
DLQHVNFGMVQGMSTRKGTVVFLDNILEETKEKMHEVMKKNENKYAQIEHPEEVADLVGISAVMI
QDMQGKRINNYEFKWERMLSFEG
>d1iq0a2 c.26.1.1 (A:97-466) Arginyl-tRNA synthetase (ArgRS) {Thermus thermophilus}
PFPRRPGVVLVEHTSVNPNKELHVGHLRNIALGDAIARILAYAGREVLVLNYIDDTGRQAAETLF
ALRHYGLTWDGKEKYDHFAGRAYVRLHQDPEYERLQPAIEEVLHALERGELREEVNRILLAQMAT
MHALNARYDLLVWESDIVRAGLLQKALALLEQSPHVFRPREGKYAGALVMDASPVIPGLEDPFFV
LLRSNGTATYYAKDIAFQFWKMGILEGLRFRPYENPYYPGLRTSAPEGEAYTPKAEETINVVDVR
QSHPQALVRAALALAGYPALAEKAHHLAYETVLLEGRQMSGRKGLAVSVDEVLEEATRRARAIVE
EKNPDHPDKEEAARMVALGAIRFSMVKTEPKKQIDFRYQEALSFE
>d1coza_ c.26.1.2 (A:) CTP:glycerol-3-phosphate cytidylyltransferase {Bacillus subtilis}
MKKVITYGTFDLLHWGHIKLLERAKQLGDYLVVAISTDEFNLQKQKKAYHSYEHRKLILETIRYV
DEVIPEKNWEQKKQDIIDHNIDVFVMGDDWEGKFDFLKDQCEVVYLPRTEGISTTKIKEEI
>d1qjca_ c.26.1.3 (A:) Phosphopantetheine adenylyltransferase {Escherichia coli}
KRAIYPGTFDPITNGHIDIVTRATQMFDHVILAIAASPSKKPMFTLEERVALAQQATAHLGNVEV
VGFSDLMANFARNQHATVLIRGLRAVADFEYEMQLAHMNRHLMPELESVFLMPSKEWSFISSSLV
KEVARHQGDVTHFLPENVHQALMAKLA
>d1f9aa_ c.26.1.3 (A:) Nicotinamide mononucleotide (NMN) adenylyltransferase {Archaeon Methanococcus jannaschii}
LRGFIIGRFQPFHKGHLEVIKKIAEEVDEIIIGIGSAQKSHTLENPFTAGERILMITQSLKDYDL
TYYPIPIKDIEFNSIWVSYVESLTPPFDIVYSGNPLVRVLFEERGYEVKRPEMFNRKEYSGTEIR

RRMLNGEKWEHLVPKAVVDVIKEIKGVERLRKLA
>d1ej2a_ c.26.1.3 (A:) Nicotinamide mononucleotide (NMN) adenylyltransferase {Archaeon Methanobacterium thermoautotrophicum}
MRGLLVGRMQPFHRGHLQVIKSILEEVDELIICIGSAQLSHSIRDPFTAGERVMMLTKALSENGI
PASRYYIIPVQDIECNALWVGHIKMLTPPFDRVYSGNPLVQRLFSEDGYEVTAPPLFYRDRYSGT
EVRRRMLDDGDWRSLLPESVVEVIDEINGVERIKHLA
>d1ihoa_ c.26.1.4 (A:) Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC) {Escherichia coli}
MLIIETLPLLRQQIRRLRMEGKRVALVPTMGNLHDGHMKLVDEAKARADVVVVSIFVNPMQFDRP
EDLARYPRTLQEDCEKLNKRKVDLVFAPSVKEIYPNGTETHTYVDVPGLSTMLEGASRPGHFRGV
STIVSKLFNLVQPDIACFGEKDFQQLALIRKMVADMGFDIEIVGVPIMRAKDGLALSSRNGYLTA
EQRKIAPGLYKVLSSIADKLQAGERDLDEIITIAGQELNEKGFRADDIQIRDADTLLEVSETSKR
AVILVAAWLGDARLIDNKMVEL
>d1g8fa2 c.26.1.5 (A:169-389) ATP sulfurylase central domain {Baker's yeast (Saccharomyces cerevisiae)}
YPGLRKTPAQLRLEFQSRQWDRVVAFQTRNPMHRAHRELTVRAAREANAKVLIHPVVGLTKPGDI
DHHTRVRVYQEIIKRYPNGIAFLSLLPLAMRMSGDREAVWHAIIRKNYGASHFIVGRDHAGPGKN
SKGVDFYGPYDAQELVESYKHELDIEVVPFRMVTYLPDEDRYAPIDQIDTTKTRTLNISGTELRR
RLRVGGEIPEWFSYPEVVKILRESNP
>d1i2da2 c.26.1.5 (A:171-390) ATP sulfurylase central domain {Fungus (Penicillium chrysogenum)}
YVALRYTPAELRVHFDKLGWSRVVAFQTRNPMHRAHRELTVRAARSRQANVLIHPVVGLTKPGDI
DHFTRVRAYQALLPRYPNGMAVLGLLGLAMRMGGPREAIWHAIIRKNHGATHFIVGRDHAGPGSN
SKGEDFYGPYDAQHAVEKYKDELGIEVVEFQMVTYLPDTDEYRPVDQVPAGVKTLNISGTELRRR
LRSGAHIPEWFSYPEVVKILRESNP
>d1jhda2 c.26.1.5 (A:174-396) ATP sulfurylase central domain {unnamed symbiont of Riftia pachyptila}
PDTFRTAVEIRNEIKEHGWSKVVAFQTRNPMHRAHEELCRMAMESLDADGVVVHMLLGKLKKGDI
PAPVRDAAIRTMAEVYFPPNTVMVTGYGFDMLYAGPREAVLHAYFRQNMGATHFIIGRDHAGVGD
YYGAFDAQTIFDDEVPEGAMEIEIFRADHTAYSKKLNKIVMMRDVPDHTKEDFVLLSGTKVREML
GQGIAPPPEFSRPEVAKILMDYYQSINS
>d1gpma1 c.26.2.1 (A:208-404) GMP synthetase, central domain {Escherichia coli}
WTPAKIIDDAVARIREQVGDDKVILGLSGGVDSSVTAMLLHRAIGKNLTCVFVDNGLLRLNEAEQ
VLDMFGDHFGLNIVHVPAEDRFLSALAGENDPEAKRKIIGRVFVEVFDEEALKLEDVKWLAQGTI
YPDVIESAASATGKAHVIKSHHNVGGLPKEMKMGLVEPLKELFKDEVRKIGLELGLPYDMLYRHP
FP
>d1ih8a_ c.26.2.1 (A:) NH3-dependent NAD+-synthetase {Bacillus subtilis}
SMQEKIMRELHVKPSIDPKQEIEDRVNFLKQYVKKTGAKGFVLGISGGQDSTLAGRLAQLAVESI
REEGGDAQFIAVRLPHGTQQDEDDAQLALKFIKPDKSWKFDIKSTVSAFSDQYQQETGDQLTDFN
KGNVKARTRMIAQYAIGGQEGLLVLGTDHAAEAVTGFFTKYGDGGADLLPLTGLTKRQGRTLLKE
LGAPERLYLKEPTADLLDEKPQQSDETELGISYDEIDDYLEGKEVSAKVSEALEKRYSMTEHKRQ
VPASMFDDWWK

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>d1ct9a1 c.26.2.1 (A:193-516) Asparagine synthetase B, C-terminal
domain {Escherichia coli}
RDWFDYDAVKDNVTDKNELRQALEDSVKSHLMSDVPYGVLLSGGLDSSIISAITKKYAARRVEDQ
ERSEAWWPQLHSFAVGLPGSPDLKAAQEVANHLGTVHHEIHFTVQEGLDAIRDVIYHIETYDVTT
IRASTPMYLMSRKIKAMGIKMVLSGEGSDEVFGGYLYFHKAPNAKELHEETVRKLLALHMYDCAR
ANKAMSAWGVEARVPFLDKKFLDVAMRINPQDKMCGNGKMEKHILRECFEAYLPASVAWRQKEQF
SDGVGYSWIDTLKEVAAQQVSDQQLETARFRFPYNTPTSKEAYLYREIFEELFPLPSAAECVPG
>d1jgta1 c.26.2.1 (A:210-508) beta-Lactam synthetase {Streptomyces
clavuligerus}
PGLSRRILPEGEAVAAVRAALEKAVAQRVTPGDTPLVVLSGGIDSSGVAACAHRAAGELDTVSMG
TDTSNEFREARAVVDHLRTRHREITIPTTELLAQLPYAVWASESVDPDIIEYLLPLTALYRALDG
PERRILTGYGADIPLGGMHREDRLPALDTVLAHDMATFDGLNEMSPVLSTLAGHWTTHPYWDREV
LDLLVSLEAGLKRRHGRDKWVLRAAMADALPAETVNRPKLGVHEGSGTTSSFSRLLLDHGVAEDR
VHEAKRQVVRELFDLTVGGGRHPSEVDTDDVVRSVADRT
>d1k92a1 c.26.2.1 (A:1-188) Argininosuccinate synthetase, N-terminal
domain {Escherichia coli}
TTILKHLPVGQRIGIAFSGGLDTSAALLWMRQKGAVPYAYTANLGQPDEEDYDAIPRRAMEYGAE
NARLIDCRKQLVAEGIAAIQCGAFHNTTGGLTYFNTTPLGRAVTGTMLVAAMKEDGVNIWGDGST
YKGNDIERFYRYGLLTNAELQIYKPWLDTDFIDELGGRHEMSEFMIACGFDYKMSVEK
>d1sur__ c.26.2.2 (-) Phosphoadenylyl sulphate (PAPS) reductase
{Escherichia coli}
SKLDLNALNELPKVDRILALAETNAELEKLDAEGRVAWALDNLPGEYVLSSSFGIQAAVSLHLVN
QIRPDIPVILTDTGYLFPETYRFIDELTDKLKLNLKVYRATESAAWQEARYGKLWEQGVEGIEKY
NDINKVEPMNRALKELNAQTWFAGLRREQSGSRANLPVLAIQRGVFKVLPIIDWDNRTIYQYLQK
HGLKYHPLWDEGYLSVGDTH
>d1dlja3 c.26.3.1 (A:295-402) UDP-glucose dehydrogenase (UDPGDH),
C-terminal (UDP-binding) domain {Streptococcus pyogenes}
AKQIINVLKEQESPVKVVGVYRLIMKSNSDNFRESAIKDVIDILKSKDIKIIIYEPMLNKLESED
QSVLVNDLENFKKQANIIVTNRYDNELQDVKNKVYSRDIFGRD
>d2tpt_2 c.27.1.1 (71-335) Thymidine phosphorylase {Escherichia coli}
DWKSLHLNGPIVDKHSTGGVGDVTSLMLGPMVAACGGYIPMISGRGLGHTGGTLDKLESIPGFDI
FPDDNRFREIIKDVGVAIIGQTSSLAPADKRFYATRDITATVDSIPLITASILAKKLAEGLDALV
MDVKVGSGAFMPTYELSEALAEAIVGVANGAGVRTTALLTDMNQVLASSAGNAVEVREAVQFLTG
EYRNPRLFDVTMALCVEMLISGKLAKDDAEARAKLQAVLDNGKAAEVFGRMVAAQKGPTDFVENY
AKYLP
>d1brwa2 c.27.1.1 (A:71-330) Pyrimidine nucleoside phosphorylase
{Bacillus stearothermophilus}
LSSIRGVKVDKHSTGGVGDTTTLVLGPLVASVGVPVAKMSGRGLGHTGGTIDKLESVPGFHVEIS
KDEFIRLVNENGIAIIGQTGDLTPADKKLYALRDVTATVNSIPLIASSIMSKKIAAGADAIVLDV
KTGAGAFMKKLDEARRLARVMVDIGKRVGRRTMAVISDMSQPLGYAVGNALEVKEAIETLKGNGP
HDLTELCLTLGSHMVYLAEKAPSLDEARRLLEEAIRSGAAIAAFKTFLAAQGGDASVVDDLDKLP
>d1dnpa2 c.28.1.1 (A:1-200) N-terminal domain of DNA photolyase
{Escherichia coli}
TTHLVWFRQDLRLHDNLALAAACRNSSARVLALYIATPRQWATHNMSPRQAELINAQLNGLQIAL
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AEKGIPLLFREVDDFVASVEIVKQVCAENSVTHLFYNYQYEVNERARDVEVERALRNVVCEGFDD
SVILPPGAVMTGNHEMYKVFTPFKNAWLKRLREGMPECVAAPKVRSSGSIEPSPSITLNYPRQSF
DTAHF
>d1iqra2 c.28.1.1 (A:2-171) N-terminal domain of DNA photolyase {Thermus thermophilus}
GPLLVWHRGDLRLHDHPALLEALARGPVVGLVVLDPNNLKTTPRRRAWFLENVRALREAYRARGG
ALWVLEGLPWEKVPEAARRLKAKAVYALTSHTPYGRYRDGRVREALPVPLHLLPAPHLLPPDLPR
AYRVYTPFSRLYRGAAPPLPPPEALPKGPEEGEIPREDPG
>d1qnf_2 c.28.1.1 (1-204) N-terminal domain of DNA photolyase {Anacystis nidulans}
MAAPILFWHRRDLRLSDNIGLAAARAQSAQLIGLFCLDPQILQSADMAPARVAYLQGCLQELQQR
YQQAGSRLLLLQGDPQHLIPQLAQQLQAEAVYWNQDIEPYGRDRDGQVAAALKTAGIRAVQLWDQ
LLHSPDQILSGSGNPYSVYGPFWKNWQAQPKPTPVATPTELVDLSPEQLTAIAPLLLSELPTLKQ
LGFDWDGGF
>d1efva1 c.29.1.1 (A:20-207) Electron transfer flavoprotein, ETFP {Human (Homo sapiens)}
QSTLVIAEHANDSLAPITLNTITAATRLGGEVSCLVAGTKCDKVAQDLCKVAGIAKVLVAQHDVY
KGLLPEELTPLILATQKQFNYTHICAGASAFGKNLLPRVAAKLEVAPISDIIAIKSPDTFVRTIY
AGNALCTVKCDEKVKVFSVRGTSFDAAATSGGSASSEKASSTSPVEISEWLDQKLTKS
>d1efvb1 c.29.1.1 (B:) Electron transfer flavoprotein, ETFP {Human (Homo sapiens)}
LRVLVAVKRVIDYAVKIRVKPDRTGVVTDGVKHSMNPFCEIAVEEAVRLKEKKLVKEVIAVSCGP
AQCQETIRTALAMGADRGIHVEVPPAEAERLGPLQVARVLAKLAEKEKVDLVLLGKQAIDDDCNQ
TGQMTAGFLDWPQGTFASQVTLEGDKLKVEREIDGGLETLRLKLPAVVTADLRLNEPRYATLPNI
MKAKKKKIEVIKPGDLGVDLTSKLSVISVEDPPQRTAGVKVETTEDLVAKLKEIGRI
>d1efpa1 c.29.1.1 (A:2-184) Electron transfer flavoprotein, ETFP {Paracoccus denitrificans}
AVLLLGEVTNGALNRDATAKAVAAVKALGDVTVLCAGASAKAAAEEAAKIAGVAKVLVAEDALYG
HRLAEPTAALIVGLAGDYSHIAAPATTDAKNVMPRVAALLDVMVLSDVSAILDADTFERPIYAGN
AIQVVKSKDAKKVFTIRTASFDAAGEGGTAPVTETAAAADPGLSSWVADEVAE
>d1efpb1 c.29.1.1 (B:) Electron transfer flavoprotein, ETFP {Paracoccus denitrificans}
MKVLVPVKRLIDYNVKARVKSDGSGVDLANVKMSMNPFDEIAVEEAIRLKEKGQAEEIIAVSIGV
KQAAETLRTALAMGADRAILVVAADDVQQDIEPLAVAKILAAVARAEGTELIIAGKQAIDNDMNA
TGQMLAAILGWAQATFASKVEIEGAKAKVTREVDGGLQTIAVSLPAVVTADLRLNEPRYASLPNI
MKAKKKPLDEKTAADYGVDVAPRLEVVSVREPEGRKAGIKVGSVDELVGKL
>d1mjha_ c.29.1.2 (A:) "Hypothetical" protein MJ0577 {Archaeon Methanococcus jannaschii}
VMYKKILYPTDFSETAEIALKHVKAFKTLKAEEVILLHVIDEREIKKRDIFSLLLGVAGLNKSVE
EFENELKNKLTEEAKNKMENIKKELEDVGFKVKDIIVVGIPHEEIVKIAEDEGVDIIIMGSHGKT
NLKEILLGSVTENVIKKSNKPVLVVKRKNS
>d1jmva_ c.29.1.2 (A:) Universal stress protein A, UspA {Haemophilus influenzae}
MYKHILVAVDLSEESPILLKKAVGIAKRHDAKLSIIHVDVNFSDLYTGLIDVNMSSMQDRISTET
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QKALLDLAESVDYPISEKLSGSGDLGQVLSDAIEQYDVDLLVTGHHQDFWSKLMSSTRQVMNTIK
IDMLVVPLRD
>d1dv1a2 c.30.1.1 (A:1-114) Biotin carboxylase (BC) subunit of acetyl-CoA carboxylase {Escherichia coli}
MLDKIVIANRGEIALRILRACKELGIKTVAVHSSADRDLKHVLLADETVCIGPAPSVKSYLNIPA
IISAAEITGAVAIHPGYGFLSENANFAEQVERSGFIFIGPKAETIRLMG
>d1gsoa2 c.30.1.1 (A:-2-103) Glycinamide ribonucleotide synthetase (GAR-syn). {Escherichia coli}
EFMKVLVIGNGGREHALAWKAAQSPLVETVFVAPGNAGTALEPALQNVAIGVTDIPALLDFAQNE
KIDLTIVGPEAPLVKGVVDTFRAAGLKIFGPTAGAAQLEG
>d1b6ra2 c.30.1.1 (A:1-78) N5-carboxyaminoimidazole ribonucleotide synthetase, AIRC, PurK {Escherichia coli}
MKQVCVLGNGQLGRMLRQAGEPLGIAVWPVGLDAEPAAVPFQQSVITAEIERWPETALTRQLARH
PAFVNRDVFPIIA
>d1eyza2 c.30.1.1 (A:2-112) Glycinamide ribonucleotide transformylase PurT {Escherichia coli}
TLLGTALRPAATRVMLLGSGELGKEVAIECQRLGVEVIAVDRYADAPAMHVAHRSHVINMLDGDA
LRRVVELEKPHYIVPEIEAIATDMLIQLEEEGLNVVPCARATKLTM
>d1a9xa3 c.30.1.1 (A:1-127) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia coli}
MPKRTDIKSILILGAGPIVIGQACEFDYSGAQACKALREEGYRVINVNSNPATIMTDPEMADATY
IEPIHWEVVRKIIEKERPDAVLPTMGGQTALNCALELERQGVLEEFGVTMIGATADAIDKAE
>d1a9xa4 c.30.1.1 (A:556-676) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia coli}
STDREKIMVLGGGPNRIGQGIEFDYCCVHASLALREDGYETIMVNCNPETVSTDYDTSDRLYFEP
VTLEDVLEIVRIEKPKGVIVQYGGQTPLKLARALEAAGVPVIGTSPDAIDRAEDRE
>d1iow_1 c.30.1.2 (1-96) D-Ala-D-Ala ligase {Escherichia coli, gene ddlB}
MTDKIAVLLGGTSAEREVSLNSGAAVLAGLREGGIDAYPVDPKEVDVTQLKSMGFQKVFIALHGR
GGEDGTLQGMLELMGLPYTGSGVMASALSMD
>d1ehia1 c.30.1.2 (A:3-134) D-alanine:D-lactate ligase, VanA {Leuconostoc mesenteroides, Ddl2}
KKRVALIFGGNSSEHDVSKRSAQNFYNAIEATGKYEIIVFAIAQNGFFLDTESSKKILALEDEQP
IVDAFMKTVDASDPLARIHALKSAGDFDIFFPVVHGNLGEDGTLQGLFKLLDKPYVGAPLRGHAV
SF
>d1e4ea1 c.30.1.2 (A:2-131) D-alanine:D-lactate ligase, VanA {Enterococcus faecium}
NRIKVAILFGGCSEEHDVSVKSAIEIAANINKEKYEPLYIGITKSGVWKMCEKPCAEWENENCYS
AVLSPDKKMHGLLVKKNHEYEINHVDVAFSALHGKSGEDGSIQGLFELSGIPFVGCDIQSSAICM
>d1gsa_1 c.30.1.3 (1-122) Prokaryotic glutathione synthetase, N-terminal domain {Escherichia coli}
MIKLGIVMDPIANINIKKDSSFAMLLEAQRRGYELHYMEMGDLYLINGEARAHTRTLNVKQNYEE
WFSFVGEQDLPLADLDVILMRKDPPFDTEFIYATYILERAEEKGTLIVNKPQSLRDC
>d2hgsa1 c.30.1.4 (A:202-303) Eukaryotic glutathione synthetase
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{Human (Homo sapiens)}
PNALVLLIAQEKERNIFDQRAIENELLARNIHVIRRTFEDISEKGSLDQDRRLFVDGQEIAVVYF
RDGYMPRQYSLQNWEARLLLERSHAAKCPDIATQLAG
>d1auva1 c.30.1.5 (A:112-213) Synapsin Ia domain {Cow (Bos taurus)}
AARVLLVIDEPHTDWAKYFKGKKIHGEIDIKVEQAEFSDLNLVAHANGGFSVDMEVLRNGVKVVR
SLKPDFVLIRQHAFSMARNGDYRSLVIGLQYAGIPSI
>d1dhs__ c.31.1.1 (-) Deoxyhypusine synthase, DHS {Human (Homo sapiens)}
APAGALAAVLKHSSTLPPESTQVRGYDFNRGVNYRALLEAFGTTGFQATNFGRAVQQVNAMIEKK
LEPLTSCTIFLGYTSNLISSGIRETIRYLVQHNMVDVLVTTAGGVEEDLIKCLAPTYLGEFSLRG
KELRENGINRIGNLLVPNENYCKFEDWLMPILDQMVMEQNTEGVKWTPSKMIARLGKEINNPESV
YYWAQKNHIPVFSPALTDGSLGDMIFFHSYKNPGLVLDIVEDLRLINTQAIFAKCTGMIILGGGV
VKHHIANANLMRNGADYAVYINTAQEFDGSDSGARPDEAVSWGKIRVDAQPVKVYADASLVFPLL
VAETFAQKMDAFMHEKNED
>d1efva2 c.31.1.2 (A:208-331) C-terminal domain of the electron transfer flavoprotein alpha subunit {Human (Homo sapiens)}
DRPELTGAKVVVSGGRGLKSGENFKLLYDLADQLHAAVGASRAAVDAGFVPNDMQVGQTGKIVAP
ELYIAVGISGAIQHLAGMKDSKTIVAINKDPEAPIFQVADYGIVADLFKVVPEMTEILK
>d1efpa2 c.31.1.2 (A:185-308) C-terminal domain of the electron transfer flavoprotein alpha subunit {Paracoccus denitrificans}
SDRPELTSARRVVSGGRGLGSKESFAIIEELADKLGAAVGASRAAVDSGYAPNDWQVGQTGKVVA
PELYVAVGISGAIQHLAGMKDSKVIVAINKDEEAPIFQIADYGLVGDLFSVVPELTGKL
>d1poxa1 c.31.1.3 (A:183-365) Pyruvate oxidase {Lactobacillus plantarum}
YASANNYQTPLLPEPDVQAVTRLTQTLLAAERPLIYYGIGARKAGKELEQLSKTLKIPLMSTYPA
KGIVADRYPAYLGSANRVAQKPANEALAQADVVLFVGNNYPFAEVSKAFKNTRYFLQIDIDPAKL
GKRHKTDIAVLADAQKTLAAILAQVSERESTPWWQANLANVKNWRAYLASLED
>d1pvda1 c.31.1.3 (A:182-360) Pyruvate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}
QTPIDMSLKPNDAESEKEVIDTILALVKDAKNPVILADACCSRHDVKAETKKLIDLTQFPAFVTP
MGKGSISEQHPRYGGVYVGTLSKPEVKEAVESADLILSVGALLSDKTKNIVEFHSDHMKIRNATF
PGVQMKFVLQKLLTNIADAAKGYKPVAVPARTPANAAVP
>d1qpba1 c.31.1.3 (A:182-360) Pyruvate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}
QTPIDMSLKPNDAESEKEVIDTILVLIKDAKNPVILADACCSRHDVKAETKKLIDLTQFPAFVTP
MGKGSIDEQHPRYGGVYVGTLSKPEVKEAVESADLILSVGALLSDFNTGSFSYSYKTKNIVEFHS
DHMKIRNATFPGVQMKFVLQKLLTAIADAAKGYKPVAVPARTPANAAVP
>d1zpda1 c.31.1.3 (A:188-362) Pyruvate decarboxylase {Zymomonas mobilis}
EASDEASLNAAVDETLKFIANRDKVAVLVGSKLRAAGAEEAAVKFTDALGGAVATMAAAKSFFPE
ENALYIGTSWGEVSYPGVEKTMKEADAVIALAPVFNDYSTTGWTDIPDPKKLVLAEPRSVVVNGI
RFPSVHLKDYLTRLAQKVSKKTGSLDFFKSLNAGELKKAAPADPS
>d1bfd_1 c.31.1.3 (182-341) Benzoylformate decarboxylase {Pseudomonas putida}
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SVRLNDQDLDILVKALNSASNPAIVLGPDVDAANANADCVMLAERLKAPVWVAPSAPRCPFPTRH
PCFRGLMPAGIAAISQLLEGHDVVLVIGAPVFRYHQYDPGQYLKPGTRLISVTCDPLEAARAPMG
DAIVADIGAMASALANLVEESSRQLPTAAP
>d1jsca1 c.31.1.3 (A:280-460) Acetohydroxyacid synthase catalytic subunit {Baker's yeast (Saccharomyces cerevisiae)}
AQDEFVMQSINKAADLINLAKKPVLYVGAGILNHADGPRLLKELSDRAQIPVTTTLQGLGSFDQE
DPKSLDMLGMHGCATANLAVQNADLIIAVGARFDDRVTGNISKFAPEARRAAAEGRGGIIHFEVS
PKNINKVVQTQIAVEGDATTNLGKMMSKIFPVKERSEWFAQINKWKKEYPY
>d1d4oa_ c.31.1.4 (A:) Transhydrogenase domain III (dIII) {Cow (Bos taurus)}
GTHTEINLDNAIDMIREANSIIITPGYGLCAAKAQYPIADLVKMLSEQGKKVRFGIHPVAGRMPG
QLNVLLAEAGVPYDIVLEMDEINHDFPDTDLVLVIGANDTVNSAAQEDPNSIIAGMPVLEVWKSK
QVIVMKRSLGVGYAAVDNPIFYKPNTAMLLGDAKKTCDALQAKVRES
>d1hzzc_ c.31.1.4 (C:) Transhydrogenase domain III (dIII) {Rhodospirillum rubrum}
SVKAGSAEDAAFIMKNASKVIIVPGYGMAVAQAQHALREMADVLKKEGVEVSYAIHPVAGRMPGH
MNVLLAEANVPYDEVFELEEINSSFQTADVAFVIGANDVTNPAAKTDPSSPIYGMPILDVEKAGT
VLFIKRSMASGYAGVENELFFRNNTMMLFGDAKKMTEQIVQAMN
>d1icia_ c.31.1.5 (A:) AF1676 sir2 homolog {Archaeon Archaeoglobus fulgidus}
GSHHHHHHGSHMDEKLLKTIAESKYLVALTGAGVSAESGIPTFRGKDGLWNRYRPEELANPQAFA
KDPEKVWKWYAWRMEKVFNAQPNKAHQAFAELERLGVLKCLITQNVDDLHERAGSRNVIHLHGSL
RVVRCTSCNNSFEVESAPKIPPLPKCDKCGSLLRPGVVWFGEMLPPDVLDRAMREVERADVIIVA
GTSAVVQPAASLPLIVKQRGGAIIEINPDETPLTPIADYSLRGKAGEVMDELVRHVRKALS
>d1j8fa_ c.31.1.5 (A:) Sirt2 histone deacetylase {Human (Homo sapiens)}
GEADMDFLRNLFSQTLSLGSQKERLLDELTLEGVARYMQSERCRRVICLVGAGISTSAGIPDFRS
PSTGLYDNLEKYHLPYPEAIFEISYFKKHPEPFFALAKELYPGQFKPTICHYFMRLLKDKGLLLR
CYTQNIDTLERIAGLEQEDLVEAHGTFYTSHCVSASCRHEYPLSWMKEKIFSEVTPKCEDCQSLV
KPDIVFFGESLPARFFSCMQSDFLKVDLLLVMGTSLQVQPFASLISKAPLSTPRLLINKEKAGQS
DPFLGMIMGLGGGMDFDSKKAYRDVAWLGECDQGCLALAELLGWKKELEDLVRREHASIDAQS
>d1fsz_1 c.32.1.1 (23-231) Cell-division protein FtsZ {Archaeon Methanococcus jannaschii}
SPEDKELLEYLQQTKAKITVVGCGGAGNNTITRLKMEGIEGAKTVAINTDAQQLIRTKADKKILI
GKKLTRGLGAGGNPKIGEEAAKESAEEIKAAIQDSDMVFITCGLGGGTGTGSAPVVAEISKKIGA
LTVAVVTLPFVMEGKVRMKNAMEGLERLKQHTDTLVVIPNEKLFEIVPNMPLKLAFKVADEVLIN
AVKGLVELITKDGL
>d1tuba1 c.32.1.1 (A:1-245) Tubulin alpha-subunit {Pig (Sus scrofa)}
MRECISIHVGQAGVQIGNACWELYCLEHGIQPDGQMPSDKTIGGGDDSFNTFFSETGAGKHVPRA
VFVDLEPTVIDEVRTGTYRQLFHPEQLITGKEDAANNYARGHYTIGKEIIDLVLDRIRKLADQCT
GLQGFSVFHSFGGGTGSGFTSLLMERLSVDYGKKSKLEFSIYPAPQVSTAVVEPYNSILTTHTTL
EHSDCAFMVDNEAIYDICRRNLDIERPTYTNLNRLIGQIVSSITASLRFD
>d1tubb1 c.32.1.1 (B:1-245) Tubulin beta-subunit {Pig (Sus scrofa)}
MREIVHIQAGQCGNQIGAKFWEVISDEHGIDPTGSYHGDSDLQLERINVYYNEAAGNKYVPRAIL
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VDLEPGTMDSVRSGPFGQIFRPDNFVFGQSGAGNNWAKGHYTEGAELVDSVLDVVRKESESCDCL
QGFQLTHSLGGGTGSGMGTLLISKIREEYPDRIMNTFSVVPSPKVSDTVVEPYNATLSVHQLVEN
TDETYCIDNEALYDICFRTLKLTTPTYGDLNHLVSATMSGVTTCLRFP
>d1nbaa_ c.33.1.1 (A:) N-carbamoylsarcosine amidohydrolase
{Arthrobacter sp.}
TFNDIEARLAAVLEEAFEAGTSIYNERGFKRRIGYGNRPAVIHIDLANAWTQPGHPFSCPGMETI
IPNVQRINEAARAKGVPVFYTTNVYRNRDASSGTNDMGLWYSKIPTETLPADSYWAQIDDRIAPA
DGEVVIEKNRASAFPGTNLELFLTSNRIDTLIVTGATAAGCVRHTVEDAIAKGFRPIIPRETIGD
RVPGVVQWNLYDIDNKFGDVESTDSVVQYLDALPQFEDTVPKTLSDPQPEVEAPADPV
>d1im5a_ c.33.1.2 (A:) Pyrazinamidase/nicotinamidase {Archaeon
Pyrococcus horikoshii}
PEEALIVVDMQRDFMPGGALPVPEGDKIIPKVNEYIRKFKEKGALIVATRDWHPENHISFRERGG
PWPRHCVQNTPGAEFVVDLPEDAVIISKATEPDKEAYSGFEGTDLAKILRGNGVKRVYICGVATE
YCVRATALDALKHGFEVYLLRDAVKGIKPEDEERALEEMKSRGIKIVQF
>d1yaca_ c.33.1.2 (A:) YcaC {Escherichia coli}
TKPYVRLDKNDAAVLLVDHQAGLLSLVRDIEPDKFKNNVLALGDLAKYFNLPTILTTSAETGPNG
PLVPELKAQFPDAPYIARPGNINAWDNEDFVKAVKATGKKQLIIAGVVTEVCVAFPALSAIEEGF
DVFVVTDASGTFNEITRHSAWDRMSQAGAQLMTWFGVACELHRDWRNDIAGLATLFSNHIPDYRN
LMTSYDTLT
>d1hi9a_ c.99.1.1 (A:) Zn-dependent D-aminopeptidase DppA {Bacillus
subtilis}
MKLYMSVDMEGISGLPDDTFVDSGKRNYERGRLIMTEEANYCIAEAFNSGCTEVLVNDSHSKMNN
LMVEKLHPEADLISGDVKPFSMVEGLDDTFRGALFLGYHARASTPGVMSHSMIFGVRHFYINDRP
VGELGLNAYVAGYYDVPVLMVAGDDRAAKEAEELIPNVTTAAVKQTISRSAVKCLSPAKRGRLLT
EKTAFALQNKDKVKPLTPPDRPVLSIEFANYGQAEWANLMPGTEIKTGTTTVQFQAKDMLEAYQA
MLVMTELAMRTSFC
>d1e20a_ c.34.1.1 (A:) Halotolerance protein Hal3 {Mouse-ear cress
(Arabidopsis thaliana)}
RKPRVLLAASGSVAAIKFGNLCHCFTEWAEVRAVVTKSSLHFLDKLSLPQEVTLYTDEDEWSSWN
KIGDPVLHIELRRWADVLVIAPLSANTLGKIAGGLCDNLLTCIIRAWDYTKPLFVAPAMNTLMWN
NPFTERHLLSLDELGITLIPPIKKRLACGDYGNGAMAEPSLIYSTVRLFWESQAH
>d1g5qa_ c.34.1.1 (A:) Epidermin modifying enzyme (peptidyl-cysteine
decarboxylase) EpiD {Staphylococcus epidermidis}
MYGKLLICATASINVININHYIVELKQHFDEVNILFSPSSKNFINTDVLKLFCDNLYDEIKDPLL
NNINIVENHEYILVLPASANTINKIANGICDNLLTTVCLTGYQKLFIFPNMNIRMWGNPFLQKNI
DLLKNNDVKVYSPDMNKSFEISSGRYKNNITMPNIENVLNFVLN
>d1k1ea_ c.108.1.5 (A:) Probable phosphatase YrbI {Haemophilus
influenzae, HI1679}
KLENIKFVITDVDGVLTDGQLHYDANGEAIKSFHVRDGLGIKMLMDADIQVAVLSGRDSPILRRR
IADLGIKLFFLGKLEKETACFDLMKQAGVTAEQTAYIGDDSVDLPAFAACGTSFAVADAPIYVKN
AVDHVLSTHGGKGAFREMSDMILQAQGKSSVFDTAQGFLKSVKSMGQ
>d1zrn__ c.108.1.1 (-) L-2-Haloacid dehalogenase, HAD {Pseudomonas
sp., strain YL}
YIKGIAFDLYGTLFDVHSVVGRCDEAFPGRGREISALWRQKQLEYTWLRSLMNRYVNFQQATEDA
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LRFTCRHLGLDLDARTRSTLCDAYLRLAPFSEVPDSLRELKRRGLKLAILSNGSPQSIDAVVSHA
GLRDGFDHLLSVDPVQVYKPDNRVYELAEQALGLDRSAILFVASNAWDATGARYFGFPTCWINRT
GNVFEEMGQTPDWEVTSLRAVVELF
>d1qq5a_ c.108.1.1 (A:) L-2-Haloacid dehalogenase, HAD {Xanthobacter autotrophicus}
MIKAVVFDAYGTLFDVQSVADATERAYPGRGEYITQVWRQKQLEYSWLRALMGRYADFWSVTREA
LAYTLGTLGLEPDESFLADMAQAYNRLTPYPDAAQCLAELAPLKRAILSNGAPDMLQALVANAGL
TDSFDAVISVDAKRVFKPHPDSYALVEEVLGVTPAEVLFVSSNGFDVGGAKNFGFSVARVARLSQ
EALARELVSGTIAPLTMFKALRMREETYAEAPDFVVPALGDLPRLVRGMA
>d1ek1a1 c.108.1.2 (A:4-225) Epoxide hydrolase, N-terminal domain {Mouse (Mus musculus)}
RVAAFDLDGVLALPSIAGAFRRSEEALALPRDFLLGAYQTEFPEGPTEQLMKGKITFSQWVPLMD
ESYRKSSKACGANLPENFSISQIFSQAMAARSINRPMLQAAIALKKKGFTTCIVTNNWLDDGDKR
DSLAQMMCELSQHFDFLIESCQVGMIKPEPQIYNFLLDTLKAKPNEVVFLDDFGSNLKPARDMGM
VTILVHNTASALRELEKVTGTQFPEAP
>d1feza_ c.108.1.3 (A:) Phosphonoacetaldehyde hydrolase {Bacillus cereus}
KIEAVIFDWAGTTVDYGCFAPLEVFMEIFHKRGVAITAEEARKPMGLLKIDHVRALTEMPRIASE
WNRVFRQLPTEADIQEMYEEFEEILFAILPRYASPINAVKEVIASLRERGIKIGSTTGYTREMMD
IVAKEAALQGYKPDFLVTPDDVPAGRPYPWMCYKNAMELGVYPMNHMIKVGDTVSDMKEGRNAGM
WTVGVILGSSELGLTEEEVENMDSVELREKIEVVRNRFVENGAHFTIETMQELESVMEHIE
>d1j97a_ c.108.1.4 (A:) Phosphoserine phosphatase {Archaeon Methanococcus jannaschii}
EKKKKLILFDFDSTLVNNETIDEIAREAGVEEEVKKITKEAMEGKLNFEQSLRKRVSLLKDLPIE
KVEKAIKRITPTEGAEETIKELKNRGYVVAVVSGGFDIAVNKIKEKLGLDYAFANRLIVKDGKLT
GDVEGEVLKENAKGEILEKIAKIEGINLEDTVAVGDGANDISMFKKAGLKIAFCAKPILKEKADI
CIEKRDLREILKYIK
>d1fs5a_ c.35.1.1 (A:) Glucosamine 6-phosphate deaminase/isomerase {Escherichia coli}
MRLIPLTTAEQVGKWAARHIVNRINAFKPTADRPFVLGLPTGGTPMTTYKALVEMHKAGQVSFKH
VVTFNMDEYVGLPKEHPESYYSFMHRNFFDHVDIPAENINLLNGNAPDIDAECRQYEEKIRSYGK
IHLFMGGVGNDGHIAFNEPASSLASRTRIKTLTHDTRVANSRFFDNDVNQVPKYALTVGVGTLLD
AEEVMILVLGSQKALALQAAVEGCVNHMWTISCLQLHPKAIMVCDEPSTMELKVKTLRYFNELEA
ENIKGL
>d1d9ta_ c.35.1.1 (A:) Glucosamine 6-phosphate deaminase/isomerase {Human (Homo sapiens)}
MKLIIILEHYSQASEWAAKYIRNRIIQFNPGPEKYFTLGLPTGSTPLGCYKKLIEYYKNGDLSFKY
VKTFNMDEYVGLPRDHPESYHSFMWNNFFKHIDIHPENTHILDGNAVDLQAECDAFEEKIKAAGG
IELFVGGIGPDGHIAFNEPGSSLVSRTRVKTLAMDTILANARFFDGELTKVPTMALTVGVGTVMD
AREVMILITGAHKAFALYKAIEEGVNHMWTVSAFQQHPRTVFVCDEDATLELKVKTVKYFKGLML
VHNKLVDPLYSIKEKETEKSQ
>d1ig3a2 c.100.1.1 (A:10-178) Thiamin pyrophosphokinase, catalytic domain {Mouse (Mus musculus)}
HSSGLVPRGSHMEHAFTPLEPLLPTGNLKYCLVVLNQPLDARFRHLWKKALLRACADGGANHLYD
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LTEGERESFLPEFVSGDFDSIRPEVKEYYTKKGCDLISTPDQDHTDFTKCLQVLQRKIEEKELQV
DVIVTLGGLGGRFDQIMASVNTLFQATHITPVPIIIIQK
>d1ig0a2 c.100.1.1 (A:3-223) Thiamin pyrophosphokinase, catalytic domain {Baker's yeast (Saccharomyces cerevisiae)}
EECIENPERIKIGTDLINIRNKMNLKELIHPNEDENSTLLILNQKIDIPRPLFYKIWKLHDLKVC
ADGAANRLYDYLDDDETLRIKYLPNYIIGDLDSLSEKVYKYYRKNKVTIIKQTTQYSTDFTKCVN
LISLHFNSPEFRSLISNKDNLQSNHGIELEKGIHTLYNTMTESLVFSKVTPISLLALGGIGGRFD
QTVHSITQLYTLSENASYFKLCYMTP
>d1f75a_ c.101.1.1 (A:) Undecaprenyl diphosphate synthase {Micrococcus luteus}
NINAAQIPKHIAIIMDGNGRWAKQKKMPRIKGHYEGMQTVRKITRYASDLGVKYLTLYAFSTENW
SRPKDEVNYLMKLPGDFLNTFLPELIEKNVKVETIGFIDDLPDHTKKAVLEAKEKTKHNTGLTLV
FALNYGGRKEIISAVQLIAERYKSGEISLDEISETHFNEYLFTANMPDPELLIRTSGEERLSNFL
IWQCSYSEFVFIDEFWPDFNEESLAQCISIYQNR
>d1jp3a_ c.101.1.1 (A:) Undecaprenyl diphosphate synthase {Escherichia coli}
LPAHGCRHVAIIMDGNGRWAKKQGKIRAFGHKAGAKSVRRAVSFAANNGIEALTLYAFSSENWNR
PAQEVSALMELFVWALDSEVKSLHRHNVRLRIIGDTSRFNSRLQERIRKSEALTAGNTGLTLNIA
ANYGGRWDIVQGVRQLAEKVQQGNLQPDQIDEEMLNQHVCMHELAPVDLVIRTGGEHRISNFLLW
QIAYAELYFTDVLWPDFDEQDFEGALNAFANRE
>d1pvda2 c.36.1.1 (A:2-181) Pyruvate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}
SEITLGKYLFERLKQVNVNTVFGLPGDFNLSLLDKIYEVEGMRWAGNANELNAAYAADGYARIKG
MSCIITTFGVGELSALNGIAGSYAEHVGVLHVVGVPSISHHTLGNGDFTVFHRMSANISETTAMI
TDIATAPAEIDRCIRTTYVTQRPVYLGLPANLVDLNVPAKLL
>d1pvda3 c.36.1.1 (A:361-556) Pyruvate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}
ASTPLKQEWMWNQLGNFLQEGDVVIAETGTSAFGINQTTFPNNTYGISQVLWGSIGFTTGATLGA
AFAAEEIDPKKRVILFIGDGSLQLTVQEISTMIRWGLKPYLFVLNNDGYTIEKLIHGPKAQYNEI
QGWDHLSLLPTFGAKDYETHRVATTGEWDKLTQDKSFNDNSKIRMIEIMLPVFDAPQNLVKQAKL
T
>d1zpda2 c.36.1.1 (A:2-187) Pyruvate decarboxylase {Zymomonas mobilis}
SYTVGTYLAERLVQIGLKHHFAVAGDYNLVLLDNLLLNKNMEQVYCCNELNCGFSAEGYARAKGA
AAAVVTYSVGALSAFDAIGGAYAENLPVILISGAPNNNDHAAGHVLHHALGKTDYHYQLEMAKNI
TAAAEAIYTPEEAPAKIDHVIKTALREKKPVYLEIACNIASMPCAAPGPASALFND
>d1zpda3 c.36.1.1 (A:363-566) Pyruvate decarboxylase {Zymomonas mobilis}
APLVNAEIARQVEALLTPNTTVIAETGDSWFNAQRMKLPNGARVEYEMQWGHIGWSVPAAFGYAV
GAPERRNILMVGDGSFQLTAQEVAQMVRLKLPVIIFLINNYGYTIEVMIHDGPYNNIKNWDYAGL
MEVFNGNGGYDSGAAKGLKAKTGGELAEAIKVALANTDGPTLIECFIGREDCTEELVKWGKRVAA
ANSRKPVNK
>d1poxa2 c.36.1.1 (A:9-182) Pyruvate oxidase {Lactobacillus plantarum}

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TNILAGAAVIKVLEAWGVDHLYGIPGGSINSIMDALSAERDRIHYIQVRHEEVGAMAAAADAKLT
GKIGVCFGSAGPGGTHLMNGLYDAREDHVPVLALIGQFGTTGMNMDTFQEMNENPIYADVADYNV
TAVNAATLPHVIDEAIRRAYAHQGVAVVQIPVDLPWQQISAEDW
>d1poxa3 c.36.1.1 (A:366-593) Pyruvate oxidase {Lactobacillus plantarum}
KQEGPLQAYQVLRAVNKIAEPDAIYSIDVGDINLNANRHLKLTPSNRHITSNLFATMGVGIPGAI
AAKLNYPERQVFNLAGDGGASMTMQDLVTQVQYHLPVINVVFTNCQYGFIKDEQEDTNQNDFIGV
EFNDIDFSKIADGVHMQAFRVNKIEQLPDVFEQAKAIAQHEPVLIDAVITGDRPLPAEKLRLDSA
MSSAADIEAFKQRYEAQDLQPLSTYLKQFGLDD
>d1bfd_2 c.36.1.1 (2-181) Benzoylformate decarboxylase {Pseudomonas putida}
ASVHGTTYELLRRQGIDTVFGNPGSNELPFLKDFPEDFRYILALQEACVVGIADGYAQASRKPAF
INLHSAAGTGNAMGALSNAWNSHSPLIVTAGQQTRAMIGVEALLTNVDAANLPRPLVKWSYEPAS
AAEVPHAMSRAIHMASMAPQGPVYLSVPYDDWDKDADPQSHHLFDRHVSS
>d1bfd_3 c.36.1.1 (342-524) Benzoylformate decarboxylase {Pseudomonas putida}
EPAKVDQDAGRLHPETVFDTLNDMAPENAIYLNESTSTTAQMWQRLNMRNPGSYYFCAAGGLGFA
LPAAIGVQLAEPERQVIAVIGDGSANYSISALWTAAQYNIPTIFVIMNNGTYGALRWFAGVLEAE
NVPGLDVPGIDFRALAKGYGVQALKADNLEQLKGSLQEALSAKGPVLIEVSTV
>d1jsca2 c.36.1.1 (A:83-270) Acetohydroxyacid synthase catalytic subunit {Baker's yeast (Saccharomyces cerevisiae)}
PDMDTSFVGLTGGQIFNEMMSRQNVDTVFGYPGGAILPVYDAIHNSDKFNFVLPKHEQGAGHMAE
GYARASGKPGVVLVTSGPGATNVVTPMADAFADGIPMVVFTGQVPTSAIGTDAFQEADVVGISRS
CTKWNVMVKSVEELPLRINEAFEIATSGRPGPVLVDLPKDVTAAILRNPIPTKTTLPS
>d1jsca3 c.36.1.1 (A:461-648) Acetohydroxyacid synthase catalytic subunit {Baker's yeast (Saccharomyces cerevisiae)}
AYMEETPGSKIKPQTVIKKLSKVANDTGRHVIVTTGVGQHQMWAAQHWTWRNPHTFITSGGLGTM
GYGLPAAIGAQVAKPESLVIDIDGDASFNMTLTELSSAVQAGTPVKILILNNEEQGMVTQWQSLF
YEHRYSHTHQLNPDFIKLAEAMGLKGLRVKKQEELDAKLKEFVSTKGPVLLEVEVDKK
>d1gpua1 c.36.1.2 (A:3-337) Transketolase, TK {Baker's yeast (Saccharomyces cerevisiae)}
QFTDIDKLAVSTIRILAVDTVSKANSGHPGAPLGMAPAAHVLWSQMRMNPTNPDWINRDRFVLSN
GHAVALLYSMLHLTGYDLSIEDLKQFRQLGSRTPGHPEFELPGVEVTTGPLGQGISNAVGMAMAQ
ANLAATYNKPGFTLSDNYTYVFLGDGCLQEGISSEASSLAGHLKLGNLIAIYDDNKITIDGATSI
SFDEDVAKRYEAYGWEVLYVENGNEDLAGIAKAIAQAKLSKDKPTLIKMTTTIGYGSLHAGSHSV
HGAPLKADDVKQLKSKFGFNPDKSFVVPQEVYDHYQKTILKPGVEANNKWNKLFSEYQKKFPELG
AELARRLSGQ
>d1gpua2 c.36.1.2 (A:338-534) Transketolase, TK {Baker's yeast (Saccharomyces cerevisiae)}
LPANWESKLPTYTAKDSAVATRKLSETVLEDVYNQLPELIGGSADLTPSNLTRWKEALDFQPPSS
GSGNYSGRYIRYGIREHAMGAIMNGISAFGANYKPYGGTFLNFVSYAAGAVRLSALSGHPVIWVA
THDSIGVGEDGPTHQPIETLAHFRSLPNIQVWRPADGNEVSAAYKNSLESKHTPSIIALSRQNLP
QL
>d1dtwa1 c.36.1.3 (A:) Branched-chain alpha-keto acid dehydrogenase
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{Human (Homo sapiens)}
PQFPGASAEFIDKLEFIQPNVISGIPIYRVMDRQGQIINPSEDPHLPKEKVLKLYKSMTLLNTMD
RILYESQRQGRISFYMTNYGEEGTHVGSAAALDNTDLVFGQYREAGVLMYRDYPLELFMAQCYGN
ISDLGKGRQMPVHYGCKERHFVTISSPLATQIPQAVGAAYAAKRANANRVVICYFGEGAASEGDA
HAGFNFAATLECPIIFFCRNNGYAISTPTSEQYRGDGIAARGPGYGIMSIRVDGNDVFAVYNATK
EARRRAVAENQPFLIEAMTYRIGHHSTSDDSSAYRSVDEVNYWDKQDHPISRLRHYLLSQGWWDE
EQEKAWRKQSRRKVMEAFEQAERKPKPNPNLLFSDVYQEMPAQLRKQQESLARHLQTYGEHYPLD
HFDK
>d1dtwb1 c.36.1.3 (B:17-204) Branched-chain alpha-keto acid
dehydrogenase {Human (Homo sapiens)}
QTQKMNLFQSVTSALDNSLAKDPTAVIFGEDVAFGGVFRCTVGLRDKYGKDRVFNTPLCEQGIVG
FGIGIAVTGATAIAEIQFADYIFPAFDQIVNEAAKYRYRSGDLFNCGSLTIRSPWGCVGHGALYH
SQSPEAFFAHCPGIKVVIPRSPFQAKGLLLSCIEDKNPCIFFEPKILYRAAAEEVPIE
>d1qs0a1 c.36.1.3 (A:) 2-oxoisovalerate dehydrogenase, E1B
{Pseudomonas putida}
NEYAPLRLHVPEPTGRPGCQTDFSYLRLNDAGQARKPPVDVDAADTADLSYSLVRVLDEQGDAQG
PWAEDIDPQILRQGMRAMLKTRIFDSRMVVAQRQKKMSFYMQSLGEEAIGSGQALALNRTDMCFP
TYRQQSILMARDVSLVEMICQLLSNERDPLKGRQLPIMYSVREAGFFTISGNLATQFVQAVGWAM
ASAIKGDTKIASAWIGDGATAESDFHTALTFAHVYRAPVILNVVNNQWAISTFQAIAGGESTTFA
GRGVGCGIASLRVDGNDFVAVYAASRWAAERARRGLGPSLIEWVTYRAGPHSTSDDPSKYRPADD
WSHFPLGDPIARLKQHLIKIGHWSEEEHQATTAEFEAAVIAAQKEAEQYGTLANGHIPSAASMFE
DVYKEMPDHLRRQRQEL
>d1qs0b1 c.36.1.3 (B:2-205) 2-oxoisovalerate dehydrogenase, E1B
{Pseudomonas putida}
ATTTMTMIQALRSAMDVMLERDDNVVVYGQDVGYFGGVFRCTEGLQTKYGKSRVFDAPISESGIV
GTAVGMGAYGLRPVVEIQFADYFYPASDQIVSEMARLRYRSAGEFIAPLTLRMPCGGGIYGGQTH
SQSPEAMFTQVCGLRTVMPSNPYDAKGLLIASIECDDPVIFLEPKRLYNGPFDGHHDRPVTPWSK
HPHSAVPDG
>d1ik6a1 c.36.1.3 (A:1-191) E1-beta subunit of pyruvate dehydrogenase
{Archaeon Pyrobaculum aerophilum}
VAGVVMMANMAKAINMALHEEMERDERVVVLGEDVGKKGGVFLVTEGLYERFGPERVIDTPLNEG
GILGFAMGMAMAGLKPVAEIQFVDFIWLGADELLNHIAKLRYRSGGNYKAPLVVRTPVGSGTRGG
LYHSNSPEAIFVHTPGLVVVMPSTPYNAKGLLKAAIRGDDPVVFLEPKILYRAPREEVPEG
>d1keka1 c.36.1.4 (A:2-258) Pyruvate-ferredoxin oxidoreductase, PFOR,
domains I and VI {Desulfovibrio africanus}
GKKMMTTDGNTATAHVAYAMSEVAAIYPITPSSTMGEEADDWAAQGRKNIFGQTLTIREMQSEAG
AAGAVHGALAAGALTTTFTASQGLLLMIPNMYKISGELLPGVFHVTARAIAAHALSIFGDHQDIY
AARQTGFAMLASSSVQEAHDMALVAHLAAIESNVPFMHFFDGFRTSHEIQKIEVLDYADMASLVN
QKALAEFRAKSMNPEHPHVRGTAQNPDIYFQGREAANPYYLKVPGIVAEYMQKVASLTGRSY
>d1keka2 c.36.1.4 (A:786-1232) Pyruvate-ferredoxin oxidoreductase,
PFOR, domains I and VI {Desulfovibrio africanus}
VKSEVLPRDSLKGSQFQEPLMEFSGACSGCGETPYVRVITQLFGERMFIANATGCSSIWGASAPS
MPYKTNRLGQGPAWGNSLFEDAAEYGFGMNMSMFARRTHLADLAAKALESDASGDVKEALQGWLA
GKNDPIKSKEYGDKLKKLLAGQKDGLLGQIAAMSDLYTKKSVWIFGGDGWAYDIGYGGLDHVLAS
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GEDVNVFVMDTEVYSNTGGQSSKATPTGAVAKFAAAGKRTGKKDLARMVMTYGYVYVATVSMGYS
KQQFLKVLKEAESFPGPSLVIAYATCINQGLRKGMGKSQDVMNTAVKSGYWPLFRYDPRLAAQGK
NPFQLDSKAPDGSVEEFLMAQNRFAVLDRSFPEDAKRLRAQVAHELDVRFKELEHMAATNIFESF
APAGGKADGSVDFGEGAEFCTRDDTPMMARPDSGEACDQNRAGTSEQQGDLSKRTKK
>d1gky__ c.37.1.1 (-) Guanylate kinase {Baker's yeast (Saccharomyces cerevisiae)}
SRPIVISGPSGTGKSTLLKKLFAEYPDSFGFSVSSTTRTPRAGEVNGKDYNFVSVDEFKSMIKNN
EFIEWAQFSGNYYGSTVASVKQVSKSGKTCILDIDMQGVKSVKAIPELNARFLFIAPPSVEDLKK
RLEGRGTETEESINKRLSAAQAELAYAETGAHDKVIVNDDLDKAYKELKDFIFAEK
>d1kgda_ c.37.1.1 (A:) Guanylate kinase-like domain of Cask {Human (Homo sapiens)}
HMRKTLVLLGAHGVGRRHIKNTLITKHPDRFAYPIPHTTRPPKKDEENGKNYYFVSHDQMMQDIS
NNEYLEYGSHEDAMYGTKLETIRKIHEQGLIAILDVEPQALKVLRTAEFAPFVVFIAAPTITPGL
NEDESLQRLQKESDILQRTYAHYFDLTIINNEIDETIRHLEEAVELVC
>d1kjwa2 c.37.1.1 (A:526-724) Guanylate kinase-like domain of Psd-95 {Rat (Rattus norvegicus)}
VTQMEVHYARPIIILGPTKDRANDDLLSEFPDKFGSCVPHTTRPKREYEIDGRDYHFVSSREKME
KDIQAHKFIEAGQYNSHLYGTSVQSVREVAEQGKHCILDVSANAVRRLQAAHLHPIAIFIRPRSL
ENVLEINKRITEEQARKAFDRATKLEQEFTECFSAIVEGDSFEEIYHKVKRVIEDLSGPYIWVPA
RERL
>d1ukz__ c.37.1.1 (-) Uridylate kinase {Baker's yeast (Saccharomyces cerevisiae)}
PAFSPDQVSVIFVLGGPGAGKGTQCEKLVKDYSFVHLSAGDLLRAEQGRAGSQYGELIKNCIKEG
QIVPQEITLALLRNAISDNVKANKHKFLIDGFPRKMDQAISFERDIVESKFILFFDCPEDIMLER
LLERGKTSGRSDDNIESIKKRFNTFKETSMPVIEYFETKSKVVRVRCDRSVEDVYKDVQDAIRDS
L
>d1deka_ c.37.1.1 (A:) Deoxynucleoside monophosphate kinase {Bacteriophage T4}
MKLIFLSGVKRSGKDTTADFIMSNYSAVKYQLAGPIKDALAYAWGVFAANTDYPCLTRKEFEGID
YDRETNLNLTKLEVITIMEQAFCYLNGKSPIKGVFVFDDEGKESVNFVAFNKITDVINNIEDQWS
VRRLMQALGTDLIVNNFDRMYWVKLFALDYLDKFNSGYDYYIVPDTRQDHEMDAARAMGATVIHV
VRPGQKSNDTHITEAGLPIRDGDLVITNDGSLEELFSKIKNTLKVL
>d1j90a_ c.37.1.1 (A:) Deoxyribonucleoside kinase {Fruit fly (Drosophila melanogaster)}
TQPFTVLIEGNIGSGKTTYLNHFEKYKNDICLLTEPVEKWRNVNGVNLLELMYKDPKKWAMPFQS
YVTLTMLQSHTAPTNKKLKIMERSIFSARYCFVENMRRNGSLEQGMYNTLEEWYKFIEESIHVQA
DLIIYLRTSPEVAYERIRQRARSEESCVPLKYLQELHELHEDWLIHQRRPQSCKVLVLDADLNLE
>d1jaga_ c.37.1.1 (A:) Deoxyguanosine kinase {Human (Homo sapiens)}
GPRRLSIEGNIAVGKSTFVKLLTKTYPEWHVATEPVATWQNIQAAGNQKACTAQSLGNLLDMMYR
EPARWSYTFQTFSFLSRLKVQLEPFPEKLLQARKPVQIFERSVYSDRYIFAKNLFENGSLSDIEW
HIYQDWHSFLLWEFASRITLHGFIYLQASPQVCLKRLYQRAREEEKGIELAYLEQLHGQHEAWLI
HKTTKLHFEALMNIPVLVLDVNDDFSEEVTKQEDLMREVNTFVKNL
>d1ckea_ c.37.1.1 (A:) CMP kinase {Escherichia coli}
AIAPVITIDGPSGAGKGTLCKAMAEALQWHLLDSGAIYRVLALAALHHHVDVASEDALVPLASHL
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DVRFVSTNGNLEVILEGEDVSGEIRTQEVANAASQVAAFPRVREALLRRQRAFRELPGLIADGRD
MGTVVFPDAPVKIFLDASSEERAHRRMLQLQVKGFSVNFERLLAEIKERDDRDRNRAVAPLVPAA
DALVLDSTTLSIEQVIEKALQYARQKLALA
>d1qf9a_ c.37.1.1 (A:) UMP/CMP kinase {Dictyostelium discoideum}
MEKSKPNVVFVLGGPGSGKGTQCANIVRDFGWVHLSAGDLLRQEQQSGSKDGEMIATMIKNGEIV
PSIVTVKLLKNAIDANQGKNFLVDGFPRNEENNNSWEENMKDFVDTKFVLFFDCPEEVMTQRLLK
RGESSGRSDDNIESIKKRFNTFNVQTKLVIDHYNKFDKVKIIPANRDVNEVYNDVENLFKSMGF
>d1e2ka_ c.37.1.1 (A:) Thymidine kinase {Herpes simplex virus type
1, different strains}
MPTLLRVYIDGPHGMGKTTTTQLLVALGSRDDIVYVPEPMTYWRVLGASETIANIYTTQHRLDQG
EISAGDAAVVMTSAQITMGMPYAVTDAVLAPHIGGEAGSSHAPPPALTLIFDRHPIAALLCYPAA
RYLMGSMTPQAVLAFVALIPPTLPGTNIVLGALPEDRHIDRLAKRQRPGERLDLAMLAAIRRVYG
LLANTVRYLQCGGSWREDWGQLSGTAVPPQGAEPQSNAGPRPHIGDTLFTLFRAPELLAPNGDLY
NVFAWALDVLAKRLRSMHVFILDYDQSPAGCRDALLQLTSGMVQTHVTTPGSIPTICDLARTFAR
EMGE
>d3adk__ c.37.1.1 (-) Adenylate kinase {Pig (Sus scrofa)}
MEEKLKKSKIIFVVGGPGSGKGTQCEKIVQKYGYTHLSTGDLLRAEVSSGSARGKMLSEIMEKGQ
LVPLETVLDMLRDAMVAKVDTSKGFLIDGYPREVKQGEEFERKIGQPTLLLYVDAGPETMTKRLL
KRGETSGRVDDNEETIKKRLETYYKATEPVIAFYEKRGIVRKVNAEGSVDDVFSQVCTHLDTLK
>d1nksa_ c.37.1.1 (A:) Adenylate kinase {Archaeon Sulfolobus
acidocaldarius}
MKIGIVTGIPGVGKSTVLAKVKEILDNQGINNKIINYGDFMLATALKLGYAKDRDEMRKLSVEKQ
KKLQIDAAKGIAEEARAGGEGYLFIDTHAVIRTPSGYLPGLPSYVITEINPSVIFLLEADPKIIL
SRQKRDTTRNRNDYSDESVILETINFARYAATASAVLAGSTVKVIVNVEGDPSIAANEIIRSMK
>d2ak3a1 c.37.1.1 (A:0-124,A:162-225) Adenylate kinase {Cow (Bos
taurus), mitochondrial izozyme-3}
GASARLLRAAIMGAPGSGKGTVSSRITKHFELKHLSSGDLLRDNMLRGTEIGVLAKTFIDQGKLI
PDDVMTRLVLHELKNLTQYNWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEVIKQRLTXDRPE
TVVKRLKAYEAQTEPVLEYYRKKGVLETFSGTETNKIWPHVYAFLQTKLPQRSQETSVTP
>d1ak2_1 c.37.1.1 (14-146,177-233) Adenylate kinase {Cow (Bos taurus),
mitochondrial izozyme-2}
PKGVRAVLLGPPGAGKGTQAPKLAKNFCVCHLATGDMLRAMVASGSELGKKLKATMDAGKLVSDE
MVLELIEKNLETPPCKNGFLLDGFPRTVRQAEMLDDLMEKRKEKLDSVIEFSIPDSLLIRRITGR
LIHXSDDNKKALKIRLEAYHTQTTPLVEYYSKRGIHSAIDASQTPDVVFASILAAFSKATS
>d1aky_1 c.37.1.1 (3-130,169-220) Adenylate kinase {Baker's yeast
(Saccharomyces cerevisiae)}
ESIRMVLIGPPGAGKGTQAPNLQERFHAAHLATGDMLRSQIAKGTQLGLEAKKIMDQGGLVSDDI
MVNMIKDELTNNPACKNGFILDGFPRTIPQAEKLDQMLKEQGTPLEKAIELKVDDELLVARITXN
ADALKKRLAAYHAQTEPIVDFYKKTGIWAGVDASQPPATVWADILNKLGKN
>d1e4ya1 c.37.1.1 (A:1-121,A:157-214) Adenylate kinase {Escherichia
coli}
MRIILLGALVAGKGTQAQFIMEKYGIPQISTGDMLRAAVKSGSELGKQAKDIMDAGKLVTDELVI
ALVKERIAQEDCRNGFLLDGFPRTIPQADAMKEAGINVDYVLEFDVPDELIVDRIVXKDDQEETV
RKRLVEYHQMTAPLIGYYSKEAEAGNTKYAKVDGTKPVAEVRADLEKILG
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>d1zaka1 c.37.1.1 (A:3-127,A:159-222) Adenylate kinase {Maize (Zea
mays)}
ADPLKVMISGAPASGKGTQCELIKTKYQLAHISAGDLLRAEIAAGSENGKRAKEFMEKGQLVPDE
IVVNMVKERLRQPDAQENGWLLDGYPRSYSQAMALETLEIRPDTFILLDVPDELLVERVVXFDDT
EEKVKLRLETYYQNIESLLSTYENIIVKVQGDATVDAVFAKIDELLGSILEKKNEMVSST
>d1zin_1 c.37.1.1 (1-125,161-217) Adenylate kinase {Bacillus
stearothermophilus}
MNLVLMGLPGAGKGTQAEKIVAAYGIPHISTGDMFRAAMKEGTPLGLQAKQYMDRGDLVPDEVTI
GIVRERLSKDDCQNGFLLDGFPRTVAQAEALETMLADIGRKLDYVIHIDVRQDVLMERLTXADDN
EATVANRLEVNMKQMKPLVDFYEQKGYLRNINGEQDMEKVFADIRELLGGLAR
>d1tmka_ c.37.1.1 (A:) Thymidylate kinase {Baker's yeast
(Saccharomyces cerevisiae)}
GRGKLILIEGLDRTGKTTQCNILYKKLQPNCKLLKFPERSTRIGGLINEYLTDDSFQLSDQAIHL
LFSANRWEIVDKIKKDLLEGKNIVMDRYVYSGVAYSAAKGTNGMDLDWCLQPDVGLLKPDLTLFL
STQDVDNNAEKSGFGDERYETVKFQEKVKQTFMKLLDKEIRKGDESITIVDVTNKGIQEVEALIW
QIVEPVLSTHIDHDKFSFF
>d1e9ea_ c.37.1.1 (A:) Thymidylate kinase {Human (Homo sapiens)}
ARRGALIVLEGVDRAGKSTQSRKLVEALCAAGHRAELLRFPERSTEIGKLLSSYLQKKSDVEDHS
VHLLFSANRWEQVPLIKEKLSQGVTLVVDRYAFSGVAYTGAKENFSLDWCKQPDVGLPKPDLVLF
LQLQLADAAKRGAFGHERYENGAFQERALRCFHQLMKDTTLNWKMVDASKSIEAVHEDIRVLSED
AIATATEKPLKELWK
>d4tmka_ c.37.1.1 (A:) Thymidylate kinase {Escherichia coli}
RSKYIVIEGLEGAGKTTARNVVVETLEQLGIRDMVFTREPGGTQLAEKLRSLLLDIKSVGDEVIT
DKAEVLMFYAARVQLVETVIKPALANGTWVIGDRHDLSTQAYQGGGRGIDQHMLATLRDAVLGDF
RPDLTLYLDVTPEVGLKRARARGELDRIEQESFDFFNRTRARYLELAAQDKSIHTIDATQPLEAV
MDAIRTTVTHWVKEL
>d1g3ua_ c.37.1.1 (A:) Thymidylate kinase {Mycobacterium
tuberculosis}
MLIAIEGVDGAGKRTLVEKLSGAFRAAGRSVATLAFPRYGQSVAADIAAEALHGEHGDLASSVYA
MATLFALDRAGAVHTIQGLCRGYDVVILDRYVASNAAYSAARLHENAAGKAAAWVQRIEFARLGL
PKPDWQVLLAVSAELAGERSRGRAQRDPGRARDNYERDAELQQRTGAVYAELAAQGWGGRWLVVG
ADVDPGRLAATLA
>d1e6ca_ c.37.1.2 (A:) Shikimate kinase {Erwinia chrysanthemi}
MTEPIFMVGARGCGMTTVGRELARALGYEFVDTDIFMQHTSGMTVADVVAAEGWPGFRRRESEAL
QAVATPNRVVATGGGMVLLEQNRQFMRAHGTVVYLFAPAEELALRLQASLQAHQRPTLTGRPIAE
EMEAVLREREALYQDVAHYVVDATQPPAAIVCELMQTMRL
>d1qhxa_ c.37.1.3 (A:) Chloramphenicol phosphotransferase
{Streptomyces venezuelae}
MTTRMIILNGGSSAGKSGIVRCLQSVLPEPWLAFGVDSLIEAMPLKMQSAEGGIEFDADGGVSIG
PEFRALEGAWAEGVVAMARAGARIIIDDVFLGGAAAQERWRSFVGDLDVLWVGVRCDGAVAEGRE
TARGDRVAGMAAKQAYVVHEGVEYDVEVDTTHKESIECAWAIAAHVVP
>d1d6ja_ c.37.1.4 (A:) Adenosine-5'phosphosulfate kinase (APS kinase)
{Penicillium chrysogenum}
HASALTRSERTELRNQRGLTIWLTGLSASGKSTLAVELEHQLVRDRRVHAYRLDGDNIRFGLNKD
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LGFSEADRNENIRRIAEVAKLFADSNSIAITSFISPYRKDRDTARQLHEVATPGEETGLPFVEVY
VDVPVEVAEQRDPKGLYKKAREGVIKEFTGISAPYEAPANPEVHVKNYELPVQDAVKQIIDYLDT
KGYLPAKK
>d1g8fa3 c.37.1.15 (A:390-511) ATP sulfurylase C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
PRPKQGFSIVLGNSLTVSREQLSIALLSTFLQFGGGRYYKIFEHNNKTELLSLIQDFIGSGSGLI
IPDQWEDDKDSVVGKQNVYLLDTSSSADIQLESADEPISHIVQKVVLFLEDNGFFVF
>d1i2da3 c.37.1.15 (A:391-573) ATP sulfurylase C-terminal domain {Fungus (Penicillium chrysogenum)}
PRATQGFTIFLTGYMNSGKDAIARALQVTLNQQGGRSVSLLLGDTVRHELSSELGFTREDRHTNI
QRIAFVATELTRAGAAVIAAPIAPYEESRKFARDAVSQAGSFFLVHVATPLEHCEQSDKRGIYAA
ARRGEIKGFTGVDDPYETPEKADLVVDFSKQSVRSIVHEIILVLESQGFLERQ
>d1aqua_ c.37.1.5 (A:) Estrogen sulfotransferase {Mouse (Mus musculus)}
EYYEVFGEFRGVLMDKRFTKYWEDVEMFLARPDDLVIATYPKSGTTWISEVVYMIYKEGDVEKCK
EDAIFNRIPYLECRNEDLINGIKQLKEKESPRIVKTHLPPKLLPASFWEKNCKMIYLCRNAKDVA
VSYYYFLLMITSYPNPKSFSEFVEKFMQGQVPYGSWYDHVKAWWEKSKNSRVLFMFYEDMKEDIR
REVVKLIEFLERKPSAELVDRIIQHTSFQEMKNNPSTNYTMMPEEMMNQKVSPFMRKGIIGDWKN
HFPEALRERFDEHYKQQMKDCTVKFRME
>d1efha_ c.37.1.5 (A:) Hydroxysteroid sulfotransferase {Human (Homo sapiens)}
DFLWFEGIAFPTMGFRSETLRKVRDEFVIRDEDVIILTYPKSGTNWLAEILCLMHSKGDAKWIQS
VPIWERSPWVESEIGYTALSETESPRLFSSHLPIQLFPKSFFSSKAKVIYLMRNPRDVLVSGYFF
WKNMKFIKKPKSWEEYFEWFCQGTVLYGSWFDHIHGWMPMREEKNFLLLSYEELKQDTGRTIEKI
CQFLGKTLEPEELNLILKNSSFQSMKENKMSNYSLLSVDYVVDKAQLLRKGVSGDWKNHFTVAQA
EDFDKLFQEKMADLPRKLAAALE
>d1cjma_ c.37.1.5 (A:) Aryl sulfotransferase sult1a3 {Human (Homo sapiens)}
SRPPLEYVKGVPLIKYFAEALGPLQSFQARPDDLLINTYPKSGTTWVSQILDMIYQGGDLEKCNR
APIYVRVPFLEVNDPGEPSGLETLKDTPPPRLIKSHLPLALLPQTLLDQKVKVVYVARNPKDVAV
SYYHFHRMEKAHPEPGTWDSFLEKFMAGEVSYGSWYQHVQEWWELSRTHPVLYLFYEDMKENPKR
EIQKILEFVGRSLPEETMDFMVQHTSFKEMKKNPMTNYTTVPQELMDHSISPFMRKGMAGDWKTT
FTVAQNERFDADYAEKMAGCSLSFRS
>d1nsta_ c.37.1.5 (A:) Heparan sulfate N-deacetylase/N-sulfotransferase domain {Human (Homo sapiens)}
DPLWQDPCEDKRHKDIWSKEKTCDRFPKLLIIGPQKTGTTALYLFLGMHPDLSSNYPSSETFEEI
QFFNGHNYHKGIDWYMEFFPIPSNTTSDFYFEKSANYFDSEVAPRRAAALLPKAKVLTILINPAD
RAYSWYQHQRAHDDPVALKYTFHEVITAGSDASSKLRALQNRCLVPGWYATHIERWLSAYHANQI
LVLDGKLLRTEPAKVMDMVQKFLGVTNTIDYHKTLAFDPKKGFWCQLLEGGKTKCLGKSKGRKYP
EMDLDSRAFLKDYYRDHNIELSKLLYKMGQTLPTWLREDLQ
>d1fmja_ c.37.1.5 (A:) Retinol dehydratase {Fall armyworm (Spodoptera frugiperda)}
PFPYEFRELNPEEDKLVKANLGAFPTTYVKLGPKGYMVYRPYLKDAANIYNMPLRPTDVFVASYQ
RSGTTMTQELVWLIENDLNFEAAKTYMSLRYIYLDGFMIYDPEKQEEYNDILPNPENLDMERYLG
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LLEYSSRPGSSLLAAVPPTEKRFVKTHLPLSLMPPNMLDTVKMVYLARDPRDVAVSSFHHARLLY
LLNKQSNFKDFWEMFHRGLYTLTPYFEHVKEAWAKRHDPNMLFLFYEDYLKDLPGCIARIADFLG
KKLSEEQIQRLCEHLNFEKFKNNGAVNMEDYREIGILADGEHFIRKGKAGCWRDYFDEEMTKQAE
KWIKDNLKDTDLRYPNM
>d1a7j__ c.37.1.6 (-) Phosphoribulokinase {Rhodobacter sphaeroides}
SKKHPIISVTGSSGAGTSTVKHTFDQIFRREGVKAVSIEGDAFHRFNRADMKAELDRRYAAGDAT
FSHFSYEANELKELERVFREYGETGQGRTRTYVHDDAEAARTGVAPGNFTDWRDFDSDSHLLFYE
GLHGAVVNSEVNIAGLADLKIGVVPVINLEWIQKIHRDRATRGYTTEAVTDVILRRMHAYVHCIV
PQFSQTDINFQRVPVVDTSNPFIARWIPTADESVVVIRFRNPRGIDFPYLTSMIHGSWMSRANSI
VVPGNKLDLAMQLILTPLIDRVVRESKV
>d1esma_ c.37.1.6 (A:) Pantothenate kinase PanK {Escherichia coli}
QTLMTPYLQFDRNQWAALRDSVPMTLSEDEIARLKGINEDLSLEEVAEIYLPLSRLLNFYISSNL
RRQAVLEQFLGTNGQRIPYIISIAGSVAVGKSTTARVLQALLSRWPEHRRVELITTDGFLHPNQV
LKERGLMKKKGFPESYDMHRLVKFVSDLKSGVPNVTAPVYSHLIYDVIPDGDKTVVQPDILILEG
LNVLQSGMDYPHDPHHVFVSDFVDFSIYVDAPEDLLQTWYINRFLKFREGAFTDPDSYFHNYAKL
TKEEAIKTAMTLWKEINWLNLKQNILPTRERASLILTKSANHAVEEVRLRK
>d1bif_1 c.37.1.7 (37-249)
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, kinase domain
{Rat (Rattus norvegicus)}
CPTLIVMVGLPARGKTYISKKLTRYLNFIGVPTREFNVGQYRRDMVKTYKSFEFFLPDNEEGLKI
RKQCALAALNDVRKFLSEEGGHVAVFDATNTTRERRAMIFNFGEQNGYKTFFVESICVDPEVIAA
NIVQVKLGSPDYVNRDSDEATEDFMRRIECYENSYESLDEEQDRDLSYIKIMDVGQSYVVNRVAD
HIQSRIVYYLMNIHVTPR
>d1ctqa_ c.37.1.8 (A:) cH-p21 Ras protein {Human (Homo sapiens)}
MTEYKLVVVGAGGVGKSALTIQLIQNHFVDEYDPTIEDSYRKQVVIDGETCLLDILDTAGQEEYS
AMRDQYMRTGEGFLCVFAINNTKSFEDIHQYREQIKRVKDSDDVPMVLVGNKCDLAARTVESRQA
QDLARSYGIPYIETSAKTRQGVEDAFYTLVREIRQH
>d1ds6a_ c.37.1.8 (A:) Rac {Human (Homo sapiens)}
MQAIKCVVVGDGAVGKTCLLISYTTNAFPGEYIPTVFDNYSANVMVDSKPVNLGLWDTAGQEDYD
RLRPLSYPQTDVFLICFSLVSPASYENVRAKWFPEVRHHCPSTPIILVGTKLDLRDDKDTIEKLK
EKKLAPITYPQGLALAKEIDSVKYLECSALTQRGLKTVFDEAIRAVLCPQP
>d1mh1__ c.37.1.8 (-) Rac {Human (Homo sapiens)}
GSPQAIKCVVVGDGAVGKTCLLISYTTNAFPGEYIPTVFDNYSANVMVDGKPVNLGLWDTAGQED
YDRLRPLSYPQTDVSLICFSLVSPASFENVRAKWYPEVRHHCPNTPIILVGTKLDLRDDKDTIEK
LKEKKLTPITYPQGLAMAKEIGAVKYLECSALTQRGLKTVFDEAIRAVLCPPP
>d1c1ya_ c.37.1.8 (A:) Rap1A {Human (Homo sapiens)}
MREYKLVVLGSGGVGKSALTVQFVQGIFVEKYDPTIEDSYRKQVEVDCQQCMLEILDTAGTEQFT
AMRDLYMKNGQGFALVYSITAQSTFNDLQDLREQILRVKDTEDVPMILVGNKCDLEDERVVGKEQ
GQNLARQWCNCAFLESSAKSKINVNEIFYDLVRQINR
>d1kao__ c.37.1.8 (-) Rap2a {Human (Homo sapiens)}
MREYKVVVLGSGGVGKSALTVQFVTGTFIEKYDPTIEDFYRKEIEVDSSPSVLEILDTAGTEQFA
SMRDLYIKNGQGFILVYSLVNQQSFQDIKPMRDQIIRVKRYEKVPVILVGNKVDLESEREVSSSE
GRALAEEWGCPFMETSAKSKTMVDELFAEIVRQMNYA
>d3raba_ c.37.1.8 (A:) Rab3a {Rat (Rattus norvegicus)}
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NFDYMFKILIIGNSSVGKTSFLFRYADDSFTPAFVSTVGIDFKVKTIYRNDKRIKLQIWDTAGQE
RYRTITTAYYRGAMGFILMYDITNEESFNAVQDWSTQIKTYSWDNAQVLLVGNKCDMEDERVVSS
ERGRQLADHLGFEFFEASAKDNINVKQTFERLVDVICEK
>d1huqa_ c.37.1.8 (A:) Rab5c {Mouse (Mus musculus)}
ICQFKLVLLGESAVGKSSLVLRFVKGQFHEYQESTIGAAFLTQTVCLDDTTVKFEIWDTAGQERY
HSLAPMYYRGAQAAIVVYDITNTDTFARAKNWVKELQRQASPNIVIALAGNKADLASKRAVEFQE
AQAYADDNSLLFMETSAKTAMNVNEIFMAIAKKL
>d1d5ca_ c.37.1.8 (A:) Rab6 {Malaria parasite (Plasmodium falciparum)}
KYKLVFLGEQAVGKTSIITRFMYDTFDNNYQSTIGIDFLSKTLYLDEGPVRLQLWDTAGQERFRS
LIPSYIRDSAAAIVVYDITNRQSFENTTKWIQDILNERGKDVIIALVGNKTDLGDLRKVTYEEGM
QKAQEYNTMFHETSAKAGHNIKVLFKKTASKL
>d1g16a_ c.37.1.8 (A:) Rab-related protein Sec4 {Baker's yeast (Saccharomyces cerevisiae)}
SIMKILLIGDSGVGKSCLLVRFVEDKFNPSFITTIGIDFKIKTVDINGKKVKLQIWDTAGQERFR
TITTAYYRGAMGIILVYDITDERTFTNIKQWFKTVNEHANDEAQLLLVGNKSDMETRVVTADQGE
ALAKELGIPFIESSAKNDDNVNEIFFTLAKLIQEKI
>d1byua_ c.37.1.8 (A:) Ran {Dog (Canis familiaris)}
EPQVQFKLVLVGDGGTGKTTFVKRHLTGEFEKKYVPTLGVEVHPLVFHTNRGPIKFNVWDTAGQE
KFGGLRDGYYIQAQCAIIMFDVTSRVTYKNVPNWHRDLVRVCENIPIVLCGNKVDIKDRKVKAKS
IVFHRKKNLQYYDISAKSNYNFEKPFLWLARKLIGDPNLEFVAMPALAPPEVVMDPALAAQYEHD
LEVAQTT
>d1i2ma_ c.37.1.8 (A:) Ran {Human (Homo sapiens)}
QVQFKLVLVGDGGTGKTTFVKRHLTGEFEKKYVATLGVEVHPLVFHTNRGPIKFNVWDTAGQEKF
GGLRDGYYIQAQCAIIMFDVTSRVTYKNVPNWHRDLVRVCENIPIVLCGNKVDIKDRKVKAKSIV
FHRKKNLQYYDISAKSNYNFEKPFLWLARKLIGDPNLEFV
>d1tx4b_ c.37.1.8 (B:) RhoA {Human (Homo sapiens)}
AIRKKLVIVGDGACGKTCLLIVNSKDQFPEVYVPTVFENYVADIEVDGAQVELALWDTAGQEDYD
RLRPLSYPDTDVILMCFSIDSPDSLENIPEKWTPEVKHFCPNVPIILVGNKKDLRNDEHTRRELA
KMKQEPVKPEEGRDMANRIGAFGYMECSAKTKDGVREVFEMATRAAL
>d1hura_ c.37.1.8 (A:) ADP-ribosylation factor {Human (Homo sapiens), ARF1}
GNIFANLFKGLFGKKEMRILMVGLDAAGKTTILYKLKLGEIVTTIPTIGFNVETVEYKNISFTVW
DVGGQDKIRPLWRHYFQNTQGLIFVVDSNDRERVNEAREELMRMLAEDELRDAVLLVFANKQDLP
NAMNAAEITDKLGLHSLRHRNWYIQATCATSGDGLYEGLDWLSNQLRNQK
>d1e0sa_ c.37.1.8 (A:) ADP-ribosylation factor {Human (Homo sapiens), ARF6}
GKVLSKIFGNKEMRILMLGLDAAGKTTILYKLKLGQSVTTIPTVGFNVETVTYKNVKFNVWDVGG
QDKIRPLWRHYYTGTQGLIFVVDCADRDRIDEARQELHRIINDREMRDAIILIFANKQDLPDAMK
PHEIQEKLGLTRIRDRNWYVQPSCATSGDGLYEGLTWLTSNYK
>d1fzqa_ c.37.1.8 (A:) ADP-ribosylation factor {Mouse (Mus musculus), ARL3}
GLLSILRKLKSAPDQEVRILLLGLDNAGKTTLLKQLASEDISHITPTQGFNIKSVQSQGFKLNVW
DIGGQRKIRPYWRSYFENTDILIYVIDSADRKRFEETGQELTELLEEEKLSCVPVLIFANKQDLL
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TAAPASEIAEGLNLHTIRDRVWQIQSCSALTGEGVQDGMNWVCKNV
>d1f6ba_ c.37.1.8 (A:) SAR1 {Chinese hamster (Cricetulus griseus)}
SSVLQFLGLYKKTGKLVFLGLDNAGKTTLLHMLKDDRLGQHVPTLHPTSEELTIAGMTFTTFDLG
GHIQARRVWKNYLPAINGIVFLVDCADHERLLESKEELDSLMTDETIANVPILILGNKIDRPEAI
SEERLREMFGLYGQTTGKGSVSLKELNARPLEVFMCSVLKRQGYGEGFRWMAQYID
>d2ngra_ c.37.1.8 (A:) CDC42 {Human (Homo sapiens)}
MQTIKCVVVGDGAVGKTCLLISYTTNKFPSEYVPTVFDNYAVTVMIGGEPYTLGLFDTAGQEDYD
RLRPLSYPQTDVFLVCFSVVSPSSFENVKEKWVPEITHHCPKTPFLLVGTQIDLRDDPSTIEKLA
KNKQKPITPETAEKLARDLKAVKYVECSALTQKGLKNVFDEAILAALEPPEPKKSRRCVLL
>d1ek0a_ c.37.1.8 (A:) Ypt51 {Baker's yeast (Saccharomyces
cerevisiae)}
VTSIKLVLLGEAAVGKSSIVLRFVSNDFAENKEPTIGAAFLTQRVTINEHTVKFEIWDTAGQERF
ASLAPMYYRNAQAALVVYDVTKPQSFIKARHWVKELHEQASKDIIIALVGNKIDMLQEGGERKVA
REEGEKLAEEKGLLFFETSAKTGENVNDVFLGIGEKIPLK
>d1h65a_ c.37.1.8 (A:) Chloroplast protein translocon GTPase Toc34
{Garden pea (Pisum sativum)}
VREWSGINTFAPATQTKLLELLGNLKQEDVNSLTILVMGKGGVGKSSTVNSIIGERVVSISPFQS
EGPRPVMVSRSRAGFTLNIIDTPGLIEGGYINDMALNIIKSFLLDKTIDVLLYVDRLDAYRVDNL
DKLVAKAITDSFGKGIWNKAIVALTHAQFSPPDGLPYDEFFSKRSEALLQVVRSGASLKKDAQAS
DIPVVLIENSGRCNKNDSDEKVLPNGIAWIPHLVQTITEVALNKSESIFVDKNLIDKLAAAD
>d1azsc2 c.37.1.8 (C:36-66,C:202-393) Transducin (alpha subunit) {Cow
(Bos taurus)}
VYRATHRLLLLGAGESGKSTIVKQMRILHVNXVLTSGIFETKFQVDKVNFHMFDVGGQRDERRKW
IQCFNDVTAIIFVVASSSYNMVIREDNQTNRLQEALNLFKSIWNNRWLRTISVILFLNKQDLLAE
KVLAGKSKIEDYFPEFARYTTPEDATPEPGEDPRVTRAKYFIRDEFLRISTASGDGRHYCYPHFT
CAVDTENIRRVFNDCRDIIQRMHLRQYEL
>d1tada2 c.37.1.8 (A:27-56,A:178-342) Transducin (alpha subunit) {Cow
(Bos taurus)}
ARTVKLLLLGAGESGKSTIVKQMKIIHQDGXTGIIETQFSFKDLNFRMFDVGGQRSERKKWIHCF
EGVTCIIFIAALSAYDMVLVEDDEVNRMHESLHLFNSICNHRYFATTSIVLFLNKKDVFSEKIKK
AHLSICFPDYNGPNTYEDAGNYIKVQFLELNMRRDVKEIYSHMTCATDTQNVKFVFDAVTDIIIK
E
>d1bof_2 c.37.1.8 (10-60,182-354) Transducin (alpha subunit) {Rat
(Rattus norvegicus)}
KAAVERSKMIDRNLREDGEKAAREVKLLLLGAGESGKSTIVKQMKIIHEAGXTGIVETHFTFKDL
HFKMFDVGGQRSERKKWIHCFEGVTAIIFCVALSDYDLVLAEDEEMNRMHESMKLFDSICNNKWF
TDTSIILFLNKKDLFEEKIKKSPLTICYPEYAGSNTYEEAAAYIQCQFEDLNKRKDTKEIYTHFT
CATDTKNVQFVFDAVTDVIIKNNLKDCGLF
>d1cipa2 c.37.1.8 (A:32-60,A:182-347) Transducin (alpha subunit) {Rat
(Rattus norvegicus)}
REVKLLLLGAGESGKSTIVKQMKIIHEAGXTGIVETHFTFKDLHFKMFDVGGQRSERKKWIHCFE
GVTAIIFCVALSDYDLVLAEDEEMNRMHESMKLFDSICNNKWFTDTSIILFLNKKDLFEEKIKKS
PLTICYPEYAGSNTYEEAAAYIQCQFEDLNKRKDTKEIYTHFTCATDTKNVQFVFDAVTDVIIKN
N
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>d1fqja2 c.37.1.8 (A:28-60,A:182-344) Transducin (alpha subunit) {Rat
(Rattus norvegicus)}
RTVKLLLLGAGESGKSTIVKQMKIIHQDGYSLEXETQFSFKDLNFRMFDVGGQRSERKKWIHCFE
GVTAIIFCVALSDYDLVLAEDEEMNRMHESMKLFDSICNNKWFTDTSIILFLNKKDLFEEKIKKS
PLTICYPEYAGSNTYEEAGNYIKVQFLELNMRRDVKEIYSHMTCATDTQNVKFVFDAVTDIIIKE
NL
>d1gota2 c.37.1.8 (A:6-60,A:182-343) Transducin (alpha subunit) {Rat
(Rattus norvegicus)}
SAEEKHSRELEKKLKEDAEKDARTVKLLLLGAGESGKSTIVKQMKIIHQDGYSLEXETQFSFKDL
NFRMFDVGGQRSERKKWIHCFEGVTAIIFCVALSDYDLVLAEDEEMNRMHESMKLFDSICNNKWF
TDTSIILFLNKKDLFEEKIKKSPLTICYPEYAGSNTYEEAGNYIKVQFLELNMRRDVKEIYSHMT
CATDTQNVKFVFDAVTDIIIKEN
>d1efca3 c.37.1.8 (A:8-204) Elongation factor Tu (EF-Tu), N-terminal
(G) domain {Escherichia coli}
TKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGAARAFDQIDNAPEEKARGITINTSHVEYDTP
TRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHILLGRQVGVPYIIVFLNKC
DMVDDEELLELVEMEVRELLSQYDFPGDDTPIVRGSALKALEGDAEWEAKILELAGFLDSYIPEP
ER
>d1efm_1 c.37.1.8 (12-190) Elongation factor Tu (EF-Tu), N-terminal
(G) domain {Escherichia coli}
VNVGTIGHVDHGKTTLTAAITTVLAKTYGGAARXXXXXXXXXXXXXXGITINTSHVEYDTPTRHY
AHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHILLGRQVGVPYIIVFLNKCDMVD
DEELLELVEMEVRELLSQYDFPGDDTPIVRGSALKALEGDAEWEAKILE
>d1etu_1 c.37.1.8 (5-200) Elongation factor Tu (EF-Tu), N-terminal
(G) domain {Escherichia coli}
FERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGAAXXXXXXXXXXXXXXXXGITINTSHVEY
DTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHILLGRQVGVPYIIVFL
NKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPIVRGSALKALEGDAEWEAKILELAGFLDSYI
P
>d1exma3 c.37.1.8 (A:3-212) Elongation factor Tu (EF-Tu), N-terminal
(G) domain {Thermus thermophilus}
GEFIRTKPHVNVGTIGHVDHGKTTLTAALTFVTAAENPNVEVKDYGDIDKAPEERARGITINTAH
VEYETAKRHYSHVDCPGHADYIKNMITGAAQMDGAILVVSAADGPMPQTREHILLARQVGVPYIV
VFMNKVDMVDDPELLDLVEMEVRDLLNQYEFPGDEVPVIRGSALLALEQMHRNPKTRRGENEWVD
KIWELLDAIDEYIPT
>d1d2ea3 c.37.1.8 (A:55-250) Elongation factor Tu (EF-Tu), N-terminal
(G) domain {Cow (Bos taurus), mitochondrial}
KPHVNVGTIGHVDHGKTTLTAAITKILAEGGGAKFKKYEEIDNAPEERARGITINAAHVEYSTAA
RHYAHTDCPGHADYVKNMITGTAPLDGCILVVAANDGPMPQTREHLLLARQIGVEHVVVYVNKAD
AVQDSEMVELVELEIRELLTEFGYKGEETPIIVGSALCALEQRDPELGLKSVQKLLDAVDTYIPV
P
>d1f60a3 c.37.1.8 (A:2-240) Elongation factor eEF-1alpha, N-terminal
(G) domain {Baker's yeast (Saccharomyces cerevisiae)}
GKEKSHINVVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAAELGKGSFKYAWVLDKLKAE
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RERGITIDIALWKFETPKYQVTVIDAPGHRDFIKNMITGTSQADCAILIIAGGVGEFEAGISKDG
QTREHALLAFTLGVRQLIVAVNKMDSVKWDESRFQEIVKETSNFIKKVGYNPKTVPFVPISGWNG
DNMIEATTNAPWYKGWEKETKAGVVKGKTLLEAIDAIEQPSRPT
>d1jnya3 c.37.1.8 (A:4-227) Elongation factor eEF-1alpha, N-terminal
(G) domain {Archaeon Sulfolobus solfataricus}
KPHLNLIVIGHVDHGKSTLVGRLLMDRGFIDEKTVKEAEEAAKKLGKESEKFAFLLDRLKEERER
GVTINLTFMRFETKKYFFTIIDAPGHRDFVKNMITGASQADAAILVVSAKKGEYEAGMSVEGQTR
EHIILAKTMGLDQLIVAVNKMDLTEPPYDEKRYKEIVDQVSKFMRSYGFNTNKVRFVPVVAPSGD
NITHKSENMKWYNGPTLEEYLDQLELPPK
>d1dar_2 c.37.1.8 (1-282) Elongation factor G (EF-G), N-terminal (G)
domain {Thermus thermophilus}
MAVKVEYDLKRLRNIGIAAHIDAGKTTTTERILYYTGRIHKIGEVHEGAATMDFMEQERERGITI
TAAVTTCFWKDHRINIIDTPGHVDFTIEVERSMRVLDGAIVVFDSSQGVEPQSETVWRQAEKYKV
PRIAFANKMDKTGADLWLVIRTMQERLGARPVVMQLPIGREDTFSGIIDVLRMKAYTYGNDLGTD
IREIPIPEEYLDQAREYHEKLVEVAADFDENIMLKYLEGEEPTEEELVAAIRKGTIDLKITPVFL
GSALKNKGVQLLLDAVVDYLPS
>d1g7sa4 c.37.1.8 (A:1-227) Initiation factor IF2/eIF5b, N-terminal
(G) domain {Archaeon Methanobacterium thermoautotrophicum}
MKIRSPIVSVLGHVDHGKTTLLDHIRGSAVASREAGGITQHIGATEIPMDVIEGICGDFLKKFSI
RETLPGLFFIDTPGHEAFTTLRKRGGALADLAILIVDINEGFKPQTQEALNILRMYRTPFVVAAN
KIDRIHGWRVHEGRPFMETFSKQDIQVQQKLDTKVYELVGKLHEEGFESERFDRVTDFASQVSII
PISAITGEGIPELLTMLMGLAQQYLREQLKIE
>d1egaa1 c.37.1.8 (A:4-182) GTPase Era, N-terminal domain
{Escherichia coli}
DKSYCGFIAIVGRPNVGKSTLLNKLLGQKISITSRKAQTTRHRIVGIHTEGAYQAIYVDTPGLHM
EEKRAINRLMNKAASSSIGDVELVIFVVEGTRWTPDDEMVLNKLREGKAPVILAVNKVDNVQEKA
DLLPHLQFLASQMNFLDIVPISAETGLNVDTIAAIVRKHLPEATHHFPE
>d1f5na2 c.37.1.8 (A:7-283) Interferon-induced guanylate-binding
protein 1 (GBP1), N-terminal domain {Human (Homo sapiens)}
MTGPMCLIENTNGRLMANPEALKILSAITQPMVVVAIVGLYRTGKSYLMNKLAGKKKGFSLGSTV
QSHTKGIWMWCVPHPKKPGHILVLLDTEGLGDVEKGDNQNDSWIFALAVLLSSTFVYNSIGTINQ
QAMDQLYYVTELTHRIRSKSSPDENENEVEDSADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEY
LTYSLKLKKGTSQKDETFNLPRLCIRKFFPKKKCFVFDRPVHRRKLAQLEKLQDEELDPEFVQQV
ADFCSYIFSNSKTKTLS
>d1jwyb_ c.37.1.8 (B:) Dynamin G domain {Slime mold (Dictyostelium
discoideum)}
DQLIPVINKLQDVFNTLGSDPLDLPQIVVVGSQSSGKSSVLENIVGRDFLPRGSGIVTRRPLILQ
LTHLPIADDGSQTQEWGEFLHKPNDMFYDFSEIREEIIRDTDRMTGKNKGISAQPINLKIYSPHV
VNLTLVDLPGITKVPVGDQPTDIEQQIRRMVMAYIKKQNAIIVAVTPANTDLANSDALQLAKEVD
PEGKRTIGVITKLDLMDKGTDAMEVLTGRVIPLTLGFIGVINRSQEDIIAKKSIRESLKSEILYF
KNHPIYKSIANRSGTAYLSKTLNKLLMFHIRDTLPDLKVKVSKMLS
>d1br2a2 c.37.1.9 (A:80-789) Myosin S1, motor domain {Chicken (Gallus
gallus), pectoral muscle}
PPKFSKVEDMAELTCLNEASVLHNLRERYFSGLIYTYSGLFCVVINPYKQLPIYSEKIIDMYKGK
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KRHEMPPHIYAIADTAYRSMLQDREDQSILCTGESGAGKTENTKKVIQYLAVVASSHKGKKDTSI
TQGPSFSYGELEKQLLQANPILEAFGNAKTVKNDNSSRFGKFIRINFDVTGYIVGANIETYLLEK
SRAIRQAKDERTFHIFYYLIAGASEQMRNDLLLEGFNNYTFLSNGHVPIPAQQDDEMFQETLEAM
TIMGFTEEEQTSILRVVSSVLQLGNIVFKKERNTDQASMPDNTAAQKVCHLMGINVTDFTRSILT
PRIKVGRDVVQKAQTKEQADFAIEALAKAKFERLFRWILTRVNKALDKTKRQGASFLGILDIAGF
EIFEINSFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGLDLQPCIELIERPTNP
PGVLALLDEECWFPKATDTSFVEKLIQEQGNHAKFQKSKQLKDKTEFCILHYAGKVTYNASAWLT
KNMDPLNDNVTSLLNQSSDKFVADLWKDVDRIVGLDQMAKMTESSLPSASKTKKGMFRTVGQLYK
EQLTKLMTTLRNTNPNFVRCIIPNHEKRAGKLDAHLVLEQLRCNGVLEGIRICRQGFPNRIVFQE
FRQRYEILAANAIPKGFMDGKQACILMIKALELDPNLYRIGQSKIFFRTGVLAHLEEERD
>d2mysa2 c.37.1.9 (A:4-33,A:80-843) Myosin S1, motor domain {Chicken
(Gallus gallus), pectoral muscle}
DAEMAAFGEAAPYLRKSEKERIEAQNKPFDXMNPPKYDKIEDMAMMTHLHEPAVLYNLKERYAAW
MIYTYSGLFCVTVNPYKWLPVYNPKVVLAYRGKKRQEAPPHIFSISDNAYQFMLTDRENQSILIT
GESGAGKTVNTKRVIQYFATIAASGEKKKEEQSGKMQGTLEDQIISANPLLEAFGNAKTVRNDNS
SRFGKFIRIHFGATGKLASADIETYLLEKSRVTFQLPAERSYHIFYQIMSNKKPELIDMLLITTN
PYDYHYVSEGEITVPSIDDQEELMATDSAIDILGFSADEKTAIYKLTGAVMHYGNLKFKQKQREE
QAEPDGTEVADKAAYLMGLNSAELLKALCYPRVGVGNEAVTKGETVSEVHNSVGALAKAVYEKMF
LWMVIRINQQLDTKQPRQYFIGVLDIAGFEIFDFNSFEQLCINFTNEKLQQFFNHHMFVLEQEEY
KKEGIEWEFIDFGMDLAACIELIEKPMGIFSILEEECMFPKATDTSFKNKLYDEHLGKSNNFQKP
KPAKGKAEAHFSLVHYAGTVDYNISGWLEKNKDPLNETVIGLYQKSSVKTLALLFATYGGEAEGG
GGKKGGKKKGSSFQTVSALFRENLNKLMANLRSTHPHFVRCIIPNETKTPGAMEHELVLHQLRCN
GVLEGIRICRKGFPSRVLYADFKQRYRVLNASAIPEGQFMDSKKASEKLLGGGDVDHTQYAFGHT
KVFFKAGLLGLLEEMRDDKLAEIITATQARCRGFLMRVEYRAMVERRESIFCIQYNVRSFMNVKH
WPWMKLFFKIKPLLK
>d1b7ta4 c.37.1.9 (A:5-28,A:77-835) Myosin S1, motor domain {Bay
scallop (Aequipecten irradians)}
FSDPDFQYLAVDRKKLMKEQTAAFXMNPPKFEKLEDMANMTYLNEASVLYNLRSRYTSGLIYTYS
GLFCIAVNPYRRLPIYTDSVIAKYRGKRKTEIPPHLFSVADNAYQNMVTDRENQSCLITGESGAG
KTENTKKVIMYLAKVACAVKKKDEEASDKKEGSLEDQIIQANPVLEAYGNAKTTRNNNSSRFGKF
IRIHFGPTGKIAGADIETYLLEKSRVTYQQSAERNYHIFYQICSNAIPELNDVMLVTPDSGLYSF
INQGCLTVDNIDDVEEFKLCDEAFDILGFTKEEKQSMFKCTASILHMGEMKFKQRPREEQAESDG
TAEAEKVAFLCGINAGDLLKALLKPKVKVGTEMVTKGQNMNQVVNSVGALAKSLYDRMFNWLVRR
VNKTLDTKAKRNYYIGVLDIAGFEIFDFNSFEQLCINYTNERLQQFFNHHMFILEQEEYKKEGIA
WEFIDFGMDLQMCIDLIEKPMGILSILEEECMFPKADDKSFQDKLYQNHMGKNRMFTKPGKPTRP
NQGPAHFELHHYAGNVPYSITGWLEKNKDPINENVVALLGASKEPLVAELFKAPEEPAGGGKKKK
GKSSAFQTISAVHRESLNKLMKNLYSTHPHFVRCIIPNELKQPGLVDAELVLHQLQCNGVLEGIR
ICRKGFPSRLIYSEFKQRYSILAPNAIPQGFVDGKTVSEKILAGLQMDPAEYRLGTTKVFFKAGV
LGNLEEMRDERLSKIISMFQAHIRGYLIRKAYKKLQDQRIGLSVIQRNIRKWLVLRNWQWWKLYS
KVKP
>d1lvk_2 c.37.1.9 (2-33,80-759) Myosin S1, motor domain {Slime mold
(Dictyostelium discoideum)}
NPIHDRTSDYHKYLKVKQGDSDLFKLTVSDKRXRNPIKFDGVEDMSELSYLNEPAVFHNLRVRYN
QDLIYTYSGLFLVAVNPFKRIPIYTQEMVDIFKGRRRNEVAPHIFAISDVAYRSMLDDRQNQSLL

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ITGESGAGKTENTKKVIQYLASVAGRNQANGSGVLEQQILQANPILEAFGNAKTTRNNNSSRFGK
FIEIQFNNAGFISGASIQSYLLEKSRVVFQSTSERNYHIFYQLLAGATAEEKKALHLAGPESFNY
LNQSGCVDIKGVSDEDEFKITRQAMDIVGFSQEEQMSIFKIIAGILHLGNIKFEKGAGEGAVLKD
KTALNAASTVFGVNPSVLEKALMEPRILAGRDLVAQHLNVEKSSSSRDALVKALYGRLFLWLVKK
INNVLCSERKAYFIGVLDISGFEIFKVNSFEQLCINYTNEKLQQFFNHHMFKVEQEKYLKEKINW
TFIDFGLDSQATIDLIDGRQPPGILALLDEQSVFPNATDNTLITKLHSHFSKKNAKYEEPRFSKT
EFGVTHYAGQVMYEIQDWLEKNKDPLQQDLELCFKDSSDNVVTKLFNDPNIASRAKKGANFLTVA
AQYKEQLASLMATLETTNPHFVRCIIPNNKQLPAKLEDKVVLDQLRCNGVLEGIRITRKGFPNRI
IYADFVKRYYDLAPNVPRDAEDSQKATDAVLKHLNIDPEQFRFGITKIFFRAGQLARIEEARE
>d1mnd_2 c.37.1.9 (2-33,80-690) Myosin S1, motor domain {Slime mold
(Dictyostelium discoideum)}
NPIHDRTSDYHKYLKVKQGDSDLFKLTVSDKRXRNPIKFDGVEDMSELSYLNEPAVFHNLRVRYN
QDLIYTYSGLFLVAVNPFKRIPIYTQEMVDIFKGRRRNEVAPHIFAISDVAYRSMLDDRQNQSLL
ITGESGAGKTENTKKVIQYLASVAGRNQANGSGVLEQQILQANPILEAFGNAKTTRNNNSSRFGK
FIEIQFNNAGFISGASIQSYLLEKSRVVFQSETERNYHIFYQLLAGATAEEKKALHLAGPESFNY
LNQSGCVDIKGVSDEDEFKITRQAMDIVGFSQEEQMSIFKIIAGILHLGNIKFEKGAGEGAVLKD
KTALNAASTVFGVNPSVLEKALMEPRILAGRDLVAQHLNVEKSSSSRDALVKALYGRLFLWLVKK
INNVLCSERAAYFIGVLDISGFEIFKVNSFEQLCINYTNEKLQQFFNHHMFKVEQEEYLKEKINW
TFIDFGLDSQATIDLIDGRQPPGILALLDEQSVFPNATDNTLITKLHSHFSKKNAKYEEPRFSKT
EFGVTHYAGQVMYEIQDWLEKNKDPLQQDLELCFKDSSDNVVTKLFNDPNIASRAKKGANFITVA
AQYKEQLASLMATLETTNPHFVRCIIPNNKQLPAKLEDKVVLDQLRCNGVLEGIRITRK
>d1bg2__ c.37.1.9 (-) Kinesin {Human (Homo sapiens)}
DLAECNIKVMCRFRPLNESEVNRGDKYIAKFQGEDTVVIASKPYAFDRVFQSSTSQEQVYNDCAK
KIVKDVLEGYNGTIFAYGQTSSGKTHTMEGKLHDPEGMGIIPRIVQDIFNYIYSMDENLEFHIKV
SYFEIYLDKIRDLLDVSKTNLSVHEDKNRVPYVKGCTERFVCSPDEVMDTIDEGKSNRHVAVTNM
NEHSSRSHSIFLINVKQENTQTEQKLSGKLYLVDLAGSEKVSKTGAEGAVLDEAKNINKSLSALG
NVISALAEGSTYVPYRDSKMTRILQDSLGGNCRTTIVICCSPSSYNESETKSTLLFGQRAKTI
>g2kin.1 c.37.1.9 (A:,B:) Kinesin {Rat (Rattus norvegicus)}
ADPAECSIKVMCRFRPLNEAEILRGDKFIPKFKGEETVVIGQGKPYVFDRVLPPNTTQEQVYNAC
AKQIVKDVLEGYNGTIFAYGQTSSGKTHTMEGKLHDPQLMGIIPRIAHDIFDHIYSMDENLEFHI
KVSYFEIYLDKIRDLLDVSKTNLAVHEDKNRVPYVKGCTERFVSSPEEVMDVIDEGKANRHVAVT
NMNEHSSRSHSIFLINIKQENVETEKKLSGKLYLVDLAGSEKVXAKNINKSLSALGNVISALAEG
TKTHVPYRDSKMTRILQDSLDGNCRTTIVICCSPSVFNEAETKSTLMFGQRAKTIKNTVSVNLEL
TAEEWKKKYEKEKE
>d1i6ia_ c.37.1.9 (A:) Kinesin {Mouse (Mus musculus), kif1a}
GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKETPKSFSFDYSYWSHTSPEDINY
ASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLCEDLFSRIND
TTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVREHPLLGPYVEDLSKLAVTSYNDIQDLMD
SGNKARTVAATNMNETSSRSHAVFNIIFTQKRHDAETNITTEKVSKISLVDLAGSERADSTGAKG
TRLKEGANINKSLTTLGKVISALAEMDSGPNKNKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAM
VAALSPADINYDETLSTLRYADRAKQIRNTVSVNHHHHHH
>d1ii6a_ c.37.1.9 (A:) Kinesin {Human (Homo sapiens), mitotic kinesin
eg5}
GKNIQVVVRCRPFNLAERKASAHSIVECDPVRKEVSVRTGGLADKSSRKTYTFDMVFGASTKQID
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VYRSVVCPILDEVIMGYNCTIFAYGQTGTGKTFTMEGERSPNEEYTWEEDPLAGIIPRTLHQIFE
KLTDNGTEFSVKVSLLEIYNEELFDLLNPSSDVSERLQMFDDPRNKRGVIIKGLEEITVHNKDEV
YQILEKGAAKRTTAATLMNAYSSRSHSVFSVTIHMKETTIDGEELVKIGKLNLVDLAGSENIGRS
GAVDKRAREAGNINQSLLTLGRVITALVERTPHVPYRESKLTRILQDSLGGRTRTSIIATISPAS
LNLEETLSTLEYAHRAKNILNKPEV
>d1goja_ c.37.1.9 (A:) Kinesin {Neurospora crassa}
SSSANSIKVVARFRPQNRVEIESGGQPIVTFQGPDTCTVDSKEAQGSFTFDRVFDMSCKQSDIFD
FSIKPTVDDILNGYNGTVFAYGQTGAGKSYTMMGTSIDDPDGRGVIPRIVEQIFTSILSSAANIE
YTVRVSYMEIYMERIRDLLAPQNDNLPVHEEKNRGVYVKGLLEIYVSSVQEVYEVMRRGGNARAV
AATNMNQESSRSHSIFVITITQKNVETGSAKSGQLFLVDLAGSEKVGKTGASGQTLEEAKKINKS
LSALGMVINALTDGKSSHVPYRDSKLTRILQESLGGNSRTTLIINCSPSSYNDAETLSTLRFGMR
AKSIKNKAKVNAELSPAELKQMLAKAKTQ
>d2ncda_ c.37.1.9 (A:) Kinesin motor Ncd (non-claret disjunctional)
{Fruit fly (Drosophila melanogaster)}
LRQRTEELLRCNEQQAAELETCKEQLFQSNMERKELHNTVMDLRGNIRVFCRIRPPLESEENRMC
CTWTYHDESTVELQSIDAQAKSKMGQQIFSFDQVFHPLSSQSDIFEMVSPLIQSALDGYNICIFA
YGQTGSGKTYTMDGVPESVGVIPRTVDLLFDSIRGYRNLGWEYEIKATFLEIYNEVLYDLLSNEQ
KDMEIRMAKNNKNDIYVSNITEETVLDPNHLRHLMHTAKMNRATASTAGNERSSRSHAVTKLELI
GRHAEKQEISVGSINLVDLAGSESPKTSTRMTETKNINRSLSELTNVILALLQKQDHIPYRNSKL
THLLMPSLGGNSKTLMFINVSPFQDCFQESVKSLRFAASVNSC
>d1f9va_ c.37.1.9 (A:) Kinesin motor Ncd (non-claret disjunctional)
{Baker's yeast (Saccharomyces cerevisiae), Kar}
GNIRVYCRIRPALKNLENSDTSLINVNEFDDNSGVQSMEVTKIQNTAQVHEFKFDKIFDQQDTNV
DVFKEVGQLVQSSLDGYNVCIFAYGQTGSGKTFTMLNPGDGIIPSTISHIFNWINKLKTKGWDYK
VNCEFIEIYNENIVDLLRSDNNNKEDTSIGLKHEIRHDQETKTTTITNVTSCKLESEEMVEIILK
KANKLRSTASTASNEHSSASHSIFIIHLSGSNAKTGAHSYGTLNLVDLAGSERINVSQVVGDRLR
ETQNINKSLSCLGDVIHALGQPDSTKRHIPFRNSKLTYLLQYSLTGDSKTLMFVNISPSSSHINE
TLNSLRFASKVNSTRLV
>d1byi__ c.37.1.10 (-) Dethiobiotin synthetase {Escherichia coli}
SKRYFVTGTDTEVGKTVASCALLQAAKAAGYRTAGYKPVASGSEKTPEGLRNSDALALQRNSSLQ
LDYATVNPYTFAEPTSPHIISAQEGRPIESLVMSAGLRALEQQADWVLVEGAGGWFTPLSDTFTF
ADWVTQEQLPVILVVGVKLGCINHAMLTAQVIQHAGLTLAGWVANDVTPPGKRHAEYMTTLTRMI
PAPLLGEIPWLAENPENAATGKYINLALL
>d1qf5a_ c.37.1.10 (A:) Adenylosuccinate synthetase, PurA
{Escherichia coli}
GNNVVVLGTQWGDEGKGKIVDLLTERAKYVVRYQGGHNAGHTLVINGEKTVLHLIPSGILRENVT
SIIGNGVVLSPAALMKEMKELEDRGIPVRERLLLSEACPLILDYHVALDNAREKARGAKAIGTTG
RGIGPAYEDKVARRGLRVGDLFDKETFAEKLKEVMEYHNFQLVNYYKAEAVDYQKVLDDTMAVAD
ILTSMVVDVSDLLDQARQRGDFVMFEGAQGTLLDIDHGTYPYVTSSNTTAGGVATGSGLGPRYVD
YVLGILKAYSTRVGAGPFPTELFDETGEFLCKQGNEFGATTGRRRRTGWLDTVAVRRAVQLNSLS
GFCLTKLDVLDGLKEVKLCVAYRMPDGREVTTTPLAADDWKGVEPIYETMPGWSESTFGVKDRSG
LPQAALNYIKRIEELTGVPIDIISTGPDRTETMILRDPFDA
>d1dj2a_ c.37.1.10 (A:) Adenylosuccinate synthetase, PurA {Mouse-ear
cress (Arabidopsis thaliana)}
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IGSLSQVSGVLGCQWGDEGKGKLVDILAQHFDIVARCQGGANAGHTIYNSEGKKFALHLVPSGIL
NEDTTCVIGNGVVVHLPGLFKEIDGLESNGVSCKGRILVSDRAHLLFDFHQEVDGLRESELAKSF
IGTTKRGIGPAYSSKVIRNGIRVGDLRHMDTLPQKLDLLLSDAAARFQGFKYTPEMLREEVEAYK
RYADRLEPYITDTVHFINDSISQKKKVLVEGGQATMLDIDFGTYPFVTSSSPSAGGICTGLGIAP
SVVGDLIGVVKAYTTRVGSGPFPTENLGTGGDLLRLAGQEFGTTTGRPRRCGWLDIVALKFSCQI
NGFASLNLTKLDVLSDLNEIQLGVAYKRSDGTPVKSFPGDLRLLEELHVEYEVLPGWKSDISSVR
NYSDLPKAAQQYVERIEELVGVPIHYIGIGPGRDALIYK
>d1dj3a_ c.37.1.10 (A:) Adenylosuccinate synthetase, PurA {Bread wheat (Triticum aestivum)}
ADRVSSLSNVSGVLGSQWGDEGKGKLVDVLAPRFDIVARCQGGANAGHTIYNSEGKKFALHLVPS
GILHEGTLCVVGNGAVIHVPGFFGEIDGLQSNGVSCDGRILVSDRAHLLFDLHQTVDGLREAELA
NSFIGTTKRGIGPCYSSKVTRNGLRVCDLRHMDTFGDKLDVLFEDAAARFEGFKYSKGMLKEEVE
RYKKFAERLEPFIADTVHVLNESIRQKKKILVEGGQATMLDIDFGTYPFVTSSSPSAGGICTGLG
IAPRVIGDLIGVVKAYTTRVGSGPFPTELLGEEGDVLRKAGMEFGTTTGRPRRCGWLDIVALKYC
CDINGFSSLNLTKLDVLSGLPEIKLGVSYNQMDGEKLQSFPGDLDTLEQVQVNYEVLPGWDSDIS
SVRSYSELPQAARRYVERIEELAGVPVHYIGVGPGRDALIYK
>d1j4ba_ c.37.1.10 (A:) Adenylosuccinate synthetase, PurA {Mouse (Mus musculus)}
AAATGSRVTVVLGAQWGDEGKGKVVDLLATDADIVSRCQGGNNAGHTVVVDGKEYDFHLLPSGII
NTKAVSFIGNGVVIHLPGLFEEAEKNEKKGLKDWEKRLIISDRAHLVFDFHQAVDGLQEVQRQAQ
EGKNIGTTKKGIGPTYSSKAARTGLRICDLLSDFDEFSARFKNLAHQHQSMFPTLEIDVEGQLKR
LKGFAERIRPMVRDGVYFMYEALHGPPKKVLVEGANAALLDIDFGTYPFVTSSNCTVGGVCTGLG
IPPQNIGDVYGVVKAYTTRVGIGAFPTEQINEIGDLLQNRGHEWGVTTGRKRRCGWLDLMILRYA
HMVNGFTALALTKLDILDVLSEIKVGISYKLNGKRIPYFPANQEILQKVEVEYETLPGWKADTTG
ARKWEDLPPQAQSYVRFVENHMGVAVKWVGVGKSRESMIQLF
>d1eg7a_ c.37.1.10 (A:) Formyltetrahydrofolate synthetase {Moorella thermoacetica}
DIEIAQAAKMKPVMELARGLGIQEDEVELYGKYKAKISLDVYRRLKDKPDGKLILVTAITPTPAG
EGKTTTSVGLTDALARLGKRVMVCLREPSLGPSFGIKGGAAGGGYAQVVPMEDINLHFTGDIHAV
TYAHNLLAAMVDNHLQQGNVLNIDPRTITWRRVIDLNERALRNIVIGLGGKANGVPRETGFDISV
ASEVMACLCLASDLMDLKERFSRKVVGYTYDGKPVTAGDLEAQGSMALLMKDAIKPNLVQTLENT
PAFIHGGPFANIAHGCNSIIATKTALKLADYVVTEAGFGADLGAEKFYDVKCRYAGFKPDATVIV
ATVRALKMHGGVPKSDLATENLEALREGFANLEKHIENIGKFGVPAVVAINAFPTDTEAELNLLY
ELCAKAGAEVALSWAKGGEGGLELARKVLQTLESRPSNFHVLYNLDLSIKDKIAKIATEIYGADG
VNYTAEADKAIQRYESLGYGNLPVVMAKTQYSFSDDMTKLGRPRNFTITVREVRLSAGGRLIVPI
TGAIMTMPGLPKRPAACNIDIDADGVITG
>d1fp6a_ c.37.1.10 (A:) Nitrogenase iron protein {Azotobacter vinelandii}
AMRQCAIYGKGGIGKSTTTQNLVAALAEMGKKVMIVGCDPKADSTRLILHSKAQNTIMEMAAEAG
TVEDLELEDVLKAGYGGVKCVESGGPEPGVGCAGRGVITAINFLEEEGAYEDDLDFVFYDVLGDV
VCGGFAMPIRENKAQEIYIVCSGEMMAMYAANNISKGIVKYANSGSVRLGGLICNSRNTDREDEL
IIALANKLGTQMIHFVPRDNVVQRAEIRRMTVIEYDPKAKQADEYRALARKVVDNKLLVIPNPIT
MDELEELLMEFGIMEVEDESIVGKTAEEV
>d1cp2a_ c.37.1.10 (A:) Nitrogenase iron protein {Clostridium

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pasteurianum}
MRQVAIYGKGGIGKSTTTQNLTSGLHAMGKTIMVVGCDPKADSTRLLLGGLAQKSVLDTLREEGE
DVELDSILKEGYGGIRCVESGGPEPGVGCAGRGIITSINMLEQLGAYTDDLDYVFYDVLGDVVCG
GFAMPIREGKAQEIYIVASGEMMALYAANNISKGIQKYAKSGGVRLGGIICNSRKVANEYELLDA
FAKELGSQLIHFVPRSPMVTKAEINKQTVIEYDPTCEQAEEYRELARKVDANELFVIPKPMTQER
LEEILMQYG
>d1hyqa_ c.37.1.10 (A:) Cell division regulator MinD {Archaeon
Archaeoglobus fulgidus}
VRTITVASGKGGTGKTTITANLGVALAQLGHDVTIVDADITMANLELILGMEGLPVTLQNVLAGE
ARIDEAIYVGPGGVKVVPAGVSLEGLRKANPEKLEDVLTQIMESTDILLLDAPAGLERSAVIAIA
AAQELLLVVNPEISSITDGLKTKIVAERLGTKVLGVVVNRITTLGIEMAKNEIEAILEAKVIGLI
PEDPEVRRAAAYGKPVVLRSPNSPAARAIVELANYIA
>d1g3qa_ c.37.1.10 (A:) Cell division regulator MinD {Archaeon
Pyrococcus furiosus}
MGRIISIVSGKGGTGKTTVTANLSVALGDRGRKVLAVDGDLTMANLSLVLGVDDPDVTLHDVLAG
EANVEDAIYMTQFDNVYVLPGAVDWEHVLKADPRKLPEVIKSLKDKFDFILIDCPAGLQLDAMSA
MLSGEEALLVTNPEISCLTDTMKVGIVLKKAGLAILGFVLNRYGRSDRDIPPEAAEDVMEVPLLA
VIPEDPAIREGTLEGIPAVKYKPESKGAKAFVKLAEEIEKLA
>d1iona_ c.37.1.10 (A:) Cell division regulator MinD {Archaeon
Pyrococcus horikoshii}
MTRIISIVSGKGGTGKTTVTANLSVALGEMGRKVLAVDGDLTMANLSLVLGVDDVNITLHDVLAG
DAKLEDAIYMTQFENVYILPGAVDWEHVIKADPRKLPEVIKSLKGKYDFILIDCPAGLQLRAMSA
MLSGEEAILVTNPEISCLTDTMKVGMVLKKAGLAILGFILNRYGRSERDIPPEAAQDVMDVPLLA
VIPEDPVIREGTLEGIPAVKYKPESKGAQAFIKLAEEVDKLAGIKAKI
>d1jpna2 c.37.1.10 (A:89-296) GTPase domain of the signal sequence
recognition protein Ffh {Thermus aquaticus}
EARLPVLKDRNLWFLVGLQGSGKTTTAAKLALYYKGKGRRPLLVAADTQRPAAREQLRLLGEKVG
VPVLEVMDGESPESIRRRVEEKARLEARDLILVDTAGRLQIDEPLMGELARLKEVLGPDEVLLVL
DAMTGQEALSVARAFDEKVGVTGLVLTKLDGDARGGAALSARHVTGKPIYFAGVSEKPEGLEPFY
PERLAGRILGMGD
>d1j8mf2 c.37.1.10 (F:87-297) GTPase domain of the signal sequence
recognition protein Ffh {Archaeon Acidianus ambivalens}
DKEPKVIPDKIPYVIMLVGVQGTGKTTTAGKLAYFYKKKGFKVGLVGADVYRPAALEQLQQLGQQ
IGVPVYGEPGEKDVVGIAKRGVEKFLSEKMEIIIVDTAGRHGYGEEAALLEEMKNIYEAIKPDEV
TLVIDASIGQKAYDLASKFNQASKIGTIIITKMDGTAKGGGALSAVAATGATIKFIGTGEKIDEL
EVFNPRRFVARLHHHH
>d1fts_2 c.37.1.10 (285-495) GTPase domain of the signal recognition
particle receptor FtsY {Escherichia coli}
PLNVEGKAPFVILMVGVNGVGKTTTIGKLARQFEQQGKSVMLAAGDTFRAAAVEQLQVWGQRNNI
PVIAQHTGADSASVIFDAIQAAKARNIDVLIADTAGRLQNKSHLMEELKKIVRVMKKLDVEAPHE
VMLTIDASTGQNAVSQAKLFHEAVGLTGITLTKLDGTAKGGVIFSVADQFGIPIRYIGVGERIED
LRPFKADDFIEALFAR
>d1ihua1 c.37.1.10 (A:1-296) Arsenite-translocating ATPase ArsA
{Escherichia coli}
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MQFLQNIPPYLFFTGKGGVGKTSISCATAIRLAEQGKRVLLVSTDPASNVGQVFSQTIGNTIQAI
ASVPGLSALEIDPQAAAQQYRARIVDPIKGVLPDDVVSSINEQLSGACTTEIAAFDEFTGLLTDA
SLLTRFDHIIFDTAPTGHTIRLLQLPGAWSSFIDSNPEGASCLGPMAGLEKQREQYAYAVEALSD
PKRTRLVLVARLQKSTLQEVARTHLELAAIGLKNQYLVINGVLPKTEAANDTLAAAIWEREQEAL
ANLPADLAGLPTDTLFLQPVNMVGVSALSRLLSTQP
>d1ihua2 c.37.1.10 (A:308-586) Arsenite-translocating ATPase ArsA
{Escherichia coli}
QRPDIPSLSALVDDIARNEHGLIMLMGKGGVGKTTMAAAIAVRLADMGFDVHLTTSDPAAHLSMT
LNGSLNNLQVSRIDPHEETERYRQHVLETKGKELDEAGKRLLEEDLRSPCTEEIAVFQAFSRVIR
EAGKRFVVMDTAPTGHTLLLLDATGAYHREIAKKMGEKGHFTTPMMLLQDPERTKVLLVTLPETT
PVLEAANLQADLERAGIHPWGWIINNSLSIADTRSPLLRMRAQQELPQIESVKRQHASRVALVPV
LASEPTGIDKLKQLAGHHH
>d2reb_1 c.37.1.11 (3-268) RecA protein, ATPase-domain {Escherichia
coli}
DENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGRIVEIYGP
ESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPDTGEQALEICDAL
ARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAGNLKQSNTLLIFINQIRM
KIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGSETRVKVVKNKIAAPFKQAEFQI
LYGEGI
>d1g19a1 c.37.1.11 (A:1-269) RecA protein, ATPase-domain
{Mycobacterium tuberculosis}
MTQTPDREKALELAVAQIEKSYGKGSVMRLGDEARQPISVIPTGSIALDVALGIGGLPRGRVIEI
YGPESSGKTTVALHAVANAQAAGGVAAFIDAEHALDPDYAKKLGVDTDSLLVSQPDTGEQALEIA
DMLIRSGALDIVVIDSVAALVPRAELEGEMGDSHVGLQARLMSQALRKMTGALNNSGTTAIFINQ
LRDKIGVMFGSPETTTGGKALKFYASVRMDVRRVETLKDGTNAVGNRTRVKVVKNKCLAPFKQAE
FDILYGKGI
>d1cr1a_ c.37.1.11 (A:) Gene 4 protein (g4p, DNA primase), helicase
domain {Bacteriophage T7}
MRERIREHLSSEESVGLLFSGCTGINDKTLGARGGEVIMVTSGSGMGKSTFVRQQALQWGTAMGK
KVGLAMLEESVEETAEDLIGLHNRVRLRQSDSLKREIIENGKFDQWFDELFGNDTFHLYDSFAEA
ETDRLLAKLAYMRSGLGCDVIILDHISIVVSASGESDERKMIDNLMTKLKGFAKSTGVVLVVICH
LKNPDKGKAHEEGRPVSITDLRGSGALRQLSDTIIALERNQQGDMPNLVLVRILKCRFTGDTGIA
GYMEYNKETGWLEPSSY
>d1g8ya_ c.37.1.11 (A:) Hexameric replicative helicase repA
{Escherichia coli, plasmid rsf1010}
ATHKPINILEAFAAAPPPLDYVLPNMVAGTVGALVSPGGAGKSMLALQLAAQIAGGPDLLEVGEL
PTGPVIYLPAEDPPTAIHHRLHALGAHLSAEERQAVADGLLIQPLIGSLPNIMAPEWFDGLKRAA
EGRRLMVLDTLRRFHIEEENASGPMAQVIGRMEAIAADTGCSIVFLHHASKGAAMMGAGDQQQAS
RGSSVLVDNIRWQSYLSSMTSAEAEEWGVDDDQRRFFVRFGVSKANYGAPFADRWFRRHDGGVLK
PA
>d1e9ra_ c.37.1.11 (A:) Bacterial conjugative coupling protein TrwB
{Escherichia coli}
VGQGEFGGAPFKRFLRGTRIVSGGKLKRMTREKAKQVTVAGVPMPRDAEPRHLLVNGATGTGKSV
LLRELAYTGLLRGDRMVIVDPNGDMLSKFGRDKDIILNPYDQRTKGWSFFNEIRNDYDWQRYALS
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VVPRGKTDEAEEWASYGRLLLRETAKKLALIGTPSMRELFHWTTIATFDDLRGFLEGTLAESLFA
GSNEASKALTSARFVLSDKLPEHVTMPDGDFSIRSWLEDPNGGNLFITWREDMGPALRPLISAWV
DVVCTSILSLPEEPKRRLWLFIDELASLEKLASLADALTKGRKAGLRVVAGLQSTSQLDDVYGVK
EAQTLRASFRSLVVLGGSRTDPKTNEDMSLSLGEHEVERDRYSKNTGKHHSTGRALERVRERVVM
PAEIANLPDLTAYVGFAGNRPIAKVPLEIKQFANRQPAFVEGT
>d1e79a3 c.37.1.11 (A:95-379) Central domain of alpha and beta subunits
of F1 ATP synthase {Cow (Bos taurus)}
VDVPVGEELLGRVVDALGNAIDGKGPIGSKARRRVGLKAPGIIPRISVREPMQTGIKAVDSLVPI
GRGQRELIIGDRQTGKTSIAIDTIINQKRFNDGTDEKKKLYCIYVAIGQKRSTVAQLVKRLTDAD
AMKYTIVVSATASDAAPLQYLAPYSGCSMGEYFRDNGKHALIIYDDLSKQAVAYRQMSLLLRRPP
GREAYPGDVFYLHSRLLERAAKMNDAFGGGSLTALPVIETQAGDVSAYIPTNVISITDGQIFLET
ELFYKGIRPAINVGLSVSRVGSAAQ
>d1e79d3 c.37.1.11 (D:82-357) Central domain of alpha and beta subunits
of F1 ATP synthase {Cow (Bos taurus)}
IRIPVGPETLGRIMNVIGEPIDERGPIKTKQFAAIHAEAPEFVEMSVEQEILVTGIKVVDLLAPY
AKGGKIGLFGGAGVGKTVLIMELINNVAKAHGGYSVFAGVGERTREGNDLYHEMIESGVINLKDA
TSKVALVYGQMNEPPGARARVALTGLTVAEYFRDQEGQDVLLFIDNIFRFTQAGSEVSALLGRIP
SAVGYQPTLATDMGTMQERITTTKKGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSRAIAE
LGIYPAVDPLDSTSRI
>d1skyb3 c.37.1.11 (B:96-371) Central domain of alpha and beta subunits
of F1 ATP synthase {Bacillus sp., strain ps3}
EVPVGETLIGRVVNPLGQPVDGLGPVETTETRPIESRAPGVMDRRSVHEPLQTGIKAIDALVPIG
RGQRELIIGDRQTGKTSVAIDTIINQKDQNMICIYVAIGQKESTVATVVETLAKHGAPDYTIVVT
ASASQPAPLLFLAPYAGVAMGEYFMIMGKHVLVVIDDLSKQAAAYRQLSLLLRRPPGREAYPGDI
FYLHSRLLERAAKLSDAKGGGSLTALPFVETQAGDISAYIPTNVISITDGQIFLQSDLFFSGVRP
AINAGLSVSRVGGAAQ
>d1skye3 c.37.1.11 (E:83-356) Central domain of alpha and beta subunits
of F1 ATP synthase {Bacillus sp., strain ps3}
ISVPVGQVTLGRVFNVLGEPIDLEGDIPADARRDPIHRPAPKFEELATEVEILETGIKVVDLLAP
YIKGGKIGLFGGAGVGKTVLIQELIHNIAQEHGGISVFAGVGERTREGNDLYHEMKDSGVISKTA
MVFGQMNEPPGARMRVALTGLTMAEYFRDEQGQDGLLFIDNIFRFTQAGSEVSALLGRMPSAIGY
QPTLATEMGQLQERITSTAKGSITSIQAIYVPADDYTDPAPATTFSHLDATTNLERKLAEMGIYP
AVDPLVSTSRALAP
>d1fx0a3 c.37.1.11 (A:97-372) Central domain of alpha and beta subunits
of F1 ATP synthase {Spinach (Spinacia oleracea), chloroplast}
QIPVSEAYLGRVINALAKPIDGRGEITASESRLIESPAPGIMSRRSVYEPLQTGLIAIDAMIPVG
RGQRELIIGDRQTGKTAVATDTILNQQGQNVICVYVAIGQKASSVAQVVTNFQERGAMEYTIVVA
ETADSPATLQYLAPYTGAALAEYFMYRERHTLIIYDDLSKQAQAYRQMSLLLRRPPGREAYPGDV
FYLHSRLLERAAKLSSLLGEGSMTALPIVETQAGDVSAYIPTNVISITDGQIFLSADLFNAGIRP
AINVGISVSRVGSAAQ
>d1fx0b3 c.37.1.11 (B:98-377) Central domain of alpha and beta subunits
of F1 ATP synthase {Spinach (Spinacia oleracea), chloroplast}
LSVPVGGPTLGRIFNVLGEPVDNLRPVDTRTTSPIHRSAPAFTQLDTKLSIFETGIKVVNLLAPY
RRGGKIGLFGGAGVGKTVLIMELINNIAKAHGGVSVFGGVGERTREGNDLYMEMKESGVINEQNI
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AESKVALVYGQMNEPPGARMRVGLTALTMAEYFRDVNEQDVLLFIDNIFRFVQAGSEVSALLGRM
PSAVGYQPTLSTEMGSLQERITSTKEGSITSIQAVYVPADDLTDPAPATTFAHLDATTVLSRGLA
AKGIYPAVDPLDSTSTMLQP
>d1cbua_ c.37.1.11 (A:) Adenosylcobinamide kinase/adenosylcobinamide phosphate guanylyltransferase CobU {Salmonella typhimurium}
MILVTGGARSGKSRHAEALIGDAPQVLYIATSQILDDEMAARIQHHKDGRPAHWRTAECWRHLDT
LITADLAPDDAILLECITTMVTNLLFALGGENDPEQWDYAAMERAIDDEIQILIAACQRCPAKVV
LVTNEVGMGIVPENRLARHFRDIAGRVNQRLAAAADEVWLVVSGIGVKIK
>d1g5ta_ c.37.1.11 (A:) ATP:corrinoid adenosyltransferase CobA {Salmonella typhimurium}
ERGIIIVFTGNGKGKTTAAFGTAARAVGHGKNVGVVQFIKGTWPNGERNLLEPHGVEFQVMATGF
TWETQNREADTAACMAVWQHGKRMLADPLLDMVVLDELTYMVAYDYLPLEEVISALNARPGHQTV
IITGRGCHRDILDLADTVSELRPVKHA
>d1g64b_ c.37.1.11 (B:) ATP:corrinoid adenosyltransferase CobA {Salmonella typhimurium}
QQRQQKVKDRVDARVAQAQEERGIIIVFTGNGKGKTTAAFGTAARAVGHGKNVGVVQFIKGTWPN
GERNLLEPHGVEFQVMATGFTWETQNREADTAACMAVWQHGKRMLADPLLDMVVLDELTYMVAYD
YLPLEEVISALNARPGHQTVIITGRGCHRDILDLADTVSELRPVKHAFDAGVKAQMGIDY
>d1b0ua_ c.37.1.12 (A:) ATP-binding subunit of the histidine permease {Salmonella typhimurium}
NKLHVIDLHKRYGGHEVLKGVSLQARAGDVISIIGSSGSGKSTFLRCINFLEKPSEGAIIVNGQN
INLVRDKDGQLKVADKNQLRLLRTRLTMVFQHFNLWSHMTVLENVMEAPIQVLGLSKHDARERAL
KYLAKVGIDERAQGKYPVHLSGGQQQRVSIARALAMEPDVLLFDEPTSALDPELVGEVLRIMQQL
AEEGKTMVVVTHEMGFARHVSSHVIFLHQGKIEEEGDPEQVFGNPQSPRLQQFLKGSLKKLEH
>d1g6ha_ c.37.1.12 (A:) MJ1267 {Archaeon Methanococcus jannaschii}
TMEILRTENIVKYFGEFKALDGVSISVNKGDVTLIIGPNGSGKSTLINVITGFLKADEGRVYFEN
KDITNKEPAELYHYGIVRTFQTPQPLKEMTVLENLLIGEICPGESPLNSLFYKKWIPKEEEMVEK
AFKILEFLKLSHLYDRKAGELSGGQMKLVEIGRALMTNPKMIVMDEPIAGVAPGLAHDIFNHVLE
LKAKGITFLIIEHRLDIVLNYIDHLYVMFNGQIIAEGRGEEEIKNVLSDPKVVEIYIGE
>d1f3oa_ c.37.1.12 (A:) MJ0796 {Archaeon Methanococcus jannaschii}
MIKLKNVTKTYKMGEEIIYALKNVNLNIKEGEFVSIMGPSGSGKSTMLNIIGCLDKPTEGEVYID
NIKTNDLDDDELTKIRRDKIGFVFQQFNLIPLLTALENVELPLIFKYRGAMSGEERRKRALECLK
MAELEERFANHKPNQLSGGQQQRVAIARALANNPPIILADEPTGALDSKTGEKIMQLLKKLNEED
GKTVVVVTHDINVARFGERIIYLKDGEVEREEKLRGF
>d1jj7a_ c.37.1.12 (A:) Peptide transporter Tap1, C-terminal ABC domain {Human (Homo sapiens)}
GLLTPLHLEGLVQFQDVSFAYPNRPDVLVLQGLTFTLRPGEVTALVGPNGSGKSTVAALLQNLYQ
PTGGQLLLDGKPLPQYEHRYLHRQVAAVGQEPQVFGRSLQENIAYGLTQKPTMEEITAAAVKSGA
HSFISGLPQGYDTEVDEAGSQLSGGQRQAVALARALIRKPCVLILDDATSALDANSQLQVEQLLY
ESPERYSRSVLLITQHLSLVEQADHILFLEGGAIREGGTHQQLMEKKGCYWAMVQA
>d1g2912 c.37.1.12 (1:1-240) Maltose transport protein MalK, N-terminal domain {Archaeon Thermococcus litoralis}
MAGVRLVDVWKVFGEVTAVREMSLEVKDGEFMILLGPSGCGKTTTLRMIAGLEEPSRGQIYIGDK
LVADPEKGIFVPPKDRDIAMVFQSYALYPHMTVYDNIAFPLKLRKVPRQEIDQRVREVAELLGLT

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ELLNRKPRELSGGQRQRVALGRAIVRKPQVFLMDEPLSNLDAKLRVRMRAELKKLQRQLGVTTIY
VTHDQVEAMTMGDRIAVMNRGVLQQVGSPDEVYDKPANTFVAGFI
>g1f2t.1 c.37.1.12 (A:,B:) Rad50 {Archaeon Pyrococcus furiosus}
MKLERVTVKNFRSHSDTVVEFKEGINLIIGQNGSGKSSLLDAILVGLYWPLRIKDIKKDEFTKVG
ARDTYIDLIFEKDGTKYRITRRFLKGYSSGEIHAMKRLVGNEWKHVTEPSSKAISAFMEKLIPYN
IFLNAIYIRQGQIDAILESXAREAALSKIGELASEIFAEFTEGKYSEVVVRAEENKVRLFVVWEG
KERPLTFLSGGERIALGLAFRLAMSLYLAGEISLLILDEPTPYLDEERRRKLITIMERYLKKIPQ
VILVSHDEELKDAADHVIRISLENGSSKVEVVS
>g1ii8.1 c.37.1.12 (A:,B:) Rad50 {Archaeon Pyrococcus furiosus}
MKLERVTVKNFRSHSDTVVEFKEGINLIIGQNGSGKSSLLDAILVGLYWPLRIKDIKKDEFTKVG
ARDTYIDLIFEKDGTKYRITRRFLKGYSSGEIHAMKRLVGNEWKHVTEPSSKAISAFMEKLIPYN
IFLNAIYIRQGQIDAILESDEAREKVVREVLNLDKFETAYKKLSELKKTINNRIKEYRDILARTE
XRERVKKEIKDLEKAKDFTEELIEKVKKYKALAREAALSKIGELASEIFAEFTEGKYSEVVVRAE
ENKVRLFVVWEGKERPLTFLSGGERIALGLAFRLAMSLYLAGEISLLILDEPTPYLDEERRRKLI
TIMERYLKKIPQVILVSHDEELKDAADHVIRISLENGSSKVEVVS
>d1e69a_ c.37.1.12 (A:) Smc head domain {Thermotoga maritima}
MRLKKLYLKGFKSFGRPSLIGFSDRVTAIVGPNGSGKSNIIDAIKWVFGEQSKKELRASEKFDMI
FAGSENLPPAGSAYVELVFEENGEEITVARELKRTGENTYYLNGSPVRLKDIRDRFAGTGLGVDF
YSIVGQGQIDRIVNASPEELRLESSKHPTSLVPRGSYQRVNESFNRFISLLFFGGEGRLNIVSEA
KSILDAGFEISIRKPGRRDQKLSLLSGGEKALVGLALLFALMEIKPSPFYVLDEVDSPLDDYNAE
RFKRLLKENSKHTQFIVITHNKIVMEAADLLHGVTMVNGVSAIVPVEV
>d1qhla_ c.37.1.12 (A:) Cell division protein MukB {Escherichia coli}
RGKFRSLTLINWNGFFARTFDLDELVTTLSGGNGAGKSTTMAAFVTALIPDLTLLHFRNTTEAGA
TSGSRDKGLHGKLKAGVCYSMLDTINSRHQRVVVGVRLQQVAGRDRKVDIKPFAIQGLPMSVQPT
QLVTETLNERQARVLPLNELKDKLEAMEGVQFKQFNSITDYHSLMFDLGIIARRLRSASDRSKFY
RLIEASLYGGISSAITRSLRDYLLPEN
>d1ewqa2 c.37.1.12 (A:542-765) DNA repair protein MutS, the C-terminal
domain {Thermus aquaticus}
YVRPRFGDRLQIRAGRHPVVERRTEFVPNDLEMAHELVLITGPNMAGKSTFLRQTALIALLAQVG
SFVPAEEAHLPLFDGIYTRIGASDDLAGGKSTFMVEMEEVALILKEATENSLVLLDEVGRGTSSL
DGVAIATAVAEALHERRAYTLFATHYFELTALGLPRLKNLHVAAREEAGGLVFYHQVLPGPASKS
YGVEVAAMAGLPKEVVARARALLQAMAAR
>d1e3ma2 c.37.1.12 (A:567-800) DNA repair protein MutS, the C-terminal
domain {Escherichia coli}
YTCPTFIDKPGIRITEGRHPVVEQVLNEPFIANPLNLSPQRRMLIITGPNMGGKSTYMRQTALIA
LMAYIGSYVPAQKVEIGPIDRIFTRVGAADDLASGRSTFMVEMTETANILHNATEYSLVLMDEIG
RGTSTYDGLSLAWACAENLANKIKALTLFATHYFELTQLPEKMEGVANVHLDALEHGDTIAFMHS
VQDGAASKSYGLAVAALAGVPKEVIKRARQKLRELESIS
>d1pjr_1 c.37.1.13 (1-318) DEXX box DNA helicase {Bacillus
stearothermophilus, PcrA}
MNFLSEQLLAHLNKEQQEAVRTTEGPLLIMAGAGSGKTRVLTHRIAYLMAEKHVAPWNILAITFT
NKAAREMRERVQSLLGGAAEDVWISTFHSMCVRILRRDIDRIGINRNFSILDPTDQLSVMKTILK
EKNIDPKKFEPRTILGTISAAKNELLPPEQFAKRASTYYEKVVSDVYQEYQQRLLRNHSLDFDDL
IMTTIQLFDRVPDVLHYYQYKFQYIHIDEYQDTNRAQYTLVKKLAERFQNICAVGDADQSIYRWR
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GADIQNILSFERDYPNAKVILLEQNYRSTKRILQAANEVIEHNVNRKPKRIWTENPEG
>d1pjr_2 c.37.1.13 (319-651) DEXX box DNA helicase {Bacillus stearothermophilus, PcrA}
KPILYYEAMNEADEAQFVAGRIREAVERGERRYRDFAVLYRTNAQSRVMEEMLLKANIPYQIVGG
LKFYDRKEIKDILAYLRVIANPDDDLSLLRIINVPKRGIGASTIDKLVRYAADHELSLFEALGEL
EMIGLGAKAAGALAAFRSQLEQWTQLQEYVSVTELVEEVLDKSGYREMLKAERTIEAQSRLENLD
EFLSVTKHFENVSDDKSLIAFLTDLALISDLDELDGTEQAAEGDAVMLMTLHAAKGLEFPVVFLI
GMEEGIFPHNRSLEDDDEMEEERRLAYVGITRAEEELVLTSAQMRTLFGNIQMDPPSRFLNEIPA
HLLETASR
>g1qhh.1 c.37.1.13 (A:,B:,C:,D:) DEXX box DNA helicase {Bacillus stearothermophilus, PcrA}
MNFLSEQLLAHLNKEQQEAVRTTEGPLLIMAGAGSGKTRVLTHRIAYLMAEKHVAPWNILAITFT
NKAAREMRERVQSLLGGAAEDVWISTFHSMCVRILRRDIDRIGINRNFSILDPTDQLSVMKTILK
EKNIDPKKFEPRTILGTISAAKNELLPPEQFAKRXYYEKVVSDVYQEYQQRLLRNHSLDFDDLIM
TTIQLFDRVPDVLHYYQYKFQYIHIDEYQDTNRAQYTLVKKLAERFQNICAVGDADQSIYRWRGA
DIQNILSFERDYPNAKVILLEQNYRSTKRILQAANEVIEHNVNRKPKRIWTENPEGKPILYYEAM
NEADEAQFVAGRIREAVERGERRYRDFAVLYRTNAQSRVMEEMLLKANIPYQIVGGLKFYDRKEI
KDILAYLRVIANPDDDLSLLRIINVPKRGIGASTIDXLFEALGELEMIGLGAKAAGALAAFRSQL
EQWTQLQEYVSVTELVEEVLDKSGYREMLKAERTIEAQSRLENLDEFLSVTKHFENVSDDKSLIA
FLTDLALISXGDAVMLMTLHAAKGLEFPVVFLIGMEEGIFPHNRSLEDDDEMEEERRLAYVGITR
AEEELVLTSAQMRTLFGNIQMDPPSRFLNEIPAHLLETASR
>d1uaaa1 c.37.1.13 (A:2-307) DEXX box DNA helicase {Escherichia coli, RepD}
RLNPGQQQAVEFVTGPCLVLAGAGSGKTRVITNKIAHLIRGCGYQARHIAAVTFTNKAAREMKER
VGQTLGRKEARGLMISTFHTLGLDIIKREYAALGMKANFSLFDDTDQLALLKELTEGLIEDDKVL
LQQLISTISNWKNDLKTPSQAAASAIGERDRIFAHCYGLYDAHLKACNVLDFDDLILLPTLLLQA
NEEVRKRWQNKIRYLLVDEYQDTNTSQYELVKLLVGSRARFTVVGDDDQSIYSWRGARPQNLVLL
SQDFPALKVIKLEQNYRSSGRILKAANILIANNPHVFEKRLFSELG
>d1uaaa2 c.37.1.13 (A:308-640) DEXX box DNA helicase {Escherichia coli, RepD}
YGAELKVLSANNEEHEAERVTGELIAHHFVNKTQYKDYAILYRGNHQSRVFEKFLMQNRIPYKIS
GGTSFFSRPEIKDLLAYLRVLTNPDDDSAFLRIVNTPKREIGPATLKKLGEWAMTRNKSMFTASF
DMGLSQTLSGRGYEALTRFTHWLAEIQRLAEREPIAAVRDLIHGMDYESWLYETSPSPKAAEMRM
KNVNQLFSWMTEMLEGSELDEPMTLTQVVTRFTLRDMMERGESEEELDQVQLMTLHASKGLEFPY
VYMVGMEEGFLPHQSSIDEDNIDEERRLAYVGITRAQKELTFTLCKERRQYGELVRPEPSRFLLE
LPQDDLIW
>d1hv8a1 c.37.1.13 (A:3-210) Putative DEAD box RNA helicase {Archaeon Methanococcus jannaschii}
VEYMNFNELNLSDNILNAIRNKGFEKPTDIQMKVIPLFLNDEYNIVAQARTGSGKTASFAIPLIE
LVNENNGIEAIILTPTRELAIQVADEIESLKGNKNLKIAKIYGGKAIYPQIKALKNANIVVGTPG
RILDHINRGTLNLKNVKYFILDEADEMLNMGFIKDVEKILNACNKDKRILLFSATMPREILNLAK
KYMGDYSFIKAKI
>d1hv8a2 c.37.1.13 (A:211-365) Putative DEAD box RNA helicase {Archaeon Methanococcus jannaschii}
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NANIEQSYVEVNENERFEALCRLLKNKEFYGLVFCKTKRDTKELASMLRDIGFKAGAIHGDLSQS
QREKVIRLFKQKKIRILIATDVMSRGIDVNDLNCVINYHLPQNPESYMHRIGRTGRAGKKGKAIS
IINRREYKKLRYIERAMKLKIKKLK
>d1gm5a3 c.37.1.13 (A:286-549) RecG helicase domain {Thermotoga
maritima}
ETLPERILEKRKLLGVKDAYYGMHFPKTFYHLEKARERLAYEELFVLQLAFQKIRKEREKHGGIP
KKIEGKLAEEFIKSLPFKLTNAQKRAHQEIRNDMISEKPMNRLLQGDVGSGKTVVAQLAILDNYE
AGFQTAFMVPTSILAIQHYRRTVESFSKFNIHVALLIGATTPSEKEKIKSGLRNGQIDVVIGTHA
LIQEDVHFKNLGLVIIDEQHRFGVKQREALMNKGKMVDTLVMSATPIPRSMALAFYGDLDVTVID
EMPP
>d1gm5a4 c.37.1.13 (A:550-755) RecG helicase domain {Thermotoga
maritima}
GRKEVQTMLVPMDRVNEVYEFVRQEVMRGGQAFIVYPLIEESDKLNVKSAVEMYEYLSKEVFPEF
KLGLMHGRLSQEEKDRVMLEFAEGRYDILVSTTVIEVGIDVPRANVMVIENPERFGLAQLHQLRG
RVGRGGQEAYCFLVVGDVGEEAMERLRFFTLNTDGFKIAEYDLKTRGPGEFFGVKQHGLSGFKVA
DLYRDLKLLEW
>d1fuka_ c.37.1.13 (A:) Initiation factor 4a {Baker's yeast
(Saccharomyces cerevisiae)}
IKQFYVNVEEEEYKYECLTDLYDSISVTQAVIFCNTRRKVEELTTKLRNDKFTVSAIYSDLPQQE
RDTIMKEFRSGSSRILISTDLLARGIDVQQVSLVINYDLPANKENYIHRIGRGGRFGRKGVAINF
VTNEDVGAMRELEKFYSTQIEELPSDIATLLN
>d1qdea_ c.37.1.13 (A:) Initiation factor 4a {Baker's yeast
(Saccharomyces cerevisiae)}
IQTNYDKVVYKFDDMELDENLLRGVFGYGFEEPSAIQQRAIMPIIEGHDVLAQAQSGTGKTGTFS
IAALQRIDTSVKAPQALMLAPTRELALQIQKVVMALAFHMDIKVHACIGGTSFVEDAEGLRDAQI
VVGTPGRVFDNIQRRRFRTDKIKMFILDEADEMLSSGFKEQIYQIFTLLPPTTQVVLLSATMPND
VLEVTTKFMRNPVRILV
>d1c4oa1 c.37.1.13 (A:2-409) Nucleotide excision repair enzyme UvrB
{Thermus thermophilus}
TFRYRGPSPKGDQPKAIAGLVEALRDGERFVTLLGATGTGKTVTMAKVIEALGRPALVLAPNKIL
AAQLAAEFRELFPENAVEYFISYYDYYQPEAYVPGKDLYIEKDASINPEIERLRHSTTRSLLTRR
DVIVVASVSAIYGLGDPREYRARNLVVERGKPYPREVLLERLLELGYQRNDIDLSPGRFRAKGEV
LEIFPAYETEPIRVELFGDEVERISQVHPVTGERLRELPGFVLFPATHYLSPEGLEEILKEIEKE
LWERVRYFEERGEVLYAQRLKERTLYDLEMLRVMGTCPGVENYARYFTGKAPGEPPYTLLDYFPE
DFLVFLDESHVTVPQLQGMYRGDYARKKTLVDYGFRLPSALDNRPLRFEEFLERVSQVVFVSATP
GPFELAHSGRVVEQIIRP
>d1c4oa2 c.37.1.13 (A:410-583) Nucleotide excision repair enzyme UvrB
{Thermus thermophilus}
TGLLDPLVRVKPTENQILDLMEGIRERAARGERTLVTVLTVRMAEELTSFLVEHGIRARYLHHEL
DAFKRQALIRDLRLGHYDCLVGINLLREGLDIPEVSLVAILDADKEGFLRSERSLIQTIGRAARN
ARGEVWLYADRVSEAMQRAIEETNRRRALQEAYNLEHGITPETV
>d1d9xa1 c.37.1.13 (A:2-414) Nucleotide excision repair enzyme UvrB
{Bacillus caldotenax}
EGRFQLVAPYEPQGDQPQAIAKLVDGLRRGVKHQTLLGATGTGKTFTISNVIAQVNKPTLVIAHN
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KTLAGQLYSELKEFFPHNAVEYFVSYYDYYQPEAYVPQTDTYIEKDAKINDEIDKLRHSATSALF
ERRDVIIVASVSCIYGLGSPEEYRELVVSLRVGMEIERNALLRRLVDIQYDRNDIDFRGTFRVRG
DVVEIFPASRDEHCIRVEFFGDEIERIRAEVDALTGKVLGEREHVAIFPASHFVTREEKMRLAIQ
NIEQELEERLAELRAQGKLLEAQRLEQRTRYDLEMMREMGFCSGIENYSRHLALRPPGSTPYTLL
DYFPDDFLIIVDESHVTLPQLRGMYNGDRARKQVLVDHGFRLPSALDNRPLTFEEFEQKINQIIY
VSATPGPYELEHSPGVVEQIIRP
>d1d9xa2 c.37.1.13 (A:415-595) Nucleotide excision repair enzyme UvrB {Bacillus caldotenax}
TGLLDPTIDVRPTKGQIDDLIGEIRERVERNERTLVTTLTKKMAEDLTDYLKEAGIKVAYLHSEI
KTLERIEIIRDLRLGKYDVLVGINLLREGLDIPEVSLVAILDADKEGFLRSERSLIQTIGRAARN
ANGHVIMYADTITKSMEIAIQETKRRRAIQEEYNRKHGIVPRTVKKEIRDV
>d1jr3a2 c.37.1.13 (A:3-242) gamma subunit of DNA polymerase III, N-domain {Escherichia coli}
YQVLARKWRPQTFADVVGQEHVLTALANGLSLGRIHHAYLFSGTRGVGKTSIARLLAKGLNCETG
ITATPCGVCDNCREIEQGRFVDLIEIDAASRTKVEDTRDLLDNVQYAPARGRFKVYLIDEVHMLS
RHSFNALLKTLEEPPEHVKFLLATTDPQKLPVTILSRCLQFHLKALDVEQIRHQLEHILNEEHIA
HEPRALQLLARAAEGSLRDALSLTDQAIASGDGQVSTQAVSAMLG
>d1a5t_2 c.37.1.13 (1-207) delta prime subunit of DNA polymerase III, N-domain {Escherichia coli}
MRWYPWLRPDFEKLVASYQAGRGHHALLIQALPGMGDDALIYALSRYLLCQQPQGHKSCGHCRGC
QLMQAGTHPDYYTLAPEKGKNTLGVDAVREVTEKLNEHARLGGAKVVWVTDAALLTDAAANALLK
TLEEPPAETWFFLATREPERLLATLRSRCRLHYLAPPPEQYAVTWLSREVTMSQDALLAALRLSA
GSPGAALALFQG
>d1jqlb_ c.37.1.13 (B:) delta subunit of DNA polymerase III, N-domain {Escherichia coli}
MIRLYPEQLRAQLNEGLRAAYLLLGNDPLLLQESQDAVRQVAAAQGFEEHHTFSIDPNTDWNAIF
SLCQAMSLFASRQTLLLLLPENGPNAAINEQLLTLTGLLHDDLLLIVRGNKLSKAQENAAWFTAL
ANRSVQVTCQ
>d1jr3d2 c.37.1.13 (D:1-211) delta subunit of DNA polymerase III, N-domain {Escherichia coli}
MIRLYPEQLRAQLNEGLRAAYLLLGNDPLLLQESQDAVRQVAAAQGFEEHHTFSIDPNTDWNAIF
SLCQAMSLFASRQTLLLLLPENGPNAAINEQLLTLTGLLHDDLLLIVRGNKLSKAQENAAWFTAL
ANRSVQVTCQTPEQAQLPRWVAARAKQLNLELDDAANQVLCYCYEGNLLALAQALERLSLLWPDG
KLTLPRVEQAVNDAAH
>d1iqpa2 c.37.1.13 (A:2-232) Replication factor C {Archaeon Pyrococcus furiosus}
SEEIREVKVLEKPWVEKYRPQRLDDIVGQEHIVKRLKHYVKTGSMPHLLFAGPPGVGKTTAALAL
ARELFGENWRHNFLELNASDERGINVIREKVKEFARTKPIGGASFKIIFLDEADALTQDAQQALR
RTMEMFSSNVRFILSCNYSSKIIEPIQSRCAIFRFRPLRDEDIAKRLRYIAENEGLELTEEGLQA
ILYIAEGDMRRAINILQAAAALDKKITDENVFMVAS
>d1hqca2 c.37.1.13 (A:5-242) Holliday junction helicase RuvB {Thermus thermophilus}
ALRPKTLDEYIGQERLKQKLRVYLEAAKARKEPLEHLLLFGPPGLGKTTLAHVIAHELGVNLRVT
SGPAIEKPGDLAAILANSLEEGDILFIDEIHRLSRQAEEHLYPAMEDFVMDIVIGQGPAARTIRL

ELPRFTLIGATTRPGLITAPLLSRFGIVEHLEYYTPEELAQGVMRDARLLGVRITEEAALEIGRR
SRGTMRVAKRLFRRVRDFAQVAGEEVITRERALEALAALGLDE
>d1in4a2 c.37.1.13 (A:17-254) Holliday junction helicase RuvB {Thermotoga maritima}
QFLRPKSLDEFIGQENVKKKLSLALEAAKMRGEVLDHVLLAGPPGLGKTTLAHIIASELQTNIHV
TSGPVLVKQGDMAAILTSLERGDVLFIDEIHRLNKAVEELLYSAIEDFQIDIMIGKGPSAKSIRI
DIQPFTLVGATTRSGLLSSPLRSRFGIILELDFYTVKELKEIIKRAASLMDVEIEDAAAEMIAKR
SRGTPRIAIRLTKRVRDMLTVVKADRINTDIVLKTMEVLNIDD
>d1fnna2 c.37.1.13 (A:1-276) CDC6, N-domain {Archaeon Pyrobaculum aerophilum}
AIVVDDSVFSPSYVPKRLPHREQQLQQLDILLGNWLRNPGHHYPRATLLGRPGTGKTVTLRKLWE
LYKDKTTARFVYINGFIYRNFTAIIGEIARSLNIPFPRRGLSRDEFLALLVEHLRERDLYMFLVL
DDAFNLAPDILSTFIRLGQEADKLGAFRIALVIVGHNDAVLNNLDPSTRGIMGKYVIRFSPYTKD
QIFDILLDRAKAGLAEGSYSEDILQMIADITGAQTPLDTNRGDARLAIDILYRSAYAAQQNGRKH
IAPEDVRKSSKEVLFG
>d1d2na_ c.37.1.13 (A:) Hexamerization domain of N-ethylmalemide-sensitive fusion (NSF) protein {Chinese hamster (Cricetulus griseus)}
EDYASYIMNGIIKWGDPVTRVLDDGELLVQQTKNSDRTPLVSVLLEGPPHSGKTALAAKIAEESN
FPFIKICSPDKMIGFSETAKCQAMKKIFDDAYKSQLSCVVVDDIERLLDYVPIGPRFSNLVLQAL
LVLLKKAPPQGRKLLIIGTTSRKDVLQEMEMLNAFSTTIHVPNIATGEQLLEALELLGNFKDKER
TTIAQQVKGKKVWIGIKKLLMLIEMSLQMDPEYRVRKFLALLREEGASPLD
>d1e32a2 c.37.1.13 (A:201-458) Membrane fusion atpase p97, D1 domain {Mouse (Mus musculus)}
VGYDDVGGCRKQLAQIKEMVELPLRHPALFKAIGVKPPRGILLYGPPGTGKTLIARAVANETGAF
FFLINGPEIMSKLAGESESNLRKAFEEAEKNAPAIIFIDELDAIAPKREKTHGEVERRIVSQLLT
LMDGLKQRAHVIVMAATNRPNSIDPALRRFGRFDREVDIGIPDATGRLEILQIHTKNMKLADDVD
LEQVANETHGHVGADLAALCSEAALQAIRKKMDLIDLEDETIDAEVMNSLAVTMDDFRWALSQ
>d1g6oa_ c.37.1.13 (A:) Hexameric traffic ATPase, HP0525 {Helicobacter pylori}
LSAEDKKFLEVERALKEAALNPLRHATEELFGDFLKMENITEICYNGNKVVWVLKNNGEWQPFDV
RDRKAFSLSRLMHFARCCASFKKKTIDNYENPILSSNLANGERVQIVLSPVTVNDETISISIRIP
SKTTYPHSFFEEQGFYNLLDNKEQAISAIKDGIAIGKNVIVCGGTGSGKTTYIKSIMEFIPKEER
IISIEDTEEIVFKHHKNYTQLFFGGNITSADCLKSCLRMRPDRIILGELRSSEAYDFYNVLCSGH
KGTLTTLHAGSSEEAFIRLANMSSSNSAARNIKFESLIEGFKDLIDMIVHINHHKQCDEFYIK
>d1ht1e_ c.37.1.13 (E:) HslU {Escherichia coli}
HSEMTPREIVSELDKHIIGQDNAKRSVAIALRNRWRRMQLNEELRHEVTPKNILMIGPTGVGKTE
IARRLAKLANAPFIKVEATKFTEVGYVGKEVDSIIRDLTDAAVKMVRVQAIEKNRYRAEELAEER
ILDVLIPPAKNNWGQTEQQQEPSAARQAFRKKLREGQLDDKEIEIDLAAAPMGVEIMAPPGMEEM
TSQLQSMFQNLGGQKQKARKLKIKDAMKLLIEEEAAKLVNPEELKQDAIDAVEQHGIVFIDEIDK
ICKRGESSGPDVSREGVQRDLLPLVEGCTVSTKHGMVKTDHILFIASGAFQIAKPSDLIPELQGR
LPIRVELQALTTSDFERILTEPNASITVQYKALMATEGVNIEFTDSGIKRIAEAAWQVNESTENI
GARRLHTVLERLMEEISYDASDLSGQNITIDADYVSKHLDALVADEDLSRFIL
>d1g41a_ c.37.1.13 (A:) HslU {Haemophilus influenzae}

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SEMTPREIVSELDQHIIGQADAKRAVAIALRNRWRRMQLQEPLRHEVTPKNILMIGPTGVGKTEI
ARRLAKLANAPFIKVEATKFTEVGYVGKEVDSIIRDLTDSAMKLVRQQEIAKNRARAEDVAEERI
LDALLPPAKNQWGEVENHDSHSSTRQAFRKKLREGQLDDKEIEIDVSAGVSMGVEIMAPPGMEEM
TNQLQSLFQNLGSDKTKKRKMKIKDALKALIDDEAAKLINPEELKQKAIDAVEQNGIVFIDEIDK
ICKKGEYSGADVSREGVQRDLLPLVEGSTVSTKHGMVKTDHILFIASGAFQVARPSDLIPELQGR
LPIRVELTALSAADFERILTEPHASLTEQYKALMATEGVNIAFTTDAVKKIAEAAFRVNEKTENI
GARRLHTVMERLMDKISFSASDMNGQTVNIDAAYVADALGEVVENEDLSRFIL
>d1g8pa_ c.37.1.13 (A:) ATPase subunit of magnesium chelatase, BchI
{Rhodobacter capsulatus}
RPVFPFSAIVGQEDMKLALLLTAVDPGIGGVLVFGDRGTGKSTAVRALAALLPEIEAVEGCPVSS
PNVEMIPDWATVLSTNVIRKPTPVVDLPLGVSEDRVVGALDIERAISKGEKAFEPGLLARANRGY
LYIDECNLLEDHIVDLLLDVAQSGENVVERDGLSIRHPARFVLVGSGNPEEGDLRPQLLDRFGLS
VEVLSPRDVETRVEVIRRRDTYDADPKAFLEEWRPKDMDIRNQILEARERLPKVEAPNTALYDCA
ALCIALGSDGLRGELTLLRSARALAALEGATAVGRDHLKRVATMALSHRLRRDPLDEAGSTARVA
RTVEETLP
>d1a1va1 c.37.1.14 (A:190-325) HCV helicase domain {Human hepatitis
C virus (HCV), different isolates}
PPAVPQSFQVAHLHAPTGSGKSTKVPAAYAAQGYKVLVLNPSVAATLGFGAYMSKAHGVDPNIRT
GVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSILGIGTVLDQAETAGARLVV
LATATP
>d1a1va2 c.37.1.14 (A:326-624) HCV helicase domain {Human hepatitis
C virus (HCV), different isolates}
PGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIKGGRHLIFCHSKKKCDELAAKLVALGINAVA
YYRGLDVSVIPTSGDVVVVATDALMTGFTGDFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDA
VSRTQRRGRTGRGKPGIYRFVAPGERPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTP
GLPVCQDHLEFWEGVFTGLTHIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCL
IRLKPTLHGPTPLLYRLGAVQNEVTLTHPITKYIMTCMS
>d1cu1a3 c.37.1.14 (A:326-631) HCV helicase domain {Human hepatitis
C virus (HCV), different isolates}
PGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEAIRGGRHLIFCHSKKKCDELAAKLSGLGINAVA
YYRGLDVSVIPTIGDVVVVATDALMTGYTGDFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDA
VSRSQRRGRTGRGRRGIYRFVTPGERPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTP
GLPVCQDHLEFWESVFTGLTHIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCL
IRLKPTLHGPTPLLYRLGAVQNEVTLTHPITKYIMACMSADLEVVT
>d1gkub1 c.37.1.16 (B:1-250) Helicase-like "domain" of reverse gyrase
{Archaeon Archaeoglobus fulgidus}
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAASLCLFPEDFLLKEFVEFFRKCVGEPRAIQKMWA
KRILRKESFAATAPTGVGKTSFGLAMSLFLALKGKRCYVIFPTSLLVIQAAETIRKYAEKAGVGT
ENLIGYYHGRIPKREKENFMQNLRNFKIVITTTQFLSKHYRELGHFDFIFVDDVDAILKASKNVD
KLLHLLGFHYDLKTKSWVGEARGCLMVSTATAKKGKKAELFRQLLNFDIGSSRIT
>d1gkub2 c.37.1.16 (B:251-498) Helicase-like "domain" of reverse
gyrase {Archaeon Archaeoglobus fulgidus}
VRNVEDVAVNDESISTLSSILEKLGTGGIIYARTGEEAEEIYESLKNKFRIGIVTATKKGDYEKF
VEGEIDHLIGTAHYYGTLVRGLDLPERIRFAVFVGCPSFRVTIEDIDSLSPQMVKLLAYLYRNVD
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EIERLLPAVERHIDEVREILKKVMGKERPQAKDVVVREGEVIFPDLRTYIQGSGRTSRLFAGGLT
KGASFLLEDDSELLSAFIERAKLYDIEFKSIDEVDFEKLSRELDESRDRYRRR
>d1gl9b1 c.37.1.16 (B:2-250) Helicase-like "domain" of reverse gyrase {Archaeon Archaeoglobus fulgidus}
IPVVYSNLCPVCGGDLESKEIEKHVCFRKKRSLCLFPEDFLLKEFVEFFRKCVGEPRAIQKMWAK
RILRKESFAATAPTGVGKTSFGLAMSLFLALKGKRCYVIFPTSLLVIQAAETIRKYAEKAGVGTE
NLIGYYHGRIPKREKENFMQNLRNFKIVITTTQFLSKHYRELGHFDFIFVDDVDAILKASKNVDK
LLHLLGFHYDLKTKSWVGEARGCLMVSTATAKKGKKAELFRQLLNFDIGSSRIT
>d1ble__ c.38.1.1 (-) Fructose permease, subunit IIb {Bacillus subtilis}
MNIVLARIDDRFIHGQILTRWIKVHAADRIIVVSDDIAQDEMRKTLILSVAPSNVKASAVSVSKM
AKAFHSPRYEGVTAMLLFENPSDIVSLIEAGVPIKTVNVGGMRFENHRRQITKSVSVTEQDIKAF
ETLSDKGVKLELRQLPSDASEDFVQILRNVT
>d1d0va_ c.39.1.1 (A:) Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) {Salmonella typhimurium}
LHALLRDIPAPDAEAMARTQQHIDGLLKPPGSLGRLETLAVQLAGMPGLNGTPQVGEKAVLVMCA
DHGVWDEGVAVSPKIVTAIQAANMTRGTTGVCVLAAQAGAKVHVIDVGIDAEPIPGVVNMRVARG
CGNIAVGPAMSRLQAEALLLEVSRYACDLAQRGVTLFGVGELGMANTTPAAAMVSVFTGSDAKEV
VGIGANLPPSRIDNKVDVVRRAIAINQPNPRDGIDVLSKVGGFDLVGMTGVMLGAARCGLPVLLD
GFLSYSAALAACQIAPAVRPYLIPSHFSAEKGARIALAHLSMEPYLHMAMRLGEGSGAALAMPIV
EAACAMFHNMGELAASNIVLP
>d1chd__ c.40.1.1 (-) Methylesterase CheB, C-terminal domain {Salmonella typhimurium}
LLSSEKLIAIGASTGGTEAIRHVLQPLPLSSPAVIITQHMPPGFTRSFAERLNKLCQISVKEAED
GERVLPGHAYIAPGDKHMELARSGANYQIKIHDGPPVNRHRPSVDVLFHSVAKHAGRNAVGVILT
GMGNDGAAGMLAMYQAGAWTIAQNEASCVVFGMPREAINMGGVSEVVDLSQVSQQMLAKISAGQA
IRI
>d1csee_ c.41.1.1 (E:) Subtilisin {Bacillus subtilis, carlsberg}
AQTVPYGIPLIKADKVQAQGFKGANVKVAVLDTGIQASHPDLNVVGGASFVAGEAYNTDGNGHGT
HVAGTVAALDNTTGVLGVAPSVSLYAVKVLNSSGSGSYSGIVSGIEWATTNGMDVINMSLGGASG
STAMKQAVDNAYARGVVVVAAAGNSGNSGSTNTIGYPAKYDSVIAVGAVDSNSNRASFSSVGAEL
EVMAPGAGVYSTYPTNTYATLNGTSMASPHVAGAAALILSKHPNLSASQVRNRLSSTATYLGSSF
YYGKGLINVEAAAQ
>d1bh6a_ c.41.1.1 (A:) Subtilisin {Bacillus licheniformis}
AQTVPYGIPLIKADKVQAQGYKGANVKVGIIDTGIASSHTDLKVVGGASFVSGESYNTDGNGHGT
HVAGTVAALDNTTGVLGVAPNVSLYAIKVLNSSGSGSYSAIVSGIEWATQNGLDVINMSLGGPSG
STALKQAVDKAYASGIVVVAAAGNSGNSGSQNTIGYPAKYDSVIAVGAVDSNKNRASFSSVGSEL
EVMAPGVSVYSTYPSNTYTSLNGTSMASPHVAGAAALILSKYPTLSASQVRNRLSSTATNLGDSF
YYGKGLINVEAAAQ
>d1gci__ c.41.1.1 (-) Subtilisin {Bacillus lentus}
AQSVPWGISRVQAPAAHNRGLTGSGVKVAVLDTGISTHPDLNIRGGASFVPGEPSTQDGNGHGTH
VAGTIAALNNSIGVLGVAPSAELYAVKVLGASGSGSVSSIAQGLEWAGNNGMHVANLSLGSPSPS
ATLEQAVNSATSRGVLVVAASGNSGAGSISYPARYANAMAVGATDQNNNRASFSQYGAGLDIVAP
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GVNVQSTYPGSTYASLNGTSMATPHVAGAAALVKQKNPSWSNVQIRNHLKNTATSLGSTNLYGSG
LVNAEAATR
>d1s01__ c.41.1.1 (-) Subtilisin {Bacillus amyloliquefaciens, Novo/BPN'}
AQSVPYGVSQIKAPALHSQGYTGSNVKVAVIDSGIDSSHPDLKVAGGASFVPSETPNFQDDNSHG
THVAGTVAALDNSIGVLGVAPSSALYAVKVLGDAGSGQYSWIINGIEWAIANNMDVINMSLGGPS
GSAALKAAVDKAVASGVVVVAAAGNEGSTGSSSTVGYPGKYPSVIAVGAVDASNQRASFSSVGPE
LDVMAPGVSICSTLPGNKYGAKSGTSMASPHVAGAAALILSKHPNWTNTQVRSSLQNTTTKLGDS
FYYGKGLINVQAAAQ
>d1sue__ c.41.1.1 (-) Subtilisin {Bacillus amyloliquefaciens, Novo/BPN'}
AKCVSYGVSQIKAPALHSQGYTGSNVKVAVIDSGIDSSHPDLNVAGGASFVPSETNPFQDNNSHG
THVAGTVLAVAPSASLYAVKVLGADGSGQYSWIINGIEWAIANNMDVINMSLGGPSGSAALKAAV
DKAVASGVVVVAAAGNEGTSGSSSTVGYPGKYPSVIAVGAVDSSNQRASFSSVGPELDVMAPGVS
ICSTLPGNKYGAKSGTSMASPHVAGAAALILSKHPNWTNTQVRSSLENTTTKLGDSFYYGKGLIN
VEAAAQ
>d1sup__ c.41.1.1 (-) Subtilisin {Bacillus amyloliquefaciens, Novo/BPN'}
AQSVPYGVSQIKAPALHSQGYTGSNVKVAVIDSGIDSSHPDLKVAGGASMVPSETNPFQDNNSHG
THVAGTVAALNNSIGVLGVAPSASLYAVKVLGADGSGQYSWIINGIEWAIANNMDVINMSLGGPS
GSAALKAAVDKAVASGVVVVAAAGNEGTSGSSSTVGYPGKYPSVIAVGAVDSSNQRASFSSVGPE
LDVMAPGVSIQSTLPGNKYGAYNGTSMASPHVAGAAALILSKHPNWTNTQVRSSLENTTTKLGDS
FYYGKGLINVQAAAQ
>d1meea_ c.41.1.1 (A:) Messentericopeptidase {Bacillus mesentericus}
AQSVPYGISQIKAPALHSQGYTGSNVKVAVIDSGIDSSHPDLNVRGGASFVPSETNPYQDGSSHG
THVAGTIAALNNSIGVLGVAPSASLYAVKVLDSTGSGQYSWIINGIEWAISNNMDVINMSLGGPT
GSTALKTVVDKAVSSGIVVAAAAGNEGSSGSTSTVGYPAKYPSTIAVGAVNSANQRASFSSAGSE
LDVMAPGVSIQSTLPGGTYGAYNGTSMATPHVAGAAALILSKHPTWTNAQVRDRLESTATYLGSS
FYYGKGLINVQAAAQ
>d1dbia_ c.41.1.1 (A:) Thermostable serine protease {Bacillus sp., AK.1}
WTPNDTYYQGYQYGPQNTYTDYAWDVTKGSSGQEIAVIDTGVDYTHPDLDGKVIKGYDFVDNDYD
PMDLNNHGTHVAGIAAAETNNATGIAGMAPNTRILAVRALDRNGSGTLSDIADAIIYAADSGAEV
INLSLGCDCHTTTLENAVNYAWNKGSVVVAAAGNNGSSTTFEPASYENVIAVGAVDQYDRLASFS
NYGTWVDVVAPGVDIVSTITGNRYAYMSGTSMASPHVAGLAALLASQGRNNIEIRQAIEQTADKI
SGTGTYFKYGRINSYNAVTY
>d1thm__ c.41.1.1 (-) Thermitase {Thermoactinomyces vulgaris}
YTPNDPYFSSRQYGPQKIQAPQAWDIAEGSGAKIAIVDTGVQSNHPDLAGKVVGGWDFVDNDSTP
QNGNGHGTHCAGIAAAVTNNSTGIAGTAPKASILAVRVLDNSGSGTWTAVANGITYAADQGAKVI
SLSLGGTVGNSGLQQAVNYAWNKGSVVVAAAGNAGNTAPNYPAYYSNAIAVASTDQNDNKSSFST
YGSWVDVAAPGSSIYSTYPTSTYASLSGTSMATPHVAGVAGLLASQGRSASNIRAAIENTADKIS
GTGTYWAKGRVNAYKAVQY
>d1ic6a_ c.41.1.1 (A:) Proteinase K {Fungus (Tritirachium album), strain limber}
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AAQTNAPWGLARISSTSPGTSTYYYDESAGQGSCVYVIDTGIEASHPEFEGRAQMVKTYYYSSRD
GNGHGTHCAGTVGSRTYGVAKKTQLFGVKVLDDNGSGQYSTIIAGMDFVASDKNNRNCPKGVVAS
LSLGGGYSSSVNSAAARLQSSGVMVAVAAGNNNADARNYSPASEPSVCTVGASDRYDRRSSFSNY
GSVLDIFGPGTDILSTWIGGSTRSISGTSMATPHVAGLAAYLMTLGKTTAASACRYIADTANKGD
LSNIPFGTVNLLAYNNYQA
>d1ga6a_ c.41.1.2 (A:) Serine-carboxyl proteinase PSCP {Pseudomonas
sp.}
AGTAKGHNPTEFPTIYDASSAPTAANTTVGIITIGGVSQTLQDLQQFTSANGLASVNTQTIQTGS
SNGDYSDDQQGQGEWDLDSQSIVGSAGGAVQQLLFYMADQSASGNTGLTQAFNQAVSDNVAKVIN
VSLGWCEADANADGTLQAEDRIFATAAAQGQTFSVSSGDEGVYECNNRGYPDGSTYSVSWPASSP
NVIAVGGTTLYTTSAGAYSNETVWNEGLDSNGKLWATGGGYSVYESKPSWQSVVSGTPGRRLLPD
ISFDAAQGTGALIYNYGQLQQIGGTSLASPIFVGLWARLQSANSNSLGFPAASFYSAISSTPSLV
HDVKSGNNGYGGYGYNAGTGWDYPTGWGSLDIAKLSAYIRSNGF
>d1d3va_ c.42.1.1 (A:) Arginase {Rat (Rattus norvegicus)}
KPIEIIGAPFSKGQPRGGVEKGPAALRKAGLVEKLKETEYNVRDHGDLAFVDVPNDSPFQIVKNP
RSVGKANEQLAAVVAETQKNGTISVVLGGDHSMAIGSISGHARVHPDLCVIWVDAHTDINTPLTT
SSGNLHGQPVAFLLKELKGKFPDVPGFSWVTPCISAKDIVYIGLRDVDPGEHYIIKTLGIKYFSM
TEVDKLGIGKVMEETFSYLLGRKKRPIHLSFDVDGLDPVFTPATGTPVVGGLSYREGLYITEEIY
KTGLLSGLDIMEVNPTLGKTPEEVTRTVNTAVALTLSCFGTKREGNHK
>d2ceva_ c.42.1.1 (A:) Arginase {Bacillus caldovelox}
KPISIIGVPMDLGQTRRGVDMGPSAMRYAGVIERLERLHYDIEDLGDIPIGKAERLHEQGDSRLR
NLKAVAEANEKLAAAVDQVVQRGRFPLVLGGDHSIAIGTLAGVAKHYERLGVIWYDAHGDVNTAE
TSPSGNIHGMPLAASLGFGHPALTQIGGYSPKIKPEHVVLIGVRSLDEGEKKFIREKGIKIYTMH
EVDRLGMTRVMEETIAYLKERTDGVHLSLDLDGLDPSDAPGVGTPVIGGLTYRESHLAMEMLAEA
QIITSAEFVEVNPILDERNKTASVAVALMGSLFGEKLM
>d1c3pa_ c.42.1.2 (A:) HDAC homologue {Aquifex aeolicus}
KKVKLIGTLDYGKYRYPKNHPLKIPRVSLLLRFKDAMNLIDEKELIKSRPATKEELLLFHTEDYI
NTLMEAERCQCVPKGAREKYNIGGYENPVSYAMFTGSSLATGSTVQAIEEFLKGNVAFNPAGGMH
HAFKSRANGFCYINNPAVGIEYLRKKGFKRILYIDLDAHHCDGVQEAFYDTDQVFVLSLHQSPEY
AFPFEKGFLEEIGEGKGKGYNLNIPLPKGLNDNEFLFALEKSLEIVKEVFEPEVYLLQLGTDPLL
EDYLSKFNLSNVAFLKAFNIVREVFGEGVYLGGGGYHPYALARAWTLIWCELSGREVPEKLNNKA
KELLKSIDFEEFDDEVDRSYMLETLKDPWRGGEVRKEVKDTLEKAKA
>d1hf2a2 c.102.1.1 (A:1-99) Cell-division inhibitor MinC, N-terminal
domain {Thermotoga maritima}
MVDFKMTKEGLVLLIKDYQNLEEVLNAISARITQMGGFFAKGDRISLMIENHNKHSQDIPRIVSH
LRNLGLEVSQILVGSTVEGKENDLKVQSRTTVES
>d1jkea_ c.110.1.1 (A:) D-Tyr tRNAtyr deacylase {Escherichia coli}
MIALIQRVTRASVTVEGEVTGEIGAGLLVLLGVEKDDDEQKANRLCERVLGYRIFSDAEGKMNLN
VQQAGGSVLVVSQFTLAADTERGMRPSFSKGASPDRAEALYDYFVERCRQQEMNTQTGRFAADMQ
VSLVNDGPVTFWLQV
>d1nocb_ c.43.1.1 (B:) Chloramphenicol acetyltransferase
{Escherichia coli}
ITGYTTVDISQWHRKEHFEAFQSVAQCTYNQTVQLDITAFLKTVKKNKHKFYPAFIHILARLMNA
HPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSSLWSEYHDDFRQFLHIYSQDVACYGENLAYF
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PKGFIENMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGF
HVGRMLNELQQYCDEWQG
>d3cla__ c.43.1.1 (-) Chloramphenicol acetyltransferase {Escherichia coli}
MNYTKFDVKNWVRREHFEFYRHRLPCGFSLTSKIDITTLKKSLDDSAYKFYPVMIYLIAQAVNQF
DELRMAIKDDELIVWDSVDPQFTVFHQETETFSALSCPYSSDIDQFMVNYLSVMERYKSDTKLFP
QGVTPENHLNISALPWVNFDSFNLNVANFTDYFAPIITMAKYQQEGDRLLLPLSVQVHHAVCDGF
HVARFINRLQELCNSKLK
>d1eaf__ c.43.1.1 (-) Dihydrolipoamide acetyltransferase {Azotobacter vinelandii}
IPPIPPVDFAKYGEIEEVPMTRLMQIGATNLHRSWLNVPHVTQFESADITELEAFRVAQKAVAKK
AGVKLTVLPLLLKACAYLLKELPDFNSSLAPSGQALIRKKYVHIGFAVDTPDGLLVPVIRNVDQK
SLLQLAAEAAELAEKARSKKLGADAMQGACFTISSLGHIGGTAFTPIVNAPEVAILGVSKASMQP
VWDGKAFQPRLMLPLSLSYDHRVINGAAAARFTKRLGDLLADIRAILL
>d1b5sa_ c.43.1.1 (A:) Dihydrolipoamide acetyltransferase {Bacillus stearothermophilus}
AAAKPATTEGEFPETREKMSGIRRAIAKAMVHSKHTAPHVTLMDEADVTKLVAHRKKFKAIAAEK
GIKLTFLPYVVKALVSALREYPVLNTSIDDETEEIIQKHYYNIGIAADTDRGLLVPVIKHADRKP
IFALAQEINELAEKARDGKLTPGEMKGASCTITNIGSAGGQWFTPVINHPEVAILGIGRIAEKPI
VRDGEIVAAPMLALSLSFDHRMIDGATAQKALNHIKRLLSDPELLLM
>d1e2o__ c.43.1.1 (-) Dihydrolipoamide succinyltransferase {Escherichia coli}
ARSEKRVPMTRLRKRVAERLLEAKNSTAMLTTFNEVNMKPIMDLRKQYGEAFEKRHGIRLGFMSF
YVKAVVEALKRYPEVNASIDGDDVVYHNYFDVSMAVSTPRGLVTPVLRDVDTLGMADIEKKIKEL
AVKGRDGKLTVEDLTGGNFTITNGGVFGSLMSTPIINPPQSAILGMHAIKDRPMAVNGQVEILPM
MYLALSYDHRLIDGRESVGFLVTIKELLEDPTRLLLDV
>d1phr__ c.44.1.1 (-) Tyrosine phosphatase {Cow (Bos taurus)}
VTKSVLFVCLGNICRSPIAEAVFRKLVTDQNISDNWVIDSGAVSDWNVGRSPDPRAVSCLRNHGI
NTAHKARQVTKEDFVTFDYILCMDESNLRDLNRKSNQVKNCRAKIELLGSYDPQKQLIIEDPYYG
NDADFETVYQQCVRCCRAFLEKVR
>d5pnt__ c.44.1.1 (-) Tyrosine phosphatase {Human (Homo sapiens)}
AEQATKSVLFVCLGNICRSPIAEAVFRKLVTDQNISENWRVDSAATSGYEIGNPPDYRGQSCMKR
HGIPMSHVARQITKEDFATFDYILCMDESNLRDLNRKSNQVKTCKAKIELLGSYDPQKQLIIEDP
YYGNDSDFETVYQQCVRCCRAFLEKAH
>d1d1qa_ c.44.1.1 (A:) Tyrosine phosphatase {Baker's yeast (Saccharomyces cerevisiae)}
IEKPKISVAFIALGNFCRSPMAEAIFKHEVEKANLENRFNKIDSFGTSNYHVGESPDHRTVSICK
QHGVKINHKGKQIKTKHFDEYDYIIGMDESNINNLKKIQPEGSKAKVCLFGDWNTNDGTVQTIIE
DPWYGDIQDFEYNFKQITYFSKQFLKKEL
>d1jf8a_ c.44.1.1 (A:) Arsenate reductase ArsC {Staphylococcus aureus}
DKKTIYFISTGNSARSQMAEGWGKEILGEGWNVYSAGIETHGVNPKAIEAMKEVDIDISNHTSDL
IDNDILKQSDLVVTLCSDADNNCPILPPNVKKEHWGFDDPAGKEWSEFQRVRDEIKLAIEKFKLR
>d1jl3a_ c.44.1.1 (A:) Arsenate reductase ArsC {Bacillus subtilis}
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NKIIYFLCTGNSCRSQMAEGWAKQYLGDEWKVYSAGIEAHGLNPNAVKAMKEVGIDISNQTSDII
DSDILNNADLVVTLCGDAADKCPMTPPHVKREHWGFDDPARAQGTEEEKWAFFQRVRDEIGNRLK
EFAETGK
>d1iiba_ c.44.2.1 (A:) Enzyme IIB-cellobiose {Escherichia coli}
KKHIYLFSSAGMSTSLLVSKMRAQAEKYEVPVIIEAFPETLAGEKGQNADVVLLGPQIAYMLPEI
QRLLPNKPVEVIDSLLYGKVDGLGVLKAAVAAIKKAAA
>d1vhra_ c.45.1.1 (A:) VH1-related dual-specificity phosphatase, VHR
{Human (Homo sapiens)}
SVQDLNDLLSDGSGCYSLPSQPCNEVTPRIYVGNASVAQDIPKLQKLGITHVLNAAEGRSFMHVN
TNANFYKDSGITYLGIKANDTQEFNLSAYFERAADFIDQALAQKNGRVLVHCREGYSRSPTLVIA
YLMMRQKMDVKSALSIVRQNREIGPNDGFLAQLCQLNDRLAKEGKLKP
>d1mkp__ c.45.1.1 (-) Mapk phosphatase Pyst1 (mkp3) {Human (Homo
sapiens)}
ASFPVEILPFLYLGCAKDSTNLDVLEEFGIKYILNVTPNLPNLFENAGEFKYKQIPISDHWSQNL
SQFFPEAISFIDEARGKNCGVLVHSLAGISRSVTVTVAYLMQKLNLSMNDAYDIVKMKKSNISPN
FNFMGQLLDFERTL
>d1d5ra2 c.45.1.1 (A:14-187) Phoshphoinositide phosphatase Pten (Pten
tumor suppressor), N-terminal domain {Human (Homo sapiens)}
RRYQEDGFDLDLTYIYPNIIAMGFPAERLEGVYRNNIDDVVRFLDSKHKNHYKIYNLCAERHYDT
AKFNCRVAQYPFEDHNPPQLELIKPFCEDLDQWLSEDDNHVAAIHCKAGKGRTGVMICAYLLHRG
KFLKAQEALDFYGEVRTRDKKGVTIPSQRRYVYYYSYLLKNHLD
>d1i9sa_ c.45.1.1 (A:) mRNA capping enzyme, triphosphatase domain
{Mouse (Mus musculus)}
KIPPRWLNCPRRGQPVAGRFLPLKTMLGPRYDSQVAEENRFHPSMLSNYLKSLKVKMSLLVDLTN
TSRFYDRNDIEKEGIKYIKLQCKGHGECPTTENTETFIRLCERFNERSPPELIGVHCTHGFNRTG
FLICAFLVEKMDWSIEAAVATFAQARPPGIYKGDYLKELFRRYGDIEEAPPPPVLPDWCFEDED
>d1fpza_ c.45.1.1 (A:) Kinase associated phosphatase (kap) {Human
(Homo sapiens)}
TPIHISWLSLSRVNCSQFLGLCALPGCKFKDVRRNVQKDTEELKSCGIQDIFVFCTRGELSKYRV
PNLLDLYQQCGIITHHHPIADGGTPDIASCCEIMEELTTCLKNYRKTLIHSYGGLGRSCLVAACL
LLYLSDTISPEQAIDSLRDLRGSGAIQTIKQYNYLHEFRDKLAAHL
>d1eeoa_ c.45.1.2 (A:) Tyrosine phosphatase {Human (Homo sapiens),
1B}
EMEKEFEQIDKSGSWAAIYQDIRHEASDFPCRVAKLPKNKNRNRYRDVSPFDHSRIKLHQEDNDY
INASLIKMEEAQRSYILTQGPLPNTCGHFWEMVWEQKSRGVVMLNRVMEKGSLKCAQYWPQKEEK
EMIFEDTNLKLTLISEDIKSYYTVRQLELENLTTQETREILHFHYTTWPDFGVPESPASFLNFLF
KVRESGSLSPEHGPVVVHSSAGIGRSGTFCLADTCLLLMDKRKDPSSVDIKKVLLEMRKFRMGLI
QTADQLRFSYLAVIEGAKFIMGDSSVQDQWKELSHED
>d1rpma_ c.45.1.2 (A:) Tyrosine phosphatase {Human (Homo sapiens),
mu}
AIRVADLLQHITQMKCAEGYGFKEEYESFFEGQSAPWDSAKKDENRMKNRYGNIIAYDHSRVRLQ
TIEGDTNSDYINGNYIDGYHRPNHYIATQGPMQETIYDFWRMVWHENTASIIMVTNLVEVGRVKC
CKYWPDDTEIYKDIKVTLIETELLAEYVIRTFAVEKRGVHEIREIRQFHFTGWPDHGVPYHATGL
LGFVRQVKSKSPPSAGPLVVHCSAGAGRTGCFIVIDIMLDMAEREGVVDIYNCVRELRSRRVNMV
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QTEEQYVFIHDAILEACL
>d1yfoa_ c.45.1.2 (A:) Tyrosine phosphatase {Mouse (Mus musculus)}
KYPPLPVDKLEEEINRRMADDNKLFREEFNALPACPIQATCEAASKEENKEKNRYVNILPYDHSR
VHLTPVEGVPDSDYINASFINGYQEKNKFIAAQGPKEETVNDFWRMIWEQNTATIVMVTNLKERK
ECKCAQYWPDQGCWTYGNVRVSVEDVTVLVDYTVRKFCIQQVGDVTNRKPQRLITQFHFTSWPDF
GVPFTPIGMLKFLKKVKACNPQYAGAIVVHCSAGVGRTGTFVVIDAMLDMMHSERKVDVYGFVSR
IRAQRCQMVQTDMQYVFIYQALLEHYLY
>d2shpa1 c.45.1.2 (A:219-525) Tyrosine phosphatase {Human (Homo sapiens), shp-2}
TRINAAEIESRVRELSKLAETTDKVKQGFWEEFETLQQQECKLLYSRKEGQRQENKNKNRYKNIL
PFDHTRVVLHDGDPNEPVSDYINANIIMPEFETKCNNSKPKKSYIATQGCLQNTVNDFWRMVFQE
NSRVIVMTTKEVERGKSKCVKYWPDEYALKEYGVMRVRNVKESAAHDYTLRELKLSKVGQGNTER
TVWQYHFRTWPDHGVPSDPGGVLDFLEEVHHKQESIMDAGPVVVHCSAGIGRTGTFIVIDILIDI
IREKGVDCDIDVPKTIQMVRSQRSGMVQTEAQYRSIYMAVQHYIETL
>d1fpra_ c.45.1.2 (A:) Tyrosine phosphatase {Human (Homo sapiens), shp-1}
GFWEEFESLQKQEVKNLHQRLEGQRPENKGKNRYKNILPFDHSRVILQGRDSNIPGSDYINANYI
KNQLLGPDENAKTYIASQGCLEATVNDFWQMAWQENSRVIVMTTREVEKGRNKCVPYWPEVGMQR
AYGPYSVTNCGEHDTTEYKLRTLQVSPLDNGDLIREIWHYQYLSWPDHGVPSEPGGVLSFLDQIN
QRQESLPHAGPIIVHSSAGIGRTGTIIVIDMLMENISTKGLDCDIDIQKTIQMVRAQRSGMVQTE
AQYKFIYVAIAQFIETTKKKLEVL
>d1jlna_ c.45.1.2 (A:) Tyrosine phosphatase {Mouse (Mus musculus), ptp-sl/br7}
GSPREKVAMEYLQSASRVLTRSQLRDVVASSHLLQSEFMEIPMNFVDPKEIDIPRHGTKNRYKTI
LPNPLSRVCLRPKNITDSLSTYINANYIRGYSGKEKAFIATQGPMINTVNDFWQMVWQEDSPVIV
MITKLKEKNEKCVLYWPEKRGIYGKVEVLVTGVTECDNYTIRNLVLKQGSHTQHVKHYWYTSWPD
HKTPDSAQPLLQLMLDVEEDRLASEGRGPVVVHCSAGIGRTGCFIATSIGCQQLKEEGVVDALSI
VCQLRVDRGGMVQTSEQYEFVHHALCLFESRLSPETV
>d1ypta_ c.45.1.2 (A:) Tyrosine phosphatase {Yersinia enterocolitica}
PEARAELSSRLTTLRNTLAPATNDPRYLQACGGEKLNRFRDIQCRRQTAVRADLNANYIQVGNTR
TIACQYPLQSQLESHFRMLAENRTPVLAVLASSSEIANQRFGMPDYFRQSGTYGSITVESKMTQQ
VGLGDGIMADMYTLTIREAGQKTISVPVVHVGNWPDQTAVSSEVTKALASLVDQTAETKRNMYES
KGSSAVADDSKLRPVIHCRAGVGRTAQLIGAMCMNDSRNSQLSVEDMVSQMRVQRNGIMVQKDEQ
LDVLIKLAEGQGRPLLNS
>d1g4us2 c.45.1.2 (S:297-539) SptP tyrosine phosphatase, catalytic domain {Salmonella typhimurium}
PQTMSGPTLGLARFAVSSIPINQQTQVKLSDGMPVPVNTLTFDGKPVALAGSYPKNTPDALEAHM
KMLLEKECSCLVVLTSEDQMQAKQLPPYFRGSYTFGEVHTNSQKVSSASQGEAIDQYNMQLSCGE
KRYTIPVLHVKNWPDHQPLPSTDQLEYLADRVKNSNQNGAPGRSSSDKHLPMIHCLGGVGRTGTM
AAALVLKDNPHSNLEQVRADFRDSRNNRMLEDASQFVQLKAMQAQLLM
>d1lara1 c.45.1.2 (A:1307-1623) RPTP Lar {Human (Homo sapiens)}
MITDLADNIERLKANDGLKFSQEYESIDPGQQFTWENSNLEVNKPKNRYANVIAYDHSRVILTSI
DGVPGSDYINANYIDGYRKQNAYIATQGPLPETMGDFWRMVWEQRTATVVMMTRLEEKSRVKCDQ
YWPARGTETCGLIQVTLLDTVELATYTVRTFALHKSGSSEKRELRQFQFMAWPDHGVPEYPTPIL
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AFLRRVKACNPLDAGPMVVHCSAGVGRTGCFIVIDAMLERMKHEKTVDIYGHVTCMRSQRNYMVQ
TEDQYVFIHEALLEAATCGHTEVPARNLYAHIQKLGQVPPGESVTAMELEFKLLASS
>d1lara2 c.45.1.2 (A:1628-1876) RPTP Lar {Human (Homo sapiens)}
SRFISANLPCNKFKNRLVNIMPYELTRVCLQPIRGVEGSDYINASFLDGYRQQKAYIATQGPLAE
STEDFWRMLWEHNSTIIVMLTKLREMGREKCHQYWPAERSARYQYFVVDPMAEYNMPQYILREFK
VTDARDGQSRTIRQFQFTDWPEQGVPKTGEGFIDFIGQVHKTKEQFGQDGPITVHCSAGVGRTGV
FITLSIVLERMRYEGVVDMFQTVKTLRTQRPAMVQTEDQYQLCYRAALEYLGSF
>d1larb1 c.45.1.2 (B:1340-1623) RPTP Lar {Human (Homo sapiens)}
TWENSNLEVNKPKNRYANVIAYDHSRVILTSIDGVPGSDYINANYIDGYRKQNAYIATQGPLPET
MGDFWRMVWEQRTATVVMMTRLEEKSRVKCDQYWPARGTETCGLIQVTLLDTVELATYTVRTFAL
HKSGSSEKRELRQFQFMAWPDHGVPEYPTPILAFLRRVKACNPLDAGPMVVHCSAGVGRTGCFIV
IDAMLERMKHEKTVDIYGHVTCMRSQRNYMVQTEDQYVFIHEALLEAATCGHTEVPARNLYAHIQ
KLGQVPPGESVTAMELEFKLLASS
>d1c25__ c.46.1.1 (-) CDC25a {Human (Homo sapiens)}
MLIGDFSKGYLFHTVAGKHQDLKYISPEIMASVLNGKFANLIKEFVIIDCRYPYEYEGGHIKGAV
NLHMEEEVEDFLLKKPIVPTDGKRVIVVFHCEFSSERGPRMCRYVRERDRLGNEYPKLHYPELYV
LKGGYKEFFMKCQSYCEPPSYRPMHHEDFKE
>d1qb0a_ c.46.1.1 (A:) CDC25b {Human (Homo sapiens)}
DHRELIGDYSKAFLLQTVDGKHQDLKYISPETMVALLTGKFSNIVDKFVIVDCRYPYEYEGGHIK
TAVNLPLERDAESFLLKSPIAPCSLDKRVILIFHCEFSSERGPRMCRFIRERDRAVNDYPSLYYP
EMYILKGGYKEFFPQHPNFCEPQDYRPMNHEAFKDELKTFRLKTRSWA
>d1hzma_ c.46.1.1 (A:) Erk2 binding domain of Mapk phosphatase mkp-3
{Human (Homo sapiens)}
MIDTLRPVPFASEMAISKTVAWLNEQLELGNERLLLMDCRPQELYESSHIESAINVAIPGIMLRR
LQKGNLPVRALFTRGEDRDRFTRRCGTDTVVLYDESSSDWNENTGGESLLGLLLKKLKDEGCRAF
YLEGGFSKFQAEFSLHCETNLDGS
>d1gmxa_ c.46.1.3 (A:) Sulfurtransferase GlpE {Escherichia coli}
MDQFECINVADAHQKLQEKEAVLVDIRDPQSFAMGHAVQAFHLTNDTLGAFMRDNDFDTPVMVMC
YHGNSSKGAAQYLLQQGYDVVYSIDGGFEAWQRQFPAEVAYGA
>d1rhs_1 c.46.1.2 (1-149) Rhodanese {Cow (Bos taurus)}
VHQVLYRALVSTKWLAESVRAGKVGPGLRVLDASWYSPGTREARKEYLERHVPGASFFDIEECRD
KASPYEVMLPSEAGFADYVGSLGISNDTHVVVYDGDDLGSFYAPRVWWMFRVFGHRTVSVLNGGF
RNWLKEGHPVTSEPSRPEP
>d1rhs_2 c.46.1.2 (150-293) Rhodanese {Cow (Bos taurus)}
AIFKATLNRSLLKTYEQVLENLESKRFQLVDSRAQGRYLGTQPEPDAVGLDSGHIRGSVNMPFMN
FLTEDGFEKSPEELRAMFEAKKVDLTKPLIATCRKGVTACHIALAAYLCGKPDVAIYDGSWFEWF
HRAPPETWVSQGKG
>d1e0ca1 c.46.1.2 (A:1-135) Sulfurtransferase {Azotobacter
vinelandii}
MDDFASLPLVIEPADLQARLSAPELILVDLTSAARYAEGHIPGARFVDPKRTQLGQPPAPGLQPP
REQLESLFGELGHRPEAVYVVYDDEGGGWAGRFIWLLDVIGQQRYHYLNGGLTAWLAEDRPLSRE
LPAPA
>d1e0ca2 c.46.1.2 (A:136-271) Sulfurtransferase {Azotobacter
vinelandii}
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GGPVALSLHDEPTASRDYLLGRLGAADLAIWDARSPQEYRGEKVLAAKGGHIPGAVNFEWTAAMD
PSRALRIRTDIAGRLEELGITPDKEIVTHCQTHHRSGLTYLIAKALGYPRVKGYAGSWGEWGNHP
DTPVEL
>d2trxa_ c.47.1.1 (A:) Thioredoxin {Escherichia coli}
SDKIIHLTDDSFDTDVLKADGAILVDFWAEWCGPCKMIAPILDEIADEYQGKLTVAKLNIDQNPG
TAPKYGIRGIPTLLLFKNGEVAATKVGALSKGQLKEFLDANLA
>d1thx__ c.47.1.1 (-) Thioredoxin {Anabaena sp., pcc 7120}
SKGVITITDAEFESEVLKAEQPVLVYFWASWCGPCQLMSPLINLAANTYSDRLKVVKLEIDPNPT
TVKKYKVEGVPALRLVKGEQILDSTEGVISKDKLLSFLDTHLN
>d1dbya_ c.47.1.1 (A:) Thioredoxin {Chlamydomonas reinhardtii}
MEAGAVNDDTFKNVVLESSVPVLVDFWAPWCGPCRIIAPVVDEIAGEYKDKLKCVKLNTDESPNV
ASEYGIRSIPTIMVFKGGKKCETIIGAVPKATIVQTVEKYLN
>d1ep7a_ c.47.1.1 (A:) Thioredoxin {Chlamydomonas reinhardtii}
GGSVIVIDSKAAWDAQLAKGKEEHKPIVVDFTATWCGPCKMIAPLFETLSNDYAGKVIFLKVDVD
AVAAVAEAAGITAMPTFHVYKDGVKADDLVGASQDKLKALVAKHAAA
>d1quwa_ c.47.1.1 (A:) Thioredoxin {Bacillus acidocaldarius}
ATMTLTDANFQQAIQGDKPVLVDFWAAWCGPCRMMAPVLEEFAEAHADKVTVAKLNVDENPETTS
QFGIMSIPTLILFKGGRPVKQLIGYQPKEQLEAQLADVLQ
>d1f9ma_ c.47.1.1 (A:) Thioredoxin {Spinach (Spinacia oleracea), thioredoxin F}
MEAIVGKVTEVNKDTFWPIVKAAGDKPVVLDMFTQWCGPCKAMAPKYEKLAEEYLDVIFLKLDCN
QENKTLAKELGIRVVPTFKILKENSVVGEVTGAKYDKLLEAIQAARS
>d1fb6a_ c.47.1.1 (A:) Thioredoxin {Spinach (Spinacia oleracea), thioredoxin M}
VQDVNDSSWKEFVLESEVPVMVDFWAPWCGPCKLIAPVIDELAKEYSGKIAVYKLNTDEAPGIAT
QYNIRSIPTVLFFKNGERKESIIGAVPKSTLTDSIEKYL
>d1erv__ c.47.1.1 (-) Thioredoxin {Human (Homo sapiens)}
MVKQIESKTAFQEALDAAGDKLVVVDFSATWCGPCKMIKPFFHSLSEKYSNVIFLEVDVDDCQDV
ASECEVKSMPTFQFFKKGQKVGEFSGANKEKLEATINELV
>d1aba__ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Bacteriophage T4}
MFKVYGYDSNIHKCGPCDNAKRLLTVKKQPFEFINIMPEKGVFDDEKIAELLTKLGRDTQIGLTM
PQVFAPDGSHIGGFDQLREYFK
>d1qfna_ c.47.1.1 (A:) Glutaredoxin (Thioltransferase) {Escherichia coli}
MQTVIFGRSGCPYSVRAKDLAEKLSNERDDFQYQYVDIRAEGITKEDLQQKAGKPVETVPQIFVD
QQHIGGYTDFAAWVKENLDA
>d3grx__ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Escherichia coli, GRX3}
ANVEIYTKETCPYSHRAKALLSSKGVSFQELPIDGNAAKREEMIKRSGRTTVPQIFIDAQHIGGY
DDLYALDARGGLDPLLK
>d1kte__ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Pig (Sus scrofa)}
AQAFVNSKIQPGKVVVFIKPTCPFCRKTQELLSQLPFKEGLLEFVDITATSDTNEIQDYLQQLTG
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ARTVPRVFIGKECIGGCTDLESMHKRGELLTRLQQVGAVK
>d1jhb__ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Human (Homo sapiens)}
AQEFVNCKIQPGKVVVFIKPTCPYCRRAQEILSQLPIKQGLLEFVDITATNHTNEIQDYLQQLTG
ARTVPRVFIGKDCIGGCSDLVSLQQSGELLTRLKQIGALQ
>d1h75a_ c.47.1.1 (A:) Glutaredoxin-like NRDH-redoxin {Escherichia coli}
MRITIYTRNDCVQCHATKRAMENRGFDFEMINVDRVPEAAEALRAQGFRQLPVVIAGDLSWSGFR
PDMINRLHPAP
>d1fo5a_ c.47.1.1 (A:) MJ0307, thioredoxin/glutaredoxin-like protein {Archaeon Methanococcus jannaschii}
MSKVKIELFTSPMCPHCPAAKRVVEEVANEMPDAVEVEYINVMENPQKAMEYGIMAVPTIVINGD
VEFIGAPTKEALVEAIKKRL
>d1iloa_ c.47.1.1 (A:) MTH985, a thioredoxin {Archaeon Methanobacterium thermoautotrophicum}
MMKIQIYGTGCANCQMLEKNAREAVKELGIDAEFEKIKEMDQILEAGLTALPGLAVDGELKIMGR
VASKEEIKKILS
>d1gh2a_ c.47.1.1 (A:) Thioredoxin-like protein, N-terminal domain {Human (Homo sapiens)}
VGVKPVGSDPDFQPELSGAGSRLAVVKFTMRGCGPCLRIAPAFSSMSNKYPQAVFLEVDVHQCQG
TAATNNISATPTFQFFRNKVRIDQYQGADAVGLEEKIKQHLE
>d1bjx__ c.47.1.2 (-) Protein disulfide isomerase, PDI {Human (Homo sapiens)}
AATTLPDGAAAESLVESSEVAVIGFFKDVESDSAKQFLQAAEAIDDIPFGITSNSDVFSKYQLDK
DGVVLFKKFDEGRNNFEGEVTKENLLDFIKHNQLPLVIEFTEQTA
>d1mek__ c.47.1.2 (-) Protein disulfide isomerase, PDI {Human (Homo sapiens)}
DAPEEEDHVLVLRKSNFAEALAAHKYLLVEFYAPWCGHCKALAPEYAKAAGKLKAEGSEIRLAKV
DATEESDLAQQYGVRGYPTIKFFRNGDTASPKEYTAGREADDIVNWLKKRTGPAA
>d1a8l_1 c.47.1.2 (1-119) Protein disulfide isomerase, PDI {Archaeon Pyrococcus furiosus}
MGLISDADKKVIKEEFFSKMVNPVKLIVFVRKDHCQYCDQLKQLVQELSELTDKLSYEIVDFDTP
EGKELAKRYRIDRAPATTITQDGKDFGVRYFGLPAGHEFAAFLEDIVDVSREET
>d1a8l_2 c.47.1.2 (120-226) Protein disulfide isomerase, PDI {Archaeon Pyrococcus furiosus}
NLMDETKQAIRNIDQDVRILVFVTPTCPYCPLAVRMAHKFAIENTKAGKGKILGDMVEAIEYPEW
ADQYNVMAVPKIVIQVNGEDRVEFEGAYPEKMFLEKLLSALS
>d1hyua3 c.47.1.2 (A:1-102) Alkyl hydroperoxide reductase subunit F (AhpF), N-terminal domain {Salmonella typhimurium}
MLDTNMKTQLRAYLEKLTKPVELIATLDDSAKSAEIKELLAEIAELSDKVTFKEDNTLPVRKPSF
LITNPGSQQGPRFAGSPLGHEFTSLVLALLWTGGHPS
>d1hyua4 c.47.1.2 (A:103-198) Alkyl hydroperoxide reductase subunit F (AhpF), N-terminal domain {Salmonella typhimurium}
KEAQSLLEQIRDIDGDFEFETYYSLSCHNCPDVVQALNLMAVLNPRIKHTAIDGGTFQNEITERN

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VMGVPAVFVNGKEFGQGRMTLTEIVAKVDTG
>d1a8y_1 c.47.1.3 (3-126) Calsequestrin {Rabbit (Oryctolagus cuniculus)}
GLDFPEYDGVDRVINVNAKNYKNVFKKYEVLALLYHEPPEDDKASQRQFEMEELILELAAQVLED
KGVGFGLVDSEKDAAVAKKLGLTEEDSIYVFKEDEVIEYDGEFSADTLVEFLLDVLEDP
>d1a8y_2 c.47.1.3 (127-228) Calsequestrin {Rabbit (Oryctolagus cuniculus)}
VELIEGERELQAFENIEDEIKLIGYFKNKDSEHYKAFKEAAEEFHPYIPFFATFDSKVAKKLTLK
LNEIDFYEAFMEEPVTIPDKPNSEEEIVNFVEEHRRS
>d1a8y_3 c.47.1.3 (229-347) Calsequestrin {Rabbit (Oryctolagus cuniculus)}
TLRKLKPESMYETWEDDMDGIHIVAFAEEADPDGYEFLEILKSVAQDNTDNPDLSIIWIDPDDFP
LLVPYWEKTFDIDLSAPQIGVVNVTDADSVWMEMDDEEDLPSAEELEDWLEDVL
>d1fvka2 c.47.1.4 (A:1-64,A:129-188) Disulphide-bond formation facilitator (DSBA) {Escherichia coli}
AQYEDGKQYTTLEKPVAGAPQVLEFFSFFCPHCYQFEEVLHISDNVKKKLPEGVKMTKYHVNFMX
FVVKSLVAQQEKAAADVQLRGVPAMFVNGKYQLNPQGMDTSNMDVFVQQYADTVKYLSEK
>d1bed_2 c.47.1.4 (1-62,127-181) Disulphide-bond formation facilitator (DSBA) {Vibrio cholerae}
AQFKEGEHYQVLKTPASSSPVVSEFFSFYCPHCNTFEPIIAQLKQQLPEGAKFQKNHVSFMGXFA
VDSMVRRFDKQFQDSGLTGVPAVVVNNRYLVQGQSVKSLDEYFDLVNYLLTLK
>d1aqwa2 c.47.1.5 (A:1-76) Glutathione S-transferase {Human (Homo sapiens), class pi}
PPYTVVYFPVRGRCAALRMLLADQGQSWKEEVVTVETWQEGSLKASCLYGQLPKFQDGDLTLYQS
NTILRHLGRTL
>d2gsra2 c.47.1.5 (A:1-76) Glutathione S-transferase {Pig (Sus scrofa), class pi}
PPYTITYFPVRGRCEAMRMLLADQDQSWKEEVVTMETWPPLKPSCLFRQLPKFQDGDLTLYQSNA
ILRHLGRSFGL
>d1glqa2 c.47.1.5 (A:1-78) Glutathione S-transferase {Mouse (Mus musculus), class pi}
PPYTIVYFPVRGRCEAMRMLLADQGQSWKEEVVTIDTWMQGLLKPTCLYGQLPKFEDGDLTLYQS
NAILRHLGRSLGL
>d1gtua2 c.47.1.5 (A:1-84) Glutathione S-transferase {Human (Homo sapiens), class mu}
PMILGYWDIRGLAHAIRLLLEYTDSSYEEKKYTMGDAPDYDRSQWLNEKFKLGLDFPNLPYLIDG
AHKITQSNAILCYIARKHN
>d1hna_2 c.47.1.5 (1-84) Glutathione S-transferase {Human (Homo sapiens), class mu}
PMTLGYWNIRGLAHSIRLLLEYTDSSYEEKKYTMGDAPDYDRSQWLNEKFKLGLDFPNLPYLIDG
THKITQSNAILRYIARKHN
>d3gtub2 c.47.1.5 (B:1-84) Glutathione S-transferase {Human (Homo sapiens), class mu}
SCESSMVLGYWDIRGLAHAIRLLLEFTDTSYEEKRYTCGEAPDYDRSQWLDVKFKLDLDFPNLPY
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LLDGKNKITQSNAILRYIA
>d2gsta2 c.47.1.5 (A:1-84) Glutathione S-transferase {Rat (Rattus
norvegicus), class mu}
PMILGYWNVRGLTHPIRLLLEYTDSSYEEKRYAMGDAPDYDRSQWLNEKFKLGLDFPNLPYLIDG
SRKITQSNAIMRYLARKHH
>d1gsua2 c.47.1.5 (A:1-84) Glutathione S-transferase {Chicken (Gallus
gallus), class mu}
VVTLGYWDIRGLAHAIRLLLEYTETPYQERRYKAGPAPDFDPSDWTNEKEKLGLDFPNLPYLIDG
DVKLTQSNAILRYIARKHN
>d1gsea2 c.47.1.5 (A:2-80) Glutathione S-transferase {Human (Homo
sapiens), class alpha (a1-1)}
AEKPKLHYFNARGKMESTRWLLAAAGVEFEEKFIKSAEDLDKLRNDGYLMFQQVPMVEIDGMKLV
QTRAILNYIASKYN
>d1gula2 c.47.1.5 (A:4-80) Glutathione S-transferase {Human (Homo
sapiens), class alpha (a1-1)}
RPKLHYPNGRGRMESVRWVLAAAGVEFDEEFLETKEQLYKLQDGNHLLFQQVPMVEIDGMKLVQT
RSILHYIADKHN
>d1f3aa2 c.47.1.5 (A:1-79) Glutathione S-transferase {Mouse (Mus
musculus), class alpha (a1-1)}
AGKPVLHYFNARGRMECIRWLLAAAGVEFEEKFIQSPEDLEKLKKDGNLMFDQVPMVEIDGMKLA
QTRAILNYIATKYD
>d1b48a2 c.47.1.5 (A:2-79) Glutathione S-transferase {Mouse (Mus
musculus), class alpha (a1-4)}
AAKPKLYYFNGRGRMESIRWLLAAAGVEFEEEFLETREQYEKMQKDGHLLFGQVPLVEIDGMMLT
QTRAILSYLAAKY
>d1ljra2 c.47.1.5 (A:1-79) Glutathione S-transferase {Human (Homo
sapiens), class theta}
MGLELFLDLVSQPSRAVYIFAKKNGIPLELRTVDLVKGQHKSKEFLQINSLGKLPTLKDGDFILT
ESSAILIYLSCKYQ
>d1pd212 c.47.1.5 (1:1-75) Glutathione S-transferase {Rat (Rattus
norvegicus), class sigma}
MPNYKLLYFNMRGRAEIIRYIFAYLDIKYEDHRIEQADWPKIKPTLPFGKIPVLEVEGLTLHQSL
AIARYLTKNT
>d2gsq_2 c.47.1.5 (1-75) Glutathione S-transferase {Squid
(Ommastrephes sloani pacificus), class sigma}
PKYTLHYFPLMGRAELCRFVLAAHGEEFTDRVVEMADWPNLKATMYSNAMPVLDIDGTKMSQSMC
IARHLAREFG
>d1eema2 c.47.1.5 (A:5-102) Glutathione S-transferase {Human (Homo
sapiens), class omega}
SARSLGKGSAPPGPVPEGSIRIYSMRFCPFAERTRLVLKAKGIRHEVININLKNKPEWFFKKNPF
GLVPVLENSQGQLIYESAITCEYLDEAYPGKKL
>d1fw1a2 c.47.1.5 (A:5-87) Glutathione S-transferase {Human (Homo
sapiens), class zeta}
KPILYSYFRSSCSWRVRIALALKGIDYKTVPINLIKDGGQQFSKDFQALNPMKQVPTLKIDGITI
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HQSLAIIEYLEETRPTPR
>d1duga2 c.47.1.5 (A:1-80) Glutathione S-transferase {Schistosoma japonicum}
SPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLT
QSMAIIRYIADKHNM
>d1fhe_2 c.47.1.5 (1-80) Glutathione S-transferase {Fasciola hepatica}
PAKLGYWKLRGLAQPVRLFLEYLGEEYEEHLYGRDDREKWMSEKFNMGLDLPNLPYYIDDKCKLT
QSVAIMRYIADKHGM
>d2fhea2 c.47.1.5 (A:1-80) Glutathione S-transferase {Fasciola hepatica}
PAKLGYWKIRGLQQPVRLLLEYLGEKYEEQIYERDDGEKWFSKKFELGLDLPNLPYYIDDKCKLT
QSLAILRYIADKHGM
>d1gnwa2 c.47.1.5 (A:2-85) Glutathione S-transferase {Mouse-ear cress (Arabidopsis thaliana)}
GIKVFGHPASIATRRVLIALHEKNLDFELVHVELKDGEHKKEPFLSRNPFGQVPAFEDGDLKLFE
SRAITQYIAHRYENQGTNL
>d1axda2 c.47.1.5 (A:1-80) Glutathione S-transferase {Maize (Zea mays), type I}
APMKLYGAVMSWNLTRCATALEEAGSDYEIVPINFATAEHKSPEHLVRNPFGQVPALQDGDLYLF
ESRAICKYAARKNKP
>d1aw9_2 c.47.1.5 (2-82) Glutathione S-transferase {Maize (Zea mays), type III}
APLKLYGMPLSPNVVRVATVLNEKGLDFEIVPVDLTTGAHKQPDFLALNPFGQIPALVDGDEVLF
ESRAINRYIASKYASE
>d1e6ba2 c.47.1.5 (A:8-87) Glutathione S-transferase {Mouse-ear cress (Arabidopsis thaliana), class zeta}
KLKLYSYWRSSCAHRVRIALALKGLDYEYIPVNLLKGDQFDSDFKKINPMGTVPALVDGDVVIND
SFAIIMYLDEKYPEP
>d1a0fa2 c.47.1.5 (A:1-80) Glutathione S-transferase {Escherichia coli}
MKLFYKPGACSLASHITLRESGKDFTLVSVDLMKKRLENGDDYFAVNPKGQVPALLLDDGTLLTE
GVAIMQYLADSVPDR
>d1pmt_2 c.47.1.5 (1-80) Glutathione S-transferase {Proteus mirabilis}
MKLYYTPGSCSLSPHIVLRETGLDFSIERIDLRTKKTESGKDFLAINPKGQVPVLQLDNGDILTE
GVAIVQYLADLKPDR
>d1f2ea2 c.47.1.5 (A:1-80) Glutathione S-transferase {Sphingomonas paucimobilis}
MKLFISPGACSLAPHIALRETGADFEAVKVDLAVRKTEAGEDFLTVNPSGKVPALTLDSGETLTE
NPAILLYIADQNPAS
>d1g7oa2 c.47.1.5 (A:1-75) Glutaredoxin 2 {Escherichia coli}
MKLYIYDHCPYCLKARMIFGLKNIPVELHVLLNDDAETPTRMVGQKQVPILQKDDSRYMPESMDI
VHYVDKLDGK

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>d1k0da2 c.47.1.5 (A:109-200) Yeast prion protein ure2p, nitrogen regulation fragment {Baker's yeast (Saccharomyces cerevisiae)}
QPLEGYTLFSHRSAPNGFKVAIVLSELGFHYNTIFLDFNLGEHRAPEFVSVNPNARVPALIDHGM
DNLSIWESGAILLHLVNKYYKETGNPL
>d1k0dd2 c.47.1.5 (D:99-200) Yeast prion protein ure2p, nitrogen regulation fragment {Baker's yeast (Saccharomyces cerevisiae)}
YSRITKFFQEQPLEGYTLFSHRSAPNGFKVAIVLSELGFHYNTIFLDFNLGEHRAPEFVSVNPNA
RVPALIDHGMDNLSIWESGAILLHLVNKYYKETGNPL
>d1k0ma2 c.47.1.5 (A:6-91) Chloride intracellular channel 1 (clic1) {Human (Homo sapiens)}
PQVELFVKAGSDGAKIGNCPFSQRLFMVLWLKGVTFNVTTVDTKRRTETVQKLCPGGELPFLLYG
TEVHTDTNKIEEFLEAVLCPP
>d2trcp_ c.47.1.6 (P:) Phosducin {Rat (Rattus norvegicus)}
EGQATHTGPKGVINDWRKFKLESEDGDSIPPSKKEILRQMSSPQSRDDKDSKERMSRKMSIQEYE
LIHQDKEDEGCLRKYRRQCMQDMHQKLSFGPRYGFVYELETGEQFLETIEKEQKVTTIVVNIYED
GVRGCDALNSSLECLAAEYPMVKFCKIRASNTGAGDRFSSDVLPTLLVYKGGELISNFISVAEQF
AEDFFAADVESFLNEYGLLPER
>d1a0rp_ c.47.1.6 (P:) Phosducin {Cow (Bos taurus)}
FEGQASHTGPKGVINDWRKFKLESEDSDSVAHSKKEILRQMSSPQSRDDKDSKERFSRKMSVQEY
ELIHKDKEDENCLRKYRRQCMQDMHQKLSFGPRYGFVYELESGEQFLETIEKEQKITTIVVHIYE
DGIKGCDALNSSLICLAAEYPMVKFCKIKASNTGAGDRFSSDVLPTLLVYKGGELLSNFISVTEQ
LAEEFFTGDVESFLNEYGLLPEK
>d1g7ea_ c.47.1.7 (A:) Endoplasmic reticulum protein ERP29, N-domain {Rat (Rattus norvegicus)}
LHTKGALPLDTVTFYKVIPKSKFVLVKFDTQYPYGEKQDEFKRLAENSASSDDLLVAEVGISDYG
DKLNMELSEKYKLDKESYPVFYLFRDGDFENPVPYSGAVKVGAIQRWLKGQGVYLGM
>d1qgva_ c.47.1.8 (A:) spliceosomal protein U5-15Kd {Human (Homo sapiens)}
SYMLPHLHNGWQVDQAILSEEDRVVVIRFGHDWDPTCMKMDEVLYSIAEKVKNFAVIYLVDITEV
PDFNKMYELYDPCTVMFFFRNKHIMIDLGTGNNNKINWAMEDKQEMVDIIETVYRGARKGRGLVV
SPKDYST
>d1eeja1 c.47.1.9 (A:61-216) Disulfide bond isomerase, DsbC, C-terminal domain {Escherichia coli}
NVTNKMLLKQLNALEKEMIVYKAPQEKHVITVFTDITCGYCHKLHEQMADYNALGITVRYLAFPR
QGLDSDAEKEMKAIWCAKDKNKAFDDVMAGKSVAPASCDVDIADHYALGVQLGVSGTPAVVLSNG
TLVPGYQPPKEMKEFLDEHQKMTSGK
>d1gp1a_ c.47.1.10 (A:) Glutathione peroxidase {Cow (Bos taurus)}
RTVYAFSARPLAGGEPFNLSSLRGKVLLIENVASLXGTTVRDYTQMNDLQRRLGPRGLVVLGFPC
NQFGHQENAKNEEILNCLKYVRPGGGFEPNFMLFEKCEVNGEKAHPLFAFLREVLPTPSDDATAL
MTDPKFITWSPVCRNDVSWNFEKFLVGPDGVPVRRYSRRFLTIDIEPDIETLLSQ
>d1qk8a_ c.47.1.10 (A:) Tryparedoxin I {Crithidia fasciculata}
GLDKYLPGIEKLRRGDGEVEVKSLAGKLVFFYFSASWCPPCRGFTPQLIEFYDKFHESKNFEVVF
CTWDEEEDGFAGYFAKMPWLAVPFAQSEAVQKLSKHFNVESIPTLIGVDADSGDVVTTRARATLV
KDPEGEQFPWKDA
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>d1i5ga_ c.47.1.10 (A:) Tryparedoxin II {Crithidia fasciculata}
SGLKKFFPYSTNVLKGAAADIALPSLAGKTVFFYFSASWCPPSRAFTPQLIDFYKAHAEKKNFEV
MLISWDESAEDFKDYYAKMPWLALPFEDRKGMEFLTTGFDVKSIPTLVGVEADSGNIITTQARTM
VVKDPEAKDFPWPN
>d1e2ya_ c.47.1.10 (A:) Tryparedoxin peroxidase (thioredoxin
peroxidase homologue) {Crithidia fasciculata}
GAAKLNHPAPEFDDMALMPNGTFKKVSLSSYKGKYVVLFFYPMDFTFVCPTEIIQFSDDAKRFAE
INTEVISCSCDSEYSHLQWTSVDRKKGGLGPMAIPMLADKTKAIARAYGVLDEDSGVAYRGVFII
DPNGKLRQIIINDMPIGRNVEEVIRLVEALQFVEEHG
>d1qq2a_ c.47.1.10 (A:) Thioredoxin peroxidase 2 (thioredoxin
peroxidase B, 2-cys peroxiredoxin) {Norway rat (Rattus norvegicus)}
SGNAKIGHPAPSFKATAVMPDGQFKDISLSDYKGKYVVFFFYPLDFTFVCPTEIIAFSDRAEEFK
KLNCQVIGASVDSHFSHLAWINTPKKQGGLGPMNIPLVSDPKRTIAQDYGVLKADEGISFRGLFI
IDDKGILRQITINDLPVGRSVDEILRLVQAFQFTDKHGEVCPA
>d1qmva_ c.47.1.10 (A:) Thioredoxin peroxidase 2 (thioredoxin
peroxidase B, 2-cys peroxiredoxin) {Human (Homo sapiens)}
SGNARIGKPAPDFKATAVVDGAFKEVKLSDYKGKYVVLFFYPLDFTFVAPTEIIAFSNRAEDFRK
LGCEVLGVSVDSQFTHLAWINTPRKEGGLGPLNIPLLADVTRRLSEDYGVLKTDEGIAYRGLFII
DGKGVLRQITVNDLPVGRSVDEALRLVQAFQYTDEHGEVCPAGWKPGSDTIKPNVDDSKEYFSKH
N
>d1hd2a_ c.47.1.10 (A:) Peroxiredoxin 5 {Human (Homo sapiens)}
APIKVGDAIPAVEVFEGEPGNKVNLAELFKGKKGVLFGVPGAFTPGCSKTHLPGFVEQAEALKAK
GVQVVACLSVNDAFVTGEWGRAHKAEGKVRLLADPTGAFGKETDLLLDDSLVSIFGNRRLKRFSM
VVQDGIVKALNVEPDGTGLTCSLAPNIISQL
>d1prxa_ c.47.1.10 (A:) HorF6 peroxidase {Human (Homo sapiens)}
LLLGDVAPNFEANTTVGRIRFHDFLGDSWGILFSHPRDFTPVCTTELGRAAKLAPEFAKRNVKLI
ALSIDSVEDHLAWSKDINAYNSEEPTEKLPFPIIDDRNRELAILLGMLDPAEKDEKGMPVTARVV
FVFGPDKKLKLSILYPATTGRNFDEILRVVISLQLTAEKRVATPVDWKDGDSVMVLPTIPEEEAK
KLFPKGVFTKELPSGKKYLRYTPQP
>d1kyga_ c.47.1.10 (A:) Alkyl hydroperoxide reductase AhpC
{Salmonella typhimurium}
SLINTKIKPFKNQAFKNGEFIEVTEKDTEGRWSVFFFYPADFTFVCPTELGDVADHYEELQKLGV
DVYSVSTDTHFTHKAWHSSSETIAKIKYAMIGDPTGALTRNFDNMREDEGLADRATFVVDPQGII
QAIEVTAEGIGRDASDLLRKIKAAQYVAAHPGEVCP
>d1jfua_ c.47.1.10 (A:) Membrane-anchored thioredoxin-like protein
TlpA, soluble domain {Bradyrhizobium japonicum}
TGDPACRAAVATAQKIAPLAHGEVAALTMASAPLKLPDLAFEDADGKPKKLSDFRGKTLLVNLWA
TWCVPCRKEMPALDELQGKLSGPNFEVVAINIDTRDPEKPKTFLKEANLTRLGYFNDQKAKVFQD
LKAIGRALGMPTSVLVDPQGCEIATIAGPAEWASEDALKLIRAATG
>d1foha3 c.47.1.10 (A:462-662) Phenol hydroxylase, C-terminal domain
{Soil-living yeast (Trichosporon cutaneum)}
NLVTDKKSSKQELAKNCVVGTRFKSQPVVRHSEGLWMHFGDRLVTDGRFRIIVFAGKATDATQMS
RIKKFSAYLDSENSVISLYTPKVSDRNSRIDVITIHSCHRDDIEMHDFPAPALHPKWQYDFIYAD
CDSWHHPHPKSYQAWGVDETKGAVVVVRPDGYTSLVTDLEGTAEIDRYFSGILVEPKEKSGAQTE
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ADWTKS
>d1f37a_ c.47.1.11 (A:) Thioredoxin-like 2Fe-2S ferredoxin {Aquifex
aeolicus}
AEFKHVFVCVQDRPPGHPQGSCAQRGSREVFQAFMEKIQTDPQLFMTTVITPTGCMNACMMGPVV
VVYPDGVWYGQVKPEDVDEIVEKHLKGGEPVERLVISKGKPPGM
>d1j9ba_ c.47.1.12 (A:) Arsenate reductase ArsC {Escherichia coli}
NITIYHNPACGTSRNTLEMIRNSGTEPTIILYLENPPSRDELVKLIADMGISVRALLRKNVEPYE
QLGLAEDKFTDDQLIDFMLQHPILINRPIVVTPLGTRLCRPSEVVLDILQDAQKGAFTKEDGEKV
VDEAGKRL
>d1qmha1 c.47.2.1 (A:185-279) RNA 3'-terminal phosphate cyclase, RPTC,
insert domain {Escherichia coli}
ERGNIVQMRGEVLLAGVPRHVAEREIATLAGSFSLHEQNIHNLPRDQGPGNTVSLEVESENITER
FFVVGEKRVSAEVVAAQLVKEVKRYLASTA
>d1gpua3 c.48.1.1 (A:535-680) Transketolase {Baker's yeast
(Saccharomyces cerevisiae)}
EGSSIESASKGGYVLQDVANPDIILVATGSEVSLSVEAAKTLAAKNIKARVVSLPDFFTFDKQPL
EYRLSVLPDNVPIMSVEVLATTCWGKYAHQSFGIDRFGASGKAPEVFKFFGFTPEGVAERAQKTI
AFYKGDKLISPLKKAF
>d1dtwb2 c.48.1.2 (B:205-342) Branched-chain alpha-keto acid
dehydrogenase {Human (Homo sapiens)}
PYNIPLSQAEVIQEGSDVTLVAWGTQVHVIREVASMAKEKLGVSCEVIDLRTIIPWDVDTICKSV
IKTGRLLISHEAPLTGGFASEISSTVQEECFLNLEAPISRVCGYDTPFPHIFEPFYIPDKWKCYD
ALRKMINY
>d1qs0b2 c.48.1.2 (B:206-339) 2-oxoisovalerate dehydrogenase E1b
{Pseudomonas putida}
YYTVPLDKAAITRPGNDVSVLTYGTTVYVAQVAAEESGVDAEVIDLRSLWPLDLDTIVESVKKTG
RCVVVHEATRTCGFGAELVSLVQEHCFHHLEAPIERVTGWDTPYPHAQEWAYFPGPSRVGAALKK
VMEV
>d1ik6a2 c.48.1.2 (A:192-326) E1-beta subunit of pyruvate
dehydrogenase {Archaeon Pyrobaculum aerophilum}
DYVVEIGKARVAREGDDVTLVTYGAVVHKALEAAERVKASVEVVDLQTLNPLDFDTVLKSVSKTG
RLIIAHDSPKTGGLGAEVRALVAEKALDRLTAPVIRLAGPDVPQSPIAADAAYAPTVERIIKAIE
YVMRY
>d1keka3 c.48.1.3 (A:259-415) Pyruvate-ferredoxin oxidoreductase,
PFOR, domain II {Desulfovibrio africanus}
KLFDYVGAPDAERVIVSMGSSCETIEEVINHLAAKGEKIGLIKVRLYRPFVSEAFFAALPASAKV
ITVLDRTKEPGAPGDPLYLDVCSAFVERGEAMPKILAGRYGLGSKEFSPAMVKSVYDNMSGAKKN
HFTVGIEDDVTGTSLPVDNAFADTTPK
>d1a49a3 c.49.1.1 (A:396-530) Pyruvate kinase, C-terminal domain
{Rabbit (Oryctolagus cuniculus)}
ELARSSSHSTDLMEAMAMGSVEASYKCLAAALIVLTESGRSAHQVARYRPRAPIIAVTRNHQTAR
QAHLYRGIFPVVCKDPVQEAWAEDVDLRVNLAMNVGKARGFFKKGDVVIVLTGWRPGSGFTNTMR
VVPVP
>d1pkla3 c.49.1.1 (A:358-498) Pyruvate kinase, C-terminal domain
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{Leishmania mexicana}
NEYVFFNSIKKLQHIPMSADEAVCSSAVNSVYETKAKAMVVLSNTGRSARLVAKYRPNCPIVCVT
TRLQTCRQLNITQGVESVFFDADKLGHDEGKEHRVAAGVEFAKSKGYVQTGDYCVVIHADHKVKG
YANQTRILLVE
>d1a3wa3 c.49.1.1 (A:367-500) Pyruvate kinase, C-terminal domain
{Baker's yeast (Saccharomyces cerevisiae)}
DMRNCTPKPTSTTETVAASAVAAVFEQKAKAIIVLSTSGTTPRLVSKYRPNCPIILVTRCPRAAR
FSHLYRGVFPFVFEKEPVSDWTDDVEARINFGIEKAKEFGILKKGDTYVSIQGFKAGAGHSNTLQ
VSTV
>d1e0ta3 c.49.1.1 (A:354-470) Pyruvate kinase, C-terminal domain
{Escherichia coli}
ITEAVCRGAVETAEKLDAPLIVVATQGGKSARAVRKYFPDATILALTTNEKTAHQLVLSKGVVPQ
LVKEITSTDDFYRLGKELALQSGLAHKGDVVVMVSGALVPSGTTNTASVHVL
>d1e79g_ c.49.2.1 (G:) ATP syntase (F1-ATPase), gamma subunit {Cow
(Bos taurus)}
ATLKDITRRLKSIKNIQKITKSMKMVAAAKYARAERELKPARVYGVGSLALYEKADIKTPEDKKK
HLIIGVSSDRGLCGAIHSSVAKQMKSEAANLAAAGKEVKIIGVGDKIRSILHRTHSDQFLVTFKE
VGRRPPTFGDASVIALELLNSGYEFDEGSIIFNRFRSVISYKTEEKPIFSLDTISSAESMSIYDD
IDADVLRNYQEYSLANIIYYSLKESTTSEQSARMTAMDNASKNASEMIDKLTLTFNRTRQAVITK
ELIEIISGAAAL
>d1mabg_ c.49.2.1 (G:) ATP syntase (F1-ATPase), gamma subunit {Rat
(Rattus norvegicus)}
RDITRRLKSIKNIQKITKSMKMVAAAKYARAERELKPARVYGTGSLALYEKAEIKGPEDKKKHLI
IGVSSDRGLCGAIHSSVAKQMKNDMAALTAAGKEVMIVGIGEKIKSILYRTHSDQFLVSFKDVGR
KPPTFGDASVIALELLNSGYEFDEGSIIFNQFKSVISYKTEEKPIFSFSTVVAAENMSIYDDIDA
DVLQNYQEYNLANIIYYSLKESTTSEQSARMTAMDNASKNASDMIDKLTLTFNRTRQAVITKELI
EIISGAAALD
>d1fs0g_ c.49.2.1 (G:) ATP syntase (F1-ATPase), gamma subunit
{Escherichia coli}
KITKAMEMVAASKMRKSQDRMAASRPYAETMRKVIGHLAHGNLEYKHPYLEDRDVKRVGYLVVST
DRGLCGGLNINLFKKLLAEMKTWTDKGVQCDLAMIGSKGVSFFNSVGGNVVAQVTGMGDNPSLSE
LIGPVKVMLQAYDEGRLDKLYIVSNKFINTMSQVPTISQLLPLPASDDDDLKHKSWDYLYEPDPK
ALLDTLLRRYVESQVYQGVVENLASEQAARMVAMK
>d1lam_1 c.50.1.1 (1-159) Leucine aminopeptidase, N-terminal domain
{Cow (Bos taurus)}
TKGLVLGIYSKEKEEDEPQFTSAGENFNKLVSGKLREILNISGPPLKAGKTRTFYGLHEDFPSVV
VVGLGKKTAGIDEQENWHEGKENIRAAVAAGCRQIQDLEIPSVEVDPCGDAQAAAEGAVLGLYEY
DDLKQKRKVVVSAKLHGSEDQEAWQRGVL
>d1kmma1 c.51.1.1 (A:326-424) Histidyl-tRNA synthetase (HisRS),
C-terminal domain {Escherichia coli}
DPVVDIYLVASGADTQSAAMALAERLRDELPGVKLMTNHGGGNFKKQFARADKWGARVAVVLGES
EVANGTAVVKDLRSGEQTAVAQDSVAAHLRTLLG
>d1qe0a1 c.51.1.1 (A:326-420) Histidyl-tRNA synthetase (HisRS),
C-terminal domain {Staphylococcus aureus}
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IEENLDLFIVTMGDQADRYAVKLLNHLRHNGIKADKDYLQRKIKGQMKQADRLGAKFTIVIGDQE
LENNKIDVKNMTTGESETIELDALVEYFKK
>d1h4vb1 c.51.1.1 (B:326-421) Histidyl-tRNA synthetase (HisRS),
C-terminal domain {Thermus thermophilus}
EKGPDLYLIPLTEEAVAEAFYLAEALRPRLRAEYALAPRKPAKGLEEALKRGAAFAGFLGEDELR
AGEVTLKRLATGEQVRLSREEVPGYLLQALG
>d1atia1 c.51.1.1 (A:395-505) Glycyl-tRNA synthetase (GlyRS),
C-terminal domain {Thermus thermophilus}
QLAPIKVAVIPLVKNRPEITEYAKRLKARLLALGLGRVLYEDTGNIGKAYRRHDEVGTPFAVTVD
YDTIGQSKDGTTRLKDTVTVRDRDTMEQIRLHVDELEGFLRERLRW
>d1qf6a1 c.51.1.1 (A:533-642) Threonyl-tRNA synthetase (ThrRS),
C-terminal domain {Escherichia coli}
FPTWLAPVQVVIMNITDSQSEYVNELTQKLSNAGIRVKADLRNEKIGFKIREHTLRRVPYMLVCG
DKEVESGKVAVRTRRGKDLGSMDVNEVIEKLQQEIRSRSLKQLEE
>d1hc7a1 c.51.1.1 (A:277-403) C-terminal domain of ProRS {Thermus
thermophilus}
RGLVLPPRLAPIQVVIVPIYKDESRERVLEAAQGLRQALLAQGLRVHLDDRDQHTPGYKFHEWEL
KGVPFRVELGPKDLEGGQAVLASRLGGKETLPLAALPEALPGKLDAFHEELYRRALAFREDH
>d1g5ha1 c.51.1.1 (A:343-469) The aaRS-like accessory subunit of
mitochondrial polymerase gamma, C-terminal domain {Mouse (Mus
musculus)}
RKVLKLHPCLAPIKVALDVGKGPTVELRQVCQGLLNELLENGISVWPGYSETVHSSLEQLHSKYD
EMSVLFSVLVTETTLENGLIQLRSRDTTMKEMMHISKLRDFLVKYLASASNVAAALDHHHHH
>d1crza2 c.51.2.1 (A:7-140) TolB, N-terminal domain {Escherichia
coli}
DSGVDSGRPIGVVPFQWAGPGAAPEDIGGIVAADLRNSGKFNPLDRARLPQQPGSAQEVQPAAWS
ALGIDAVVVGQVTPNPDGSYNVAYQLVDTGGAPGTVLAQNSYKVNKQWLRYAGHTASDEVFEKLT
GIKG
>d1eexb_ c.51.3.1 (B:) Diol dehydratase, beta subunit {Klebsiella
oxytoca}
GFLTEVGEARQGTQQDEVIIAVGPAFGLAQTVNIVGIPHKSILREVIAGIEEEGIKARVIRCFKS
SDVAFVAVEGNRLSGSGISIGIQSKGTTVIHQQGLPPLSNLELFPQAPLLTLETYRQIGKNAARY
AKRESPQPVPTLNDQMARPKYQAKSAILHIKETKYVVTGKNPQELRVA
>d1b78a_ c.51.4.1 (A:) XTP pyrophosphatase {Archaeon Methanococcus
jannaschii}
KIYFATGNPNKIKEANIILKDLKDVEIEQIKISYPEIQGTLEEVAEFGAKWVYNILKKPVIVEDS
GFFVEALNGFPGTYSKFVQETIGNEGILKLLEGKDNRNAYFKTVIGYCDENGVRLFKGIVKGRVS
EEIRSKGYGFAYDSIFIPEEEERTFAEMTTEEKSQISHRKKAFEEFKKFLLDRI
>d1ex2a_ c.51.4.2 (A:) Maf protein {Bacillus subtilis}
MTKPLILASQSPRRKELLDLLQLPYSIIVSEVEEKLNRNFSPEENVQWLAKQKAKAVADLHPHAI
VIGADTMVCLDGECLGKPQDQEEAASMLRRLSGRSHSVITAVSIQAENHSETFYDKTEVAFWSLS
EEEIWTYIETKEPMDKAGAYGIQGRGALFVKKIDGDYYSVMGLPISKTMRALRHF
>d1ihna_ c.103.1.1 (A:) Hypothetical protein MT938 (MTH938) {Archaeon
Methanobacterium thermoautotrophicum}
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SHMFSDCRFGSVTYRGREYRSDIVVHVDGSVTPRRKEISRRKYGTSHVMAEEELEELLEEKPESI
IIGSGVHGALETGFRSDATVLPTCEAIKRYNEERSAGRRVAAIIHVTC
>d1ckqa_ c.52.1.1 (A:) Restriction endonuclease EcoRI {Escherichia
coli}
SQGVIGIFGDYAKAHDLAVGEVSKLVKKALSNEYPQLSFRYRDSIKKTEINEALKKIDPDLGGTL
FVSNSSIKPDGGIVEVKDDYGEWRVVLVAEAKHQGKDIINIRNGLLVGKRGDQDLMAAGNAIERS
HKNISEIANFMLSESHFPYVLFLEGSNFLTENISITRPDGRVVNLEYNSGILNRLDRLTAANYGM
PINSNLCINKFVNHKDKSIMLQAASIYTQGDGREWDSKIMFEIMFDISTTSLRVLGRDLFEQLTS
K
>d1az3a_ c.52.1.2 (A:) Restriction endonuclease EcoRV {Escherichia
coli}
SLRSDLINALYDENQKYDVCGIISAEGKIYPLGSDTKVLSTIFELFSRPIINKIAEKHGYIVEEP
KQQNHYPDFTLYKPSEPNKKIAIDIKTTYTNKENEKIKFTLGGYTSFIRNNTKNIVYPFDQYIAH
WIIGYVYTRVATRKSSLKTYNINELNEIPKPYKGVKVFLQDKWVIAGDLAGSGNTTNIGSIHAHY
KDFVEGKGIFDSEDEFLDYWR
>d1eona_ c.52.1.2 (A:) Restriction endonuclease EcoRV {Escherichia
coli}
SLRSDLINALYDENQKYDVCGIISAEGKIYPLGSDTKVLSTIFELFSRPIINKIAEKHGYIVEEP
KQQNHYPDFTLYKPSEPNKKIAIDIKTTYTNKENEKIKFTLGGYTSFIRNNTKNIVYPFDQYIAH
WIIGYVYTRVATRKSSLKTYNINELNEIPKPYKGVKVFLQDKWVIAGDLAGSGNTTNIGSIHAHY
KDFVEGKGIFDSEDEFLDYWRNYERTSQLRNDKYNNISEYRNWIYRGRK
>d1bam__ c.52.1.3 (-) Restriction endonuclease BamHI {Bacillus
amyloliquefaciens}
MEVEKEFITDEAKELLSKDKLIQQAYNEVKTSICSPIWPATSKTFTINNTEKNCNGVVPIKELCY
TLLEDTYNWYREKPLDILKLEKKKGGPIDVYKEFIENSELKRVGMEFETGNISSAHRSMNKLLLG
LKHGEIDLAIILMPIKQLAYYLTDRVTNFEELEPYFELTEGQPFIFIGFNAEAYNSNVPLIPKGS
DGMSKRSIKKWKDKVENK
>d1dmua_ c.52.1.4 (A:) Restriction endonuclease BglI {Bacillus
subtilis}
MYNLHREKIFMSYNQNKQYLEDNPEIQEKIELYGLNLLNEVISDNEEEIRADYNEANFLHPFWMN
YPPLDRGKMPKGDQIPWIEVGEKAVGSKLTRLVSQREDITVREIGLPTGPDERYLLTSPTIYSLT
NGFTDSIMMFVDIKSVGPRDSDYDLVLSPNQVSGNGDWAQLEGGIQNNQQTIQGPRSSQIFLPTI
PPLYILSDGTIAPVVHLFIKPIYAMRSLTKGDTGQSLYKIKLASVPNGLGLFCNPGYAFDSAYKF
LFRPGKDDRTKSLLQKRVRVDLRVLDKIGPRVMTIDMDK
>d1dfma_ c.52.1.5 (A:) Restriction endonuclease BglII {Bacillus
subtilis}
MKIDITDYNHADEILNPQLWKEIEETLLKMPLHVKASDQASKVGSLIFDPVGTNQYIKDELVPKH
WKNNIPIPKRFDFLGTDIDFGKRDTLVEVQFSNYPFLLNNTVRSELFHKSNMDIDEEGMKVAIII
TKGHMFPASNSSLYYEQAQNQLNSLAEYNVFDVPIRLVGLIEDFETDIDIVSTTYADKRYSRTIT
KRDTVKGKVIDTNTPNTRRRKRGTIVTY
>d3pvia_ c.52.1.6 (A:) Restriction endonuclease PvuII {Proteus
vulgaris}
SHPDLNKLLELWPHIQEYQDLALKHGINDIFQGNGGKLLQVLLITGLTVLPGREGNDAVDNAGQE
YELKSINIDLTKGFSTHHHMNPVIIAKYRQVPWIFAIYRGIAIEAIYRLEPKDLEFYYDKWERKW
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YSDGHKDINNPKIPVKYVMEHGTKIY
>d1cfr__ c.52.1.7 (-) Restriction endonuclease Cfr10I {Citrobacter freundii}
MDIISKSGEGNKYTINSAIAFVAYASHIDINTTEFSKVLSGLRDFINDEAIRLGGKISDGSFNKC
NGDWYEWLIGIRAIEFFLESETNFIVVKMPNATSFDVMSIYKSCLSEFIYDLRSKLSLNNVNLIT
SNPDFSIIDIRGRREELKSMLKDISFSNISLSTISEIDNLYKNFIDYAELEHIKSFLSVKTTFRP
DRRLQLAHEGSLMKALYTHLQTRTWTINPTGIRYYAAATSIGNADVIGLKTVATHSITDVKSLPQ
SAVDEIFKINSVLDVDSCLSHIL
>d1knva_ c.52.1.7 (A:) Restriction endonuclease Bse634I {Bacillus stearothermophilus}
NLTNSNCVEEYKENGKTKIRIKPFNALIELYHHQTPTGSIKENLDKLENYVKDVVKAKGLAIPTS
GAFSNTRGTWFEVMIAIQSWNYRVKRELNDYLIIKMPNVKTFDFRKIFDNETREKLHQLEKSLLT
HKQQVRLITSNPDLLIIRQKDLIKSEYNLPINKLTHENIDVALTLFKDIEGKCKWDSLVAGVGLK
TSLRPDRRLQLVHEGNILKSLFAHLKMRYWNPKAEFKYYGASSEPVSKADDDALQTAATHTIVNV
NSTPERAVDDIFSLTSFEDIDKMLDQIIKK
>d1d02a_ c.52.1.8 (A:) Restriction endonuclease MunI {Eubacteria (Mycoplasma unidentified)}
LSGRLNWQALAGLKASGAEQNLYNVFNAVFEGTKYVLYEKPKHLKNLYAQVVLPDDVIKEIFNPL
IDLSTTQWGVSPAFAIENTETHKILFGEIKRQDGWVEGKDPSAGRGNAHERSCKLFTPGLLKAYR
TIGGINDEEILPFWVVFEGDITRDPKRVREITFWYDHYQDNYFMWRPNESGEKLVQHFNEKLKKY
LD
>d1ev7a_ c.52.1.9 (A:) Restriction endonuclease NaeI {Nocardia aerocolonigenes}
EPDDDLERVRATLYSLDPDGDRTAGVLRDTLDQLYDGQRTGRWNFDQLHKTEKTHMGTLVEINLH
REFQFGDGFETDYEIAGVQVDCKFSMSQGAWMLPPESIGHICLVIWASDQQCAWTAGLVKVIPQF
LGTANRDLKRRLTPEGRAQVVKLWPDHGKLQENLLLHIPGDVRDQIFSAKSSRGNQHGQARVNEL
FRRVHGRLIGRAVIATVAQQDDFMKRVRGSGGARSILRPEGIIILGHQDNDPKVANDLGLPVPRK
GQVVAARVVPADEGDQRQTAEIQGRRWAVAVPGDPIVEAPVV
>d1fiua_ c.52.1.10 (A:) Restriction endonuclease NgoIV {Neisseria gonorrhoeae}
MQPLFTQERRIFHKKLLDGNILATNNRGVVSNADGSNTRSFNIAKGIADLLHSETVSERLPGQTS
GNAFEAICSEFVQSAFEKLQHIRPGDWNVKQVGSRNRLEIARYQQYAHLTALAKAAEENPELAAA
LGSDYTITPDIIVTRNLIADAEINRNEFLVDENIATYASLRAGNGNMPLLHASISCKWTIRSDRA
QNARSEGLNLVRNRKGRLPHIVVVTAEPTPSRISSIALGTGEIDCVYHFALYELEQILQSLNYED
ALDLFYIMVNGKRLKDISDLPLDLAV
>d1dc1a_ c.52.1.11 (A:) Restriction endonuclease BsobI {Bacillus stearothermophilus}
KPFENHLKSVDDLKTTYEEYRAGFIAFALEKNKRSTPYIERARALKVAASVAKTPKDLLYLEDIQ
DALLYASGISDKAKKFLTEDDKKESINNLIENFLEPAGEEFIDELIFRYLLFQGDSLGGTMRNIA
GALAQQKLTRAIISALDIANIPYKWLDSRDKKYTNWMDKPEDDYELETFAKGISWTINGKHRTLM
YNITVSLVKKNVDICLFNCEPEIYTPQKVHQQPEKYLLLGELKGGIDPAGADEHWKTANTALTRI
RNKFSEKGLSPKTIFIGAAIEHSMAEEIWDQLQSGSLTNSANLTKTEQVGSLCRWIINI
>d1kc6a_ c.52.1.19 (A:) Restriction endonuclease HincII {Haemophilus influenzae}
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SFIKPIYQDINSILIGQKVKRPKSGTLSGHAAGEPFEKLVYKFLKENLSDLTFKQYEYLNDLFMK
NPAIIGHEARYKLFNSPTLLFLLSRGKAATENWSIENLFEEKQNDTADILLVKDQFYELLDVKTR
NISKSAQAPNIISAYKLAQTCAKMIDNKEFDLFDINYLEVDWELNGEDLVCVSTSFAELFKSEPS
ELYINWAAAMQIQFHVRDLDQGFNGTREEWAKSYLKHFVTQAEQRAISMIDKFVKPFKKYIL
>d2foka4  c.52.1.12  (A:387-579)  Restriction  endonuclease  FokI,
C-terminal (catalytic) domain {Flavobacterium okeanokoites}
KSELEEKKSELRHKLKYVPHEYIELIEIARNSTQDRILEMKVMEFFMKVYGYRGKHLGGSRKPDG
AIYTVGSPIDYGVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRNKHINPNEWWKVYPSSVTEFK
FLFVSGHFKGNYKAQLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLTLEEVRRKFNNGEINF
>d1avqa_ c.52.1.13 (A:) lambda exonuclease {Bacteriophage lambda}
SHMTPDIILQRTGIDVRAVEQGDDAWHKLRLGVITASEVHNVIAKPRSGKKWPDMKMSYFHTLLA
EVCTGVAPEVNAKALAWGKQYENDARTLFEFTSGVNVTESPIIYRDESMRTACSPDGLCSDGNGL
ELKCPFTSRDFMKFRLGGFEAIKSAYMAQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDE
KYMASFDEIVPEFIEKMDEALAEIGFVFGEQWR
>d1azo__  c.52.1.14  (-)  DNA  mismatch  repair  protein  MutH  from
{Escherichia coli}
PRPLLSPPETEEQLLAQAQQLSGYTLGELAALVGLVTPENLKRDKGWIGVLLEIWLGASAGSKPE
QDFAALGVELKTIPVDSLGRPLETTFVCVAPLTGNSGVTWETSHVRHKLKRVLWIPVEGEASIPL
AQRRVGSPLLWSPNEEEDRQLREDWEELMDMIVLGQVERITARHGEYLQIRPKAANAKALTEAIG
ARGERILTLPRGFYLKKNFTSALLARHFLIQ
>d1cw0a_ c.52.1.15 (A:) Very short patch repair (VSR) endonuclease
{Escherichia coli}
ADVHDKATRSKNMRAIATRDTAIEKRLASLLTGQGLAFRVQDASLPGRPDFVVDEYRCVIFTHGC
FWHHHHCYLFKVPATRTEFWLEKIGKNVERDRRDISRLQELGWRVLIVWECALRGREKLTDEALT
ERLEEWICGEGASAQIDTQGIHLLA
>d1vsra_ c.52.1.15 (A:) Very short patch repair (VSR) endonuclease
{Escherichia coli}
AIEKRLASLLTGQGLAFRVQDASLPGRPDFVVDEYRCVIFTHGCFWHHHHCYLFKVPATRTEFWL
EKIGKNVERDRRDISRLQELGWRVLIVWECALRGREKLTDEALTERLEEWICGEGASAQIDTQGI
HLLA
>d1f1za2 c.52.1.16 (A:8-168) TnsA endonuclease, N-terminal domain
{Escherichia coli}
FSEVQIARRIKEGRGQGHGKDYIPWLTVQEVPSSGRSHRIYSHKTGRVHHLLSDLELAVFLSLEW
ESSVLDIREQFPLLPSDTRQIAIDSGIKHPVIRGVDQVMSTDFLVDCKDGPFEQFAIQVKPAAAL
QDERTLEKLELERRYWQQKQIPWFIFTDKEI
>d1fzra_ c.52.1.17 (A:) Endonuclease I (Holliday junction resolvase)
{Bacteriophage T7}
SGLEDKVSKQLESKGIKFEYEEWKVPYVIPASNHTYTPDFLLPNGIFVKTKGLWESDDRKKHLLI
REQHPELDIRIVFSSSRTKLYKGSPTSYGEFCEKHGIKFADKLIPAEWIKEPKKEVPFDRLKRK
>d1gefa_  c.52.1.18  (A:)  Archaeal  Holliday  junction  resolvase  Hjc
{Archaeon Pyrococcus furiosus}
MYRKGAQAERELIKLLEKHGFAVVRSAGSKKVDLVAGNGKKYLCIEVKVTKKDHLYVGKRDMGRL
IEFSRRFGGIPVLAVKFLNVGWRFIEVSPKIEKFVFTPSSGVSLEVLLGIQKTLE
>d1hh1a_  c.52.1.18  (A:)  Archaeal  Holliday  junction  resolvase  Hjc
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{Archaeon Sulfolobus solfataricus}
SAVERNIVSRLRDKGFAVVRAPASGSKRKDPIPDIIALKNGVIILIEMKSRKDIEGKIYVRREQA
EGIIEFARKSGGSLFLGVKKPGVLKFIPFEKLRRTETGNYVADSEIEGLDLEDLVRLVEAKISRT
LD
>d1a79a1 c.52.2.1 (A:83-179) tRNA splicing endonuclease, C-terminal
domain {Archaeon Methanococcus jannaschii}
ERLCLKYLVYKDLRTRGYIVKTGLKYGADFRLYERGANIDKEHSVYLVKVFPEDSSFLLSELTGF
VRVAHSVRKKLLIAIVDADGDIVYYNMTYVKP
>d1dzfa1 c.52.3.1 (A:5-143) Eukaryotic RPB5 N-terminal domain
{Baker's yeast (Saccharomyces cerevisiae)}
NERNISRLWRAFRTVKEMVKDRGYFITQEEVELPLEDFKAKYCDSMGRPQRKMMSFQANPTEESI
SKFPDMGSLWVEFCDEPSVGVKTMKTFVIHIQEKNFQTGIFVYQNNITPSAMKLVPSIPPATIET
FNEAALVVN
>d1gdta2 c.53.1.1 (A:1-140) gamma,delta resolvase, catalytic domain
{Escherichia coli}
MRLFGYARVSTSQQSLDIQVRALKDAGVKANRIFTDKASGSSSDRKGLDLLRMKVEEGDVILVKK
LDRLGRDTADMIQLIKEFDAQGVSIRFIDDGISTDGEMGKMVVTILSAVAQAERQRILERTNEGR
QEAMAKGVVF
>d1hx7a_ c.53.1.1 (A:) gamma,delta resolvase, catalytic domain
{Escherichia coli}
MRLFGYARVSTSQQSLDIQVRALKDAGVKANRIFTDKASGSSSDRKGLDLLRMKVEEGDVILVKK
LDRLGRDTADMIQLIKEFDAQGVSIRFIDDGISTDGEMGK
>d2rsla_ c.53.1.1 (A:) gamma,delta resolvase, catalytic domain
{Escherichia coli}
MRLFGYARVSTSQQSLDIQVRALKDAGVKANRIFTDKASGSSSDRKGLDLLRMKVEEGDVILVKK
LDRLGRDTADMIQLIKEFDAQGVSIRFIDDGISTDGEMGKMVVTILSAVAQAERQRI
>d1tfr_2 c.53.1.2 (12-180) T4 RNase H {Bacteriophage T4}
KEGICLIDFSQIALSTALVNFPDKEKINLSMVRHLILNSIKFNVKKAKTLGYTKIVLCIDNAKSG
YWRRDFAYYYKKNRGKAREESTWDWEGYFESSHKVIDELKAYMPYIVMDIDKYEADDHIAVLVKK
FSLEGHKILIISSDGDFTQLHKYPNVKQWSPMHKKWVKI
>d1bgxt2 c.53.1.2 (T:1-173) 5' to 3' exonuclease domain of DNA
polymerase <i>Taq</i> {Thermus aquaticus}
MRGMLPLFEPKGRVLLVDGHHLAYRTFHALKGLTTSRGEPVQAVYGFAKSLLKALKEDGDAVIVV
FDAKAPSFRHEAYGGYKAGRAPTPEDFPRQLALIKELVDLLGLARLEVPGYEADDVLASLAKKAE
KEGYEVRILTADKDLYQLLSDRIHVLHPEGYLITPAWLWEKYG
>d1xo1a2 c.53.1.2 (A:19-185) T5 5'-exonuclease {Bacteriophage T5}
RRNLMIVDGTNLGFRFKHNNSKKPFASSYVSTIQSLAKSYSARTTIVLGDKGKSVFRLEHLPEYA
GNRDEKYAQRTEEEKALDEQFFEYLKDAFELCKTTFPTFTIRGVEADDMAAYIVKLIGHLYDHVW
LISTDGDWDTLLTDKVSRFSFTTRREYHLRDMYEHHN
>d1a77_2 c.53.1.2 (2-208) Flap endonuclease-1 {Archaeon Methanococcus
jannaschii}
GVQFGDFIPKNIISFEDLKGKKVAIDGMNALYQFLTSIRLRDGSPLRNRKGEITSAYNGVFYKTI
HLLENDITPIWVFDGEPPKLKEKTRKVRREMKEKAELKMKEAIKKEDFEEAAKYAKRVSYLTPKM
VENCKYLLSLMGIPYVEAPSEGEAQASYMAKKGDVWAVVSQDYDALLYGAPRVVRNLTTTKEMPE
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LIELNEVLEDLR
>d1b43a2 c.53.1.2 (A:1-219) Fen-1 nuclease {Archaeon Pyrococcus furiosus}
GVPIGEIIPRKEIELENLYGKKIAIDALNAIYQFLSTIRQKDGTPLMDSKGRITSHLSGLFYRTI
NLMEAGIKPVYVFDGEPPEFKKKELEKRREAREEAEEKWREALEKGEIEEARKYAQRATRVNEML
IEDAKKLLELMGIPIVQAPSEGEAQAAYMAAKGSVYASASQDYDSLLFGAPRLVRNLTITGKRKL
PGKNVYYVEIKPELIILEEVLKELK
>d1ekja_ c.53.2.1 (A:) beta-carbonic anhydrase {Pea (Pisum sativum)}
EASERIKTGFLHFKKEKYDKNPALYGELAKGQSPPFMVFACSDSRVCPSHVLDFQPGEAFVVRNV
ANLVPPYDQAKYAGTGAAIEYAVLHLKVSNIVVIGHSACGGIKGLLSFPFDGTYSTDFIEEWVKI
GLPAKAKVKAQHGDAPFAELCTHCEKEAVNASLGNLLTYPFVREGLVNKTLALKGGYYDFVKGSF
ELWGLEFGLSSTFSV
>d1g5ca_ c.53.2.1 (A:) beta-carbonic anhydrase {Archaeon Methanobacterium thermoautotrophicum}
IIKDILRENQDFRFRDLSDLKHSPKLCIITCMDSRLIDLLERALGIGRGDAKVIKNAGNIVDDGV
IRSAAVAIYALGDNEIIIVGHTDCGMARLDEDLIVSRMRELGVEEEVIENFSIDVLNPVGDEEEN
VIEGVKRLKSSPLIPESIGVHGLIIDINTGRLKPLYLDE
>d1i6pa_ c.53.2.1 (A:) beta-carbonic anhydrase {Escherichia coli}
KDIDTLISNNALWSKMLVEEDPGFFEKLAQAQKPRFLWIGCSDSRVPAERLTGLEPGELFVHRNV
ANLVIHTDLNCLSVVQYAVDVLEVEHIIICGHYGCGGVQAAVENPELGLINNWLLHIRDIWFKHS
SLLGEMPQERRLDTLCELNVMEQVYNLGHSTIMQSAWKRGQKVTIHGWAYGIHDGLLRDLDVTAT
NRETLEQRYRHGISNLKLK
>d1ddza1 c.53.2.1 (A:84-325) beta-carbonic anhydrase {Red alga (Porphyridium purpureum)}
VMSDLEKKFIELEAKLVAQPAGQAMPGKSNIFANNEAWRQEMLKQDPEFFNRLANGQSPEYLWIG
CADSRVPANQLLDLPAGEVFVHRNIANQCIHSDISFLSVLQYAVQYLKVKHILVCGHYGCGGAKA
ALGDSRLGLIDNWLRHIRDVRRMNAKYLDKCKDGDEELNRLIELNVLEQVHNVCATSIVQDAWDA
GQELTVQGVVYGVGDGKLRDLGVVVNSSDDISKFYRTKSDSGALKAG
>d1ddza2 c.53.2.1 (A:326-564) beta-carbonic anhydrase {Red alga (Porphyridium purpureum)}
NPNAPLVQVTKGGESELDSTMEKLTAELVQQTPGKLKEGANRVFVNNENWRQKMLKQDPQFFSNL
AHTQTPEILWIGCADSRVPANQIINLPAGEVFVHRNIANQCIHSDMSFLSVLQYAVQYLKVKRVV
VCGHYACGGCAAALGDSRLGLIDNWLRHIRDVRRHNQAELSRITDPKDSLNRLIEINVLEQMHNV
CATSIVQDAWDAGQELEVQGVVYGVGDGKLRDMGVVAKANDDIG
>d1pdo__ c.54.1.1 (-) IIA domain of mannose transporter, IIA-Man {Escherichia coli}
TIAIVIGTHGWAAEQLLKTAEMLLGEQENVGWIDFVPGENAETLIEKYNAQLAKLDTTKGVLFLV
DTWGGSPFNAASRIVVDKEHYEVIAGVNIPMLVETLMARDDDPSFDELVALAVETGREGVKALK
>d1bupa1 c.55.1.1 (A:4-188) Heat shock protein 70kDa, ATPase fragment {Cow (Bos taurus)}
GPAVGIDLGSTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVAMNPTNTVF
DAKRLIGRRFDDAVVQSDMKHWPFMVVNDAGRPKVQVEYKGETKSFYPEEVSSMVLTKMKEIAEA
YLGKTVTNAVVTVPAYFNDSQRQATKDAGTIAGLNVLRIINEPTAAAIAYGLDKK
>d1bupa2 c.55.1.1 (A:189-381) Heat shock protein 70kDa, ATPase
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fragment {Cow (Bos taurus)}
VGAERNVLIFDLGGGTFDVSILTIEDGIFEVKSTAGDTHLGGEDFDNRMVNHFIAEFKRKHKKDI
SENKRAVRRLRTACERAKRTLSSSTQASIEIDSLYEGIDFYTSITRARFEELNADLFRGTLDPVE
KALRDAKLDKSQIHDIVLVGGSTRIPKIQKLLQDFFNGKELNKSINPDEAVAYGAAVQAAILS
>d1hjoa1 c.55.1.1 (A:3-188) Heat shock protein 70kDa, ATPase fragment {Human (Homo sapiens)}
KAAAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPQNTV
FDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEISSMVLTKMKEIAE
AYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGLDRT
>d1hjoa2 c.55.1.1 (A:189-382) Heat shock protein 70kDa, ATPase fragment {Human (Homo sapiens)}
GKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNHFVEEFKRKHKKDI
SQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRARFEELCSDLFRSTLEPVE
KALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLNKSINPDEAVAYGAAVQAAILMG
>d1dkgd1 c.55.1.1 (D:3-185) Heat shock protein 70kDa, ATPase fragment {Escherichia coli, gene dnaK}
KIIGIDLGTTNSCVAIMDGTTPRVLENAEGDRTTPSIIAYTQDGETLVGQPAKRQAVTNPQNTLF
AIKRLIGRRFQDEEVQRDVSIMPFKIIAADNGDAWVEVKGQKMAPPQISAEVLKKMKKTAEDYLG
EPVTEAVITVPAYFNDAQRQATKDAGRIAGLEVKRIINEPTAAALAYGLDKGT
>d1dkgd2 c.55.1.1 (D:186-383) Heat shock protein 70kDa, ATPase fragment {Escherichia coli, gene dnaK}
GNRTIAVYDLGGGTFDISIIEIDEVDGEKTFEVLATNGDTHLGGEDFDSRLINYLVEEFKKDQGI
DLRNDPLAMQRLKEAAEKAKIELSSAQQTDVNLPYITADATGPKHMNIKVTRAKLESLVEDLVNR
SIELLKVALQDAGLSVSDIDDVILVGGQTRMPMVQKKVAEFFGKEPRKDVNPDEAVAIGAAVQGG
VLT
>d1j6za1 c.55.1.1 (A:4-146) Actin {Rabbit (Oryctolagus cuniculus)}
ETTALVCDNGSGLVKAGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQKDSYVGDEAQSKRGILTLK
YPIEHGIITNWDDMEKIWHHTFYNELRVAPEEHPTLLTEAPLNPKANREKMTQIMFETFNVPAMY
VAIQAVLSLYASG
>d1j6za2 c.55.1.1 (A:147-372) Actin {Rabbit (Oryctolagus cuniculus)}
RTTGIVLDSGDGVTHNVPIYEGYALPHAIMRLDLAGRDLTDYLMKILTERGYSFVTTAEREIVRD
IKEKLCYVALDFENEMATAASSSSLEKSYELPDGQVITIGNERFRCPETLFQPSFIGMESAGIHE
TTYNSIMKCDIDIRKDLYANNVMSGGTTMYPGIADRMQKEITALAPSTMKIKIIAPPERKYSVWI
GGSILASLSTFQQMWITKQEYDEAGPSIVHR
>d1d4xa1 c.55.1.1 (A:4-146) Actin {Nematode (Caenorhabditis elegans)}
EVAALVVDNGSGMCKAGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQKDSYVGDEAQSKRGILTLK
YPIEHGIVTNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAPLNPKANREKMTQIMFETFNTPAMY
VAIQAVLSLYASG
>d1d4xa2 c.55.1.1 (A:147-375) Actin {Nematode (Caenorhabditis elegans)}
RTTGVVLDSGDGVTHTVPIYEGYALPHAILRLDLAGRDLTDYLMKILTERGYSFTTTAEREIVRD
IKEKLCYVALDFEQEMATAASSSSLEKSYELPDGQVITVGNERFRCPEAMFQPSFLGMESAGIHE
TSYNSIMKCDIDIRKDLYANTVLSGGTTMYPGIADRMQKEITALAPSTMKIKIIAPPERKYSVWI
GGSILASLSTFQQMWISKQEYDESGPSIVHRKCF

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>d1c0fa1 c.55.1.1 (A:1-146) Actin {Slime mold (Dictyostelium discoideum)}
DGEDVQALVIDNGSGMCKAGFAGDDAPRAVFPSIVGRPRHTGKDSYVGDEAQSKRGILTLKYPIE
HGIVTNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAPLNPKANREKMTQIMFETFNTPAMYVAIQ
AVLSLYASG
>d1dgaa2 c.55.1.1 (A:147-375) Actin {Slime mold (Dictyostelium discoideum)}
RTTGIVMDSGDGVSHTVPIYEGYALPHAILRLDLAGRDLTDYMMKILTERGYSFTTTAEREIVRD
IKEKLAYVALDFEQEMATAASSSALEKSYELPDGQVITIGNERFRCPEALFQPSFLGMESAGIHE
TTYNSIMKCDVDIRKDLYGNVVLSGGTTMFPGIADRMNKELTALAPSTMKIKIIAPPERKYSVWI
GGSILASLSTFQQMWISKEEYDESGPSIVHRKCF
>d1yaga1 c.55.1.1 (A:4-146) Actin {Baker's yeast (Saccharomyces cerevisiae)}
EVAALVIDNGSGMCKAGFAGDDAPRAVFPSIVGRPRHQGIMVGMGQKDSYVGDEAQSKRGILTLR
YPIEHGIVTNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAPMNPKSNREKMTQIMFETFNVPAFY
VSIQAVLSLYSSG
>d1yaga2 c.55.1.1 (A:147-375) Actin {Baker's yeast (Saccharomyces cerevisiae)}
RTTGIVLDSGDGVTHVVPIYAGFSLPHAILRIDLAGRDLTDYLMKILSERGYSFSTTAEREIVRD
IKEKLCYVALDFEQEMQTAAQSSSIEKSYELPDGQVITIGNERFRAPEALFHPSVLGLESAGIDQ
TTYNSIMKCDVDVRKELYGNIVMSGGTTMFPGIAERMQKEITALAPSSMKVKIIAPPERKYSVWI
GGSILASLTTFQQMWISKQEYDESGPSIVHHKCF
>d1jcfa1 c.55.1.1 (A:1-140) Prokaryotic actin homolog MreB {Thermotoga maritima}
MLRKDIGIDLGTANTLVFLRGKGIVVNEPSVIAIDSTTGEILKVGLEAKNMIGKTPATIKAIRPM
RDGVIADYTVALVMLRYFINKAKGGMNLFKPRVVIGVPIGITDVERRAILDAGLEAGASKVFLIE
EPMAAAIGSN
>d1jcfa2 c.55.1.1 (A:141-336) Prokaryotic actin homolog MreB {Thermotoga maritima}
LNVEEPSGNMVVDIGGGTTEVAVISLGSIVTWESIRIAGDEMDEAIVQYVRETYRVAIGERTAER
VKIEIGNVFPSKENDELETTVSGIDLSTGLPRKLTLKGGEVREALRSVVVAIVESVRTTLEKTPP
ELVSDIIERGIFLTGGGSLLRGLDTLLQKETGISVIRSEEPLTAVAKGAGMVLDKVNILKKLQGA
G
>d1k8ka1 c.55.1.1 (A:3-160) Actin-related protein 3, Arp3 {Cow (Bos taurus)}
GRLPACVVDCGTGYTKLGYAGNTEPQFIIPSCIAIKESAKVGDQAQRRVMKGVDDLDFFIGDEAI
EKPTYATKWPIRHGIVEDWDLMERFMEQVIFKYLRAEPEDHYFLLTEPPLNTPENREYTAEIMFE
SFNVPGLYIAVQAVLALAASWTSRQVGE
>d1k8ka2 c.55.1.1 (A:161-418) Actin-related protein 3, Arp3 {Cow (Bos taurus)}
RTLTGTVIDSGDGVTHVIPVAEGYVIGSCIKHIPIAGRDITYFIQQLLRDREVGIPPEQSLETAK
AVKERYSYVCPDLVKEFNKYDTDGSKWIKQYTGINAISKKEFSIDVGYERFLGPEIFFHPEFANP
DFTQPISEVVDEVIQNCPIDVRRPLYKNIVLSGGSTMFRDFGRRLQRDLKRTVDARLKLSEELSG
GRLKPKPIDVQVITHHMQRYAVWFGGSMLASTPEFYQVCHTKKDYEEIGPSICRHNPVFGVMS
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>d1k8kb1 c.55.1.1 (B:154-343) Actin-related protein 2, Arp2 {Cow (Bos taurus)}
GVVVDSGDGVTHICPVYEGFSLPHLTRRLDIAGRDITRYLIKLLLLRGYAFNHSADFETVRMIKE
KLCYVGYNIEQEQKLALETTVLVESYTLPDGRIIKVGGERFEAPEALFQPHLINVEGVGVAELLF
NTIQAADIDTRSEFYKHIVLSGGSTMYPGLPSRLERELKQLYLERVLKGDVEKLSKFKIR
>d1e4ft1 c.55.1.1 (T:7-199) Cell division protein FtsA {Thermotoga maritima}
TVFYTSIDIGSRYIKGLVLGKRDQEWEALAFSSVKSRGLDEGEIKDAIAFKESVNTLLKELEEQL
QKSLRSDFVISFSSVSFEREDTVIERDFGEEKRSITLDILSEMQSEALEKLKENGKTPLHIFSKR
YLLDDERIVFNPLDMKASKIAIEYTSIVVPLKVYEMFYNFLQDTVKSPFQLKSSLVSTAEGVL
>d1e4ft2 c.55.1.1 (T:200-390) Cell division protein FtsA {Thermotoga maritima}
TTPEKDRGVVVVNLGYNFTGLIAYKNGVPIKISYVPVGMKHVIKDVSAVLDTSFEESERLIITHG
NAVYNDLKEEEIQYRGLDGNTIKTTTAKKLSVIIHARLREIMSKSKKFFREVEAKIVEEGEIGIP
GGVVLTGGGAKIPRINELATEVFKSPVRTGCYANSDRPSIINADEVANDPSFAAAFGNVFA
>d1huxa_ c.55.1.5 (A:) Hydroxyglutaryl-CoA dehydratase component A {Acidaminococcus fermentans}
SIYTLGIDVGSTASKCIILKDGKEIVAKSLVAVGTGTSGPARSISEVLENAHMKKEDMAFTLATG
YGRNSLEGIADKQMSELSCHAMGASFIWPNVHTVIDIGGQDVKVIHVENGTMTNFQMNDKCAAGT
GRFLDVMANILEVKVSDLAELGAKSTKRVAISSTCTVFAESEVISQLSKGTDKIDIIAGIHRSVA
SRVIGLANRVGIVKDVVMTGGVAQNYGVRGALEEGLGVEIKTSPLAQYNGALGAALYAYKKAAK
>d1g99a1 c.55.1.2 (A:1-156) Acetate kinase {Archaeon Methanosarcina thermophila}
MKVLVINAGSSSLKYQLIDMTNESALAVGLCERIGIDNSIITQKKFDGKKLEKLTDLPTHKDALE
EVVKALTDDEFGVIKDMGEINAVGHRVVHGGEKFTTSALYDEGVEKAIKDCFELAPLHNPPNMMG
ISACAEIMPGTPMVIVFDTAFHQTMP
>d1g99a2 c.55.1.2 (A:157-398) Acetate kinase {Archaeon Methanosarcina thermophila}
PYAYMYALPYDLYEKHGVRKYGFHGTSHKYVAERAALMLGKPAEETKIITCHLGNGSSITAVEGG
KSVETSMGFTPLEGLAMGTRCGSIDPAIVPFLMEKEGLTTREIDTLMNKKSGVLGVSGLSNDFRD
LDEAASKGNRKAELALEIFAYKVKKFIGEYSAVLNGADAVVFTAGIGENSASIRKRILTGLDGIG
IKIDDEKNKIRGQEIDISTPDAKVRVFVIPTNEELAIARETKEIVET
>d1ig8a1 c.55.1.3 (A:18-224) Hexokinase {Baker's yeast (Saccharomyces cerevisiae), pII}
DVPKELMQQIENFEKIFTVPTETLQAVTKHFISELEKGLSKKGGNIPMIPGWVMDFPTGKESGDF
LAIDLGGTNLRVVLVKLGGDRTFDTTQSKYRLPDAMRTTQNPDELWEFIADSLKAFIDEQFPQGI
SEPIPLGFTFSFPASQNKINEGILQRWTKGFDIPNIENHDVVPMLQKQITKRNIPIEVVALINDT
TGTLVASYYTDP
>d1ig8a2 c.55.1.3 (A:225-486) Hexokinase {Baker's yeast (Saccharomyces cerevisiae), pII}
ETKMGVIFGTGVNGAYYDVCSDIEKLQGKLSDDIPPSAPMAINCEYGSFDNEHVVLPRTKYDITI
DEESPRPGQQTFEKMSSGYYLGEILRLALMDMYKQGFIFKNQDLSKFDKPFVMDTSYPARIEEDP
FENLEDTDDLFQNEFGINTTVQERKLIRRLSELIGARAARLSVCGIAAICQKRGYKTGHIAADGS
VYNRYPGFKEKAANALKDIYGWTQTSLDDYPIKIVPAEDGSGAGAAVIAALAQKRIAEGKSVGII
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GA
>d1bdg_1 c.55.1.3 (13-222) Hexokinase {Blood fluke (Schistosoma mansoni)}
FSDQQLFEKVVEILKPFDLSVVDYEEICDRMGESMRLGLQKSTNEKSSIKMFPSYVTKTPNGTET
GNFLALDLGGTNYRVLSVTLEGKGKSPRIQERTYCIPAEKMSGSGTELFKYIAETLADFLENNGM
KDKKFDLGFTFSFPCVQKGLTHATLVRWTKGFSADGVEGHNVAELLQTELDKRELNVKCVAVVND
TVGTLASCALEDP
>d1bdg_2 c.55.1.3 (223-460) Hexokinase {Blood fluke (Schistosoma mansoni)}
KCAVGLIVGTGTNVAYIEDSSKVELMDGVKEPEVVINTEWGAFGEKGELDCWRTQFDKSMDIDSL
HPGKQLYEKMVSGMYLGELVRHIIVYLVEQKILFRGDLPERLKVRNSLLTRYLTDVERDPAHLLY
NTHYMLTDDLHVPVVEPIDNRIVRYACEMVVKRAAYLAGAGIACILRRINRSEVTVGVDGSLYKF
HPKFCERMTDMVDKLKPKNTRFCLRLSEDGSGKGAAAIAASC
>d1czan1 c.55.1.3 (N:16-222) Mammalian type I hexokinase {Human (Homo sapiens)}
DDQVKKIDKYLYAMRLSDETLIDIMTRFRKEMKNGLSRDFNPTATVKMLPTFVRSIPDGSEKGDF
IALDLGGSSFRILRVQVNHEKNQNVHMESEVYDTPENIVHGSGSQLFDHVAECLGDFMEKRKIKD
KKLPVGFTFSFPCQQSKIDEAILITWTKRFKASGVEGADVVKLLNKAIKKRGDYDANIVAVVNDT
VGTMMTCGYDDQ
>d1czan2 c.55.1.3 (N:223-465) Mammalian type I hexokinase {Human (Homo sapiens)}
HCEVGLIIGTGTNACYMEELRHIDLVEGDEGRMCINTEWGAFGDDGSLEDIRTEFDRAIDAYSLN
PGKQLFEKMVSGMYLGELVRLILVKMAKEGLLFEGRITPELLTRGKFNTSDVSAIEKNKEGLHNA
KEILTRLGVEPSDDDCVSVQHVCTIVSFRSANLVAATLGAILNRLRDNKGTPRLRTTVGVDGSLY
KTHPQYSRRFHKTLRRLVPDSDVRFLLSESGSGKGAAMVTAVAYRLAE
>d1czan3 c.55.1.3 (N:466-670) Mammalian type I hexokinase {Human (Homo sapiens)}
QHRQIEETLAHFHLTKDMLLEVKKRMRAEMELGLRKQTHNNAVVKMLPSFVRRTPDGTENGDFLA
LDLGGTNFRVLLVKIRSGKKRTVEMHNKIYAIPIEIMQGTGEELFDHIVSCISDFLDYMGIKGPR
MPLGFTFSFPCQQTSLDAGILITWTKGFKATDCVGHDVVTLLRDAIKRREEFDLDVVAVVNDTVG
TMMTCAYEEP
>d1czan4 c.55.1.3 (N:671-913) Mammalian type I hexokinase {Human (Homo sapiens)}
TCEVGLIVGTGSNACYMEEMKNVEMVEGDQGQMCINMEWGAFGDNGCLDDIRTHYDRLVDEYSLN
AGKQRYEKMISGMYLGEIVRNILIDFTKKGFLFRGQISETLKTRGIFETKFLSQIESDRLALLQV
RAILQQLGLNSTCDDSILVKTVCGVVSRRAAQLCGAGMAAVVDKIRENRGLDRLNVTVGVDGTLY
KLHPHFSRIMHQTVKELSPKCNVSFLLSEDGSGKGAALITAVGVRLRT
>d1bg3a1 c.55.1.3 (A:1-222) Mammalian type I hexokinase {Rat (Rattus norvegicus)}
MIAAQLLAYYFTELKDDQVKKIDKYLYAMRLSDEILIDILTRFKKEMKNGLSRDYNPTASVKMLP
TFVRSIPDGSEKGDFIALDLGGSSFRILRVQVNHEKNQNVSMESEIYDTPENIVHGSGTQLFDHV
ADCLGDFMEKKKIKDKKLPVGFTFSFPCRQSKIDEAVLITWTKRFKASGVEGADVVKLLNKAIKK
RGDYDANIVAVVNDTVGTMMTCGYDDQ
>d1bg3a2 c.55.1.3 (A:223-465) Mammalian type I hexokinase {Rat (Rattus

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norvegicus)}
QCEVGLIIGTGTNACYMEELRHIDLVEGDEGRMCINTEWGAFGDDGSLEDIRTEFDRELDRGSLN
PGKQLFEKMVSGMYMGELVRLILVKMAKEGLLFEGRITPELLTRGKFNTSDVSAIEKDKEGIQNA
KEILTRLGVEPSDVDCVSVQHICTIVSFRSANLVAATLGAILNRLRDNKGTPRLRTTVGVDGSLY
KMHPQYSRRFHKTLRRLVPDSDVRFLLSESGTGKGAAMVTAVAYRLAE
>d1bg3a3 c.55.1.3 (A:466-670) Mammalian type I hexokinase {Rat (Rattus
norvegicus)}
QHIRQIEETLAHFRLSKQTLMEVKKRLRTEMEMGLRKETNSKATVKMLPSFVRSIPDGTEHGDFL
ALDLGGTNFRVLLVKIRSGKKRTVEMHNKIYSIPLEIMQGTGDELFDHIVSCISDFLDYMGIKGP
RMPLGFTFSFPCHQTNLDCGILISWTKGFKATDCEGHDVASLLRDAVKRREEFDLDVVAVVNDTV
GTMMTCAYEEP
>d1bg3a4 c.55.1.3 (A:671-911) Mammalian type I hexokinase {Rat (Rattus
norvegicus)}
TCEIGLIVGTGTNACYMEEMKNVEMVEGNQGQMCINMEWGAFGDNGCLDDIRTDFDKVVDEYSLN
SGKQRFEKMISGMYLGEIVRNILIDFTKKGFLFRGQISEPLKTRGIFETKFLSQIESDRLALLQV
RAILQQLGLNSTCDDSILVKTVCGVVSKRAAQLCGAGMAAVVEKIRENRGLDHLNVTVGVDGTLY
KLHPHFSRIMHQTVKELSPKCTVSFLLSEDGSGKGAALITAVGVRL
>d1bu6o1 c.55.1.4 (O:3-253) Glycerol kinase {Escherichia coli}
KKYIVALDQGTTSSRAVVMDHDANIISVSQREFEQIYPKPGWVEHDPMEIWATQSSTLVEVLTKA
DISSDQIAAIGITNQRETTIVWEKETGKPIYNAIVWQCRRTAEICEHLKRDGLEDYIRSNTGLVI
DPYFSGTKVKWILDHVEGSRERARRGELLFGTVDTWLIWKMTQGRVHVTDYTNASRTMLFNIHTL
DWDDKMLEVLDIPREMLPEVRRSSEVYGQTNIGGKGGTRIPISGIAGDQQAALFGQ
>d1bu6o2 c.55.1.4 (O:254-499) Glycerol kinase {Escherichia coli}
LCVKEGMAKNTYGTGCFMLMNTGEKAVKSENGLLTTIACGPTGEVNYALEGAVFMAGASIQWLRD
EMKLINDAYDSEYFATKVQNTNGVYVVPAFTGLGAPYWDPYARGAIFGLTRGVNANHIIRATLES
IAYQTRDVLEAMQADSGIRLHALRVDGGAVANNFLMQFQSDILGTRVERPEVREVTALGAAYLAG
LAVGFWQNLDELQEKAVIEREFRPGIETTERNYRYAGWKKAVKRAMAWEEH
>d1chma1 c.55.2.1 (A:2-156) Creatinase {Pseudomonas putida}
QMPKTLRIRNGDKVRSTFSAQEYANRQARLRAHLAAENIDAAIFTSYHNINYYSDFLYCSFGRPY
ALVVTEDDVISISANIDGGQPWRRTVGTDNIVYTDWQRDNYFAAIQQALPKARRIGIEHDHLNLQ
NRDKLAARYPDAELVDVAAACMRMR
>d1az9_1 c.55.2.1 (1-176) Aminopeptidase P {Escherichia coli}
SEISRQEFQRRRQALVEQMQPGSAALIFAAPEVTRSADSEYPYRQNSDFWYFTGFNEPEAVLVLI
KSDDTHNHSVLFNRVRDLTAEIWFGRRLGQDAAPEKLGVDRALAFSEINQQLYQLLNGLDVVYHA
QGEYAYADVIVNSALEKLRKGSRQNLTAPATMIDWRPVVHEMRLFK
>d1jl1a_ c.55.3.1 (A:) RNase H (RNase HI) {Escherichia coli}
KQVEIFTAGSALGNPGPGGYGAILRYRGREKTFSAGYTRTTNNRMELMAAIVALEALKEHAEVIL
STDSQYVRQGITQWIHNWKKRGWKTADKKPVKNVDLWQRLDAALGQHQIKWEWVKGHAGHPENER
ADELARAAAMNPTLEDTGYQVE
>d1ril__ c.55.3.1 (-) RNase H (RNase HI) {Thermus thermophilus}
RKRVALFTDGACLGNPGPGGWAALLRFHAHEKLLSGGEACTTNNRMELKAAIEGLKALKEPCEVD
LYTDSHYLKKAFTEGWLEGWRKRGWRTAEGKPVKNRDLWEALLLAMAPHRVRFHFVKGHTGHPEN
ERVDREARRQAQSQAKT
>d1jl2a_ c.55.3.1 (A:) RNase H (RNase HI) {Chimeric (Escherichia
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coli/Thermus thermophilus)}
KQVEIFTDGSALGNPGPGGYGAILRYRGREKTFSAGYTRTTNNRMELKAAIEGLKALKEPAEVDL
YTDSHYLKKAFTEGWLEGWRKRGWRTAEGKPVKNRDLWEALLLAMAPHRVRFHFVKGHAGHPENE
RADELARAAAMNPTLEDTGY
>d1ekea_ c.55.3.1 (A:) Class II ribonuclease H (RNase HII) {Archaeon
Methanococcus jannaschii}
MIIIGIDEAGRGPVLGPMVVCAFAIEKEREEELKKLGVKDSKELTKNKRAYLKKLLENLGYVEKR
ILEAEEINQLMNSINLNDIEINAFSKVAKNLIEKLNIRDDEIEIYIDACSTNTKKFEDSFKDKIE
DIIKERNLNIKIIAEHKADAKYPVVSAASIIAKAERDEIIDYYKKIYGDIGSGYPSDPKTIKFLE
DYFKKHKKLPDIARTHWKTCKRILDKSKQT
>d1i39a_ c.55.3.1 (A:) Class II ribonuclease H (RNase HII) {Archaeon
Archaeoglobus fulgidus}
MKAGIDEAGKGCVIGPLVVAGVACSDEDRLRKLGVKDSKKLSQGRREELAEEIRKICRTEVLKVS
PENLDERMAAKTINEILKECYAEIILRLKPEIAYVDSPDVIPERLSRELEEITGLRVVAEHKADE
KYPLVAAASIIAKVEREREIERLKEKFGDFGSGYASDPRTREVLKEWIASGRIPSCVRMRWKTVS
NLRQK
>d1io2a_ c.55.3.1 (A:) Class II ribonuclease H (RNase HII) {Archaeon
Thermococcus kodakaraensis}
MKIAGIDEAGRGPVIGPMVIAAVVVDENSLPKLEELKVRDSKKLTPKRREKLFNEILGVLDDYVI
LELPPDVIGSREGTLNEFEVENFAKALNSLKVKPDVIYADAADVDEERFARELGERLNFEAEVVA
KHKADDIFPVVSAASILAKVTRDRAVEKLKEEYGEIGSGYPSDPRTRAFLENYYREHGEFPPIVR
KGWKTLKKIAEKVESEKK
>d1c9ra1 c.55.3.1 (A:430-558) HIV RNase H (Domain of reverse
transcriptase) {Human immunodeficiency virus type 1}
EKEPIVGAETFYVDGAANAATKLGKAGYVTNKGRQKVVPLTNTTNQKTELQAIYLALQDSGLEVN
IVTDSQYALGIIQAQPDKSESELVNQIIEALIKKEAVYLAWVPAHAGIGGNAAVDALVSAGIAA
>d1hrha1 c.55.3.1 (A:432-556) HIV RNase H (Domain of reverse
transcriptase) {Human immunodeficiency virus type 1}
EPIVGAETFYVDGAANRETKLGKAGYVTNKGRQKVVPLTNTTNQKTELQAIYLALQDSGLEVNIV
TDSQYALGIIQAQPDKSESELVNQIIEQLIKKEKVYLAWVPAHKGIGGNEQVDKLVSAGI
>d1jlaa1 c.55.3.1 (A:430-553) HIV RNase H (Domain of reverse
transcriptase) {Human immunodeficiency virus type 1}
EKEPIVGAETFYVDGAANRETKLGKAGYVTNRGRQKVVTLTDTTNQKTELQAIYLALQDSGLEVN
IVTDSQYALGIIQAQPDQSESELVNQIIEQLIKKEKVYLAWVPAHKGIGGNEQVDKLVS
>d1vrta1 c.55.3.1 (A:430-539) HIV RNase H (Domain of reverse
transcriptase) {Human immunodeficiency virus type 1}
EKEPIVGAETFYVDGAANRETKLGKAGYVTNRGRQKVVTLTDTTNQKTELQAIYLALQDSGLEVN
IVTDSQYALGIIQAQPDQSESELVNQIIEQLIKKEKVYLAWVPAH
>d1asu__ c.55.3.2 (-) Retroviral integrase, catalytic domain {Rous
sarcoma virus (RSV, avian sarcoma virus)}
PLREPRGLGPLQIWQTDFTLEPRMAPRSWLAVTVDTASSAIVVTQHGRVTSVAAQHHWATAIAVL
GRPKAIKTDNGSCFTSKSTREWLARWGIAHTTGIPGNSQGQAMVERANRLLKDKIRVLAEGDGFM
KRIPTSKQGELLAKAMYALNHFERGENTKTNL
>d1c0ma2 c.55.3.2 (A:49-216) Retroviral integrase, catalytic domain
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{Rous sarcoma virus (RSV, avian sarcoma virus)}
GVNPRGLGPLQIWQTDFTLEPRMAPRSWLAVTVDTASSAIVVTQHGRVTSVAVQHHWATAIAVLG
RPKAIKTDNGSCFTSKSTREWLARWGIAHTTGIPGNSQGQAMVERANRLLKDRIRVLAEGDGFMK
RIPTSKQGELLAKAMYALNHKERGENTKTPIQKHWRPT
>d1cxqa_ c.55.3.2 (A:) Retroviral integrase, catalytic domain {Rous sarcoma virus (RSV, avian sarcoma virus)}
GRGLGPLQIWQTDFTLEPRMAPRSWLAVTVDTASSAIVVTQHGRVTSVAAQHHWATAIAVLGRPK
AIKTDNGSCFTSKSTREWLARWGIAHTTGIPGNSQGQAMVERANRLLKDKIRVLAEGDGFMKRIP
TSKQGELLAKAMYALNH
>d1exqa_ c.55.3.2 (A:) Retroviral integrase, catalytic domain {Human immunodeficiency virus type 1}
SSPGIWQLDCTHLEGKVILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKTIHTDNGSN
FTGATVRAACDWAGIKQEDGIPYNPQSQGVVESMNKELKKIIGQVRDQAEHLKTAVQMAVFIHNK
KRKGGIGGYSAGERIVDIIATDIQ
>d1hyva_ c.55.3.2 (A:) Retroviral integrase, catalytic domain {Human immunodeficiency virus type 1}
SPGIWQLDCTHLEGKVILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKTVHTDNGSNF
TSTTVKAACWWAGIKQEFGIPYNPQSQGVIESMNKELKKIIGQVRDQAEHLKTAVQMAVFIHNKK
RKGGIGGYSAGERIVDIIATDIQT
>d1c6va_ c.55.3.2 (A:) Retroviral integrase, catalytic domain {Simian immunodeficiency virus}
NSDLGTWQMDCTHLEGKIVIVAVHVASGFIEAEVIPQETGRQTALFLLKLAGRWPITHLHTDNGA
NFASQEVKMVAWWAGIEHTFGVPYNPQSQGVVEAMNHHLKNQIDRIREQANSVETIVLMAVHCMN
HKRRGGIGDMTPAERLINMITTEQEIQFQ
>d1bco_2 c.55.3.3 (258-480) mu transposase, core domain {Bacteriophage mu}
EHLDAMQWINGDGYLHNVFVRWFNGDVIRPKTWFWQDVKTRKILGWRCDVSENIDSIRLSFMDVV
TRYGIPEDFHITIDNTRGAANKWLTGGAPNRYRFKVKEDDPKGLFLLMGAKMHWTSVVAGKGWGQ
AKPVERAFGVGGLEEYVDKHPALAGAYTGPNPQAKPDNYGDRAVDAELFLKTLAEGVAMFNARTG
RETEMCGGKLSFDDVFEREYARTIVRKP
>d1b7ea_ c.55.3.4 (A:) Transposase inhibitor (Tn5 transposase) {Escherichia coli}
SAEAIRKAGAMQTVKLAQEFPELLAIEDTTSLSYRHQVAEELGKLGSIQDKSRGWWVHSVLLLEA
TTFRTVGLLHQEWWMRPDDPADADEKESGKWLAAAATSRLRMGSMMSNVIAVCDREADIHAYLQD
KLAHNERFVVRSKHPRKDVESGLYLYDHLKNQPELGGYQISIPQKGVVDKRGKRKNRPARKASLS
LRSGRITLKQGNITLNAVLAEEINPPKGETPLKWLLLTSEPVESLAQALRVIDIYTHRWRIEEFH
KAWKTGAGAERQRMEEPDNLERMVSILSFVAVRLLQLRESFTLPQALRAQGLLKEAEHVESQSAE
TVLTPDECQLLGYLDKGKRKRKEKGSLQWAYMAIARLGGFMDSKRTGIASWGALWEGWEALQSKL
DGFLAAKDLMAQ
>d1f3ia_ c.55.3.4 (A:) Transposase inhibitor (Tn5 transposase) {Escherichia coli}
ALHRAADWAKSVFSSAALGDPRRTARLVNVAAQLAKYSGKSITISSEGSKAAQEGAYRFIRNPNV
SAEAIRKAGAMQTVKLAQEFPELLAIEDTTSLSYRHQVAEELGKLGSIQDKSRGWWVHSVLLLEA
TTFRTVGLLHQEWWMRPDDPADADEKESGKWLAAAATSRLRMGSMMSNVIAVCDREADIHAYLQD

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KLAHNERFVVRSKHPRKDVESGLYLYDHLKNQPELGGYQISIPQKGVVDKRGKRKNRPARKASLS
LRSGRITLKQGNITLNAVLAEEINPPKGETPLKWLLLTSEPVESLAQALRVIDIYTHRWRIEEFH
KAWKTGAGAERQRMEEPDNLERMVSILSFVAVRLLQLRESFTLPQALRAQGLLKEAEHVESQSAE
TVLTPDECQLLGYLDKGKRKRKEKAGSLQWAYMAIARLGGFMDSKRTGIASWGALWEGWEALQSK
LDGFLAAKDLMAQGIKIG
>d1kfsa1 c.55.3.5 (A:324-518) Exonuclease domain of prokaryotic DNA
polymerase {Escherichia coli}
MISYDNYVTILDEETLKAWIAKLEKAPVFAFDTETDSLDNISANLVGLSFAIEPGVAAYIPVAHD
YLDAPDQISRERALELLKPLLEDEKALKVGQNLKYDRGILANYGIELRGIAFDTMLESYILNSVA
GRHDMDSLAERWLKHKTITFEEIAGKGKNQLTFNQIALEEAGRYAAEDADVTLQLHLKMWPDLQK
>d1qtma1 c.55.3.5 (A:293-422) Exonuclease domain of prokaryotic DNA
polymerase {Thermus aquaticus}
ALEEAPWPPPEGAFVGFVLSRKEPMWADLLALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLS
VLALREGLGLPPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEEAGERAALSERLFANLWGRLEG
>d1xwl_1 c.55.3.5 (297-468) Exonuclease domain of prokaryotic DNA
polymerase {Bacillus stearothermophilus, newly identified strain as
yet unnamed}
AKMAFTLADRVTEEMLADKAALVVEVVEENYHDAPIVGIAVVNEHGRFFLRPETALADPQFVAWL
GDETKKKSMFDSKRAAVALKWKGIELCGVSFDLLLAAYLLDPAQGVDDVAAAAKMKQYEAVRPDE
AVYGKGAKRAVPDEPVLAEHLVRKAAAIWELERPFLDELRRN
>d1t7pa1 c.55.3.5 (A:1-210) Exonuclease domain of T7 DNA polymerase
{Bacteriophage T7}
MIVSDIEANALLESVTKFHCGVIYDYSTAEYVSYRPSDFGAYLDALEAEVARGGLIVFHNGHKYD
VPALTKLAKLQLNREFHLPRENCIDTLVLSRLIHSNLKDTDMGLLRSGKLPGALEAWGYRLGEMK
GEYKDDFKRMLEEQGEEYVDGMEWWNFNEEMMDYNVQDVVVTKALLEKLLSDKHYFPPEIDFTDV
GYTTFWSES
>d1noya_ c.55.3.5 (A:) Exonuclease domain of family B (archaeal and
phage) DNA polymerases {Bacteriophage T4}
DEFYISIETVGNNIVERYIDENGKERTREVEYLPTMFRHCKEESKYKDIYGKNCAPQKFPSMKDA
RDWMKRMEDIGLEALGMNDFKLAYISDTYGSEIVYDRKFVRVANCDIEVTGDKFPDPMKAEYEID
AITHYDSIDDRFYVFDLLNSMYGSVSKWDAKLAAKLDCEGGDEVPQEILDRVIYMPFDNERDMLM
EYINLWEQKRPAIFTGWNIEGFDVPYIMNRVKMILGERSMKRFSPIGRVKSKLLQNMYGSKEIYS
IDGVSILDYLDLYKKFAFTNLPSFSLESVAQHETKKGKLPYDGPINKLRETNHQRYISYNIIDVE
SVQAIDKIRGFIDLVLSMSYYAKMPFSGVMSPIKTWDAIIFNSLKGE
>d1ih7a1 c.55.3.5 (A:1-375) Exonuclease domain of family B (archaeal
and phage) DNA polymerases {Bacteriophage RB69}
MKEFYLTVEQIGDSIFERYIDSNGRERTREVEYKPSLFAHCPESQATKYFDIYGKPCTRKLFANM
RDASQWIKRMEDIGLEALGMDDFKLAYLSDTYNYEIKYDHTKIRVANFDIEVTSPDGFPEPSQAK
HPIDAITHYDSIDDRFYVFDLLNSPYGNVEEWSIEIAAKLQEQGGDEVPSEIIDKIIYMPFDNEK
ELLMEYLNFWQQKTPVILTGWNVESFDIPYVYNRIKNIFGESTAKRLSPHRKTRVKVIENMYGSR
EIITLFGISVLDYIDLYKKFSFTNQPSYSLDYISEFELNVGKLKYDGPISKLRESNHQRYISYNI
IDVYRVLQIDAKRQFINLSLDMGYYAKIQIQSVFSPIKTWDAIIFNSLKE
>d1tgoa1 c.55.3.5 (A:1-347) Exonuclease domain of family B (archaeal
and phage) DNA polymerases {Archaeon Thermococcus gorgonarius}
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MILDTDYITEDGKPVIRIFKKENGEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTVRV
VRAEKVKKKFLGRPIEVWKLYFTHPQDVPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPME
GDEELKMLAFDIETLYHEGEEFAEGPILMISYADEEGARVITWKNIDLPYVDVVSTEKEMIKRFL
KVVKEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFILGREGSEPKIQRMGDRFAVEVKGRIHFDL
YPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEEIAQAWETGEGLERVARYSMEDAKVTYELGKE
FFPMEAQLSRLVGQSLWDVSRS
>d1qhta1 c.55.3.5 (A:1-347) Exonuclease domain of family B (archaeal
and phage) DNA polymerases {Archaeon Thermococcus sp., 9on-7}
MILDTDYITENGKPVIRVFKKENGEFKIEYDRTFEPYFYALLKDDSAIEDVKKVTAKRHGTVVKV
KRAEKVQKKFLGRPIEVWKLYFNHPQDVPAIRDRIRAHPAVVDIYEYDIPFAKRYLIDKGLIPME
GDEELTMLAFAIATLYHEGEEFGTGPILMISYADGSEARVITWKKIDLPYVDVVSTEKEMIKRFL
RVVREKDPDVLITYNGDNFDFAYLKKRCEELGIKFTLGRDGSEPKIQRMGDRFAVEVKGRIHFDL
YPVIRRTINLPTYTLEAVYEAVFGKPKEKVYAEEIAQAWESGEGLERVARYSMEDAKVTYELGRE
FFPMEAQLSRLIGQSLWDVSRS
>d1d5aa1 c.55.3.5 (A:1-347) Exonuclease domain of family B (archaeal
and phage) DNA polymerases {Archaeon Desulfurococcus tok}
MILDADYITEDGKPVIRVFKKEKGEFKIDYDRDFEPYIYALLKDDSAIEDIKKITAERHGTTVRV
TRAERVKKKFLGRPVEVWKLYFTHPQDVPAIRDKIREHPAVVDIYEYDIPFAKRYLIDRGLIPME
GDEELRMLAFDIETLAHAGAAAGAGPILMISYADEEGARVITWKNIDLPYVESVSTEKEMIKRFL
KVIQEKDPDVLITYNGDNFDFAYLKKRSEMLGVKFILGRDGSEPKIQRMGDRFAVEVKGRIHFDL
YPVIRRTINLPTYTLETVYEPVFGQPAEKVYAEEIAEAWASGEGLERVARYSMEDAKATYELGKE
FFPMEAQLSRLVGQSLWDVSRS
>d1gcxa1 c.55.3.5 (A:1-347) Exonuclease domain of family B (archaeal
and phage) DNA polymerases {Archaeon Pyrococcus kodakaraensis}
MILDTDYITEDGKPVIRIFKKENGEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTV
KRVEKVQKKFLGRPVEVWKLYFTHPQDVPAIRDKIREHPAVIDIYEYDIPFAKRYLIDKGLVPME
GDEELKMLAFDIETLYHEGEEFAEGPILMISYADEEGARVITWKNVDLPYVDVVSTEREMIKRFL
RVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGINFALGRDGSEPKIQRMGDRFAVEVKGRIHFDL
YPVIRRTINLPTYTLEAVYEAVFGQPKEKVYAEEITTAWETGENLERVARYSMEDAKVTYELGKE
FLPMEAQLSRLIGQSLWDVSRS
>d1fxxa_ c.55.3.5 (A:) Exonuclease I {Escherichia coli}
QSTFLFHDYETFGTHPALDRPAQFAAIRTDSEFNVIGEPEVFYCKPADDYLPQPGAVLITGITPQ
EARAKGENEAAFAARIHSLFTVPKTCILGYNNVRFDDEVTRNIFYRNFYDPYAWSWQHDNSRWDL
LDVMRACYALRPEGINWPENDDGLPSFRLEHLTKANGIEHSNAHDAMADVYATIAMAKLVKTRQP
RLFDYLFTHRNKHKLMALIDVPQMKPLVHVSGMFGAWRGNTSWVAPLAWHPENRNAVIMVDLAGD
ISPLLELDSDTLRERLYTAKTDLGDNAAVPVKLVHINKCPVLAQANTLRPEDADRLGINRQHCLD
NLKILRENPQVREKVVAIFAEAEPFTPSDNVDAQLYNGFFSDADRAAMKIVLETEPRNLPALDIT
FVDKRIEKLLFNYRARNFPGTLDYAEQQRWLEHRRQVFTPEFLQGYADELQMLVQQYADDKEKVA
LLKALWQYADEIVEH
>d1hjra_ c.55.3.6 (A:) RuvC resolvase {Escherichia coli}
AIILGIDPGSRVTGYGVIRQVGRQLSYLGSGCIRTKVDDLPSRLKLIYAGVTEIITQFQPDYFAI
EQVFMAKNADSALKLGQARGVAIVAAVNQELPVFEYAARQVKQTVVGIGSAEKSQVQHMVRTLLK
LPANPQADAADALAIAITHCHVSQNAMQ
>d1kcfa2 c.55.3.7 (A:39-256) Mitochondrial resolvase ydc2 catalytic

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domain {Fission yeast (Schizosaccharomyces pombe)}
TSRVLGIDLGIKNFSYCFASQNEDSKVIIHNWSVENLTEKNGLDIQWTEDFQPSSMADLSIQLFN
TLHEKFNPHVILMERQRYRSGIATIPEWTLRVNMLESMLYALHYAEKRNSIEQKIQYPFLLSLSP
KSTYSYWASVLNTKASFSKKKSRVQMVKELIDGQKILFENEEALYKWNNGSRVEFKKDDMADSAL
IASGWMRWQAQLKHYRNFCKQFL
>d1jj2m_ c.55.4.1 (M:) Ribosomal protein L18 (L18p) {Archaeon
Haloarcula marismortui}
ATGPRYKVPMRRRREARTDYHQRLRLLKSGKPRLVARKSNKHVRAQLVTLGPNGDDTLASAHSSD
LAEYGWEAPTGNMPSAYLTGLLAGLRAQEAGVEEAVLDIGLNSPTPGSKVFAIQEGAIDAGLDIP
HNDDVLADWQRTRGAHIAEYDEQLEEPLYSGDFDAADLPEHFDELRETLLDGDIEL
>d1fjgk_ c.55.4.1 (K:) Ribosomal protein S11 {Thermus thermophilus}
KRQVASGRAYIHASYNNTIVTITDPDGNPITWSSGGVIGYKGSRKGTPYAAQLAALDAAKKAMAY
GMQSVDVIVRGTGAGREQAIRALQASGLQVKSIVDDTPVPHNGCRPKKKFRKAS
>d1dt9a1 c.55.4.2 (A:143-276) Middle domain of eukaryotic peptide
chain release factor subunit 1, ERF1 {Human (Homo sapiens)}
DSKFGFIVIDGSGALFGTLQGNTREVLHKFTVDLPKKHGRGGQSALRFARLRMEKRHNYVRKVAE
TAVQLFISGDKVNVAGLVLAGSADFKTELSQSDMFDQRLQSKVLKLVDISYGGENGFNQAIELST
EVLS
>d1eo1a_ c.55.5.1 (A:) Hypothetical protein MTH1175 {Archaeon
Methanobacterium thermoautotrophicum}
MKIAIASSGTDLGSEVSRFFGRAPYFMIVEMKKGNIESSEVIENPSASASGGAGIRTAQIIANNG
VKAVIASSPGPNAFEVLNELGIKIYRATGTSVEENLKLFTEGNLEEIRSPGSGRGRRRR
>d1ewqa3 c.55.6.1 (A:121-266) DNA repair protein MutS, domain II
{Thermus aquaticus}
LLQESLLPREANYLAAIATGDGWGLAFLDVSTGEFKGTVLKSKSALYDELFRHRPAEVLLAPELL
ENGAFLDEFRKRFPVMLSEAPFEPEGEGPLALRRARGALLAYAQRTQGGALSLQPFRFYDPGAFM
RLPEATLRALEVFEPL
>d1e3ma3 c.55.6.1 (A:117-269) DNA repair protein MutS, domain II
{Escherichia coli}
GTISDEALLQERQDNLLAAIWQDSKGFGYATLDISSGRFRLSEPADRETMAAELQRTNPAELLYA
EDFAEMSLIEGRRGLRRRPLWEFEIDTARQQLNLQFGTRDLVGFGVENAPRGLCAAGCLLQYAKD
TQRTTLPHIRSITMEREQDSIIM
>d1sfe_2 c.55.7.1 (12-92) Ada DNA repair protein {Escherichia coli}
LAVRYALADCELGRCLVAESERGICAILLGDDDATLISELQQMFPAADNAPADLMFQQHVREVIA
SLNQRDTPLTLPLDIR
>d1qnta2 c.55.7.1 (A:6-91) O6-alkylguanine-DNA alkyltransferase
{Human (Homo sapiens)}
EMKRTTLDSPLGKLELSGCEQGLHEIKLLGKGTSAADAVEVPAPAAVLGGPEPLMQCTAWLNAYF
HQPEAIEEFPVPALHHPVFQQ
>d1mgta2 c.55.7.1 (A:1-88) O6-alkylguanine-DNA alkyltransferase
{Archaeon Pyrococcus kodakaraensis}
MLSVEKFRVGERVVWIGVIFSGRVQGIAFAFDRGTLMKRIHDLAEHLGKRGVSISLDVQPSDYPE
KVFKVLIGELDNASFLRELSFEG
>d1cfza_ c.56.1.1 (A:) Hydrogenase maturating endopeptidase HybD
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{Escherichia coli}
MRILVLGVGNILLTDEAIGVRIVEALEQRYILPDYVEILDGGTAGMELLGDMANRDHLIIADAIV
SKKNAPGTMMILRDEEVPALFTNKISPHQLGLADVLSALRFTGEFPKKLTLVGVIPESLEPHIGL
TPTVEAMIEPALEQVLAALRESGVEAIPRSDS
>d1c8ba_ c.56.1.2 (A:) Germination protease {Bacillus megaterium}
MEKELDLSQYSVRTDLAVEAKDIALENQPKPNNQSEIKGVIVKEKEEQGVKISMVEITEEGAEAI
GKKKGRYVTLESVGIREQDTEKQEEAMEEVFAKELNFFIKSLNIPDDASCLVVGLGNLSVTPDAL
GPKAVDNLLITRHLFELQPESVQDGFRPVSAIVPGVMGMTGIETSDIIFGVVKKVNPDFIIAIDA
LAARSIERVNATIQISDSGIHPGSGVGNKRKEISYETLGIPVIAIGIPTVVDAVSITSDTIDFIL
KHFGREMKEQGKPSKSLLPSGMTFGEKKKLTEDDLPNEEQRQTYLGMIGTLPDEEKRRLIHEVLA
PLGHNLMVTPKEVDMFIEDMANVVAGGLNAALHHEVDQENFGAYTH
>d1ulb__ c.56.2.1 (-) Purine nucleoside phosphorylase, PNP {Human
(Homo sapiens)}
MENGYTYEDYKNTAEWLLSHTKHRPQVAIICGSGLGGLTDKLTQAQIFDYSEIPNFPRSTVPGHA
GRLVFGFLNGRACVMMQGRFHMYEGYPLWKVTFPVRVFHLLGVDTLVVTNAAGGLNPKFEVGDIM
LIRDHINLPGFSGQNPLRGPNDERFGDRFPAMSDAYDRTMRQRALSTWKQMGEQRELQEGTYVMV
AGPSFETVAECRVLQKLGADAVGMSTVPEVIVARHCGLRVFGFSLITNKVIMDYESLEKANHEEV
LAAGKQAAQKLEQFVSILMASIPLPDKAS
>d1b8oa_ c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP {Cow (Bos
taurus)}
NGYTYEDYQDTAKWLLSHTEQRPQVAVICGSGLGGLVNKLTQAQTFDYSEIPNFPESTVPGHAGR
LVFGILNGRACVMMQGRFHMYEGYPFWKVTFPVRVFRLLGVETLVVTNAAGGLNPNFEVGDIMLI
RDHINLPGFSGENPLRGPNEERFGVRFPAMSDAYDRDMRQKAHSTWKQMGEQRELQEGTYVMLGG
PNFETVAECRLLRNLGADAVGMSTVPEVIVARHCGLRVFGFSLITNKVIMDYESQGKANHEEVLE
AGKQAAQKLEQFVSLLMASI
>d1k9sa_ c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP
{Escherichia coli}
ATPHINAEMGDFADVVLMPGDPLRAKYIAETFLEDAREVNNVRGMLGFTGTYKGRKISVMGHGMG
IPSCSIYTKELITDFGVKKIIRVGSCGAVLPHVKLRDVVIGMGACTDSKVNRIRFKDHDFAAIAD
FDMVRNAVDAAKALGIDARVGNLFSADLFYSPDGEMFDVMEKYGILGVEMEAAGIYGVAAEFGAK
ALTICTVSDHIRTHEQTTAAERQTTFNDMIKIALESVLLGDK
>d1qe5a_ c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP
{Cellulomonas sp.}
PPLDDPATDPFLVARAAADHIAQATGVEGHDMALVLGSGWGGAAELLGEVVAEVPTHEIPGFSSV
TRSIRVERADGSVRHALVLGSRTHLYEGKGVRAVVHGVRTAAATGAETLILTNGCGGLNQEWGAG
TPVLLSDHINLTARSPLEGPTFVDLTDVYSPRLRELAHRVDPTLPEGVYAQFPGPHYETPAEVRM
AGILGADLVGMSTTLEAIAARHCGLEVLGVSLVTNLAAGISPTPLSHAEVIEAGQAAGPRISALL
ADIAKR
>d1g2oa_ c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP
{Mycobacterium tuberculosis}
DPDELARRAAQVIADRTGIGEHDVAVVLGSGWLPAVAALGSPTTVLPQAELPGFVPPTAAGHAGE
LLSVPIGAHRVLVLAGRIHAYEGHDLRYVVHPVRAARAAGAQIMVLTNAAGGLRADLQVGQPVLI
SDHLNLTARSPLVGGEFVDLTDAYSPRLRELARQSDPQLAEGVYAGLPGPHYETPAEIRMLQTLG
ADLVGMSTVHETIAARAAGAEVLGVSLVTNLAAGITGEPLSHAEVLAAGAASATRMGALLADVIA
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RF
>d1k3fa_ c.56.2.1 (A:) Uridine phosphorylase {Escherichia coli}
MSKSDVFHLGLTKNDLQGATLAIVPGDPDRVEKIAALMDKPVKLASHREFTTWRAELDGKPVIVC
STGIGGPSTSIAVEELAQLGIRTFLRIGTTGAIQPHINVGDVLVTTASVRLDGASLHFAPLEFPA
VADFECTTALVEAAKSIGATTHVGVTASSDTFYPGQERYDTYSGRVVRHFKGSMEEWQAMGVMNY
EMESATLLTMCASQGLRAGMVAGVIVNRTQQEIPNAETMKQTESHAVKIVVEAARRLL
>d1cb0a_ c.56.2.1 (A:) 5'-deoxy-5'-methylthioadenosine phosphorylase
{Human (Homo sapiens)}
AVKIGIIGGTGLDDPEILEGRTEKYVDTPFGKPSDALILGKIKNVDCVLLARHGRQHTIMPSKVN
YQANIWALKEEGCTHVIVTTACGSLREEIQPGDIVIIDQFIDRTTMRPQSFYDGSHSCARGVCHI
PMAEPFCPKTREVLIETAKKLGLRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVV
LAKEAGICYASIAMATDYDCWKEHEEAVSVDRVLKTLKENANKAKSLLLTTIPQIGSTEWSETLH
NLKNMAQFSVLLP
>d1je0a_ c.56.2.1 (A:) 5'-deoxy-5'-methylthioadenosine phosphorylase
{Archaeon Sulfolobus solfataricus}
PVHILAKKGEVAERVLVVGDPGRARLLSTLLQNPKLTNENRGFLVYTGKYNGETVSIATHGIGGP
SIAIVLEELAMLGANVFIRYGTTGALVPYINLGEYIIVTGASYNQGGLFYQYLRDNACVASTPDF
ELTNKLVTSFSKRNLKYYVGNVFSSDAFYAEDEEFVKKWSSRGNIAVEMECATLFTLSKVKGWKS
ATVLVVSDNLAKGGIWITKEELEKSVMDGAKAVLDTLTS
>d2pth__ c.56.3.1 (-) Peptidyl-tRNA hydrolase {Escherichia coli}
TIKLIVGLANPGAEYAATRHNAGAWFVDLLAERLRAPLREEAKFFGYTSRVTLGGEDVRLLVPTT
FMNLSGKAVAAMASFFRINPDEILVAHDELDLPPGVAKFKLGGGHGGHNGLKDIISKLGNNPNFH
RLRIGIGHPGDKNKVVGFVLGKPPVSEQKLIDEAIDEAARCTEMWFTDGLTKATNRLHAFKAQ
>d1a2za_ c.56.4.1 (A:) Pyrrolidone carboxyl peptidase (pyroglutamate
aminopeptidase) {Archaeon Thermococcus litoralis}
MKKVLITGFEPFGGDSKNPTEQIAKYFDRKQIGNAMVYGRVLPVSVKRATIELKRYLEEIKPEIV
INLGLAPTYSNITVERIAVNIIDARIPDNDGYQPIDEKIEEDAPLAYMATLPVRAITKTLRDNGI
PATISYSAGTYLCNYVMFKTLHFSKIEGYPLKAGFIHVPYTPDQVVNKFFLLGKNTPSMCLEAEI
KAIELAVKVSLDYLEKDRDDIKIPL
>d1auga_ c.56.4.1 (A:) Pyrrolidone carboxyl peptidase (pyroglutamate
aminopeptidase) {Bacillus amyloliquefaciens}
MEKKVLLTGFDPFGGETVNPSWEAVKRLNGAAEGPASIVSEQVPTVFYKSLAVLREAIKKHQPDI
IICVGQAGGRMQITPERVAINLNEARIPDNEGNQPVGEDISQGGPAAYWTGLPIKRIVEEIKKEG
IPAAVSYTAGTFVCNHLFYGLMDEISRHHPHIRGGFIHIPYIPEQTLQKSAPSLSLDHITKALKI
AAVTAAVHEDDIETG
>d1iofa_ c.56.4.1 (A:) Pyrrolidone carboxyl peptidase (pyroglutamate
aminopeptidase) {Archaeon Pyrococcus furiosus}
MKVLVTGFEPFGGEKINPTERIAKDLDGIKIGDAQVFGRVLPVVFGKAKEVLEKTLEEIKPDIAI
HVGLAPGRSAISIERIAVNAIDARIPDNEGKKIEDEPIVPGAPTAYFSTLPIKKIMKKLHERGIP
AYISNSAGLYLCNYVMYLSLHHSATKGYPKMSGFIHVPYIPEQIIDKIGKGQVPPSMCYEMELEA
VKVAIEVALEELL
>d2ctc__ c.56.5.1 (-) Carboxypeptidase A {Cow (Bos taurus)}
ARSTNTFNYATYHTLDEIYDFMDLLVAEHPQLVSKLQIGRSYEGRPIYVLKFSTGGSNRPAIWID
LGIHSREWITQATGVWFAKKFTEDYGQDPSFTAILDSMDIFLEIVTNPDGFAFTHSQNRLWRKTR
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SVTSSSLCVGVDANRNWDAGFGKAGASSSPCSETYHGKYANSEVEVKSIVDFVKDHGNFKAFLSI
HSYSQLLLYPYGYTTQSIPDKTELNQVAKSAVEALKSLYGTSYKYGSIITTIYQASGGSIDWSYN
QGIKYSFTFELRDTGRYGFLLPASQIIPTAQETWLGVLTIMEHTLNN
>d1pca_1 c.56.5.1 (1-308) Carboxypeptidase A {Pig (Sus scrofa)}
ARTTSTFNYATYHTLEEIYDFMDILVAEHPALVSKLQIGRSYEGRPIYVLKFSTGGSNRPAIWID
SGIHSREWITQASGVWFAKKITENYGQNSSFTAILDSMDIFLEIVTNPNGFAFTHSDNRLWRKTR
SKASGSLCVGSDSNRNWDAGFGGAGASSSPCAETYHGKYPNSEVEVKSITDFVKNNGNIKAFISI
HSYSQLLLYPYGYKTQSPADKSELNQIAKSAVAALKSLYGTSYKYGSIITVIYQASGGVIDWTYN
QGIKYSFSFELRDTGRRGFLLPASQIIPTAQETWLALLTIMEHTLNNS
>d1dtda_ c.56.5.1 (A:) Carboxypeptidase A {Human (Homo sapiens)}
FNFGAYHTLEEISQEMDNLVAEHPGLVSKVNIGSSFENRPMNVLKFSTGGDKPAIWLDAGIHARE
WVTQATALWTANKIVSDYGKDPSITSILDALDIFLLPVTNPDGYVFSQTKNRMWRKTRSKVSAGS
LCVGVDPNRNWDAGFGGPGASSNPCSDSYHGPSANSEVEVKSIVDFIKSHGKVKAFIILHSYSQL
LMFPYGYKCTKLDDFDELSEVAQKAAQSLSRLHGTKYKVGPICSVIYQASGGSIDWSYDYGIKYS
FAFELRDTGRYGFLLPARQILPTAEETWLGLKAIMEHVRDHPY
>d1nsa_1 c.56.5.1 (4-308) Carboxypeptidase B {Pig (Sus scrofa)}
TTGHSYEKYNNWETIEAWTEQVTSKNPDLISRSAIGTTFDGDNIYLLKVGKPGSNKPAIFMDCGF
HAREWISQAFCQWFVRDAVRTYGYEAHMTEFLDNLDFYVLPVLNIDGYIYTWTKNRMWRKTRSTN
AGSSCTGTDPNRNFNAGWCTVGASVNPCNETYCGSAAESEKETKALADFIRNNLSSIKAYLTIHS
YSQMILYPYSYDYKLPENDAELNSLAKGAVKELASLYGTSYSYGPGSTTIYPAAGGSDDWAYNQG
IKYSFTFELRDKGRFGFVLPESQIQATCQETMLAVKYVTNYTLEHL
>d1cpb__ c.56.5.1 (-) Carboxypeptidase B {Cow (Bos taurus)}
TTGHSYEKYNNWETIEAWTEQVASENPDLISRSAIGTTFLGNTIYLLKVGKPGSNKPAVFMDCGF
HAREWISPAFCQWFVREXXXXXXXEIHMTEFLDKLDFYVLPVVNIDGYIYTWTTNRMWRKTRSTR
AGSSCTGTDLNRNFDAGWCSIGASNNPCSETYCGSAAESEKESKAVADFIRNHLSSIKAYLTIHS
YSQMMLYPYSYDYKLPKNNVELNTLAKGAVKKLASLHGTTYSYGPGATTIYPASGGSDDWAYDQG
IKYSFTFELRDKGRYGFVLPESQIQPTCEETMLAIKYVTSYVLEHL
>d1h8la2 c.56.5.1 (A:4-304) Carboxypeptidase D, catalytic domain
{Crested duck (Lophonetta specularioides)}
QAVQPVDFRHHHFSDMEIFLRRYANEYPSITRLYSVGKSVELRELYVMEISDNPGIHEAGEPEFK
YIGNMHGNEVVGRELLLNLIEYLCKNFGTDPEVTDLVQSTRIHIMPSMNPDGYEKSQEGDRGGTV
GRNNSNNYDLNRNFPDQFFQVTDPPQPETLAVMSWLKTYPFVLSANLHGGSLVVNYPFDDDEQGI
AIYSKSPDDAVFQQLALSYSKENKKMYQGSPCKDLYPTEYFPHGITNGAQWYNVPGGMQDWNYLN
TNCFEVTIELGCVKYPKAEELPKYWEQNRRSLLQFIKQVHR
>d1obr__ c.56.5.2 (-) Carboxypeptidase T {Thermoactinomyces vulgaris}
DFPSYDSGYHNYNEMVNKINTVASNYPNIVKKFSIGKSYEGRELWAVKISDNVGTDENEPEVLYT
ALHHAREHLTVEMALYTLDLFTQNYNLDSRITNLVNNREIYIVFNINPDGGEYDISSGSYKSWRK
NRQPNSGSSYVGTDLNRNYGYKWGCCGGSSGSPSSETYRGRSAFSAPETAAMRDFINSRVVGGKQ
QIKTLITFHTYSELILYPYGYTYTDVPSDMTQDDFNVFKTMANTMAQTNGYTPQQASDLYITDGD
MTDWAYGQHKIFAFTFEMYPTSYNPGFYPPDEVIGRETSRNKEAVLYVAEKADCPYSVIGKSC
>d1lam_2 c.56.5.3 (160-484) Leucine aminopeptidase, C-terminal domain
{Cow (Bos taurus)}
FASGQNLARRLMETPANEMTPTKFAEIVEENLKSASIKTDVFIRPKSWIEEQEMGSFLSVAKGSE
EPPVFLEIHYKGSPNASEPPLVFVGKGITFDSGGISIKAAANMDLMRADMGGAATICSAIVSAAK
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LDLPINIVGLAPLCENMPSGKANKPGDVVRARNGKTIQVDNTDAEGRLILADALCYAHTFNPKVI
INAATLTGAMDIALGSGATGVFTNSSWLWNKLFEASIETGDRVWRMPLFEHYTRQVIDCQLADVN
NIGKYRSAGACTAAAFLKEFVTHPKWAHLDIAGVMTNKDEVPYLRKGMAGRPTRTLIEFLFRFSQ
>d1amp__ c.56.5.4 (-) Aminopeptidase {Aeromonas proteolytica}
MPPITQQATVTAWLPQVDASQITGTISSLESFTNRFYTTTSGAQASDWIASEWQALSASLPNASV
KQVSHSGYNQKSVVMTITGSEAPDEWIVIGGHLDSTIGSHTNEQSVAPGADDDASGIAAVTEVIR
VLSENNFQPKRSIAFMAYAAEEVGLRGSQDLANQYKSEGKNVVSALQLDMTNYKGSAQDVVFITD
YTDSNFTQYLTQLMDEYLPSLTYGFDTCGYACSDHASWHNAGYPAAMPFESKFNDYNPRIHTTQD
TLANSDPTGSHAKKFTQLGLAYAIEMGSATG
>d1qq9a_ c.56.5.4 (A:) Aminopeptidase {Streptomyces griseus}
APDIPLANVKAHLTQLSTIAANNGGNRAHGRPGYKASVDYVKAKLDAAGYTTTLQQFTSGGATGY
NLIANWPGGDPNKVLMAGAHLDSVSSGAGINDNGSGSAAVLETALAVSRAGYQPDKHLRFAWWGA
EELGLIGSKFYVNNLPSADRSKLAGYLNFDMIGSPNPGYFVYDDDPVIEKTFKNYFAGLNVPTEI
ETEGDGRSDHAPFKNVGVPVGGLFTGAGYTKSAAQAQKWGGTAGQAFDRCYHSSCDSLSNINDTA
LDRNSDAAAHAIWTLSS
>d1cg2a1 c.56.5.4 (A:26-213,A:327-414) Carboxypeptidase G2,
catalytic domain {Pseudomonas sp., strain rs-16}
QKRDNVLFQAATDEQPAVIKTLEKLVNIETGTGDAEGIAAAGNFLEAELKNLGFTVTRSKSAGLV
VGDNIVGKIKGRGGKNLLLMSHMDTVYLKGILAKAPFRVEGDKAYGPGIADDKGGNAVILHTLKL
LKEYGVRDYGTITVLFNTDEEKGSFGSRDLIQEEAKLADYVLSFEPTSAGDEKLSLGTXFNAGEG
GKKLVDKAVAYYKEAGGTLGVEERTGGGTDAAYAALSGKPVIESLGLPGFGYHSDKAEYVDISAI
PRRLYMAARLIMDLGAG
>d1de4c3 c.56.5.5 (C:122-189,C:383-608) Transferrin receptor
ectodomain, protease-like domain {Human (Homo sapiens)}
LYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSKVWRDQH
FVKXEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGVGTALLLKLAQMFSDMVLKDGFQ
PSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTYINLDKAVLGTSNFKVSASPLLYTLIEK
TMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAAFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTY
KELIERIPELNKVARAAAEVAGQFVIKLTHDVELN
>d1boub_ c.56.6.1 (B:) LigB subunit of an aromatic-ring-opening
dioxygenase LigAB {Pseudomonas paucimobilis}
ARVTTGITSSHIPALGAAIQTGTSDNDYWGPVFKGYQPIRDWIKQPGNMPDVVILVYNDHASAFD
MNIIPTFAIGCAETFKPADEGWGPRPVPDVKGHPDLAWHIAQSLILDEFDMTIMNQMDVDHGCTV
PLSMIFGEPEEWPCKVIPFPVNVVTYPPPSGKRCFALGDSIRAAVESFPEDLNVHVWGTGGMSHQ
LQGPRAGLINKEFDLNFIDKLISDPEELSKMPHIQYLRESGSEGVELVMWLIMRGALPEKVRDLY
TFYHIPASNTALGAMILQPEETAGTPLEPRKVMSGHSL
>d1di6a_ c.57.1.1 (A:) MogA {Escherichia coli}
ATLRIGLVSISDRASSGVYQDKGIPALEEWLTSALTTPFELETRLIPDEQAIIEQTLCELVDEMS
CHLVLTTGGTGPARRDVTPDATLAVADREMPGFGEQMRQISLHFVPTAILSRQVGVIRKQALILN
LPGQPKSIKETLEGVKDAEGNVVVHGIFASVPYCIQLLEGPYVETAPEVVAAFRPKSARR
>d1jlja_ c.57.1.1 (A:) Gephyrin N-terminal domain {Human (Homo
sapiens)}
HQIRVGVLTVSDSCFRNLAEDRSGINLKDLVQDPSLLGGTISAYKIVPDEIEEIKETLIDWCDEK
ELNLILTTGGTGFAPRDVTPEATKEVIEREAPGMALAMLMGSLNVTPLGMLSRPVCGIRGKTLII
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NLPGSKKGSQECFQFILPALPHAIDLLRDAIVKVKEVHD
>d1eava_ c.57.1.1 (A:) Plant CNX1 G domain {Mouse-ear cress
(Arabidopsis thaliana)}
GPEYKVAILTVSDTVSAGAGPDRSGPRAVSVVDSSSEKLGGAKVVATAVVPDEVERIKDILQKWS
DVDEMDLILTLGGTGFTPRDVTPEATKKVIERETPGLLFVMMQESLKITPFAMLSRSAAGIRGST
LIINMPGNPNAVAECMEALLPALKHALKQI
>d1g8la3 c.57.1.2 (A:178-326) MoeA, central domain {Escherichia coli}
VRVALFSTGDELQLPGQPLGDGQIYDTNRLAVHLMLEQLGCEVINLGIIRDDPHALRAAFIEADS
QADVVISSGGVSVGEADYTKTILEELGEIAFWKLAIKPGKPFAFGKLSNSWFCGLPGNPVSATLT
FYQLVQPLLAKLSGNTASG
>d1bgva2 c.58.1.1 (A:1-194) Glutamate dehydrogenase {Clostridium
symbiosum}
SKYVDRVIAEVEKKYADEPEFVQTVEEVLSSLGPVVDAHPEYEEVALLERMVIPERVIEFRVPWE
DDNGKVHVNTGYRVQFNGAIGPYKGGLRFAPSVNLSIMKFLGFEQAFKDSLTTLPMGGAKGGSDF
DPNGKSDREVMRFCQAFMTELYRHIGPDIDVPAGDLGVGAREIGYMYGQYRKIVGGFYNGVLTG
>d1gtma2 c.58.1.1 (A:3-180) Glutamate dehydrogenase {Archaeon
Pyrococcus furiosus}
ADPYEIVIKQLERAAQYMEISEEALEFLKRPQRIVEVTIPVEMDDGSVKVFTGFRVQHNWARGPT
KGGIRWHPEETLSTVKALAAWMTWKTAVMDLPYGGGKGGIIVDPKKLSDREKERLARGYIRAIYD
VISPYEDIPAPDVYTNPQIMAWMMDEYETISRRKTPAFGIITGKPLSI
>d1euza2 c.58.1.1 (A:4-180) Glutamate dehydrogenase {Archaeon
Thermococcus profundus}
IDPFEMAVKQLERAAQYMDISEEALEWLKKPMRIVEVSVPIEMDDGSVKVFTGFRVQHNWARGPT
KGGIRWHPAETLSTVKALATWMTWKVAVVDLPYGGGKGGIIVNPKELSEREQERLARAYIRAVYD
VIGPWTDIPAPDVYTNPKIMGWMMDEYETIMRRKGPAFGVITGKPLS
>d1bvua2 c.58.1.1 (A:3-180) Glutamate dehydrogenase {Archaeon
Thermococcus litoralis}
QDPFEIAVKQLERAAQYMDISEEALEFLKRPQRIVEVSIPVEMDDGSVKVFTGFRVQYNWARGPT
KGGIRWHPEETLSTVKALAAWMTWKTAVMDLPYGGGKGGVICNPKEMSDREKERLARGYVRAIYD
VISPYTDIPAPDVYTNPQIMAWMMDEYETISRRKDPSFGVITGKPPSV
>d1b26a2 c.58.1.1 (A:4-178) Glutamate dehydrogenase {Thermotoga
maritima}
SLYEMAVEQFNRAASLMDLESDLAEVLRRPKRVLIVEFPVRMDDGHVEVFTGYRVQHNVARGPAK
GGIRYHPDVTLDEVKALAFWMTWKTAVMNLPFGGGKGGVRVDPKKLSRNELERLSRRFFSEIQVI
IGPYNDIPAPDVNTNADVIAWYMDTYSMNVGHTVLGIVTGKPVEL
>d1hwxa2 c.58.1.1 (A:1-208) Glutamate dehydrogenase {Cow (Bos
taurus)}
ADREDDPNFFKMVEGFFDRGASIVEDKLVEDLKTRQTQEQKRNRVRGILRIIKPCNHVLSLSFPI
RRDDGSWEVIEGYRAQHSHQRTPCKGGIRYSTDVSVDEVKALASLMTYKCAVVDVPFGGAKAGVK
INPKNYTDEDLEKITRRFTMELAKKGFIGPGVDVPAPNMSTGEREMSWIADTYASTIGHYDINAH
ACVTGKPISQGGI
>d1leha2 c.58.1.1 (A:1-134) Leucine dehydrogenase {Bacillus
sphaericus}
MEIFKYMEKYDYEQLVFCQDEASGLKAVIAIHDTTLGPALGGARMWTYNAEEEAIEDALRLARGM
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TYKNAAAGLNLGGGKTVIIGDPFADKNEDMFRALGRFIQGLNGRYITAEDVGTTVDDMDLIHQET
DYVT
>d1c1da2 c.58.1.1 (A:1-148) Phenylalanine dehydrogenase {Rhodococcus sp., M4}
SIDSALNWDGEMTVTRFDAMTGAHFVIRLDSTQLGPAAGGTRAAQYSNLADALTDAGKLAGAMTL
KMAVSNLPMGGGKSVIALPAPRHSIDPSTWARILRIHAENIDKLSGNYWTGPDVNTNSADMDTLN
DTTEFVFGRSLERGGAGS
>d1a4ia2 c.58.1.2 (A:2-126) Tetrahydrofolate dehydrogenase/cyclohydrolase {Human (Homo sapiens)}
APAEILNGKEISAQIRARLKNQVTQLKEQVPGFTPRLAILQVGNRDDSNLYINVKLKAAEEIGIK
ATHIKLPRTTTESEVMKYITSLNEDSTVHGFLVQLPLDSENSINTEEVINAIAPEKDVDG
>d1b0aa2 c.58.1.2 (A:2-122) Tetrahydrofolate dehydrogenase/cyclohydrolase {Escherichia coli}
AAKIIDGKTIAQQVRSEVAQKVQARIAAGLRAPGLAVVLVGSNPASQIYVASKRKACEEVGFVSR
SYDLPETTSEAELLELIDTLNADNTIDGILVQLPLPAGIDNVKVLERIHPDKDVDG
>d1edza2 c.58.1.2 (A:3-148) Tetrahydrofolate dehydrogenase/cyclohydrolase {Baker's yeast (Saccharomyces cerevisiae)}
KPGRTILASKVAETFNTEIINNVEEYKKTHNGQGPLLVGFLANNDPAAKMYATWTQKTSESMGFR
YDLRVIEDKDFLEEAIIQANGDDSVNGIMVYFPVFGNAQDQYLQQVVCKEKDVEGLNHVYYQNLY
HNVRYLDKENRLKSIL
>d1do8a2 c.58.1.3 (A:21-279) Mitochondrial NAD(P)-dependenent malic enzyme {Human (Homo sapiens)}
IKEKGKPLMLNPRTNKGMAFTLQERQMLGLQGLLPPKIETQDIQALRFHRNLKKMTSPLEKYIYI
MGIQERNEKLFYRILQDDIESLMPIVYTPTVGLACSQYGHIFRRPKGLFISISDRGHVRSIVDNW
PENHVKAVVVTDGERILGLGDLGVYGMGIPVGKLCLYTACAGIRPDRCLPVCIDVGTDNIALLKD
PFYMGLYQKRDRTQQYDDLIDEFMKAITDRYGRNTLIQFEDFGNHNAFRFLRKYREKYCTFNDD
>d2uaga2 c.59.1.1 (A:298-437) UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase MurD {Escherichia coli}
GLPHRFEVVLEHNGVRWINDSKATNVGSTEAALNGLHVDGTLHLLLGGDGKSADFSPLARYLNGD
NVRLYCFGRDGAQLAALRPEVAEQTETMEQAMRLLAPRVQPGDMVLLSPACASLDQFKNFEQRGN
EFARLAKELG
>d1e8ca2 c.59.1.1 (A:338-497) UDP-N-acetylmuramyl tripeptide synthetase MurE {Escherichia coli}
VCGRMEVFTAPGKPTVVVDYAHTPDALEKALQAARLHCAGKLWCVFGCGGDRDKGKRPLMGAIAE
EFADVAVVTDDNPRTEEPRAIINDILAGMLDAGHAKVMEGRAEAVTCAVMQAKENDVVLVAGKGH
EDYQIVGNQRLDYSDRVTVARLLGVIARSH
>d1gg4a1 c.59.1.1 (A:313-447) UDP-murNac-tripeptide D-alanyl-D-alanine-adding enzyme MurF {Escherichia coli}
VPGRLFPIQLAENQLLLDDSYNANVGSMTAAVQVLAEMPGYRVLVVGDMAELGAESEACHVQVGE
AAKAAGIDRVLSVGKQSHAISTASGVGEHFADKTALITRLKLLIAEQQVITILVKGSRSAAMEEV
VRALQ
>d1jbwa1 c.59.1.2 (A:297-425) Folylpolyglutamate synthetase,
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C-terminal domain {Lactobacillus casei}
WPARLEKISDTPLIVIDGAHNPDGINGLITALKQLFSQPITVIAGILADKDYAAMADRLTAAFST
VYLVPVPGTPRALPEAGYEALHEGRLKDSWQEALAASLNDVPDQPIVITGSLYLASAVRQTLLG
>d1qhfa_ c.60.1.1 (A:) Phosphoglycerate mutase {Baker's yeast
(Saccharomyces cerevisiae)}
PKLVLVRHGQSEWNEKNLFTGWVDVKLSAKGQQEAARAGELLKEKKVYPDVLYTSKLSRAIQTAN
IALEKADRLWIPVNRSWRLNERHYGDLQGKDKAETLKKFGEEKFNTYRRSFDVPPPPIDASSPFS
QKGDERYKYVDPNVLPETESLALVIDRLLPYWQDVIAKDLLSGKTVMIAAHGNSLRGLVKHLEGI
SDADIAKLNIPTGIPLVFELDENLKPSKPSYYLDPEAAAAGAAAV
>d3pgm__ c.60.1.1 (-) Phosphoglycerate mutase {Baker's yeast
(Saccharomyces cerevisiae)}
PKLVLVRHGQSEWNEKNLFTGWVDVKLSAKGQQEAARAGELLKEKGVNVLVDYTSKLSRAIQTAN
IALEKADRLWIPVNRSWRLNERHYGDLQGKDKAQTLKKFGEEKFNTYRRSFDVPPPPIDASSPFS
QKGDERYKYVDPNVLPETESLALVIDRLLPYWQDVIAKLVGKTSMIAAHGNSLRGLVKHLEGISD
ADIAKLNIPPGTILVFELDENLKPSKPSYYLDPEA
>d1fzta_ c.60.1.1 (A:) Phosphoglycerate mutase {Yeast
(Schizosaccharomyces pombe)}
MTTEAAPNLLVLTRHGESEWNKLNLFTGWKDPALSETGIKEAKLGGERLKSRGYKFDIAFTSALQ
RAQKTCQIILEEVGEPNLETIKSEKLNERYYGDLQGLNKDDARKKWGAEQVQIWRRSYDIAPPNG
ESLKDTAERVLPYYKSTIVPHILKGEKVLIAAHGNSLRALIMDLEGLTGDQIVKRELATGVPIVY
HLDKDGKYVSKELIDN
>d1e58a_ c.60.1.1 (A:) Phosphoglycerate mutase {Escherichia coli}
AVTKLVLVRHGESQWNKENRFTGWYDVDLSEKGVSEAKAAGKLLKEEGYSFDFAYTSVLKRAIHT
LWNVLDELDQAWLPVEKSWKLNERHYGALQGLNKAETAEKYGDEQVKQWRRGFAVTPPELTKDDE
RYPGHDPRYAKLSEKELPLTESLALTIDRVIPYWNETILPRMKSGERVIIAAHGNSLRALVKYLD
NMSEEEILELNIPTGVPLVYEFDENFKPLKRYYLGNADEIAAKAAAVANQGK
>d1ebba_ c.60.1.1 (A:) Broad specificity phosphatase YhfR {Bacillus
stearothermophilus}
ATTLYLTRHGETKWNVERRMQGWQDSPLTEKGRQDAMRLGKRLEAVELAAIYTSTSGRALETAEI
VRGGRLIPIYQDERLREIHLGDWEGKTHDEIRQMDPIAFDHFWQAPHLYAPQRGERFCDVQQRAL
EAVQSIVDRHEGETVLIVTHGVVLKTLMAAFKDTPLDHLWSPPYMYGTSVTIIEVDGGTFHVAVE
GDVSHIE
>d1rpa__ c.60.1.2 (-) Acid phosphatase {Rat (Rattus norvegicus)}
KELKFVTLVFRHGDRGPIETFPNDPIKESSWPQGFGQLTKWGMGQHYELGSYIRRRYGRFLNNSY
KHDQVYIRSTDVDRTLMSAMTNLAALFPPEGNSIWNPRLLWQPIPVHTVSLSEDRLLYLPFRDCP
RFQELKSETLKSEEFLKRLQPYKSFIDTLPSLSGFEDQDLFEIWSRLYDPLYCESVHNFTLPTWA
TEDAMTKLKELSELSLLSLYGIHKQKEKSRLQGGVLVNEILKNMKLATQPQKARKLIMYSAHDTT
VSGLQMALDVYNGLLPPYASCHIMELYQDNGGHFVEMYYRNETQNEPYPLTLPGCTHSCPLEKFA
ELLDPVIPQDWATECMG
>d2hpaa_ c.60.1.2 (A:) Acid phosphatase {Human (Homo sapiens)}
KELKFVTLVFRHGDRSPIDTFPTDPIKESSWPQGFGQLTQLGMEQHYELGEYIRKRYRKFLNESY
KHEQVYIRSTDVDRTLMSAMTNLAALFPPEGVSIWNPILLWQPIPVHTVPLSEDQLLYLPFRNCP
RFQELESETLKSEEFQKRLHPYKDFIATLGKLSGLHGQDLFGIWSKVYDPLYCESVHNFTLPSWA
TEDTMTKLRELSELSLLSLYGIHKQKEKSRLQGGVLVNEILNHMKRATQIPSYKKLIMYSAHDTT
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VSGLQMALDVYNGLLPPYASCHLTELYFEKGEYFVEMYYRNETQHEPYPLMLPGCSPSCPLERFA
ELVGPVIPQDWSTECMT
>d1ihp__ c.60.1.3 (-) Phytase
(myo-inositol-hexakisphosphate-3-phosphohydrolase) {Aspergillus
ficuum}
SCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKK
YSALIEEIQQNATTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIR
SSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELA
DTVEANFTATFVPSIRQRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDE
WINYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNST
LYADFSHDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQE
PLVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA
>d1qfxa_ c.60.1.3 (A:) Phytase
(myo-inositol-hexakisphosphate-3-phosphohydrolase) {Aspergillus
niger}
KQFSQEFRDGYSILKHYGGNGPYSERVSYGIARDPPTSCEVDQVIMVKRHGERYPSPSAGKDIEE
ALAKVYSINTTEYKGDLAFLNDWTYYVPNECYYNAETTSGPYAGLLDAYNHGNDYKARYGHLWNG
ETVVPFFSSGYGRVIETARKFGEGFFGYNYSTNAALNIISESEVMGADSLTPTCDTDNDQTTCDN
LTYQLPQFKVAAARLNSQNPGMNLTASDVYNLMVMASFELNARPFSNWINAFTQDEWVSFGYVED
LNYYYCAGPGDKNMAAVGAVYANASLTLLNQGPKEAGSLFFNFAHDTNITPILAALGVLIPNEDL
PLDRVAFGNPYSIGNIVPMGGHLTIERLSCQATALSDEGTYVRLVLNEAVLPFNDCTSGPGYSCP
LANYTSILNKNLPDYTTTCNVSASYPQYLSFWWNYNTTTELNYRSSPIACQEGDAMD
>d1dkla_ c.60.1.3 (A:) Phytase
(myo-inositol-hexakisphosphate-3-phosphohydrolase) {Escherichia
coli}
SEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWPTWPVKLGWLTPRGGELIAYLGHYQRQRL
VADGLLAKKGCPQSGQVAIIADVDERTRKTGEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTG
VCQLDNANVTDAILSRAGGSIADFTGHRQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPS
ELKVSADNVSLTGAVSLASMLTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTP
EVARSRATPLLDLIKTALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDN
TPPGGELVFERWRRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMC
SLAGFTQIVNEARIPACSL
>d1bif_2 c.60.1.4 (250-468)
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase
domain {Rat (Rattus norvegicus)}
SIYLCRHGESELNLKGRIGGDPGLSPRGREFSKHLAQFISDQNIKDLKVFTSQMKRTIQTAEALS
VPYEQFKVLNEIDAGVCEEMTYEEIQDHYPLEFALRDQDKYRYRYPKGESYEDLVQRLEPVIMEL
ERQENVLVICHQAVMRCLLAYFLDKAAEELPYLKCPLHTVLKLTPVAYGCKVESIFLNVAAVNTH
RDRPQNVDISRPSEEALVTVPAHQ
>d1fbta_ c.60.1.4 (A:)
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase
domain {Rat (Rattus norvegicus)}
RSIYLCRHGESELNLRGRIGGDSGLSARGKQYAYALANFIRSQGISSLKVWTSHMKRTIQTAEAL
GVPYEQWKALNEIDAGVCEEMTYEEIQEHYPEEFALRDQDKYRYRYPKGESYEDLVQRLEPVIME
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LERQENVLVICHQAVMRCLLAYFLDKSSDELPYLKCPLHTVLKLTPVAYGCRVESIYLNV
>d1nula_ c.61.1.1 (A:) Xantine-guanine PRTase (XPRTase) {Escherichia
coli}
EKYIVTWDMLQIHARKLASRLMPSEQWKGIIAVSRGGLVPGALLARELGIRHVDTVCISSYDHDN
QRELKVLKRAEGDGEGFIVIDDLVDTGGTAVAIREMYPKAHFVTIFAKPAGRPLVDDYVVDIPQD
TWIEQPWDMGVVFVPPISGR
>d1hgxa_ c.61.1.1 (A:) Hypoxantine-guanine-xanthine PRTase
{Tritrichomonas foetus}
MDDLERVLYNQDDIQKRIRELAAELTEFYEDKNPVMICVLTGAVFFYTDLLKHLDFQLEPDYIIC
SSYSGTKSTGNLTISKDLKTNIEGRHVLVVEDIIDTGLTMYQLLNNLQMRKPASLKVCTLCDKDI
GKKAYDVPIDYCGFVVENRYIIGYGFDFHNKYRNLPVIGILKE
>d1fsga_ c.61.1.1 (A:) Hypoxantine-guanine-xanthine PRTase
{Toxoplasma gondii}
GSHMASKPIEDYGKGKGRIEPMYIPDNTFYNADDFLVPPHCKPYIDKILLPGGLVKDRVEKLAYD
IHRTYFGEELHIICILKGSRGFFNLLIDYLATIQKYSGRESSVPPFFEHYVRLKSYQNDNSTGQL
TVLSDDLSIFRDKHVLIVEDIVDTGFTLTEFGERLKAVGPKSMRIATLVEKRTDRSNSLKGDFVG
FSIEDVWIVGCCYDFNEMFRDFDHVAVLSDAARKKFEK
>d1gph11 c.61.1.1 (1:235-465) Glutamine PRPP amidotransferase,
C-terminal domain {Bacillus subtilis}
ICSMEYIYFSRPDSNIDGINVHSARKNLGKMLAQESAVEADVVTGVPDSSISAAIGYAEATGIPY
ELGLIKNRYVGRTFIQPSQALREQGVRMKLSAVRGVVEGKRVVMVDDSIVRGTTSRRIVTMLREA
GATEVHVKISSPPIAHPCFYGIDTSTHEELIASSHSVDEIRQEIGADTLSFLSVEGLLKGIGRKY
DDSNCGQCLACFTGKYPTEIYQDTVLPHVKEAVLTK
>d1ecfa1 c.61.1.1 (A:250-492) Glutamine PRPP amidotransferase,
C-terminal domain {Escherichia coli}
NPCLFEYVYFARPDSFIDKISVYSARVNMGTKLGEKIAREWEDLDIDVVIPIPETSCDIALEIAR
ILGKPYRQGFVKNRYVGRTFIMPGQQLRRKSVRRKLNANRAEFRDKNVLLVDDSIVRGTTSEQII
EMAREAGAKKVYLASAAPEIRFPNVYGIDMPSATELIAHGREVDEIRQIIGADGLIFQDLNDLID
AVRAENPDIQQFECSVFNGVYVTKDVDQGYLDFLDTLRNDDAKAVQRQ
>d1dqna_ c.61.1.1 (A:) Guanine PRTase {Giardia lamblia}
MICSVTGKPVKDVLSTFFKDRNDVLESEVKKFHLLATFEECKALAADTARRMNEYYKDVAEPVTL
VALLTGAYLYASLLTVHLTFPYTLHFVKVSSYKGTRQESVVFDEEDLKQLKEKREVVLIDEYVDS
GHTIFSIQEQIKHAKICSCFVKDVDAIKKHSALADTKMFYGYTPMPKGSWLIGFGLDDNGLRRGW
AHLFDINLSESEVTEFRRRLTEHIKGLNINGVNRY
>d1bzya_ c.61.1.1 (A:) Hypoxantine-guanine PRTase (HGPRTase) {Human
(Homo sapiens)}
SPGVVISDDEPGYDLDLFCIPNHYAEDLERVFIPHGLIMDRTERLARDVMKEMGGHHIVALCVLK
GGYKFFADLLDYIKALNRNSDRSIPMTVDFIRLKSYCNDQSTGDIKVIGGDDLSTLTGKNVLIVE
DIIDTGKTMQTLLSLVRQYNPKMVKVASLLVKRTPRSVGYKPDFVGFEIPDKFVVGYALDYNEYF
RDLNHVCVISETGKAKYKA
>d1cjba_ c.61.1.1 (A:) Hypoxantine-guanine PRTase (HGPRTase)
{Plasmodium falciparum}
PIPNNPGAGENAFDPVFVNDDDGYDLDSFMIPAHYKKYLTKVLVPNGVIKNRIEKLAYDIKKVYN
NEEFHILCLLKGSRGFFTALLKHLSRIHNYSAVETSKPLFGEHYVRVKSYCNDQSTGTLEIVSED
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LSCLKGKHVLIVEDIIDTGKTLVKFCEYLKKFEIKTVAIACLFIKRTPLWNGFKADFVGFSIPDH
FVVGYSLDYNEIFRDLDHCCLVNDEGKKKYKAT
>d1tc1a_ c.61.1.1 (A:) Hypoxanthine PRTase {Trypanosoma cruzi}
YEFAEKILFTEEEIRTRIKEVAKRIADDYKGKGLRPYVNPLVLISVLKGSFMFTADLCRALCDFN
VPVRMEFICVSSYGEGLTSSGQVRMLLDTRHSIEGHHVLIVEDIVDTALTLNYLYHMYFTRRPAS
LKTVVLLDKREGRRVPFSADYVVANIPNAFVIGYGLDYDDTYRELRDIVVLRPE
>d1qb7a_ c.61.1.1 (A:) Adenine PRTase {Leishmania donovani}
PFKEVSPNSFLLDDSHALSQLLKKSYRWYSPVFSPRNVPRFADVSSITESPETLKAIRDFLVQRY
RAMSPAPTHILGFDARGFLFGPMIAVELEIPFVLMRKADKNAGLLIRSEPYEKEYKEAAPEVMTI
RYGSIGKGSRVVLIDDVLATGGTALSGLQLVEASDAVVVEMVSILSIPFLKAAEKIHSTANSRYK
DIKFISLLSDDALTEENCGDSKNYTGPRVLSCGDVLAEHPH
>d1g2qa_ c.61.1.1 (A:) Adenine PRTase {Baker's yeast (Saccharomyces cerevisiae)}
MPIASYAQELKLALHQYPNFPSEGILFEDFLPIFRNPGLFQKLIDAFKLHLEEAFPEVKIDYIVG
LESRGFLFGPTLALALGVGFVPVRKAGKLPGECFKATYEKEYGSDLFEIQKNAIPAGSNVIIVDD
IIATGGSAAAAGELVEQLEANLLEYNFVMELDFLKGRSKLNAPVFTLL
>d1oroa_ c.61.1.1 (A:) Orotate PRTase {Escherichia coli}
MKPYQRQFIEFALSKQVLKFGEFTLKSGRKSPYFFNAGLFNTGRDLALLGRFYAEALVDSGIEFD
LLFGPAYKGIPIATTTAVALAEHHDLDLPYCFNRKEAKDHGEGGNLVGSALQGRVMLVDDVITAG
TAIRESMEIIQANGATLAGVLISLDRQERGRGEISAIQEVERDYNCKVISIITLKDLIAYLEEKP
EMAEHLAAVKAYREEFGV
>d1a3c__ c.61.1.1 (-) Uracil PRTase {Bacillus subtilis}
QKAVILDEQAIRRALTRIAHEMIERNKGMNNCILVGIKTRGIYLAKRLAERIEQIEGNPVTVGEI
DITLYRDDLSKKTSNDEPLVKGADIPVDITDQKVILVDDVLYTGRTVRAGMDALVDVGRPSSIQL
AVLVDRGHRELPIRADYIGKNIPTSKSEKVMVQLDEVDQNDLVAIYEN
>d1bd3a_ c.61.1.1 (A:) Uracil PRTase {Toxoplasma gondii}
QEESILQDIITRFPNVVLMKQTAQLRAMMTIIRDKETPKEEFVFYADRLIRLLIEEALNELPFQK
KEVTTPLDVSYHGVSFYSKICGVSIVRAGESMESGLRAVCRGVRIGKILIQRDETTAEPKLIYEK
LPADIRERWVMLLDPMCATAGSVCKAIEVLLRLGVKEERIIFVNILAAPQGIERVFKEYPKVRMV
TAAVDICLNSRYYIVPGIGDFGDRYFGTM
>d1dkra1 c.61.1.2 (A:8-166) Phosphoribosylpyrophosphate synthetase {Bacillus subtilis}
NLKIFSLNSNPELAKEIADIVGVQLGKCSVTRFSDGEVQINIEESIRGCDCYIIQSTSDPVNEHI
MELLIMVDALKRASAKTINIVIPYYGYARQDRKARSREPITAKLFANLLETAGATRVIALDLHAP
QIQGFFDIPIDHLMGVPILGEYFEGKNLE
>d1dkra2 c.61.1.2 (A:167-316) Phosphoribosylpyrophosphate synthetase {Bacillus subtilis}
DIVIVSPDHGGVTRARKLADRLKAPIAIIDKRRPRPNVAEVMNIVGNIEGKTAILIDDIIDTAGT
ITLAANALVENGAKEVYACCTHPVLSGPAVERINNSTIKELVVTNSIKLPEEKKIERFKQLSVGP
LLAEAIIRVHEQQSVSYLFS
>d1lfaa_ c.62.1.1 (A:) Integrin CD11a/CD18 (Leukocyte function associated antigen-1, LFA-1) {Human (Homo sapiens)}
GNVDLVFLFDGSMSLQPDEFQKILDFMKDVMKKLSNTSYQFAAVQFSTSYKTEFDFSDYVKRKDP
DALLKHVKHMLLLTNTFGAINYVATEVFREELGARPDATKVLIIITDGEATDSGNIDAAKDIIRY

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IIGIGKHFQTKESQETLHKFASKPASEFVKILDTFEKLKDLFTELQKKIYVIE
>d1atza_ c.62.1.1 (A:) von Willebrand factor A3 domain {Human (Homo sapiens)}
QPLDVILLLDGSSSFPASYFDEMKSFAKAFISKANIGPRLTQVSVLQYGSITTIDVPWNVVPEKA
HLLSLVDVMQREGGPSQIGDALGFAVRYLTSEMHGARPGASKAVVILVTDVSVDSVDAAADAARS
NRVTVFPIGIGDRYDAAQLRILAGPAGDSNVVKLQRIEDLPTMVTLGNSFLHKL
>d1fnsa_ c.62.1.1 (A:) von Willebrand factor A1 domain {Human (Homo sapiens)}
MYCSRLLDLVFLLDGSSRLSEAEFEVLKAFVVDMMERLRVSQKWVRVAVVEYHDGSHAYIGLKDR
KRPSELRRIASQVKYAGSQVASTSEVLKYTLFQIFSKIDRPEASRIALLLMASQEPQRMSRNFVR
YVQGLKKKKVIVIPVGIGPHANLKQIRLIEKQAPENKAFVLSSVDELEQQRDEIVSYLCDLAPEA
P
>d1ido__ c.62.1.1 (-) Integrin CR3 (CD11b/CD18, Mac-1), alpha subunit {Human (Homo sapiens)}
DSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFKEFQNNPNPR
SLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEADR
EGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNQLREK
>d1qc5a_ c.62.1.1 (A:) Integrin alpha1-beta1 {Human (Homo sapiens)}
STQLDIVIVLDGSNSIYPWDSVTAFLNDLLERMDIGPKQTQVGIVQYGENVTHEFNLNKYSSTEE
VLVAAKKIVQRGGRQTMTALGTDTARKEAFTEARGARRGVKKVMVIVTDGESHDNHRLKKVIQDC
EDENIQRFSIAILGSYNRGNLSTEKFVEEIKSIASEPTEKHFFNVSDEIALVTIVKTLGERI
>d1ck4a_ c.62.1.1 (A:) Integrin alpha1-beta1 {Rat (Rattus norvegicus)}
TQLDIVIVLDGSNSIYPWESVIAFLNDLLKRMDIGPKQTQVGIVQYGENVTHEFNLNKYSSTEEV
LVAANKIGRQGGLQTMTALGIDTARKEAFTEARGARRGVKKVMVIVTDGESHDNYRLKQVIQDCE
DENIQRFSIAILGHYNRGNLSTEKFVEEIKSIASEPTEKHFFNVSDELALVTIVKALGERIFA
>d1aoxa_ c.62.1.1 (A:) Integrin alpha2-beta1 {Human (Homo sapiens)}
SCPSLIDVVVVCDESNSIYPWDAVKNFLEKFVQGLDIGPTKTQVGLIQYANNPRVVFNLNTYKTK
EEMIVATSQTSQYGGDLTNTFGAIQYARKYAYSAASGGRRSATKVMVVVTDGESHDGSMLKAVID
QCNHDNILRFGIAVLGYLNRNALDTKNLIKEIKAIASIPTERYFFNVSDEAALLEKAGTLGEQIF
SIEGGT
>d1jv2b2 c.62.1.1 (B:107-354) Integrin beta A domain {Human (Homo sapiens)}
VEDYPVDIYYLMDLSYSMKDDLWSIQNLGTKLATQMRKLTSNLRIGFGAFVDKPVSPYMYISPPE
ALENPCYDMKTTCLPMFGYKHVLTLTDQVTRFNEEVKKQSVSRNRDAPEGGFDAIMQATVCDEKI
GWRNDASHLLVFTTDAKTHIALDGRLAGIVQPNDGQCHVGSDNHYSASTTMDYPSLGLMTEKLSQ
KNINLIFAVTENVVNLYQNYSELIPGTTVGVLSMDSSNVLQLIVDAYGKIRSK
>d1poia_ c.63.1.1 (A:) Glutaconate-CoA transferase alpha {Acidaminococcus fermentans}
SKVMTLKDAIAKYVHSGDHIALGGFTTDRKPYAAVFEILRQGITDLTGLGGAAGGDWDMLIGNGR
VKAYINCYTANSGVTNVSRRFRKWFEAGKLTMEDYSQDVIYMMWHAAALGLPFLPVTLMQGSGLT
DEWGISKEVRKTLDKVPDDKFKYIDNPFKPGEKVVAVPVPQVDVAIIHAQQASPDGTVRIWGGKF
QDVDIAEAAKYTIVTCEEIISDEEIRRDPTKNDIPGMCVDAVVLAPYGAHPSQCYGLYDYDNPFL
KVYDKVSKTQEDFDAFCKEWVFDLKDHDEYLNKLGATRLINLKVVPGLGYHIDMTKE
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>d1poib_ c.63.1.1 (B:) Glutaconate-CoA transferase beta
{Acidaminococcus fermentans}
DYTNYTNKEMQAVTIAKQIKNGQVVTVGTGLPLIGASVAKRVYAPDCHIIVESGLMDCSPVEVPR
SVGDLRFMAHCGCIWPNVRFVGFEINEYLHKANRLIAFIGGAQIDPYGNVNSTSIGDYHHPKTRF
TGSGGANGIATYSNTIIMMQHEKRRFMNKIDYVTSPGWIDGPGGRERLGLPGDVGPQLVVTDKGI
LKFDEKTKRMYLAAYYPTSSPEDVLENTGFDLDVSKAVELEAPDPAVIKLIREEIDPGQAFIQVP
>d1keka4 c.64.1.1 (A:416-668) Pyruvate-ferredoxin oxidoreductase,
PFOR, domain III {Desulfovibrio africanus}
GTIQCQFWGLGADGTVGANKQAIKIIGDNTDLFAQGYFSYDSKKSGGITISHLRFGEKPIQSTYL
VNRADYVACHNPAYVGIYDILEGIKDGGTFVLNSPWSSLEDMDKHLPSGIKRTIANKKLKFYNID
AVKIATDVGLGGRINMIMQTAFFKLAGVLPFEKAVDLLKKSIHKAYGKKGEKIVKMNTDAVDQAV
TSLQEFKYPDSWKDAPAETKAEPMTNEFFKNVVKPILTQQGDKLPVSAFEADGRFPLG
>d1jkxa_ c.65.1.1 (A:) Glycinamide ribonucleotide transformylase,
GART {Escherichia coli}
MNIVVLISGNGSNLQAIIDACKTNKIKGTVRAVFSNKADAFGLERARQAGIATHTLIASAFDSRE
AYDRELIHEIDMYAPDVVVLAGFMRILSPAFVSHYAGRLLNIHPSLLPKYPGLHTHRQALENGDE
EHGTSVHFVTDELDGGPVILQAKVPVFAGDSEDDITARVQTQEHAIYPLVISWFADGRLKMHENA
AWLDGQRLPPQGYA
>d1fmta2 c.65.1.1 (A:1-206) Methionyl-tRNAfmet formyltransferase
{Escherichia coli}
SESLRIIFAGTPDFAARHLDALLSSGHNVVGVFTQPDRPAGRGKKLMPSPVKVLAEEKGLPVFQP
VSLRPQENQQLVAELQADVMVVVAYGLILPKAVLEMPRLGCINVHGSLLPRWRGAAPIQRSLWAG
DAETGVTIMQMDVGLDTGDMLYKLSCPITAEDTSGTLYDKLAELGPQGLITTLKQLADGTAKPEV
QDETLVTYAEK
>d1vid__ c.66.1.1 (-) Catechol O-methyltransferase, COMT {Rat (Rattus
norvegicus)}
TKEQRILRYVQQNAKPGDPQSVLEAIDTYCTQKEWAMNVGDAKGQIMDAVIREYSPSLVLELGAY
CGYSAVRMARLLQPGARLLTMEMNPDYAAITQQMLNFAGLQDKVTILNGASQDLIPQLKKKYDVD
TLDMVFLDHWKDRYLPDTLLLEKCGLLRKGTVLLADNVIVPGTPDFLAYVRGSSSFECTHYSSYL
EYMKVVDGLEKAIYQGPS
>d1fp1d2 c.66.1.12 (D:129-372) Chalcone O-methyltransferase {Alfalfa
(Medicago sativa)}
RGYLASFTTFLCYPALLQVWMNFKEAVVDEDIDLFKNVHGVTKYEFMGKDKKMNQIFNKSMVDVC
ATEMKRMLEIYTGFEGISTLVDVGGGSGRNLELIISKYPLIKGINFDLPQVIENAPPLSGIEHVG
GDMFASVPQGDAMILKAVCHNWSDEKCIEFLSNCHKALSPNGKVIIVEFILPEEPNTSEESKLVS
TLDNLMFITVGGRERTEKQYEKLSKLSGFSKFQVACRAFNSLGVMEFYK
>d1fp2a2 c.66.1.12 (A:109-352) Isoflavone O-methyltransferase
{Alfalfa (Medicago sativa)}
LCLAPMVECVLDPTLSGSYHELKKWIYEEDLTLFGVTLGSGFWDFLDKNPEYNTSFNDAMASDSK
LINLALRDCDFVFDGLESIVDVGGGTGTTAKIICETFPKLKCIVFDRPQVVENLSGSNNLTYVGG
DMFTSIPNADAVLLKYILHNWTDKDCLRILKKCKEAVTNDGKRGKVTIIDMVIDKKKDENQVTQI
KLLMDVNMACLNGKERNEEEWKKLFIEAGFQHYKISPLTGFLSLIEIYP
>d1ej0a_ c.66.1.2 (A:) RNA methyltransferase FtsJ {Escherichia coli}
GLRSRAWFKLDEIQQSDKLFKPGMTVVDLGAAPGGWSQYVVTQIGGKGRIIACDLLPMDPIVGVD
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FLQGDFRDELVMKALLERVGDSKVQVVMSDMAPNMSGTPAVDIPRAMYLVELALEMCRDVLAPGG
SFVVKVFQGEGFDEYLREIRSLFTKVKVRKPDSSRARSREVYIVATGRKP
>d1fbna_ c.66.1.3 (A:) Fibrillarin homologue {Archaeon Methanococcus
jannaschii}
MEDIKIKEIFENIYEVDLGDGLKRIATKSIVKGKKVYDEKIIKIGDEEYRIWNPNKSKLAAAIIK
GLKVMPIKRDSKILYLGASAGTTPSHVADIADKGIVYAIEYAPRIMRELLDACAERENIIPILGD
ANKPQEYANIVEKVDVIYEDVAQPNQAEILIKNAKWFLKKGGYGMIAIKARSIDVTKDPKEIFKE
QKEILEAGGFKIVDEVDIEPFEKDHVMFVGIWEGK
>d1dusa_ c.66.1.4 (A:) Hypothetical protein MJ0882 {Archaeon
Methanococcus jannaschii}
FSEKPTTKSDVKIVEDILRGKKLKFKTDSGVFSYGKVDKGTKILVENVVVDKDDDILDLGCGYGV
IGIALADEVKSTTMADINRRAIKLAKENIKLNNLDNYDIRVVHSDLYENVKDRKYNKIITNPPIR
AGKEVLHRIIEEGKELLKDNGEIWVVIQTKQGAKSLAKYMKDVFGNVETVTIKGGYRVLKSKKL
>d1im8a_ c.66.1.14 (A:) Hypothetical protein HI0319 (YecO)
{Haemophilus influenzae}
FIFDENVAEVFPDMIQRSVPGYSNIITAIGMLAERFVTADSNVYDLGCSRGAATLSARRNINQPN
VKIIGIDNSQPMVERCRQHIAAYHSEIPVEILCNDIRHVEIKNASMVILNFTLQFLPPEDRIALL
TKIYEGLNPNGVLVLSEKFRFEDTKINHLLIDLHHQFKRANGYSELEVSQKRTALENVMRTDSIE
THKVRLKNVGFSQVELWFQCFNFGSMIAVK
>d1d2ha_ c.66.1.5 (A:) Glycine <i>N</i>-methyltransferase {Rat
(Rattus norvegicus)}
TAEYKAWLLGLLRQHGCHRVLDVACGTGVDSIMLVEEGFSVTSVDASDKMLKYALKERWNRRKEP
AFDKWVIEEANWLTLDKDVPAGDGFDAVICLGNSFAHLPDSKGDQSEHRLALKNIASMVRPGGLL
VIDHKNYDYILSTGCAPPGKNIYYKSDLTKDITTSVLTVNNKAHMVTLDYTVQVPGAGRDGAPGF
SKFRLSYYPHCLASFTELVQEAFGGRCQHSVLGDFKPYRPGQAYVPCYFIHVLKKTG
>d1xvaa_ c.66.1.5 (A:) Glycine <i>N</i>-methyltransferase {Rat
(Rattus norvegicus)}
VDSVYRTRSLGVAAEGIPDQYADGEAARVWQLYIGDTRSRTAEYKAWLLGLLRQHGCHRVLDVAC
GTGVDSIMLVEEGFSVTSVDASDKMLKYALKERWNRRKEPAFDKWVIEEANWLTLDKDVPAGDGF
DAVICLGNSFAHLPDSKGDQSEHRLALKNIASMVRPGGLLVIDHRNYDYILSTGCAPPGKNIYYK
SDLTKDITTSVLTVNNKAHMVTLDYTVQVPGAGRDGAPGFSKFRLSYYPHCLASFTELVQEAFGG
RCQHSVLGDFKPYRPGQAYVPCYFIHVLKKTG
>d1hnna_ c.66.1.15 (A:) Phenylethanolamine N-methyltransferase,
PNMTase {Human (Homo sapiens)}
AVASAYQRFEPRAYLRNNYAPPRGDLCNPNGVGPWKLRCLAQTFATGEVSGRTLIDIGSGPTVYQ
LLSACSHFEDITMTDFLEVNRQELGRWLQEEPGAFNWSMYSQHACLIEGKGECWQDKERQLRARV
KRVLPIDVHQPQPLGAGSPAPLPADALVSAFCLEAVSPDLASFQRALDHITTLLRPGGHLLLIGA
LEESWYLAGEARLTVVPVSEEEVREALVRSGYKVRDLRTYIMPAHLQTGVDDVKGVFFAWAQKVG
L
>d1khha_ c.66.1.16 (A:) Guanidinoacetate methyltransferase {Rat
(Rattus norvegicus)}
RWETPYMHSLAAAAASRGGRVLEVGFGMAIAASRVQQAPIKEHWIIECNDGVFQRLQNWALKQPH
KVVPLKGLWEEVAPTLPDGHFDGILYDTYPLSEETWHTHQFNFIKTHAFRLLKPGGILTYCNLTS
WGELMKSKYTDITAMFEETQVPALLEAGFQRENICTEVMALVPPADCRYYAFPQMITPLVTKH
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>d1g6q1_ c.66.1.6 (1:) Arginine methyltransferase, HMT1 {Baker's
yeast (Saccharomyces cerevisiae)}
DYYFDSYDHYGIHEEMLQDTVRTLSYRNAIIQNKDLFKDKIVLDVGCGTGILSMFAAKHGAKHVI
GVDMSSIIEMAKELVELNGFSDKITLLRGKLEDVHLPFPKVDIIISEWMGYFLLYESMMDTVLYA
RDHYLVEGGLIFPDKCSIHLAGLEDSQYKDEKLNYWQDVYGFDYSPFVPLVLHEPIVDTVERNNV
NTTSDKLIEFDLNTVKISDLAFKSNFKLTAKRQDMINGIVTWFDIVFPAPKGKRPVEFSTGPHAP
YTHWKQTIFYFPDDLDAETGDTIEGELVCSPNEKNNRDLNIKISYKFESNGIDGNSRSRKNEGSY
LMH
>d1f3la_ c.66.1.6 (A:) Arginine methyltransferase, HMT1 {Rat (Rattus
norvegicus)}
DLQEDEDGVYFSSYGHYGIHEEMLKDKVRTESYRDFIYQNPHIFKDKVVLDVGCGTGILSMFAAK
AGAKKVIAVDQSEILYQAMDIIRLNKLEDTIVLIKGKIEEVSLPVEKVDVIISEWMGYFLLFESM
LDSVLYAKSKYLAKGGSVYPDICTISLVAVSDVSKHADRIAFWDDVYGFNMSCMKKAVIPEAVVE
VVDHKTLISDPCDIKHIDCHTTSISDLEFSSDFTLRTTKTAMCTAVAGYFDIYFEKNCHNRVVFS
TGPQSTKTHWKQTIFLLEKPFPVKAGEALKGKITVHKNKKDPRSLIVTLTLNSSTQTYSLQ
>d1dl5a1 c.66.1.7 (A:1-213) Protein-L-isoaspartyl
O-methyltransferase {Thermotoga maritima}
MREKLFWILKKYGVSDHIAKAFLEIPREEFLTKSYPLSYVYEDIVLVSYDDGEEYSTSSQPSLMA
LFMEWVGLDKGMRVLEIGGGTGYNAAVMSRVVGEKGLVVSVEYSRKICEIAKRNVERLGIENVIF
VCGDGYYGVPEFSPYDVIFVTVGVDEVPETWFTQLKEGGRVIVPINLKLSRRQPAFLFKKKDPYL
VGNYKLETRFITAGGNLG
>d1jg1a_ c.66.1.7 (A:) Protein-L-isoaspartyl O-methyltransferase
{Archaeon Pyrococcus furiosus}
EKELYEKWMRTVEMLKAEGIIRSKEVERAFLKYPRYLSVEDKYKKYAHIDEPLPIPAGQTVSAPH
MVAIMLEIANLKPGMNILEVGTGSGWNAALISEIVKTDVYTIERIPELVEFAKRNLERAGVKNVH
VILGDGSKGFPPKAPYDVIIVTAGAPKIPEPLIEQLKIGGKLIIPVGSYHLWQELLEVRKTKDGI
KIKNHGGVAFVPLIGEYGWK
>d1kr5a_ c.66.1.7 (A:) Protein-L-isoaspartyl O-methyltransferase
{Human (Homo sapiens)}
ASHSELIHNLRKNGIIKTDKVFEVMLATDRSHYAKCNPYMDSPQSIGFQATISAPHMHAYALELL
FDQLHEGAKALDVGSGSGILTACFARMVGCTGKVIGIDHIKELVDDSVNNVRKDDPTLLSSGRVQ
LVVGDGRMGYAEEAPYDAIHVGAAAPVVPQALIDQLKPGGRLILPVGPAGGNQMLEQYDKLQDGS
IKMKPLMGVIYVPLTDKEKQWSR
>d1i9ga_ c.66.1.13 (A:) Probable methyltransferase Rv2118c
{Mycobacterium tuberculosis}
TGPFSIGERVQLTDAKGRRYTMSLTPGAEFHTHRGSIAHDAVIGLEQGSVVKSSNGALFLVLRPL
LVDYVMSMPRGPQVIYPKDAAQIVHEGDIFPGARVLEAGAGSGALTLSLLRAVGPAGQVISYEQR
ADHAEHARRNVSGCYGQPPDNWRLVVSDLADSELPDGSVDRAVLDMLAPWEVLDAVSRLLVAGGV
LMVYVATVTQLSRIVEALRAKQCWTEPRAWETLQRGWNVVGLAVRPQHSMRGHTAFLVATRRLAP
GAVA
>d1af7_2 c.66.1.8 (92-284) Chemotaxis receptor methyltransferase CheR,
C-terminal domain {Salmonella typhimurium}
NLTAFFREAHHFPILAEHARRRHGEYRVWSAAASTGEEPYSIAITLADALGMAPGRWKVFASDID
TEVLEKARSGIYRLSELKTLSPQQLQRYFMRGTGPHEGLVRVRQELANYVEFSSVNLLEKQYNVP
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GPFDAIFCRNVMIYFDKTTQEDILRRFVPLLKPDGLLFAGHSENFSNLVREFSLRGQTVYALS
>d3mag__ c.66.1.9 (-) Polymerase regulatory subunit VP39 {Vaccinia virus}
MDVVSLDKPFMYFEEIDNELDYEPESANEVAKKLPYQGQLKLLLGELFFLSKLQRHGILDGATVV
YIGSAPGTHIRYLRDHFYNLGVIIKWMLIDGRHHDPILNGLRDVTLVTRFVDEEYLRSIKKQLHP
SKIILISDVRSPKRGGNESTADLLSNYALQNVMISILNPVASSLKWRCPFPDQWIKDFYIPHGNK
MLQPFAPSYSAEMRLLSIYTGENMRLTRVTKSDAVNYEKKMYYLNKIVRNKVVVNFDYPNQEYDY
FHMYFMLRTVYCNKTFPTTKAKVLFLQQSIFRFLNIP
>d1yub__ c.66.1.9 (-) rRNA methyltransferase {Streptococcus pneumoniae, Ermam}
MNKNIKYSQNFLTSEKVLNQIIKQLNLKETDTVYEIGTGKGHLTTKLAKISKQVTSIELDSHLFN
LSSEKLKLNTRVTLIHQDILQFQFPNKQRYKIVGNIPYHLSTQIIKKVVFESRASDIYLIVEEGF
YKRTLDIHRTLGLLLHTQVSIQQLLKLPAECFHPKPKVNSVLIKLTRHTTDVPDKYWKLYTYFVS
KWVNREYRQLFTKNQFHQAMKHAKVNNLSTITYEQVLSIFNSYLLFNGRK
>d1qama_ c.66.1.9 (A:) rRNA methyltransferase {Bacillus subtilis, Ermc'}
QNFITSKHNIDKIMTNIRLNEHDNIFEIGSGKGHFTLELVQRCNFVTAIEIDHKLCKTTENKLVD
HDNFQVLNKDILQFKFPKNQSYKIFGNIPYNISTDIIRKIVFDSIADEIYLIVEYGFAKRLLNTK
RSLALFLMAEVDISILSMVPREYFHPKPKVNSSLIRLNRKKSRISHKDKQKYNYFVMKWVNKEYK
KIFTKNQFNNSLKHAGIDDLNNISFEQFLSLFNSYKLFNK
>d1i4wa_ c.66.1.9 (A:) Transcription factor sc-mtTFB {Baker's yeast (Saccharomyces cerevisiae)}
PIPGIKDISKLKFFYGFKYLWNPTVYNKIFDKLDLTKTYKHPEELKVLDLYPGVGIQSAIFYNKY
CPRQYSLLEKRSSLYKFLNAKFEGSPLQILKRDPYDWSTYSNLIDEERIFVPEVQSSDHINDKFL
TVANVTGEGSEGLIMQWLSCIGNKNWLYRFGKVKMLLWMPSTTARKLLARPGMHSRSKCSVVREA
FTDTKLIAISDANELKGFDSQCIEEWDPILFSAAEIWPTKGKPIALVEMDPIDFDFDVDNWDYVT
RHLMILKRTPLNTVMDSLGHGGQQYFNSRITDKDLLKKCPIDLTNDEFIYLTKLFMEWPFKP
>d6mhta_ c.66.1.10 (A:) DNA methylase HhaI, coenzyme-binding domain {Haemophilus haemolyticus}
MIEIKDKQLTGLRFIDLFAGLGGFRLALESCGAECVYSNEWDKYAQEVYEMNFGEKPEGDITQVN
EKTIPDHDILCAGFPCQAFSISGKQKGFEDSRGTLFFDIARIVREKKPKVVFMENVKNFASHDNG
NTLEVVKNTMNELDYSFHAKVLNALDYGIPQKRERIYMICFRNDLNIQNFQFPKPFELNTFVKDL
LLPDSEVEHLVIDRKDLVMTNQEIEQTTPKTVRLGIVGKGGQGERIYSTRGIAITLSAYGGGIFA
KTGGYLVNGKTRKLHPRECARVMGYPDSYKVHPSTSQAYKQFGNSVVINVLQYIAYNIGSSLNFK
PY
>d1g38a_ c.66.1.10 (A:) DNA methylase TaqI, coenzyme-binding domain {Thermus aquaticus}
VETPPEVVDFMVSLAEAPRGGRVLEPACAHGPFLRAFREAHGTGYRFVGVEIDPKALDLPPWAEG
ILADFLLWEPGEAFDLILGNPPYGIVGEASKYPIHVFKAVKDLYKKAFSTWKGKYNLYGAFLEKA
VRLLKPGGVLVFVVPATWLVLEDFALLREFLAREGKTSVYYLGEVFPQKKVSAVVIRFQKSGKGL
SLWDTQESESGFTPILWAEYPHWEGEIIRFETEETRKLEISGMPLGDLFHIRFAARSPEFKKHPA
VRKEPGPGLVPVLTGRNLKPGWVDYEKNHSGLWMPKERAKELRDFYATPHLVVAHTKGTRVVAAW
DERAYPWREEFHLLPKEGVRLDPSSLVQWLNSEAMQKHVRTLYRDFVPHLTLRMLERLPVRREYG
FHT
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>d1dcta_ c.66.1.10 (A:) DNA methylase HaeIII, coenzyme-binding domain {Haemophilus aegyptius}
MNLISLFSGAGGLDLGFQKAGFRIICANEYDKSIWKTYESNHSAKLIKGDISKISSDEFPKCDGI
IGGPPCQSWSEGGSLRGIDDPRGKLFYEYIRILKQKKPIFFLAENVKGMMAQRHNKAVQEFIQEF
DNAGYDVHIILLNANDYGVAQDRKRVFYIGFRKELNINYLPPIPHLIKPTFKDVIWDLKDNPIPA
LDKNKTNGNKCIYPNHEYFIGSYSTIFMSRNRVRQWNEPAFTVQASGRQCQLHPQAPVMLKVSKN
LNKFVEGKEHLYRRLTVRECARVQGFPDDFIFHYESLNDGYKMIGNAVPVNLAYEIAKTIKSAL
>d2dpma_ c.66.1.10 (A:) DpnM DNA adenine methyltransferase {Streptococcus pneumoniae}
TLQPFTKWTGGKRQLLPVIRELIPKTYNRYFEPFVGGGALFFDLAPKDAVINDFNAELINCYQQI
KDNPQELIEILKVHQEYNSKEYYLDLRSADRDERIDMMSEVQRAARILYMLRVNFNGLYRVNSKN
QFNVPYGRYKNPKIVDEELISAISVYINNNQLEIKVGDFEKAIVDVRTGDFVYFDPPYIPLSETS
AFTSYTHEGFSFADQVRLRDAFKRLSDTGAYVMLSNSSSALVEELYKDFNIHYVEATRTNGAKSS
SRGKISEIIVTNYEK
>d1g55a_ c.66.1.10 (A:) DNMT2 {Human (Homo sapiens)}
EPLRVLELYSGVGGMHHALRESCIPAQVVAAIDVNTVANEVYKYNFPHTQLLAKTIEGITLEEFD
RLSFDMILMSPPCQPFTRIGRQGDMTDSRTNSFLHILDILPRLQKLPKYILLENVKGFEVSSTRD
LLIQTIENCGFQYQEFLLSPTSLGIPNSRLRYFLIAKLQSEPLPFQAPGQVLMEFPKIEIHRKNQ
QDSDLSVKMLKDFLEDDTDVNQYLLPPKSLLRYALLLDIVQPTCRRSVCFTKGYGSYIEGTGSVL
QTAEDVQVENIYKSLTNLSQEEQITKLLILKLRYFTPKEIANLLGFPPEFGFPEKITVKQRYRLL
GNSLNVHVVAKLIKILYE
>d1booa_ c.66.1.11 (A:) m.PvuII N4 cytosine-specific DNA methyltransferase {Proteus vulgaris}
NFGKKPAYTTSNGSMYIGDSLELLESFPEESISLVMTSPPFALQRKKEYGNLEQHEYVDWFLSFA
KVVNKKLKPDGSFVVDFGGAYMKGVPARSIYNFRVLIRMIDEVGFFLAEDFYWFNPSKLPSPIEW
VNKRKIRVKDAVNTVWWFSKTEWPKSDITKVLAPYSDRMKKLIEDPDKFYTPKTRPSGHDIGKSF
SKDNGGSIPPNLLQISNSESNGQYLANCKLMGIKAHPARFPAKLPEFFIRMLTEPDDLVVDIFGG
SNTTGLVAERESRKWISFEMKPEYVAASAFRFLDNNISEEKITDIYNRILNGESLDLNSI
>d1eg2a_ c.66.1.11 (A:) m.RsrI N6 adenosine-specific DNA methyltransferase {Rhodobacter sphaeroides}
GTTRHVYDVCDCLDTLAKLPDDSVQLIICDPPYNIMLADWDDHMDYIGWAKRWLAEAERVLSPTG
SIAIFGGLQYQGEAGSGDLISIISHMRQNSKMLLANLIIWNYPNGMSAQRFFANRHEEIAWFAKT
KKYFFDLDAVREPYDEETKAAYMKDKRLNPESVEKGRNPTNVWRMSRLNGNSLERVGHPTQKPAA
VIERLVRALSHPGSTVLDFFAGSGVTARVAIQEGRNSICTDAAPVFKEYYQKQLTFLQDDGLIDK
ARSYEIVEGAANFGAALQR
>d1inla_ c.66.1.17 (A:) Spermidine synthase {Thermotoga maritima}
RTLKELERELQPRQHLWYFEYYTGNNVGLFMKMNRVIYSGQSDIQRIDIFENPDLGVVFALDGIT
MTTEKDEFMYHEMLAHVPMFLHPNPKKVLIIGGGDGGTLREVLKHDSVEKAILCEVDGLVIEAAR
KYLKQTSCGFDDPRAEIVIANGAEYVRKFKNEFDVIIIDSTDPTAGQGGHLFTEEFYQACYDALK
EDGVFSAETEDPFYDIGWFKLAYRRISKVFPITRVYLGFMTTYPSGMWSYTFASKGIDPIKDFDP
EKVRKFNKELKYYNEEVHVASFALPNFVKKELGLM
>d1kpga_ c.66.1.18 (A:) Mycolic acid cyclopropane synthase CmaA1 {Mycobacterium tuberculosis}
DELKPHFANVQAHYDLSDDFFRLFLDPTQTYSCAYFERDDMTLQEAQIAKIDLALGKLGLQPGMT
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LLDVGCGWGATMMRAVEKYDVNVVGLTLSKNQANHVQQLVANSENLRSKRVLLAGWEQFDEPVDR
IVSIGAFEHFGHERYDAFFSLAHRLLPADGVMLLHTITGLHPKEIHERGLPMSFTFARFLKFIVT
EIFPGGRLPSIPMVQECASANGFTVTRVQSLQPHYAKTLDLWSAALQANKGQAIALQSEEVYERY
MKYLTGCAEMFRIGYIDVNQFTCQK
>d1kpia_ c.66.1.18 (A:) Mycolic acid cyclopropane synthase CmaA1
{Mycobacterium tuberculosis}
QLKPPVEAVRSHYDKSNEFFKLWLDPSMTYSCAYFERPDMTLEEAQYAKRKLALDKLNLEPGMTL
LDIGCGWGSTMRHAVAEYDVNVIGLTLSENQYAHDKAMFDEVDSPRRKEVRIQGWEEFDEPVDRI
VSLGAFEHFADGAGDAGFERYDTFFKKFYNLTPDDGRMLLHTITIPDKEEAQELGLTSPMSLLRF
IKFILTEIFPGGRLPRISQVDYYSSNAGWKVERYHRIGANYVPTLNAWADALQAHKDEAIALKGQ
ETCDIYMHYLRGCSDLFRDKYTDVCQFTLVK
>d7aata_ c.67.1.1 (A:) Aspartate aminotransferase, AAT {Chicken
(Gallus gallus), mitochondria}
SSWWSHVEMGPPDPILGVTEAFKRDTNSKKMNLGVGAYRDDNGKPYVLNCVRKAEAMIAAKKMDK
EYLPIAGLADFTRASAELALGENSEAFKSGRYVTVQGISGTGSLRVGANFLQRFFKFSRDVYLPK
PSWGNHTPIFRDAGLQLQAYRYYDPKTCSLDFTGAMEDISKIPEKSIILLHACAHNPTGVDPRQE
QWKELASVVKKRNLLAYFDMAYQGFASGDINRDAWALRHFIEQGIDVVLSQSYAKNMGLYGERAG
AFTVICRDAEEAKRVESQLKILIRPMYSNPPMNGARIASLILNTPELRKEWLVEVKGMADRIISM
RTQLVSNLKKEGSSHNWQHITDQIGMFCFTGLKPEQVERLTKEFSIYMTKDGRISVAGVASSNVG
YLAHAIHQVTK
>d2csta_ c.67.1.1 (A:) Aspartate aminotransferase, AAT {Chicken
(Gallus gallus), cytosolic form}
AASIFAAVPRAPPVAVFKLTADFREDGDSRKVNLGVGAYRTDEGQPWVLPVVRKVEQLIAGDGSL
NHEYLPILGLPEFRANASRIALGDDSPAIAQKRVGSVQGLGGTGALRIGAEFLRRWYNGNNNTAT
PVYVSSPTWENHNSVFMDAGFKDIRTYRYWDAAKRGLDLQGLLDDMEKAPEFSIFILHACAHNPT
GTDPTPDEWKQIAAVMKRRCLFPFFDSAYQGFASGSLDKDAWAVRYFVSEGFELFCAQSFSKNFG
LYNERVGNLSVVGKDEDNVQRVLSQMEKIVRTTWSNPPSQGARIVATTLTSPQLFAEWKDNVKTM
ADRVLLMRSELRSRLESLGTPGTWNHITDQIGMFSFTGLNPKQVEYMIKEKHIYLMASGRINMCG
LTTKNLDYVAKSIHEAVTKIQ
>d1ajsa_ c.67.1.1 (A:) Aspartate aminotransferase, AAT {Pig (Sus
scrofa), cytosolic form}
APPSVFAEVPQAQPVLVFKLIADFREDPDPRKVNLGVGAYRTDDCQPWVLPVVRKVEQRIANNSS
LNHEYLPILGLAEFRTCASRLALGDDSPALQEKRVGGVQSLGGTGALRIGAEFLARWYNGTNNKD
TPVYVSSPTWENHNGVFTTAGFKDIRSYRYWDTEKRGLDLQGFLSDLENAPEFSIFVLHACAHNP
TGTDPTPEQWKQIASVMKRRFLFPFFDSAYQGFASGNLEKDAWAIRYFVSEGFELFCAQSFSKNF
GLYNERVGNLTVVAKEPDSILRVLSQMQKIVRVTWSNPPAQGARIVARTLSDPELFHEWTGNVKT
MADRILSMRSELRARLEALKTPGTWNHITDQIGMFSFTGLNPKQVEYLINQKHIYLLPSGRINMC
GLTTKNLDYVATSIHEAVTKIQ
>d1yaaa_ c.67.1.1 (A:) Aspartate aminotransferase, AAT {Baker's yeast
(Saccharomyces cerevisiae), cytosolic form}
SATLFNNIELLPPDALFGIKQRYGQDQRATKVDLGIGAYRDDNGKPWVLPSVKAAEKLIHNDSSY
NHEYLGITGLPSLTSNAAKIIFGTQSDALQEDRVISVQSLSGTGALHISAKFFSKFFPDKLVYLS
KPTWANHMAIFENQGLKTATYPYWANETKSLDLNGFLNAIQKAPEGSIFVLHSCAHNPTGLDPTS
EQWVQIVDAIASKNHIALFDTAYQGFATGDLDKDAYAVRLGVEKLSTVSPVFVCQSFAKNAGMYG
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ERVGCFHLALTKQAQNKTIKPAVTSQLAKIIRSEVSNPPAYGAKIVAKLLETPELTEQWHKDMVT
MSSRITKMRHALRDHLVKLGTPGNWDHIVNQCGMFSFTGLTPQMVKRLEETHAVYLVASGRASIA
GLNQGNVEYVAKAIDEVVRFYA
>d1qisa_ c.67.1.1 (A:) Aspartate aminotransferase, AAT {Escherichia coli}
MFENITAAPADPILGLADLFRADERPGKINLGIGVYKDETGKTPVLTSVKKAEQYLLENETTKNY
LGIDGIPEFGRCTQELLFGKGSALINDKRARTAQTPGGTGALRVAADFLAKNTSVKRVWVSNPSW
PNHKSVFNSAGLEVREYAYYDAENHTLDFDALINSLNEAQAGDVVLFHGFCHNPTGIDPTLEQWQ
TLAQLSVEKGWLPLFDFAYQGFARGLEEDAEGLRAFAAMHKELIVASSYSKNFGLYNERVGACTL
VAADSETVDRAFSQMKAAIRANYSNPPAHGASVVATILSNDALRAIWEQELTDMRQRIQRMRQLF
VNTLQEKGANRDFSFIIKQNGMFSFSGLTKEQVLRLREEFGVYAVASGRVNVAGMTPDNMAPLCE
AIVAVL
>d1bjwa_ c.67.1.1 (A:) Aspartate aminotransferase, AAT {Thermus thermophilus}
MRGLSRRVQAMKPSATVAVNAKALELRRQGVDLVALTAGEPDFDTPEHVKEAARRALAQGKTKYA
PPAGIPELREALAEKFRRENGLSVTPEETIVTVGGKQALFNLFQAILDPGDEVIVLSPYWVSYPE
MVRFAGGVVVEVETLPEEGFVPDPERVRRAITPRTKALVVNSPNNPTGAVYPKEVLEALARLAVE
HDFYLVSDEIYEHLLYEGEHFSPGRVAPEHTLTVNGAAKAFAMTGWRIGYACGPKEVIKAMASVS
SQSTTSPDTIAQWATLEALTNQEASRAFVEMAREAYRRRRDLLLEGLTALGLKAVRPSGAFYVLM
DTSPIAPDEVRAAERLLEAGVAVVPGTDFAAFGHVRLSYATSEENLRKALERFARVL
>d2ay1a_ c.67.1.1 (A:) Aromatic aminoacid aminotransferase, AroAT {Paracoccus denitrificans}
MLGNLKPQAPDKILALMGEFRADPRQGKIDLGVGVYKDATGHTPIMRAVHAAEQRMLETETTKTY
AGLSGEPEFQKAMGELILGDGLKSETTATLATVGGTGALRQALELARMANPDLRVFVSDPTWPNH
VSIMNFMGLPVQTYRYFDAETRGVDFEGMKADLAAAKKGDMVLLHGCCHNPTGANLTLDQWAEIA
SILEKTGALPLIDLAYQGFGDGLEEDAAGTRLIASRIPEVLIAASCSKNFGIYRERTGCLLALCA
DAATRELAQGAMAFLNRQTYSFPPFHGAKIVSTVLTTPELRADWMAELEAVRSGMLRLREQLAGE
LRDLSGSDRFGFVAEHRGMFSRLGATPEQVKRIKEEFGIYMVGDSRINIAGLNDNTIPILARAII
EVGV
>d3tata_ c.67.1.1 (A:) Aromatic aminoacid aminotransferase, AroAT {Escherichia coli}
MFQKVDAYAGDPILTLMERFKEDPRSDKVNLSIGLYYNEDGIIPQLQAVAEAEARLNAQPHGASL
YLPMEGLNCYRHAIAPLLFGADHPVLKQQRVATIQTLGGSGALKVGADFLKRYFPESGVWVSDPT
WENHVAIFAGAGFEVSTYPWYDEATNGVRFNDLLATLKTLPARSIVLLHPCCHNPTGADLTNDQW
DAVIEILKARELIPFLDIAYQGFGAGMEEDAYAIRAIASAGLPALVSNSFSKIFSLYGERVGGLS
VMCEDAEAAGRVLGQLKATVRRNYSSPPNFGAQVVAAVLNDEALKASWLAEVEEMRTRILAMRQE
LVKVLSTEMPERNFDYLLNQRGMFSYTGLSAAQVDRLREEFGVYLIASGRMCVAGLNTANVQRVA
KAFAAVM
>d1gdea_ c.67.1.1 (A:) Aromatic aminoacid aminotransferase, AroAT {Archaeon Pyrococcus horikoshii}
ALSDRLELVSASEIRKLFDIAAGMKDVISLGIGEPDFDTPQHIKEYAKEALDKGLTHYGPNIGLL
ELREAIAEKLKKQNGIEADPKTEIMVLLGANQAFLMGLSAFLKDGEEVLIPTPAFVSYAPAVILA
GGKPVEVPTYEEDEFRLNVDELKKYVTDKTRALIINSPCNPTGAVLTKKDLEEIADFVVEHDLIV
ISDEVYEHFIYDDARHYSIASLDGMFERTITVNGFSKTFAMTGWRLGFVAAPSWIIERMVKFQMY
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NATCPVTFIQYAAAKALKDERSWKAVEEMRKEYDRRRKLVWKRLNEMGLPTVKPKGAFYIFPRIR
DTGLTSKKFSELMLKEARVAVVPGSAFGKAGEGYVRISYATAYEKLEEAMDRMERVLKERKLV
>d1bw0a_ c.67.1.1 (A:) Tyrosine aminotransferase (TAT) {Trypanosoma
cruzi}
WDVSMSNHAGLVFNPIRTVSDNAKPSPSPKPIIKLSVGDPTLDKNLLTSAAQIKKLKEAIDSQEC
NGYFPTVGSPEAREAVATWWRNSFVHKEELKSTIVKDNVVLCSGGSHGILMAITAICDAGDYALV
PQPGFPHYETVCKAYGIGMHFYNCRPENDWEADLDEIRRLKDDKTKLLIVTNPSNPCGSNFSRKH
VEDIVRLAEELRLPLFSDEIYAGMVFKGKDPNATFTSVADFETTVPRVILGGTAKNLVVPGWRLG
WLLYVDPHGNGPSFLEGLKRVGMLVCGPCTVVQAALGEALLNTPQEHLDQIVAKIEESAMYLYNH
IGECIGLAPTMPRGAMYLMSRIDLEKYRDIKTDVEFFEKLLEEENVQVLPGTIFHAPGFTRLTTT
RPVEVYREAVERIKAFCQRHAA
>d1fg7a_ c.67.1.1 (A:) Histidinol-phosphate aminotransferase
{Escherichia coli}
TVTITDLARENVRNLTPYQSARRLGGNGDVWLNANEYPTAVEFQLTQQTLNRYPECQPKAVIENY
AQYAGVKPEQVLVSRGADEGIELLIRAFCEPGKDAILYCPPTYGMYSVSAETIGVECRTVPTLDN
WQLDLQGISDKLDGVKVVYVCSPNNPTGQLINPQDFRTLLELTRGKAIVVADEAYIEFCPQASLA
GWLAEYPHLAILRTLSKAFALAGLRCGFTLANEEVINLLMKVIAPYPLSTPVADIAAQALSPQGI
VAMRERVAQIIAEREYLIAALKEIPCVEQVFDSETNYILARFKASSAVFKSLWDQGIILRDQNKQ
PSLSGCLRITVGTREESQRVIDALRAEQV
>d1kusa_ c.67.1.1 (A:) L-threonine-O-3-phosphate decarboxylase CobD
{Salmonella enterica}
HGGNIREPATVLGISPDQLLDFSANINPLGMPVSVKRALIDNLDCIERYPDADYFHLHQALARHH
QVPASWILAGNGETESIFTVASGLKPRRAMIVTPGFAEYGRALAQSGCEIRRWSLREADGWQLTD
AILEALTPDLDCLFLCTPNNPTGLLPERPLLQAIADRCKSLNINLILDEAFIDFIPHETGFIPAL
KDNPHIWVLRSLTKFYAIPGLRLGYLVNSDDAAMARMRRQQMPWSVNALAALAGEVALQDSAWQQ
ATWHWLREEGARFYQALCQLPLLTVYPGRANYLLLRCEREDIDLQRRLLTQRILIRSCANYPGLD
SRYYRVAIRSAAQNERLLAALRNVLTGIAP
>d1jg8a_ c.67.1.1 (A:) Low-specificity threonine aldolase {Thermatoga
maritima}
MIDLRSDTVTKPTEEMRKAMAQAEVGDDVYGEDPTINELERLAAETFGKEAALFVPSGTMGNQVS
IMAHTQRGDEVILEADSHIFWYEVGAMAVLSGVMPHPVPGKNGAMDPDDVRKAIRPRNIHFPRTS
LIAIENTHNRSGGRVVPLENIKEICTIAKEHGINVHIDGARIFNASIASGVPVKEYAGYADSVMF
CLSKGLCAPVGSVVVGDRDFIERARKARKMLGGGMRQAGVLAAAGIIALTKMVDRLKEDHENARF
LALKLKEIGYSVNPEDVKTNMVILRTDNLKVNAHGFIEALRNSGVLANAVSDTEIRLVTHKDVSR
NDIEEALNIFEKLFRKFS
>d1tpla_ c.67.1.2 (A:) Tyrosine phenol-lyase {Citrobacter
intermedius}
MNYPAEPFRIKSVETVSMIPRDERLKKMQEAGYNTFLLNSKDIYIDLLTDSGTNAMSDKQWAGMM
MGDEAYAGSENFYHLERTVQELFGFKHIVPTHQGRGAENLLSQLAIKPGQYVAGNMYKNGAVFVD
IVRDEAHDAGLNIAFKGDIDLKKLQKLIDEKGAENIAYICLAVTVNLAGGQPVSMANMRAVRELT
AAHGIKVFYDATRCVENAYFIKEQEQGFENKSIAEIVHEMFSYADGCTMSGKKDCLVNIGGFLCM
NDDEMFSSAKELVVVYEGMPSYGGLAGRDMEAMAIGLREAMQYEYIEHRVKQVRYLGDKLKAAGV
PIVEPVGGHAVFLDARRFCEHLTQDEFPAQSLAASIYVETGVRSMERGIKLETVRLTIPRRVYTY
AHMDVVADGIIKLYQHKEDIRGLKFIYFFTARFDYI
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>d1ax4a_ c.67.1.2 (A:) Tryptophan indol-lyase (tryptophanase) {Proteus vulgaris}
AKRIVEPFRIKMVEKIRVPSREEREAALKEAGYNPFLLPSSAVYIDLLTDSGTNAMSDHQWAAMI
TGDEAYAGSRNYYDLKDKAKELFNYDYIIPAHQGRGAENILFPVLLKYKQKEGKAKNPVFISNFH
FDTTAAHVELNGCKAINIVTEKAFDSETYDDWKGDFDIKKLKENIAQHGADNIVAIVSTVTCNSA
GGQPVSMSNLKEVYEIAKQHGIFVVMDSARFCENAYFIKARDPKYKNATIKEVIFDMYKYADALT
MSAKKDPLLNIGGLVAIRDNEEIFTLARQRCVPMEGFVTYGGLAGRDMAAMVQGLEEGTEEEYLH
YRIGQVKYLGDRLREAGIPIQYPTGGHAVFVDCKKLVPQIPGDQFPAQAVINALYLESGVRAVEI
GSFLLGRDPATGEQKHADMEFMRLTIARRVYTNDHMDYIADALIGLKEKFATLKGLEFEYEPPVL
RHFTARLKPI
>d1js3a_ c.67.1.6 (A:) DOPA decarboxylase {Pig (Sus scrofa)}
MNASDFRRRGKEMVDYMADYLEGIEGRQVYPDVQPGYLRPLIPATAPQEPDTFEDILQDVEKIIM
PGVTHWHSPYFFAYFPTASSYPAMLADMLCGAIGCIGFSWAASPACTELETVMMDWLGKMLQLPE
AFLAGEAGEGGGVIQGSASEATLVALLAARTKVVRRLQAASPGLTQGAVLEKLVAYASDQAHSSV
ERAGLIGGVKLKAIPSDGKFAMRASALQEALERDKAAGLIPFFVVATLGTTSCCSFDNLLEVGPI
CHEEDIWLHVDAAYAGSAFICPEFRHLLNGVEFADSFNFNPHKWLLVNFDCSAMWVKRRTDLTGA
FKLDPVYLKHSHQGSGLITDYRHWQLPLGRRFRSLKMWFVFRMYGVKGLQAYIRKHVQLSHEFEA
FVLQDPRFEVCAEVTLGLVCFRLKGSDGLNEALLERINSARKIHLVPCRLRGQFVLRFAICSRKV
ESGHVRLAWEHIRGLAAELLA
>d1cl1a_ c.67.1.3 (A:) Cystathionine beta-lyase, CBL {Escherichia coli}
KLDTQLVNAGRSKKYTLGAVNSVIQRASSLVFDSVEAKKHATRNRANGELFYGRRGTLTHFSLQQ
AMCELEGGAGCVLFPCGAAAVANSILAFIEQGDHVLMTNTAYEPSQDFCSKILSKLGVTTSWFDP
LIGADIVKHLQPNTKIVFLESPGSITMEVHDVPAIVAAVRSVVPDAIIMIDNTWAAGVLFKALDF
GIDVSIQAATKYLVGHSDAMIGTAVCNARCWEQLRENAYLMGQMVDADTAYITSRGLRTLGVRLR
QHHESSLKVAEWLAEHPQVARVNHPALPGSKGHEFWKRDFTGSSGLFSFVLKKKLNNEELANYLD
NFSLFSMAYSWGGYESLILANQPEHIAAIRPQGEIDFSGTLIRLHIGLEDVDDLIADLDAGFARI
V
>d1ibja_ c.67.1.3 (A:) Cystathionine beta-lyase, CBL {Thale cress (Arabidopsis thaliana)}
ASVSTLLVNLDNKFDPFDAMSTPLYQTATFKQPSAIENGPYDYTRSGNPTRDALESLLAKLDKAD
RAFCFTSGMAALSAVTHLIKNGEEIVAGDDVYGGSDRLLSQVVPRSGVVVKRVNTTKLDEVAAAI
GPQTKLVWLESPTNPRQQISDIRKISEMAHAQGALVLVDNSIMSPVLSRPLELGADIVMHSATKF
IAGHSDVMAGVLAVKGEKLAKEVYFLQNSEGSGLAPFDCWLCLRGIKTMALRIEKQQENARKIAM
YLSSHPRVKKVYYAGLPDHPGHHLHFSQAKGAGSVFSFITGSVALSKHLVETTKYFSIAVSFGSV
KSLISMPCFMSHASIPAEVREARGLTEDLVRISAGIEDVDDLISDLDIAFKTFPL
>d1cs1a_ c.67.1.3 (A:) Cystathionine gamma-synthase, CGS {Escherichia coli}
RKQATIAVRSGLNDDEQYGCVVPPIHLSSTYNFTGFNEPRAHDYSRRGNPTRDVVQRALAELEGG
AGAVLTNTGMSAIHLVTTVFLKPGDLLVAPHDCYGGSYRLFDSLAKRGCYRVLFVDQGDEQALRA
ALAEKPKLVLVESPSNPLLRVVDIAKICHLAREVGAVSVVDNTFLSPALQNPLALGADLVLHSCT
KYLNGHSDVVAGVVIAKDPDVVTELAWWANNIGVTGGAFDSYLLLRGLRTLVPRMELAQRNAQAI
VKYLQTQPLVKKLYHPSLPENQGHEIAARQQKGFGAMLSFELDGDEQTLRRFLGGLSLFTLAESL
GGVESLISHAATMTHAGMAPEARAAAGISETLLRISTGIEDGEDLIADLENGFRAANKG
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>d1qgna_ c.67.1.3 (A:) Cystathionine gamma-synthase, CGS {Common
tobacco (Nicotiana tabacum)}
MKYASFLNSDGSVAIHAGERLGRGIVTDAITTPVVNTSAYFFNKTSELIDFKEKRRASFEYGRYG
NPTTVVLEEKISALEGAESTLLMASGMCASTVMLLALVPAGGHIVTTTDCYRKTRIFIETILPKM
GITATVIDPADVGALELALNQKKVNLFFTESPTNPFLRCVDIELVSKLCHEKGALVCIDGTFATP
LNQKALALGADLVLHSATKFLGGHNDVLAGCISGPLKLVSEIRNLHHILGGALNPNAAYLIIRGM
KTLHLRVQQQNSTALRMAEILEAHPKVRHVYYPGLQSHPEHHIAKKQMTGFGGAVSFEVDGDLLT
TAKFVDALKIPYIAPSFGGCESIVDQPAIMSYWDLSQSDRAKYGIMDNLVRFSFGVEDFDDLKAD
ILQALDSI
>d1e5ea_ c.67.1.3 (A:) Methionine gamma-lyase, MGL {Trichomonas
vaginalis}
ERMTPATACIHANPQKDQFGAAIPPIYQTSTFVFDNCQQGGNRFAGQESGYIYTRLGNPTVSNLE
GKIAFLEKTEACVATSSGMGAIAATVLTILKAGDHLISDECLYGCTHALFEHALTKFGIQVDFIN
TAIPGEVKKHMKPNTKIVYFETPANPTLKIIDMERVCKDAHSQEGVLVIADNTFCSPMITNPVDF
GVDVVVHSATKYINGHTDVVAGLICGKADLLQQIRMVGIKDITGSVISPHDAWLITRGLSTLNIR
MKAESENAMKVAEYLKSHPAVEKVYYPGFEDHEGHDIAKKQMRMYGSMITFILKSGFEGAKKLLD
NLKLITLAVSLGGCESLIQHPASMTHAVVPKEEREAAGITDGMIRLSVGIEDADELIADFKQGLD
ALLR
>d1d2fa_ c.67.1.3 (A:) Modulator in mal gene expression, MalY
{Escherichia coli}
LLPFTISDMDFATAPCIIEALNQRLMHGVFGYSRWKNDEFLAAIAHWFSTQHYTAIDSQTVVYGP
SVIYMVSELIRQWSETGEGVVIHTPAYDAFYKAIEGNQRTVMPVALEKQADGWFCDMGKLEAVLA
KPECKIMLLCSPQNPTGKVWTCDELEIMADLCERHGVRVISDEIHMDMVWGEQPHIPWSNVARGD
WALLTSGSKSFNIPALTGAYGIIENSSSRDAYLSALKGRDGLSSPSVLALTAHIAAYQQGAPWLD
ALRIYLKDNLTYIADKMNAAFPELNWQIPQSTYLAWLDLRPLNIDDNALQKALIEQEKVAIMPGY
TYGEEGRGFVRLNAGCPRSKLEKGVAGLINAIRAVR
>d1c7na_ c.67.1.3 (A:) Cystalysin {Treponema denticola}
MIYDFTTKISRKNLGSLKWDLMYSQNPEVGNEVVPLSVADMEFKNPPELIEGLKKYLDETVLGYT
GPTEEYKKTVKKWMKDRHQWDIQTDWIINTAGVVPAVFNAVREFTKPGDGVIIITPVYYPFFMAI
KNQERKIIECELLEKDGYYTIDFQKLEKLSKDKNNKALLFCSPHNPVGRVWKKDELQKIKDIVLK
SDLMLWSDEIHFDLIMPGYEHTVFQSIDEQLADKTITFTAPSKTFNIAGMGMSNIIIKNPDIRER
FTKSRDATSGMPFTTLGYKACEICYKECGKWLDGCIKVIDKNQRIVKDFFEVNHPEIKAPLIEGT
YLQWIDFRALKMDHKAMEEFMIHKAQIFFDEGYIFGDGGIGFERINLAAPSSVIQESLERLNKAL
KDLK
>d1eg5a_ c.67.1.3 (A:) NifS-like protein/selenocysteine lyase
{Thermotoga maritima}
MRVYFDNNATTRVDDRVLEEMIVFYREKYGNPNSAHGMGIEANLHMEKAREKVAKVLGVSPSEIF
FTSCATESINWILKTVAETFEKRKRTIITTPIEHKAVLETMKYLSMKGFKVKYVPVDSRGVVKLE
ELEKLVDEDTFLVSIMAANNEVGTIQPVEDVTRIVKKKNKETLVHVDAVQTIGKIPFSLEKLEVD
YASFSAHKFHGPKGVGITYIRKGVPIRPLIHGGGQERGLRSGTQNVPGIVGAARAMEIAVEELSE
AAKHMEKLRSKLVSGLMNLGAHIITPLEISLPNTLSVSFPNIRGSTLQNLLSGYGIYVSTSSACT
SKDERLRHVLDAMGVDRRIAQGAIRISLCKYNTEEEVDYFLKKIEEILSFL
>d1jf9a_ c.67.1.3 (A:) NifS-like protein/selenocysteine lyase
{Escherichia coli}
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IFSVDKVRADFPVLSREVNGLPLAYLDSAASAQKPSQVIDAEAEFYRHGYAAVHRGIHTLSAQAT
EKMENVRKRASLFINARSAEELVFVRGTTEGINLVANSWGNSNVRAGDNIIISQMEHHANIVPWQ
MLCARVGAELRVIPLNPDGTLQLETLPTLFDEKTRLLAITHVSNVLGTENPLAEMITLAHQHGAK
VLVDGAQAVMHHPVDVQALDCDFYVFSGHKLYGPTGIGILYVKEALLQEMPPWEGGGSMIATVSL
SEGTTWTKAPWRFEAGTPNTGGIIGLGAALEYVSALGLNNIAEYEQNLMHYALSQLESVPDLTLY
GPQNRLGVIAFNLGKHHAYDVGSFLDNYGIAVRTGHHCAMPLMAYYNVPAMCRASLAMYNTHEEV
DRLVTGLQRIHRLLG
>d1elua_ c.67.1.3 (A:) Cystine C-S lyase {Synechocystis sp.}
QFPGLANKTYFNFGGQGILPTVALEAITAMYGYLQENGPFSIAANQHIQQLIAQLRQALAETFNV
DPNTITITDNVTTGCDIVLWGLDWHQGDEILLTDCEHPGIIAIVQAIAARFGITYRFFPVAATLN
QGDAAAVLANHLGPKTRLVILSHLLWNTGQVLPLAEIMAVCRRHQGNYPVRVLVDGAQSAGSLPL
DFSRLEVDYYAFTGHKWFAGPAGVGGLYIHGDCLGEINPTYVGWRSITYGAKGEPTGWAEGGKRF
EVATSAYPQYAGLLAALQLHQRQGTAEERYQAICQRSEFLWRGLNQLPHVHCLATSAPQAGLVSF
TVDSPLGHRAIVQKLEEQRIYLRTIADPDCIRACCHYITDEEEINHLLARLADFGP
>d2dkb__ c.67.1.4 (-) Dialkylglycine decarboxylase {Pseudomonas cepacia}
LNDDATFWRNARHHLVRYGGTFEPMIIERAKGSFVYDADGRAILDFTSGQMSAVLGHCHPEIVSV
IGEYAGKLDHLFSEMLSRPVVDLATRLANITPPGLDRALLLSTGAESNEAAIRMAKLVTGKYEIV
GFAQSWHGMTGAAASATYSAGRKGVGPAAVGSFAIPAPFTYRPRFERNGAYDYLAELDYAFDLID
RQSSGNLAAFIAEPILSSGGIIELPDGYMAALKRKCEARGMLLILDEAQTGVGRTGTMFACQRDG
VTPDILTLSKTLGAGLPLAAIVTSAAIEERAHELGYLFYTTHVSDPLPAAVGLRVLDVVQRDGLV
ARANVMGDRLRRGLLDLMERFDCIGDVRGRGLLLGVEIVKDRRTKEPADGLGAKITRECMNLGLS
MNIVQLPGMGGVFRIAPPLTVSEDEIDLGLSLLGQAIERAL
>d2gsaa_ c.67.1.4 (A:) Glutamate-1-semialdehyde aminomutase (aminotransferase) {Synechococcus sp., strain GR6}
FKTIKSDEIFAAAQKLMPGGVSSPVRAFKSVGGQPIVFDRVKDAYAWDVDGNRYIDYVGTWGPAI
CGHAHPEVIEALKVAMEKGTSFGAPCALENVLAEMVNDAVPSIEMVRFVNSGTEACMAVLRLMRA
YTGRDKIIKFEGCYHGHADMFLVKAGSGVATLGLPSSPGVPKKTTANTLTTPYNDLEAVKALFAE
NPGEIAGVILEPIVGNSGFIVPDAGFLEGLREITLEHDALLVFDEVMTGFRIAYGGVQEKFGVTP
DLTTLGKIIGGGLPVGAYGGKREIMQLVAPAGPMYQAGTLSGNPLAMTAGIKTLELLRQPGTYEY
LDQITKRLSDGLLAIAQETGHAACGGQVSGMFGFFFTEGPVHNYEDAKKSDLQKFSRFHRGMLEQ
GIYLAPSQFEAGFTSLAHTEEDIDATLAAARTVMSAL
>d2oata_ c.67.1.4 (A:) Ornithine aminotransferase {Human (Homo sapiens)}
GPPTSDDIFEREYKYGAHNYHPLPVALERGKGIYLWDVEGRKYFDFLSSYSAVNQGHCHPKIVNA
LKSQVDKLTLTSRAFYNNVLGEYEEYITKLFNYHKVLPMNTGVEAGETACKLARKWGYTVKGIQK
YKAKIVFAAGNFWGRTLSAISSSTDPTSYDGFGPFMPGFDIIPYNDLPALERALQDPNVAAFMVE
PIQGEAGVVVPDPGYLMGVRELCTRHQVLFIADEIQTGLARTGRWLAVDYENVRPDIVLLGKALS
GGLYPVSAVLCDDDIMLTIKPGEHGSTYGGNPLGCRVAIAALEVLEEENLAENADKLGIILRNEL
MKLPSDVVTAVRGKGLLNAIVIKETKDWDAWKVCLRLRDNGLLAKPTHGDIIRFAPPLVIKEDEL
RESIEIINKTILSF
>d1gtxa_ c.67.1.4 (A:) 4-aminobutyrate aminotransferase, GABA-aminotransferase {Pig (Sus scrofa)}
FDYDGPLMKTEVPGPRSRELMKQLNIIQNAEAVHFFCNYEESRGNYLVDVDGNRMLDLYSQISSI
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PIGYSHPALVKLVQQPQNVSTFINRPALGILPPENFVEKLRESLLSVAPKGMSQLITMACGSCSN
ENAFKTIFMWYRSKERGQSAFSKEELETCMINQAPGCPDYSILSFMGAFHGRTMGCLATTHSKAI
HKIDIPSFDWPIAPFPRLKYPLEEFVKENQQEEARCLEEVEDLIVKYRKKKKTVAGIIVEPIQSE
GGDNHASDDFFRKLRDISRKHGCAFLVDEVQTGGGSTGKFWAHEHWGLDDAADVMTFSKKMMTGG
FFHKEEFRPNAPYRIFNTWLGDPSKNLLLAEVINIIKREDLLSNAAHAGKVLLTGLLDLQARYPQ
FISRVRGRGTFCSFDTPDESIRNKLISIARNKGVMLGGCGDKSIRFRPTLVFRDHHAHLFLNIFS
DILADFK
>d1bt4a_ c.67.1.4 (A:) Phosphoserine aminotransferase, PSAT {Bacillus
circulans, subsp. alkalophilus}
SERAYNFNAGPAALPLEVLERAQAEFVDYQHTGMSIMEMSHRGAVYEAVHNEAQARLLALLGNPT
GYKVLFIQGGASTQFAMIPMNFLKEGQTANYVMTGSWASKALKEAKLIGDTHVAASSEASNYMTL
PKLQEIQLQDNAAYLHLTSNETIEGAQFKAFPDTGSVPLIGDMSSDILSRPFDLNQFGLVYAGAQ
KNLGPSGVTVVIVREDLVAESPKHLPTMLRYDTYVKNNSLYNTPPSFGIYMVNEVLKWIEERGGL
EGVQQANRKKASLIYDAIDQSGGFYRGCVDVDSRSDMNITFRLASEELEKEFVKASEQEGFVGLK
GHRSVGGLRASIYNAVPYESCEALVQFMEHFKRSRG
>d1bjna_ c.67.1.4 (A:) Phosphoserine aminotransferase, PSAT
{Escherichia coli}
QIFNFSSGPAMLPAEVLKQAQQELRDWNGLGTSVMEVSHRGKEFIQVAEEAEKDFRDLLNVPSNY
KVLFCHGGGRGQFAAVPLNILGDKTTADYVDAGYWAASAIKEAKKYCTPNVFDAKVTVDGLRAVK
PMREWQLSDNAAYMHYCPNETIDGIAIDETPDFGADVVVAADFSSTILSRPIDVSRYGVIYAGAQ
KNIGPAGLTIVIVREDLLGKANIACPSILDYSILNDNGSMFNTPPTFAWYLSGLVFKWLKANGGV
AEMDKINQQKAELLYGVIDNSDFYRNDVAKRNRSRMNVPFQLADSALDKLFLEESFAAGLHALKG
HRVVGGMRASIYNAMPLEGVKALTDFMVEFERRHG
>d1cj0a_ c.67.1.4 (A:) Serine hydroxymethyltransferase {Rabbit
(Oryctolagus cuniculus)}
WSSHEQMLAQPLKDSDAEVYDIIKKESNRQRVGLELIASENFASRAVLEALGSCLNNKYSEGYPG
QRYYGGTEHIDELETLCQKRALQAYGLDPQCWGVNVQPYSGSPANFAVYTALVEPHGRIMGLDLP
DGGHLTHGFMTDKKKISATSIFFESMAYKVNPDTGYIDYDRLEENARLFHPKLIIAGTSCYSRNL
DYGRLRKIADENGAYLMADMAHISGLVVAGVVPSPFEHCHVVTTTTHKTLRGCRAGMIFYRRGVR
SVDPKTGKEILYNLESLINSAVFPGLQGGPHNHAIAGVAVALKQAMTPEFKEYQRQVVANCRALS
AALVELGYKIVTGGSDNHLILVDLRSKGTDGGRAEKVLEACSIACNKNTCPGDKSALRPSGLRLG
TPALTSRGLLEKDFQKVAHFIHRGIELTVQIQDDTGPRATLKEFKEKLAGDEKHQRAVRALRQEV
ESFAALFPLPGLPGF
>d1ejia_ c.67.1.4 (A:) Serine hydroxymethyltransferase {Mouse (Mus
musculus)}
MADRDATLWASHEKMLSQPLKDSDAEVYSIIKKESNRQRVGLELIASENFASRAVLEALGSSLNN
KYSEGYPGQRYYGGTEFIDELEMLCQKRALQAYHLDPQCWGVNVQPYSGSPANFAVYTALVEPHG
RIMGLDLPDGGHLTHGFMTDKKKISATSIFFESMPYKVYPETGYINYDQLEENASLFHPKLIIAG
TSCYSRNLDYARLRKIADDNGAYLMADMAHISGLVAAGVVPSPFEHCHVVTTTTHKTLRGCRAGM
IFYRKGVRSVDPKTGKETYYELESLINSAVFPGLQGGPHNHAIAGVAVALKQAMTTEFKIYQLQV
LANCRALSDALTELGYKIVTGGSDNHLILMDLRSKGTDGGRAEKVLEACSIACNKNTCPGDKSAL
RPSGLRLGTPALTSRGLLEEDFQKVAHFIHRGIELTLQIQSHMATKATLKEFKEKLAGDEKIQSA
VATLREEVENFASNFSLPGLPDF
>d1bj4a_ c.67.1.4 (A:) Serine hydroxymethyltransferase {Human (Homo
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sapiens)}
DADLWSSHDAMLAQPLKDSDVEVYNIIKKESNRQRVGLELIASENFASRAVLEALGSCLNNKYSE
GYPGQRYYGGTEFIDELETLCQKRALQAYKLDPQCWGVNVQPYSGSPANFAVYTALVEPHGRIMG
LDLPDGGHLTHGFMTDKKKISATSIFFESMPYKVNPDTGYINYDQLEENARLFHPKLIIAGTSCY
SRNLEYARLRKIADENGAYLMADMAHISGLVAAGVVPSPFEHCHVVTTTTHKTLRGCRAGMIFYR
KGVKSVDPATGKEILYNLESLINSAVFPGLQGGPHNHAIAGVAVALKQAMTLEFKVYQHQVVANC
RALSEALTELGYKIVTGGSDNHLILVDLRSKGTDGGRAEKVLEACSIACNKNTCPGDRSALRPSG
LRLGTPALTSRGLLEKDFQKVAHFIHRGIELTLQIQSDTGVAATLKEFKERLAGDKYQAAVQALR
EEVESFASLFPLPGL
>d1dfoa_ c.67.1.4 (A:) Serine hydroxymethyltransferase {Escherichia
coli}
LKREMNIADYDAELWQAMEQEKVRQEEHIELIASENYTSPRVMQAQGSQLTNKYAEGYPGKRYYG
GCEYVDIVEQLAIDRAKELFGADYANVQPHSGSQANFAVYTALLEPGDTVLGMNLAHGGHLTHGS
PVNFSGKLYNIVPYGIDATGHIDYADLEKQAKEHKPKMIIGGFSAYSGVVDWAKMREIADSIGAY
LFVDMAHVAGLVAAGVYPNPVPHAHVVTTTTHKTLAGPRGGLILAKGGSEELYKKLNSAVFPGGQ
GGPLMHVIAGKAVALKEAMEPEFKTYQQQVAKNAKAMVEVFLERGYKVVSGGTDNHLFLVDLVDK
NLTGKEADAALGRANITVNKNSVPNDPKSPFVTSGIRVGTPAITRRGFKEAEAKELAGWMCDVLD
SINDEAVIERIKGKVLDICARYPVYA
>d1b9ha_ c.67.1.4 (A:) 3-amino-5-hydroxybenzoic acid synthase (AHBA
synthase) {Amycolatopsis mediterranei}
KAPEFPAWPQYDDAERNGLVRALEQGQWWRMGGDEVNSFEREFAAHHGAAHALAVTNGTHALELA
LQVMGVGPGTEVIVPAFTFISSSQAAQRLGAVTVPVDVDAATYNLDPEAVAAAVTPRTKVIMPVH
MAGLMADMDALAKISADTGVPLLQDAAHAHGARWQGKRVGELDSIATFSFQNGKLMTAGEGGAVV
FPDGETEKYETAFLRHSCGRPRDDRRYFHKIAGSNMRLNEFSASVLRAQLARLDEQIAVRDERWT
LLSRLLGAIDGVVPQGGDVRADRNSHYMAMFRIPGLTEERRNALVDRLVEAGLPAFAAFRAIYRT
DAFWELGAPDESVDAIARRCPNTDAISSDCVWLHHRVLLAGEPELHATAEIIADAVARA
>d1fc4a_ c.67.1.4 (A:) 2-amino-3-ketobutyrate CoA ligase {Escherichia
coli}
GSHMRGEFYQQLTNDLETARAEGLFKEERIITSAQQADITVADGSHVINFCANNYLGLANHPDLI
AAAKAGMDSHGFGMASVRFICGTQDSHKELEQKLAAFLGMEDAILYSSCFDANGGLFETLLGAED
AIISDALNHASIIDGVRLCKAKRYRYANNDMQELEARLKEAREAGARHVLIATDGVFSMDGVIAN
LKGVCDLADKYDALVMVDDSHAVGFVGENGRGSHEYCDVMGRVDIITGTLGKALGGASGGYTAAR
KEVVEWLRQRSRPYLFSNSLAPAIVAASIKVLEMVEAGSELRDRLWANARQFREQMSAAGFTLAG
ADHAIIPVMLGDAVVAQKFARELQKEGIYVTGFFYPVVPKGQARIRTQMSAAHTPEQITRAVEAF
TRIGKQLGVIA
>d1bs0a_ c.67.1.4 (A:) PLP-dependent acyl-CoA synthase
(8-amino-7-oxonanoate synthase, AONS) {Escherichia coli}
SWQEKINAALDARRAADALRRRYPVAQGAGRWLVADDRQYLNFSSNDYLGLSHHPQIIRAWQQGA
EQFGIGSGGSGHVSGYSVVHQALEEELAEWLGYSRALLFISGFAANQAVIAAMMAKEDRIAADRL
SHASLLEAASLSPSQLRRFAHNDVTHLARLLASPCPGQQMVVTEGVFSMDGDSAPLAEIQQVTQQ
HNGWLMVDDAHGTGVIGEQGRGSCWLQKVKPELLVVTFGKGFGVSGAAVLCSSTVADYLLQFARH
LIYSTSMPPAQAQALRASLAVIRSDEGDARREKLAALITRFRAGVQDLPFTLADSCSAIQPLIVG
DNSRALQLAEKLRQQGCWVTAIRPPTVPAGTARLRLTLTAAHEMQDIDRLLEVLHGNG
>d1qj5a_ c.67.1.4 (A:) Adenosylmethionine-8-amino-7-oxononanoate

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aminotransferase, BioA {Escherichia coli}
MTTDDLAFDQRHILHPYTSMTSPLPVYPVVSAEGCELILSDGRRLVDGMSSWWAAIHGYNHPQLN
AAMKSQIDAMSHVMFGGITHAPAIELCRKLVAMTPQPLECVFLADSGSVAVEVAMKMALQYWQAK
GEARQRFLTFRNGYHGDTFGAMSVCDPDNSMHSLWKGYLPENLFAPAPQSRMDGEWDERDMVGFA
RLMAAHRHEIAAVIIEPIVQGAGGMRMYHPEWLKRIRKICDREGILLIADEIATGFGRTGKLFAC
EHAEIAPDILCLGKALTGGTMTLSATLTTREVAETISNGEAGCFMHGPTFMGNPLACAAANASLA
ILESGDWQQQVADIEVQLREQLAPARDAEMVADVRVLGAIGVVETTHPVNMAALQKFFVEQGVWI
RPFGKLIYLMPPYIILPQQLQRLTAAVNRAVQDETFFCQ
>d1b8ga_ c.67.1.4 (A:) 1-aminocyclopropane-1-carboxylate synthase
(ACC synthase) {Apple (Malus domestica)}
MLSRNATFNSHGQDSSYFLGWQEYEKNPYHEVHNTNGIIQMGLAENQLCFDLLESWLAKNPEAAA
FKKNGESIFAELALFQDYHGLPAFKKAMVDFMAEIRGNKVTFDPNHLVLTAGATSANETFIFCLA
DPGEAVLIPTPYYPGFDRDLKWRTGVEIVPIHCTSSNGFQITETALEEAYQEAEKRNLRVKGVLV
TNPSNPLGTTMTRNELYLLLSFVEDKGIHLISDEIYSGTAFSSPSFISVMEVLKDRNCDENSEVW
QRVHVVYSLSKDLGLPGFRVGAIYSNDDMVVAAATKMSSFGLVSSQTQHLLSAMLSDKKLTKNYI
AENHKRLKQRQKKLVSGLQKSGISCLNGNAGLFCWVDMRHLLRSNTFEAEMELWKKIVYEVHLNI
SPGSSCHCTEPGWFRVCFANLPERTLDLAMQRLKAFVG
>d1iaya_ c.67.1.4 (A:) 1-aminocyclopropane-1-carboxylate synthase
(ACC synthase) {Tomato (Lycopersicon esculentum)}
ILSKLATNEEHGENSPYFDGWKAYDSDPFHPLKNPNGVIQMGLAENQLCLDLIEDWIKRNPKGSI
CSEGIKSFKAIANFQDYHGLPEFRKAIAKFMEKTRGGRVRFDPERVVMAGGATGANETIIFCLAD
PGDAFLVPSPYYPAFNRDLRWRTGVQLIPIHCESSNNFKITSKAVKEAYENAQKSNIKVKGLILT
NPSNPLGTTLDKDTLKSVLSFTNQHNIHLVCDEIYAATVFDTPQFVSIAEILDEQEMTYCNKDLV
HIVYSLSKDMGLPGFRVGIIYSFNDDVVNCARKMSSFGLVSTQTQYFLAAMLSDEKFVDNFLRES
AMRLGKRHKHFTNGLEVVGIKCLKNNAGLFCWMDLRPLLRESTFDSEMSLWRVIINDVKLNVSPG
SSFECQEPGWFRVCFANMDDGTVDIALARIRRFVGVEK
>d1c4ka2 c.67.1.5 (A:108-569) Ornithine decarboxylase major domain
{Lactobacillus sp., strain 30a}
PPFFKSLKEYVSRYLIQFDCPGHQGGQYYRKHPAGREFYDFFGETVFRADLCNADVALGDLLIHE
GPAVAAEKHAARVYNADKTYFVLGGSSNANNTVTSALVSNGDLVLFDRNNHKSVYNSALAMAGGR
PVYLQTNRNPYGFIGGIYDSDFDEKKIRELAAKVDPERAKWKRPFRLAVIQLGTYDGTIYNAHEV
VKRIGHLCDYIEFDSAWVGYEQFIPMMRNSSPLLIDDLGPEDPGIIVVQSVHKQQAGFSQTSQIH
KKDSHIKGQLRYCDHKHFNNSFNLFMSTSPFYPMYAALDVNAAMQEGEAGRKLWHDLLITTIEAR
KKLIKAGSMFRPFVPPVVNGKKWEDGDTEDMANNIDYWRFEKGAKWHAYEGYGDNQYYVDPNKFM
LTTPGINPETGDYEDFGVPATIVANYLRDHGIIPEKSDLNSILFLMTPAETPAKMNNLITQLLQL
QRLIEED
>d1qg8a_ c.68.1.1 (A:) Spore coat polysaccharide biosynthesis protein
SpsA {Bacillus subtilis}
PKVSVIMTSYNKSDYVAKSISSILSQTFSDFELFIMDDNSNEETLNVIRPFLNDNRVRFYQSDIS
GVKERTEKTRYAALINQAIEMAEGEYITYATDDNIYMPDRLLKMVRELDTHPEKAVIYSASKTYH
LNENRDIVKETVRPAAQVTWNAPCAIDHCSVMHRYSVLEKVKEKFGSYWDESPAFYRIGDARFFW
RVNHFYPFYPLDEELDLNYITDQSIHFQLFELEKNEFVRNLPPQRNCRELRESLKKLGMG
>d1j8wb_ c.68.1.2 (B:) beta 1,4 galactosyltransferase (b4GalT1) {Cow
(Bos taurus)}
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TACPEESPLLVGPMLIEFNIPVDLKLVEQQNPKVKLGGRYTPMDCISPHKVAIIIPFRNRQEHLK
YWLYYLHPILQRQQLDYGIYVINQAGESMFNRAKLLNVGFKEALKDYDYNCFVFSDVDLIPMNDH
NTYRCFSQPRHISVAMDKFGFSLPYVQYFGGVSALSKQQFLSINGFPNNYWGWGGEDDDIYNRLA
FRGMSVSRPNAVIGKCRMIRHSRDKKNEPNPQRFDRIAHTKETMLSDGLNSLTYMVLEVQRYPLY
TKITVDIGTPS
>d1ezia_ c.68.1.3 (A:) CMP acylneuraminate synthetase {Neisseria meningitidis}
MEKQNIAVILARQNSKGLPLKNLRKMNGISLLGHTINAAISSKCFDRIIVSTDGGLIAEEAKNFG
VEVVLRPAELASDTASSISGVIHALETIGSNSGTVTLLQPTSPLRTGAHIREAFSLFDEKIKGSV
VSACPMEHHPLKTLLQINNGEYAPMRHLSDLEQPRQQLPQAFRPNGAIYINDTASLIANNCFFIA
PTKLYIMSHQDSIDIDTELDLQQAENILN
>d1ga8a_ c.68.1.4 (A:) Galactosyltransferase LgtC {Neisseria meningitidis}
MDIVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLDAGISEANRAAVAANLRGGGGNIRFIDVN
PEDFAGFPLNIRHISITTYARLKLGEYIADCDKVLYLDIDVLVRDSLTPLWDTDLGDNWLGASID
LFVERQEGYKQKIGMADGEYYFNAGVLLINLKKWRRHDIFKMSSEWVEQYKDVMQYQDQDILNGL
FKGGVCYANSRFNFMPTNYAFMANWFASRHTDPLYRDRTNTVMPVAVSHYCGPAKPWHRDCTAWG
AERFTELAGSLTTVPEEWRGKL
>d1g93a_ c.68.1.9 (A:) alpha-1,3-galactosyltransferase catalytic domain {Cow (Bos taurus)}
KLKLSDWFNPFKRPEVVTMTKWKAPVVWEGTYNRAVLDNYYAKQKITVGLTVFAVGRYIEHYLEE
FLTSANKHFMVGHPVIFYIMVDDVSRMPLIELGPLRSFKVFKIKPEKRWQDISMMRMKTIGEHIV
AHIQHEVDFLFCMDVDQVFQDKFGVETLGESVAQLQAWWYKADPNDFTYERRKESAAYIPFGEGD
FYYHAAIFGGTPTQVLNITQECFKGILKDKKNDIEAQWHDESHLNKYFLLNKPTKILSPEYCWDY
HIGLPADIKLVKMSWQT
>d1hv9a2 c.68.1.5 (A:4-251) N-acetylglucosamine 1-phosphate uridyltransferase GlmU, N-terminal domain {Escherichia coli}
NAMSVVILAAGKGTRMYSDLPKVLHTLAGKAMVQHVIDAANELGAAHVHLVYGHGGDLLKQALKD
DNLNWVLQAEQLGTGHAMQQAAPFFADDEDILMLYGDVPLISVETLQRLRDAKPQGGIGLLTVKL
DDPTGYGRITRENGKVTGIVEHKDATDEQRQIQEINTGILIANGADMKRWLAKLTNNNAQGEYYI
TDIIALAYQEGREIVAVHPQRLSEVEGVNNRLQLSRLERVYQSEQAEKLLLAG
>d1hm9a2 c.68.1.5 (A:2-251) N-acetylglucosamine 1-phosphate uridyltransferase GlmU, N-terminal domain {Streptococcus pneumoniae}
SNFAIILAAGKGTRMKSDLPKVLHKVAGISMLEHVFRSVGAIQPEKTVTVVGHKAELVEEVLAGQ
TEFVTQSEQLGTGHAVMMTEPILEGLSGHTLVIAGDTPLITGESLKNLIDFHINHKNVATILTAE
TDNPFGYGRIVRNDNAEVLRIVEQKDATDFEKQIKEINTGTYVFDNERLFEALKNINTNNAQGEY
YITDVIGIFRETGEKVGAYTLKDFDESLGVNDRVALATAESVMRRRINHKHMVNG
>d1fxoa_ c.68.1.6 (A:) glucose-1-phosphate thymidylyltransferase RmlA {Pseudomonas aeruginosa}
KRKGIILAGGSGTRLHPATLAISKQLLPVYDKPMIYYPLSTLMLAGIREILIISTPQDTPRFQQL
LGDGSNWGLDLQYAVQPSPDGLAQAFLIGESFIGNDLSALVLGDNLYYGHDFHELLGSASQRQTG
ASVFAYHVLDPERYGVVEFDQGGKAISLEEKPLEPKSNYAVTGLYFYDQQVVDIARDLKPSPRGE
LEITDVNRAYLERGQLSVEIMGRGYAWLDTGTHDSLLEAGQFIATLENRQGLKVACPEEIAYRQK
WIDAAQLEKLAAPLAKNGYGQYLKRLLTETVY

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>d1iina_ c.68.1.6 (A:) glucose-1-phosphate thymidylyltransferase
RmlA {Salmonella enterica}
MKTRKGIILAGGSGTRLYPVTMAVSQQLLPIYDKPMIYYPLSTLMLAGIRDILIISTPQDTPRFQ
QLLGDGSQWGLNLQYKVQPSPDGLAQAFIIGEEFIGHDDCALVLGDNIFYGHDLPKLMEAAVNKE
SGATVFAYHVNDPERYGVVEFDQKGTAVSLEEKPLQPKSNYAVTGLYFYDNSVVEMAKNLKPSAR
GELEITDINRIYMEQGRLSVAMMGRGYAWLDTGTHQSLIEASNFIATIEERQGLKVSCPEEIAFR
KNFINAQQVIELAGPLSKNDYGKYLLKMV
>d1h5ra_ c.68.1.6 (A:) glucose-1-phosphate thymidylyltransferase
RmlA {Escherichia coli}
KMRKGIILAGGSGTRLYPVTMAVSKQLLPIYDKPMIYYPLSTLMLAGIRDILIISTPQDTPRFQQ
LLGDGSQWGLNLQYKVQPSPDGLAQAFIIGEEFIGGDDCALVLGDNIFYGHDLPKLMEAAVNKES
GATVFAYHVNDPERYGVVEFDKNGTAISLEEKPLEPKSNYAVTGLYFYDNDVVQMAKNLKPSARG
ELEITDINRIYLEQGRLSVAMMGRGYAWLDTGTHQSLIEASNFIATIEERQGLKVSCPEEIAFRK
GFIDVEQVRKLAVPLIKNNYGQYLYKMTKD
>d1fgga_ c.68.1.7 (A:) 1,3-Glucuronyltransferase I (glcAT-I) {Human
(Homo sapiens)}
MTIYVVTPTYARLVQKAELVRLSQTLSLVPRLHWLLVEDAEGPTPLVSGLLAASGLLFTHLVVLT
PKAQRLREGEPGWVHPRGVEQRNKALDWLRGRGGAVGGEKDPPPPGTQGVVYFADDDNTYSRELF
EEMRWTRGVSVWPVGLVGGLRFEGPQVQDGRVVGFHTAWEPSRPFPVDMAGFAVALPLLLDKPNA
QFDSTAPRGHLESSLLSHLVDPKDLEPRAANCTRVLVWHTRTEKPKMKQEEQLQRQGRGSDPAIE
V
>d1fo8a_ c.68.1.10 (A:) N-acetylglucosaminyltransferase I {Rabbit
(Oryctolagus cuniculus)}
LAVIPILVIACDRSTVRRCLDKLLHYRPSAELFPIIVSQDCGHEETAQVIASYGSAVTHIRQPDL
SNIAVQPDHRKFQGYYKIARHYRWALGQIFHNFNYPAAVVVEDDLEVAPDFFEYFQATYPLLKAD
PSLWCVSAWNDNGKEQMVDSSKPELLYRTDFFPGLGWLLLAELWAELEPKWPKAFWDDWMRRPEQ
RKGRACVRPEISRTMTFGRKGVSHGQFFDQHLKFIKLNQQFVPFTQLDLSYLQQEAYDRDFLARV
YGAPQLQVEKVRTNDRKELGEVRVQYTGRDSFKAFAKALGVMDDLKSGVPRAGYRGIVTFLFRGR
RVHLAPPQTWDGYDPSWT
>d1e5ka_ c.68.1.8 (A:) Molybdenum cofactor biosynthesis protein MobA
{Escherichia coli}
MTTITGVVLAGGKARRMGGVDKGLLELNGKPLWQHVADALMTQLSHVVVNANRHQEIYQASGLKV
IEDSLADYPGPLAGMLSVMQQEAGEWFLFCPCDTPYIPPDLAARLNHQRKDAPVVWVHDGERDHP
TIALVNRAIEPLLLEYLQAGERRVMVFMRLAGGHAVDFSDHKDAFVNVNTPEELARWQ
>d1i52a_ c.68.1.13 (A:) 4-diphosphocytidyl-2-c-methylerythritol
(CDP-me) synthase (YgbP) {Escherichia coli}
HLDVCAVVPAAGFGRRMQTECPKQYLSIGNQTILEHSVHALLAHPRVKRVVIAISPGDSRFAQLP
LANHPQITVVDGGDERADSVLAGLKAAGDAQWVLVHDAARPCLHQDDLARLLALSETSRTGGILA
APVRDTMKRAEPGKNAIAHTVDRNGLWHALTPQFFPRELLHDCLTRALNEGATITDEASALEYCG
FHPQLVEGRADNIKVTRPEDLALAEFYLTR
>d1h7ea_ c.68.1.13 (A:) CMP:2-keto-3-deoxy-manno-octonic acid
(CMP-KDO)synthetase, KdsB {Escherichia coli}
SKAVIVIPARYGSSRLPGKPLLDIVGKPMIQHVYERALQVAGVAEVWVATDDPRVEQAVQAFGGK
AIMTRNDHESGTDRLVEVMHKVEADIYINLQGDEPMIRPRDVETLLQGMRDDPALPVATLCHAIS
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AAEAAEPSTVKVVVNTRQDALYFSRSPIPYPRNAEKARYLKHVGIYAYRRDVLQNYSQLPESMPE
QAESLEQLRLMNAGINIRTFEVAATGPGVDTPACLEKVRALMAQELAENA
>d1jyka_ c.68.1.13 (A:) CTP:phosphocholine cytidylytransferase LicC
{Streptococcus pneumoniae}
EIRVKAIILAAGLGTRLRPLTENTPKALVQVNQKPLIEYQIEFLKEKGINDIIIIVGYLKEQFDY
LKEKYGVRLVFNDKYADYNNFYSLYLVKEELANSYVIDADNYLFKNMFRNDLTRSTYFSVYREDC
TNEWFLVYGDDYKVQDIIVDSKAGRILSGVSFWDAPTAEKIVSFIDKAYVSGEFVDLYWDNMVKD
NIKELDVYVEELEGNSIYEIDSVQDYRKLEEILK
>d1jw9b_ c.111.1.1 (B:) Molybdenum cofactor biosynthesis protein MoeB
{Escherichia coli}
AELSDQEMLRYNRQIILRGFDFDGQEALKDSRVLIVGLGGLGCAASQYLASAGVGNLTLLDFDTV
SLSNLQRQTLHSDATVGQPKVESARDALTRINPHIAITPVNALLDDAELAALIAEHDLVLDCTDN
VAVRNQLNAGCFAAKVPLVSGAAIRMEGQITVFTYQDGEPCYRCLSRLFGENALTCVEAGVMAPL
IGVIGSLQAMEAIKMLAGYGKPASGKIVMYDAMTCQFREMKLMRNPGCEVCG
>d1ea5a_ c.69.1.1 (A:) Acetylcholinesterase {Electric ray (Torpedo
californica)}
SELLVNTKSGKVMGTRVPVLSSHISAFLGIPFAEPPVGNMRFRRPEPKKPWSGVWNASTYPNNCQ
QYVDEQFPGFSGSEMWNPNREMSEDCLYLNIWVPSPRPKSTTVMVWIYGGGFYSGSSTLDVYNGK
YLAYTEEVVLVSLSYRVGAFGFLALHGSQEAPGNVGLLDQRMALQWVHDNIQFFGGDPKTVTIFG
ESAGGASVGMHILSPGSRDLFRRAILQSGSPNCPWASVSVAEGRRRAVELGRNLNCNLNSDEELI
HCLREKKPQELIDVEWNVLPFDSIFRFSFVPVIDGEFFPTSLESMLNSGNFKKTQILLGVNKDEG
SFFLLYGAPGFSKDSESKISREDFMSGVKLSVPHANDLGLDAVTLQYTDWMDDNNGIKNRDGLDD
IVGDHNVICPLMHFVNKYTKFGNGTYLYFFNHRASNLVWPEWMGVIHGYEIEFVFGLPLVKELNY
TAEEEALSRRIMHYWATFAKTGNPNEPHSQESKWPLFTTKEQKFIDLNTEPMKVHQRLRVQMCVF
WNQFLPKLLNAT
>d1maaa_ c.69.1.1 (A:) Acetylcholinesterase {Mouse (Mus musculus)}
EDPQLLVRVRGGQLRGIRLKAPGGPVSAFLGIPFAEPPVGSRRFMPPEPKRPWSGVLDATTFQNV
CYQYVDTLYPGFEGTEMWNPNRELSEDCLYLNVWTPYPRPASPTPVLIWIYGGGFYSGAASLDVY
DGRFLAQVEGAVLVSMNYRVGTFGFLALPGSREAPGNVGLLDQRLALQWVQENIAAFGGDPMSVT
LFGESAGAASVGMHILSLPSRSLFHRAVLQSGTPNGPWATVSAGEARRRATLLARLVGCPPGGAG
GNDTELIACLRTRPAQDLVDHEWHVLPQESIFRFSFVPVVDGDFLSDTPEALINTGDFQDLQVLV
GVVKDEGSYFLVYGVPGFSKDNESLISRAQFLAGVRIGVPQASDLAAEAVVLHYTDWLHPEDPTH
LRDAMSAVVGDHNVVCPVAQLAGRLAAQGARVYAYIFEHRASTLTWPLWMGVPHGYEIEFIFGLP
LDPSLNYTTEERIFAQRLMKYWTNFARTGDPNDPRDRKSPQWPPYTTAAQQYVSLNLKPLEVRRG
LRAQTCAFWNRFLPKLLSAT
>d1f8ua_ c.69.1.1 (A:) Acetylcholinesterase {Human (Homo sapiens)}
DAELLVTVRGGRLRGIRLKTPGGPVSAFLGIPFAEPPMGPRRFLPPEPKQPWSGVVDATTFQSVC
YQYVDTLYPGFEGTEMWNPNRELSEDCLYLNVWTPYPRPTSPTPVLVWIYGGGFYSGASSLDVYD
GRFLVQAERTVLVSMNYRVGAFGFLALPGSREAPGNVGLLDQRLALQWVQENVAAFGGDPTSVTL
FGQSAGAASVGMHLLSPPSRGLFHRAVLQSGAPNGPWATVGMGEARRRATQLAHLVGCPPGGTGG
NDTELVACLRTRPAQVLVNHEWHVLPQESVFRFSFVPVVDGDFLSDTPEALINAGDFHGLQVLVG
VVKDEGSYFLVYGAPGFSKDNESLISRAEFLAGVRVGVPQVSDLAAEAVVLHYTDWLHPEDPARL
REALSDVVGDHNVVCPVAQLAGRLAAQGARVYAYVFEHRASTLSWPLWMGVPHGYEIEFIFGIPL
DPSRNYTAEEKIFAQRLMRYWANFARTGDPNEPRDPKAPQWPPYTAGAQQYVSLDLRPLEVRRGL
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RAQACAFWNRFLPKLLSAT
>d1dx4a_ c.69.1.1 (A:) Acetylcholinesterase {Fruit fly (Drosophila melanogaster)}
DRLVVQTSSGPVRGRSVTVQGREVHVYTGIPYAKPPVEDLRFRKPVPAEPWHGVLDATGLSATCV
QERYEYFPGFSGEEIWNPNTNVSEDCLYINVWAPAKARLRHGRGANGGEHPNGKQADTDHLIHNG
NPQNTTNGLPILIWIYGGGFMTGSATLDIYNADIMAAVGNVIVASFQYRVGAFGFLHLAPEMPSE
FAEEAPGNVGLWDQALAIRWLKDNAHAFGGNPEWMTLFGESAGSSSVNAQLMSPVTRGLVKRGMM
QSGTMNAPWSHMTSEKAVEIGKALINDCNCNASMLKTNPAHVMSCMRSVDAKTISVQQWNSYSGI
LSFPSAPTIDGAFLPADPMTLMKTADLKDYDILMGNVRDEGTYFLLYDFIDYFDKDDATALPRDK
YLEIMNNIFGKATQAEREAIIFQYTSWEGNPGYQNQQQIGRAVGDHFFTCPTNEYAQALAERGAS
VHYYYFTHRTSTSLWGEWMGVLHGDEIEYFFGQPLNNSLQYRPVERELGKRMLSAVIEFAKTGNP
AQDGEEWPNFSKEDPVYYIFSTDDKIEKLARGPLAARCSFWNDYLPKVRSW
>d2bce__ c.69.1.1 (-) Bile-salt activated lipase (cholesterol esterase) {Cow (Bos taurus)}
AKLGSVYTEGGFVEGVNKKLSLFGDSVDIFKGIPFAAAPKALEKPERHPGWQGTLKAKSFKKRCL
QATLTQDSTYGNEDCLYLNIWVPQGRKEVSHDLPVMIWIYGGAFLMGASQGANFLSNYLYDGEEI
ATRGNVIVVTFNYRVGPLGFLSTGDSNLPGNYGLWDQHMAIAWVKRNIEAFGGDPDNITLFGESA
GGASVSLQTLSPYNKGLIKRAISQSGVGLCPWAIQQDPLFWAKRIAEKVGCPVDDTSKMAGCLKI
TDPRALTLAYKLPLGSTEYPKLHYLSFVPVIDGDFIPDDPVNLYANAADVDYIAGTNDMDGHLFV
GMDVPAINSNKQDVTEEDFYKLVSGLTVTKGLRGANATYEVYTEPWAQDSSQETRKKTMVDLETD
ILFLIPTKIAVAQHKSHAKSANTYTYLFSQPSRMPIYPKWMGADHADDLQYVFGKPFATPLGYRA
QDRTVSKAMIAYWTNFARTGDPNTGHSTVPANWDPYTLEDDNYLEINKQMDSNSMKLHLRTNYLQ
FWTQTYQALPTVTSAGASLLPPEDNSQASPVPPADNSGAPTEPSAGDSEVAQMPVVIGF
>d1f6wa_ c.69.1.1 (A:) Bile-salt activated lipase (cholesterol esterase) {Human (Homo sapiens)}
AKLGAVYTEGGFVEGVNKKLGLLGDSVDIFKGIPFAAPTKALENPQPHPGWQGTLKAKNFKKRCL
QATITQDSTYGDEDCLYLNIWVPQGRKQVSRDLPVMIWIYGGAFLMGSGHGANFLNNYLYDGEEI
ATRGNVIVVTFNYRVGPLGFLSTGDANLPGNYGLRDQHMAIAWVKRNIAAFGGDPDNITLFGESA
GGASVSLQTLSPYNKGLIRRAISQSGVALSPWVIQKNPLFWAKKVAEKVGCPVGDAARMAQCLKV
TDPRALTLAYKVPLAGLEYPMLHYVGFVPVIDGDFIPDDPINLYANAADIDYIAGTNNMDGHIFA
SIDMPAINKGNKKVTEEDFYKLVSEFTITKGLRGAKTTFDVYTESWAQDPSQENKKKTVVDFETD
VLFLVPTEIALAQHRANAKSAKTYAYLFSHPSRMPVYPKWVGADHADDIQYVFGKPFATPTGYRP
QDRTVSKAMIAYWTNFAKTGDPNMGDSAVPTHWEPYTTENSGYLEITKKMGSSSMKRSLRTNFLR
YWTLTYLALPTVT
>d1qe3a_ c.69.1.1 (A:) Thermophylic para-nitrobenzyl esterase (PNB esterase) {Bacillus subtilis}
THQIVTTQYGKVKGTTENGVHKWKGIPYAKPPVGQWRFKAPEPPEVWEDVLDATAYGPICPQPSD
LLSLSYTELPRQSEDCLYVNVFAPDTPSQNLPVMVWIHGGAFYLGAGSEPLYDGSKLAAQGEVIV
VTLNYRLGPFGFLHLSSFDEAYSDNLGLLDQAAALKWVRENISAFGGDPDNVTVFGESAGGMSIA
ALLAMPAAKGLFQKAIMESGASRTMTKEQAASTAAAFLQVLGINESQLDRLHTVAAEDLLKAADQ
LRIAEKENIFQLFFQPALDPKTLPEEPEKSIAEGAASGIPLLIGTTRDEGYLFFTPDSDVHSQET
LDAALEYLLGKPLAEKAADLYPRSLESQIHMMTDLLFWRPAVAYASAQSHYAPVWMYRFDWHPEK
PPYNKAFHALELPFVFGNLDGLERMAKAEITDEVKQLSHTIQSAWITFAKTGNPSTEAVNWPAYH
EETRETVILDSEITIENDPESEKRQKLF
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>d1jkma_ c.69.1.2 (A:) Carboxylesterase {Bacillus subtilis, brefeldin A esterase}
PGRLGDESSGPRTDPRFSPAMVEALATFGLDAVAAAPPVSASDDLPTVLAAVGASHDGFQAVYDS
IALDLPTDRDDVETSTETILGVDGNEITLHVFRPAGVEGVLPGLVYTHGGGMTILTTDNRVHRRW
CTDLAAAGSVVVMVDFRNAWTAEGHHPFPSGVEDCLAAVLWVDEHRESLGLSGVVVQGESGGGNL
AIATTLLAKRRGRLDAIDGVYASIPYISGGYAWDHERRLTELPSLVENDGYFIENGGMALLVRAY
DPTGEHAEDPIAWPYFASEDELRGLPPFVVAVNELDPLRDEGIAFARRLARAGVDVAARVNIGLV
HGADVIFRHWLPAALESTVRDVAGFAADRARLR
>d1evqa_ c.69.1.2 (A:) Carboxylesterase {Alicyclobacillus acidocaldarius}
LDPVIQQVLDQLNRMPAPDYKHLSAQQFRSQQSLFPPVKKEPVAEVREFDMDLPGRTLKVRMYRP
EGVEPPYPALVYYHGGGWVVGDLETHDPVCRVLAKDGRAVVFSVDYRLAPEHKFPAAVEDAYDAL
QWIAERAADFHLDPARIAVGGDSAGGNLAAVTSILAKERGGPALAFQLLIYPSTGYDPAHPPASI
EENAEGYLLTGGMMLWFRDQYLNSLEELTHPWFSPVLYPDLSGLPPAYIATAQYDPLRDVGKLYA
EALNKAGVKVEIENFEDLIHGFAQFYSLSPGATKALVRIAEKLRDALA
>d1jjia_ c.69.1.2 (A:) Carboxylesterase {Archaeon Archaeoglobus fulgidus}
MLDMPIDPVYYQLAEYFDSLPKFDQFSSAREYREAINRIYEERNRQLSQHERVERVEDRTIKGRN
GDIRVRVYQQKPDSPVLVYYHGGGFVICSIESHDALCRRIARLSNSTVVSVDYRLAPEHKFPAAV
YDCYDATKWVAENAEELRIDPSKIFVGGDSAGGNLAAAVSIMARDSGEDFIKHQILIYPVVNFVA
PTPSLLEFGEGLWILDQKIMSWFSEQYFSREEDKFNPLASVIFADLENLPPALIITAEYDPLRDE
GEVFGQMLRRAGVEASIVRYRGVLHGFINYYPVLKAARDAINQIAALLVFD
>d1jjfa_ c.69.1.2 (A:) Feruloyl esterase domain of the cellulosomal xylanase z {Clostridium thermocellum}
SLPTMPPSGYDQVRNGVPRGQVVNISYFSTATNSTRPARVYLPPGYSKDKKYSVLYLLHGIGGSE
NDWFEGGGRANVIADNLIAEGKIKPLIIVTPNTNAAGPGIADGYENFTKDLLNSLIPYIESNYSV
YTDREHRAIAGLSMGGGQSFNIGLTNLDKFAYIGPISAAPNTYPNERLFPDGGKAAREKLKLLFI
ACGTNDSLIGFGQRVHEYCVANNINHVYWLIQGGGHDFNVWKPGLWNFLQMADEAGLTRD
>d1gkla_ c.69.1.2 (A:) Feruloyl esterase domain of the cellulosomal xylanase y {Clostridium thermocellum}
SFKYESAVQYRPAPDSYLNPCPQAGRIVKETYTGINGTKSLNVYLPYGYDPNKKYNIFYLMHGGG
ENENTIFSNDVKLQNILDHAIMNGELEPLIVVTPTFNGGNCTAQNFYQEFRQNVIPFVESKYSTY
AESTTPQGIAASRMHRGFGGFAMGGLTTWYVMVNCLDYVAYFMPLSGDYWYGNSPQDKANSIAEA
INRSGLSKREYFVFAATGSEDIAYANMNPQIEAMKALPHFDYTSDFSKGNFYFLVAPGATHWWGY
VRHYIYDALPYFFHELEHHHHHH
>d1f0na_ c.69.1.3 (A:) Antigen 85b {Mycobacterium tuberculosis}
SRPGLPVEYLQVPSPSMGRDIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYYQSGL
SIVMPVGGQSSFYSDWYSPACGKAGCQTYKWETFLTSELPQWLSANRAVKPTGSAAIGLSMAGSS
AMILAAYHPQQFIYAGSLSALLDPSQGMGPSLIGLAMGDAGGYKAADMWGPSSDPAWERNDPTQQ
IPKLVANNTRLWVYCGNGTPNELGGANIPAEFLENFVRSSNLKFQDAYNAAGGHNAVFNFPPNGT
HSWEYWGAQLNAMKGDLQSSLGAG
>d1dqza_ c.69.1.3 (A:) Antigen 85c {Mycobacterium tuberculosis}
RPGLPVEYLQVPSASMGRDIKVQFQGGGPHAVYLLDGLRAQDDYNGWDINTPAFEEYYQSGLSVI
MPVGGQSSFYTDWYQPSQSNGQNYTYKWETFLTREMPAWLQANKGVSPTGNAAVGLSMSGGSALI
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LAAYYPQQFPYAASLSGFLNPSESWWPTLIGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPR
LVANNTRIWVYCGNGTPSDLGGDNIPAKFLEGLTLRTNQTFRDTYAADGGRNGVFNFPPNGTHSW
PYWNEQLVAMKADIQHVLNG
>d1ju3a2 c.69.1.21 (A:5-351) Bacterial cocaine esterase N-terminal
domain {Rhodococcus sp. mb1}
NYSVASNVMVPMRDGVRLAVDLYRPDADGPVPVLLVRNPYDKFDVFAWSTQSTNWLEFVRDGYAV
VIQDTRGLFASEGEFVPHVDDEADAEDTLSWILEQAWCDGNVGMFGVSYLGVTQWQAAVSGVGGL
KAIAPSMASADLYRAPWYGPGGALSVEALLGWSALIGTGLITSRSDARPEDAADFVQLAAILNDV
AGAASVTPLAEQPLLGRLIPWVIDQVVDHPDNDESWQSISLFERLGGLATPALITAGWYDGFVGE
SLRTFVAVKDNADARLVVGPWSHSNLTGRNADRKFGIAATYPIQEATTMHKAFFDRHLRGETDAL
AGVPKVRLFVMGIDEWRDETDW
>d1qfma2 c.69.1.4 (A:431-710) Prolyl oligopeptidase, C-terminal
domain {Pig (Sus scrofa)}
DASDYQTVQIFYPSKDGTKIPMFIVHKKGIKLDGSHPAFLYGYGGFNISITPNYSVSRLIFVRHM
GGVLAVANIRGGGEYGETWHKGGILANKQNCFDDFQCAAEYLIKEGYTSPKRLTINGGSNGGLLV
ATCANQRPDLFGCVIAQVGVMDMLKFHKYTIGHAWTTDYGCSDSKQHFEWLIKYSPLHNVKLPEA
DDIQYPSMLLLTADHDDRVVPLHSLKFIATLQYIVGRSRKQNNPLLIHVDTKAGHGAGKPTAKVI
EEVSDMFAFIARCLNIDWIP
>g1wht.1 c.69.1.5 (A:,B:) Serine carboxypeptidase II {Wheat (Triticum
vulgaris)}
GHAADRIARLPGQPAVDFDMYSGYITVDEGAGRSLFYLLQEAPEDAQPAPLVLWLNGGPGCSSVA
YGASEELGAFRVKPRGAGLVLNEYRWNKVANVLFLDSPAGVGFSYTNTSSDIYTSGDNRTAHDSY
AFLAKWFERFPHYKYRDFYIAGESYAGHYVPELSQLVHRSKNPVINLKGFMVGNGLIDDYHDYVG
TFEFWWNHGIVSDDTYRRLKEACLHDSFIHPSPACDAATDVATAEQGNIDMYSLYTPVCNIXSYD
PCTERYSTAYYNRRDVQMALHANVTGAMNYTWATCSDTINTHWHDAPRSMLPIYRELIAAGLRIW
VFSGDTDAVVPLTATRYSIGALGLPTTTSWYPWYDDQEVGGWSQVYKGLTLVSVRGAGHEVPLHR
PRQALVLFQYFLQGKPMPGQ
>d1cpy__ c.69.1.5 (-) Serine carboxypeptidase II {Baker's yeast
(Saccharomyces cerevisiae)}
KIKDPKILGIDPNVTQYTGYLDVEDEDKHFFFWTFESRNDPAKDPVILWLNGGPGCSSLTGLFFA
LGPSSIGPDLKPIGNPYSWNSNATVIFLDQPVNVGFSYSGSSGVSNTVAAGKDVYNFLELFFDQF
PEYVNKGQDFHIAGASYAGHYIPVFASEILSHKDRNFNLTSVLIGNGLTDPLTQYNYYEPMACGE
GGEPSVLPSEECSAMEDSLERCLGLIESCYDSQSVWSCVPATIYCNNAQLAPYQRTGRNVYDIRK
DCEGGNLCYPTLQDIDDYLNQDYVKEAVGAEVDHYESCNFDINRNFLFAGDWMKPYHTAVTDLLN
QDLPILVYAGDKDFICNWLGNKAWTDVLPWKYDEEFASQKVRNWTASITDEVAGEVKSYKHFTYL
RVFNGGHMVPFDVPENALSMVNEWIHGGFSL
>d1ac5__ c.69.1.5 (-) Serine carboxypeptidase II {Baker's yeast
(Saccharomyces cerevisiae), kex1(delta)p}
LPSSEEYKVAYELLPGLSEVPDPSNIPQMHAGHIPLRSEDADEQDSSDLEYFFWKFTNNDSNGNV
DRPLIIWLNGGPGCSSMDGALVESGPFRVNSDGKLYLNEGSWISKGDLLFIDQPTGTGFSVEQNK
DEGKIDKNKFDEDLEDVTKHFMDFLENYFKIFPEDLTRKIILSGESYAGQYIPFFANAILNHNKF
SKIDGDTYDLKALLIGNGWIDPNTQSLSYLPFAMEKKLIDESNPNFKHLTNAHENCQNLINSAST
DEAAHFSYQECENILNLLLSYTRESSQKGTADCLNMYNFNLKDSYPSCGMNWPKDISFVSKFFST
PGVIDSLHLDSDKIDHWKECTNSVGTKLSNPISKPSIHLLPGLLESGIEIVLFNGDKDLICNNKG
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VLDTIDNLKWGGIKGFSDDAVSFDWIHKSKSTDDSEEFSGYVKYDRNLTFVSVYNASHMVPFDKS
LVSRGIVDIYSNDVMIIDNNGKNVMITT
>d1ivya_ c.69.1.5 (A:) Human 'protective protein', HPP {Human (Homo
sapiens)}
APDQDEIQRLPGLAKQPSFRQYSGYLKSSGSKHLHYWFVESQKDPENSPVVLWLNGGPGCSSLDG
LLTEHGPFLVQPDGVTLEYNPYSWNLIANVLYLESPAGVGFSYSDDKFYATNDTEVAQSNFEALQ
DFFRLFPEYKNNKLFLTGESYAGIYIPTLAVLVMQDPSMNLQGLAVGNGLSSYEQNDNSLVYFAY
YHGLLGNRLWSSLQTHCCSQNKCNFYDNKDLECVTNLQEVARIVGNSGLNIYNLYAPCAGGVPSH
FRYEKDTVVVQDLGNIFTRLPLKRMWHQALLRSGDKVRMDPPCTNTTAASTYLNNPYVRKALNIP
EQLPQWDMCNFLVNLQYRRLYRSMNSQYLKLLSSQKYQILLYNGDVDMACNFMGDEWFVDSLNQK
MEVQRRPWLVKYGDSGEQIAGFVKEFSHIAFLTIKGAGHMVPTDKPLAAFTMFSRFLNKQPY
>d1hlga_ c.69.1.6 (A:) Gastric lipase {Human (Homo sapiens)}
SPEVTMNISQMITYWGYPNEEYEVVTEDGYILEVNRIPYGKKNSGNTGQRPVVFLQHGLLASATN
WISNLPNNSLAFILADAGYDVWLGNSRGNTWARRNLYYSPDSVEFWAFSFDEMAKYDLPATIDFI
VKKTGQKQLHYVGHSQGTTIGFIAFSTNPSLAKRIKTFYALAPVATVKYTKSLINKLRFVPQSLF
KFIFGDKIFYPHNFFDQFLATEVCSREMLNLLCSNALFIICGFDSKNFNTSRLDVYLSHNPAGTS
VQNMFHWTQAVKSGKFQAYDWGSPVQNRMHYDQSQPPYYNVTAMNVPIAVWNGGKDLLADPQDVG
LLLPKLPNLIYHKEIPFYNHLDFIWAMDAPQEVYNDIVSMISEDKK
>d1azwa_ c.69.1.7 (A:) Proline iminopeptidase {Xanthomonas campestris,
pv. citri}
MRTLYPEITPYQQGSLKVDDRHTLYFEQCGNPHGKPVVMLHGGPGGGCNDKMRRFHDPAKYRIVL
FDQRGSGRSTPHADLVDNTTWDLVADIERLRTHLGVDRWQVFGGSWGSTLALAYAQTHPQQVTEL
VLRGIFLLRRFELEWFYQEGASRLFPDAWEHYLNAIPPVERADLMSAFHRRLTSDDEATRLAAAK
AWSVWEGATSFLHVDEDFVTGHEDAHFALAFARIENHYFVNGGFFEVEDQLLRDAHRIADIPGVI
VHGRYDVVCPLQSAWDLHKAWPKAQLQISPASGHSAFEPENVDALVRATDGFA
>d1qtra_ c.69.1.7 (A:) Proline iminopeptidase {Serratia marcescens}
LRGLYPPLAAYDSGWLDTGDGHRIYWELSGNPNGKPAVFIHGGPGGGISPHHRQLFDPERYKVLL
FDQRGCGRSRPHASLDNNTTWHLVADIERLREMAGVEQWLVFGGSWGSTLALAYAQTHPERVSEM
VLRGIFTLRKQRLHWYYQDGASRFFPEKWERVLSILSDDERKDVIAAYRQRLTSADPQVQLEAAK
LWSVWEGETVTLLPSRESASFGEDDFALAFARIENHYFTHLGFLESDDQLLRNVPLIRHIPAVIV
HGRYDMACQVQNAWDLAKAWPEAELHIVEGAGHSYDEPGILHQLMIATDRFAGK
>d1b6g__ c.69.1.8 (-) Haloalkane dehalogenase {Xanthobacter
autotrophicus}
MVNAIRTPDQRFSNLDQYPFSPNYLDDLPGYPGLRAHYLDEGNSDAEDVFLCLHGEPTWSYLYRK
MIPVFAESGARVIAPDFFGFGKSDKPVDEEDYTFEFHRNFLLALIERLDLRNITLVVQDWGGFLG
LTLPMADPSRFKRLIIMNACLMTDPVTQPAFSAFVTQPADGFTAWKYDLVTPSDLRLDQFMKRWA
PTLTEAEASAYAAPFPDTSYQAGVRKFPKMVAQRDQACIDISTEAISFWQNDWNGQTFMAIGMKD
KLLGPDVMYPMKALINGCPEPLEIADAGHFVQEFGEQVAREALKHFAETE
>d1bn7a_ c.69.1.8 (A:) Haloalkane dehalogenase {Rhodococcus sp.}
IGTGFPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYLWRNIIPHVAPSHRCIAPDLIG
MGKSDKPDLDYFFDDHVRYLDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIACMEFIR
PIPTWDEWPEFARETFQAFRTADVGRELIIDQNAFIEGVLPKCVVRPLTEVEMDHYREPFLKPVD
REPLWRFPNEIPIAGEPANIVALVEAYMNWLHQSPVPKLLFWGTPGVLIPPAEAARLAESLPNCK
TVDIGPGLHYLQEDNPDLIGSEIARWLPGLA
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>d1cv2a_ c.69.1.8 (A:) Haloalkane dehalogenase {Sphingomonas
paucimobilis, UT26, LinB}
GAKPFGEKKFIEIKGRRMAYIDEGTGDPILFQHGNPTSSYLWRNIMPHCAGLGRLIACDLIGMGD
SDKLDPSGPERYAYAEHRDYLDALWEALDLGDRVVLVVHDWGSALGFDWARRHRERVQGIAYMEA
IAMPIEWADFPEQDRDLFQAFRSQAGEELVLQDNVFVEQVLPGLILRPLSEAEMAAYREPFLAAG
EARRPTLSWPRQIPIAGTPADVVAIARDYAGWLSESPIPKLFINAEPGALTTGRMRDFCRTWPNQ
TEITVAGAHFIQEDSPDEIGAAIAAFVRRLRPA
>d1din__ c.69.1.9 (-) Dienelactone hydrolase {Pseudomonas sp., B13}
MLTEGISIQSYDGHTFGALVGSPAKAPAPVIVIAQEIFGVNAFMRETVSWLVDQGYAAVCPDLYA
RQAPGTALDPQDERQREQAYKLWQAFDMEAGVGDLEAAIRYARHQPYSNGKVGLVGYALGGALAF
LVAAKGYVDRAVGYYGVGLEKQLNKVPEVKHPALFHMGGQDHFVPAPSRQLITEGFGANPLLQVH
WYEEAGHSFARTSSSGYVASAAALANERTLDFLAPLQS
>d1c4xa_ c.69.1.10 (A:) 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate
hydrolase (BPHD) {Rhodococcus sp., strain rha1}
TVEIIEKRFPSGTLASHALVAGDPQSPAVVLLHGAGPGAHAASNWRPIIPDLAENFFVVAPDLIG
FGQSEYPETYPGHIMSWVGMRVEQILGLMNHFGIEKSHIVGNSMGGAVTLQLVVEAPERFDKVAL
MGSVGAPMNARPPELARLLAFYADPRLTPYRELIHSFVYDPENFPGMEEIVKSRFEVANDPEVRR
IQEVMFESMKAGMESLVIPPATLGRLPHDVLVFHGRQDRIVPLDTSLYLTKHLKHAELVVLDRCG
HWAQLERWDAMGPMLMEHFRA
>d1ek1a2 c.69.1.11 (A:226-544) Mammalian epoxide hydrolase,
C-terminal domain {Mouse (Mus musculus)}
LPVPCNPNDVSHGYVTVKPGIRLHFVEMGSGPALCLCHGFPESWFSWRYQIPALAQAGFRVLAID
MKGYGDSSSPPEIEEYAMELLCKEMVTFLDKLGIPQAVFIGHDWAGVMVWNMALFYPERVRAVAS
LNTPFMPPDPDVSPMKVIRSIPVFNYQLYFQEPGVAEAELEKNMSRTFKSFFRASDETGFIAVHK
ATEIGGILVNTPEDPNLSKITTEEEIEFYIQQFKKTGFRGPLNWYRNTERNWKWSCKGLGRKILV
PALMVTAEKDIVLRPEMSKNMEKWIPFLKRGHIEDCGHWTQIEKPTEVNQILIKWLQTE
>d1ehya_ c.69.1.11 (A:) Bacterial epoxide hydrolase {Agrobacterium
radiobacter}
AIRRPEDFKHYEVQLPDVKIHYVREGAGPTLLLLHGWPGFWWEWSKVIGPLAEHYDVIVPDLRGF
GDSEKPDLNDLSKYSLDKAADDQAALLDALGIEKAYVVGHDFAAIVLHKFIRKYSDRVIKAAIFD
PIQPDFGPVYFGLGHVHESWYSQFHQLDMAVEVVGSSREVCKKYFKHFFDHWSYRDELLTEEELE
VHVDNCMKPDNIHGGFNYYRANIRPDAALWTDLDHTMSDLPVTMIWGLGDTCVPYAPLIEFVPKY
YSNYTMETIEDCGHFLMVEKPEIAIDRIKTAFR
>d1qo7a_ c.69.1.11 (A:) Bacterial epoxide hydrolase {Aspergillus
niger}
KAFAKFPSSASISPNPFTVSIPDEQLDDLKTLVRLSKIAPPTYESLQADGRFGITSEWLTTMREK
WLSEFDWRPFEARLNSFPQFTTEIEGLTIHFAALFSEREDAVPIALLHGWPGSFVEFYPILQLFR
EEYTPETLPFHLVVPSLPGYTFSSGPPLDKDFGLMDNARVVDQLMKDLGFGSGYIIQGGDIGSFV
GRLLGVGFDACKAVHLNLCAMRAPPEGPSIESLSAAEKEGIARMEKFMTDGLAYAMEHSTRPSTI
GHVLSSSPIALLAWIGEKYLQWVDKPLPSETILEMVSLYWLTESFPRAIHTYRETTPTASAPNGA
TMLQKELYIHKPFGFSFFPKDLCPVPRSWIATTGNLVFFRDHAEGGHFAALERPRELKTDLTAFV
EQVW
>d1brt__ c.69.1.12 (-) Bromoperoxidase A2 {Streptomyces aureofaciens}
PFITVGQENSTSIDLYYEDHGTGQPVVLIHGFPLSGHSWERQSAALLDAGYRVITYDRRGFGQSS
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QPTTGYDYDTFAADLNTVLETLDLQDAVLVGFSTGTGEVARYVSSYGTARIAKVAFLASLEPFLL
KTDDNPDGAAPQEFFDGIVAAVKADRYAFYTGFFNDFYNLDENLGTRISEEAVRNSWNTAASGGF
FAAAAAPTTWYTDFRADIPRIDVPALILHGTGDRTLPIENTARVFHKALPSAEYVEVEGAPHGLL
WTHAEEVNTALLAFLAK
>d1a8q__ c.69.1.12 (-) Bromoperoxidase A1 {Streptomyces aureofaciens}
PICTTRDGVEIFYKDWGQGRPVVFIHGWPLNGDAWQDQLKAVVDAGYRGIAHDRRGHGHSTPVWD
GYDFDTFADDLNDLLTDLDLRDVTLVAHSMGGGELARYVGRHGTGRLRSAVLLSAIPPVMIKSDK
NPDGVPDEVFDALKNGVLTERSQFWKDTAEGFFSANRPGNKVTQGNKDAFWYMAMAQTIEGGVRC
VDAFGYTDFTEDLKKFDIPTLVVHGDDDQVVPIDATGRKSAQIIPNAELKVYEGSSHGIAMVPGD
KEKFNRDLLEFLNK
>d1a88a_ c.69.1.12 (A:) Chloroperoxidase L {Streptomyces lividans}
GTVTTSDGTNIFYKDWGPRDGLPVVFHHGWPLSADDWDNQMLFFLSHGYRVIAHDRRGHGRSDQP
STGHDMDTYAADVAALTEALDLRGAVHIGHSTGGGEVARYVARAEPGRVAKAVLVSAVPPVMVKS
DTNPDGLPLEVFDEFRAALAANRAQFYIDVPSGPFYGFNREGATVSQGLIDHWWLQGMMGAANAH
YECIAAFSETDFTDDLKRIDVPVLVAHGTDDQVVPYADAAPKSAELLANATLKSYEGLPHGMLST
HPEVLNPDLLAFVKS
>d1a8s__ c.69.1.12 (-) Chloroperoxidase F {Pseudomonas fluorescens}
TTFTTRDGTQIYYKDWGSGQPIVFSHGWPLNADSWESQMIFLAAQGYRVIAHDRRGHGRSSQPWS
GNDMDTYADDLAQLIEHLDLRDAVLFGFSTGGGEVARYIGRHGTARVAKAGLISAVPPLMLKTEA
NPGGLPMEVFDGIRQASLADRSQLYKDLASGPFFGFNQPGAKSSAGMVDWFWLQGMAAGHKNAYD
CIKAFSETDFTEDLKKIDVPTLVVHGDADQVVPIEASGIASAALVKGSTLKIYSGAPHGLTDTHK
DQLNADLLAFIKG
>d1thta_ c.69.1.13 (A:) Myristoyl-ACP-specific thioesterase {Vibrio
harveyi}
QCKTIAHVLRVNNGQELHVWETPPKENVPFKNNTILIASGFARRMDHFAGLAEYLSTNGFHVFRY
DSLHHVGLSSGSIDEFTMTTGKNSLCTVYHWLQTKGTQNIGLIAASLSARVAYEVISDLELSFLI
TAVGVVNLRDTLEKALGFDYLSLPIDELPNDLDFEGHKLGSEVFVRDCFEHHWDTLDSTLDKVAN
TSVPLIAFTANNDDWVKQEEVYDMLAHIRTGHCKLYSLLGSSHDLGENLVVLRNFYQSVTKAAIA
MDGGSLEIDVDFIEPDFEQLTIATVNERRLKAEIENRTPEMA
>d1ei9a_ c.69.1.13 (A:) Palmitoyl protein thioesterase 1 {Cow (Bos
taurus)}
DPPAPLPLVIWHGMGDSCCNPLSMGAIKKMVEKKIPGIHVLSLEIGKTLREDVENSFFLNVNSQV
TTVCQILAKDPKLQQGYNAMGFSQGGQFLRAVAQRCPSPPMVNLISVGGQHQGVFGLPRCPGESS
HICDFIRKTLNAGAYNKAIQERLVQAEYWHDPIREDIYRNHSIFLADINQERGVNESYKKNLMAL
KKFVMVKFLNDTIVDPVDSEWFGFYRSGQAKETIPLQESTLYTQDRLGLKAMDKAGQLVFLALEG
DHLQLSEEWFYAHIIPFLE
>d1auoa_ c.69.1.14 (A:) Carboxylesterase {Pseudomonas fluorescens}
MTEPLILQPAKPADACVIWLHGLGADRYDFMPVAEALQESLLTTRFVLPQAPTRPVTINGGYEMP
SWYDIKAMSPARSISLEELEVSAKMVTDLIEAQKRTGIDASRIFLAGFSQGGAVVFHTAFINWQG
PLGGVIALSTYAPTFGDELELSASQQRIPALCLHGQYDDVVQNAMGRSAFEHLKSRGVTVTWQEY
PMGHEVLPQEIHDIGAWLAARLG
>d1fj2a_ c.69.1.14 (A:) Acyl protein thioesterase 1 {Human (Homo
sapiens)}
MDPEFMSTPLPAIVPAARKATAAVIFLHGLGDTGHGWAEAFAGIRSSHIKYICPHAPVRPVTLNM
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NVAMPSWFDIIGLSPDSQEDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQGGALSLYTAL
TTQQKLAGVTALSCWLPLRASFPQGPIGGANRDISILQCHGDCDPLVPLMFGSLTVEKLKTLVNP
ANVTFKTYEGMMHSSCQQEMMDVKQFIDKLLPPI
>d1qlwa_ c.69.1.15 (A:) A novel bacterial esterase {Alcaligenes sp.}
VPKTPAGPLTLSGQGSFFVGGRDVTSETLSLSPKYDAHGTVTVDQMYVRYQIPQRAKRYPITLIH
GCCLTGMTWETTPDGRMGWDEYFLRKGYSTYVIDQSGRGRSATDISAINAVKLGKAPASSLPDLF
AAGHEAAWAIFRFGPRYPDAFKDTQFPVQAQAELWQQMVPDWLGSMPTPNPTVANLSKLAIKLDG
TVLLSHSQSGIYPFQTAAMNPKGITAIVSVEPGECPKPEDVKPLTSIPVLVVFGDHIEEFPRWAP
RLKACHAFIDALNAAGGKGQLMSLPALGVHGNSHMMMQDRNNLQVADLILDWIGRNTA
>d1jfra_ c.69.1.16 (A:) Lipase {Streptomyces exfoliatus}
NPYERGPAPTNASIEASRGPYATSQTSVSSLVASGFGGGTIYYPTSTADGTFGAVVISPGFTAYQ
SSIAWLGPRLASQGFVVFTIDTNTTLDQPDSRGRQLLSALDYLTQRSSVRTRVDATRLGVMGHSM
GGGGSLEAAKSRTSLKAAIPLTGWNTDKTWPELRTPTLVVGADGDTVAPVATHSKPFYESLPGSL
DKAYLELRGASHFTPNTSDTTIAKYSISWLKRFIDSDTRYEQFLCPIPRPSLTIAEYRGTCPHTS
>d1tca__ c.69.1.17 (-) Triacylglycerol lipase {Yeast (Candida
antarctica), form b}
LPSGSDPAFSQPKSVLDAGLTCQGASPSSVSKPILLVPGTGTTGPQSFDSNWIPLSTQLGYTPCW
ISPPPFMLNDTQVNTEYMVNAITALYAGSGNNKLPVLTWSQGGLVAQWGLTFFPSIRSKVDRLMA
FAPDYKGTVLAGPLDALAVSAPSVWQQTTGSALTTALRNAGGLTQIVPTTNLYSATDEIVQPQVS
NSPLDSSYLFNGKNVQAQAVCGPLFVIDHAGSLTSQFSYVVGRSALRSTTGQARSADYGITDCNP
LPANDLTPEQKVAAAALLAPAAAAIVAGPKQNCEPDLMPYARPFAVGKRTCSGIVTP
>d3tgl__ c.69.1.17 (-) Triacylglycerol lipase {Rhizomucor miehei}
GIRAATSQEINELTYYTTLSANSYCRTVIPGATWDCIHCDATEDLKIIKTWSTLIYDTNAMVARG
DSEKTIYIVFRGSSSIRNWIADLTFVPVSYPPVSGTKVHKGFLDSYGEVQNELVATVLDQFKQYP
SYKVAVTGHSLGGATVLLCALDLYQREEGLSSSNLFLYTQGQPRVGDPAFANYVVSTGIPYRRTV
NERDIVPHLPPAAFGFLHAGEEYWITDNSPETVQVCTSDLETSDCSNSIVPFTSVLDHLSYFGIN
TGLCT
>d1tia__ c.69.1.17 (-) Triacylglycerol lipase {Penicillium
camembertii}
DVSTSELDQFEFWVQYAAASYYEADYTAQVGDKLSCSKGNCPEVEATGATVSYDFSDSTITDTAG
YIAVDHTNSAVVLAFRGSYSVRNWVADATFVHTNPGLCDGCLAELGFWSSWKLVRDDIIKELKEV
VAQNPNYELVVVGHSLGAAVATLAATDLRGKGYPSAKLYAYASPRVGNAALAKYITAQGNNFRFT
HTNDPVPKLPLLSMGYVHVSPEYWITSPNNATVSTSDIKVIDGDVSFDGNTGTGLPLLTDFEAHI
WYFVQVDAGKG
>d1tib__ c.69.1.17 (-) Triacylglycerol lipase {Thermomyces (Humicola)
lanuginosa}
EVSQDLFNQFNLFAQYSAAAYCGKNNDAPAGTNITCTGNACPEVEKADATFLYSFEDSGVGDVTG
FLALDNTNKLIVLSFRGSRSIENWIGNLNFDLKEINDICSGCRGHDGFTSSWRSVADTLRQKVED
AVREHPDYRVVFTGHSLGGALATVAGADLRGNGYDIDVFSYGAPRVGNRAFAEFLTVQTGGTLYR
ITHTNDIVPRLPPREFGYSHSSPEYWIKSGTLVPVTRNDIVKIEGIDATGGNNQPNIPDIPAHLW
YFGLIGTCL
>d1lgya_ c.69.1.17 (A:) Triacylglycerol lipase {Rhizopus niveus}
KVVAATTAQIQEFTKYAGIAATAYCRSVVPGNKWDCVQCQKWVPDGKIITTFTSLLSDTNGYVLR
SDKQKTIYLVFRGTNSFRSAITDIVFNFSDYKPVKGAKVHAGFLSSYEQVVNDYFPVVQEQLTAH
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PTYKVIVTGHSLGGAQALLAGMDLYQREPRLSPKNLSIFTVGGPRVGNPTFAYYVESTGIPFQRT
VHKRDIVPHVPPQSFGFLHPGVESWIKSGTSNVQICTSEIETKDCSNSIVPFTSILDHLSYFDIN
EGSCL
>d1thg__ c.69.1.17 (-) Type-B carboxylesterase/lipase {Fungus (Geotrichum candidum), ATCC 34614}
EAPTAVLNGNEVISGVLEGKVDTFKGIPFADPPLNDLRFKHPQPFTGSYQGLKANDFSPACMQLD
PGNSLTLLDKALGLAKVIPEEFRGPLYDMAKGTVSMNEDCLYLNVFRPAGTKPDAKLPVMVWIYG
GAFVYGSSAAYPGNSYVKESINMGQPVVFVSINYRTGPFGFLGGDAITAEGNTNAGLHDQRKGLE
WVSDNIANFGGDPDKVMIFGESAGAMSVAHQLIAYGGDNTYNGKKLFHSAILQSGGPLPYHDSSS
VGPDISYNRFAQYAGCDTSASANDTLECLRSKSSSVLHDAQNSYDLKDLFGLLPQFLGFGPRPDG
NIIPDAAYELFRSGRYAKVPYISGNQEDEGTAFAPVALNATTTPHVKKWLQYIFYDASEASIDRV
LSLYPQTLSVGSPFRTGILNALTPQFKRVAAILSDMLFQSPRRVMLSATKDVNRWTYLSTHLHNL
VPFLGTFHGNELIFQFNVNIGPANSYLRYFISFANHHDPNVGTNLLQWDQYTDEGKEMLEIHMTD
NVMRTDDYRIEGISNFETDVNLYG
>d1lpp__ c.69.1.17 (-) Type-B carboxylesterase/lipase {Fungus (Candida rugosa), formerly Cylindracea}
APTATLANGDTITGLNAIINEAFLGIPFAEPPVGNLRFKDPVPYSGSLDGQKFTSYGPSCMQQNP
EGTYEENLPKAALDLVMQSKVFEAVSPSSEDCLTINVVRPPGTKAGANLPVMLWIFGGGFEVGGT
STFPPAQMITKSIAMGKPIIHVSVNYRVSSWGFLAGDEIKAEGSANAGLKDQRLGMQWVADNIAA
FGGDPTKVTIFGESAGSMSVMCHILWNDGDNTYKGKPLFRAGIMQSGAMVPSDAVDGIYGNEIFD
LLASNAGCGSASDKLACLRGVSSDTLEDATNNTPGFLAYSSLRLSYLPRPDGVNITDDMYALVRE
GKYANIPVIIGDQNDEGTFFGTSSLNVTTDAQAREYFKQSFVHASDAEIDTLMTAYPGDITQGSP
FDTGILNALTPQFKRISAVLGDLGFTLARRYFLNHYTGGTKYSFLSKQLSGLPVLGTFHSNDIVF
QDYLLGSGSLIYNNAFIAFATDLDPNTAGLLVKWPEYTSSSQSGNNLMMINALGLYTGKDNFRTA
GYDALFSNPPSFFV
>d1clea_ c.69.1.17 (A:) Type-B carboxylesterase/lipase {Candida cylindracea, cholesterol esterase}
APTAKLANGDTITGLNAIINEAFLGIPFAEPPVGNLRFKDPVPYSGSLNGQKFTSYGPSCMQQNP
EGTFEENLGKTALDLVMQSKVFQAVLPQSEDCLTINVVRPPGTKAGANLPVMLWIFGGGFEIGSP
TIFPPAQMVTKSVLMGKPIIHVAVNYRVASWGFLAGDDIKAEGSGNAGLKDQRLGMQWVADNIAG
FGGDPSKVTIFGESAGSMSVLCHLIWNDGDNTYKGKPLFRAGIMQSGAMVPSDPVDGTYGNEIYD
LFVSSAGCGSASDKLACLRSASSDTLLDATNNTPGFLAYSSLRLSYLPRPDGKNITDDMYKLVRD
GKYASVPVIIGDQNDEGTVFGLSSLNVTTNAQARAYFKQSFIHASDAEIDTLMAAYPQDITQGSP
FDTGIFNAITPQFKRISAVLGDLAFIHARRYFLNHFQGGTKYSFLSKQLSGLPIMGTFHANDIVW
QDYLLGSGSVIYNNAFIAFATDLDPNTAGLLVNWPKYTSSSQSGNNLMMINALGLYTGKDNFRTA
GYDALMTNPSSFFV
>d1i6wa_ c.69.1.18 (A:) Lipase A {Bacillus subtilis}
HNPVVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETG
AKKVDIVAHSMGGANTLYYIKNLDGGNKVANVVTLGGANRLTTGKALPGTDPNQKILYTSIYSSA
DMIVMNYLSRLDGARNVQIHGVGHIGLLYSSQVNSLIKEGLNGGGQNTN
>d4lipd_ c.69.1.18 (D:) Lipase {Burkholderia cepacia (formerly Pseudomonas cepacia)}
DNYAATRYPIILVHGLTGTDKYAGVLEYWYGIQEDLQQRGATVYVANLSGFQSDDGPNGRGEQLL
AYVKTVLAATGATKVNLVGHSQGGLTSRYVAAVAPDLVASVTTIGTPHRGSEFADFVQGVLAYDP

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TGLSSTVIAAFVNVFGILTSSSNNTNQDALAALKTLTTAQAATYNQNYPSAGLGAPGSCQTGAPT
ETVGGNTHLLYSWAGTAIQPTISVFGVTGATDTSTIPLVDPANALDPSTLALFGTGTVMVNRGSG
QNDGVVSKCSALYGQVLSTSYKWNHLDEINQLLGVRGANAEDPVAVIRTHANRLKLAGV
>d1ex9a_ c.69.1.18 (A:) Lipase {Pseudomonas aeruginosa}
STYTQTKYPIVLAHGMLGFDNILGVDYWFGIPSALRRDGAQVYVTEVSQLDTSEVRGEQLLQQVE
EIVALSGQPKVNLIGHSHGGPTIRYVAAVRPDLIASATSVGAPHKGSDTADFLRQIPPGSAGEAV
LSGLVNSLGALISFLSSGSTGTQNSLGSLESLNSEGAARFNAKYPQGIPTSACGEGAYKVNGVSY
YSWSGSSPLTNFLDPSDAFLGASSLTFKNGTANDGLVGTCSSHLGMVIRDNYRMNHLDEVNQVFG
LTSLFETSPVSVYRQHANRLKNASL
>d1cvl__ c.69.1.18 (-) Lipase {Chromobacterium viscosum}
ADTYAATRYPVILVHGLAGTDKFANVVDYWYGIQSDLQSHGAKVYVANLSGFQSDDGPNGRGEQL
LAYVKQVLAATGATKVNLIGHSQGGLTSRYVAAVAPQLVASVTTIGTPHRGSEFADFVQDVLKTD
PTGLSSTVIAAFVNVFGTLVSSSHNTDQDALAALRTLTTAQTATYNRNFPSAGLGAPGSCQTGAA
TETVGGSQHLLYSWGGTAIQPTSTVLGVTGATDTSTGTLDVANVTDPSTLALLATGAVMINRASG
QNDGLVSRCSSLFGQVISTSYHWNHLDEINQLLGVRGANAEDPVAVIRTHVNRLKLQGV
>d1hpla2 c.69.1.19 (A:1-336) Pancreatic lipase, N-terminal domain
{Horse (Equus caballus)}
NEVCYERLGCFSDDSPWAGIVERPLKILPWSPEKVNTRFLLYTNENPDNFQEIVADPSTIQSSNF
NTGRKTRFIIHGFIDKGEESWLSTMCQNMFKVESVNCICVDWKSGSRTAYSQASQNVRIVGAEVA
YLVGVLQSSFDYSPSNVHIIGHSLGSHAAGEAGRRTNGAVGRITGLDPAEPCFQGTPELVRLDPS
DAQFVDVIHTDIAPFIPNLGFGMSQTAGHLDFFPNGGKEMPGCQKNVLSQIVDIDGIWQGTRDFA
ACNHLRSYKYYTDSILNPDGFAGFSCASYSDFTANKCFPCSSEGCPQMGHYADRFPGRTKGVGQL
FYLNTGDASNFA
>d1etha2 c.69.1.19 (A:1-336) Pancreatic lipase, N-terminal domain
{Pig (Sus scrofa)}
SEVCFPRLGCFSDDAPWAGIVQRPLKILPWSPKDVDTRFLLYTNQNQNNYQELVADPSTITNSNF
RMDRKTRFIIHGFIDKGEEDWLSNICKNLFKVESVNCICVDWKGGSRTGYTQASQNIRIVGAEVA
YFVEVLKSSLGYSPSNVHVIGHSLGSHAAGEAGRRTNGTIERITGLDPAEPCFQGTPELVRLDPS
DAKFVDVIHTDAAPIIPNLGFGMSQTVGHLDFFPNGGKQMPGCQKNILSQIVDIDGIWEGTRDFV
ACNHLRSYKYYADSILNPDGFAGFPCDSYNVFTANKCFPCPSEGCPQMGHYADRFPGKTNGVSQV
FYLNTGDASNF
>d1lpbb2 c.69.1.19 (B:1-336) Pancreatic lipase, N-terminal domain
{Human (Homo sapiens)}
KEVCYERLGCFSDDSPWSGITERPLHILPWSPKDVNTRFLLYTNENPNNFQEVAADSSSISGSNF
KTNRKTRFIIHGFIDKGEENWLANVCKNLFKVESVNCICVDWKGGSRTGYTQASQNIRIVGAEVA
YFVEFLQSAFGYSPSNVHVIGHSLGAHAAGEAGRRTNGTIGRITGLDPAEPCFQGTPELVRLDPS
DAKFVDVIHTDGAPIVPNLGFGMSQVVGHLDFFPNGGVEMPGCKKNILSQIVDIDGIWEGTRDFA
ACNHLRSYKYYTDSIVNPDGFAGFPCASYNVFTANKCFPCPSGGCPQMGHYADRYPGKTNDVGQK
FYLDTGDASNFA
>d1gpl_2 c.69.1.19 (1-336) Pancreatic lipase, N-terminal domain
{Guinea pig (Cavia porcellus)}
AEVCYSHLGCFSDEKPWAGTSQRPIKSLPSDPKKINTRFLLYTNENQNSYQLITATDIATIKASN
FNLNRKTRFIIHGFTDSGENSWLSDMCKNMFQVEKVNCICVDWKGGSKAQYSQASQNIRVVGAEV
AYLVQVLSTSLNYAPENVHIIGHSLGAHTAGEAGKRLNGLVGRITGLDPAEPYFQDTPEEVRLDP
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SDAKFVDVIHTDISPILPSLGFGMSQKVGHMDFFPNGGKDMPGCKTGISCNHHRSIEYYHSSILN
PEGFLGYPCASYDEFQESGCFPCPAKGCPKMGHFADQYPGKTNAVEQTFFLNTGASDNFT
>d1rp1_2 c.69.1.19 (1-336) Pancreatic lipase, N-terminal domain {Dog (Canis familiaris)}
KEVCYEQIGCFSDAEPWAGTAIRPLKVLPWSPERIGTRFLLYTNKNPNNFQTLLPSDPSTIGASN
FQTDKKTRFIIHGFIDKGEENWLLDMCKNMFKVEEVNCICVDWKKGSQTSYTQAANNVRVVGAQV
AQMLSMLSANYSYSPSQVQLIGHSLGAHVAGEAGSRTPGLGRITGLDPVEASFQGTPEEVRLDPT
DADFVDVIHTDAAPLIPFLGFGTSQQMGHLDFFPNGGEEMPGCKKNALSQIVDLDGIWEGTRDFV
ACNHLRSYKYYSESILNPDGFASYPCASYRAFESNKCFPCPDQGCPQMGHYADKFAQKYFLNTGD
SSNFA
>d1bu8a2 c.69.1.19 (A:1-336) Pancreatic lipase, N-terminal domain {Rat (Rattus norvegicus)}
KEVCYGHLGCFSNDKPWAGMLQRPLKIFPWSPEDIDTRFLLYTNENPNNYQKISATEPDTIKFSN
FQLDRKTRFIVHGFIDKGEDGWLLDMCKKMFQVEKVNCICVDWRRGSRTEYTQASYNTRVVGAEI
AFLVQVLSTEMGYSPENVHLIGHSLGAHVVGEAGRRLEGHVGRITGLDPAEPCFQGLPEEVRLDP
SDAMFVDVIHTDSAPIIPYLGFGMSQKVGHLDFFPNGGKEMPGCQKNILSTIVDINGIWEGTQNF
VACNHLRSYKYYASSILNPDGFLGYPCSSYEKFQQNDCFPCPEEGCPKMGHYADQFEGKTATVEQ
TVYLNTGDSGNFT
>d1qj4a_ c.69.1.20 (A:) Hydroxynitrile lyase {Rubber tree (Hevea brasiliensis)}
AFAHFVLIHTICHGAWIWHKLKPLLEALGHKVTALDLAASGVDPRQIEEIGSFDEYSEPLLTFLE
ALPPGEKVILVGESCGGLNIAIAADKYCEKIAAAVFHNSVLPDTEHCPSYVVDKLMEVFPDWKDT
TYFTYTKDGKEITGLKLGFTLLRENLYTLCGPEEYELAKMLTRKGSLFQNILAKRPFFTKEGYGS
IKKIYVWTDQDEIFLPEFQLWQIENYKPDKVYKVEGGDHKLQLTKTKEIAEILQEVADTYN
>d1e89a_ c.69.1.20 (A:) Hydroxynitrile lyase {Cassava (Manihot esculenta)}
PISKMVTAHFVLIHTICHGAWIWHKLKPALERAGHKVTALDMAASGIDPRQIEQINSFDEYSEPL
LTFLEKLPQGEKVIIVGEACAGLNIAIAADRYVDKIAAGVFHNSLLPDTVHSPSYTVEKLLESFP
DWRDTEYFTFTNITGETITTMKLGFVLLRENLFTKCTDGEYELAKMVMRKGSLFQNVLAQRPKFT
EKGYGSIKKVYIWTDQDKIFLPDFQRWQIANYKPDKVYQVQGGDHKLQLTKTEEVAHILQEVADA
YA
>d1keza_ c.69.1.22 (A:) Erythromycin polyketide synthase {Saccharopolyspora erythraea}
SSALRDGYRQAGVSGRVRSYLDLLAGLSDFREHFDGSDGFSLDLVDMADGPGEVTVICCAGTAAI
SGPHEFTRLAGALRGIAPVRAVPQPGYEEGEPLPSSMAAVAAVQADAVIRTQGDKPFVVAGHSAG
ALMAYALATELLDRGHPPRGVVLIDVYPPGHQDAMNAWLEELTATLFDRETVRMDDTRLTALGAY
DRLTGQWRPRETGLPTLLVSAGEPMGPWPDDSWKPTWPFEHDTVAVPGDHFTMVQEHADAIARHI
DAWLGGG
>d2masa_ c.70.1.1 (A:) Inosine-uridine nucleoside N-ribohydrolase, IU-NH {Crithidia fasciculata}
AKKIILDCDPGLDDAVAILLAHGNPEIELLAITTVVGNQTLAKVTRNAQLVADIAGITGVPIAAG
CDKPLVRKIMTAGHIHGESGMGTVAYPAEFKNKVDERHAVNLIIDLVMSHEPKTITLVPTGGLTN
IAMAARLEPRIVDRVKEVVLMGGGYHEGNATSVAEFNIIIDPEAAHIVFNESWQVTMVGLDLTHQ
ALATPPILQRVKEVDTNPARFMLEIMDYYTKIYQSNRYMAAAAVHDPCAVAYVIDPSVMTTERVP

VDIELTGKLTLGMTVADFRNPRPEHCHTQVAVKLDFEKFWGLVLDALERIGDP
>d1ezra_ c.70.1.1 (A:) Nucleoside hydrolase {Leishmania major}
PRKIILDCDPGIDDAVAIFLAHGNPEIELLAITTVVGNQSLEKVTQNARLVADVAGIVGVPVAAG
CTKPLVRGVRNASHIHGETGMGNVSYPPEFKTKLDGRHAVQLIIDLIMSHEPKTITLVPTGGLTN
IAMAVRLEPRIVDRVKEVVLMGGGYHTGNASPVAEFNVFIDPEAAHIVFNESWNVTMVGLDLTHL
ALATPAVQKRVREVGTKPAAFMLQILDFYTKVYEKEHDTYGKVHDPCAVAYVIDPTVMTTERVPV
DIELNGALTTGMTVADFRYPRPKNCRTQVAVKLDFDKFWCLVIDALERIGDP
>d1hoza_ c.70.1.1 (A:) Inosine-adenosine-guanosine preferring nucleoside hydrolase {Trypanosoma vivax}
GSAKNVVLDHDGNLDDFVAMVLLASNTEKVRLIGALCTDADCFVENGFNVTGKIMCLMHNNMNLP
LFPIGKSAATAVNPFPKEWRCLAKNMDDMPILNIPENVELWDKIKAENEKYEGQQLLADLVMNSE
EKVTICVTGPLSNVAWCIDKYGEKFTSKVEECVIMGGAVDVRGNVFLPSTDGTAEWNIYWDPASA
KTVFGCPGLRRIMFSLDSTNTVPVRSPYVQRFGEQTNFLLSILVGTMWAMCTHCELLRDGDGYYA
WDALTAAYVVDQKVANVDPVPIDVVVDKQPNEGATVRTDAENYPLTFVARNPEAEFFLDMLLRSA
RAC
>d1ra9__ c.71.1.1 (-) Dihydrofolate reductase, prokaryotic type {Escherichia coli}
MISLIAALAVDRVIGMENAMPWNLPADLAWFKRNTLDKPVIMGRHTWESIGRPLPGRKNIILSSQ
PGTDDRVTWVKSVDEAIAACGDVPEIMVIGGGRVYEQFLPKAQKLYLTHIDAEVEGDTHFPDYEP
DDWESVFSEFHDADAQNSHSYCFEILERR
>d3dfr__ c.71.1.1 (-) Dihydrofolate reductase, prokaryotic type {Lactobacillus casei}
TAFLWAQNRNGLIGKDGHLPWHLPDDLHYFRAQTVGKIMVVGRRTYESFPKRPLPERTNVVLTHQ
EDYQAQGAVVVHDVAAVFAYAKQHLDQELVIAGGAQIFTAFKDDVDTLLVTRLAGSFEGDTKMIP
LNWDDFTKVSSRTVEDTNPALTHTYEVWQKKA
>d1df7a_ c.71.1.1 (A:) Dihydrofolate reductase, prokaryotic type {Mycobacterium tuberculosis}
MVGLIWAQATSGVIGRGGDIPWRLPEDQAHFREITMGHTIVMGRRTWDSLPAKVRPLPGRRNVVL
SRQADFMASGAEVVGSLEEALTSPETWVIGGGQVYALALPYATRCEVTEVDIGLPREAGDALAPV
LDETWRGETGEWRFSRSGLRYRLYSYHRS
>d1d1ga_ c.71.1.1 (A:) Dihydrofolate reductase, prokaryotic type {Thermotoga maritima}
AKVIFVLAMDVSGKIASSVESWSSFEDRKNFRKITTEIGNVVMGRITFEEIGRPLPERLNVVLTR
RPKTSNNPSLVFFNGSPADVVKFLEGKGYERVAVIGGKTVFTEFLREKLVDELFVTVEPYVFGKG
IPFFDEFEGYFPLKLLEMRRLNERGTLFLKYSVE
>d1vdra_ c.71.1.1 (A:) Dihydrofolate reductase, prokaryotic type {Haloferax volcanii}
ELVSVAALAENRVIGRDGELPWPSIPADKKQYRSRIADDPVVLGRTTFESMRDDLPGSAQIVMSR
SERSFSVDTAHRAASVEEAVDIAASLDAETAYVIGGAAIYALFQPHLDRMVLSRVPGEYEGDTYY
PEWDAAEWELDAETDHEGFTLQEWVRS
>d8dfr__ c.71.1.1 (-) Dihydrofolate reductases, eukaryotic type {Chicken (Gallus gallus)}
VRSLNSIVAVCQNMGIGKDGNLPWPPLRNEYKYFQRMTSTSHVEGKQNAVIMGKKTWFSIPEKNR
PLKDRINIVLSRELKEAPKGAHYLSKSLDDALALLDSPELKSKVDMVWIVGGTAVYKAAMEKPIN

HRLFVTRILHEFESDTFFPEIDYKDFKLLTEYPGVPADIQEEDGIQYKFEVYQKSV
>d1hfq__ c.71.1.1 (-) Dihydrofolate reductases, eukaryotic type {Human (Homo sapiens)}
VGSLNCIVAVSQNMGIGKNGDLPWPPLRNESRYFQRMTTTSSVEGKQNLVIMGKKTWFSIPEKNR
PLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTEQPELANKVDMVWIVGGSSVYKEAMNHPGH
LKLFVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSDVQEEKGIKYKFEVYEKND
>d1dyr__ c.71.1.1 (-) Dihydrofolate reductases, eukaryotic type {Fungus (Pneumocystis carinii)}
NQQKSLTLIVALTTSYGIGRSNSLPWKLKKEISYFKRVTSFVPTFDSFESMNVVLMGRKTWESIP
LQFRPLKGRINVVITRNESLDLGNGIHSAKSLDHALELLYRTYGSESSVQINRIFVIGGAQLYKA
AMDHPKLDRIMATIIYKDIHCDVFFPLKFRDKEWSSVWKKEKHSDLESWVGTKVPHGKINEDGFD
YEFEMWTRDL
>d1aoea_ c.71.1.1 (A:) Dihydrofolate reductases, eukaryotic type {Yeast (Candida albicans)}
MLKPNVAIIVAALKPALGIGYKGKMPWRLRKEIRYFKDVTTRTTKPNTRNAVIMGRKTWESIPQK
FRPLPDRLNIILSRSYENEIIDDNIIHASSIESSLNLVSDVERVFIIGGAEIYNELINNSLVSHL
LITEIEHPSPESIEMDTFLKFPLESWTKQPKSELQKFVGDTVLEDDIKEGDFTYNYTLWTRK
>d1ekqa_ c.72.1.2 (A:) Hydroxyethylthiazole kinase (THZ kinase, ThiK) {Bacillus subtilis}
MDAQSAAKCLTAVRRHSPLVHSITNNVVTNFTANGLLALGASPVMAYAKEEVADMAKIAGALVLN
IGTLSKESVEAMIIAGKSANEHGVPVILDPVGAGATPFRTESARDIIREVRLAAIRGNAAEIAHT
VGVTDWLIKGVDAGEGGGDIIRLAQQAAQKLNTVIAITGEVDVIADTSHVYTLHNGHKLLTKVTG
AGCLLTSVVGAFCAVEENPLFAAIAAISSYGVAAQLAAQQTADKGPGSFQIELLNKLSTVTEQDV
QEWATIERV
>d1jxha_ c.72.1.2 (A:) 4-amino-5-hydroxymethyl-2-methylpyrimidine phosphate kinase (HMP-phosphate kinase, ThiD) {Salmonella typhimurium}
MQRINALTIAGTDPSGGAGIQADLKTFSALGAYGCSVITALVAENTCGVQSVYRIEPDFVAAQLD
SVFSDVRIDTTKIGMLAETDIVEAVAERLQRHHVRNVVLDTVMLAKSGDPLLSPSAIETLRVRLL
PQVSLITPNLPEAAALLDAPHARTEQEMLAQGRALLAMGCEAVLMKGGHLEDAQSPDWLFTREGE
QRFSAPRVNTKNTHGTGCTLSAALAALRPRHRSWGETVNEAKAWLSAALAQADTLEVGKGIGPVH
HFHAWW
>d1rkd__ c.72.1.1 (-) Ribokinase {Escherichia coli}
AGSLVVLGSINADHILNLQSFPTPGETVTGNHYQVAFGGKGANQAVAAGRSGANIAFIACTGDDS
IGESVRQQLATDNIDITPVSVIKGESTGVALIFVNGEGENVIGIHAGANAALSPALVEAQRERIA
NASALLMQLESPLESVMAAAKIAHQNKTIVALNPAPARELPDELLALVDIITPNETEAEKLTGIR
VENDEDAAKAAQVLHEKGIRTVLITLGSRGVWASVNGEGQRVPGFRVQAVDTIAAGDTFNGALIT
ALLEEKPLPEAIRFAHAAAAIAVTRKGAQPSVPWREEIDAFLDRQR
>d1bx4a_ c.72.1.1 (A:) Adenosine kinase {Human (Homo sapiens)}
VRENILFGMGNPLLDISAVVDKDFLDKYSLKPNDQILAEDKHKELFDELVKKFKVEYHAGGSTQN
SIKVAQWMIQQPHKAATFFGCIGIDKFGEILKRKAAEAHVDAHYYEQNEQPTGTCAACITGDNRS
LIANLAAANCYKKEKHLDLEKNWMLVEKARVCYIAGFFLTVSPESVLKVAHHASENNRIFTLNLS
APFISQFYKESLMKVMPYVDILFGNETEAATFAREQGFETKDIKEIAKKTQALPKMNSKRQRIVI
FTQGRDDTIMATESEVTAFAVLDQDQKEIIDTNGAGDAFVGGFLSQLVSDKPLTECIRAGHYAAS

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IIIRRTGCTFPEKPDFH
>d1dgya_ c.72.1.1 (A:) Adenosine kinase {Toxoplasma gondii}
GPMRVFAIGNPILDLVAEVPSSFLDEFFLKRGDATLATPEQMRIYSTLDQFNPTSLPGGSALNSV
RVVQKLLRKPGSAGYMGAIGDDPRGQVLKELCDKEGLATRFMVAPGQSTGTCAVLINEKERTLCT
HLGACGSFRIPENWTTFASGALIFYATAYTLTATPKNALEVAGYAHGIPNAIFTLNLSAPFCVEL
YKDAMQSLLLHTNILFGNEEEFAHLAKVHNLVAAEKVALSVANKEHAVEVCTGALRLLTAGQNTG
ATKLVVMTRGHNPVIAAEQTADGTVVVHEVGVPVVAAEKIVDTNGAGDAFVGGFLYGLSQGKTVK
QCIMCGNACAQDVIQHVGFSLSF
>d1gc5a_ c.72.1.3 (A:) ADP-dependent glucokinase {Archaeon
Thermococcus litoralis}
MKESLKDRIRLWKRLYVNAFENALNAIPNVKGVLLAYNTNIDAIKYLDADDLEKRVTEKGKEKVF
EIIENPPEKISSIEELLGGILRSIKLGKAMEWFVESEEVRRYLREWGWDELRIGGQAGIMANLLG
GVYRIPTIVHVPQNPKLQAELFVDGPIYVPVFEGNKLKLVHPKDAIAEEEELIHYIYEFPRGFQV
FDVQAPRENRFIANADDYNARVYMRREFREGFEEITRNVELAIISGLQVLKEYYPDGTTYKDVLD
RVESHLNILNRYNVKSHFEFAYTANRRVREALVELLPKFTSVGLNEVELASIMEIIGDEELAKEV
LEGHIFSVIDAMNVLMDETGIERIHFHTYGYYLALTQYRGEEVRDALLFASLAAAAKAMKGNLER
IEQIRDALSVPTNERAIVLEEELEKEFTEFENGLIDMVDRQLAFVPTKIVASPKSTVGIGDTISS
SAFVSEFGMRKR
>d2uaga3 c.72.2.1 (A:94-297)
UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase MurD {Escherichia
coli}
DIELFCREAQAPIVAITGSNGKSTVTTLVGEMAKAAGVNVGVGGNIGLPALMLLDDECELYVLEL
SSFQLETTSSLQAVAATILNVTEDHMDRYPFGLQQYRAAKLRIYENAKVCVVNADDALTMPIRGA
DERCVSFGVNMGDYHLNHQQGETWLRVKGEKVLNVKEMKLSGQHNYTNALAALALADAAGLPRAS
SLKALTTFT
>d1e8ca3 c.72.2.1 (A:88-337) UDP-N-acetylmuramyl tripeptide
synthetase MurE {Escherichia coli}
QLNERLSALAGRFYHEPSDNLRLVGVTGTNGKTTTTQLLAQWSQLLGEISAVMGTVGNGLLGKVI
PTENTTGSAVDVQHELAGLVDQGATFCAMEVSSHGLVQHRVAALKFAASVFTNLSRDHLDYHGDM
EHYEAAKWLLYSEHHCGQAIINADDEVGRRWLAKLPDAVAVSMEDHINPNCHGRWLKATEVNYHD
SGATIRFSSSWGDGEIESHLMGAFNVSNLLLALATLLALGYPLADLLKTAARLQP
>d1gg4a4 c.72.2.1 (A:82-312) UDP-murNac-tripeptide
D-alanyl-D-alanine-adding enzyme MurF {Escherichia coli}
DTRLAFGELAAWVRQQVPARVVALTGSSGKTSVKEMTAAILSQCGNTLYTAGNLNNDIGVPMTLL
RLTPEYDYAVIELGANHQGEIAWTVSLTRPEAALVNNLAAAHLEGFGSLAGVAKAKGEIFSGLPE
NGIAIMNADNNDWLNWQSVIGSRKVWRFSPNAANSDFTATNIHVTSHGTEFTLQTPTGSVDVLLP
LPGRHNIANALAAAALSMSVGATLDAIKAGLANLKA
>d1jbwa2 c.72.2.2 (A:1-296) Folylpolyglutamate synthetase
{Lactobacillus casei}
MNYTETVAYIHSFPRLAKTGDHRRILTLLHALGNPQQQGRYIHVTGTNGKGSAANAIAHVLEASG
LTVGLYTSPFIMRFNERIMIDHEPIPDAALVNAVAFVRAALERLQQQQADFNVTEFEFITALAYW
YFRQRQVDVAVIEVGIGGDTDSTNVITPVVSVLTEVALDHQKLLGHTITAIAKHKAGIIKRGIPV
VTGNLVPDAAAVVAAKVATTGSQWLRFDRDFSVPKAKLHGWGQRFTYEDQDGRISDLEVPLVGDY
QQRNMAIAIQTAKVYAKQTEWPLTPQNIRQGLAASH
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>d1jzta_ c.104.1.1 (A:) Hypothetical protein YNL200c (YNU0_YEAST) {Baker's yeast (Saccharomyces cerevisiae)}
LKVVSSKLAAEIDKELMGPQIGFTLQQLMELAGFSVAQAVCRQFPLRGKTETEKGKHVFVIAGPG
NNGGDGLVCARHLKLFGYNPVVFYPKRSERTEFYKQLVHQLNFFKVPVLSQDEGNWLEYLKPEKT
LCIVDAIFGFSFKPPMREPFKGIVEELCKVQNIIPIVSVDVPTGWDVDKGPISQPSINPAVLVSL
TVPKPCSSHIRENQTTHYVGGRFIPRDFANKFGFEPFGYESTDQILKL
>d1b7ba_ c.73.1.1 (A:) Carbamate kinase {Enterococcus faecium}
GKKMVVALGGNAILSNDASAHAQQQALVQTSAYLVHLIKQGHRLIVSHGNGPQVGNLLLQQQAAD
SEKNPAMPLDTCVAMTQGSIGYWLSNALNQELNKAGIKKQVATVLTQVVVDPADEAFKNPTKPIG
PFLTEAEAKEAMQAGAIFKEDAGRGWRKVVPSPKPIDIHEAETINTLIKNDIITISCGGGGIPVV
GQELKGVEAVIDKDFASEKLAELVDADALVILTGVDYVCINYGKPDEKQLTNVTVAELEEYKQAG
HFAPGSMLPKIEAAIQFVESQPNKQAIITSLENLGSMSGDEIVGTVV
>d1e19a_ c.73.1.1 (A:) Carbamate kinase {Archaeon Pyrococcus furiosus}
GKRVVIALGGNALQQRGQKGSYEEMMDNVRKTARQIAEIIARGYEVVITHGNGPQVGSLLLHMDA
GQATYGIPAQPMDVAGAMSQGWIGYMIQQALKNELRKRGMEKKVVTIITQTIVDKNDPAFQNPTK
PVGPFYDEETAKRLAREKGWIVKEDSGRGWRRVVPSPDPKGHVEAETIKKLVERGVIVIASGGGG
VPVILEDGEIKGVEAVIDKDLAGEKLAEEVNADIFMILTDVNGAALYYGTEKEQWLREVKVEELR
KYYEEGHFKAGSMGPKVLAAIRFIEWGGERAIIAHLEKAVEALEGKTGTQVLP
>d1eqja1 c.105.1.1 (A:77-310) 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain {Bacillus stearothermophilus}
QSLTRINIAIREGEFDRNETFLAAMNHVKQHGTSLHLFGLLSDGGVHSHIHHLYALLRLAAKEGV
KRVYIHGFLDGRDVGPQTAPQYIKELQEKIKEYGVGEIATLSGRYYSMDRDKRWDRVEKAYRAMV
YGEGPTYRDPLECIEDSYKHGIYDEFVLPSVIVREDGRPVATIQDNDAIIFYNFRPDRAIQISNT
FTNEDFREFDRGPKHPKHLFFVCLTHFSETVAGYVAFKP
>d1eqja2 c.76.1.3 (A:3-76,A:311-510) 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain {Bacillus stearothermophilus}
KKPVALIILDGFALRDETYGNAVAQANKPNFDRYWNEYPHTTLKACGEAVGLPEGQMGNSEVGHL
NIGAGRIVYXTNLDNTIGEVLSQHGLRQLRIAETEKYPHVTFFMSGGREEEFPGEDRILINSPKV
PTYDLKPEMSAYEVTDALLKEIEADKYDAIILNYANPDMVGHSGKLEPTIKAVEAVDECLGKVVD
AILAKGGIAIITADHGNADEVLTPDGKPQTAHTTNPVPVIVTKKGIKLRDGGILGDLAPTMLDLL
GLPQPKEMTGKSLIV
>d1ed8a_ c.76.1.1 (A:) Alkaline phosphatase {Escherichia coli}
TPEMPVLENRAAQGDITAPGGARRLTGDQTAALRDSLSDKPAKNIILLIGDGMGDSEITAARNYA
EGAGGFFKGIDALPLTGQYTHYALNKKTGKPDYVTDSAASATAWSTGVKTYNGALGVDIHEKDHP
TILEMAKAAGLATGNVSTAELQDATPAALVAHVTSRKCYGPSATSEKCPGNALEKGGKGSITEQL
LNARADVTLGGGAKTFAETATAGEWQGKTLREQAQARGYQLVSDAASLNSVTEANQQKPLLGLFA
DGNMPVRWLGPKATYHGNIDKPAVTCTPNPQRNDSVPTLAQMTDKAIELLSKNEKGFFLQVEGAS
IDKQDHAANPCGQIGETVDLDEAVQRALEFAKKEGNTLVIVTADHAHASQIVAPDTKAPGLTQAL
NTKDGAVMVMSYGNSEEDSQEHTGSQLRIAAYGPHAANVVGLTDQTDLFYTMKAALGLK
>d1ew2a_ c.76.1.1 (A:) Alkaline phosphatase {Human (Homo sapiens)}
IIPVEEENPDFWNREAAEALGAAKKLQPAQTAAKNLIIFLGDGMGVSTVTAARILKGQKKDKLGP

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EIPLAMDRFPYVALSKTYNVDKHVPDSGATATAYLCGVKGNFQTIGLSAAARFNQCNTTRGNEVI
SVMNRAKKAGKSVGVVTTTRVQHASPAGTYAHTVNRNWYSDADVPASARQEGCQDIATQLISNMD
IDVILGGGRKYMFRMGTPDPEYPDDYSQGGTRLDGKNLVQEWLAKRQGARYVWNRTELMQASLDP
SVTHLMGLFEPGDMKYEIHRDSTLDPSLMEMTEAALRLLSRNPRGFFLFVEGGRIDHGHHESRAY
RALTETIMFDDAIERAGQLTSEEDTLSLVTADHSHVFSFGGYPLRGSSIFGLAPGKARDRKAYTV
LLYGNGPGYVLKDGARPDVTESESGSPEYRQQSAVPLDEETHAGEDVAVFARGPQAHLVHGVQEQ
TFIAHVMAFAACLEPYTACDLAPP
>d1auk__ c.76.1.2 (-) Arylsulfatase A {Human (Homo sapiens)}
RPPNIVLIFADDLGYGDLGCYGHPSSTTPNLDQLAAGGLRFTDFYVPVSLCTPSRAALLTGRLPV
RMGMYPGVLVPSSRGGLPLEEVTVAEVLAARGYLTGMAGKWHLGVGPEGAFLPPHQGFHRFLGIP
YSHDQGPCQNLTCFPPATPCDGGCDQGLVPIPLLANLSVEAQPPWLPGLEARYMAFAHDLMADAQ
RQDRPFFLYYASHHTHYPQFSGQSFAERSGRGPFGDSLMELDAAVGTLMTAIGDLGLLEETLVIF
TADNGPETMRMSRGGCSGLLRCGKGTTYEGGVREPALAFWPGHIAPGVTHELASSLDLLPTLAAL
AGAPLPNVTLDGFDLSPLLLGTGKSPRQSLFFYPSYPDEVRGVFAVRTGKYKAHFFTQGSAHSDT
TADPACHASSSLTAHEPPLLYDLSKDPGENYNLLGGVAGATPEVLQALKQLQLLKAQLDAAVTFG
PSQVARGEDPALQICCHPGCTPRPACCHCP
>d1fsu__ c.76.1.2 (-) Arylsulfatase B (4-sulfatase) {Human (Homo
sapiens)}
SRPPHLVFLLADDLGWNDVGFHGSRIRTPHLDALAAGGVLLDNYYTQPLXTPSRSQLLTGRYQIR
TGLQHQIIWPCQPSCVPLDEKLLPQLLKEAGYTTHMVGKWHLGMYRKECLPTRRGFDTYFGYLLG
SEDYYSHERCTLIDALNVTRCALDFRDGEEVATGYKNMYSTNIFTKRAIALITNHPPEKPLFLYL
ALQSVHEPLQVPEEYLKPYDFIQDKNRHHYAGMVSLMDEAVGNVTAALKSSGLWNNTVFIFSTDN
GGQTLAGGNNWPLRGRKWSLWEGGVRGVGFVASPLLKQKGVKNRELIHISDWLPTLVKLARGHTN
GTKPLDGFDVWKTISEGSPSPRIELLHNIDPNFVDSSPCPRNSMAPAKDDSSLPEYSAFNTSVHA
AIRHGNWKLLTGYPGCGYWFPPPSQYNVSEIPSSDPPTKTLWLFDIDRDPEERHDLSREYPHIVT
KLLSRLQFYHKHSVPVYFPAQDPRCDPKATGVWGPWM
>d1hdha_ c.76.1.2 (A:) Arylsulfatase B (4-sulfatase) {Pseudomonas
aeruginosa}
KRPNFLVIVADDLGFSDIGAFGGEIATPNLDALAIAGLRLTDFHTASTCSPTRSMLLTGTDHHIA
GIGTMAEALTPELEGKPGYEGHLNERVVALPELLREAGYQTLMAGKWHLGLKPEQTPHARGFERS
FSLLPGAANHYGFEPPYDESTPRILKGTPALYVEDERYLDTLPEGFYSSDAFGDKLLQYLKERDQ
SRPFFAYLPFSAPHWPLQAPREIVEKYRGRYDAGPEALRQERLARLKELGLVEADVEAHPVLALT
REWEALEDEERAKSARAMEVYAAMVERMDWNIGRVVDYLRRQGELDNTFVLFMSDNGAEGALLEA
FPKFGPDLLGFLDRHYDNSLENIGRANSYVWYGPRWAQAATAPSRLYKAFTTQGGIRVPALVRYP
RLSRQGAISHAFATVMDVTPTLLDLAGVRHPGKRWRGREIAEPRGRSWLGWLSGETEAAHDENTV
TGWELFGMRAIRQGDWKAVYLPAPVGPATWQLYDLARDPGEIHDLADSQPGKLAELIEHWKRYVS
ETGVV
>d1k30a_ c.112.1.1 (A:) Glycerol-3-phosphate (1)-acyltransferase
{Cushaw squash (Cucurbita moschata)}
SHSRKFLDVRSEEELLSCIKKETEAGKLPPNVAAGMEELYQNYRNAVIESGNPKADEIVLSNMTV
ALDRILLDVEDPFVFSSHHKAIREPFDYYIFGQNYIRPLIDFGNSFVGNLSLFKDIEEKLQQGHN
VVLISNHQTEADPAIISLLLEKTNPYIAENTIFVAGDRVLADPLCKPFSIGRNLICVYSKKHMFD
IPELTETKRKANTRSLKEMALLLRGGSQLIWIAPSGGRDRPDPSTGEWYPAPFDASSVDNMRRLI
QHSDVPGHLFPLALLCHDIMPPPSQVEIEIGEKRVIAFNGAGLSVAPEISFEEIAATHKNPEEVR
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EAYSKALFDSVAMQYNVLKTAISGKQGLGASTADVSLSQPW
>d1e4bp_ c.74.1.1 (P:) L-fuculose-1-phosphate aldolase {Escherichia coli}
MERNKLARQIIDTCLEMTRLGLNQGTAGQVSVRYQDGMLITPTGIPYEKLTESHIVFIDGNGKHE
EGKLPSSEWRFHMAAYQSRPDANAVVHNHAVHCTAVSILNRSIPAIHYMIAAAGGNSIPCAPYAT
FGTRELSEHVALALKNRKATLLQHHGLIACEVNLEKALWLAHEVEVLAQLYLTTLAITDPVPVLS
DEEIAVVLEKF
>d1jdia_ c.74.1.1 (A:) L-ribulose-5-phosphate 4-epimerase {Escherichia coli}
MLEDLKRQVLEANLALPKHNLVTLTWGNVSAVDRERGVFVIKPSGVDYSIMTADDMVVVSIETGE
VVEGAKKPSSDTPTHRLLYQAFPSIGGIVHTHSRHATIWAQAGQSIPATGTTHADYFYGTIPCTR
KMTDAEINGEYEWETGNVIVETFEKQGIDAAQMPGVLVHSHGPFAWGKNAEDAVHNAIVLEEVAY
MGIFCRQLAPQLPDMQQTLLNKHYLRKH
>d1j9la_ c.106.1.1 (A:) SurE homolog TM1662 (TM107 ?) {Thermotoga maritima}
MRILVTNDDGIQSKGIIVLAELLSEEHEVFVVAPDKERSATGHSITIHVPLWMKKVFISERVVAY
STTGTPADCVKLAYNVVMDKRVDLIVSGVNRGPNMGMDILHSGTVSGAMEGAMMNIPSIAISSAN
YESPDFEGAARFLIDFLKEFDFSLLDPFTMLNINVPAGEIKGWRFTRQSRRRWNDYFEERVSPFG
EKYYWMMGEVIEDDDRDDVDYKAVREGYVSITPIHPFLTNEQCLKKLREVYD
>d1cjya2 c.75.1.1 (A:142-721) Cytosolic phospholipase A2 catalytic domain {Human (Homo sapiens)}
PDLRFSMALCDQEKTFRQQRKEHIRESMKKLLGPKNSEGLHSARDVPVVAILGSGGGFRAMVGFS
GVMKALYESGILDCATYVAGLSGSTWYMSTLYSHPDFPEKGPEEINEELMKNVSHNPLLLLTPQK
VKRYVESLWKKKSSGQPVTFTDIFGMLIGETLIHNRMNTTLSSLKEKVNTAQCPLPLFTCLHVKP
DVSELMFADWVEFSPYEIGMAKYGTFMAPDLFGSKFFMGTVVKKYEENPLHFLMGVWGSAFSILF
NRVLGVSGSQSRGSTMEEELENITTKHIVSNDSSDSDDESHEPKGTENEDAGSDYQSDNQASWIH
RMIMALVSDSALFNTREGRAGKVHNFMLGLNLNTSYPLSPLSDFATQDSFDDDELDAAVADPDEF
ERIYEPLDVKSKKIHVVDSGLTFNLPYPLILRPQRGVDLIISFDFSARPSDSSPPFKELLLAEKW
AKMNKLPFPKIDPYVFDREGLKECYVFKPKNPDMEKDCPTIIHFVLANINFRKYKAPGVPRETEE
EKEIADFDIFDDPESPFSTFNFQYPNQAFKRLHDLMHFNTLNNIDVIKEAMVESIEYRRQ
>d1xaa__ c.77.1.1 (-) 3-isopropylmalate dehydrogenase, IPMDH {Thermus thermophilus}
MKVAVLPGDGIGPEVTEAALKVLRALDEAEGLGLAYEVFPFGGAAIDAFGEPFPEPTRKGVEEAE
AVLLGSVGGPKWDGLPRKIRPETGLLSLRKSQDLFANLRPAKVFPGLERLSPLKEEIARGVDVLI
VRELTGGIYFGEPRGMSEAEAWNTERYSKPEVERVARVAFEAARKRRKHVVSVDKANVLEVGEFW
RKTVEEVGRGYPDVALEHQYVDAMAMHLVRSPARFDVVVTGNIFGDILSDLASVLPGSLGLLPSA
SLGRGTPVFEPVHGSAPDIAGKGIANPTAAILSAAMMLEHAFGLVELARKVEDAVAKALLETPPP
DLGGSAGTEAFTATVLRHLA
>d1xad__ c.77.1.1 (-) 3-isopropylmalate dehydrogenase, IPMDH {Chimera (Thermus thermophilus) and (Bacillus subtilis)}
MKVAVLPGDGIGPEVTEAALKVLRALDEAEGLGLAYEVFPFGGAAIDAFGEPFPEPTRKGVEEAE
AVLLGSVGGPKWDQNPRELRPEKGLLSIRKQLDLFANLRPVKVFESLSDASPLKKEYIDNVDFVI
VRELTGGIYFGEPRGMSEAEAWNTERYSKPEVERVARVAFEAARKRRKHVVSVDKANVLEVGEFW
RKTVEEVGRGYPDVALEHQYVDAMAMHLVRSPARFDVVVTGNIFGDILSDLASVLPGSLGLLPSA
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SLGRGTPVFEPVHGSAPDIAGKGIANPTAAILSAAMMLEHAFGLVELARKVEDAVAKALLETPPP
DLGGSAGTEAFTATVLRHLA
>d2ayqa_ c.77.1.1 (A:) 3-isopropylmalate dehydrogenase, IPMDH
{Bacillus coagulans}
MKMKLAVLPGDGIGPEVMDAAIRVLKTVLDNDGHEAVFENALIGGAAIDEAGTPLPEETLDICRR
SDAILLGAVGGPKWDHNPASLRPEKGLLGLRKEMGLFANLRPVKAYATLLNASPLKRERVENVDL
VIVRELTGGLYFGRPSERRGPGENEVVDTLAYTREEIERIIEKAFQLAQIRRKKLASVDKANVLE
SSRMWREIAEETAKKYPDVELSHMLVDSTSMQLIANPGQFDVIVTENMFGDILSDEASVITGSLG
MLPSASLRSDRFGMYEPVHGSAPDIAGQGKANPLGTVLSAALMLRYSFGLEKEAAAIEKAVDDVL
QDGYCTGDLQVANGKVVSTIELTDRLIEKLN
>d1a05a_ c.77.1.1 (A:) 3-isopropylmalate dehydrogenase, IPMDH
{Thiobacillus ferrooxidans}
MKKIAIFAGDGIGPEIVAAARQVLDAVDQAAHLGLRCTEGLVGGAALDASDDPLPAASLQLAMAA
DAVILGAVGGPRWDAYPPAKRPEQGLLRLRKGLDLYANLRPAQIFPQLLDASPLRPELVRDVDIL
VVRELTGDIYFGQPRGLEVIDGKRRGFNTMVYDEDEIRRIAHVAFRAAQGRRKQLCSVDKANVLE
TTRLWREVVTEVARDYPDVRLSHMYVDNAAMQLIRAPAQFDVLLTGNMFGDILSDEASQLTGSIG
MLPSASLGEGRAMYEPIHGSAPDIAGQDKANPLATILSVAMMLRHSLNAEPWAQRVEAAVQRVLD
QGLRTADIAAPGTPVIGTKAMGAAVVNALNLK
>d1cnza_ c.77.1.1 (A:) 3-isopropylmalate dehydrogenase, IPMDH
{Salmonella typhimurium}
MSKNYHIAVLPGDGIGPEVMAQALKVMDAVRSRFDMRITTSHYDVGGIAIDNHGHPLPKATVEGC
EQADAILFGSVGGPKWENLPPESQPERGALLPLRKHFKLFSNLRPAKLYQGLEAFCPLRADIAAN
GFDILCVRELTGGIYFGQPKGREGSGQYEKAFDTEVYHRFEIERIARIAFESARKRRRKVTSIDK
ANVLQSSILWREIVNDVAKTYPDVELAHMYIDNATMQLIKDPSQFDVLLCSNLFGDILSDECAMI
TGSMGMLPSASLNEQGFGLYEPAGGSAPDIAGKNIANPIAQILSLALLLRYSLDANDAATAIEQA
INRALEEGVRTGDLARGAAAVSTDEMGDIIARYVAEGV
>d1cm7a_ c.77.1.1 (A:) 3-isopropylmalate dehydrogenase, IPMDH
{Escherichia coli}
MSKNYHIAVLPGDGIGPEVMTQALKVLDAVRNRFAMRITTSHYDVGGAAIDNHGQPLPPATVEGC
EQADAVLFGSVGGPKWEHLPPDQQPERGALLPLRKHFKLFSNLRPAKLYQGLEAFCPLRADIAAN
GFDILCVRELTGGIYFGQPKGREGSGQYEKAFDTEVYHRFEIERIARIAFESARKRRHKVTSIDK
ANVLQSSILWREIVNEIATEYPDVELAHMYIDNATMQLIKDPSQFDVLLCSNLFGDILSDECAMI
TGSMGMLPSASLNEQGFGLYEPAGGSAPDIAGKNIANPIAQILSLALLLRYSLDADDAACAIERA
INRALEEGIRTGDLARGAAAVSTDEMGDIIARYVAEGV
>d1iso__ c.77.1.1 (-) Isocitrate dehydrogenase, ICDH {Escherichia
coli}
SKVVVPAQGKKITLQNGKLNVPENPIIPYIEGDGIGVDVTPAMLKVVDAAVEKAYKGERKISWME
IYTGEKSTQVYGQDVWLPAETLDLIREYRVAIKGPLTTPVGGGIRSLNVALRQELDLYICLRPVR
YYQGTPSPVKHPELTDMVIFRENSEDIYAGIEWKADSADAEKVIKFLREEMGVKKIRFPEHCGIG
IKPMSEEGTKRLVRAAIEYAIANDRDSVTLVHKGNIMKFTEGAFKDWGYQLAREEFGGELIDGGP
WLKVKNPNTGKEIVIKDVIADAFLQQILLRPAEYDVIACMNLNGDYISDALAAQVGGIGIAPGAN
IGDEYALFEATHGTAPDIAGQDKANPGSIILSAEMMLRHMGWTEAADLIVKGMEGAINAKTVTKD
FESLMDGAKLLKCSEFGDAIIENM
>d1hqsa_ c.77.1.1 (A:) Isocitrate dehydrogenase, ICDH {Bacillus
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subtilis}
MAQGEKITVSNGVLNVPNNPIIPFIEGDGTGPDIWNAASKVLEAAVEKAYKGEKKITWKEVYAGE
KAYNKTGEWLPAETLDVIREYFIAIKGPLTTPVGGGIRSLNVALRQELDLFVCLRPVRYFTGVPS
PVKRPEDTDMVIFRENTEDIYAGIEYAKGSEEVQKLISFLQNELNVNKIRFPETSGIGIKPVSEE
GTSRLVRAAIDYAIEHGRKSVTLVHKGNIMKFTEGAFKNWGYELAEKEYGDKVFTWAQYDRIAEE
QGKDAANKAQSEAEAAGKIIIKDSIADIFLQQILTRPNEFDVVATMNLNGDYISDALAAQVGGIG
IAPGANINYETGHAIFEATHGTAPKYAGLDKVNPSSVILSGVLLLEHLGWNEAADLVIKSMEKTI
ASKVVTYDFARLMDGATEVKCSEFGEELIKNMD
>d1ekxa1 c.78.1.1 (A:1-150) Aspartate carbamoyltransferase catalytic
subunit {Escherichia coli}
ANPLYQKHIISINDLSRDDLNLVLATAAKLKANPQPELLKHKVIASCFFEASTRTRLSFETSMHR
LGASVVGFSDSANTSLGKKGETLADTISVISTYVDAIVMRHPQEGAARLATEFSGNVPVLNAGDG
SNQHPTQTLLDLFTIQETQG
>d1ekxa2 c.78.1.1 (A:151-310) Aspartate carbamoyltransferase
catalytic subunit {Escherichia coli}
RLDNLHVAMVGDLKYGRTVHSLTQALAKFDGNRFYFIAPDALAMPQYILDMLDEKGIAWSLHSSI
EEVMAEVDILYMTRVQKERLDPSEYANVKAQFVLRASDLHNAKANMKVLHPLPRVDEIATDVDKT
PHAWYFQQAGNGIFARQALLALVLNRDLVL
>d2atca2 c.78.1.1 (A:151-305) Aspartate carbamoyltransferase
catalytic subunit {Escherichia coli}
RLNNLHVAMVGDLKYGRTVHSLTQALAKFDGNRFYFIAPDALAMPEYILDMLDEKGIAWSLHSSI
EEVMTRVQKERLDPSEYABVKAQFLVRANSLGGLHNAKMNAKVLHPLPRVDEIATDVDKTPHAWY
FQQAGNGIFARQALLALVLNRDLVL
>d2at2a1 c.78.1.1 (A:1-144) Aspartate carbamoyltransferase catalytic
subunit {Bacillus subtilis}
MKHLTTMSELSTEEIKDLLQTAQELKSGKTDNQLTGKFAANLFFEPSTRTRFSFEVAEKKLGMNV
LNLDGTSTSVQKGETLYDTIRTLESIGVDVCVIRHSEDEYYEELVSQVNIPILNAGDGCGQHPTQ
SLLDLMTIYEEFNT
>d2at2a2 c.78.1.1 (A:145-295) Aspartate carbamoyltransferase
catalytic subunit {Bacillus subtilis}
FKGLTVSIHGDIKHSRVARSNAEVLTRLGARVLFSGPSEWQDEENTFGTYVSMDEAVESSDVVML
LRIQNERHQSAVSQEGYLNKYGLTVERAERMKRHAIIMHPAPVNRGVEIDDSLVESEKSRIFKQM
KNGVFIRMAVIQCALQTNVKR
>d1dxha1 c.78.1.1 (A:1-150) Ornithine transcarbamoylase {Pseudomonas
aeruginosa}
AFNMHNRNLLSLMHHSTRELRYLLDLSRDLKRAKYTGTEQQHLKRKNIALIFEKTSTRTRCAFEV
AAYDQGANVTYIDPNSSQIGHKESMKDTARVLGRMYDAIEYRGFKQEIVEELAKFAGVPVFNGLT
DEYHPTQMLADVLTMREHSD
>d1dxha2 c.78.1.1 (A:151-335) Ornithine transcarbamoylase
{Pseudomonas aeruginosa}
KPLHDISYAYLGDARNNMGNSLLLIGAKLGMDVRIAAPKALWPHDEFVAQCKKFAEESGAKLTLT
EDPKEAVKGVDFVHTDVWVSMGEPVEAWGERIKELLPYQVNMEIMKATGNPRAKFMHCLPAFHNS
ETKVGKQIAEQYPNLANGIEVTEDVFESPYNIAFEQAENRMHTIKAILVSTLADI
>d1duvg1 c.78.1.1 (G:1-150) Ornithine transcarbamoylase {Escherichia
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coli}
SGFYHKHFLKLLDFTPAELNSLLQLAAKLKADKKSGKEEAKLTGKNIALIFEKDSTRTRCSFEVA
AYDQGARVTYLGPSGSQIGHKESIKDTARVLGRMYDGIQYRGYGQEIVETLAEYASVPVWNGLTN
EFHPTQLLADLLTMQEHLPG
>d1duvg2 c.78.1.1 (G:151-333) Ornithine transcarbamoylase {Escherichia coli}
KAFNEMTLVYAGDARNNMGNSMLEAAALTGLDLRLVAPQACWPEAALVTECRALAQQNGGNITLT
EDVAKGVEGADFIYTDVWVSMGEAKEKWAERIALLREYQVNSKMMQLTGNPEVKFLHCLPAFHDD
QTTLGKKMAEEFGLHGGMEVTDEVFESAASIVFDQAENRMHTIKAVMVATLSK
>d1a1s_1 c.78.1.1 (1-150) Ornithine transcarbamoylase {Archaeon Pyrococcus furiosus}
VVSLAGRDLLCLQDYTAEEIWTILETAKMFKIWQKIGKPHRLLEGKTLAMIFQKPSTRTRVSFEV
AMAHLGGHALYLNAQDLQLRRGETIADTARVLSRYVDAIMARVYDHKDVEDLAKYATVPVINGLS
DFSHPCQALADYMTIWEKKG
>d1a1s_2 c.78.1.1 (151-313) Ornithine transcarbamoylase {Archaeon Pyrococcus furiosus}
TIKGVKVVYVGDGNNVAHSLMIAGTKLGADVVVATPEGYEPDEKVIKWAEQNAAESGGSFELLHD
PVKAVKDADVIYTDVWASMGQEAEAEERRKIFRPFQVNKDLVKHAKPDYMFMHCLPAHRGEEVTD
DVIDSPNSVVWDQAENRLHAQKAVLALVMGGIK
>d1otha1 c.78.1.1 (A:34-184) Ornithine transcarbamoylase {Human (Homo sapiens)}
KVQLKGRDLLTLKNFTGEEIKYMLWLSADLKFRIKQKGEYLPLLQGKSLGMIFEKRSTRTRLSTE
TGFALLGGHPCFLTTQDIHLGVNESLTDTARVLSSMADAVLARVYKQSDLDTLAKEASIPIINGL
SDLYHPIQILADYLTLQEHYS
>d1otha2 c.78.1.1 (A:185-354) Ornithine transcarbamoylase {Human (Homo sapiens)}
SLKGLTLSWIGDGNNILHSIMMSAAKFGMHLQAATPKGYEPDASVTKLAEQYAKENGTKLLLTND
PLEAAHGGNVLITDTWISMGREEEKKKRLQAFQGYQVTMKTAKVAASDWTFLHCLPRKPEEVDDE
VFYSPRSLVFPEAENRKWTIMAVMVSLLTDYSPQLQKPKF
>d1b74a1 c.78.2.1 (A:1-105) Glutamate racemase {Aquifex pyrophilus}
MKIGIFDSGVGGLTVLKAIRNRYRKVDIVYLGDTARVPYGIRSKDTIIRYSLECAGFLKDKGVDI
IVVACNTASAYALERLKKEINVPVFGVIEPGVKEALKKSR
>d1b74a2 c.78.2.1 (A:106-252) Glutamate racemase {Aquifex pyrophilus}
NKKIGVIGTPATVKSGAYQRKLEEGGADVFAKACPLFAPLAEEGLLEGEITRKVVEHYLKEFKGK
IDTLILGCTHYPLLKKEIKKFLGDAEVVDSSEALSLSLHNFIKDDGSSSLELFFTDLSPNLQFLI
KLILGRDYPVKLAEGVF
>d1qopb_ c.79.1.1 (B:) Tryptophan synthase, beta-subunit {Salmonella typhimurium}
TTLLNPYFGEFGGMYVPQILMPALNQLEEAFVSAQKDPEFQAQFADLLKNYAGRPTALTKCQNIT
AGTRTTLYLKREDLLHGGAHKTNQVLGQALLAKRMGKSEIIAETGAGQHGVASALASALLGLKCR
IYMGAKDVERQSPNVFRMRLMGAEVIPVHSGSATLKDACNEALRDWSGSYETAHYMLGTAAGPHP
YPTIVREFQRMIGEETKAQILDKEGRLPDAVIACVGGGSNAIGMFADFINDTSVGLIGVEPGGHG
IETGEHGAPLKHGRVGIYFGMKAPMMQTADGQIEESYSISAGLDFPSVGPQHAYLNSIGRADYVS
ITDDEALEAFKTLCRHEGIIPALESSHALAHALKMMREQPEKEQLLVVNLSGRGDKDIFTVHDIL

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>d1fcja_ c.79.1.1 (A:) O-acetylserine sulfhydrylase (Cystein synthase)
{Salmonella typhimurium}
SKIYEDNSLTIGHTPLVRLNRIGNGRILAKVESRNPSFSVKCRIGANMIWDAEKRGVLKPGVELV
EPTNGNTGIALAYVAAARGYKLTLTMPETMSIERRKLLKALGANLVLTEGAKGMKGAIQKAEEIV
ASDPQKYLLLQQFSNPANPEIHEKTTGPEIWEDTDGQVDVFISGVGTGGTLTGVTRYIKGTKGKT
DLITVAVEPTDSPVIAQALAGEEIKPGPHKIQGIGAGFIPGNLDLKLIDKVVGITNEEAISTARR
LMEEEGILAGISSGAAVAAALKLQEDESFTNKNIVVILPSSG
>d1tdj_1 c.79.1.1 (5-335) Allosteric threonine deaminase N-terminal
domain {Escherichia coli}
QPLSGAPEGAEYLRAVLRAPVYEAAQVTPLQKMEKLSSRLDNVILVKREDRQPVHSFKLRGAYAM
MAGLTEEQKAHGVITASAGNHAQGVAFSSARLGVKALIVMPTATADIKVDAVRGFGGEVLLHGAN
FDEAKAKAIELSQQQGFTWVPPFDHPMVIAGQGTLALELLQQDAHLDRVFVPVGGGGLAAGVAVL
IKQLMPQIKVIAVEAEDSACLKAALDAGHPVDLPRVGLFAEGVAVKRIGDETFRLCQEYLDDIIT
VDSDAICAAMKDLFEDVRAVAEPSGALALAGMKKYIALHNIRGERLAHILSGANVNFHGLRYVSE
RCELGE
>d1e5xa_ c.79.1.1 (A:) Threonine synthase {Mouse-ear cress
(Arabidopsis thaliana)}
IETAVKPPHRTEDNIRDEARRNRSNAVNPFSAKYVPFNAAPGSTESYSLDEIVYRSRSGGLLDVE
HDMEALKRFDGAYWRDLFDSRVGKSTWPYGSGVWSKKEWVLPEIDDDDIVSAFEGNSNLFWAERF
GKQFLGMNDLWVKHCGISHTGSFKDLGMTVLVSQVNRLRKMKRPVVGVGCASTGDTSAALSAYCA
SAGIPSIVFLPANKISMAQLVQPIANGAFVLSIDTDFDGCMKLIREITAELPIYLANSLNSLRLE
GQKTAAIEILQQFDWQVPDWVIVPGGNLGNIYAFYKGFKMCQELGLVDRIPRMVCAQAANANPLY
LHYKSGWKDFKPMTASTTFASAIQIGDPVSIDRAVYALKKCNGIVEEATEEELMDAMAQADSTGM
FICPHTGVALTALFKLRNQGVIAPTDRTVVVSTAHGLKFTQSKIDYHSNAIPDMACRFSNPPVDV
KADFGAVMDVLKSYLGSNTLTS
>d1f2da_ c.79.1.1 (A:) 1-aminocyclopropane-1-carboxylate deaminase
{Yeast (Hansenula saturnus)}
AGVAKFAKYPLTFGPSPISNLNRLSQHLGSKVNVYAKREDCNSGLAFGGNKLRKLEYIVPDIVEG
DYTHLVSIGGRQSNQTRMVAALAAKLGKKCVLIQEDWVPIPEAEKDVYNRVGNIELSRIMGADVR
VIEDGFDIGMRKSFANALQELEDAGHKPYPIPAGCSEHKYGGLGFVGFADEVINQEVELGIKFDK
IVVCCVTGSTTAGILAGMAQYGRQDDVIAIDASFTSEKTKEQTLRIANNTAKLIGVEHEFKDFTL
DTRFAYPCYGVPNEGTIEAIRTCAEQEGVLTDPVYEGKSMQGLIALIKEDYFKPGANVLYVHLGG
APALSAYSSFFPTKTA
>d1jbqa_ c.79.1.1 (A:) Cystathionine beta-synthase {Human (Homo
sapiens)}
WIRPDAPSRCTWQLGRPASESPHHHTAPAKSPKILPDILKKIGDTPMVRINKIGKKFGLKCELLA
KCEFFNAGGSVKDRISLRMIEDAERDGTLKPGDTIIEPTSGNTGIGLALAAAVRGYRCIIVMPEK
MSSEKVDVLRALGAEIVRTPTNARFDSPESHVGVAWRLKNEIPNSHILDQYRNASNPLAHYDTTA
DEILQQCDGKLDMLVASVGTGGTITGIARKLKEKCPGCRIIGVDPEGSILAEPEELNQTEQTTYE
VEGIGYDFIPTVLDRTVVDKWFKSNDEEAFTFARMLIAQEGLLCGGSAGSTVAVAVKAAQELQEG
QRCVVILPDSVRNYMTKFLSDRWMLQKGFL
>d1jeoa_ c.80.1.3 (A:) Probable 3-hexulose-6-phosphate isomerase
MJ1247 {Archaeon Methanococcus jannaschii}
LEELDIVSNNILILKKFYTNDEWKNKLDSLIDRIIKAKKIFIFGVGRSGYIGRCFAMRLMHLGFK
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SYFVGETTTPSYEKDDLLILISGSGRTESVLTVAKKAKNINNNIIAIVCECGNVVEFADLTIPLE
VKKSKYLPMGTTFEETALIFLDLVIAEIMKRLNLDESEIIKRHCNLL
>d1moq__ c.80.1.1 (-) "Isomerase domain" of glucosamine 6-phosphate synthase (GLMS) {Escherichia coli}
GDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSELGPNADELLSKVEHIQILACGTSYNSG
MVSRYWFESLAGIPCDVEIASEFRYRKSAVRRNSLMITLSQSGETADTLAGLRLSKELGYLGSLA
ICNVPGSSLVRESDLALMTNAGTEIGVASTKAFTTQLTVLLMLVAKLSRLKGLDASIEHDIVHGL
QALPSRIEQMLSQDKRIEALAEDFSDKHHALFLGRGDQYPIALEGALKLKEISYIHAEAYAAGEL
KHGPLALIDADMPVIVVAPNNELLEKLKSNIEEVRARGGQLYVFADQDAGFVSSDNMHIIEMPHV
EEVIAPIFYTVPLQLLAYHVALIKGTDVDQPRNLAKSVTVE
>d1g98a_ c.80.1.2 (A:) Phosphoglucose isomerase, PGI {Rabbit (Oryctolagus cuniculus)}
AALTRNPQFQKLQQWHREHGSELNLRHLFDTDKERFNHFSLTLNTNHGHILLDYSKNLVTEEVMH
MLLDLAKSRGVEAARESMFNGEKINSTEDRAVLHVALRNRSNTPIVVDGKDVMPEVNKVLDKMKA
FCQRVRSGDWKGYTGKTITDVINIGIGGSDLGPLMVTEALKPYSSGGPRVWFVSNIDGTHIAKTL
ACLNPESSLFIIASKTFTTQETITNAKTAKDWFLLSAKDPSTVAKHFVALSTNTAKVKEFGIDPQ
NMFEFWDWVGGRYSLWSAIGLSIALHVGFDNFEQLLSGAHWMDQHFRTTPLEKNAPVLLAMLGIW
YINCFGCETQAVLPYDQYLHRFAAYFQQGDMESNGKYITKSGARVDHQTGPIVWGEPGTNGQHAF
YQLIHQGTKMIPCDFLIPVQTQHPIRKGLHHKILLANFLAQTEALMKGKSTEEARKELQAAGKSP
EDLMKLLPHKVFEGNRPTNSIVFTKLTPFILGALIAMYEHKIFVQGVVWDINSFDQWGVELGKQL
AKKIEPELDGSSPVTSHDSSTNGLINFIKQQREAK
>d1iata_ c.80.1.2 (A:) Phosphoglucose isomerase, PGI {Human (Homo sapiens)}
AALTRDPQFQKLQQWYREHRSELNLRRLFDANKDRFNHFSLTLNTNHGHILVDYSKNLVTEDVMR
MLVDLAKSRGVEAARERMFNGEKINYTEGRAVLHVALRNRSNTPILVDGKDVMPEVNKVLDKMKS
FCQRVRSGDWKGYTGKTITDVINIGIGGSDLGPLMVTEALKPYSSGGPRVWYVSNIDGTHIAKTL
AQLNPESSLFIIASKTFTTQETITNAETAKEWFLQAAKDPSAVAKHFVALSTNTTKVKEFGIDPQ
NMFEFWDWVGGRYSLWSAIGLSIALHVGFDNFEQLLSGAHWMDQHFRTTPLEKNAPVLLALLGIW
YINCFGCETHAMLPYDQYLHRFAAYFQQGDMESNGKYITKSGTRVDHQTGPIVWGEPGTNGQHAF
YQLIHQGTKMIPCDFLIPVQTQHPIRKGLHHKILLANFLAQTEALMRGKSTEEARKELQAAGKSP
EDLERLLPHKVFEGNRPTNSIVFTKLTPFMLGALVAMYEHKIFVQGIIWDINSFDQWGVELGKQL
AKKIEPELDGSAQVTSHDASTNGLINFIKQQREARV
>d1c7qa_ c.80.1.2 (A:) Phosphoglucose isomerase, PGI {Bacillus stearothermophilus}
AISFDYSNALPFMQENELDYLSEFVKAAHHMLHERKGPGSDFLGWVDWPIRYDKNEFSRIKQAAE
RIRNHSDALVVIGIGGSYLGARAAIEALSHTFHNQMNDTTQIYFAGQNISSTYISHLLDVLEGKD
LSINVISKSGTTTEPAIAFRIFRDYMEKKYGKEEARKRIYVTTDRTKGALKKLADQEGYETFVIP
DNIGGRYSVLTAVGLLPIAVAGLNIDRMMEGAASAYHKYNNPDLLTNESYQYAAVRNILYRKGKA
IELLVNYEPSLHYVSEWWKQLFGESEGKDQKGLFPASVDFTTDLHSMGQYVQEGRRNLIETVLHV
KKPQIELTIQEDPENIDGLNFLAGKTLDEVNKKAFQGTLLAHVDGGVPNLIVELDEMNEYTFGEM
VYFFEKACGISGHLLGVNPFDQPGVEAYKKNMFALLGKPGFEDEKAALMKRL
>d1eu1a2 c.81.1.1 (A:4-625) Dimethylsulfoxide reductase (DMSO reductase) {Rhodobacter sphaeroides}
ANGEVMSGCHWGVFKARVENGRAVAFEPWDKDPAPSHQLPGVLDSIYSPTRIKYPMVRREFLEKG

VNADRSTRGNGDFVRVTWDEALDLVARELKRVQESYGPTGTFGGSYGWKSPGRLHNCQVLMRRAL
NLAGGFVNSSGDYSTAAAQIIMPHVMGTLEVYEQQTAWPVVVENTDLMVFWAADPMKTNEIGWVI
PDHGAYAGMKALKEKGTRVIAINPVRTETADYFGADVVSPRPQTDVALMLGMAHTLYSEDLHDKD
FLENCTTGFDLFAAYLTGESDGTPKTAEWAAEICGLPAEQIRELARSFVAGRTMLAAGWSIQRMH
HGEQAHWMLVTLASMIGQIGLPGGGFGLSYHYSNGGSPTSDGPALGGISDGGKAVEGAAWLSESG
ATSIPCARVVDMLLNPGGEFQFNGATATYPDVKLAYWAGGNPFAHHQDRNRMLKAWEKLETFIVQ
DFQWTATARHADIVLPATTSYERNDIESVGDYSNRAILAMKKVVDPLYEARSDYDIFAALAERLG
KGAEFTEGRDEMGWISSFYEAAVKQAEFKNVAMPSFEDFWSEGIVEFPITEGANFVRYADFREDP
LFNPLGTPSGLIEIYSKNIEKMGYDDCPAHPTWMEPA
>d1dmr_2 c.81.1.1 (3-625) Dimethylsulfoxide reductase (DMSO reductase) {Rhodobacter capsulatus}
LANGTVMSGSHWGVFTATVENGRATAFTPWEKDPHPSPMLAGVLDSIYSPTRIKYPMVRREFLEK
GVNADRSTRGNGDFVRVSWDQALDLVAAEVKRVEETYGPEGVFGGSYGWKSPGRLHNCTTLLRRM
LTLAGGYVNGAGDYSTGAAQVIMPHVVGTLEVYEQQTAWPVLAENTEVMVFWAADPIKTSQIGWV
IPEHGAYPGLEALKAKGTKVIVIDPVRTKTVEFFGAEHITPKPQTDVAIMLGMAHTLVAEDLYDK
DFIANYTSGFDKFLPYLDGETDSTPKTAEWAEGISGVPAETIKELARLFESKRTMLAAGWSMQRM
HHGEQAHWMLVTLASMLGQIGLPGGGFGLSYHYSGGGTPSTSGPALAGITDGGAATKGPEWLAAS
GASVIPVARVVDMLENPGAEFDFNGTRSKFPDVKMAYWVGGNPFVHHQDRNRMVKAWEKLETFVV
HDFQWTPTARHADIVLPATTSYERNDIETIGDYSNTGILAMKKIVEPLYEARSDYDIFAAVAERL
GKGAEFTEGKDEMGWIKSFYDDAAKQGKAAGVQMPAFDAFWAEGIVEFPVTDGADFVRYASFRED
PLLNPLGTPTGLIEIYSKNIEKMGYDDCPAHPTWMEPL
>d1aa6_2 c.81.1.1 (1-564) Formate dehydrogenase H {Escherichia coli}
MKKVVTVCPYCASGCKINLVVDNGKIVRAEAAQGKTNQGTLCLKGYYGWDFINDTQILTPRLKTP
MIRRQRGGKLEPVSWDEALNYVAERLSAIKEKYGPDAIQTTGSSRGTGNETNYVMQKFARAVIGT
NNVDCCARVCHGPSVAGLHQSVGNGAMSNAINEIDNTDLVFVFGYNPADSHPIVANHVINAKRNG
AKIIVCDPRKIETARIADMHIALKNGSNIALLNAMGHVIIEENLYDKAFVASRTEGFEEYRKIVE
GYTPESVEDITGVSASEIRQAARMYAQAKSAAILWGMGVTQFYQGVETVRSLTSLAMLTGNLGKP
HAGVNPVRGQNNVQGACDMGALPDTYPGYQYVKDPANREKFAKAWGVESLPAHTGYRISELPHRA
AHGEVRAAYIMGEDPLQTDAELSAVRKAFEDLELVIVQDIFMTKTASAADVILPSTSWGEHEGVF
TAADRGFQRFFKAVEPKWDLKTDWQIISEIATRMGYPMHYNNTQEIWDELRHLCPDFYGATYEKM
GELGFIQWPCRDTSDADQGTSYLFKEKFDTPNGLAQFFTCDWVA
>d1tmo_2 c.81.1.1 (5-631) Trimethylamine N-oxide reductase {Shewanella massilia}
NEDEWLTTGSHFGAFKMKRKNGVIAEVKPFDLDKYPTDMINGIRGMVYNPSRVRYPMVRLDFLLK
GHKSNTHQRGDFRFVRVTWDKALTLFKHSLDEVQTQYGPSGLHAGQTGWRATGQLHSSTSHMQRA
VGMHGNYVKKIGDYSTGAGQTILPYVLGSTEVYAQGTSWPLILEHSDTIVLWSNDPYKNLQVGWN
AETHESFAYLAQLKEKVKQGKIRVISIDPVVTKTQAYLGCEQLYVNPQTDVTLMLAIAHEMISKK
LYDDKFIQGYSLGFEEFVPYVMGTKDGVAKTPEWAAPICGVEAHVIRDLAKTLVKGRTQFMMGWC
IQRQQHGEQPYWMAAVLATMIGQIGLPGGGISYGHHYSSIGVPSSGAAAPGAFPRNLDENQKPLF
DSSDFKGASSTIPVARWIDAILEPGKTIDANGSKVVYPDIKMMIFSGNNPWNHHQDRNRMKQAFH
KLECVVTVDVNWTATCRFSDIVLPACTTYERNDIDVYGAYANRGILAMQKMVEPLFDSLSDFEIF
TRFAAVLGKEKEYTRNMGEMEWLETLYNECKAANAGKFEMPDFATFWKQGYVHFGDGEVWTRHAD
FRNDPEINPLGTPSGLIEIFSRKIDQFGYDDCKGHPTWMEKT
>d1g8ka2 c.81.1.1 (A:4-682) Arsenite oxidase large subunit

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{Alcaligenes faecalis}
NDRITLPPANAQRTNMTCHFCIVGCGYHVYKWPELEEGGRAPEQNALGLDFRKQLPPLAVTLTPA
MTNVVTEHDGARYDIMVVPDKACVVNSGLSSTRGGKMASYMYTPTGDGKERLSAPRLYAADEWVD
TTWDHAMALYAGLIKKTLDKDGPQGVFFSCFDHGGAGGGFENTWGTGKLMFSAIQTPMVRIHNRP
AYNSECHATREMGIGELNNAYEDAQLADVIWSIGNNPYESQTNYFLNHWLPNLQGATTSKKKERF
PNENFPQARIIFVDPRETPSVAIARHVAGNDRVLHLAIEPGTDTALFNGLFTYVVEQGWIDKPFI
EAHTKGFDDAVKTNRLSLDECSNITGVPVDMLKRAAEWSYKPKASGQAPRTMHAYEKGIIWGNDN
YVIQSALLDLVIATHNVGRRGTGCVRMGGHQEGYTRPPYPGDKKIYIDQELIKGKGRIMTWWGCN
NFQTSNNAQALREAILQRSAIVKQAMQKARGATTEEMVDVIYEATQNGGLFVTSINLYPTKLAEA
AHLMLPAAHPGEMNLTSMNGERRIRLSEKFMDPPGTAMADCLIAARIANALRDMYQKDGKAEMAA
QFEGFDWKTEEDAFNDGFRRAGQPGAPAIDSQGGSTGHLVTYDRLRKSGNNGVQLPVVSWDESKG
LVGTEMLYTEGKFDTDDGKAHFKPAPWNG
>d2napa2 c.81.1.1 (A:4-600) Dissimilatory nitrate reductase (NAP)
{Desulfovibrio desulfuricans}
RPEKWVKGVCRYCGTGCGVLVGVKDGKAVAIQGNPNNHNAGLLCLKGSLLIPVLNSKERVTQPLV
RRHKGGKLEPVSWDEALDLMASRFRSSIDMYGPNSVAWYGSGQCLTEESYVANKIFKGGFGTNNV
DGNPRLCMASAVGGYVTSFGKDEPMGTYADIDQATCFFIIGSNTSEAHPVLFRRIARRKQVEPGV
KIIVADPRRTNTSRIADMHVAFRPGTDLAFMHSMAWVIINEELDNPRFWQRYVNFMDAEGKPSDF
EGYKAFLENYRPEKVAEICRVPVEQIYGAARAFAESAATMSLWCMGINQRVQGVFANNLIHNLHL
ITGQICRPGATSFSLTGQPNACGGVRDGGALSHLLPAGRAIPNAKHRAEMEKLWGLPEGRIAPEP
GYHTVALFEALGRGDVKCMIICETNPAHTLPNLNKVHKAMSHPESFIVCIEAFPDAVTLEYADLV
LPPAFWCERDGVYGCGERRYSLTEKAVDPPGQCRPTVNTLVEFARRAGVDPQLVNFRNAEDVWNE
WRMVSKGTTYDFWGMTRERLRKESGLIWPCPSEDHPGTSLRYVRGQDPCVPADHPDRFFFYGKPD
GRAVIWMRPAKG
>d1ad3a_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Rat
(Rattus norvegicus)}
SISDTVKRAREAFNSGKTRSLQFRIQQLEALQRMINENLKSISGALASDLGKNEWTSYYEEVAHV
LEELDTTIKELPDWAEDEPVAKTRQTQQDDLYIHSEPLGVVLVIGAWNYPFNLTIQPMVGAVAAG
NAVILKPSEVSGHMADLLATLIPQYMDQNLYLVVKGGVPETTELLKERFDHIMYTGSTAVGKIVM
AAAAKHLTPVTLELGGKSPCYVDKDCDLDVACRRIAWGKFMNSGQTCVAPDYILCDPSIQNQIVE
KLKKSLKDFYGEDAKQSRDYGRIINDRHFQRVKGLIDNQKVAHGGTWDQSSRYIAPTILVDVDPQ
SPVMQEEIFGPVMPIVCVRSLEEAIQFINQREKPLALYVFSNNEKVIKKMIAETSSGGVTANDVI
VHITVPTLPFGGVGNSGMGAYHGKKSFETFSHRRSCLVKSLLNEEAHKARYPPSPA
>d1bi9a_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Rat
(Rattus norvegicus), retinal type II}
MASLQLLPSPTPNLEIKYTKIFINNEWQNSESGRVFPVCNPATGEQVCEVQEADKVDIDKAVQAA
RLAFSLGSVWRRMDASERGRLLDKLADLVERDRATLATMESLNGGKPFLQAFYIDLQGVIKTLRY
YAGWADKIHGMTIPVDGDYFTFTRHEPIGVCGQIIPWNFPLLMFTWKIAPALCCGNTVVIKPAEQ
TPLSALYMGALIKEAGFPPGVVNILPGYGPTAGAAIASHIGIDKIAFTGSTEVGKLIQEAAGRSN
LKRVTLELGGKSPNIIFADADLDYAVEQAHQGVFFNQGQCCTAGSRIFVEESIYEEFVKRSVERA
KRRIVGSPFDPTTEQGPQIDKKQYNKILELIQSGVAEGAKLECGGKGLGRKGFFIEPTVFSNVTD
DMRIAKEEIFGPVQEILRFKTMDEVIERANNSDFGLVAAVFTNDINKALMVSSAMQAGTVWINCY
NALNAQSPFGGFKMSGNGREMGEFGLREYSEVKTVTVKIPQKNS
>d1ag8a_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Cow
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(Bos taurus), mitochondrial}
VPTPNQQPEVLYNQIFINNEWHDAVSKKTFPTVNPSTGDVICHVAEGDKADVDRAVKAARAAFQL
GSPWRRMDASERGRLLNRLADLIERDRTYLAALETLDNGKPYIISYLVDLDMVLKCLRYYAGWAD
KYHGKTIPIDGDYFSYTRHEPVGVCGQIIPWNFPLLMQAWKLGPALATGNVVVMKVAEQTPLTAL
YVANLIKEAGFPPGVVNVIPGFGPTAGAAIASHEDVDKVAFTGSTEVGHLIQVAAGKSNLKRVTL
EIGGKSPNIIMSDADMDWAVEQAHFALFFNQGQCCCAGSRTFVQEDIYAEFVERSVARAKSRVVG
NPFDSRTEQGPQVDETQFKKVLGYIKSGKEEGLKLLCGGGAAADRGYFIQPTVFGDLQDGMTIAK
EEIFGPVMQILKFKSMEEVVGRANNSKYGLAAAVFTKDLDKANYLSQALQAGTVWVNCYDVFGAQ
SPFGGYKLSGSGRELGEYGLQAYTEVKTVTVRVPQKNS
>d1cw3a_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH
{Human (Homo sapiens), mitochondrial}
AVPAPNQQPEVFCNQIFINNEWHDAVSRKTFPTVNPSTGEVICQVAEGDKEDVDKAVKAARAAFQ
LGSPWRRMDASHRGRLLNRLADLIERDRTYLAALETLDNGKPYVISYLVDLDMVLKCLRYYAGWA
DKYHGKTIPIDGDFFSYTRHEPVGVCGQIIPWNFPLLMQAWKLGPALATGNVVVMKVAEQTPLTA
LYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDKVAFTGSTEIGRVIQVAAGSSNLKRVT
LELGGKSPNIIMSDADMDWAVEQAHFALFFNQGQCCCAGSRTFVQEDIYDEFVERSVARAKSRVV
GNPFDSKTEQGPQVDETQFKKILGYINTGKQEGAKLLCGGGIAADRGYFIQPTVFGDVQDGMTIA
KEEIFGPVMQILKFKTIEEVVGRANNSTYGLAAAVFTKDLDKANYLSQALQAGTVWVNCYDVFGA
QSPFGGYKMSGSGRELGEYGLQAYTEVKTVTVKVPQKNS
>d1bxsa_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH
{Sheep (Ovis aries)}
DVPAPLTNLQFKYTKIFINNEWHSSVSGKKFPVFNPATEEKLCEVEEGDKEDVDKAVKAARQAFQ
IGSPWRTMDASERGRLLNKLADLIERDRLLLATMEAMNGGKLFSNAYLMDLGGCIKTLRYCAGWA
DKIQGRTIPMDGNFFTYTRSEPVGVCGQIIPWNFPLLMFLWKIGPALSCGNTVVVKPAEQTPLTA
LHMGSLIKEAGFPPGVVNIVPGYGPTAGAAISSHMDVDKVAFTGSTEVGKLIKEAAGKSNLKRVS
LELGGKSPCIVFADADLDNAVEFAHQGVFYHQGQCCIAASRLFVEESIYDEFVRRSVERAKKYVL
GNPLTPGVSQGPQIDKEQYEKILDLIESGKKEGAKLECGGGPWGNKGYFIQPTVFSDVTDDMRIA
KEEIFGPVQQIMKFKSLDDVIKRANNTFYGLSAGIFTNDIDKAITVSSALQSGTVWVNCYSVVSA
QCPFGGFKMSGNGRELGEYGFHEYTEVKTVTIKISQKNS
>d1a4sa_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH
{Baltic cod (Gadus callarias)}
AQLVDSMPSASTGSVVVTDDLNYWGGRRIKSKDGATTEPVFEPATGRVLCQMVPCGAEEVDQAVQ
SAQAAYLKWSKMAGIERSRVMLEAARIIRERRDNIAKLEVINNGKTITEAEYDIDAAWQCIEYYA
GLAPTLSGQHIQLPGGAFAYTRREPLGVCAGILAWNYPFMIAAWKCAPALACGNAVVFKPSPMTP
VTGVILAEIFHEAGVPVGLVNVVQGGAETGSLLCHHPNVAKVSFTGSVPTGKKVMEMSAKTVKHV
TLELGGKSPLLIFKDCELENAVRGALMANFLTQGQVCTNGTRVFVQREIMPQFLEEVVKRTKAIV
VGDPLLTETRMGGLISKPQLDKVLGFVAQAKKEGARVLCGGEPLTPSDPKLKNGYFMSPCVLDNC
RDDMTCVKEEIFGPVMSVLPFDTEEEVLQRANNTTFGLASGVFTRDISRAHRVAANLEAGTCYIN
TYSISPVEVPFGGYKMSGFGRENGQATVDYYSQLKTVIVEMGDVDSLF
>d1euha_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH
{Streptococcus mutans}
TKQYKNYVNGEWKLSENEIKIYEPASGAELGSVPAMSTEEVDYVYASAKKAQPAWRALSYIERAA
YLHKVADILMRDKEKIGAILSKEVAKGYKSAVSEVVRTAEIINYAAEEGLRMEGEVLEGGSFEAA
SKKKIAVVRREPVGLVLAISPFNYPVNLAGSKIAPALIAGNVIAFKPPTQGSISGLLLAEAFAEA
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GLPAGVFNTITGRGSEIGDYIVEHQAVNFINFTGSTGIGERIGKMAGMRPIMLELGGKDSAIVLE
DADLELTAKNIIAGAFGYSGQRCTAVKRVLVMESVADELVEKIREKVLALTIGNPEDDADITPLI
DTKSADYVEGLINDANDKGATALTEIKREGNLICPILFDKVTTDMRLAWEEPFGPVLPIIRVTSV
EEAIEISNKSEYGLQASIFTNDFPRAFGIAEQLEVGTVHINNKTQRGTDNFPFLGAKKSGAGIQG
VKYSIEAMTTVKSVVFDIK
>d1ez0a_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Vibrio harveyi}
TDNVFYATNAFTGEALPLAFPVHTEVEVNQAATAAAKVARDFRRLNNSKRASLLRTIASELEARS
DDIIARAHLETALPEVRLTGEIARTANQLRLFADVVNSGSYHQAILDTPNPTRAPLPKPDIRRQQ
IALGPVAVFGASNFPLAFSAAGGDTASALAAGCPVIVKGHTAHPGTSQIVAECIEQALKQEQLPQ
AIFTLLQGNQRALGQALVSHPEIKAVGFTGSVGGGRALFNLAHERPEPIPFYGELGAINPTFIFP
SAMRAKADLADQFVASMTMGCGQFCTKPGVVFALNTPETQAFIETAQSLIRQQSPSTLLTPGIRD
SYQSQVVSRGSDDGIDVTFSQAESPCVASALFVTSSENWRKHPAWEEEIFGPQSLIVVCENVADM
LSLSEMLAGSLTATIHATEEDYPQVSQLIPRLEEIAGRLVFNGWPTGVEVGYAMVHGGPYPASTH
SASTSVGAEAIHRWLRPVAYQALPESLLPDSLKAENPLEIARAVDGKAA
>d1k75a_ c.82.1.2 (A:) L-histidinol dehydrogenase HisD {Escherichia coli}
NTIIDWNSCTAEQQRQLLMRPAISASESITRTVNDILDNVKARGDEALREYSAKFDKTTVTALKV
SAEEIAAASERLSDELKQAMAVAVKNIETFHTAQKLPPVDVETQPGVRCQQVTRPVASVGLYIPG
GSAPLFSTVLMLATPASIAGCKKVVLCSPPPIADEILYAAQLCGVQDVFNVGGAQAIAALAFGTE
SVPKVDKIFGPGNAFVTEAKRQVSQRLDGAAIDMPAGPSEVLVIADSGATPDFVASDLLSQAEHG
PDSQVILLTPAADMARRVAEAVERQLAELPRAETARQALNASRLIVTKDLAQCVEISNQYGPEHL
IIQTRNARELVDSITSAGSVFLGDWSPESAGDYASGTNHVLPTYGYTATCSSLGLADFQKRMTVQ
ELSKEGFSALASTIETLAAAERLTAHKNAVTLRVNALKEQA
>d1aco_2 c.83.1.1 (2-528) Aconitase, first 3 domains {Cow (Bos taurus)}
RAKVAMSHFEPHEYIRYDLLEKNIDIVRKRLNRPLTLSEKIVYGHLDDPANQEIERGKTYLRLRP
DRVAMQDATAQMAMLQFISSGLPKVAVPSTIHCDHLIEAQLGGEKDLRRAKDINQEVYNFLATAG
AKYGVGFWRPGSGIIHQIILENYAYPGVLLIGTDSHTPNGGGLGGICIGVGGADAVDVMAGIPWE
LKCPKVIGVKLTGSLSGWTSPKDVILKVAGILTVKGGTGAIVEYHGPGVDSISCTGMATICNMGA
EIGATTSVFPYNHRMKKYLSKTGRADIANLADEFKDHLVPDSGCHYDQLIEINLSELKPHINGPF
TPDLAHPVAEVGSVAEKEGWPLDIRVGLIGSCTNSSYEDMGRSAAVAKQALAHGLKCKSQFTITP
GSEQIRATIERDGYAQVLRDVGGIVLANACGPCIGQWDRKDIKKGEKNTIVTSYNRNFTGRNDAN
PETHAFVTSPEIVTALAIAGTLKFNPETDFLTGKDGKKFKLEAPDADELPRAEFDPGQDTYQHPP
KDSSGQR
>d3pmga1 c.84.1.1 (A:1-190) Phosphoglucomutase {Rabbit (Oryctolagus cuniculus)}
VKIVTVKTKAYPDQKPGTSGLRKRVKVFQSSTNYAENFIQSIISTVEPAQRQEATLVVGGDGRFY
MKEAIQLIVRIAAANGIGRLVIGQNGILSTPAVSCIIRKIKAIGGIILTASHNPGGPNGDFGIKF
NISNGGPAPEAITDKIFQISKTIEEYAICPDLKVDLGVLGKQQFDLENKFKPFTVEIVDS
>d3pmga2 c.84.1.1 (A:191-303) Phosphoglucomutase {Rabbit (Oryctolagus cuniculus)}
VEAYATMLRNIFDFNALKELLSGPNRLKIRIDAMHGVVGPYVKKILCEELGAPANSAVNCVPLED
FGGHHPDPNLTYAADLVETMKSGEHDFGAAFDGDGDRNMILGKHGFFV
>d3pmga3 c.84.1.1 (A:304-420) Phosphoglucomutase {Rabbit
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(Oryctolagus cuniculus)}
NPSDSVAVIAANIFSIPYFQQTGVRGFARSMPTSGALDRVANATKIALYETPTGWKFFGNLMDAS
KLSLCGEESFGTGSDHIREKDGLWAVLAWLSILATRKQSVEDILKDHWHKFG
>d1kfia1 c.84.1.1 (A:3-205) Exocytosis-sensitive phosphoprotein, pp63/parafusin {Paramecium tetraurelia}
QVIPAPRVQVTQPYAGQKPGTSGLRKKVSEATQPNYLENFVQSIFNTLRKDELKPKNVLFVGGDG
RYFNRQAIFSIIRLAYANDISEVHVGQAGLMSTPASSHYIRKVNEEVGNCIGGIILTASHNPGGK
EHGDFGIKFNVRTGAPAPEDFTDQIYTHTTKIKEYLTVDYEFEKHINLDQIGVYKFEGTRLEKSH
FEVKVVDT
>d1kfia2 c.84.1.1 (A:206-323) Exocytosis-sensitive phosphoprotein, pp63/parafusin {Paramecium tetraurelia}
VQDYTQLMQKLFDFDLLKGLFSNKDFSFRFDGMHGVAGPYAKHIFGTLLGCSKESLLNCDPSEDF
GGGHPDPNLTYAHDLVELLDIHKKKDVGTVPQFGAACDGDADRNMILGRQFFV
>d1kfia3 c.84.1.1 (A:324-443) Exocytosis-sensitive phosphoprotein, pp63/parafusin {Paramecium tetraurelia}
TPSDSLAVIAANANLIFKNGLLGAARSMPTSGALDKVAAKNGIKLFETPTGWKFFGNLMDAGLIN
LCGEESFGTGSNHIREKDGIWAVLAWLTILAHKNKNTDHFVTVEEIVTQYWQQFG
>d1k2yx1 c.84.1.1 (X:5-154) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}
KAPTLPASIFRAYDIRGVVGDTLTAETAYWIGRAIGSESLARGEPCVAVGRDGRLSGPELVKQLI
QGLVDCGCQVSDVGMVPTPVLYYAANVLEGKSGVMLTGAHNPPDYNGFKIVVAGETLANEQIQAL
RERIEKNDLASGVGSVEQVD
>d1k2yx2 c.84.1.1 (X:155-258) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}
ILPRYFKQIRDDIAMAKPMKVVVDCGNGVAGVIAPQLIEALGCSVIPLYCEVDGNFPNHHPDPGK
PENLKDLIAKVKAENADLGLAFDGDGDRVGVVTNTGTII
>d1k2yx3 c.84.1.1 (X:259-367) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}
YPDRLLMLFAKDVVSRNPGADIIFDVKCTRRLIALISGYGGRPVMWKTGHSLIKKKMKETGALLA
GEMSGHVFFKERWFGFDDGIYSAARLLEILSQDQRDSEHVFSAF
>d1k2yx4 c.84.1.1 (X:368-463) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}
PSDISTPEINITVTEDSKFAIIEALQRDAQWGEGNITTLDGVRVDYPKGWGLVRASNTTPVLVLR
FEADTEEELERIKTVFRNQLKAVDSSLPVPF
>d1fuia2 c.85.1.1 (A:1-355) L-fucose isomerase, N-terminal and second domains {Escherichia coli}
MKKISLPKIGIRPVIDGRRMGVRESLEEQTMNMAKATAALLTEKLRHACGAAVECVISDTCIAGM
AEAAACEEKFSSQNVGLTITVTPCWCYGSETIDMDPTRPKAIWGFNGTERPGAVYLAAALAAHSQ
KGIPAFSIYGHDVQDADDTSIPADVEEKLLRFARAGLAVASMKGKSYLSLGGVSMGIAGSIVDHN
FFESWLGMKVQAVDMTELRRRIDQKIYDEAELEMALAWADKNFRYGEDENNKQYQRNAEQSRAVL
RESLLMAMCIRDMMQGNSKLADIGRVEESLGYNAIAAGFQGQRHWTDQYPNGDTAEAILNSSFDW
NGVREPFVVATENDSLNGVAMLMGHQLTGT
>d1fw8a_ c.86.1.1 (A:) Phosphoglycerate kinase {Baker's yeast (Saccharomyces cerevisiae)}

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SKYSLAPVAKELQSLLGKDVTFLNDCVGPEVEAAVKASAPGSVILLENLRYHIEEEGSRKVDGQK
VKASKEDVQKFRHELSSLADVYINDAFGTAHRAHSSMVGFDLPQRAAGFLLEKELKYFGKALENP
TRPFLAILGGAKVADKIQLIDNLLDKVDSIIIGGGMAFTFKKVLENTEIGDSIFDKAGAEIVPKL
MEKAKAKGVEVVLPVDFIIADAFSADANTKTVTDKEGIPAGWQGLDNGPESRKLFAATVAKAKTI
VWNGPPGVFEFEKFAAGTKALLDEVVKSSAAGNTVIIGGGDTATVAKKYGVTDKISHVSTGGGAS
LELLEGKELPGVAFLSEKKSLSSKLSVQDLDLKDKRVFIRVDFNVPLDGKKITSNQRIVAALPTI
KYVLEHHPRYVVLASHLGRPNGERN
>d1qpg__ c.86.1.1 (-) Phosphoglycerate kinase {Baker's yeast (Saccharomyces cerevisiae)}
SLSSKLSVQDLDLKDKRVFIRVDFNVPLDGKKITSNQRIVAALPTIKYVLEHHPRYVVLASHLGQ
PNGERNEKYSLAPVAKELQSLLGKDVTFLNDCVGPEVEAAVKASAPGSVILLENLRYHIEEEGSR
KVDGQKVKASKEDVQKFRHELSSLADVYINDAFGTAHRAHSSMVGFDLPQRAAGFLLEKELKYFG
KALENPTRPFLAILGGAKVADKIQLIDNLLDKVDSIIIGGGMAFTFKKVLENTEIGDSIFDKAGA
EIVPKLMEKAKAKGVEVVLPVDFIIADAFSADANTKTVTDKEGIPAGWQGLDNGPESRKLFAATV
AKAKTIVWNGPPGVFEFEKFAAGTKALLDEVVKSSAAGNTVIIGGGDTATVAKKYGVTDKISHVS
TGGGASLELLEGKELPGVAFLSEKK
>d1php__ c.86.1.1 (-) Phosphoglycerate kinase {Bacillus stearothermophilus}
MNKKTIRDVDVRGKRVFCRVDFNVPMEQGAITDDTRIRAALPTIRYLIEHGAKVILASHLGRPKG
KVVEELRLDAVAKRLGELLERPVAKTNEAVGDEVKAAVDRLNEGDVLLLENVRFYPGEEKNDPEL
AKAFAELADLYVNDAFGAAHRAHASTEGIAHYLPAVAGFLMEKELEVLGKALSNPDRPFTAIIGG
AKVKDKIGVIDNLLEKVDNLIIGGGLAYTFVKALGHDVGKSLLEEDKIELAKSFMEKAKEKGVRF
YMPVDVVVADRFANDANTKVVPIDAIPADWSALDIGPKTRELYRDVIRESKLVVWNGPMGVFEMD
AFAHGTKAIAEALAEALDTYSVIGGGDSAAAVEKFGLADKMDHISTGGGASLEFMEGKQLPGVVA
LEDK
>d1vpe__ c.86.1.1 (-) Phosphoglycerate kinase {Thermotoga maritima}
EKMTIRDVDLKGKRVIMRVDFNVPVKDGVVQDDTRIRAALPTIKYALEQGAKVILLSHLGRPKGE
PSPEFSLAPVAKRLSELLGKEVKFVPAVVGDEVKKAVEELKEGEVLLLENTRFHPGETKNDPELA
KFWASLADIHVNDAFGTAHRAHASNVGIAQFIPSVAGFLMEKEIKFLSKVTYNPEKPYVVVLGGA
KVSDKIGVITNLMEKADRILIGGAMMFTFLKALGKEVGSSRVEEDKIDLAKELVEKAKEKGVEIV
LPVDAVIAQKIEPGVEKKVVRIDDGIPEGWMGLDIGPETIELFKQKLSDAKTVVWNGPMGVFEID
DFAEGTKQVALAIAALTEKGAITVVGGGDSAAAVNKFGLEDKFSHVSTGGGASLEFLEGKELPGI
ASMRIKKA
>d16pk__ c.86.1.1 (-) Phosphoglycerate kinase {Trypanosoma brucei}
EKKSINECDLKGKKVLIRVDFNVPVKNGKITNDYRIRSALPTLKKVLTEGGSCVLMSHLGRPKGI
PMAQAGKIRSTGGVPGFQQKATLKPVAKRLSELLLRPVTFAPDCLNAADVVSKMSPGDVVLLENV
RFYKEEGSKKAKDREAMAKILASYGDVYISDAFGTAHRDSATMTGIPKILGNGAAGYLMEKEISY
FAKVLGNPPRPLVAIVGGAKVSDKIQLLDNMLQRIDYLLIGGAMAYTFLKAQGYSIGKSKCEESK
LEFARSLLKKAEDRKVQVILPIDHVCHTEFKAVDSPLITEDQNIPEGHMALDIGPKTIEKYVQTI
GKCKSAIWNGPMGVFEMVPYSKGTFAIAKAMGRGTHEHGLMSIIGGGDSASAAELSGEAKRMSHV
STGGGASLELLEGKTLPGVTVLDDK
>d1hdia_ c.86.1.1 (A:) Phosphoglycerate kinase {Pig (Sus scrofa)}
NKLTLDKLNVKGKRVVMRVDFNVPMAAAQITNNARIKAAVPSIKFCLDDGAKSVVLMSHLGRPDG
SPMPDKYSLQPVAAELKSALGKAVLFLKDCVGPAVEKACADPAAGSVILLENLRFHVEEEGKGKD
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ASGNKAAGEPAKIKAFRASLSALGDVYVNDAFGTAHRAHSSMVGVNLPKKAGAFLMKKELNYFAA
AAESPERPFLAILGGAKVADKIQLINNMLDKVNEMIIGGGMAFTFLKVLNNMEIGTSLFDEAGKK
IVKNLMSKAAANGVKITLPVDFVTADKFDEQAKIGQATVASGIPAGWMGLDCGPKSSAKYSEAVA
RAKQIVWNGPVGVFEWEAFAQGTKALMDEVVKATSRGCITIIGGGDTATCCAKWNTEDNVSHVST
GGGASLELLEGKVLPGVDALSNV
>d1jixa_ c.87.1.1 (A:) beta-Glucosyltransferase (DNA-modifying) {Bacteriophage T4}
MKIAIINMGNNVINFKTVPSSETIYLFKVISEMGLNVDIISLKNGVYTKSFDEVDVNDYDRLIVV
NSSINFFGGKPNLAILSAQKFMAKYKSKIYYLFTDIRLPFSQSWPNVKNRPWAYLYTEEELLIKS
PIKVISQGINLDIAKAAHKKVDNVIEFEYFPIEQYKIHMNDFQLSKPTKKTLDVIYGGSFRSGQR
ESKMVEFLFDTGLNIEFFGNAREKQFKNPKYPWTKAPVFTGKIPMNMVSEKNSQAIAALIIGDKN
YNDNFITLRVWETMASDAVMLIDEEFDTKHRIINDARFYVNNRAELIDRVNELKHSDVLRKEMLS
IQHDILNKTRAKKAEWQDAFKKAIDL
>d1f0ka_ c.87.1.2 (A:) Peptidoglycan biosynthesys glycosyltransferase MurG {Escherichia coli}
KRLMVMAGGTGGHVFPGLAVAHHLMAQGWQVRWLGTADRMEADLVPKHGIEIDFIRISGLRGKGI
KALIAAPLRIFNAWRQARAIMKAYKPDVVLGMGGYVSGPGGLAAWSLGIPVVLHEQNGIAGLTNK
WLAKIATKVMQAFPGAFPNAEVVGNPVRTDVLALPLPQQRLAGREGPVRVLVVGGSQGARILNQT
MPQVAAKLGDSVTIWHQSGKGSQQSVEQAYAEAGQPQHKVTEFIDDMAAAYAWADVVVCRSGALT
VSEIAAAGLPALFVPFQHKDRQQYWNALPLEKAGAAKIIEQPQLSVDAVANTLAGWSRETLLTMA
ERARAASIPDATERVANEVSRVARAL
>d1f6da_ c.87.1.3 (A:) UDP-N-acetylglucosamine 2-epimerase {Escherichia coli}
MKVLTVFGTRPEAIKMAPLVHALAKDPFFEAKVCVTAQHREMLDQVLKLFSIVPDYDLNIMQPGQ
GLTEITCRILEGLKPILAEFKPDVVLVHGDTTTTLATSLAAFYQRIPVGHVEAGLRTGDLYSPWP
EEANRTLTGHLAMYHFSPTETSRQNLLRENVADSRIFITGNTVIDALLWVRDQVMSSDKLRSELA
ANYPFIDPDKKMILVTGHRRESFGRGFEEICHALADIATTHQDIQIVYPVHLNPNVREPVNRILG
HVKNVILIDPQEYLPFVWLMNHAWLILTDSGGIQEEAPSLGKPVLVMRDTTERPEAVTAGTVRLV
GTDKQRIVEEVTRLLKDENEYQAMSRAHNPYGDGQACSRILEALKNNRISL
>d1iira_ c.87.1.5 (A:) UDP-glucosyltransferase GtfB {Amycolatopsis orientalis}
MRVLLATCGSRGDTEPLVALAVRVRDLGADVRMCAPPDCAERLAEVGVPHVPVGPSARAPIQRAK
PLTAEDVRRFTTEAIATQFDEIPAAAEGCAAVVTTGLLAAAIGVRSVAEKLGIPYFYAFHCPSYV
PSPYYPPPPLGEPSTQDTIDIPAQWERNNQSAYQRYGGLLNSHRDAIGLPPVEDIFTFGYTDHPW
VAADPVLAPLQPTDLDAVQTGAWILPDERPLSPELAAFLDAGPPPVYLGFGSLGAPADAVRVAID
AIRAHGRRVILSRGWADLVLPDDGADCFAIGEVNHQVLFGRVAAVIHHGGAGTTHVAARAGAPQI
LLPQMADQPYYAGRVAELGVGVAHDGPIPTFDSLSAALATALTPETHARATAVAGTIRTDGAAVA
ARLLLDAVSRE
>d1em6a_ c.87.1.4 (A:) Glycogen phosphorylase {Human (Homo sapiens)}
ENVAELKKSFNRHLHFTLVKDRNVATTRDYYFALAHTVRDHLVGRWIRTQQHYYDKCPKRVYYLS
LEFYMGRTLQNTMINLGLQNACDEAIYQLGLDIEELEEIEEDAGLGNGGLGRLAACFLDSMATLG
LAAYGYGIRYEYGIFNQKIRDGWQVEEADDWLRYGNPWEKSRPEFMLPVHFYGKVEHTNTGTKWI
DTQVVLALPYDTPVPGYMNNTVNTMRLWSARAPNDFNLRDFNVGDYIQAVLDRNLAENISRVLYP
NDNFFEGKELRLKQEYFVVAATLQDIIRRFKASKFGSTRGAGTVFDAFPDQVAIQLNDTHPALAI
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PELMRIFVDIEKLPWSKAWELTQKTFAYTNHTVLPEALERWPVDLVEKLLPRHLEIIYEINQKHL
DRIVALFPKDVDRLRRMSLIEEEGSKRINMAHLCIVGSHAVNGVAKIHSDIVKTKVFKDFSELEP
DKFQNKTNGITPRRWLLLCNPGLAELIAEKIGEDYVKDLSQLTKLHSFLGDDVFLRELAKVKQEN
KLKFSQFLETEYKVKINPSSMFDVQVKRIHEYKRQLLNCLHVITMYNRIKKDPKKLFVPRTVIIG
GKAAPGYHMAKMIIKLITSVADVVNNDPMVGSKLKVIFLENYRVSLAEKVIPATDLSEQISTAGT
EASGTGNMKFMLNGALTIGTMDGANVEMAEEAGEENLFIFGMRIDDVAALDKKGYEAKEYYEALP
ELKLVIDQIDNGFFSPKQPDLFKDIINMLFYHDRFKVFADYEAYVKCQDKVSQLYMNPKAWNTMV
LKNIAASGKFSSDRTIKEYAQNIWNVEPS
>d1a8i__ c.87.1.4 (-) Glycogen phosphorylase {Rabbit (Oryctolagus cuniculus)}
QEKRKQISVRGLAGVENVTELKKNFNRHLHFTLVKDRNVATPRDYYFALAHTVRDHLVGRWIRTQ
QHYYEKDPKRIYYLSLEFYMGRTLQNTMVNLALENACDEATYQLGLDMEELEEIEEDAGLGNGGL
GRLAACFLDSMATLGLAAYGYGIRYEFGIFNQKICGGWQMEEADDWLRYGNPWEKARPEFTLPVH
FYGRVEHTSQGAKWVDTQVVLAMPYDTPVPGYRNNVVNTMRLWSAKAPNDFNLKDFNVGGYIQAV
LDRNLAENISRVLYPNDNFFEGKELRLKQEYFVVAATLQDIIRRFKSSKFGCRDPVRTNFDAFPD
KVAIQLNDTHPSLAIPELMRVLVDLERLDWDKAWEVTVKTCAYTNHTVIPEALERWPVHLLETLL
PRHLQIIYEINQRFLNRVAAAFPGDVDRLRRMSLVEEGAVKRINMAHLCIAGSHAVNGVARIHSE
ILKKTIFKDFYELEPHKFQNKTNGITPRRWLVLCNPGLAEIIAERIGEEYISDLDQLRKLLSYVD
DEAFIRDVAKVKQENKLKFAAYLEREYKVHINPNSLFDVQVKRIHEYKRQLLNCLHVITLYNRIK
KEPNKFVVPRTVMIGGKAAPGYHMAKMIIKLITAIGDVVNHDPVVGDRLRVIFLENYRVSLAEKV
IPAADLSEQISTAGTEASGTGNMKFMLNGALTIGTMDGANVEMAEEAGEENFFIFGMRVEDVDRL
DQRGYNAQEYYDRIPELRQIIEQLSSGFFSPKQPDLFKDIVNMLMHHDRFKVFADYEEYVKCQER
VSALYKNPREWTRMVIRNIATSGKFSSDRTIAQYAREIWGVEPSRQRLP
>d1ygpa_ c.87.1.4 (A:) Glycogen phosphorylase {Baker's yeast (Saccharomyces cerevisiae)}
TRRLTGFLPQEIKSIDTMIPLLSRALWNKHQVKKFNKAEDFQDRFIDHVETTLARSLYNCDDMVA
YEAASMSIRDNLVIDWNKTQQKFTTRDPKRVYYLSLEFLMGRALDNALINMKIEDPEDPAASKGK
PREMIKGALDELGFKLEDVLDQEPDAGLGNGGLGRLAACFVDSMATEGIPAWGYGLRYEYGIFAQ
KIIDGYQVETPDYWLNSGNPWEIERNEVQIPVTFYGYVDRPEGGKTTLSASQWIGGERVLAVAYD
FPVPGFKTSNVNNLRLWQARPTTEFDLNKFNNGDYKNSVAQQQRAESITAVLYPNDNFAQGKELR
LKQQYFWCAASLHDILRRFKKSKRPWTEFPDQVAIQLNDTHPTLAIVELQRVLVDLEKLDWHEAW
DIVTKTFAYTNHTVMQEALEKWPRRLFGHLLPRHLEIIYDINWFFLEDVAKKFPKDVDLLSRISI
IEENSPERQIRMAFLAIVGSHKVNGVVELHSELIKTTIFKDFIKFYGPSKFVNVTNGITPRRWLK
QANPSLAKLISETLNDPTEEYLLDMAKLTQLEKYVEDKEFLKKWNQVKLNNKIRLVDLIKKENDG
VDIINREYLDDTLFDMQVKRIHEYKRQQLNVFGIIYRYLAMKNMLKNGASIEEVARKYPRKVSIF
GGKSAPGYYMAKLIIKLINCVADIVNNDESIEHLLKVVFVADYNVSKAEIIIPASDLSEHISTAG
TEASGTSNMKFVMNGGLIIGTVDGANVEITREIGEDNVFLFGNLSENVEELRYNHQYHPQDLPSS
LDSVLSYIESGQFSPENPNEFKPLVDSIKYHGDYYLVSDDFESYLATHELVDQEFHNQRSEWLKK
SVLSLANVGFFSSDRCIEEYSDTIWNVEPVT
>d1qm5a_ c.87.1.4 (A:) Maltodextrin phosphorylase (MALP) {Escherichia coli}
SQPIFNDKQFQEALSRQWQRYGLNSAAEMTPRQWWLAVSEALAEMLRAQPFAKPVANQRHVNYIS
MEFLIGRLTGNNLLNLGWYQDVQDSLKAYDINLTDLLEEEIDPALGNGGLGRLAACFLDSMATVG
QSATGYGLNYQYGLFRQSFVDGKQVEAPDDWHRSNYPWFRHNEALDVQVGIGGKVTKDGRWEPEF

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TITGQAWDLPVVGYRNGVAQPLRLWQATHAHPFDLTKFNDGDFLRAEQQGINAEKLTKVLYPNDN
HTAGKKLRLMQQYFQCACSVADILRRHHLAGRKLHELADYEVIQLNDTHPTIAIPELLRVLIDEH
QMSWDDAWAITSKTFAYTNHTLMPEALERWDVKLVKGLLPRHMQIINEINTRFKTLVEKTWPGDE
KVWAKLAVVHDKQVHMANLCVVGGFAVNGVAALHSDLVVKDLFPEYHQLWPNKFHNVTNGITPRR
WIKQCNPALAALLDKSLQKEWANDLDQLINLEKFADDAKFRDQYREIKQANKVRLAEFVKVRTGI
EINPQAIFDIQIKRLHEYKRQHLNLLHILALYKEIRENPQADRVPRVFLFGAKAAPGYYLAKNII
FAINKVADVINNDPLVGDKLKVVFLPDYCVSAAEKLIPAADISEQISTAGKEASGTGNMKLALNG
ALTVGTLDGANVEIAEKVGEENIFIFGHTVEQVKAILAKGYDPVKWRKKDKVLDAVLKELESGKY
SDGDKHAFDQMLHSIGKQGGDPYLVMADFAAYVEAQKQVDVLYRDQEAWTRAAILNTARCGMFSS
DRSIRDYQARIWQAKR
>d4ecaa_ c.88.1.1 (A:) Asparaginase type II {Escherichia coli}
LPNITILATGGTIAGGGDSATKSNYTVGKVGVENLVNAVPQLKDIANVKGEQVVNIGSQDMNDNV
WLTLAKKINTDCDKTDGFVITHGVDTMEETAYFLDLTVKCDKPVVMVGAMRPSTSMSADGPFNLY
NAVVTAADKASANRGVLVVMNDTVLDGRDVTKTNTTDVATFKSVNYGPLGYIHNGKIDYQRTPAR
KHTSDTPFDVSKLNELPKVGIVYNYANASDLPAKALVDAGYDGIVSAGVGNGNLYKSVFDTLATA
AKTGTAVVRSSRVPTGATTQDAEVDDAKYGFVASGTLNPQKARVLLQLALTQTKDPQQIQQIFNQ
Y
>d1wsaa_ c.88.1.1 (A:) Asparaginase type II {Wolinella succinogenes}
KPQVTILATGGTIAGSGESSVKSSYSAGAVTVDKLLAAVPAINDLATIKGEQISSIGSQEMTGKV
WLKLAKRVNELLAQKETEAVIITHGTDTMEETAFFLNLTVKSQKPVVLVGAMRPGSSMSADGPMN
LYNAVNVAINKASTNKGVVIVMNDEIHAAREATKLNTTAVNAFASPNTGKIGTVYYGKVEYFTQS
VRPHTLASEFDISKIEELPRVDILYAHPDDTDVLVNAALQAGAKGIIHAGMGNGNPFPLTQNALE
KAAKSGVVVARSSRVGSGSTTQEAEVDDKKLGFVATESLNPQKARVLLMLALTKTSDREAIQKIF
STY
>d1jsra_ c.88.1.1 (A:) Asparaginase type II {Erwinia chrysanthemi}
LPNIVILATGGTIAGSAATGTQTTGYKAGALGVDTLINAVPEVKKLANVKGEQFSNMASENMTGD
VVLKLSQRVNELLARDDVDGVVITHGTDTVEESAYFLHLTVKSDKPVVFVAAMRPATAISADGPM
NLLEAVRVAGDKQSRGRGVMVVINDRIGSARYITKTNASTLDTFRANEEGYLGVIIGNRIYYQNR
IDKLHTTRSVFDVRGLTSLPKVDILYGYQDDPEYLYDAAIQHGVKGIVYAGMGAGSVSVRGIAGM
RKALEKGVVVMRSTRTGNGIVPPDEELPGLVSDSLNPAHARILLMLALTRTSDPKVIQEYFHTY
>d1agx__   c.88.1.1   (-)   Glutaminase-asparaginase   {Acinetobacter
glutaminasificans}
KNNVVIVATGGTIAGAGASSTNSATYSAAKVPVDALIKAVPQVNDLANITGIQALQVASESITDK
ELLSLARQVNDLVKKPSVNGVVITHGTDTMEETAFFLNLVVHTDKPIVLVGSMRPSTALSADGPL
NLYSAVALASSNEAKNKGVMVLMNDSIFAARDVTKGINIHTHAFVSQWGALGTLVEGKPYWFRSS
VKKHTNNSEFNIEKIQGDALPGVQIVYGSDNMMPDAYQAFAKAGVKAIIHAGTGNGSMANYLVPE
VRKLHDEQGLQIVRSSRVAQGFVLRNAEQPDDKYGWIAAHDLNPQKARLLMALALTKTNDAKEIQ
NMFWNY
>d4pgaa_ c.88.1.1 (A:) Glutaminase-asparaginase {Pseudomonas sp., 7A}
KLANVVILATGGTIAGAGASAANSATYQAAKVGVDKLIAGVPELADLANVRGEQVMQIASESITN
DDLLKLGKRVAELADSNDVDGIVITHGTDTLEETAYFLNLVQKTDKPIVVVGSMRPGTAMSADGM
LNLYNAVAVASNKDSRGKGVLVTMNDEIQSGRDVSKSINIKTEAFKSAWGPLGMVVEGKSYWFRL
PAKRHTVNSEFDIKQISSLPQVDIAYSYGNVTDTAYKALAQNGAKALIHAGTGNGSVSSRVVPAL
QQLRKNGTQIIRSSHVNQGGFVLRNAEQPDDKNDWVVAHDLNPEKARILAMVAMTKTQDSKELQR
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IFWEY
>d1pfka_ c.89.1.1 (A:) Phosphofructokinase {Escherichia coli}
MIKKIGVLTSGGDAPGMNAAIRGVVRSALTEGLEVMGIYDGYLGLYEDRMVQLDRYSVSDMINRG
GTFLGSARFPEFRDENIRAVAIENLKKRGIDALVVIGGDGSYMGAMRLTEMGFPCIGLPGTIDND
IKGTDYTIGFFTALSTVVEAIDRLRDTSSSHQRISVVEVMGRYCGDLTLAAAIAGGCEFVVVPEV
EFSREDLVNEIKAGIAKGKKHAIVAITEHMCDVDELAHFIEKETGRETRATVLGHIQRGGSPVPY
DRILASRMGAYAIDLLLAGYGGRCVGIQNEQLVHHDIIDAIENMKRPFKGDWLDCAKKLY
>d3pfk__ c.89.1.1 (-) Phosphofructokinase {Bacillus
stearothermophilus}
MKRIGVLTSGGDSPGMNAAIRSVVRKAIYHGVEVYGVYHGYAGLIAGNIKKLEVGDVGDIIHRGG
TILYTARCPEFKTEEGQKKGIEQLKKHGIQGLVVIGGDGSYQGAKKLTEHGFPCVGVPGTIDNDI
PGTDFTIGFDTALNTVIDAIDKIRDTATSHERTYVIEVMGRHAGDIALWSGLAGGAETILIPEAD
YDMNDVIARLKRGHERGKKHSIIIVAEGVGSGVDFGRQIQEATGFETRVTVLGHVQRGGSPTAFD
RVLASRLGARAVELLLEGKGGRCVGIQNNQLVDHDIAEALANKHTIDQRMYALSKELSI
>d1cbf__ c.90.1.1 (-) Cobalt precorrin-4 methyltransferase CbiF
{Bacillus megaterium}
GLVPRGSHMKLYIIGAGPGDPDLITVKGLKLLQQADVVLYADSLVSQDLIAKSKPGAEVLKTAGM
HLEEMVGTMLDRMREGKMVVRVHTGDPAMYGAIMEQMVLLKREGVDIEIVPGVTSVFAAAAAAEA
ELTIPDLTQTVILTRAEGRTPVPEFEKLTDLAKHKCTIALFLSSTLTKKVMKEFINAGWSEDTPV
VVVYKATWPDEKIVRTTVKDLDDAMRTNGIRKQAMILAGWALDP
>d1i74a_ c.107.1.1 (A:) Manganese-dependent inorganic
pyrophosphatase (family II) {Streptococcus mutans}
SKILVFGHQNPDSDAIGSSMAYAYLKRQLGVDAQAVALGNPNEETAFVLDYFGIQAPPVVKSAQA
EGAKQVILTDHNEFQQSIADIREVEVVEVVDHHRVANFETANPLYMRLEPVGSASSIVYRLYKEN
GVAIPKEIAGVMLSGLISDTLLLKSPTTHASDPAVAEDLAKIAGVDLQEYGLAMLKAGTNLASKT
AAQLVDIDAKTFELNGSQVRVAQVNTVDINEVLERQNEIEEAIKASQAANGYSDFVLMITDILNS
NSEILALGNNTDKVEAAFNFTLKNNHAFLAGAVSRKKQVVPQLTESFNG
>d1k20a_ c.107.1.1 (A:) Manganese-dependent inorganic
pyrophosphatase (family II) {Streptococcus gordonii}
SKILVFGHQNPDSDAIGSSYAFAYLAREAYGLDTEAVALGEPNEETAFVLDYFGVAAPRVITSAK
AEGAEQVILTDHNEFQQSVADIAEVEVYGVVDHHRVANFETANPLYMRLEPVGSASSIVYRMFKE
HSVAVSKEIAGLMLSGLISDTLLLKSPTTHPTDKAIAPELAELAGVNLEEYGLAMLKAGTNLASK
SAEELIDIDAKTFELNGNNVRVAQVNTVDIAEVLERQAEIEAAIEKAIADNGYSDFVLMITDIIN
SNSEILAIGSNMDKVEAAFNFVLENNHAFLAGAVSRKKQVVPQLTESFNA
>d1k23a_ c.107.1.1 (A:) Manganese-dependent inorganic
pyrophosphatase (family II) {Bacillus subtilis}
MEKILIFGHQNPDTDTICSAIAYADLKNKLGFNAEPVRLGQVNGETQYALDYFKQESPRLVETAA
NEVNGVILVDHNERQQSIKDIEEVQVLEVIDHHRIANFETAEPLYYRAEPVGCTATILNKMYKEN
NVKIEKEIAGLMLSAIISDSLLFKSPTCTDQDVAAAKELAEIAGVDAEEYGLNMLKAGADLSKKT
VEELISLDAKEFTLGSKKVEIAQVNTVDIEDVKKRQAELEAVISKVVAEKNLDLFLLVITDILEN
DSLALAIGNEAAKVEKAFNVTLENNTALLKGVVSRKKQVVPVLTDAM
>d1ayl_1 c.91.1.1 (228-540) Phosphoenolpyruvate (PEP) carboxykinase
(ATP-oxaloacetate carboxy-liase) {Escherichia coli}
IASMHCSANVGEKGDVAVFFGLSGTGKTTLSTDPKRRLIGDDEHGWDDDGVFNFEGGCYAKTIKL
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SKEAEPEIYNAIRRDALLENVTVREDGTIDFDDGSKTENTRVSYPIYHIDNIVKPVSKAGHATKV
IFLTADAFGVLPPVSRLTADQTQYHFLSGFTAKLAGTERGITEPTPTFSACFGAAFLSLHPTQYA
EVLVKRMQAAGAQAYLVNTGWNGTGKRISIKDTRAIIDAILNGSLDNAETFTLPMFNLAIPTELP
GVDTKILDPRNTYASPEQWQEKAETLAKLFIDNFDKYTDTPAGAALVAAGPKL
>d1ii2a1 c.91.1.1 (A:201-523) Phosphoenolpyruvate (PEP)
carboxykinase (ATP-oxaloacetate carboxy-liase) {Trypanosoma cruzi}
HLCMHASANVGKQGDVTVFFGLSGTGKTTLSADPHRNLIGDDEHVWTDRGVFNIEGGCYAKAIGL
NPKTEKDIYDAVRFGAVAENCVLDKRTGEIDFYDESICKNTRVAYPLSHIEGALSKAIAGHPKNV
IFLTNDAFGVMPPVARLTSAQAMFWFVMGYTANVPGVEAGGTRTARPIFSSCFGGPFLVRHATFY
GEQLAEKMQKHNSRVWLLNTGYAGGRADRGAKRMPLRVTRAIIDAIHDGTLDRTEYEEYPGWGLH
IPKYVAKVPEHLLNPRKAWKDVRQFNETSKELVAMFQESFSARFAAKASQEMKSAVPRYVEFA
>d1khba1 c.91.1.1 (A:260-622) Cytosolic phosphoenolpyruvate
carboxykinase (GTP-hydrolysing) {Human (Homo sapiens)}
WLAEHMLVLGITNPEGEKKYLAAAFPSACGKTNLAMMNPSLPGWKVECVGDDIAWMKFDAQGHLR
AINPENGFFGVAPGTSVKTNPNAIKTIQKNTIFTNVAETSDGGVYWEGIDEPLASGVTITSWKNK
EWSSEDGEPCAHPNSRFCTPASQCPIIDAAWESPEGVPIEGIIFGGRRPAGVPLVYEALSWQHGV
FVGAAMRSEATAAAEHKGKIIMHDPFAMRPFFGYNFGKYLAHWLSMAQHPAAKLPKIFHVNWFRK
DKEGKFLWPGFGENSRVLEWMFNRIDGKASTKLTPIGYIPKEDALNLKGLGHINMMELFSISKEF
WDKEVEDIEKYLVDQVNADLPCEIEREILALKQRISQM
>d1jb1a_ c.91.1.2 (A:) HPr kinase HprK C-terminal domain
{Lactobacillus casei}
ERRSMHGVLVDIYGLGVLITGDSGVGKSETALELVQRGHRLIADDRVDVYQQDEQTIVGAAPPIL
SHLLEIRGLGIIDVMNLFGAGAVREDTTISLIVHLENWTPDKTFDRLGSGEQTQLIFDVPVPKIT
VPVKVGRNLAIIIEVAAMNFRAKSMGYDATKTFEKNLNHLIEH
>d1ayl_2 c.109.1.1 (1-227) Phosphoenolpyruvate (PEP) carboxykinase
(ATP-oxaloacetate carboxy-liase) {Escherichia coli}
MRVNNGLTPQELEAYGISDVHDIVYNPSYDLLYQEELDPSLTGYERGVLTNLGAVAVDTGIFTGR
SPKDKYIVRDDTTRDTFWWADKGKGKNDNKPLSPETWQHLKGLVTRQLSGKRLFVVDAFCGANPD
TRLSVRFITEVAWQAHFVKNMFIRPSDEELAGFKPDFIVMNGAKCTNPQWKEQGLNSENFVAFNL
TERMQLIGGTWYGGEMKKGMFSMMNYLLPLKG
>d1ii2a2 c.109.1.1 (A:2-200) Phosphoenolpyruvate (PEP) carboxykinase
(ATP-oxaloacetate carboxy-liase) {Trypanosoma cruzi}
PPTIHRNLLSPELVQWALKIEKDSRLTARGALAVMSYAKTGRSPLDKRIVDTDDVRENVDWGKVN
MKLSEESFARVRKIAKEFLDTREHLFVVDCFAGHDERYRLKVRVFTTRPYHALFMRDMLIVPTPE
ELATFGEPDYVIYNAGECKADPSIPGLTSTTCVALNFKTREQVILGTEYAGEMKKGILTVMFELM
PQMN
>d1khba2 c.109.1.1 (A:10-259) Cytosolic phosphoenolpyruvate
carboxykinase (GTP-hydrolysing) {Human (Homo sapiens)}
NLSAKVVQGSLDSLPQAVREFLENNAELCQPDHIHICDGSEEENGRLLGQMEEEGILRRLKKYDN
CWLALTDPRDVARIESKTVIVTQEQRDTVPIPKTGLSQLGRWMSEEDFEKAFNARFPGCMKGRTM
YVIPFSMGPLGSPLSKIGIELTDSPYVVASMRIMTRMGTPVLEALGDGEFVKCLHSVGCPLPLQK
PLVNNWPCNPELTLIAHLPDRREIISFGSGYGGNSLLGKKCFALRMASRLAKEEG
>d1doza_ c.92.1.1 (A:) Ferrochelatase {Bacillus subtilis}
SRKKMGLLVMAYGTPYKEEDIERYYTHIRRGRKPEPEMLQDLKDRYEAIGGISPLAQITEQQAHN
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LEQHLNEIQDEITFKAYIGLKHIEPFIEDAVAEMHKDGITEAVSIVLAPHFSTFSVQSYNKRAKE
EAEKLGGLTITSVESWYDEPKFVTYWVDRVKETYASMPEDERENAMLIVSAHSLPEKIKEFGDPY
PDQLHESAKLIAEGAGVSEYAVGWQSEGNTPDPWLGPDVQDLTRDLFEQKGYQAFVYVPVGFVAD
HLEVLYDNDYECKVVTDDIGASYYRPEMPNAKPEFIDALATVVLKKLGR
>d1hrka_ c.92.1.1 (A:) Ferrochelatase {Human (Homo sapiens)}
RKPKTGILMLNMGGPETLGDVHDFLLRLFLDRDLMTLPIQNKLAPFIAKRLTPKIQEQYRRIGGG
SPIKIWTSKQGEGMVKLLDELSPNTAPHKYYIGFRYVHPLTEEAIEEMERDGLERAIAFTQYPQY
SCSTTGSSLNAIYRYYNQVGRKPTMKWSTIDRWPTHHLLIQCFADHILKELDHFPLEKRSEVVIL
FSAHSLPMSVVNRGDPYPQEVSATVQKVMERLEYCNPYRLVWQSKVGPMPWLGPQTDESIKGLCE
RGRKNILLVPIAFTSDHIETLYELDIEYSQVLAKECGVENIRRAESLNGNPLFSKALADLVHSHI
QSNELCSKQLTLSCPLCVNPVCRETKSFFTSQQL
>d1qgoa_ c.92.1.2 (A:) Cobalt chelatase CbiK {Salmonella typhimurium}
KKALLVVSFGTSYHDTCEKNIVACERDLAASCPDRDLFRAFTSGMIIRKLRQRDGIDIDTPLQAL
QKLAAQGYQDVAIQSLHIINGDEYEKIVREVQLLRPLFTRLTLGVPLLSSHNDYVQLMQALRQQM
PSLRQTEKVVFMGHGASHHAFAAYACLDHMMTAQRFPARVGAVESYPEVDILIDSLRDEGVTGVH
LMPLMLVAGDHAINDMASDDGDSWKMRFNAAGIPATPWLSGLGENPAIRAMFVAHLHQALNM
>d1efdn_ c.92.2.1 (N:) Periplasmic ferric siderophore binding protein FhuD {Escherichia coli}
GIDPNRIVALEWLPVELLLALGIVPYGVADTINYRLWVSEPPLPDSVIDVGLRTEPNLELLTEMK
PSFMVWSAGYGPSPEMLARIAPGRGFNFSDGKQPLAMARKSLTEMADLLNLQSAAETHLAQYEDF
IRSMKPRFVKRGARPLLLTTLIDPRHMLVFGPNSLFQEILDEYGIPNAWQGETNFWGSTAVSIDR
LAAYKDVDVLCFDHDNSKDMDALMATPLWQAMPFVRAGRFQRVPAVWFYGATLSAMHFVRVLDNA
IG
>d1toaa_ c.92.2.2 (A:) Periplasmic zinc binding protein TroA {Treponema pallidum}
GKPLVVTTIGMIADAVKNIAQGDVHLKGLMGPGVDPHLYTATAGDVEWLGNADLILYNGLHLETK
MGEVFSKLRGSRLVVAVSETIPVSQRLSLEEAEFDPHVWFDVKLWSYSVKAVYESLCKLLPGKTR
EFTQRYQAYQQQLDKLDAYVRRKAQSLPAERRVLVTAHDAFGYFSRAYGFEVKGLQGVSTASEAS
AHDMQELAAFIAQRKLPAIFIESSIPHKNVEALRDAVQARGHVVQIGGELFSDAMGDAGTSEGTY
VGMVTHNIDTIVAALAR
>d1psza_ c.92.2.2 (A:) Pneumococcal surface antigen PssA {Pneumococcus (Streptococcus pneumoniae)}
KKDTTSGQKLKVVATNSIIADITKNIAGDKIDLHSIVPIGQDPHEYEPLPEDVKKTSEADLIFYN
GINLETGGNAWFTKLVENAKKTENKDYFAVSDGVDVIYLEGQNEKGKEDPHAWLNLENGIIFAKN
IAKQLSAKDPNNKEFYEKNLKEYTDKLDKLDKESKDKFNKIPAEKKLIVTSEGAFKYFSKAYGVP
SAYIWEINTEEEGTPEQIKTLVEKLRQTKVPSLFVESSVDDRPMKTVSQDTNIPIYAQIFTDSIA
EQGKEGDSYYSMMKYNLDKIAEGLAK
>d1mioa_ c.92.2.3 (A:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Clostridium pasteurianum}
SENLKDEILEKYIPKTKKTRSGHIVIKTEETPNPEIVANTRTVPGIITARGCAYAGCKGVVMGPI
KDMVHITHGPIGCSFYTWGGRRFKSKPENGTGLNFNEYVFSTDMQESDIVFGGVNKLKDAIHEAY
EMFHPAAIGVYATCPVGLIGDDILAVAATASKEIGIPVHAFSCEGYKGVSQSAGHHIANNTVMTD
IIGKGNKEQKKYSINVLGEYNIGGDAWEMDRVLEKIGYHVNATLTGDATYEKVQNADKADLNLVQ
CHRSINYIAEMMETKYGIPWIKCNFIGVDGIVETLRDMAKCFDDPELTKRTEEVIAEEIAAIQDD
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LDYFKEKLQGKTACLYVGGSRSHTYMNMLKSFGVDSLVAGFEFAHRDDYEGREVIPTIKIDADSK
NIPEITVTPDEQKYRVVIPEDKVEELKKAGVPLSSYGGMMKEMHDGTILIDDMNHHDMEVVLEKL
KPDMFFAGIKEKFVIQKGGVLSKQLHSYDYNGPYAGFRGVVNFGHELVNGIYTPAWKMITPPWKK
ASSES
>d1miob_ c.92.2.3 (B:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Clostridium pasteurianum}
LDATPKEIVERKALRINPAKTCQPVGAMYAALGIHNCLPHSHGSQGCCSYHRTVLSRHFKEPAMA
STSSFTEGASVFGGGSNIKTAVKNIFSLYNPDIIAVHTTCLSETLGDDLPTYISQMEDAGSIPEG
KLVIHTNTPSYVGSHVTGFANMVQGIVNYLSENTGAKNGKINVIPGFVGPADMREIKRLFEAMDI
PYIMFPDTSGVLDGPTTGEYKMYPEGGTKIEDLKDTGNSDLTLSLGSYASDLGAKTLEKKCKVPF
KTLRTPIGVSATDEFIMALSEATGKEVPASIEEERGQLIDLMIDAQQYLQGKKVALLGDPDEIIA
LSKFIIELGAIPKYVVTGTPGMKFQKEIDAMLAEAGIEGSKVKVEGDFFDVHQWIKNEGVDLLIS
NTYGKFIAREENIPFVRFGFPIMDRYGHYYNPKVGYKGAIRLVEEITNVILDKIERECTEEDFEV
VR
>d2mina_ c.92.2.3 (A:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Azotobacter vinelandii}
SREEVESLIQEVLEVYPEKARKDRNKHLAVNDPAVTQSKKCIISNKKSQPGLMTIRGCAYAGSKG
VVWGPIKDMIHISHGPVGCGQYSRAGRRNYYIGTTGVNAFVTMNFTSDFQEKDIVFGGDKKLAKL
IDEVETLFPLNKGISVQSECPIGLIGDDIESVSKVKGAELSKTIVPVRCEGFRGVSQSLGHHIAN
DAVRDWVLGKRDEDTTFASTPYDVAIIGDYNIGGDAWSSRILLEEMGLRCVAQWSGDGSISEIEL
TPKVKLNLVHCYRSMNYISRHMEEKYGIPWMEYNFFGPTKTIESLRAIAAKFDESIQKKCEEVIA
KYKPEWEAVVAKYRPRLEGKRVMLYIGGLRPRHVIGAYEDLGMEVVGTGYEFAHNDDYDRTMKEM
GDSTLLYDDVTGYEFEEFVKRIKPDLIGSGIKEKFIFQKMGIPFREMHSWDYSGPYHGFDGFAIF
ARDMDMTLNNPCWKKLQAPWE
>d2minb_ c.92.2.3 (B:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Azotobacter vinelandii}
SQQVDKIKASYPLFLDQDYKDMLAKKRDGFEEKYPQDKIDEVFQWTTTKEYQELNFQREALTVNP
AKACQPLGAVLCALGFEKTMPYVHGSQGCVAYFRSYFNRHFREPVSCVSDSMTEDAAVFGGQQNM
KDGLQNCKATYKPDMIAVSTTCMAEVIGDDLNAFINNSKKEGFIPDEFPVPFAHTPSFVGSHVTG
WDNMFEGIARYFTLKSMDDKVVGSNKKINIVPGFETYLGNFRVIKRMLSEMGVGYSLLSDPEEVL
DTPADGQFRMYAGGTTQEEMKDAPNALNTVLLQPWHLEKTKKFVEGTWKHEVPKLNIPMGLDWTD
EFLMKVSEISGQPIPASLTKERGRLVDMMTDSHTWLHGKRFALWGDPDFVMGLVKFLLELGCEPV
HILCHNGNKRWKKAVDAILAASPYGKNATVYIGKDLWHLRSLVFTDKPDFMIGNSYGKFIQRDTL
HKGKEFEVPLIRIGFPIFDRHHLHRSTTLGYEGAMQILTTLVNSILERLDEETRGMQATDYNHDL
VR
>d1qgua_ c.92.2.3 (A:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Klebsiella pneumoniae}
TNATGERNLALIQEVLEVFPETARKERRKHMMVSDPKMKSVGKCIISNRKSQPGVMTVRGCAYAG
SKGVVFGPIKDMAHISHGPVGCGQYSRAGRRNYYTGVSGVDSFGTLNFTSDFQERDIVFGGDKKL
SKLIEEMELLFPLTKGITIQSECPVGLIGDDISAVANASSKALDKPVIPVRCEGFRGVSQSLGHH
IANDVVRDWILNNREGQPFETTPYDVAIIGDYNIGGDAWASRILLEEMGLRVVAQWSGDGTLVEM
ENTPFVKLNLVHCYRSMNYIARHMEEKHQIPWMEYNFFGPTKIAESLRKIADQFDDTIRANAEAV
IARYEGQMAAIIAKYRPRLEGRKVLLYMGGLRPRHVIGAYEDLGMEIIAAGYEFAHNDDYDRTLP
DLKEGTLLFDDASSYELEAFVKALKPDLIGSGIKEKYIFQKMGVPFRQMHSWDYSGPYHGYDGFA

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IFARDMDMTLNNPAWNELTAPWL
>d1qgub_ c.92.2.3 (B:) Nitrogenase iron-molybdenum protein, alpha and
beta chains {Klebsiella pneumoniae}
SQTIDKINSCYPLFEQDEYQELFRNKRQLEEAHDAQRVQEVFAWTTTAEYEALNFRREALTVDPA
KACQPLGAVLCSLGFANTLPYVHGSQGCVAYFRTYFNRHFKEPIACVSDSMTEDAAVFGGNNNMN
LGLQNASALYKPEIIAVSTTCMAEVIGDDLQAFIANAKKDGFVDSSIAVPHAHTPSFIGSHVTGW
DNMFEGFAKTFTADYQGQPGKLPKLNLVTGFETYLGNFRVLKRMMEQMAVPCSLLSDPSEVLDTP
ADGHYRMYSGGTTQQEMKEAPDAIDTLLLQPWQLLKSKKVVQEMWNQPATEVAIPLGLAATDELL
MTVSQLSGKPIADALTLERGRLVDMMLDSHTWLHGKKFGLYGDPDFVMGLTRFLLELGCEPTVIL
SHNANKRWQKAMNKMLDASPYGRDSEVFINCDLWHFRSLMFTRQPDFMIGNSYGKFIQRDTLAKG
KAFEVPLIRLGFPLFDRHHLHRQTTWGYEGAMNIVTTLVNAVLEKLDSDTSQLGKTDYSFDLVR
>d1jr2a_ c.113.1.1 (A:) Uroporphyrinogen III synthase (U3S, HemD)
{Human (Homo sapiens)}
MKVLLLKDAKEDDCGQDPYIRELGLYGLEATLIPVLSFEFLSLPSFSEKLSHPEDYGGLIFTSPR
AVEAAELCLEQNNKTEVWERSLKEKWNAKSVYVVGNATASLVSKIGLDTEGETCGNAEKLAEYIC
SRESSALPLLFPCGNLKREILPKALKDKGIAMESITVYQTVAHPGIQGNLNSYYSQQGVPASITF
FSPSGLTYSLKHIQELSGDNIDQIKFAAIGPTTARALAAQGLPVSCTAESPTPQALATGIRKALQ
>d2dri__ c.93.1.1 (-) D-ribose-binding protein {Escherichia coli,
strain k-12}
KDTIALVVSTLNNPFFVSLKDGAQKEADKLGYNLVVLDSQNNPAKELANVQDLTVRGTKILLINP
TDSDAVGNAVKMANQANIPVITLDRQATKGEVVSHIASDNVLGGKIAGDYIAKKAGEGAKVIELQ
GIAGTSAARERGEGFQQAVAAHKFNVLASQPADFDRIKGLNVMQNLLTAHPDVQAVFAQNDEMAL
GALRALQTAGKSDVMVVGFDGTPDGEKAVNDGKLAATIAQLPDQIGAKGVETADKVLKGEKVQAK
YPVDLKLVVKQ
>d8abp__ c.93.1.1 (-) L-arabinose-binding protein {Escherichia coli}
NLKLGFLVKQPEEPWFQTEWKFADKAGKDLGFEVIKIAVPDGEKTLNAIDSLAASGAKGFVICTP
DPKLGSAIVAKARGYDMKVIAVDDQFVNAKGKPMDTVPLVMLAATKIGERQGQELYKEMQKRGWD
VKESAVMAITANELDTARRRTTGSMDALKAAGFPEKQIYQVPTKSNDIPGAFDAANSMLVQHPEV
KHWLIVGMNDSTVLGGVRATEGQGFKAADIIGIGINGVDAVSELSKAQATGFYGSLLPSPDVHGY
KSSEMLYNWVAKDVEPPKFTEVTDVVLITRDNFKEELEKKGLGGK
>d1rpja_ c.93.1.1 (A:) D-allose-binding protein {Escherichia coli}
AAEYAVVLKTLSNPFWVDMKKGIEDEAKTLGVSVDIFASPSEGDFQSQLQLFEDLSNKNYKGIAF
APLSSVNLVMPVARAWKKGIYLVNLDEKIDMDNLKKAGGNVEAFVTTDNVAVGAKGASFIIDKLG
AEGGEVAIIEGKAGNASGEARRNGATEAFKKASQIKLVASQPADWDRIKALDVATNVLQRNPNIK
AIYCANDTMAMGVAQAVANAGKTGKVLVVGTDGIPEARKMVEAGQMTATVAQNPADIGATGLKLM
VDAEKSGKVIPLDKAPEFKLVDSILVTQ
>d2gbp__ c.93.1.1 (-) Galactose/glucose-binding protein {Escherichia
coli}
ADTRIGVTIYKYDDNFMSVVRKAIEQDAKAAPDVQLLMNDSQNDQSKQNDQIDVLLAKGVKALAI
NLVDPAAAGTVIEKARGQNVPVVFFNKEPSRKALDSYDKAYYVGTDSKESGIIQGDLIAKHWAAN
QGWDLNKDGQIQFVLLKGEPGHPDAEARTTYVIKELNDKGIKTEQLQLDTAMWDTAQAKDKMDAW
LSGPNANKIEVVIANNDAMAMGAVEALKAHNKSSIPVFGVDALPEALALVKSGALAGTVLNDANN
QAKATFDLAKNLADGKGAADGTNWKIDNKVVRVPYVGVDKDNLAEFSKK
>d1gca__ c.93.1.1 (-) Galactose/glucose-binding protein {Salmonella
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typhimurium, strain lt2}
ADTRIGVTIYKYDDNFMSVVRKAIEKDGKSAPDVQLLMNDSQNDQSKQNDQIDVLLAKGVKALAI
NLVDPAAAGTVIEKARGQNVPVVFFNKEPSRKALDSYDKAYYVGTDSKESGVIQGDLIAKHWQAN
QGWDLNKDGKIQYVLLKGEPGHPDAEARTTYVVKELNDKGIQTEQLALDTAMWDTAQAKDKMDAW
LSGPNANKIEVVIANNDAMAMGAVEALKAHNKSSIPVFGVDALPEALALVKSGAMAGTVLNDANN
QAKATFDLAKNLAEGKGAADGTSWKIENKIVRVPYVGVDKDNLSEFTQK
>d1pea__ c.93.1.1 (-) Amide receptor/negative regulator of the amidase operon (AmiC) {Pseudomonas aeruginosa}
PLIGLLFSETGVTADIERSQRYGALLAVEQLNREGGVGGRPIETLSQDPGGDPDRYRLCAEDFIR
NRGVRFLVGCYMSHTRKAVMPVVERADALLCYPTPYEGFEYSPNIVYGGPAPNQNSAPLAAYLIR
HYGERVVFIGSDYIYPRESNHVMRHLYRQHGGTVLEEIYIPLYPSDDDLQRAVERIYQARADVVF
STVVGTGTAELYRAIARRYGDGRRPPIASLTTSEAEVAKMESDVAEGQVVVAPYFSSIDTPASRA
FVQACHGFFPENATITAWAEAAYWQTLLLGRAAQAAGNWRVEDVQRHLYDIDIDAPQGPVRVERQ
NNHSRLSSRIAEIDARGVFQVRWQSPEPIRPDPYVVVHNLDDW
>d1jx6a_ c.93.1.1 (A:) Quorum-sensing signal (autoinducer-2) binding protein LuxP {Vibrio harveyi}
GYWGYQEFLDEFPEQRNLTNALSEAVRAQPVPLSKPTQRPIKISVVYPGQQVSDYWVRNIASFEK
RLYKLNINYQLNQVFTRPNADIKQQSLSLMEALKSKSDYLIFTLDTTRHRKFVEHVLDSTNTKLI
LQNITTPVREWDKHQPFLYVGFDHAEGSRELATEFGKFFPKHTYYSVLYFSEGYISDVRGDTFIH
QVNRDNNFELQSAYYTKATKQSGYDAAKASLAKHPDVDFIYACSTDVALGAVDALAELGREDIMI
NGWGGGSAELDAIQKGDLDITVMRMNDDTGIAMAEAIKWDLEDKPVPTVYSGDFEIVTKADSPER
IEALKKRAFRYSD
>d1dbqa_ c.93.1.1 (A:) Purine repressor (PurR), C-terminal domain {Escherichia coli}
KSIGLLATSSEAAYFAEIIEAVEKNCFQKGYTLILGNAWNNLEKQRAYLSMMAQKRVDGLLVMCS
EYPEPLLAMLEEYRHIPMVVMDWGEAKADFTDAVIDNAFEGGYMAGRYLIERGHREIGVIPGPLE
RNTGAGRLAGFMKAMEEAMIKVPESWIVQGDFEPESGYRAMQQILSQPHRPTAVFCGGDIMAMGA
LCAADEMGLRVPQDVSLIGYDNVRNARYFTPALTTIHQPKDSLGETAFNMLLDRIVNKREEPQSI
EVHPRLIERRSVADGPFRDYRR
>d1jyea_ c.93.1.1 (A:) Lac-repressor (lacR) core (C-terminal domain) {Escherichia coli}
LLIGVATSSLALHAPSQIVAAILSRADQLGASVVVSMVERSGVEACKTAVHNLLAQRVSGLIINY
PLDDQDAIAVEAACTNVPALFLDVSDQTPINSIIFSHEDGTRLGVEHLVALGHQQIALLAGPLSS
VSARLRLAGWHKYLTRNQIQPIAEREGDWSAMSGFQQTMQMLNEGIVPTAMLVANDQMALGAMRA
ITESGLRVGADISVVGYDDTEDSSCYIPPLTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLPV
SLVKRKTTLAP
>d1tlfa_ c.93.1.1 (A:) Lac-repressor (lacR) core (C-terminal domain) {Escherichia coli}
SLLIGVATSSLALHAPSQIVAAIKSRADQLGASVVVSMVERSGVEACKAAVHNLLAQRVSGLIIN
YPLDDQDAIAVEAACTNVPALFLDVSDQTPINSIIFSHEDGTRLGVEHLVALGHQQIALLAGPLS
SVSARLRLAGWHKYLTRNQIQPIAEREGDWSAMSGFQQTMQMLNEGIVPTAMLVANDQMALGAMR
AITESGLRVGADISVVGYDDTEDSSCYIPPLTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLP
VSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRL
>d1byka_ c.93.1.1 (A:) Trehalose repressor, C-terminal domain

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{Escherichia coli}
SDKVVAIIVTRLDSLSENLAVQTMLPAFYEQGYDPIMMESQFSPQLVAEHLGVLKRRNIDGVVLF
GFTGITEEMLAHWQSSLVLLARDAKGFASVCYDDEGAIKILMQRLYDQGHRNISYLGVPHSDVTT
GKRRHEAYLAFCKAHKLHPVAALPGLAMKQGYENVAKVITPETTALLCATDTLALGASKYLQEQR
IDTLQLASVGNTPLMKFLHPEIVTVDPGYAEAGRQAACQLIAQVTGRSEPQQIIIPATLS
>d2liv__ c.93.1.1 (-) Leucine-,isoleucine-,valine-binding (LIV)
protein {Escherichia coli}
EDIKVAVVGAMSGPVAQYGDQEFTGAEQAVADINAKGGIKGNKLQIAKYDDACDPKQAVAVANKV
VNDGIKYVIGHLCSSSTQPASDIYEDEGILMITPAATAPELTARGYQLILRTTGLDSDQGPTAAK
YILEKVKPQRIAIVHDKQQYGEGLARAVQDGLKKGNANVVFFDGITAGEKDFSTLVARLKKENID
FVYYGGYHPEMGQILRQARAAGLKTQFMGPEGVANVSLSNIAGESAEGLLVTKPKNYDQVPANKP
IVDAIKAKKQDPSGAFVWTTYAALQSLQAGLNQSDDPAEIAKYLKANSVDTVMGPLTWDEKGDLK
GFEFGVFDWHANGTATDAK
>d2lbp__ c.93.1.1 (-) Leucine-binding protein {Escherichia coli}
DDIKVAVVGAMSGPIAQWGIMEFNGAEQAIKDINAKGGIKGDKLVGVEYDDACDPKQAVAVANKI
VNDGIKYVIGHLCSSSTQPASDIYEDEGILMISPGATAPELTQRGYQHIMRTAGLDSSQGPTAAK
YILETVKPQRIAIIHDKQQYGEGLARSVQDGLKAANANVVFFDGITAGEKDFSALIARLKKENID
FVYYGGYYPEMGQMLRQARSVGLKTQFMGPEGVGNASLSNIAGDAAEGMLVTMPKRYDQDPANQG
IVDALKADKKDPSGPYVWITYAAVQSLATALERTGSDEPLALVKDLKANGANTVIGPLNWDEKGD
LKGFDFGVFQWHADGSSTKAK
>d1dp4a_ c.93.1.1 (A:) Hormone binding domain of the atrial natriuretic
peptide receptor {Rat (Rattus norvegicus)}
SDLTVAVVLPLTNTSYPWSWARVGPAVELALARVKARPDLLPGWTVRMVLGSSENAAGVCSDTAA
PLAAVDLKWEHSPAVFLGPGCVYSAAPVGRFTAHWRVPLLTAGAPALGIGVKDEYALTTRTGPSH
VKLGDFVTALHRRLGWEHQALVLYADRLGDDRPCFFIVEGLYMRVRERLNITVNHQEFVEGDPDH
YPKLLRAVRRKGRVIYICSSPDAFRNLMLLALNAGLTGEDYVFFHLDVFGQSLKSAQGLVPQKPW
ERGDGQDRSARQAFQAAKIITYKEPDNPEYLEFLKQLKLLADKKFNFTVEDGLKNIIPASFHDGL
LLYVQAVTETLAQGGTVTDGENITQRMWNRSFQGVTGYLKIDRNGDRDTDFSLWDMDPETGAFRV
VLNYNGTSQELMAVSEHKLYWPLGYPPPDVPKCGF
>d1jdpa_ c.93.1.1 (A:) Hormone binding domain of the atrial natriuretic
peptide receptor {Human (Homo sapiens)}
EALPPQKIEVLVLLPQDDSYLFSLTRVRPAIEYALRSVEGNGTGRRLLPPGTRFQVAYEDSDCGN
RALFSLVDRVAAARGAKPDLILGPVCEYAAAPVARLASHWDLPMLSAGALAAGFQHKDSEYSHLT
RVAPAYAKMGEMMLALFRHHHWSRAALVYSDDKLERNCYFTLEGVHEVFQEEGLHTSIYSFDETK
DLDLEDIVRNIQASERVVIMCASSDTIRSIMLVAHRHGMTSGDYAFFNIELFNSSSYGDGSWKRG
DKHDFEAKQAYSSLQTVTLLRTVKPEFEKFSMEVKSSVEKQGLNMEDYVNMFVEGFHDAILLYVL
ALHEVLRAGYSKKDGGKIIQQTWNRTFEGIAGQVSIDANGDRYGDFSVIAMTDVEAGTQEVIGDY
FGKEGRFEMRP
>d1ewka_ c.93.1.1 (A:) Metabotropic glutamate receptor subtype 1 {Rat
(Rattus norvegicus)}
RSVARMDGDVIIGALFSVHHQPPAEKVPERKCGEIREQYGIQRVEAMFHTLDKINADPVLLPNIT
LGSEIRDSCWHSSVALEQSIEFIRDSLISIRDEKDGLNRCLPDGQTLPPGRTKKPIAGVIGPGSS
SVAIQVQNLLQLFDIPQIAYSATSIDLSDKTLYKYFLRVVPSDTLQARAMLDIVKRYNWTYVSAV
HTEGNYGESGMDAFKELAAQEGLCIAHSDKIYSNAGEKSFDRLLRKLRERLPKARVVVCFCEGMT
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VRGLLSAMRRLGVVGEFSLIGSDGWADRDEVIEGYEVEANGGITIKLQSPEVRSFDDYFLKLRLD
TNTRNPWFPEFWQHRFQCRLPGHLLENPNFKKVCTGNESLEENYVQDSKMGFVINAIYAMAHGLQ
NMHHALCPGHVGLCDAMKPIDGRKLLDFLIKSSFVGVSGEEVWFDEKGDAPGRYDIMNLQYTEAN
RYDYVHVGTWHEGVLNIDDYKI

>d1jeta_ c.94.1.1 (A:) Oligo-peptide binding protein (OPPA) {Salmonella typhimurium}

ADVPAGVQLADKQTLVRNNGSEVQSLDPHKIEGVPESNVSRDLFEGLLISDVEGHPSPGVAEKWE
NKDFKVWTFHLRENAKWSDGTPVTAHDFVYSWQRLADPNTASPYASYLQYGHIANIDDIIAGKKP
ATDLGVKALDDHTFEVTLSEPVPYFYKLLVHPSVSPVPKSAVEKFGDKWTQPANIVTNGAYKLKN
WVVNERIVLERNPQYWDNAKTVINQVTYLPISSEVTDVNRYRSGEIDMTYNNMPIELFQKLKKEI
PNEVRVDPYLCTYYYEINNQKAPFNDVRVRTALKLALDRDIIVNKVKNQGDLPAYSYTPPYTDGA
KLVEPEWFKWSQQKRNEEAKKLLAEAGFTADKPLTFDLLYNTSDLHKKLAIAVASIWKKNLGVNV
NLENQEWKTFLDTRHQGTFDVARAGWCADYNEPTSFLNTMLSDSSNNTAHYKSPAFDKLIADTLK
VADDTQRSELYAKAEQQLDKDSAIVPVYYYVNARLVKPWVGGYTGKDPLDNIYVKNLYIIKH

>d1pda_1 c.94.1.1 (3-219) Porphobilinogen deaminase (hydroxymethylbilane synthase), N-terminal domain {Escherichia coli}

DNVLRIATRQSPLALWQAHYVKDKLMASHPGLVVELVPMVTRGDVILDTPLAKVGGKGLFVKELE
VALLENRADIAVHSMKDVPVEFPQGLGLVTICEREDPRDAFVSNNYDSLDALPAGSIVGTSSLRR
QCQLAERRPDLIIRSLRGNVGTRLSKLDNGEYDAIILAVAGLKRLGLESRIRAALPPEISLPAVG
QGAVGIECRLDDSRTRELLAAL

>d1lst__ c.94.1.1 (-) Lysine-,arginine-,ornithine-binding (LAO) protein {Salmonella typhimurium}

ALPQTVRIGTDTTYAPFSSKDAKGEFIGFDIDLGNEMCKRMQVKCTWVASDFDALIPSLKAKKID
AIISSLSITDKRQQEIAFSDKLYAADSRLIAAKGSPIQPTLESLKGKHVGVLQGSTQEAYANDNW
RTKGVDVVAYANQDLIYSDLTAGRLDAALQDEVAASEGFLKQPAGKEYAFAGPSVKDKKYFGDGT
GVGLRKDDTELKAAFDKALTELRQDGTYDKMAKKYFDFNVYGDK

>d1sbp__ c.94.1.1 (-) Sulphate-binding protein {Salmonella typhimurium}

KDIQLLNVSYDPTRELYEQYNKAFSAHWKQETGDNVVIDQSHGGSGKQATSVINGIEADTVTLAL
AYDVNAIAERGRIDKNWIKRLPDDSAPYTSTIVFLVRKGNPKQIHDWNDLIKPGVSVITPNPKSS
GGARWNYLAAWGYALHHNNNDQAKAEDFVKALFKNVEVLDSGARGSTNTFVERGIGDVLIAWENE
ALLATNELGKDKFEIVTPSESILAEPTVSVVDKVVEKKDTKAVAEAYLKYLYSPEGQEIAAKNFY
RPRDADVAKKYDDAFPKLKLFTIDEVFGGWAKAQKDHFADGGTFDQISK

>d1ixh__ c.94.1.1 (-) Phosphate-binding protein {Escherichia coli}

EASLTGAGATFPAPVYAKWADTYQKETGNKVNYQGIGSSGGVKQIIANTVDFGASDAPLSDEKLA
QEGLFQFPTVIGGVVLAVNIPGLKSGELVLDGKTLGDIYLGKIKKWDDEAIAKLNPGLKLPSQNI
AVVRRADGSGTSFVFTSYLAKVNEEWKNNVGTGSTVKWPIGLGGKGNDGIAAFVQRLPGAIGYVE
YAYAKQNNLAYTKLISADGKPVSPTEENFANAAKGADWSKTFAQDLTNQKGEDAWPITSTTFILI
HKDQKKPEQGTEVLKFFDWAYKTGAKQANDLDYASLPDSVVEQVRAAWKTNIKDSSGKPLY

>d3mbp__ c.94.1.1 (-) D-maltodextrin-binding protein, MBP {Escherichia coli}

KIEEGKLVIWINGDKGYNGLAEVGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPDIIFWAHD
RFGGYAQSGLLAEITPDKAFQDKLYPFTWDAVRYNGKLIAYPIAVEALSLIYNKDLLPNPPKTWE
EIPALDKELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENGKYDIKDVGVDNAGAKAGLTFL

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VDLIKNKHMNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSKVNYGVTVLPTFKGQPSKPFVG
VLSAGINAASPNKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRIAATMENAQ
KGEIMPNIPQMSAFWYAVRTAVINAASGRQTVDEALKDAQTRITK
>d1elja_ c.94.1.1 (A:) D-maltodextrin-binding protein, MBP {Archaeon
Pyrococcus furiosus}
MKIEEGKVVIWHAMQPNELEVFQSLAEEYMALCPEVEIVFEQKPNLEDALKAAIPTGQGPDLFIW
AHDWIGKFAEAGLLEPIDEYVTEDLLNEFAPMAQDAMQYKGHYYALPFAAETVAIIYNKEMVSEP
PKTFDEMKAIMEKYYDPANEKYGIAWPINAYFISAIAQAFGGYYFDDKTEQPGLDKPETIEGFKF
FFTEIWPYMAPTGDYNTQQSIFLEGRAPMMVNGPWSINDVKKAGINFGVVPLPPIIKDGKEYWPR
PYGGVKLIYFAAGIKNKDAAWKFAKWLTTSEESIKTLALELGYIPVLTKVLDDPEIKNDPVIYGF
GQAVQHAYLMPKSPKMSAVWGGVDGAINEILQDPQNADIEGILKKYQQEILNNMQ
>d1eu8a_ c.94.1.1 (A:) D-maltodextrin-binding protein, MBP {Archaeon
Thermococcus litoralis}
IEEGKIVFAVGGAPNEIEYWKGVIAEFEKKYPGVTVELKRQATDTEQRRLDLVNALRGKSSDPDV
FLMDVAWLGQFIASGWLEPLDDYVQKDNYDLSVFFQSVINLADKQGGKLYALPVYIDAGLLYYRK
DLLEKYGYSKPPETWQELVEMAQKIQSGERETNPNFWGFVWQGKQYEGLVCDFVEYVYSNGGSLG
EFKDGKWVPTLNKPENVEALQFMVDLIHKYKISPPNTYTEMTEEPVRLMFQQGNAAFERNWPYAW
GLHNADDSPVKGKVGVAPLPHFPGHKSAATLGGWHIGISKYSDNKALAWEFVKFVESYSVQKGFA
MNLGWNPGRVDVYDDPAVVSKSPHLKELRAVFENAVPRPIVPYYPQLSEIIQKYVNSALAGKISP
QEALDKAQKEAEELVKQ
>d3thia_ c.94.1.1 (A:) Thiaminase I {Paenibacillus thiaminolyticus}
ITLKVAIYPYVPDPARFQAAVLDQWQRQEPGVKLEFTDWDSYSADPPDDLDVFVLDSIFLSHFVD
AGYLLPFGSQDIDQAEDVLPFALQGAKRNGEVYGLPQILCTNLLFYRKGDLKIGQVDNIYELYKK
IGTSHSEQIPPPQNKGLLINMAGGTTKASMYLEALIDVTGQYTEYDLLPPLDPLNDKVIRGLRLL
INMAGEKPSQYVPEDGDAYVRASWFAQGSGRAFIGYSESMMRMGDYAEQVRFKPISSSAGQDIPL
FYSDVVSVNSKTAHPELAKKLANVMASADTVEQALRPQADGQYPQYLLPARHQVYEALMQDYPIY
SELAQIVNKPSNRVFRLGPEVRTWLKDAKQVLPEALG
>d1mrp__ c.94.1.1 (-) Ferric-binding protein {Haemophilus influenzae}
DITVYNGQHKEAATAVAKAFEQETGIKVTLNSGKSEQLAGQLKEEGDKTPADVFYTEQTATFADL
SEAGLLAPISEQTIQQTAQKGVPLAPKKDWIALSGRSRVVVYDHTKLSEKDMEKSVLDYATPKWK
GKIGYVSTSGAFLEQVVALSKMKGDKVALNWLKGLKENGKLYAKNSVALQAVENGEVPAALINNY
YWYNLAKEKGVENLKSRLYFVRHQDPGALVSYSGAAVLKASKNQAEAQKFVDFLASKKGQEALVA
ARAEYPLRADVVSPFNLEPYEKLEAPVVSATTAQDKEHAIKLIEEAGLK
>d1d9ya_ c.94.1.1 (A:) Ferric-binding protein {Neisseria gonorrhoeae}
DITVYNGQHKEAAQAVADAFTRATGIKVKLNCAKGDQLAGQIKEEGSRSPADVFYSEQIPALATL
SAANLLEPLPASTINETRGKGVPVAAKKDWVALSGRSRVVVYDTRKLSEKDLEKSVLNYATPKWK
NRIGYVPTSGAFLEQIVAIVKLKGEAAALKWLKGLKEYGKPYAKNSVALQAVENGEIDAALINNY
YWHAFAREKGVQNVHTRLNFVRHRDPGALVTYSGAAVLKSSQNKDEAKKFVAFLAGKEGQRALTA
VRAEYPLNPHVVSTFNLEPIAKLEAPQVSATTVSEKEHATRLLEQAGMK
>d1dpe__ c.94.1.1 (-) Dipeptide-binding protein {Escherichia coli}
KTLVYCSEGSPEGFNPQLFISGTTYDASSVPLYNRLVEFKIGTTEVIPGLAEKWEVSEDGKTYTF
HLRKGVKWHDNKEFKPTRELNADDVVFSFDRQKNAQNPYHKVSGGSYEYFEGMGLPELISEVKKV
DDNTVQFVLTRPEAPFLADLAMDFASILSKEYADAMMKAGTPEKLDLNPIGTGPFQLQQYQKDSR
IRYKAFDGYWGTKPQIDTLVFSITPDASVRYAKLQKNECQVMPYPNPADIARMKQDKSINLMEMP
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GLNVGYLSYNVQKKPLDDVKVRQALTYAVNKDAIIKAVYQGAGVSAKNLIPPTMWGYNDDVQDYT
YDPEKAKALLKEAGLEKGFSIDLWAMPVQRPYNPNARRMAEMIQADWAKVGVQAKIVTYEWGEYL
KRAKDGEHQTVMMGWTGDNGDPDNFFATEFSCAASEQGSNYSKWCYKPFEDLIQPARATDDHNKR
VELYKQAQVVMHDQAPALIIAHSTVFEPVRKEVKGYVVDPLGKHHFENVSIE
>d1hsla_ c.94.1.1 (A:) Histidine-binding protein {Escherichia coli}
AIPQKIRIGTDPTYAPFESKNAQGELVGFDIDLAKELCKRINTQCTFVENPLDALIPSLKAKKID
AIMSSLSITEKRQQEIAFTDKLYAADSRLVVAKNSDIQPTVASLKGKRVGVLQGTTQETFGNEHW
APKGIEIVSYQGQDNIYSDLTAGRIDAAFQDEVAASEGFLKQPVGKDYKFGGPAVKDEKLFGVGT
GMGLRKEDNELREALNKAFAEMRADGTYEKLAKKYFDFDVYGG
>d1pot__ c.94.1.1 (-) Spermidine/putrescine-binding protein PotD {Escherichia coli}
NNTLYFYNWTEYVPPGLLEQFTKETGIKVIYSTYESNETMYAKLKTYKDGAYDLVVPSTYYVDKM
RKEGMIQKIDKSKLTNFSNLDPDMLNKPFDPNNDYSIPYIWGATAIGVNGDAVDPKSVTSWADLW
KPEYKGSLLLTDDAREVFQMALRKLGYSGNTTDPKEIEAAYNELKKLMPNVAAFNSDNPANPYME
GEVNLGMIWNGSAFVARQAGTPIDVVWPKEGGIFWMDSLAIPANAKNKEGALKLINFLLRPDVAK
QVAETIGYPTPNLAARKLLSPEVANDKTLYPDAETIKNGEWQNDVGAASSIYEEYYQKLKAG
>d1a99a_ c.94.1.1 (A:) Putrescine receptor (PotF) {Escherichia coli}
QKTLHIYNWSDYIAPDTVANFEKETGIKVVYDVFDSNEVLEGKLMAGSTGFDLVVPSASFLERQL
TAGVFQPLDKSKLPEWKNLDPELLKLVAKHDPDNKFAMPYMWATTGIGYNVDKVKAVLGENAPVD
SWDLILKPENLEKLKSCGVSFLDAPEEVFATVLNYLGKDPNSTKADDYTGPATDLLLKLRPNIRY
FHSSQYINDLANGDICVAIGWAGDVWQASNRAKEAKNGVNVSFSIPKEGAMAFFDVFAMPADAKN
KDEAYQFLNYLLRPDVVAHISDHVFYANANKAATPLVSAEVRENPGIYPPADVRAKLFTLKVQDP
KIDRVRTRAWTKVKSG
>d1wdna_ c.94.1.1 (A:) Glutamine-binding protein {Escherichia coli}
KLVVATDTAFVPFEFKQGDLYVGFDVDLWAAIAKELKLDYELKPMDFSGIIPALQTKNVDLALAG
ITITDERKKAIDFSDGYYKSGLLVMVKANNNDVKSVKDLDGKVVAVKSGTGSVDYAKANIKTKDL
RQFPNIDNAYMELGTNRADAVLHDTPNILYFIKTAGNGQFKAVGDSLEAQQYGIAFPKGSDELRD
KVNGALKTLRENGTYNEIYKKWFGTEPK
>d1ftka_ c.94.1.1 (A:) Glutamate receptor ligand binding core {Rat (Rattus norvegicus), GluR2}
KTVVVTTILESPYVMMKKNHEMLEGNERYEGYCVDLAAEIAKHCGFKYKLTIVGDGKYGARDADT
KIWNGMVGELVYGKADIAIAPLTITLVREEVIDFSKPFMSLGISIMIKKPGTDGNPIESAEDLSK
QTEIAYGTLDSGSTKEFFRRSKIAVFDKMWTYMRSAEPSVFVRTTAEGVARVRKSKGKYAYLLES
TMNEYIEQRKPCDTMKVGGNLDSKGYGIATPKGSSLGNAVNLAVLKLNEQGLLDKLKNKWWYDKG
EC
>d1ii5a_ c.94.1.1 (A:) Glutamate receptor ligand binding core {Synechocystis sp., GluR0}
GSAMALKVGVVGNPPFVFYGEGKNAAFTGISLDVWRAVAESQKWNSEYVRQNSISAGITAVAEGE
LDILIGPISVTPERAAIEGITFTQPYFSSGIGLLIPGTATPLFRSVGDLKNKEVAVVRDTTAVDW
ANFYQADVRETNNLTAAITLLQKKQVEAVMFDRPALIYYTRQNPNLNLEVTEIRVSLEPYGFVLK
ENSPLQKTINVEMLNLLYSRVIAEFTERWLG
>d1amf__ c.94.1.1 (-) Molybdate-binding protein, ModA {Escherichia coli}
GKITVFAAASLTNAMQDIATQFKKEKGVDVVSSFASSSTLARQIEAGAPADLFISADQKWMDYAV

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DKKAIDTATRQTLLGNSLVVVAPKASVQKDFTIDSKTNWTSLLNGGRLAVGDPEHVPAGIYAKEA
LQKLGAWDTLSPKLAPAEDVRGALALVERNEAPLGIVYGSDAVASKGVKVVATFPEDSHKKVEYP
VAVVEGHNNATVKAFYDYLKGPQAAEIFKRYGFTIK
>d1atg__ c.94.1.1 (-) Molybdate-binding protein, ModA {Azotobacter
vinelandii}
ELKVVTATNFLGTLEQLAGQFAKQTGHAVVISSGSSGPVYAQIVNGAPYNVFFSADEKSPEKLDN
QGFALPGSRFTYAIGKLVLWSAKPGLVDNQGKVLAGNGWRHIAISNPQIAPYGLAGTQVLTHLGL
LDKLTAQERIVEANSVGQAHSQTASGAADLGFVALAQIIQAAAKIPGSHWFPPANYYEPIVQQAV
ITKSTAEKANAEQFMSWMKGPKAVAIIKAAGYVLPQ
>d1al3__ c.94.1.1 (-) Cofactor-binding fragment of CysB {Klebsiella
aerogenes}
TWPDKGSLYVATTHTQARYALPGVIKGFIERYPRVSLHMHQGSPTQIAEAVSKGNADFAIATEAL
HLYDDLVMLPCYHWNRSIVVTPEHPLATKGSVSIEELAQYPLVTYTFGFTGRSELDTAFNRAGLT
PRIVFTATDADVIKTYVRLGLGVGVIASMAVDPVSDPDLVKLDANGIFSHSTTKIGFRRSTFLRS
YMYDFIQRFAPHLTRDVVDTAVALRSNEDIEAMFKDIKLPEK
>d1i6aa_ c.94.1.1 (A:) Hydrogen peroxide-inducible genes activator
OxyR, regulatory domain {Escherichia coli}
ETMSGPLHIGLIPTVGPYLLPHIIPMLHQTFPKLEMYLHEAQTHQLLAQLDSGKLDAVILALVKE
SEAFIEVPLFDEPMLLAIYEDHPWANREAVPMADLAGEKLLMLEDGHCLRDQAMGFCFEAGADED
THFRATSLETLRNMVAAGSGITLLPALAVPPERKRDGVVYLPAIKPEPRRTIGLVYRPGSPLRSR
YEQLAEAIRARMDGHFD
>d1kwha_ c.94.1.1 (A:) Alginate-binding periplasmic protein AlgQ2
{Sphingomonas sp.}
KEATWVTDKPLTLKIHMHFRDKWVWDENWPVAKESFRLTNVKLQSVANKAATNSQEQFNLMMASG
DLPDVVGGDNLKDKFIQYGQEGAFVPLNKLIDQYAPHIKAFFKSHPEVERAIKAPDGNIYFIPYV
PDGVVARGYFIREDWLKKLNLKPPQNIDELYTVLKAFKEKDPNGNGKADEVPFIDRHPDEVFRLV
NFWGARSSGSDNYMDFYIDNGRVKHPWAETAFRDGMKHVAQWYKEGLIDKEIFTRKAKAREQMFG
GNLGGFTHDWFASTMTFNEGLAKTVPGFKLIPIAPPTNSKGQRWEEDSRQKVRPDGWAITVKNKN
PVETIKFFDFYFSRPGRDISNFGVPGVTYDIKNGKAVFKDSVLKSPQPVNNQLYDMGAQIPIGFW
QDYDYERQWTTPEAQAGIDMYVKGKYVMPGFEGVNMTREERAIYDKYWADVRTYMYEMGQAWVMG
TKDVDKTWDEYQRQLKLRGLYQVLQMMQQAYDRQYKN
>d1cb6a2 c.94.1.2 (A:1335-1691) Lactoferrin {Human (Homo sapiens)}
EEEVAARRARVVWCAVGEQELRKCNQWSGLSEGSVTCSSASTTEDCIALVLKGEADAMSLDGGYV
YTAGKCGLVPVLAENYKSQQSSDPDPNCVDRPVEGYLAVAVVRRSDTSLTWNSVKGKKSCHTAVD
RTAGWNIPMGLLFNQTGSCKFDEYFSQSCAPGSDPRSNLCALCIGDEQGENKCVPNSNERYYGYT
GAFRCLAENAGDVAFVKDVTVLQNTDGNNNEAWAKDLKLADFALLCLDGKRKPVTEARSCHLAMA
PNHAVVSRMDKVERLKQVLLHQQAKFGRNGSDCPDKFCLFQSETKNLLFNDNTECLARLHGKTTY
EKYLGPQYVAGITNLKKCSTSPLLEACEFLRK
>d1lct__ c.94.1.2 (-) Lactoferrin {Human (Homo sapiens)}
RSVQWCAVSNPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQAIAENRADAVTLDGGFIYEAG
LAPYKLRPVAAEVYGTERQPRTHYYAVAVVKKGGSFQLNELQGLKSCHTGLRRTAGWNVPIGTLR
PFLNWTGPPEPIEAAVARFFSASCVPGADKGQFPNLCRLCAGTGENKCAFSSQEPYFSYSGAFKC
LRDGAGDVAFIRESTVFEDLSDEAERDEYELLCPDNTRKPVDKFKDCHLARVPSHAVVARSVNGK
EDAIWNLLRQAQEKFGKDKSPKFQLFGSPSGQKDLLFKDSAIGFSRVPPRIDSGLYLGSGYFTA
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>d1lgbc_ c.94.1.2 (C:) Lactoferrin {Human (Homo sapiens)}
HYYAVAVVKKGGSFQLNELQGLKSCHTGLRRTAGWNVPIGTLRPFLNWTGPPEPIEAAVARFFSA
SCVPGADKGQFPNLCRLCAGTGENKCAFSSQEPYFSYSGAFKCLKDGAGDVAFIRESTVFEDLSD
EAERDEYELLCPDNTRKPVDKFKDCHLAR
>d1ce2a1  c.94.1.2  (A:1-333)  Lactoferrin  {Domestic  water  buffalo
(Bubalus arnee bubalis)}
APRKNVRWCTISQPEWLKCHRWQWRMKKLGAPSITCVRRASVLECIRAITEKKADAVTLDGGMVF
EAGRDPYKLRPVAAEIYGTKESPQTHYYAVAVVKKGSNFQLDQLQGRNSCHTGLGRSAGWNIPMG
ILRPYLSWTESLEPLQGAVAKFFSASCVPCVDRQAYPNLCQLCKGEGENQCACSPREPYFGYSGA
FKCLQDGAGDVAFVKETTVFENLPEKADRDQYELLCLNNTRAPVDAFKECHLAQVPSHAVVARSV
DGKEDLIWKLLSKAQEKFGKNKSGSFQLFGSPPGQRDLLFKDSALGFLRIPSKVDSALYLGSRYL
TALKNLRE
>d1ce2a2 c.94.1.2 (A:334-689) Lactoferrin {Domestic water buffalo
(Bubalus arnee bubalis)}
TAEEVQARRARVVWCAVGPEEQKKCQQWSQQSGQIVTCATASTTDDCIALVLKGEADALSLDGGY
IYTAGKCGLVPVLAENRKSSKHSSLDCVLRPTEGYLAVAVVKKANEGLTWNSLKGKKSCHTAVDR
TAGWNIPMGLIANQTGSCAFDEFFSQSCAPGADPKSRLCALCAGDDQGLDKCVPNSKEKYYGYTG
AFRCLAEDVGDVAFVKNDTVWENTNGESTADWAKNLNREDFRLLCLDGTRKPVTEAQSCHLAVAP
NHAVVSLSERAAHVEQVLLHQQALFGENGKNCPDKFCLFKSETKNLLFNDNTECLAKLGGRPTYE
EYLGTEYVTAIANLKKCSTSPLLEACAFLTR
>d1b1xa1 c.94.1.2 (A:1-333) Lactoferrin {Horse (Equus caballus)}
APRKSVRWCTISPAEAAKCAKFQRNMKKVRGPSVSCIRKTSSFECIQAIAANKADAVTLDGGLVY
EAGLHPYKLRPVAAEVYQTRGKPQTRYYAVAVVKKGSGFQLNQLQGVKSCHTGLGRSAGWNIPIG
TLRPYLNWTGPPEPLQKAVANFFSASCVPCADGKQYPNLCRLCAGTEADKCACSSQEPYFGYSGA
FKCLENGAGDVAFVKDSTVFENLPDEAERDKYELLCPDNTRKPVDAFKECHLARVPSHAVVARSV
DGREDLIWKLLHRAQEEFGRNKSSAFQLFGSTPGEQDLLFKDSALGFVRIPSQIDSGLYLGANYL
TATQNLRE
>d1b1xa2 c.94.1.2 (A:334-689) Lactoferrin {Horse (Equus caballus)}
TAAEVAARRERVVWCAVGPEEERKCKQWSDVSNRKVACASASTTEECIALVLKGEADALNLDGGF
IYVAGKCGLVPVLAENQKSQNSNAPDCVHRPPEGYLAVAVVRKSDADLTWNSLSGKKSCHTGVGR
TAAWNIPMGLLFNQTGSCKFDKFFSQSCAPGADPQSSLCALCVGNNENENKCMPNSEERYYGYTG
AFRCLAEKAGDVAFVKDVTVLQNTDGKNSEPWAKDLKQEDFELLCLDGTRKPVAEAESCHLARAP
NHAVVSQSDRAQHLKKVLFLQQDQFGGNGPDCPGKFCLFKSETKNLLFNDNTECLAELQGKTTYE
QYLGSEYVTSITNLRRCSSSPLLEACAFLRA
>d1dtza1  c.94.1.2  (A:1-333)  Lactoferrin  {Arabian  camel  (Camelus
dromedarius)}
ASKKSVRWCTTSPAESKKCAQWQRRMKKVRGPSVTCVKKTSRFECIQAISTEKADAVTLDGGLVY
DAGLDPYKLRPIAAEVYGTENQPQTHYYAVAIAKKGTNFQLNQLQGLKSCHTGLGRSAGWNIPMG
LLRPFLDWTGPPEPLQKAVAKFFSASCVPCVDGKEYPNLCQLCAGTGENKCACSSQEPYFGYSGA
FKCLQDGAGDVAFVKDSTVFESLPAKADRDQYELLCPNNTRKPVDAFQECHLARVPSHAVVARSV
NGKEDLIWKLLVKAQEKFGRGKPSAFQLFGSPAGQKDLLFKDSALGLLRIPKKIDSGLYLGSNYI
TAIRGLRE
>d1dtza2 c.94.1.2 (A:334-689) Lactoferrin {Arabian camel (Camelus
dromedarius)}
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TAAEVELRRAQVVWCAVGSDEQLKCQEWSRQSNQSVVCATASTTEDCIALVLKGEADALSLDGGY
IYIAGKCGLVPVLAESQQSPESSGLDCVHRPVKGYLAVAVVRKANDKITWNSLRGKKSCHTAVDR
TAGWNIPMGPLFKDTDSCRFDEFFSQSCAPGSDPRSKLCALCAGNEEGQLKCVPNSSERLYGYTG
AFRCLAENVGDVAFVKDVTVLDNTDGKGTEQWAKDLKLGDFELLCLNGTRKPVTEAESCHLPVAP
NHAVVSRIDKVAHLRQVLLRQQAHFGRNGEDCPGKFCLFQSKTKNLLFNDNTECLAKLQGKTTYD
EYLGPQYVTAIAKLRRCSTSPLLEACAFLMR
>d1dot_1 c.94.1.2 (1-334) Ovotransferrin {Duck (Anas platyrhynchos)}
APPKTTVRWCTISSAEEKKCNSLKDHMQQERVTLSCVQKATYLDCIKAISNNEADAISLDGGQVF
EAGLAPYKLKPIAAEVYERSGGSTTSYYAVAVVKKGTDFMIKDLRGKTSCHTGLGRSAGWNIPIG
TLIHREDIEWEGIESGISEQAVAKFFSASCVPGATIEQKLCRQCKGDAKTKCLRNGPYSGYSGAF
QCLKDGKGDVAFVKHTTVQENAPEEKDEYELLCLDGSRQPVDSYKTCNWARVAAHAVVARDDSKI
DDIWSFLGMQAYSLGVDTTSDFHLFGPPGKKDPVLKDLLFKDSAIMLKRVPELMDSQLYLGFEYY
SAIQSLRKD
>d1dot_2 c.94.1.2 (335-686) Ovotransferrin {Duck (Anas
platyrhynchos)}
QLTVGPRENKIQWCAVGKDEKSKCDRWSVVSNGEVECTILDDNKDCIVKITKGEADAISLDGGFV
YTAGVCGLVPVVGESYEDETQCSKDEEQPAYYFAVAVVKKSSAITWNNLQGKKSCHTAVGRTAGW
NIPMGLIHNKTGSCDFDDYFSEGCAPGSPPNSRLCKLCQGSGENLLEKCVASSHEKYYGYTGALR
CLVEQGDVAFIKHSTVGENVSGSNKDDWAKGLTRDDFELLCTNGKRAKTMDYKTCHLAKVPTHAV
VARPEKANKIRELLEGQEKLFGLHGTEKERFMMFQSQTKDLLFKALTKCLVKLRQGITYKEFLGD
EYYASVASLNTCNPSDLLQVCTFLEDK
>d1gv8a_ c.94.1.2 (A:) Ovotransferrin {Duck (Anas platyrhynchos)}
SYYAVAVVKKGTDFMIKDLRGKTSCHTGLGRSAGWNIPIGTLIHRGDIEWEGIESGSVEQAVAKF
FSASCVPGATTEQKLCRQCKGDAKTKCLRNAPYSGYSGAFQCLKDGKGDVAFVKHTTVQENAPEE
KDEYELLCLDGTRQPVDSYKTCNWARVAA
>d1ieja_ c.94.1.2 (A:) Ovotransferrin {Chicken (Gallus gallus)}
KSVIRWCTISSPEEKKCNNLRDLTQQERISLTCVQKATYLDCIKAIANNEADAITLDGGQVFEAG
LAPYKLKPIAAEVYEHTEGSTTSYYAVAVVKKGTEFTVNDLQGKTSCHTGLGRSAGWNIPIGTLL
HRGAIEWEGIESGSVEQAVAKFFSASCVPGATIEQKLCRQCKGDPKTKCARNAPYSGYSGAFHCL
KDGKGDVAFVKHTTVNENAPDQKDEYELLCLDGSRQPVDNYKTCNWARVAAHAVVARDDNKVEDI
WSFLSKAQSDFGVDTKSDFHLFGPPGKKDPVLKDLLFKDSAIMLKRVPSLMDSQLYLGFEYYSAI
QSMR
>d1iq7a_ c.94.1.2 (A:) Ovotransferrin {Chicken (Gallus gallus)}
RIQWCAVGKDEKSKCDRWSVVSNGDVECTVVDETKDCIIKIMKGEADAVALDGGLVYTAGVCGLV
PVMAERYDDESQCSKTDERPASYFAVAVARKDSNVNWNNLKGKKSCHTAVGRTAGWVIPMGLIHN
RTGTCNFDEYFSEGCAPGSPPNSRLCQLCQGSGGIPPEKCVASSHEKYFGYTGALRCLVEKGDVA
FIQHSTVEENTGGKNKADWAKNLQMDDFELLCTDGRRANVMDYRECNLAEVPTHAVVVRPEKANK
IRDLLERQEKRFGVNGSEKSKFMMFESQNKDLLFKDLTKCLFKVREGTTYKEFLGDKFYTVISSL
KTCNPSDILQMCSFLEGK
>d1jnfa1 c.94.1.2 (A:3-334) Transferrin {Rabbit (Oryctolagus
cuniculus)}
EKTVRWCAVNDHEASKCANFRDSMKKVLPEDGPRIICVKKASYLDCIKAIAAHEADAVTLDAGLV
HEAGLTPNNLKPVVAEFYGSKENPKTFYYAVALVKKGSNFQLNELQGKKSCHTGLGRSAGWNIPI
GLLLCDLPEPRKPLEKAVASFFSGSCVPCADGADFPQLCQLCPGCGCSSVQPYFGYSGAFKCLKD
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GLGDVAFVKQETIFENLPSKDERDQYELLCLDNTRKPVDEYEQCHLARVPSHAVVARSVDGKEDL
IWELLNQAQEHFGKDKSGDFQLFSSPHGKNLLFKDSAYGFFKVPPRMDANLYLGYEYVTAVRNLR
EGICPDP
>d1jnfa2 c.94.1.2 (A:335-676) Transferrin {Rabbit (Oryctolagus
cuniculus)}
LQDECKAVKWCALGHHERLKCDEWSVTSGGLIECESAETPEDCIAKIMNGEADAMSLDGGYVYIA
GQCGLVPVLAENYESTDCKKAPEEGYLSVAVVKKSNPDINWNNLEGKKSCHTAVDRTAGWNIPMG
LLYNRINHCRFDEFFRQGCAPGSQKNSSLCELCVGPSVCAPNNREGYYGYTGAFRCLVEKGDVAF
VKSQTVLQNTGGRNSEPWAKDLKEEDFELLCLDGTRKPVSEAHNCHLAKAPNHAVVSRKDKAACV
KQKLLDLQVEFGNTVADCSSKFCMFHSKTKDLLFRDDTKCLVDLRGKNTYEKYLGADYIKAVSNL
RKCSTSRLLEACTFHKH
>d1tfd__ c.94.1.2 (-) Transferrin {Rabbit (Oryctolagus cuniculus)}
VRWCAVNDHEASKCANFRDSMKKVLPEDGPRIICVKKASYLDCIKAIAAHEADAVTLDAGLVHEA
GLTPNNLKPVVAEFYGSKENPKTFYYAVALVKKGSNFQLNELQGKKSCHTGLGRSAGWNIPIGLL
YCDLPEPRKPLEKAVASFFSGSCVPCADGADFPQLCQLCPGCGCSSSQPYFGYSGAFKCLKDGLG
DVAFVKQETIFENLPSKDERDQYELLCLDNTRKPVDEYEQCHLARVPSHAVVARSVDGKEDLIWE
LLNQAQEHFGKDKSGDFQLFSSPHGKNLLFKDSAYGFFK
>d1a8e__ c.94.1.2 (-) Transferrin {Human (Homo sapiens)}
DKTVRWCAVSEHEATKCQSFRDHMKSVIPSDGPSVACVKKASYLDCIRAIAANEADAVTLDAGLV
YDAYLAPNNLKPVVAEFYGSKEDPQTFYYAVAVVKKDSGFQMNQLRGKKSCHTGLGRSAGWNIPI
GLLYCDLPEPRKPLEKAVANFFSGSCAPCADGTDFPQLCQLCPGCGCSTLNQYFGYSGAFKCLKD
GAGDVAFVKHSTIFENLANKADRDQYELLCLDNTRKPVDEYKDCHLAQVPSHTVVARSMGGKEDL
IWELLNQAQEHFGKDKSKEFQLFSSPHGKDLLFKDSAHGFLKVPPRMDAKMYLGYEYVTAIRNLR
EGTC
>d1h76a1 c.94.1.2 (A:3-333) Transferrin {Pig (Sus scrofa)}
QKTVRWCTISNQEANKCSSFRENMSKAVKNGPLVSCVKKSSYLDCIKAIRDKEADAVTLDAGLVF
EAGLAPYNLKPVVAEFYGQKDNPQTHYYAVAVVKKGSNFQWNQLQGKRSCHTGLGRSAGWIIPMG
LLYDQLPEPRKPIEKAVASFFSSSCVPCADPVNFPKLCQQCAGKGAEKCACSNHEPYFGYAGAFN
CLKEDAGDVAFVKHSTVLENLPDKADRDQYELLCRDNTRRPVDDYENCYLAQVPSHAVVARSVDG
QEDSIWELLNQAQEHFGRDKSPDFQLFSSSHGKDLLFKDSANGFLKIPSKMDSSLYLGYQYVTAL
RNLREE
>d1h76a2 c.94.1.2 (A:342-687) Transferrin {Pig (Sus scrofa)}
ECKKVRWCAIGHEETQKCDAWSINSGGKIECVSAENTEDCIAKIVKGEADAMSLDGGYIYIAGKC
GLVPVLAENYKTEGENCVNTPEKGYLAVAVVKKSSGPDLNWNNLKGKKSCHTAVDRTAGWNIPMG
LLYNKINSCKFDQFFGEGCAPGSQRNSSLCALCIGSERAPGRECLANNHERYYGYTGAFRCLVEK
GDVAFVKDQVVQQNTDGKNKDDWAKDLKQMDFELLCQNGAREPVDNAENCHLARAPNHAVVARDD
KVTCVAEELLKQQAQFGRHVTDCSSSFCMFKSNTKDLLFRDDTQCLARVGKTTYESYLGADYITA
VANLRKCSTSKLLEACTFHSA
>d1afwa1 c.95.1.1 (A:25-293) Thiolase {Baker's yeast (Saccharomyces
cerevisiae)}
KNSLLEKRPEDVVIVAANRSAIGKGFKGAFKDVNTDYLLYNFLNEFIGRFPEPLRADLNLIEEVA
CGNVLNVGAGATEHRAACLASGIPYSTPFVALNRQCSSGLTAVNDIANKIKVGQIDIGLALGVES
MTNNYKNVNPLGMISSEELQKNREAKKCLIPMGITNENVAANFKISRKDQDEFAANSYQKAYKAK
NEGLFEDEILPIKLPDGSICQSDEGPRPNVTAESLSSIRPAFIKDRGTTTAGNASQVSDGVAGVL
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LARRSVANQ
>d1afwa2 c.95.1.1 (A:294-417) Thiolase {Baker's yeast (Saccharomyces
cerevisiae)}
LNLPVLGRYIDFQTVGVPPEIMGVGPAYAIPKVLEATGLQVQDIDIFEINEAFAAQALYCIHKLG
IDLNKVNPRGGAIALGHPLGCTGARQVATILRELKKDQIGVVSMCIGTGMGAAAIFIKE
>d1qfla1 c.95.1.1 (A:4-268) Biosynthetic thiolase {Zoogloea ramigera}
SIVIASAARTAVGSFNGAFANTPAHELGATVISAVLERAGVAAGEVNEVILGQVLPAGEGQNPAR
QAAMKAGVPQEATAWGMNQLCGSGLRAVALGMQQIATGDASIIVAGGMESMSMAPHCAHLRGGVK
MGDFKMIDTMIKDGLTDAFYGYHMGTTAENVAKQWQLSRDEQDAFAVASQNKAEAAQKDGRFKDE
IVPFIVKGRKGDITVDADEYIRHGATLDSMAKLRPAFDKEGTVTAGNASGLNDGAAAALLMSEAE
ASRRG
>d1qfla2 c.95.1.1 (A:269-392) Biosynthetic thiolase {Zoogloea
ramigera}
IQPLGRIVSWATVGVDPKVMGTGPIPASRKALERAGWKIGDLDLVEANEAFAAQACAVNKDLGWD
PSIVNVNGGAIAIGHPIGASGARILNTLLFEMKRRGARKGLATLCIGGGMGVAMCIESL
>d1ek4a1 c.95.1.1 (A:1-253) Beta-ketoacyl-ACP synthase I {Escherichia
coli}
MKRVVITGLGIVSSIGNNQQEVLASLREGRSGITFSQELKDSGMRSHVWGNVKLDTTGLIDRKVV
RFMSDASIYAFLSMEQAIADAGLSPEAYQNNPRVGLIAGSGGGSPRFQVFGADAMRGPRGLKAVG
PYVVTKAMASGVSACLATPFKIHGVNYSISSASATSAHCIGNAVEQIQLGKQDIVFAGGGEELCW
EMACEFDAMGALSTKYNDTPEKASRTYDAHRDGFVIAGGGGMVVVEELEHALARGAHI
>d1ek4a2 c.95.1.1 (A:254-406) Beta-ketoacyl-ACP synthase I
{Escherichia coli}
YAEIVGYGATSDGADMVAPSGEGAVRCMKMAMHGVDTPIDYLNSHGTSTPVGDVKELAAIREVFG
DKSPAISATKAMTGHSLGAAGVQEAIYSLLMLEHGFIAPSINIEELDEQAAGLNIVTETTDRELT
TVMSNSFGFGGTNATLVMRKLKD
>d1kas_1 c.95.1.1 (2-251) Beta-ketoacyl-ACP synthase II {Escherichia
coli}
KRRVVVTGLGMLSPVGNTVESTWKALLAGQSGISLIDHFDTSAYATKFAGLVKDFNCEDIISRKE
QRKMDAFIQYGIVAGVQAMQDSGLEITEENATRIGAAIGSGIGGLGLIEENHTSLMNGGPRKISP
FFVPSTIVNMVAGHLTIMYGLRGPSISIATACTSGVHNIGHAARIIAYGDADVMVAGGAEKASTP
LGVGGFGAARALSTRNDNPQAASRPWDKERDGFVLGDGAGMLVLEEYEHAKKRGA
>d1kas_2 c.95.1.1 (252-412) Beta-ketoacyl-ACP synthase II
{Escherichia coli}
KIYAELVGFGMSSDAYHMTSPPENGAGAALAMANALRDAGIEASQIGYVNAHGTSTPAGDKAEAQ
AVKTIFGEAASRVLVSSTKSMTGHLLGAAGAVESIYSILALRDQAVPPTINLDNPDEGCDLDFVP
HEARQVSGMEYTLCNSFGFGGTNGSLIFKKI
>d1e5ma1 c.95.1.1 (A:6-255) Beta-ketoacyl-ACP synthase II
{Synechocystis sp.}
KKRVVVTGLGAITPIGNTLQDYWQGLMEGRNGIGPITRFDASDQACRFGGEVKDFDATQFLDRKE
AKRMDRFCHFAVCASQQAINDAKLVINELNADEIGVLIGTGIGGLKVLEDQQTILLDKGPSRCSP
FMIPMMIANMASGLTAINLGAKGPNNCTVTACAAGSNAIGDAFRLVQNGYAKAMICGGTEAAITP
LSYAGFASARALSFRNDDPLHASRPFDKDRDGFVMGEGSGILILEELESALARGA
>d1e5ma2 c.95.1.1 (A:256-416) Beta-ketoacyl-ACP synthase II
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{Synechocystis sp.}
KIYGEMVGYAMTCDAYHITAPVPDGRGATRAIAWALKDSGLKPEMVSYINAHGTSTPANDVTETR
AIKQALGNHAYNIAVSSTKSMTGHLLGGSGGIEAVATVMAIAEDKVPPTINLENPDPECDLDYVP
GQSRALIVDVALSNSFGFGGHNVTLAFKKYQ
>d1hnja1 c.95.1.1 (A:1-174) Ketoacyl-ACP synthase III (FabH) {Escherichia coli}
MYTKIIGTGSYLPEQVRTNADLEKMVDTSDEWIVTRTGIRERHIAAPNETVSTMGFEAATRAIEM
AGIEKDQIGLIVVATTSATHAFPSAACQIQSMLGIKGCPAFDVAAACAGFTYALSVADQYVKSGA
VKYALVVGSDVLARTCDPTDRGTIIIFGDGAGAAVLAASEEPGI
>d1hnja2 c.95.1.1 (A:175-317) Ketoacyl-ACP synthase III (FabH) {Escherichia coli}
ISTHLHADGSYGELLTLPNADRVNPENSIHLTMAGNEVFKVAVTELAHIVDETLAANNLDRSQLD
WLVPHQANLRIISATAKKLGMSMDNVVVTLDRHGNTSAASVPCALDEAVRDGRIKPGQLVLLEAF
GGGFTWGSALVRF
>d1hzpa1 c.95.1.1 (A:-10-174) Ketoacyl-ACP synthase III (FabH) {Mycobacterium tuberculosis}
MTEIATTSGARSVGLLSVGAYRPERVVTNDEICQHIDSSDEWIYTRTGIKTRRFAADDESAASMA
TEACRRALSNAGLSAADIDGVIVTTNTHFLQTPPAAPMVAASLGAKGILGFDLSAGCAGFGYALG
AAADMIRGGGAATMLVVGTEKLSPTIDMYDRGNCFIFADGAAAVVVGETPFQGI
>d1hzpa2 c.95.1.1 (A:175-317) Ketoacyl-ACP synthase III (FabH) {Mycobacterium tuberculosis}
GPTVAGSDGEQADAIRQDIDWITFAQNPSGPRPFVRLEGPAVFRWAAFKMGDVGRRAMDAAGVRP
DQIDVFVPHQANSRINELLVKNLQLRPDAVVANDIEHTGNTSAASIPLAMAELLTTGAAKPGDLA
LLIGYGAGLSYAAQVVRM
>d1bi5a1 c.95.1.2 (A:1-235) Chalcone synthase {Alfalfa (Medicago sativa)}
MVSVSEIRKAQRAEGPATILAIGTANPANCVEQSTYPDFYFKITNSEHKTELKEKFQRMCDKSMI
KRRYMYLTEEILKENPNVCEYMAPSLDARQDMVVVEVPRLGKEAAVKAIKEWGQPKSKITHLIVC
TTSGVDMPGADYQLTKLLGLRPYVKRYMMYQQGAFAGGTVLRLAKDLAENNKGARVLVVCSEVTA
VTFRGPSDTHLDSLVGQALFGDGAAALIVGSDPVPEIEKP
>d1bi5a2 c.95.1.2 (A:236-389) Chalcone synthase {Alfalfa (Medicago sativa)}
IFEMVWTAQTIAPDSEGAIDGHLREAGLTFHLLKDVPGIVSKNITKALVEAFEPLGISDYNSIFW
IAHPGGPAILDQVEQKLALKPEKMNATREVLSEYGNMSSACVLFILDEMRKKSTQNGLKTTGEGL
EWGVLFGFGPGLTIETVVLRSVAI
>d1ee0a1 c.95.1.2 (A:20-235) Pyrone synthase (PyS, chalcone synthase 2) {Gerbera hybrida}
GLATILAIGTATPPNCVAQADYADYYFRVTKSEHMVDLKEKFKRICEKTAIKKRYLALTEDYLQE
NPTMCEFMAPSLNARQDLVVTGVPMLGKEAAVKAIDEWGLPKSKITHLIFCTTAGVDMPGADYQL
VKLLGLSPSVKRYMLYQQGAAAGGTVLRLAKDLAENNKGSRVLIVCSEITAILFHGPNENHLDSL
VAQALFGDGAAALIVGSGPHL
>d1ee0a2 c.95.1.2 (A:236-395) Pyrone synthase (PyS, chalcone synthase 2) {Gerbera hybrida}
AVERPIFEIVSTDQTILPDTEKAMKLHLREGGLTFQLHRDVPLMVAKNIENAAEKALSPLGITDW
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NSVFWMVHPGGRAILDQVERKLNLKEDKLRASRHVLSEYGNLISACVLFIIDEVRKRSMAEGKST
TGEGLDCGVLFGFGPGMTVETVVLRSVRVT
>d1feha1 c.96.1.1 (A:210-574) Fe-only hydrogenase, catalytic domain
{Clostridium pasteurianum}
HMDRVKNALNAPEKHVIVAMAPSVRASIGELFNMGFGVDVTGKIYTALRQLGFDKIFDINFGADM
TIMEEATELVQRIENNGPFPMFTSCCPGWVRQAENYYPELLNNLSSAKSPQQIFGTASKTYYPSI
SGLDPKNVFTVTVMPCTSKKFEADRPQMEKDGLRDIDAVITTRELAKMIKDAKIPFAKLEDSEAD
PAMGEYSGAGAIFGATGGVMEAALRSAKDFAENAELEDIEYKQVRGLNGIKEAEVEINNNKYNVA
VINGASNLFKFMKSGMINEKQYHFIEVMACHGGCVNGGGQPHVNPKDLEKVDIKKVRASVLYNQD
EHLSKRKSHENTALVKMYQNYFGKPGEGRAHEILHFKYKK
>d1hfel1 c.96.1.1 (L:87-398) Fe-only hydrogenase larger subunit,
C-domain {Desulfovibrio desulfuricans}
WVPEVEKKLKDGKVKCIAMPAPAVRYALGDAFGMPVGSVTTGKMLAALQKLGFAHCWDTEFTADV
TIWEEGSEFVERLTKKSDMPLPQFTSCCPGWQKYAETYYPELLPHFSTCKSPIGMNGALAKTYGA
ERMKYDPKQVYTVSIMPCIAKKYEGLRPELKSSGMRDIDATLTTRELAYMIKKAGIDFAKLPDGK
RDSLMGESTGGATIFGVTGGVMEAALRFAYEAVTGKKPDSWDFKAVRGLDGIKEATVNVGGTDVK
VAVVHGAKRFKQVCDDVKAGKSPYHFIEYMACPGGCVCGGGQPVMPGVLEAM
>d1aln_1 c.97.1.1 (1-150) Cytidine deaminase {Escherichia coli}
MHPRFQTAFAQLADNLQSALEPILADKYFPALLTGEQVSSLKSATGLDEDALAFALLPLAAACAR
TPLSNFNVGAIARGVSGTWYFGANMEFIGATMQQTVHAEQSAISHAWLSGEKALAAITVNYTPCG
HCRQFMNELNSGLDLRIHLP
>d1aln_2 c.97.1.1 (151-294) Cytidine deaminase {Escherichia coli}
GREAHALRDYLPDAFGPKDLEIKTLLMDEQDHGYALTGDALSQAAIAAANRSHMPYSKSPSGVAL
ECKDGRIFSGSYAENAAFNPTLPPLQGALILLNLKGYDYPDIQRAVLAEKADAPLIQWDATSATL
KALGCHSIDRVLLA
>d1g8ma2 c.97.2.1 (A:201-593) AICAR transformylase domain of
bifunctional purine biosynthesis enzyme ATIC {Chicken (Gallus
gallus)}
GVSQLPLRYGMNPHQSPAQLYTTRPKLPLTVVNGSPGFINLCDALNAWQLVKELKQALGIPAAAS
FKHVSPAGAAVGIPLSEEEAQVCMVHDLHKTLTPLASAYARSRGADRMSSFGDFIALSDICDVPT
AKIISREVSDGVVAPGYEEEALKILSKKKNGGYCVLQMDPNYEPDDNEIRTLYGLQLMQKRNNAV
IDRSLFKNIVTKNKTLPESAVRDLIVASIAVKYTQSNSVCYAKDGQVIGIGAGQQSRIHCTRLAG
DKANSWWLRHHPRVLSMKFKAGVKRAEVSNAIDQYVTGTIGEDEDLVKWQAMFEEVPAQLTEAEK
KQWIAKLTAVSLSSDAFFPFRDNVDRAKRIGVQFIVAPSGSAADEVVIEACNELGITLIHTNLRL
FHH
>d1rgea_ d.1.1.1 (A:) RNase Sa {Streptomyces aureofaciens}
DVSGTVCLSALPPEATDTLNLIASDGPFPYSQDGVVFQNRESVLPTQSYGYYHEYTVITPGARTR
GTRRIITGEATQEDYYTGDHYATFSLIDQTC
>d1fus__ d.1.1.1 (-) RNase F1 {Fusarium moniliforme}
ESATTCGSTNYSASQVRAAANAACQYYQNDDTAGSSTYPHTYNNYEGFDFPVDGPYQEFPIKSGG
VYTGGSPGADRVVINTNCEYAGAITHTGASGNNFVGCSGTN
>d1i0va_ d.1.1.1 (A:) RNase T1 {Aspergillus oryzae}
ACDYTCGSNCYSSSDVSTAQAAGYKLHEDGETVGSNSYPHKYNNYEGFDFSVSSPYYEWPILSSG
DVYSGGSPGADRVVFNENNQLAGVITHTGASGNNFVECT
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>d1rtu__ d.1.1.1 (-) RNase U2 {Ustilago sphaerogena}
CDIPQSTNCGGNVYSNDDINTAIQGALDDVANGDRPDNYPHQYYXEASEDITLCCGSGPWSEFPL
VYNGPYYSSRDNYVSPGPDRVIYQTNTGEFCATVTHTGAASYDGFTQCS
>d1a2pa_ d.1.1.1 (A:) Barnase/Binase {Bacillus amyloliquefaciens}
VINTFDGVADYLQTYHKLPDNYITKSEAQALGWVASKGNLADVAPGKSIGGDIFSNREGKLPGKS
GRTWREADINYTSGFRNSDRILYSSDWLIYKTTDHYQTFTKIR
>d1goua_ d.1.1.1 (A:) Barnase/Binase {Bacillus intermedius}
AVINTFDGVADYLIRYKRLPNDYITKSQASALGWVASKGDLAEVAPGKSIGGDVFSNREGRLPSA
GSRTWREADINYVSGFRNADRLVYSSDWLIYKTTDHYATFTRIR
>d2rbia_ d.1.1.1 (A:) Barnase/Binase {Bacillus intermedius}
VINTFDGVADYLIRYKRLPDNYITKSQASALGWVASKGNLAEVAPGKSIGGDVFSNREGRLPSAS
GRTWREADINYVSGFRNADRLVYSSDWLIYKTTDNYATFTRIR
>d1rds__ d.1.1.1 (-) RNase Ms {Molsin (Aspergillus saitoi)}
ESCEYTCGSTCYWSSDVSAAKAKGYSLYESGDTIDDYPHEYHDYEGFDFPVSGTYYEYPIMSDYD
VYTGGSPGADRVIFNGDDELAGVITHTGASGDDFVACSSS
>d0rst__ d.1.1.1 (-) RNase St {Streptomyces erythreus}
QAPCGDTSGFEEVRLADLPPEATDTYELIEKGGPYPYPEDGTVFENREGILPDCAEGYYHEYTVK
TPSGDDRGARRFVVGDGGEYFYTEDHYESFRLTIVN
>d1aqza_ d.1.1.1 (A:) Ribotoxin {Fungus (Aspergillus restrictus),
restrictocin}
ATWTCINQQLNPKTNKWEDKRLLYSQAKAESNSHHAPLSDGKTGSSYPHWFTNGYDGNGKLIKGR
TPIKFGKADCDRPPKHSQNGMGKDDHYLLEFPTFPDGHDYKFDSKKPKENPGPARVIYTYPNKVF
CGIVAHQRGNQGDLRLCSH
>d1de3a_ d.1.1.1 (A:) Ribotoxin {Fungus (Aspergillus giganteus),
alpha-Sarcin}
AVTWTCLNDQKNPKTNKYETKRLLYNQNKAESNSHHAPLSDGKTGSSYPHWFTNGYDGDGKLPKG
RTPIKFGKSDCDRPPKHSKDGNGKTDHYLLEFPTFPDGHDYKFDSKKPKENPGPARVIYTYPNKV
FCGIIAHTKENQGELKLCSH
>d1cnsa_ d.2.1.1 (A:) Plant class II chitinase {Barley (Hordeum
vulgare)}
SVSSIVSRAQFDRMLLHRNDGACQAKGFYTYDAFVAAAAAFSGFGTTGSADVQKREVAAFLAQTS
HETTGGWATAPDGAFAWGYCFKQERGASSDYCTPSAQWPCAPGKRYYGRGPIQLSHNYNYGPAGR
AIGVDLLANPDLVATDATVSFKTAMWFWMTAQPPKPSSHAVIVGQWSPSGADRAAGRVPGFGVIT
NIINGGIECGHGQDSRVADRIGFYKRYCDILGVGYGNNLDCYSQRPFA
>d1dxja_ d.2.1.1 (A:) Plant class II chitinase {Jack bean (Canavalia
ensiformis)}
DVGSVIDASLFDQLLKHRNDPACEGKGFYSYNAFVTAARSFGGFGTTGDTNTRKREVAAFLAQTS
HETTGGAAGSPDGPYAWGYCFVTERDKSNKYCDPGTPCPAGKSYYGRGPIQLTHNYNYAQAGRAL
GVDLINNPDLVARDAVISFKTAIWFWMTPQGNKPSCHDVITNRWTPSAADVAANRTPGFGVITNI
INGGIECGRGPSPASGDRIGFYKRYCDVLHLSYGPNLNCRDQRPFGG
>d1lsg_1 d.2.1.2 (1-144) Lysozyme {Chicken (Gallus gallus)}
MKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWC
NDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCRL
QQHHLGGAKQAGDV
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>d3lzt__ d.2.1.2 (-) Lysozyme {Chicken (Gallus gallus)}
KVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCN
DGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCRL
>d1jse__ d.2.1.2 (-) Lysozyme {Turkey (Meleagris gallopavo)}
KVYGRCELAAAMKRLGLDNYRGYSLGNWVCAAKFESNFNTHATNRNTDGSTDYGILQINSRWWCN
DGRTPGSKNLCNIPCSALLSSDITASVNCAKKIASGGNGMNAWVAWRNRCKGTDVHAWIRGCRL
>d1hhl__ d.2.1.2 (-) Lysozyme {Guinea fowl (Numida meleagris)}
KVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNSQATNRNTDGSTDYGVLQINSRWWCN
DGRTPGSRNLCNIPCSALQSSDITATANCAKKIVSDGDGMNAWVAWRKHCKGTDVRVWIKGCRL
>d1ghla_ d.2.1.2 (A:) Lysozyme {Pheasant (Phasianus colchicus)}
GKVYGRCELAAAMKRMGLDNYRGYSLGNWVCAAKFESNFNTGATNRNTDGSTDYGILQINSRWWC
NDGRTPGSKNLCHIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRKHCKGTDVNVWIRGCRL
>d1jsf__ d.2.1.2 (-) Lysozyme {Human (Homo sapiens)}
KVFERCELARTLKRLGMDGYRGISLANWMCLAKWESGYNTRATNYNAGDRSTDYGIFQINSRYWC
NDGKTPGAVNACHLSCSALLQDNIADAVACAKRVVRDPQGIRAWVAWRNRCQNRDVRQYVQGCGV
>d2eql__ d.2.1.2 (-) Lysozyme {Horse (Equus caballus), milk}
KVFSKCELAHKLKAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWC
KDNKRSSSNACNIMCSKLLDENIDDDISCAKRVVRDPKGMSAWKAWVKHCKDKDLSEYLASCNL
>d1qqya_ d.2.1.2 (A:) Lysozyme {Dog (Canis familiaris), milk}
MKIFSKCELARKLKSMGMDGFHGYSLANWVCMAEYESNFNTQAFNGRNSNGSSDYGIFQLNSKWW
CKSNSHSSANACNIMCSKFLDDNIDDDIACAKRVVKDPNGMSAWVAWVKHCKGKDLSKYLASCNL
>d1jug__ d.2.1.2 (-) Lysozyme {Australian echidna (Tachyglossus
aculeatus)}
KILKKQELCKNLVAQGMNGYQHITLPNWVCTAFHESSYNTRATNHNTDGSTDYGILQINSRYWCH
DGKTPGSKNACNISCSKLLDDDITDDLKCAKKIAGEAKGLTPWVAWKSKCRGHDLSKFKC
>d1lmq__ d.2.1.2 (-) Lysozyme {Rainbow trout (Oncorhynchus mykiss)}
KVYDRCELARALKASGMDGYAGNSLPNWVCLSKWESSYNTQATNRNTDGSTDYGIFQINSRYWCD
DGRTPGAKNVCGIRCSQLLTDDLTVAIRCAKRVVLDPNGIGAWVAWRLHCQNQDLRSYVAGCGV
>d1gd6a_ d.2.1.2 (A:) Lysozyme {Silkworm (Bombyx mori)}
KTFTRCGLVHELRKHGFEENLMRNWVCLVEHESSRDTSKTNTNRNGSKDYGLFQINDRYWCSKGA
SPGKDCNVKCSDLLTDDITKAAKCAKKIYKRHRFDAWYGWKNHCQGSLPDISSC
>d1iiza_ d.2.1.2 (A:) Lysozyme {Tasar silkworm (Antheraea mylitta)}
KRFTRCGLVNELRKQGFDENLMRDWVCLVENESARYTDKIANVNKNGSRDYGLFQINDKYWCSKG
STPGKDCNVTCSQLLTDDITVASTCAKKIYKRTKFDAWSGWDNHCNHSNPDISSC
>d1alc__ d.2.1.2 (-) alpha-Lactalbumin {Baboon (Papio cynocephalus)}
KQFTKCELSQNLYDIDGYGRIALPELICTMFHTSGYDTQAIVENDESTEYGLFQISNALWCKSSQ
SPQSRNICDITCDKFLDDDITDDIMCAKKILDIKGIDYWIAHKALCTEKLEQWLCEK
>d1b9oa_ d.2.1.2 (A:) alpha-Lactalbumin {Human (Homo sapiens)}
KQFTKCELSQLLKDIDGYGGIALPELICTMFHTSGYDTQAIVENDESTEYGLFQISNKLWCKSSQ
VPQSRNICDISCDKFLDDDITDDIMCAKKILDIKGIDYWLAHKALCTEKLEQWLCEKL
>d1hfx__ d.2.1.2 (-) alpha-Lactalbumin {Guinea pig (Cavia porcellus)}
KQLTKCALSHELNDLAGYRDITLPEWLCIIFHISGYDTQAIVKNSDHKEYGLFQINDKDFCESST
TVQSRNICDISCDKLLDDDLTDDIMCVKKILDIKGIDYWLAHKPLCSDKLEQWYCEAQ
>d1fkqa_ d.2.1.2 (A:) alpha-Lactalbumin {Goat (Capra hircus)}
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MEQLTKCEVFQKLKDLKDYGGVSLPEWVCVAFHTSGYDTQAIVQNNDSTEYGLFQINNKIWCKDD
QNPHSRNICNISCDKFLDDDLTDDIVCAKKILDKVGINYWLAHKALCSEKLDQWLCEKL
>d1f6ra_ d.2.1.2 (A:) alpha-Lactalbumin {Cow (Bos taurus)}
EQLTKCEVFRELKDLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNNDSTEYGLFQINNKIWCKDDQ
NPHSSNICNISCDKFLDDDLTDDIMCVKKILDKVGINYWLAHKALCSEKLDQWLCEKL
>d1j8wa_ d.2.1.2 (A:) alpha-Lactalbumin {Mouse (Mus musculus)}
TELTKCKVSHAIKDMDGYQGISLLEWTCVLFHTSGYDSQAVVNDNGSTEYGLFQISERFWCKSSE
FPESENICGISCDKLLDDELDDDIVCAKKIVAIKGIDYWKAYKPMCSEKLEQWRCEKP
>d169la_ d.2.1.3 (A:) Phage T4 lysozyme {Bacteriophage T4}
MNIFEMLRIDEGLRLKIYKDTEGYYTIGIGHLLTKSPSLNAAKSELDKAIGRNCNGVITKDEAEK
LFNQDVDAAVRGILRNAKLKPVYDSLDAVRRCALINMVFQMGETGVAGFTNSLRMLQQKRWDAAA
AALAAAAWAAATPNRAKRVITTFRTGTWDAYK
>d174la_ d.2.1.3 (A:) Phage T4 lysozyme {Bacteriophage T4}
MNIFEMLRIDEGLRLKIYKDTEGYYTIGIGHLLAAAADLAAAKAALAAAIGRNTNGVITKDEAEK
LFNQDVDAAVRGILRNAKLKPVYDSLDAVRRAALINMVFQMGETGVAGFTNSLRMLQQKRWDEAA
VNLAKSRWYNQTPNRAKRVITTFRTGTWDAYKNL
>d176la_ d.2.1.3 (A:) Phage T4 lysozyme {Bacteriophage T4}
MNIFEMLRIDEGLRLKIYKDTEGYYTIGIGHTLKVDGNSNAAKSELDKAIGRNTNGVITKDEAEK
LFNQDVDAAVRGILRNAKLKPVYDSLDAVRRAALINMVFQMGETGVAGFTNSLRMLQQKRWDEAA
VNLAKSRWYNQTPNRAKRVITTFRTGTWDAYKNL
>d189l__ d.2.1.3 (-) Phage T4 lysozyme {Bacteriophage T4}
MNLFEMLRIDEGLRLKIYKDTEGYYTIGIGHLLTKSPDLNVAKSELDKAIGRNCNGVITKDEAEK
LFNQDVDAAVRGILRNPKLKPVYDSLDAVRRCALINMVFQMGETGVAGFTDSLRMLQQKRWDEAA
ANLAKSRWYNQTPDRAKRVITTFRTGTWDAYKNL
>d191l__ d.2.1.3 (-) Phage T4 lysozyme {Bacteriophage T4}
MNIFEMLRIDEGLRLKIYKDTEGYYTIGIGHLLTKSPSLNAAKSELDKAIGRACAGAITKDEAEK
LFNQDVDAAVRGILRNAKLKPVYDSLDAVRRCALINMVFQMGETGVAGFTNSLRMLQQKRWDAAA
AALAKSRWYNQTPNRAKRVITTFRTGTWDAYK
>d192l__ d.2.1.3 (-) Phage T4 lysozyme {Bacteriophage T4}
MNIFEMLRIDEGLRLKIYKDTEGYYTIGIGHLLTKSPSLAAAKAALAAAIGRNTNGVITKDEAEK
LFNQDVDAAVRGILRNAKLKPVYDSLDAVRRAALINMVFQMGETGVAGFTNSLRMLQQKRWAAAA
AALAKSRWYNQTPNRAKRVITTFRTGTWDAYK
>d217l__ d.2.1.3 (-) Phage T4 lysozyme {Bacteriophage T4}
MNIFEMLRIDEGLRLKIYKDTEGYYTIGIGHLLTKSPSLNAAKEELDKAIGRNTNGVITKDEAEK
LFNQDVDAAVRGILRNAKLKPVYDSLDAVRRAALINMVFQMGETGVAGFTNSLRMLQQKRWDEAA
VNLAKSRWYNQTPNRAKRVITTFRTGTWDAYK
>d1k28a3 d.2.1.3 (A:130-345) Tail-associated lysozyme gp5, catalytic
domain {Bacteriophage T4}
NVLNQGGEVGYDSSSNVIQDSNLDTAINPDDRPLSEIPTDDNPNMSMAEMLRRDEGLRLKVYWDT
EGYPTIGIGHLIMKQPVRDMAQINKVLSKQVGREITGNPGSITMEEATTLFERDLADMQRDIKSH
SKVGPVWQAVNRSRQMALENMAFQMGVGGVAKFNTMLTAMLAGDWEKAYKAGRDSLWYQQTKGRA
SRVTMIILTGNLESYGVEVKT
>d1am7a_ d.2.1.4 (A:) Lambda lysozyme {Bacteriophage lambda}
MVEINNQRKAFLDMLAWSEGTDNGRQKTRNHGYDVIVGGELFTDYSDHPRKLVTLNPKLKSTGAG
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RYQLLSRWWDAYRKQLGLKDFSPKSQDAVALQQIKERGALPMIDRGDIRQAIDRCSNIWASLPGA
GYGQFEHKADSLIAKFKEAGGTVR
>d153l__ d.2.1.5 (-) Lysozyme {Goose (Anser anser anser)}
RTDCYGNVNRIDTTGASCKTAKPEGLSYCGVSASKKIAERDLQAMDRYKTIIKKVGEKLCVEPAV
IAGIISRESHAGKVLKNGWGDRGNGFGLMQVDKRSHKPQGTWNGEVHITQGTTILINFIKTIQKK
FPSWTKDQQLKGGISAYNAGAGNVRSYARMDIGTTHDDYANDVVARAQYYKQHGY
>d1qsaa2 d.2.1.6 (A:451-618) 70 kDa soluble lytic transglycosylase,
SLT70 {Escherichia coli}
LAYNDLFKRYTSGKEIPQSYAMAIARQESAWNPKVKSPVGASGLMQIMPGTATHTVKMFSIPGYS
SPGQLLDPETNINIGTSYLQYVYQQFGNNRIFSSAAYNAGPGRVRTWLGNSAGRIDAVAFVESIP
FSETRGYVKNVLAYDAYYRYFMGDKPTLMSATEWGRRY
>d1qusa_ d.2.1.6 (A:) 36 kDa soluble lytic transglycosylase, SLT35
{Escherichia coli}
MVEPQHNVMQMGGDFANNPNAQQFIDKMVNKHGFDRQQLQEILSQAKRLDSVLRLMDNQAPTTSV
KPPSGPNGAWLRYRKKFITPDNVQNGVVFWNQYEDALNRAWQVYGVPPEIIVGIIGVETRWGRVM
GKTRILDALATLSFNYPRRAEYFSGELETFLLMARDEQDDPLNLKGSFAGAMGYGQFMPSSYKQY
AVDFSGDGHINLWDPVDAIGSVANYFKAHGWVKGDQVAVMANGQAPGLPNGFKTKYSISQLAAAG
LTPQQPLGNHQQASLLRLDVGTGYQYWYGLPNFYTITRYNHSTHYAMAVWQLGQAVALARVQ
>d1chka_ d.2.1.7 (A:) Endochitosanase {Streptomyces sp., strain N174}
AGAGLDDPHKKEIAMELVSSAENSSLDWKAQYKYIEDIGDGRGYTGGIIGFCSGTGDMLELVQHY
TDLEPGNILAKYLPALKKVNGSASHSGLGTPFTKDWATAAKDTVFQQAQNDERDRVYFDPAVSQA
KADGLRALGQFAYYDAIVMHGPGNDPTSFGGIRKTAMKKARTPAQGGDETTYLNGFLDARKAAML
TEAAHDDTSRVDTEQRVFLKAGNLDLNPPLKWKTYGDPYVINS
>d1qgia_ d.2.1.7 (A:) Endochitosanase {Bacillus circulans}
ASPDDNFSPETLQFLRNNTGLDGEQWNNIMKLINKPEQDDLNWIKYYGYCEDIEDERGYTIGLFG
ATTGGSRDTHPDGPDLFKAYDAAKGASNPSADGALKRLGINGKMKGSILEIKDSEKVFCGKIKKL
QNDAAWRKAMWETFYNVYIRYSVEQARQRGFTSAVTIGSFVDTALNQGATGGSDTLQGLLARSGS
SSNEKTFMKNFHAKRTLVVDTNKYNKPPNGKNRVKQWDTLVDMGKMNLKNVDSEIAQVTDWEMK
>d1aec__ d.3.1.1 (-) Actinidin {Chinese gooseberry or kiwifruit
(Actinidia chinensis)}
LPSYVDWRSAGAVVDIKSQGECGGCWAFSAIATVEGINKIVTGVLISLSEQELIDCGRTQNTRGC
NGGYITDGFQFIINNGGINTEENYPYTAQDGECNVDLQNEKYVTIDTYENVPYNNEWALQTAVTY
QPVSVALDAAGDAFKQYSSGIFTGPCGTAIDHAVTIVGYGTEGGIDYWIVKNSWDTTWGEEGYMR
ILRNVGGAGTCGIATMPSYPVKY
>d2act__ d.3.1.1 (-) Actinidin {Chinese gooseberry or kiwifruit
(Actinidia chinensis)}
LPSYVDWRSAGAVVDIKSQGECGGCWAFSAIATVEGINKITSGSLISLSEQELIDCGRTQNTRGC
DGGYITDGFQFIINDGGINTEENYPYTAQDGDCDVALQDQKYVTIDTYENVPYNNEWALQTAVTY
QPVSVALDAAGDAFKQYASGIFTGPCGTAVDHAIVIVGYGTEGGVDYWIVKNSWDTTWGEEGYMR
ILRNVGGAGTCGIATMPSYPVKY
>d1ppn__ d.3.1.1 (-) Papain {Papaya (Carica papaya)}
IPEYVDWRQKGAVTPVKNQGSCGSCWAFSAVVTIEGIIKIRTGNLNEYSEQELLDCDRRSYGCNG
GYPWSALQLVAQYGIHYRNTYPYEGVQRYCRSREKGPYAAKTDGVRQVQPYNEGALLYSIANQPV
SVVLEAAGKDFQLYRGGIFVGPCGNKVDHAVAAVGYGPNYILIKNSWGTGWGENGYIRIKRGTGN
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SYGVCGLYTSSFYPVKN
>d1pcia_ d.3.1.1 (A:) Caricain (protease omega) {Papaya (Carica
papaya)}
LTSTERLIQLFNSWMLNHNKFYENVDEKLYRFEIFKDNLNYIDETNKKNNSYWLGLNEFADLSND
EFNEKYVGSLIDATIEQSYDEEFINEDIVNLPENVDWRKKGAVTPVRHQGSCGSCWAFSAVATVE
GINKIRTGKLVELSEQELVDCERRSHGCKGGYPPYALEYVAKNGIHLRSKYPYKAKQGTCRAKQV
GGPIVKTSGVGRVQPNNEGNLLNAIAKQPVSVVVESKGRPFQLYKGGIFEGPCGTKVDGAVTAVG
YGKSGGKGYILIKNSWGTAWGEKGYIRIKRAPGNSPGVCGLYKSSYYPTKN
>d1ppo__ d.3.1.1 (-) Caricain (protease omega) {Papaya (Carica
papaya)}
LPENVDWRKKGAVTPVRHQGSCGSCWAFSAVATVEGINKIRTGKLVELSEQELVDCERRSHGCKG
GYPPYALEYVAKNGIHLRSKYPYKAKQGTCRAKQVGGPIVKTSGVGRVQPNNEGNLLNAIAKQPV
SVVVESKGRPFQLYKGGIFEGPCGTKVDHAVTAVGYGKSGGKGYILIKNSWGTAWGEKGYIRIKR
APGNSPGVCGLYKSSYYPTKN
>d1yal__ d.3.1.1 (-) Chymopapain {Papaya (Carica papaya)}
YPQSIDWRAKGAVTPVKNQGACGSCWAFSTIATVEGINKIVTGNLLELSEQELVDCDKHSYGCKG
GYQTTSLQYVANNGVHTSKVYPYQAKQYKCRATDKPGPKVKITGYKRVPSNCETSFLGALANQPL
SVLVEAGGKPFQLYKSGVFDGPCGTKLDHAVTAVGYGTSDGKNYIIIKNSWGPNWGEKGYMRLKR
QSGNSQGTCGVYKSSYYPFKGFA
>d1gece_ d.3.1.1 (E:) Glycyl endopeptidase {Papaya (Carica papaya)}
LPESVDWRAKGAVTPVKHQGYCESCWAFSTVATVEGINKIKTGNLVELSEQELVDCDLQSYGCNR
GYQSTSLQYVAQNGIHLRAKYPYIAKQQTCRANQVGGPKVKTNGVGRVQSNNEGSLLNAIAHQPV
SVVVESAGRDFQNYKGGIFEGSCGTKVDHAVTAVGYGKSGGKGYILIKNSWGPGWGENGYIRIRR
ASGNSPGVCGVYRSSYYPIKN
>d1cqda_ d.3.1.1 (A:) Proline-specific cysteine protease {Ginger
rhizome (Zingiber officinale)}
LPDSIDWRENGAVVPVKNQGGCGSCWAFSTVAAVEGINQIVTGDLISLSEQQLVDCTTANHGCRG
GWMNPAFQFIVNNGGINSEETYPYRGQDGICNSTVNAPVVSIDSYENVPSHNEQSLQKAVANQPV
SVTMDAAGRDFQLYRSGIFTGSCNISANHALTVVGYGTENDKDFWIVKNSWGKNWGESGYIRAER
NIENPDGKCGITRFASYPVKK
>d3gcb__ d.3.1.1 (-) Bleomycin hydrolase {Baker's yeast
(Saccharomyces cerevisiae), Gal6}
AFQGAMASSIDISKINSWNKEFQSDLTHQLATTVLKNYNADDALLNKTRLQKQDNRVFNTVVSTD
STPVTNQKSSGRAWLFAATNQLRLNVLSELNLKEFELSQAYLFFYDKLEKANYFLDQIVSSADQD
IDSRLVQYLLAAPTEDGGQYSMFLNLVKKYGLIPKDLYGDLPYSTTASRKWNSLLTTKLREFAET
LRTALKERSADDSIIVTLREQMQREIFRLMSLFMDIPPVQPNEQFTWEYVDKDKKIHTIKSTPLE
FASKYAKLDPSTPVSLINDPRHPYGKLIKIDRLGNVLGGDAVIYLNVDNETLSKLVVKRLQNNKA
VFFGSHTPKFMDKKTGVMDIELWNYPAIGYNLPQQKASRIRYHESLMTHAMLITGCHVDETSKLP
LRYRVENSWGKDSGKDGLYVMTQKYFEEYCFQIVVDINELPKELASKFTSGKEEPIVLPIWDPMG
ALA
>d2cb5a_ d.3.1.1 (A:) Bleomycin hydrolase {Human (Homo sapiens)}
SSSGLNSEKVAALIQKLNSDPQFVLAQNVGTTHDLLDICLKRATVQRAQHVFQHAVPQEGKPITN
QKSSGRSWIFSCLNVMRLPFMKKLNIEEFEFSQSYLFFWDKVERCYFFLSAFVDTAQRKEPEDGR
LVQFLLMNPANDGGQWDMLVNIVEKYGVIPKKCFPESYTTEATRRMNDILNHKMREFCIRLRNLV
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HSGATKGEISATQDVMMEEIFRVVCICLGNPPETFTWEYRDKDKNYEKIGPITPLEFYREHVKPL
FNMEDKICLVNDPRPQHKHNKLYTVEYLSNMVGGRKTLYNNQPIDFLKKMVAASIKDGEAVWFGC
DVGKHFNSKLGLSDMNLYDHELVFGVSLKNMNKAERLTFGESLMTHAMTFTAVSEKDDQDGAFTK
WRVENSWGEDHGHKGYLCMTDEWFSEYVYEVVVDRKHVPEEVLAVLEQEPIILPAWDPMGALA
>d1f2aa_ d.3.1.1 (A:) Cruzain {Trypanosoma cruzi}
APAAVDWRARGAVTAVKDQGQCGSCWAFSAIGNVECQWFLAGHPLTNLSEQMLVSCDKTDSGCSG
GLMNNAFEWIVQENNGAVYTEDSYPYASGEGISPPCTTSGHTVGATITGHVELPQDEAQIAAWLA
VNGPVAVAVDASSWMTYTGGVMTSCVSEQLDHGVLLVGYNDSAAVPYWIIKNSWTTQWGEEGYIR
IAKGSNQCLVKEEASSAVVG
>d3pbh__ d.3.1.1 (-) (Pro)cathepsin B {Human (Homo sapiens)}
MRSRPSFHPLSDELVNYVNKRNTTWQAGHNFYNVDMSYLKRLCGTFLGGPKPPQRVMFTEDLKLP
ASFDAREQWPQCPTIKEIRDQGSCGSCWAFGAVEAISDRICIHTNAHVSVEVSAEDLLTCCGSMC
GDGCNGGYPAEAWNFWTRKGLVSGGLYESHVGCRPYSIPPCEHHVNGSRPPCTGEGDTPKCSKIC
EPGYSPTYKQDKHYGYNSYSVSNSEKDIMAEIYKNGPVEGAFSVYSDFLLYKSGVYQHVTGEMMG
GHAIRILGWGVENGTPYWLVANSWNTDWGDNGFFKILRGQDHCGIESEVVAGIPRTD
>g1huc.1 d.3.1.1 (A:,B:) (Pro)cathepsin B {Human (Homo sapiens)}
LPASFDAREQWPQCPTIKEIRDQGSCGSCWAFGAVEAISDRICIHTNXVSVEVSAEDLLTCCGSM
CGDGCNGGYPAEAWNFWTRKGLVSGGLYESHVGCRPYSIPPCEHHVNGSRPPCTGEGDTPKCSKI
CEPGYSPTYKQDKHYGYNSYSVSNSEKDIMAEIYKNGPVEGAFSVYSDFLLYKSGVYQHVTGEMM
GGHAIRILGWGVENGTPYWLVANSWNTDWGDNGFFKILRGQDHCGIESEVVAGIPRTD
>d1mira_ d.3.1.1 (A:) (Pro)cathepsin B {Rat (Rattus norvegicus)}
SDDMINYINKQNTTWQAGRNFYNVDISYLKKLCGTVLGGPKLPERVGFSEDINLPESFDAREQWS
NCPTIAQIRDQGSCGSSWAFGAVEAMSDRICIHTNGRVNVEVSAEDLLTCCGIQCGDGCNGGYPS
GAWNFWTRKGLVSGGVYNSHIGCLPYTIPPCEHHVNGARPPCTGEGDTPKCNKMCEAGYSTSYKE
DKHYGYTSYSVSDSEKEIMAEIYKNGPVEGAFTVFSDFLTYKSGVYKHEAGDVMGGHAIRILGWG
IENGVPYWLVANSWNADWGDNGFFKILRGENHCGIESEIVAGIPRTQQYWGRF
>d1thea_ d.3.1.1 (A:) (Pro)cathepsin B {Rat (Rattus norvegicus)}
LPESFDAREQWSNCPTIAQIRDQGSCGSCWAFGAVEAMSDRICIHTNGRVNVEVSAEDLLTCCGI
QCGDGCNGGYPSGAWNFWTRKGLVSGGVYNSHIGCLPYTIPPCEHHVNGARPPCTGEGDTPKCNK
MCEAGYSTSYKEDKHYGYTSYSVSDSEKEIMAEIYKNGPVEGAFTVFSDFLTYKSGVYKHEAGDV
MGGHAIRILGWGIENGVPYWLVANSWNADWGDNGFFKILRGENHCGIESEIVAGIPRT
>d1qdqa_ d.3.1.1 (A:) (Pro)cathepsin B {Cow (Bos taurus)}
LPESFDAREQWPNCPTIKEIRDQGSCGSCWAFGAVEAISDRICIHSNGRVNVEVSAEDMLTCCGG
ECGDGCNGGEPSGAWNFWTKKGLVSGGLYNSHVGCRPYSIPPCEHHVNGSRPPCTGEGDTPKCSK
TCEPGYSPSYKEDKHFGCSSYSVANNEKEIMAEIYKNGPVEGAFSVYSDFLLYKSGVYQHVSGEI
MGGHAIRILGWGVENGTPYWLVANSWNTDWGDNGFFKILRGQDHCGIESEIVAGMPCT
>d1cs8a_ d.3.1.1 (A:) (Pro)cathepsin L {Human (Homo sapiens)}
SLTFDHSLEAQWTKWKAMHNRLYGMNEEGWRRAVWEKNMKMIELHNQEYREGKHSFTMAMNAFGD
MTSEEFRQVMNGFQNRKPRKGKVFQEPLFYEAPRSVDWREKGYVTPVKNQGQCGSCWAFSATGAL
EGQMFRKTGRLISLSEQNLVDCSGPQGNEGCNGGLMDYAFQYVQDNGGLDSEESYPYEATEESCK
YNPKYSVANDAGFVDIPKQEKALMKAVATVGPISVAIDAGHESFLFYKEGIYFEPDCSSEDMDHG
VLVVGYGFESTESDNNKYWLVKNSWGEEWGMGGYVKMAKDRRNHCGIASAASYPTV
>g1icf.1 d.3.1.1 (A:,B:) (Pro)cathepsin L {Human (Homo sapiens)}
APRSVDWREKGYVTPVKNQGQCGSCWAFSATGALEGQMFRKTGRLISLSEQNLVDCSGPQGNEGC
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NGGLMDYAFQYVQDNGGLDSEESYPYEATEESCKYNPKYSVANDTGFVDIPKQEKALMKAVATVG
PISVAIDAGHESFLFYKEGIYFEPDCSSEDMDHGVLVVGYGFESTXNNKYWLVKNSWGEEWGMGG
YVKMAKDRRNHCGIASAASYPTV
>d1mema_ d.3.1.1 (A:) (Pro)cathepsin K {Human (Homo sapiens)}
APDSVDYRKKGYVTPVKNQGQCGSCWAFSSVGALEGQLKKKTGKLLNLSPQNLVDCVSENDGCGG
GYMTNAFQYVQKNRGIDSEDAYPYVGQEESCMYNPTGKAAKCRGYREIPEGNEKALKRAVARVGP
VSVAIDASLTSFQFYSKGVYYDESCNSDNLNHAVLAVGYGIQKGNKHWIIKNSWGENWGNKGYIL
MARNKNNACGIANLASFPKM
>d7pcka_ d.3.1.1 (A:) (Pro)cathepsin K {Human (Homo sapiens)}
LYPEEILDTHWELWKKTHRKQYNNKVDEISRRLIWEKNLKYISIHNLEASLGVHTYELAMNHLGD
MTSEEVVQKMTGLKVPLSHSRSNDTLYIPEWEGRAPDSVDYRKKGYVTPVKNQGQCGSCWAFSSV
GALEGQLKKKTGKLLNLSPQNLVDCVSENDGCGGGYMTNAFQYVQKNRGIDSEDAYPYVGQEESC
MYNPTGKAAKCRGYREIPEGNEKALKRAVARVGPVSVAIDASLTSFQFYSKGVYYDESCNSDNLN
HAVLAVGYGIQKGNKHWIIKNSWGENWGNKGYILMARNKNNACGIANLASFPKM
>d8pcha_ d.3.1.1 (A:) (Pro)cathepsin K {Pig (Sus scrofa)}
YPPSMDWRKKGNFVSPVKNQGSCGSCWTFSTTGALESAVAIATGKMLSLAEQQLVDCAQNFNNHG
CQGGLPSQAFEYIRYNKGIMGEDTYPYKGQDDHCKFQPDKAIAFVKDVANITMNDEEAMVEAVAL
YNPVSFAFEVTNDFLMYRKGIYSSTSCHKTPDKVNHAVLAVGYGEENGIPYWIVKNSWGPQWGMN
GYFLIERGKNMCGLAACASYPIPLV
>d1fh0a_ d.3.1.1 (A:) (Pro)cathepsin V {Human (Homo sapiens)}
LPKSVDWRKKGYVTPVKNQKQCGSCWAFSATGALEGQMFRKTGKLVSLSEQNLVDCSRPQGNQGC
NGGFMARAFQYVKENGGLDSEESYPYVAVDEICKYRPENSVAQDTGFTVVAPGKEKALMKAVATV
GPISVAMDAGHSSFQFYKSGIYFEPDCSSKNLDHGVLVVGYGFEGANSDNSKYWLVKNSWGPEWG
SNGYVKIAKDKNNHCGIATAASYPNV
>d1deua_ d.3.1.1 (A:) (Pro)cathepsin X {Human (Homo sapiens)}
RGQTCYRPLRGDGLAPLGRTTYPRPHEYLSPADLPKSWDWRNVDGVNYASITRNQHIPQYCGSCW
AHASTSAMADRINIKRKGAWPSTLLSVQNVIDCGNAGSCEGGNDLSVWDYAHQHGIPDETCNNYQ
AKDQECDKFNQCGTCNEFKECHAIRNYTLWRVGDYGSLSGREKMMAEIYANGPISCGIMATERLA
NYTGGIYAEYQDTTYINHVVSVAGWGISDGTEYWIVRNSWGEPWGERGWLRIVTSTYKDGKGARY
NLAIEEHCTFGDPIV
>d1ef7a_ d.3.1.1 (A:) (Pro)cathepsin X {Human (Homo sapiens)}
LPKSWDWRNVDGVNYASITRNQHIPQYCGSCWAHASTSAMADRINIKRKGAWPSTLLSVQNVIDC
GNAGSCEGGNDLSVWDYAHQHGIPDETCNNYQAKDQECDKFNQCGTCNEFKECHAIRNYTLWRVG
DYGSLSGREKMMAEIYANGPISCGIMATERLANYTGGIYAEYQDTTYINHVVSVAGWGISDGTEY
WIVRNSWGEPWGERGWLRIVTSTYKDGKGARYNLAIEEHCTFGDPIV
>d1cv8__ d.3.1.1 (-) Staphopain {Staphylococcus aureus}
NEQYVNKLENFKIRETQGNNGWCAGYTMSALLNATYNTNKYHAEAVMRFLHPNLQGQQFQFTGLT
PREMIYFGQTQGRSPQLLNRMTTYNEVDNLTKNNKGIAILGSRVESRNGMHAGHAMAVVGNAKLN
NGQEVIIIWNPWDNGFMTQDAKNNVIPVSNGDHYQWYSSIYGY
>d1dkia_ d.3.1.1 (A:) Streptococcal pyrogenic exotoxin B {Streptococcus pyogenes}
LDKVNLGGELSGSNMYVYNISTGGFVIVSGDKRSPEILGYSTSGSFDVNGKENIASFMESYVEQI
KENKKLDSTYAGTAEIKQPVVKSLLDSKGIHYNQGNPYNLLTPVIEKVKPGEQSFVGQHAATGSV
ATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFAAISTRQYNWNNILPTYSGRESNVQK

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MAISELMADVGISVDMDYGPSSGSAGSSRVQRALKENFGYNQSVHQINRGDFSKQDWEAQIDKEL
SQNQPVYYQGVGKVGGHAFVIDGADGRNFYHVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNG
YQSAVVGIKP
>d1qmya_ d.3.1.2 (A:) FMDV leader protease {Foot-and-mouth disease virus}
MELTLYNGEKKTFYSRPNNHDNAWLNAILQLFRYVEEPFFDWVYSSPENLTLEAIKQLEDLTGLE
LHEGGPPALVIWNIKHLLHTGIGTASRPSEVCVVDGTDMSLADFHAGIFLKGQEHAVFACVTSNG
WYAIDDEDFYPWTPDPSDVLVFVPYD
>d1qola_ d.3.1.2 (A:) FMDV leader protease {Foot-and-mouth disease virus}
MELTLYNGEKKTFYSRPNNHDNAWLNAILQLFRYVEEPFFDWVYSSPENLTLEAIKQLEDLTGLE
LHEGGPPALVIWNIKHLLHTGIGTASRPSEVCVVDGTDMCLADFHAGIFLKGQEHAVFACVTSNG
WYAIDDEDFYPWTPDPSDVLVFVPYDQEPLNGEWKAKVQRKLK
>d1kful3 d.3.1.3 (L:2-355) Calpain large subunit, catalytic domain (domain II) {Human (Homo sapiens)}
AGIAAKLAKDREAAEGLGSHERAIKYLNQDYEALRNECLEAGTLFQDPSFPAIPSALGFKELGPY
SSKTRGMRWKRPTEICADPQFIIGGATRTDICQGALGDCWLLAAIASLTLNEEILARVVPLNQSF
QENYAGIFHFQFWQYGEWVEVVVDDRLPTKDGELLFVHSAEGSEFWSALLEKAYAKINGCYEALS
GGATTEGFEDFTGGIAEWYELKKPPPNLFKIIQKALQKGSLLGCSIDITSAADSEAITFQKLVKG
HAYSVTGAEEVESNGSLQKLIRIRNPWGEVEWTGRWNDNCPSWNTIDPEERERLTRRHEDGEFWM
SFSDFLRHYSRLEICNLTPDTLTSDTYKK
>d1df0a3 d.3.1.3 (A:2-355) Calpain large subunit, catalytic domain (domain II) {Rat (Rattus norvegicus)}
AGIAMKLAKDREAAEGLGSHERAIKYLNQDYETLRNECLEAGALFQDPSFPALPSSLGFKELGPY
SSKTRGIEWKRPTEICADPQFIIGGATRTDICQGALGDSWLLAAIASLTLNEEILARVVPLDQSF
QENYAGIFHFQFWQYGEWVEVVVDDRLPTKDGELLFVHSAEGSEFWSALLEKAYAKINGCYEALS
GGATTEGFEDFTGGIAEWYELRKPPPNLFKIIQKALEKGSLLGCSIDITSAADSEAVTYQKLVKG
HAYSVTGAEEVESSGSLQKLIRIRNPWGQVEWTGKWNDNCPSWNTVDPEVRANLTERQEDGEFWM
SFSDFLRHYSRLEICNLTPDTLTCDSYKK
>d1f13a4 d.3.1.4 (A:191-515) Transglutaminase catalytic domain {Human (Homo sapiens)}
DAVYLDNEKEREEYVLNDIGVIFYGEVNDIKTRSWSYGQFEDGILDTCLYVMDRAQMDLSGRGNP
IKVSRVGSAMVNAKDDEGVLVGSWDNIYAYGVPPSAWTGSVDILLEYRSSENPVRYGQCWVFAGV
FNTFLRCLGIPARIVTNYFSAHDNDANLQMDIFLEEDGNVNSKLTKDSVWNYHCWNEAWMTRPDL
PVGFGGWQAVDSTPQENSDGMYRCGPASVQAIKHGHVCFQFDAPFVFAEVNSDLIYITAKKDGTH
VVENVDATHIGKLIVTKQIGGDGMMDITDTYKFQEGQEEERLALETALMYGAKKPLNTEGVMKSR
>d1g0da4 d.3.1.4 (A:141-461) Transglutaminase catalytic domain {Red sea bream (Chrysophrys major)}
DMVYLPDESKLQEYVMNEDGVIYMGTWDYIRSIPWNYGQFEDYVMDICFEVLDNSPAALKNSEMD
IEHRSDPVYVGRTITAMVNSNGDRGVLTGRWEEPYTDGVAPYRWTGSVPILQQWSKAGVRPVKYG
QCWVFAAVACTVLRCLGIPTRPITNFASAHDVDGNLSVDFLLNERLESLDSRQRSDSSWNFHCWV
ESWMSREDLPEGNDGWQVLDPTPQELSDGEFCCGPCPVAAIKEGNLGVKYDAPFVFAEVNADTIY
WIVQKDGQRRKITEDHASVGKNISTKSVYGNHREDVTLHYKYPEGSQKEREVYKKAGRRVT
>d1e2ta_ d.3.1.5 (A:) Arylamine N-acetyltransferase {Salmonella
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typhimurium}
HMTSFLHAYFTRLHCQPLGVPTVEALRTLHLAHNCAIPFENLDVLLPREIQLDETALEEKLLYAR
RGGYCFELNGLFERALRDIGFNVRSLLGRVILSHPASLPPRTHRLLLVDVEDEQWIADVGFGGQT
LTAPLRLQAEIAQQTPHGEYRLMQEGSTWILQFRHHEHWQSMYCFDLGVQQQSDHVMGNFWSAHW
PQSHFRHHLLMCRHLPDGGKLTLTNFHFTRYHQGHAVEQVNVPDVPSLYQLLQQQFGLGVNDVKH
GFTEAELAAVMAAF
>d1uch__ d.3.1.6 (-) Ubiquitin C-terminal hydrolase UCH-l3 {Human
(Homo sapiens)}
RWLPLEANPEVTNQFLKQLGLHPNWQFVDVYGMDPELLSMVPRPVCAVLLLFPITEKYEVFRTEE
EEKIKSQGQDVTSSVYFMKQTISNACGTIGLIHAIANNKDKMHFESGSTLKKFLEESVSMSPEER
ARYLENYDAIRVTHETSAHEGQTEAPSIDEKVDLHFIALVHVDGHLYELDGRKPFPINHGETSDE
TLLEDAIEVCKKFMERDPDELRFNAIALSAA
>d1cmxa_ d.3.1.6 (A:) Ubiquitin C-terminal hydrolase UCH-l3
{Synthetic, based on Saccharomyces cerevisiae sequence}
RAVVPIESNPEVFTNFAHKLGLKNEWAYFDIYSLTEPELLAFLPRPVKAIVLLFPINEDRKSSTS
QQITSSYDVIWFKQSVKNACGLYAILHSLSNNQSLLEPGSDLDNFLKSQSDTSSSKNRFDDVTTD
QFVLNVIKENVQTFSTGQSEAPEATADTNLHYITYVEENGGIFELDGRNLSGPLYLGKSDPTATD
LIEQELVRVRVASYMENANEEDVLNFAMLGLGPN
>d1avpa_ d.3.1.7 (A:) Human adenovirus 2 proteinase {Mastadenovirus
H2}
MGSSEQELKAIVKDLGCGPYFLGTYDKRFPGFVSPHKLACAIVNTAGRETGGVHWMAFAWNPRSK
TCYLFEPFGFSDQRLKQVYQFEYESLLRRSAIASSPDRCITLEKSTQSVQGPNSAACGLFCCMFL
HAFANWPQTPMDHNPTMNLITGVPNSMLNSPQVQPTLRRNQEQLYSFLERHSPYFRSHSAQIRSA
TSFCHLKNM
>d1euva_ d.3.1.7 (A:) Ulp1 protease C-terminal domain {Baker's yeast
(Saccharomyces cerevisiae)}
GSLVPELNEKDDDQVQKALASRENTQLMNRDNIEITVRDFKTLAPRRWLNDTIIEFFMKYIEKST
PNTVAFNSFFYTNLSERGYQGVRRWMKRKKTQIDKLDKIFTPINLNQSHWALGIIDLKKKTIGYV
DSLSNGPNAMSFAILTDLQKYVMEESKHTIGEDFDLIHLDCPQQPNGYDCGIYVCMNTLYGSADA
PLDFDYKDAIRMRRFIAHLILTDALK
>d7ceib_ d.4.1.1 (B:) DNase domain of colicin E7 {Escherichia coli}
RNKPGKATGKGKPVNNKWLNNAGKDLGSPVPDRIANKLRDKEFKSFDDFRKKFWEEVSKDPELSK
QFSRNNNDRMKVGKAPKTRTQDVSGKRTSFELHHEKPISQNGGVYDMDNISVVTPKRHIDIH
>d1emvb_ d.4.1.1 (B:) DNase domain of colicin E9 {Escherichia coli}
MESKRNKPGKATGKGKPVGDKWLDDAGKDSGAPIPDRIADKLRDKEFKSFDDFRKAVWEEVSKDP
ELSKNLNPSNKSSVSKGYSPFTPKNQQVGGRKVYELHHDKPISQGGEVYDMDNIRVTTPKRHIDI
H
>d1ql0a_ d.4.1.2 (A:) Sm endonuclease {Serratia marcescens}
SIDNCAVGCPTGGSSKVSIVRHAYTLNNNSTTKFANWVAYHITKDTPASGKTRNWKTDPALNPAD
TLAPADYTGANAALKVDRGHQAPLASLAGVSDWESLNYLSNITPQKSDLNQGAWARLEDQERKLI
DRADISSVYTVTGPLYERDMGKLPGTQKAHTIPSAYWKVIFINNSPAVNHYAAFLFDQNTPKGAD
FCQFRVTVDEIEKRTGLIIWAGLPDDVQASLKSKPGVLPELMGCKN
>d1a73a_ d.4.1.3 (A:) Intron-encoded homing endonuclease I-PpoI
{Slime mold (Physarum polycephalum)}
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ALTNAQILAVIDSWEETVGQFPVITHHVPLGGGLQGTLHCYEIPLAAPYGVGFAKNGPTRWQYKR
TINQVVHRWGSHTVPFLLEPDNINGKTCTASHLCHNTRCHNPLHLCWESLDDNKGRNWCPGPNGG
CVHAVVCLRQGPLYGPGATVAGPQQRGSHFVV
>d1e7la2 d.4.1.5 (A:1-103) Recombination endonuclease VII, C-terminal
and dimerization domains {Bacteriophage T4}
MLLTGKLYKEEKQKFYDAQNGKCLICQRELNPDVQANHLDHDHELNGPKAGKVRGLLCNLCDAAE
GQMKHKFNRSGLKGQGVDYLEWLENLLTYLKSDYTQNN
>d1dy5a_ d.5.1.1 (A:) Ribonuclease A (also ribonuclease B, S) {Cow
(Bos taurus)}
KETAAAKFERQHMDSSTSAASSSNYCNQMMKSRNLTKDRCKPVNTFVHESLADVQAVCSQKNVAC
KNGQTNCYQSYSTMSITDCRETGSSKYPNCAYKTTQANKHIIVACEGNPYVPVHFDASV
>d1h8xa_ d.5.1.1 (A:) Ribonuclease A (also ribonuclease B, S) {Cow
(Bos taurus)}
KESAAAKFERQHMDSGNSPSSSSTYCNQMMRRRNMTQGRCKPVNTFVHEPLVDVQNVCFQEKVTC
KNGQGNCYKSNSSMHITDCRLTNGSRYPNCAYRTSQKERHIIVACEGSPYVPVHFDASVE
>d1rbd__ d.5.1.1 (-) Ribonuclease A (also ribonuclease B, S) {Cow (Bos
taurus)}
SSSNYCNQMMKSRNLTKDRCKPVNTFVHESLADVQAVCSQKNVACKNGQTNCYQSYSTMSITDCR
ETGSSKYPNCAYKTTQANKHIIVACEGNPYVPVHFDASV
>g1d5d.1 d.5.1.1 (A:,B:) Ribonuclease A (also ribonuclease B, S) {Cow
(Bos taurus)}
KETAAAKMERQHLDSXNYCNQMMKSRNLTKDRCKPVNTFVHESLADVQAVCSQKNVACKNGQTNC
YQSYSTMSITDCRETGSSKYPNCAYKTTQANKHIIVACEGNPYVPVHFDASV
>d1e21a_ d.5.1.1 (A:) Ribonuclease A (also ribonuclease B, S) {Human
(Homo sapiens), des1-7}
AFQRQHMDSDSSPSSSSTYCNQMMRRRNMTQGRCKPVNTFVHEPLVDVQNVCFQEKVTCKNGQGN
CYKSNSSMHITDCRLTNGSRYPNCAYRTSPKERHIIVACEGSPYVPVHFDASVE
>d1rraa_ d.5.1.1 (A:) Ribonuclease A (also ribonuclease B, S) {Rat
(Rattus norvegicus)}
AESSADKFKRQHMDTEGPSKSSPTYCNQMMKRQGMTKGSCKPVNTFVHEPLEDVQAICSQGQVTC
KNGRNNCHKSSSTLRITDCRLKGSSKYPNCDYTTTDSQKHIIIACDGNPYVPVHFDASV
>d1onc__ d.5.1.1 (-) P-30 protein {Frog (Rana pipiens)}
EDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTSEFYL
SDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC
>d1bc4__ d.5.1.1 (-) Cytotoxic ribonuclease {Bullfrog (Rana
catesbeiana)}
ENWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLSTTR
FQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
>d11bga_ d.5.1.1 (A:) Seminal ribonucleasease {Cow (Bos taurus)}
KESAAAKFERQHMDSGNSPSSSSNYCNLMMCCRKMTQGKCKPVNTFVHESLADVKAVCSQKKVTC
KNGQTNCYQSKSTMRITDCRETGSSKYPNCAYKTTQVEKHIIVACGGKPSVPVHFDASV
>d1b6va_ d.5.1.1 (A:) Hybrid between ribonuclease A and seminal
ribonuclease {Cow (Bos taurus)}
KETAAAKFERQHMDSSTSAASSSNYCNQMMKSRNLTKDRCKPVNTFVHESLADVKAVCSQKKVTC
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KNGQTNCYQSKSTMRITDCRETGSSKYPNCAYKTTQANKHIIVACGGKPYVPVHFDASV
>d1dyta_ d.5.1.1 (A:) Eosinophil cationic protein (ECP), ribonuclease
3 {Human (Homo sapiens)}
RPPQFTRAQWFAIQHISLNPPRCTIAMRAINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHN
RTLNNCHRSRFRVPLLHCDLINPGAQNISNCRYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLD
TTI
>d1hi2a_ d.5.1.1 (A:) Eosinophil-derived neurotoxin (EDN) {Human
(Homo sapiens)}
MKPPQFTWAQWFETQHINMTSQQCTNAMQVINNYQRRCKNQNTFLLTTFANVVNVCGNPNMTCPS
NKTRKNCHHSGSQVPLIHCNLTTPSPQNISNCRYAQTPANMFYIVACDNRDQRRDPPQYPVVPVH
LDRII
>d1rnfa_ d.5.1.1 (A:) Ribonuclease 4 {Human (Homo sapiens)}
MQDGMYQRFLRQHVHPEETGGSDRYCNLMMQRRKMTLYHCKRFNTFIHEDIWNIRSICSTTNIQC
KNGKMNCHEGVVKVTDCRDTGSSRAPNCRYRAIASTRRVVIACEGNPQVPVHFDG
>d1b1ia_ d.5.1.1 (A:) Angiogenin {Human (Homo sapiens)}
EDNSRYTHFLTQHYDAKPQGRDDRYCESIMRRRGLTSPCKDINTFIHGNKRSIKAICENKNGNPH
RENLRISKSSFQVTTCKLHGGSPWPPCQYRATAGFRNVVVACENGLPVHLDQSIFRRP
>d1agi__ d.5.1.1 (-) Angiogenin {Cow (Bos taurus)}
AQDDYRYIHFLTQHYDAKPKGRNDEYCFNMMKNRRLTRPCKDRNTFIHGNKNDIKAICEDRNGQP
YRGDLRISKSEFQITICKHKGGSSRPPCRYGATEDSRVIVVGCENGLPVHFDESFITPRH
>d1ag2__ d.6.1.1 (-) Prion protein domain {Mouse (Mus musculus)}
GLGGYMLGSAMSRPMIHFGNDWEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHT
VTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYY
>d1b10a_ d.6.1.1 (A:) Prion protein domain {Golden hamster
(Mesocricetus auratus)}
LGGYMLGSAMSRPMMHFGNDWEDRYYRENMNRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTV
TTTTKGENFTETDIKIMERVVEQMCTTQYQKESQAYYDG
>d1fo7a_ d.6.1.1 (A:) Prion protein domain {Human (Homo sapiens)}
LGGYMLGSAMSRPIIHFGSDYEDRYYRENMHRYPNQVYYRPMDEYSNQNNFVHDCVNITIKQHTV
TTTTKGENFTKTDVKMMERVVEQMCITQYERESQAYYQRGSS
>d1i4ma_ d.6.1.1 (A:) Prion protein domain {Human (Homo sapiens)}
GAVVGGLGGYMLGSAMSRPIIHFGSDYEDRYYRENMHRYPNQVYYRPMDEYSNQNNFVHDCVNIT
IKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYERESQAYY
>d1dwya_ d.6.1.1 (A:) Prion protein domain {Cow (Bos taurus)}
GLGGYMLGSAMSRPLIHFGSDYEDRYYRENMHRYPNQVYYRPVDQYSNQNNFVHDCVNITVKEHT
VTTTTKGENFTETDIKMMERVVEQMCITQYQRESQAYYQ
>d1i17a_ d.6.1.1 (A:) Prion-like protein Doppel {Mouse (Mus musculus)}
RVAENRPGAFIKQGRKLDIDFGAEGNRYYAANYWQFPDGIYYEGCSEANVTKEMLVTSCVNATQA
ANQAEFSREKQDSKLHQRVLWRLIKEICSAKHCDFWLERGAA
>d1e01a_ d.7.1.1 (A:) Membrane-bound lytic murein transclycosylase
D, MltD {Escherichia coli}
DSITYRVRKGDSLSSIAKRHGVNIKDVMRWNSDTANLQPGDKLTLFVK
>d1hywa_ d.186.1.1 (A:) Head-to-tail joining protein W, gpW
{Bacteriophage lambda}
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MTRQEELAAARAALHDLMTGKRVATVQKDGRRVEFTATSVSDLKKYIAELEVQTGMTQ
>d1ejra_ d.8.1.1 (A:) Urease, gamma-subunit {Klebsiella aerogenes}
MELTPREKDKLLLFTAALVAERRLARGLKLNYPESVALISAFIMEGARDGKSVASLMEEGRHVLT
REQVMEGVPEMIPDIQVEATFPDGSKLVTVHNPII
>d4ubpa_ d.8.1.1 (A:) Urease, gamma-subunit {Bacillus pasteurii}
MHLNPAEKEKLQIFLASELLLRRKARGLKLNYPEAVAIITSFIMEGARDGKTVAMLMEEGKHVLT
RDDVMEGVPEMIDDIQAEATFPDGTKLVTVHNPIS
>d1e9ya2 d.8.1.1 (A:1-105) Urease, gamma-subunit {Helicobacter
pylori}
MKLTPKELDKLMLHYAGELAKKRKEKGIKLNYVEAVALISAHIMEEARAGKKTAAELMQEGRTLL
KPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGK
>d1qe6b_ d.9.1.1 (B:) Interleukin-8, IL-8 {Human (Homo sapiens)}
AKECRCQCIKTYSKPFHPKFIKELRVIESGPCCANTEIIVKLSDGRELCLDPKENWVQRVVEKFL
KRAENS
>d3il8__ d.9.1.1 (-) Interleukin-8, IL-8 {Human (Homo sapiens)}
LRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRELCLDPKENWVQRVVEKFLKRA
ENS
>d1plfa_ d.9.1.1 (A:) Platelet factor 4, PF4 {Cow (Bos taurus)}
LQCVCLKTTSGINPRHISSLEVIGAGLHCPSPQLIATLKTGRKICLDQQNPLYKKIIKRLLKS
>d1pfma_ d.9.1.1 (A:) Platelet factor 4, PF4 {Human (Homo sapiens)}
MSAKELRCQCVKTTSQVRPRHITSLEVIKAGPHCPTAQLIATLKNGRKICLDLQAPLYKKIIKKL
LES
>d1rhpa_ d.9.1.1 (A:) Platelet factor 4, PF4 {Human (Homo sapiens)}
DLQCLCVKTTSQVRPRHITSLEVIKAGPHCPTAQLIATLKNGRKICLDLQAPLYKKIIKKLLES
>d1mgsa_ d.9.1.1 (A:) Melanoma growth stimulating activity (MGSA)
{Human (Homo sapiens)}
ASVATELRCQCLQTLQGIHPKNIQSVNVKSPGPHCAQTEVIATLKNGRKACLNPASPIVKKIIEK
MLNSDKSN
>d1roda_ d.9.1.1 (A:) IL-8/MGSA chimeric protein CIL-8M {Human (Homo
sapiens)}
SAKELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRELCLDPASPIVKKIIEKM
LNSDKSN
>d1huna_ d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Human
(Homo sapiens), 1-beta}
APMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQPAVVFQTKRSKQVCADPSESWVQEYVYD
LELN
>d1b50a_ d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Human
(Homo sapiens), 1-alpha}
SLAADTPTACCFSYTSRQIPQNFIAAYFETSSQCSKPGVIFLTKRSRQVCADPSEEWVQKYVSDL
ELSA
>d1ha6a_ d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Mouse (Mus
musculus), ccl20/mip-3a}
ASNYDCCLSYIQTPLPSRAIVGFTRQMADEACDINAIIFHTKKRKSVCADPKQNWVKRAVNLLSL
RVKKM
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>d1cm9a_ d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Kaposi's
sarcoma herpes virus, VMIP-II}
SWHRPDKCCLGYQKRPLPQVLLSSWYPTSQLCSKPGVIFLTKRGRQVCADKSKDWVKKLMQQLPV
TAR
>d1b3aa_ d.9.1.1 (A:) RANTES (regulated upon activation, normal T-cell
expressed and secreted) {Human (Homo sapiens)}
PYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNPAVVFVTRKNRQVCANPEKKWVREYINSLE
MS
>d1doka_ d.9.1.1 (A:) Monocyte chemoattractant protein-1 (MCP-1, MCAF)
{Human (Homo sapiens)}
MQPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWVQDSM
DHLDKQT
>d1esra_ d.9.1.1 (A:) Monocyte chemoattractant protein-2 (MCP-2)
{Human (Homo sapiens)}
EPDSVSIPITCCFNVINRKIPIQRLESYTRITNIQCPKEAVIFKTQRGKEVCADPKERWVRDSMK
HLDQIFQNLKP
>d1el0a_ d.9.1.1 (A:) CC chemokine I-309 {Human (Homo sapiens)}
SKSMQVPFSRCCFSFAEQEIPLRAILCYRNTSSICSNEGLIFKLKRGKEACALDTVGWVQRHRKM
LRHCPSKRK
>d1eot__ d.9.1.1 (-) Eotaxin {Human (Homo sapiens)}
GPASVPTTCCFNLANRKIPLQRLESYRRITSGKCPQKAVIFKTKLAKDICADPKKKWVQDSMKYL
DQKSPTPKP
>d1eiha_ d.9.1.1 (A:) Eotaxin-2 {Human (Homo sapiens)}
VVIPSPCCMFFVSKRIPENRVVSYQLSSRSTCLKAGVIFTTKKGQQSCGDPKQEWVQRYMKNLDA
KQKKASPR
>d1j9oa_ d.9.1.1 (A:) Lymphotactin {Human (Homo sapiens)}
VGSEVSDKRTCVSLTTQRLPVSRIKTYTITEGSLRAVIFITKRGLKVCADPQATWVRDVVRSMDR
KSNTRNNMIQTKPTGTQQSTNTAVTLTG
>d1bo0__ d.9.1.1 (-) Monocyte chemoattractant protein-3 (MCP-3)
{Human (Homo sapiens)}
QPVGINTSTTCCYRFINKKIPKQRLESYRRTTSSHCPREAVIFKTKLDKEICADPTQKWVQDFMK
HLDKKTQTPKL
>d1b2ta_ d.9.1.1 (A:) Chemokine domain of fractalkine {Human (Homo
sapiens)}
MQHHGVTKCNITCSKMTSKIPVALLIHYQQNQASCGKRAIILETRQHRLFCADPKEQWVKDAMQH
LDRQAAALTRNG
>d1f2la_ d.9.1.1 (A:) Chemokine domain of fractalkine {Human (Homo
sapiens)}
VTKCNITCSKMTSKIPVALLIHYQQNQASCGKRAIILETRQHRLFCADPKEQWVKDAMQHLDRQ
>d1tvxa_ d.9.1.1 (A:) Neutrophil-activating peptide-2 (NAP-2) {Human
(Homo sapiens)}
LRCLCIKTTSGIHPKNIQSLEVIGKGTHCNQVEVIATLKDGRKICLDPDAPRIKKIVQKKLAGD
>d1tvxb_ d.9.1.1 (B:) Neutrophil-activating peptide-2 (NAP-2) {Human
(Homo sapiens)}
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DSDLYAELRCLCIKTTSGIHPKNIQSLEVIGKGTHCNQVEVIATLKDGRKICLDPDAPRIKKIVQKKLAGD

>d1a15a_ d.9.1.1 (A:) Stromal cell-derived factor-1 (SDF-1) {Human (Homo sapiens)}

KPVSLSYRCPCRFFESHVARANVKHLKILNTPACALQIVARLKNNNRQVCIDPKLKWIQEYLEKALN

>d1a15b_ d.9.1.1 (B:) Stromal cell-derived factor-1 (SDF-1) {Human (Homo sapiens)}

RCPCRFFESHVARANVKHLKILNTPACALQIVARLKNNNRQVCIDPKLKWIQEYLEK

>d1qg7a_ d.9.1.1 (A:) Stromal cell-derived factor-1 (SDF-1) {Human (Homo sapiens)}

SYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQEYLEKALN

>d1mi2a_ d.9.1.1 (A:) Macrophage inflammatory protein-2 {Mouse (Mus musculus)}

AVVASELRCQCLKTLPRVDFKNIQSLSVTPPGPHCAQTEVIATLKGGQKVCLDPEAPLVQKIIQKILNKGKAN

>d2hcc__ d.9.1.1 (-) Chemokine hcc-2 (macrophage inflammatory protein-5) {Human (Homo sapiens)}

HFAADCCTSYISQSIPCSLMKSYFETSSECSKPGVIFLTKKGRQVCAKPSGPGVQDCMKKLKPYSI

>d1qnka_ d.9.1.1 (A:) Gro beta {Human (Homo sapiens)}

TELRCQCLQTLQGIHLKNIQSVKVKSPGPHCAQTEVIATLKNGQKACLNPASPMVKKIIEKMLKNGKSN

>d1g91a_ d.9.1.1 (A:) Myeloid progenitor inhibitory factor-1 (MPIF-1) {Human (Homo sapiens)}

MDRFHATSADCCISYTPRSIPCSLLESYFETNSECSKPGVIFLTKKGRRFCANPSDKQVQVCMRMLKLDTRIKTRKN

>d1bf4a_ d.9.2.1 (A:) DNA-binding protein {Archaeon Sulfolobus solfataricus, Sso7d}

ATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKK

>d1azpa_ d.9.2.1 (A:) DNA-binding protein {Archaeon Sulfolobus acidocaldarius, Sac7d}

MVKVKFKYKGEEKEVDTSKIKKVWRVGKMVSFTYDDNGKTGRGAVSEKDAPKELLDMLARAEREKK

>d1ap0__ d.9.2.2 (-) Modifier protein 1 (M31, HP1 beta) {Mouse (Mus musculus)}

HMVEEVLEEEEEEYVVEKVLDRRVVKGKVEYLLKWKGFSDEDNTWEPEENLDCPDLIAEFLQSQKTAHETDKS

>d1dz1a_ d.9.2.2 (A:) Modifier protein 1 (M31, HP1 beta) {Mouse (Mus musculus)}

HMKEESEKPRGFARGLEPERIIGATDSSGELMFLMKWKNSDEADLVPAKEANVKCPQVVISFYEERLTWH

>d1e0ba_ d.9.2.2 (A:) HP1 homologue SWI6 {Fission yeast (Schizosaccharomyces pombe)}

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QVENYDSWEDLVSSIDTIERKDDGTLEIYLTWKNGAISHHPSTITNKKCPQKMLQFYESHL
>d1g6za_ d.9.2.2 (A:) Histone methyltransferase clr4 chromo domain
{Fission yeast (Schizosaccharomyces pombe)}
ISSPKQEEYEVERIVDEKLDRNGAVKLYRIRWLNYSSRSDTWEPPENLSGCSAVLAEWKRRKRRL
KGSNS
>d1bb8__ d.10.1.1 (-) DNA-binding domain from tn916 integrase
{Enterococcus faecalis}
EKRRDNRGRILKTGESQRKDGRYLYKYIDSFGEPQFVYSWKLVATDRVPAGKRDCISLREKIAEL
QKDIHD
>d1gcca_ d.10.1.2 (A:) GCC-box binding domain {Mouse-ear cress
(Arabidopsis thaliana)}
KHYRGVRQRPWGKFAAEIRDPAKNGARVWLGTFETAEDAALAYDRAAFRMRGSRALLNFPLRV
>d1qk9a_ d.10.1.3 (A:) Methyl-CpG-binding protein 2, MECP2 {Human
(Homo sapiens)}
ASASPKQRRSIIRDRGPMYDDPTLPEGWTRKLKQRKSGRSAGKYDVYLINPQGKAFRSKVELIAY
FEKVGDTSLDPNDFDFTVTGRGSGSGC
>d1d9na_ d.10.1.3 (A:) Methylation-dependent transcriptional
repressor MBD1/PCM1 {Human (Homo sapiens)}
MAEDWLDCPALGPGWKRREVFRKSGATCGRSDTYYQSPTGDRIRSKVELTRYLGPACDLTLFDFK
QGILCYPAPK
>d1k25a1 d.11.1.1 (A:632-692) Penicillin-binding protein 2x (pbp-2x),
c-terminal domain {Streptococcus pneumoniae}
TESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGTKIKETSVEEGTNLAPNQQVLLLSDK
>d1k25a2 d.11.1.1 (A:693-750) Penicillin-binding protein 2x (pbp-2x),
c-terminal domain {Streptococcus pneumoniae}
VEEIPDMYGWKKETAETFAKWLDIELEFEGSGSVVQKQDVRTNTAIKNIKKIKLTLGD
>d1qmea1 d.11.1.1 (A:632-692) Penicillin-binding protein 2x (pbp-2x),
c-terminal domain {Streptococcus pneumoniae}
QQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQQVLILSDK
>d1qmea2 d.11.1.1 (A:693-750) Penicillin-binding protein 2x (pbp-2x),
c-terminal domain {Streptococcus pneumoniae}
AEEVPDMYGWTKETAETLAKWLNIELEFQGSGSTVQKQDVRANTAIKDIKKITLTLGD
>d1jj2r_ d.12.1.1 (R:) Ribosomal protein L23 {Archaeon Haloarcula
marismortui}
SWDVIKHPHVTEKAMNDMDFQNKLQFAVDDRASKGEVADAVEEQYDVTVEQVNTQNTMDGEKKAV
VRLSEDDDAQEVASRI
>d1ffki_ d.12.1.2 (I:) Ribosomal protein L15e {Archaeon Haloarcula
marismortui}
MKSMYAYIREAWKRPYEGYVGELMWHRLQKWRREPAVVRIPRPTRLDRARALGYKAKKGIIVVRV
RIRRGGRRATRPNKGRKSKKMMVNRRPRKKNLQWIAEERANRKYPNMEVLNSYWVGEDGRYKWFE
VILVDRDHPAIKSDPQLSWVSRTRGRVYRGLTSAGRKARGLRRKGRGAEKVRPSLRANFRKKRR
>d1jj2l_ d.12.1.2 (L:) Ribosomal protein L15e {Archaeon Haloarcula
marismortui}
ARSAYSYIREAWKRPKEGQIAELMWHRMQEWRNEPAVVRIERPTRLDRARSLGYKAKQGIIVVRV
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AIRKGSSRRTRFNKGRRSKRMMVNRITRKKNIQRIAEERANRKFPNLRVLNSYSVGEDGRHKWHE
VILIDPDHPAIKSDDQLSWISRTRHRLRTFRGLTSAGRRCRGLRGQGKGSEKVRPSLRVNGAKA
>d4rhn__ d.13.1.1 (-) Histidine triad nucleotide-binding protein
(HINT) {Rabbit (Oryctolagus cuniculus)}
RPGGDTIFGKIIRKEIPAKIIFEDDQCLAFHDISPQAPTHFLVIPKKHISQISAAEDADESLLGH
LMIVGKKCAADLGLKKGYRMVVNEGSDGGQSVYHVHLHVLGGRQMNWPPG
>d1fit__ d.13.1.1 (-) FHIT (fragile histidine triad protein) {Human
(Homo sapiens)}
SFRFGQHLIKPSVVFLKTELSFALVNRKPVVPGHVLVCPLRPVERFHDLRPDEVADLFQTTQRVG
TVVEKHFHGTSLTFSMQDGPEAGQTVKHVHVHVLPRKAGDFHRNDSIYEELQKHDKEDFPASWRS
EEEMAAEAAALRVYFQ
>d1kpf__ d.13.1.1 (-) Protein kinase C inhibitor-1, PKCI-1 {Human (Homo
sapiens)}
DTIFGKIIRKEIPAKIIFEDDRCLAFHDISPQAPTHFLVIPKKHISQISVAEDDDESLLGHLMIV
GKKCAADLGLNKGYRMVVNEGSDGGQSVYHVHLHVLGGRQMHWPPG
>d1emsa1 d.13.1.1 (A:281-440) NIT-FHIT fusion protein, C-terminal
domain {Nematode (Caenorhabditis elegans)}
RSDLYTLHINEKSSETGGLKFARFNIPADHIFYSTPHSFVFVNLKPVTDGHVLVSPKRVVPRLTD
LTDAETADLFIVAKKVQAMLEKHHNVTSTTICVQDGKDAGQTVPHVHIHILPRRAGDFGDNEIYQ
KLASHDKEPERKPRSNEQMAEEAVVYRNLM
>d1guqa1 d.13.1.2 (A:2-177) Galactose-1-phosphate
uridylyltransferase {Escherichia coli}
TQFNPVDHPHRRYNPLTGQWILVSPHRAKRPWQGAQETPAKQVLPAHDPDCFLCAGNVRVTGDKN
PDYTGTYVFTNDFAALMSDTPDAPESHDPLMRCQSARGTSRVICFSPDHSKTLPELSVAALTEIV
KTWQEQTAELGKTYPWVQVFENKGAAMGCSNPHPGGQIWANSFLPN
>d1guqa2 d.13.1.2 (A:178-348) Galactose-1-phosphate
uridylyltransferase {Escherichia coli}
EAEREDRLQKEYFAEQKSPMLVDYVQRELADGSRTVVETEHWLAVVPYWAAWPFETLLLPKAHVL
RITDLTDAQRSDLALALKKLTSRYDNLFQCSFPYSMGWHGAPFNGEENQHWQLHAHFYPPLLRSA
TVRKFMVGYEMLAETQRDLTAEQAAERLRAVSDIHFRESGV
>d1jyaa_ d.198.1.1 (A:) YopE chaperone SycE {Yersinia pestis}
YSFEQAITQLFQQLSLSIPDTIEPVIGVKVGEFACHITEHPVGQILMFTLPSLDNNDEKETLLSH
NIFSQDILKPILSWDEVGGHPVLWNRQPLNSLDNNSLYTQLEMLVQGAERLQ
>d1k6za_ d.198.1.1 (A:) YopE chaperone SycE {Yersinia pestis}
SFEQAITQLFQQLSLSIPDTIEPVIGVKVGEFACHITEHPVGQILMFTLPSLDNNDEKETLLSHN
IFSQDILKPILSWDEVGGHPVLWNRQPLNSLDNNSLYTQLEMLVQGAERLQTSSLISPPRSFSHH
>d1jyoa_ d.198.1.1 (A:) Virulence effector SptP secretion chaperone
SicP {Salmonella typhimurium}
LQAHQDIIANIGEKLGLPLTFDDNNQCLLLLDSDIFTSIEAKDDIWLLNGMIIPLSPVCGDSIWR
QIMVINGELAANNEGTLAYIDAAETLLLIHAITDLTNTYHIISQLESFVNQQEALKNILQEYAKV
>d1k3ea_ d.198.1.1 (A:) Secretion chaperone CesT {Escherichia coli}
MSSRSELLLEKFAEKIGIGSISFNENRLCSFAIDEIYYISLSDANDEYMMIYGVCGKFPTDNSNF
ALEILNANLWFAENGGPYLCYEAGAQSLLLALRFPLDDATPEKLENEIEVVVKSMENLYLVLHNQ
GITLENEHMKIEEISS
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>d1k3sa_ d.198.1.1 (A:) Secretion chaperone SigE {Salmonella enterica}
MESLLNRLYDALGLDAPEDEPLLIIDDGIQVYFNESDHTLEMCCPFMPLPDDILTLQHFLRLNYT
SAVTIGADADNTALVALYRLPQTSTEEEALTGFELFISNVKQLKEHYA
>d1k8kf_ d.198.2.1 (F:) ARPC4 (20 kDa subunit) {Cow (Bos taurus)}
TATLRPYLSAVRATLQAALCLENFSSQVVERHNKPEVEVRSSKELLLQPVTISRNEKEKVLIEGS
INSVRVSIAVKQADEIEKILCHKFMRFMMMRAENFFILRRKPVEGYDISFLITNFHTEQMYKHKL
VDFVIHFMEEIDKEISEMKLSVNARARIVAEEFLKNF
>d1k8kd1 d.198.2.1 (D:1-120) ARPC2 (34 kDa subunit) {Cow (Bos taurus)}
MILLEVNNRIIEETLALKFENAAAGNKPEAVEVTFADFDGVLYHISNPNGDKTKVMVSISLKFYK
ELQAHGADELLKRVYGSYLVNPESGYNVSLLYDLENLPASKDSIVHQAGMLKRNC
>d1k8kd2 d.198.2.1 (D:121-284) ARPC2 (34 kDa subunit) {Cow (Bos taurus)}
FASVFEKYFQFQEEGKEGENRAVIHYRDDETMYVESKKDRVTVVFSTVFKDDDDVVIGKVFMQEF
KEGRRASHTAPQVLFSHREPPLELKDTDAAVGDNIGYITFVLFPRHTNASARDNTINLIHTFRDY
LHYHIKCSKAYIHTRMRAKTSDFLKVLNRARPDA
>d1kafa_ d.199.1.1 (A:) DNA-binding C-terminal domain of the transcription factor MotA {Bacteriophage T4}
MEITSDMEEDKDLMLKLLDKNGFVLKKVEIYRSNYLAILEKRTNGIRNFEINNNGNMRIFGYKMM
EHHIQKFTDIGMSCKIAKNGNVYLDIKRSAENIEAVITVASEL
>d1dar_3 d.14.1.1 (476-599) Elongation factor G (EF-G), domain IV {Thermus thermophilus}
VGKPQVAYRETITKPVDVEGKFIRQTGGRGQYGHVKIKVEPLPRGSGFEFVNAIVGGVIPKEYIP
AVQKGIEEAMQSGPLIGFPVVDIKVTLYDGSYHEVDSSEMAFKIAGSMAIKEAVQKGDP
>d1pkp_1 d.14.1.1 (78-148) Ribosomal protein S5, C-terminal domain {Bacillus stearothermophilus}
GTTIPHEVIGHFGAGEIILKPASEGTGVIAGGPARAVLELAGISDILSKSIGSNTPINMVRATFD
GLKQLK
>d1fjge1 d.14.1.1 (E:74-154) Ribosomal protein S5, C-terminal domain {Thermus thermophilus}
GTIPHEIEVEFGASKIVLKPAAPGTGVIAGAVPRAILELAGVTDILTKELGSRNPINIAYATMEA
LRQLRTKADVERLRKG
>d1fjgi_ d.14.1.1 (I:) Ribosomal protein S9 {Thermus thermophilus}
EQYYGTGRRKEAVARVFLRPGNGKVTVNGQDFNEYFQGLVRAVAALEPLRAVDALGRFDAYITVR
GGGKSGQIDAIKLGIARALVQYNPDYRAKLKPLGFLTRDARVVERKKYGKHKARRAPQYSKR
>d1a6f__ d.14.1.2 (-) RNase P protein {Bacillus subtilis}
AHLKKRNRLKKNEDFQKVFKHGTSVANRQFVLYTLDQPENDELRVGLSVSKKIGNAVMRNRIKRL
IRQAFLEEKERLKEKDYIIIARKPASQLTYEETKKSLQHLFRKSSLYK
>d1d6ta_ d.14.1.2 (A:) RNase P protein {Staphylococcus aureus}
MLLEKAYRIKKNADFQRIYKKGHSVANRQFVVYTCNNKEIDHFRLGISVSKKLGNAVLRNKIKRA
IRENFKVHKSHILAKDIIVIARQPAKDMTTLQIQNSLEHVLKIAKVFNKKIK
>d1b63a1 d.14.1.3 (A:217-331) DNA mismatch repair protein MutL {Escherichia coli}
GTAFLEQALAIEWQHGDLTLRGWVADPNHTTPALAEIQYCYVNGRMMRDRLINHAIRQACEDKLG
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ADQQPAFVLYLEIDPHQVDVNVHPAKHEVRFHQSRLVHDFIYQGVLSVLQ
>d1h7sa1 d.14.1.3 (A:232-365) DNA mismatch repair protein PMS2 {Human
(Homo sapiens)}
GQKQLQSLIPFVQLPPSDSVCEEYGLSCSDALHNLFYISGFISQCTHGVGRSSTDRQFFFINRRP
CDPAKVCRLVNEVYHMYNRHQYPFVVLNISVDSECVDINVTPDKRQILLQEEKLLLAVLKTSLIG
MFDS
>d1ei1a1 d.14.1.3 (A:221-392) DNA gyrase B {Escherichia coli}
GIKAFVEYLNKNKTPIHPNIFYFSTEKDGIGVEVALQWNDGFQENIYCFTNNIPQRDGGTHLAGF
RAAMTRTLNAYMDKEGYSKKAKVSATGDDAREGLIAVVSVKVPDPKFSSQTKDKLVSSEVKSAVE
QQMNELLAEYLLENPTDAKIVVGKIIDAARAREAARRAREMT
>d1e3ha2 d.14.1.4 (A:3-151) Polynucleotide phosphorylase/guanosine
pentaphosphate synthase (PNPase/GPSI), domains 1 and 4 {Streptomyces
antibioticus}
NETHYAEAVIDNGAFGTRTIRFETGRLARQAAGSAVAYLDDDTMVLSATTASKNPKDQLDFFPLT
VDVEERMYAAGKIPGSFFRREGRPSEDAILTCRLIDRPLRPSFKKGLRNEIQVVATIMALNPDHL
YDVVAINAASASTQLAGLP
>d1e3ha3 d.14.1.4 (A:346-482) Polynucleotide phosphorylase/guanosine
pentaphosphate synthase (PNPase/GPSI), domains 1 and 4 {Streptomyces
antibioticus}
TDIRTLAAEVEAIPRVHGSALFERGETQILGVTTLNMLRMEQQLDTLSPVTRKRYMHNYNFPPYS
VGETGRVGSPKRREIGHGALAERAIVPVLPTREEFPYAIRQVSEALGSNGSTSMGSVCASTMSLL
NAGVPLK
>d1h72c1 d.14.1.5 (C:5-167) Homoserine kinase {Archaeon Methanococcus
jannaschii}
MKVRVKAPCTSANLGVGFDVFGLCLKEPYDVIEVEAIDDKEIIIEVDDKNIPTDPDKNVAGIVAK
KMIDDFNIGKGVKITIKKGVKAGSGLGSSAASSAGTAYAINELFKLNLDKLKLVDYASYGELASS
GAKHADNVAPAIFGGFTMVTNYEPLEVLHIPID
>d1fi4a1 d.14.1.5 (A:3-190) Mevalonate 5-diphosphate decarboxylase
{Baker's yeast (Saccharomyces cerevisiae)}
VYTASVTAPVNIATLKYWGKRDTKLNLPTNSSISVTLSQDDLRTLTSAATAPEFERDTLWLNGEP
HSIDNERTQNCLRDLRQLRKEMESKDASLPTLSQWKLHIVSENNFPTAAGLASSAAGFAALVSAI
AKLYQLPQSTSEISRIARKGSGSACRSLFGGYVAWEMGKAEDGHDSMAVQIADSSDWP
>d1c3ta_ d.15.1.1 (A:) Ubiquitin {Human (Homo sapiens)}
MQLFVKTLTGKTLTVELEPSDTVENLKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNLQKES
TIHLVLRLRGG
>d1gjza_ d.15.1.1 (A:) Ubiquitin {Human (Homo sapiens)}
GSMQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLE
>d1ubi__ d.15.1.1 (-) Ubiquitin {Human (Homo sapiens)}
MQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNIQKES
TLHLVLRLRGG
>d1ud7a_ d.15.1.1 (A:) Ubiquitin {Human (Homo sapiens)}
MQVFLKTLTGKTVTIEVEPSDTVENFKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNIQKES
TIHLVLRLRGG
>d1a5r__ d.15.1.1 (-) SUMO-1 (smt3 homologue) {Human (Homo sapiens)}
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GSMSDQEAKPSTEDLGDKKEGEYIKLKVIGQDSSEIHFKVKMTTHLKKLKESYCQRQGVPMNSLR
FLFEGQRIADNHTPKELGMEEEDVIEVYQEQTGGHSTV
>d1euvb_ d.15.1.1 (B:) SUMO-1 (smt3 homologue) {Baker's yeast
(Saccharomyces cerevisiae)}
PETHINLKVSDGSSEIFFKIKKTTPLRRLMEAFAKRQGKEMDSLRFLYDGIRIQADQTPEDLDME
DNDIIEAHREQIGG
>d1ndda_ d.15.1.1 (A:) Nedd8 {Human (Homo sapiens)}
MLIKVKTLTGKEIEIDIEPTDKVERIKERVEEKEGIPPQQQRLIYSGKQMNDEKTAADYKILGGS
VLHLVLALR
>d1vcba_ d.15.1.1 (A:) Elongin B {Human (Homo sapiens)}
MDVFLMIRRHKTTIFTDAKESSTVFELKRIVEGILKRPPDEQRLYKDDQLLDDGKTLGECGFTSQ
TARPQAPATVGLAFRADDTFEALCIEPFSSPPE
>d1bt0a_ d.15.1.1 (A:) Rub1 {Mouse-ear cress (Arabidopsis thaliana)}
MLIKVKTLTGKEIEIDIEPTDTIDRIKERVEEKEGIPPVQQRLIYAGKQLADDKTAKDYNIEGGS
VLHLVLAL
>d1h8ca_ d.15.1.2 (A:) Fas-assosiated factor 1, Faf1 {Human (Homo
sapiens)}
NAEPVSKLRIRTPSGEFLERRFLASNKLQIVFDFVASKGFPWDEYKLLSTFPRRDVTQLDPNKSL
LEVKLFPQETLFLEAKE
>d1i42a_ d.15.1.2 (A:) p47 {Rat (Rattus norvegicus)}
KASSSILINEAEPTTNIQIRLADGGRLVQKFNHSHRISDIRLFIVDARPAMAATSFVLMTTFPNK
ELADENQTLKEANLLNAVIVQRLT
>d1eo6a_ d.15.1.3 (A:) Golgi-associated ATPase enhancer of 16 kD,
Gate-16 {Cow (Bos taurus)}
MKWMFKEDHSLEHRCVESAKIRAKYPDRVPVIVEKVSGSQIVDIDKRKYLVPSDITVAQFMWIIR
KRIQLPSEKAIFLFVDKTVPQSSLTMGQLYEKEKDEDGFLYVAYSGENTFG
>d1gnua_ d.15.1.3 (A:) GABA(A) receptor associated protein GABARAP
{Human (Homo sapiens)}
MKFVYKEEHPFEKRRSEGEKIRKKYPDRVPVIVEKAPKARIGDLDKKKYLVPSDLTVGQFYFLIR
KRIHLRAEDALFFFVNNVIPPTSATMGQLYQEHHEEDFFLYIAYSDESVYGL
>d1ef1a3 d.15.1.4 (A:4-87) Moesin {Human (Homo sapiens)}
TISVRVTTMDAELEFAIQPNTTGKQLFDQVVKTIGLREVWFFGLQYQDTKGFSTWLKLNKKVTAQ
DVRKESPLLFKFRAKFYPE
>d1gc7a3 d.15.1.4 (A:1-87) Radixin {Mouse (Mus musculus)}
MPKPINVRVTTMDAELEFAIQPNTTGKQLFDQVVKTVGLREVWFFGLQYVDSKGYSTWLKLNKKV
TQQDVKKENPLQFKFRAKFFPE
>d1gg3a3 d.15.1.4 (A:1-81) Erythroid membrane protein 4.1R {Human
(Homo sapiens)}
MHCKVSLLDDTVYECVVEKHAKGQDLLKRVCEHLNLLEEDYFGLAIWDNATSKTWLDSAKEIKKQ
VRGVPWNFTFNVKFYP
>d1h4ra3 d.15.1.4 (A:20-103) Merlin {Human (Homo sapiens)}
KTFTVRIVTMDAEMEFNCEMKWKGKDLFDLVCRTLGLRETWFFGLQYTIKDTVAWLKMDKKVLDH
DVSKEEPVTFHFLAKFYPE
>d1c1yb_ d.15.1.5 (B:) c-Raf1 RBD {Human (Homo sapiens)}
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SNTIRVFLPNKQRTVVNVRNGMSLHDCLMKALKVRGLQPECCAVFRLLHEHKGKKARLDWNTDAA
SLIGEELQVDFL
>d1lfda_ d.15.1.5 (A:) Ral guanosine-nucleotide exchange factor,
RalGDS {Rat (Rattus norvegicus)}
GDCCIIRVSLDVDNGNMYKSILVTSQDKAPTVIRKAMDKHNLDEDEPEDYELLQIISEDHKLKIP
ENANVFYAMNSAANYDFILKKR
>d1raxa_ d.15.1.5 (A:) Ral guanosine-nucleotide exchange factor,
RalGDS {Human (Homo sapiens)}
QQVGDCCIIRVSLDVDNGNMYKSILVTSQDKAPAVIRKAMDKHNLEEEEPEDYELLQILSDDRKL
KIPENANVFYAMNSTANYDFVLKKRTFT
>d1rlf__ d.15.1.5 (-) RalGDS-like factor, Rlf {Mouse (Mus musculus)}
GSSDCRIIRVQMELGEDGSVYKSILVTSQDKAPSVISRVLKKNNRDSAVASEFELVQLLPGDREL
TIPHSANVFYAMDGASHDFLLRQRR
>d1ef5a_ d.15.1.5 (A:) Rgl {Mouse (Mus musculus)}
EDTCIIRISVEDNNGNMYKSIMLTSQDKTPAVIQRAMSKHNLESDPAEEYELVQVISEDKELVIP
DSANVFYAMNSQVNFDFILRKKN
>d1e8xa3 d.15.1.5 (A:142-321) Phoshoinositide 3-kinase (PI3K) {Pig
(Sus scrofa)}
AASEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPKLYAMHPWVTSKP
LPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFTKMAKKKSLMDIPESQNERDFV
LRVCGRDEYLVGETPIKNFQWVRQCLKNGEEIHLVLDTPPDPALDEVRKE
>d1e8ya3 d.15.1.5 (A:143-322) Phoshoinositide 3-kinase (PI3K) {Human
(Homo sapiens)}
MSEESQAFQRQLTALIGYDVTDVSNVHDDELEFTRRGLVTPRMAEVASRDPKLYAMHPWVTSKPL
PEYLWKKIANNCIFIVIHRSTTSQTIKVSPDDTPGAILQSFFTKMAKKKSLMDIPESQSEQDFVL
RVCGRDEYLVGETPIKNFQWVRHCLKNGEEIHVVLDTPPDPALDEVRKEE
>d1i35a_ d.15.1.5 (A:) Protein kinase byr2 {Yest (Schizosaccharomyces
pombe)}
CILRFIACNGQTRAVQSRGDYQKTLAIALKKFSLEDASKFIVCVSQSSRIKLITEEEFKQICFNS
SSPERDRLIIVPKEKPCPSFEDLRRSWEIE
>d1d4ba_ d.15.2.1 (A:) Cell death-inducing effector B (CIDE-B),
N-terminal domain {Human (Homo sapiens)}
MEYLSALNPSDLLRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATRQELLAKALE
TLLLNGVLTLVLEEDGTAVDSEDFFQLLEDDTCLMVLQSGQSWSPTRSGVLHHHHHH
>d1c9fa_ d.15.2.1 (A:) Caspase-activated DNase (CAD), DFF40,
N-terminal domain {Mouse (Mus musculus)}
MCAVLRQPKCVKLRALHSACKFGVAARSCQELLRKGCVRFQLPMPGSRLCLYEDGTEVTDDCFPG
LPNDAELLLLTAGETWHGYVSD
>d1ibxa_ d.15.2.1 (A:) Caspase-activated DNase (CAD), DFF40,
N-terminal domain {Human (Homo sapiens)}
MLQKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPD
NAELVLLTLGQAWQGH
>d1f2ri_ d.15.2.1 (I:) Inhibitor of caspase-activated DNase (ICAD),
DFF45, N-terminal domain {Mouse (Mus musculus)}
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MELSRGASAPDPDDVRPLKPCLLRRNHSRDQHGVAASSLEELRSKACELLAIDKSLTPITLVLAEDGTIVDDDDYFLCLPSNTKFVALACNEKWTYNDSD
>d1ibxb_ d.15.2.1 (B:) Inhibitor of caspase-activated DNase (ICAD), DFF45, N-terminal domain {Human (Homo sapiens)}
SGEIRTLKPCLLRRNYSREQHGVAASCLEDLRSKACDILAIDKSLTPVTLVLAEDGTIVDDDDYFLCLPSNTKFVALASNEKWAYNNSD
>d1ip9a_ d.15.2.2 (A:) Bud emergence mediator Bemp1 {Baker's yeast (Saccharomyces cerevisiae)}
GAMGSSTSGLKTTKIKFYYKDDIFALMLKGDTTYKELRSKIAPRIDTDNFKLQTKLFDGSGEEIKTDSQVSNIIQAKLKISVHDI
>d1fm0d_ d.15.3.1 (D:) Molybdopterin synthase subunit MoaD {Escherichia coli}
MIKVLFFAQVRELVGTDATEVAADFPTVEALRQHMAAQSDRWALALEDGKLLAAVNQTLVSFDHPLTDGDEVAFFPPVTGG
>d1f0za_ d.15.3.2 (A:) Thiamin biosynthesis sulfur carrier protein ThiS {Escherichia coli}
MQILFNDQAMQCAAGQTVHELLEQLDQRQAGAALAINQQIVPREQWAQHIVQDGDQILLFQVIAGG
>d1jsba_ d.15.3.2 (A:) Hypothetical protein MTH1743 {Archaeon Methanobacterium thermoautotrophicum}
MVIGMKFTVITDDGKKILESGAPRRIKDVLGELEIPIETVVVKKNGQIVIDEEEIFDGDIIEVIRVIYGG
>d1czpa_ d.15.4.1 (A:) 2Fe-2S ferredoxin {Cyanobacterium (Anabaena sp.), pcc 7119 and 7120}
ATFKVTLINEAEGTKHEIEVPDDEYILDAAEEQGYDLPFSCRAGACSTCAGKLVSGTVDQSDQSFLDDDQIEAGYVLTCVAYPTSDVVIQTHKEEDLY
>d1frd__ d.15.4.1 (-) 2Fe-2S ferredoxin {Cyanobacterium (Anabaena sp.), pcc 7119 and 7120}
ASYQVRLINKKQDIDTTIEIDEETTILDGAEENGIELPFSCHSGSCSSCVGKVVEGEVDQSDQIFLDDEQMGKGFALLCVTYPRSNCTIKTHQEPYLA
>d4fxc__ d.15.4.1 (-) 2Fe-2S ferredoxin {Spirulina platensis}
ATYKVTLINEAEGINETIDCDDDTYILDAAEEAGLDLPYSCRAGACSTCAGTITSGTIDQSDQSFLDDDQIEAGYVLTCVAYPTSDCTIKTHQEEGLY
>d1fxia_ d.15.4.1 (A:) 2Fe-2S ferredoxin {Cyanobacterium (Aphanothece sacrum)}
ASYKVTLKTPDGDNVITVPDDEYILDVAEEEGLDLPYSCRAGACSTCAGKLVSGPAPDEDQSFLDDDQIQAGYILTCVAYPTGDCVIETHKEEALY
>d1dox__ d.15.4.1 (-) 2Fe-2S ferredoxin {Synechocystis sp., pcc 6803}
ASYTVKLITPDGESSIECSDDTYILDAAEEAGLDLPYSCRAGACSTCAGKITAGSVDQSDQSFLDDDQIEAGYVLTCVAYPTSDCTIETHKEEDLY
>d2cjn__ d.15.4.1 (-) 2Fe-2S ferredoxin {Synechococcus elongatus}
ATYKVTLVRPDGSETTIDVPEDEYILDVAEEQGLDLPFSCRAGACSTCAGKLLEGEVDQSDQSFLDDDQIEKGFVLTCVAYPRSDCKILTNQEEELY
>d1awd__ d.15.4.1 (-) 2Fe-2S ferredoxin {Chlorella fusca}

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YKVTLKTPSGEETIECPEDTYILDAAEEAGLDLPYSCRAGACSSCAGKVESGEVDQSDQSFLDDA
QMGKGFVLTCVAYPTSDVTILTHQEAALY
>d1frra_ d.15.4.1 (A:) 2Fe-2S ferredoxin {Equisetum arvense}
AYKTVLKTPSGEFTLDVPEGTTILDAAEEAGYDLPFSCRAGACSSCLGKVVSGSVDESEGSFLDD
GQMEEGFVLTCIAIPESDLVIETHKEEELF
>d1doi__ d.15.4.1 (-) 2Fe-2S ferredoxin {Archaeon Haloarcula
marismortui}
PTVEYLNYEVVDDNGWDMYDDDVFGEASDMDLDDEDYGSLEVNEGEYILEAAEAQGYDWPFSCRA
GACANCAAIVLEGDIDMDMQQILSDEEVEDKNVRLTCIGSPDADEVKIVYNAKHLDYLQNRVI
>d1e0za_ d.15.4.1 (A:) 2Fe-2S ferredoxin {Archaeon Halobacterium
halobium}
PTVEYLNYETLDDQGWDMDDDDLFEKAADAGLDGEDYGTMEVAEGEYILEAAEAQGYDWPFSCRA
GACANCASIVKEGEIDMDMQQILSDEEVEEKDVRLTCIGSPAADEVKIVYNAKHLDYLQNRVI
>d1pfd__ d.15.4.1 (-) 2Fe-2S ferredoxin {Parsley (Petroselinum
crispum)}
ATYNVKLITPDGEVEFKCDDDVYVLDQAEEEGIDIPYSCRAGSCSSCAGKVVSGSIDQSDQSFLD
DEQMDAGYVLTCHAYPTSDVVIETHKEEEIV
>d1a70__ d.15.4.1 (-) 2Fe-2S ferredoxin {Spinach (Spinacia oleracea)}
AAYKVTLVTPTGNVEFQCPDDVYILDAAEEEGIDLPYSCRAGSCSSCAGKLKTGSLNQDDQSFLD
DDQIDEGWVLTCAAYPVSDVTIETHKKEELTA
>d1gaqb_ d.15.4.1 (B:) 2Fe-2S ferredoxin {Maize (Zea mays)}
ATYNVKLITPEGEVELQVPDDVYILDQAEEDGIDLPYSCRAGSCSSCAGKVVSGSVDQSDQSYLD
DGQIADGWVLTCHAYPTSDVVIETHKEEELTGA
>d1e9ma_ d.15.4.1 (A:) Ferredoxin VI {Rhodobacter capsulatus}
AKIIFIEHNGTRHEVEAKPGLTVMEAARDNGVPGIDADCGGACACSTCHAYVDPAWVDKLPKALP
TETDMIDFAYEPNPATSRLTCQIKVTSLLDGLVVHLPEKQI
>d1put__ d.15.4.1 (-) Putidaredoxin {Pseudomonas putida}
SKVVYVSHDGTRRQLDVADGVSLMQAAVSNGIYDIVGDCGGSASCATCHVYVNEAFTDKVPAANE
REIGMLECVTAELKPNSRLCCQIIMTPELDGIVVDVPDRQW
>d1b9ra_ d.15.4.1 (A:) Terpredoxin {Pseudomonas sp.}
PRVVFIDEQSGEYAVDAQDGQSLMEVATQNGVPGIVAECGGSCVCATCRIEIEDAWVEIVGEANP
DENDLLQSTGEPMTAGTRLSCQVFIDPSMDGLIVRVPLPA
>d1ayfa_ d.15.4.1 (A:) Adrenodoxin {Cow (Bos taurus)}
KITVHFINRDGETLTTKGKIGDSLLDVVVQNNLDIDGFGACEGTLACSTCHLIFEQHIFEKLEAI
TDEENDMLDLAYGLTDRSRLGCQICLTKAMDNMTVRVP
>d1feha2 d.15.4.2 (A:1-126) Fe-only hydrogenase, N-terminal domain
{Clostridium pasteurianum}
MKTIIINGVQFNTDEDTTILKFARDNNIDISALCFLNNCNNDINKCEICTVEVEGTGLVTACDTL
IEDGMIINTNSDAVNEKIKSRISQLLDIHEFKCGPCNRRENCEFLKLVIKYKARASKPFLP
>d1hlra2 d.15.4.2 (A:1-80) Aldehyde oxidoreductase, N-terminal domain
{Desulfovibrio gigas}
MIQKVITVNGIEQNLFVDAEALLSDVLRQQLGLTGVKVGCEQGQCGACSVILDGKVVRACVTKMK
RVADGAQITTIEGVG
>d1dgja2 d.15.4.2 (A:1-80) Aldehyde oxidoreductase, N-terminal domain
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{Desulfovibrio desulfuricans}
METKTLIVNGMARRLLVSPNDLLVDVLRSQLQLTSVKVGCGKGQCGACTVILDGKVVRACIIKMS
RVAENASVTTLEGIG
>d1fo4a2 d.15.4.2 (A:3-92) Xanthine oxidase, N-terminal domain {Cow (Bos taurus)}
ADELVFFVNGKKVVEKNADPETTLLAYLRRKLGLRGTKLGCGEGGCGACTVMLSKYDRLQDKIIH
FSANACLAPICTLHHVAVTTVEGIG
>d1jroa2 d.15.4.2 (A:1-84) Xanthine dehydrogenase chain A, N-terminal domain {Rhodobacter capsulatus}
MEIAFLLNGETRRVRIEDPTQSLLELLRAEGLTGTKEGCNEGDCGACTVMIRDAAGSRAVNACLM
MLPQIAGKALRTIEGIAAP
>d1qj2a2 d.15.4.2 (A:3-81) Carbone monoxide (CO) dehydrogenase iron-sulfur protein, N-domain {Pseudomonas carboxydovorans}
KAHIELTINGHPVEALVEPRTLLIHFIREQQNLTGAHIGCDTSHCGACTVDLDGMSVKSCTMFAV
QANGASITTIEGMA
>d1ffva2 d.15.4.2 (A:3-81) Carbone monoxide (CO) dehydrogenase iron-sulfur protein, N-domain {Hydrogenophaga pseudoflava}
KKIITVNVNGKAQEKAVEPRTLLIHFLREELNLTGAHIGCETSHCGACTVDIDGRSVKSCTHLAV
QCDGSEVLTVEGLA
>d2pia_3 d.15.4.2 (224-321) Phthalate dioxygenase reductase, C-terminal domain {Pseudomonas cepacia, db01}
SFGATNTNARENTPFTVRLSRSGTSFEIPANRSILEVLRDANVRVPSSCESGTCGSCKTALCSGE
ADHRDMVLRDDEKGTQIMVCVSRAKSAELVLDL
>d1fumb2 d.15.4.2 (B:1-105) Fumarate reductase iron-sulfur protein, N-terminal domain {Escherichia coli}
AEMKNLKIEVVRYNPEVDTAPHSAFYEVPYDATTSLLDALGYIKDNLAPDLSYRWSCRMAICGSC
GMMVNNVPKLACKTFLRDYTDGMKVEALANFPIERDLVVD
>d1qlab2 d.15.4.2 (B:1-106) Fumarate reductase iron-sulfur protein, N-terminal domain {Wolinella succinogenes}
MGRMLTIRVFKYDPQSAVSKPHFQEYKIEEAPSMTIFIVLNMIRETYDPDLNFDFVCRAGICGSC
GMMINGRPSLACRTLTKDFEDGVITLLPLPAFKLIKDLSVD
>d1jq4a_ d.15.4.2 (A:) Methane monooxygenase reductase N-terminal domain {Methylococcus capsulatus}
MQRVHTITAVTEDGESLRFECRSDEDVITAALRQNIFLMSSCREGGCATCKALCSEGDYDLKGCS
VQALPPEEEEEGLVLLCRTYPKTDLEIELPYTH
>d1ssn__ d.15.5.1 (-) Staphylokinase {Staphylococcus aureus}
SSSFDKGKYKKGDDASYFEPTGPYLMVNVTGVDSKGNELLSPHYVEFPIKPGTTLTKEKIEYYVE
WALDATAYKEFRVVELDPSAKIEVTYYDKNKKKEETKSFPITEKGFVVPDLSEHIKNPGFNLITK
VVIEKK
>d2sak__ d.15.5.1 (-) Staphylokinase {Staphylococcus aureus}
SYFEPTGPYLMVNVTGVDSKGNELLSPHYVEFPIKPGTTLTKEKIEYYVEWALDATAYKEFRVVE
LDPSAKIEVTYYDKNKKKEETKSFPITEKGFVVPDLSEHIKNPGFNLITKVVIEKK
>d1bmlc1 d.15.5.1 (C:12-148) Streptokinase {Streptococcus equisimilis}

SVNNSQLVVSVAGTVEGTNQDISLKFFEIDLTSRPAHGGKTEQGLSPKSKPFATDSGAMPHKLEK
ADLLKAIQEQLIANVHSNDDYFEVIDFASDATITDRNGKVYFADKDGSVTLPTQPVQEFLLSGHV
RVRPYKE
>d1bmlc3 d.15.5.1 (C:285-372) Streptokinase {Streptococcus equisimilis}
DPFDRSHLKLFTIKYVDVNTNELLKSEQLLTASERNLDFRDLYDPRDKAKLLYNNLDAFGIMDYT
LTGKVEDNHDDTNRIITVYMGKR
>d1c4pc_ d.15.5.1 (C:) Streptokinase {Streptococcus equisimilis}
KPIQNQAKSVDVEYTVQFTPLNPDDDFRPGLKDTKLLKTLAIGDTITSQELLAQAQSILNKTHPG
YTIYERDSSIVTHDNDIFRTILPMDQEFTYHVKNREQAYEINKKSGLNEEINNTDLISEKYYVLK
KG
>d1qqra_ d.15.5.1 (A:) Streptokinase {Streptococcus equisimilis}
IQNQAKSVDVEYTVQFTPLNPDDDFRPGLKLTKLLKTLAIGDTITSQELLAQAQSILNKNHPGYT
IYERDSSIVTHDNDIFRTILPMDQEFTYRVKNREQAYRINKKSGLNEEINNTDLISEKYYVLKKG
EKPYDPFD
>d1esfa2 d.15.6.1 (A:121-233) Staphylococcal enterotoxin A, SEA {Staphylococcus aureus}
EEKKVPINLWLDGKQNTVPLETVKTNKKNVTVQELDLQARRYLQEKYNLYNSDVFDGKVQRGLIV
FHTSTEPSVNYDLFGAQGQYSNTLLRIYRDNKTINSENMHIDIYLYTS
>d1i4pa2 d.15.6.1 (A:121-239) Staphylococcal enterotoxin C2, SEC2 {Staphylococcus aureus}
NHFDNGNLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEFNSSPYETGY
IKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEVHLTTKNG
>d3tss_2 d.15.6.1 (94-194) Toxic shock syndrome toxin-1 (TSST-1) {Staphylococcus aureus}
LPTPIELPLKVKVHGKDSPLKYWPKFDKKQLAISTLDFKIRHQLTQTHGLYRSSDKTGGYWKITM
NDGSTYQSDLSKKFEYNTEKPPINIDEIKTIEAEIN
>d1sebd2 d.15.6.1 (D:127-235) Staphylococcal enterotoxin B, SEB {Staphylococcus aureus}
DKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYETGYIKFIENENSFWY
DMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLT
>d3seb_2 d.15.6.1 (122-238) Staphylococcal enterotoxin B, SEB {Staphylococcus aureus}
NGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFNNSPYETGY
IKFIENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLTTKK
>d1enfa2 d.15.6.1 (A:102-213) Staphylococcal enterotoxin H, SEH {Staphylococcus aureus}
EKLAQERVIGANVWVDGIQKETELIRTNKKNVTLQELDIKIRKILSDKYKIYYKDSEISKGLIEF
DMKTPRDYSFDIYDLKGENDYEIDKIYEDNKTLKSDDISHIDVNLYT
>d1an8_2 d.15.6.1 (96-208) Streptococcal superantigen Spe-C {Streptococcus pyogenes}
NKVNHKLLGNLFISGESQQNLNNKIILEKDIVTFQEIDFKIRKYLMDNYKIYDATSPYVSGRIEI
GTKDGKHEQIDLFDSPNEGTRSDIFAKYKDNRIINMKNFSHFDIYLEK
>d1et9a2 d.15.6.1 (A:96-204) Streptococcal superantigen Spe-H

{Streptococcus pyogenes}
EKKEIKVPVNVWDKSKQQPPMFITVNKPKVTAQEVDIKVRKLLIKKYDIYNNREQKYSKGTVTLD
LNSGKDIVFDLYYFGNGDFNSMLKIYSNNERIDSTQFHVDVSIS
>d1eu3a2 d.15.6.1 (A:97-209) Streptococcal superantigen Smez-2 {Streptococcus pyogenes}
TSIPKNIPVNLWINGKQISVPYNEISTNKTTVTAQEIDLKVRKFLIAQHQLYSSGSSYKSGRLVF
HTNDNSDKYSFDLFYVGYRDKESIFKVYKDNKSFNIDKIGHLDIEIDS
>d1bxta2 d.15.6.1 (A:120-234) Streptococcal superantigen SSA {Streptococcus pyogenes}
QIEGKFPNITVKVYEDNENILSFDITTNKKQVTVQELDCKTRKILVSRKNLYEFNNSPYETGYIK
FIESSGDSFWYDMMPAPGAIFDQSKYLMLYNDNKTVSSSAIAIEVHLTKK
>d1fnua2 d.15.6.1 (A:108-221) Streptococcal pyrogenic exotoxin A1 {Streptococcus pyogenes}
GNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYTIDNKQLYTNGPSKYETGYI
KFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDNKTSQIEVYLTTK
>d1fcla_ d.15.7.1 (A:) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}
TTFKLIINGKTLKGETTTEAVDAATAEKVLKQYINDNGIDGEWTYDDATKTWTVTE
>d1fd6a_ d.15.7.1 (A:) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}
MTTFKLIINGKTLKGETTTEAVDAATAEKVFKQYANDNGIDGEWTYDDATKTFTVTE
>d1gb4__ d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}
MTTFKLIINGKTLKGEITIEAVDAAEAEKIFKQYANDNGIDGEWTYDDATKTFTVTE
>d1pgb__ d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}
MTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTE
>d1pgx__ d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}
ELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTYDDATKTFTVTEMVT
EVPVA
>d1qkza_ d.15.7.1 (A:) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}
VTTYKLVINGKTLKGETTTKAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTEK
>d2igd__ d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}
MTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTYDDATKTFTVTE
>d2igg__ d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}
LTPAVTTYKLVINGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTEKPE
>d1heze_ d.15.7.1 (E:) Immunoglobulin light chain-binding domain of protein L {Peptostreptococcus magnus}
EVTIKVNLIFADGKIQTAEFKGTFEEATAEAYRYADLLAKVNGEYTADLEDGGNHMNIKFA
>d1hz6a_ d.15.7.1 (A:) Immunoglobulin light chain-binding domain of

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protein L {Peptostreptococcus magnus}
HHAMEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEWTVDVADKGYTLNIKF
AG
>d1jmla_ d.15.7.1 (A:) Immunoglobulin light chain-binding domain of
protein L {Peptostreptococcus magnus}
MHHHHHHGMEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEWTVDVVPKAYT
LNIKFAG
>d1k52a_ d.15.7.1 (A:) Immunoglobulin light chain-binding domain of
protein L {Peptostreptococcus magnus}
MHHHHHHAMEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEWTVDVADGGYT
LNIKFAG
>d1kh0a_ d.15.7.1 (A:) Immunoglobulin light chain-binding domain of
protein L {Peptostreptococcus magnus}
EEVTIKANLIFANGSTQTAEFKGTKEKALSEVLAYADTLKKDNGEWTIDKRVTNGVIILNIKFAG
>d2ptl__ d.15.7.1 (-) Immunoglobulin light chain-binding domain of
protein L {Peptostreptococcus magnus}
ENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDV
ADKGYTLNIKFAG
>d1tif__ d.15.8.1 (-) Translation initiation factor IF3, N-terminal
domain {Bacillus stearothermophilus}
KDFIINEQIRAREVRLIDQNGDQLGIKSKQEALEIAARRNLDLVLVAPNAKPPVCRIMDYGKFRF
EQQKKEKEARK
>d1f52a1 d.15.9.1 (A:1-100) Glutamine synthetase, N-terminal domain
{Salmonella typhimurium}
SAEHVLTMLNEHEVKFVDLRFTDTKGKEQHVTIPAHQVNAEFFEEGKMFDGSSIGGWKGINESDM
VLMPDASTAVIDPFFADSTLIIRCDILEPGTLQGY
>d1coy_2 d.16.1.1 (319-450) Cholesterol oxidase {Brevibacterium
sterolicum}
GNNGNIMVGRANHMWDATGSKQATIPTMGIDNWADPTAPIFAEIAPLPAGLETYVSLYLAITKNP
ERARFQFNSGTGKVDLTWAQSQNQKGIDMAKKVFDKINQKEGTIYRTDLFGVYYKTWGDDFTYHP
LG
>d1ijha2 d.16.1.1 (A:319-450) Cholesterol oxidase {Streptomyces sp.}
GPNGNIMTARANHMWNPTGAHQSSIPALGIDAWDNSDSSVFAEIAPMPAGLETWVSLYLAITKNP
QRGTFVYDAATDRAKLNWTRDQNAPAVNAAKALFDRINKANGTIYRYDLFGTQLKAFADDFCYHP
LG
>d1k0ia2 d.16.1.2 (A:174-275) p-Hydroxybenzoate hydroxylase (PHBH)
{Pseudomonas aeruginosa}
LKVFERVYPFGWLGLLADTPPVSHELIYANHPRGFALCSQRSATRSQYYVQVPLSEKVEDWSDER
FWTELKARLPSEVAEKLVTGPSLEKSIAPLRSFVVEP
>d1foha4 d.16.1.2 (A:241-341) Phenol hydroxylase {Soil-living yeast
(Trichosporon cutaneum)}
GEQTDYIWGVLDAVPASNFPDIRSRCAIHSAESGSIMIIPRENNLVRFYVQLQARAEKGGRVDRT
KFTPEVVIANAKKIFHPYTFDVQQLDWFTAYHIGQR
>d1an9a2 d.16.1.3 (A:195-287) D-amino acid oxidase {Pig (Sus scrofa)}
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LQPGRGQIIKVDAPWLKNFIITHDLERGIYNSPYIIPGLQAVTLGGTFQVGNWNEINNIQDHNTI
WEGCCRLEPTLKDAKIVGEYTGFRPVRP
>d1c0pa2 d.16.1.3 (A:1194-1288) D-amino acid oxidase {Yeast
(Rhodotorula gracilis)}
AEPIRGQTVLVKSPCKRCTMDSSDPASPAYIIPRPGGEVICGGTYGVGDWDLSVNPETVQRILKH
CLRLDPTISSDGTIEGIEVLRHNVGLRPAR
>d1el8a2 d.16.1.3 (A:218-321) Sarcosine oxidase {Bacillus sp., strain
b0618}
LQPYRQVVGFFESDESKYSNDIDFPGFMVEVPNGIYYGFPSFGGCGLKLGYHTFGQKIDPDTINR
EFGVYPEDESNLRAFLEEYMPGANGELKRGAVCMYTKTL
>d1i8ta2 d.16.1.7 (A:245-313) UDP-galactopyranose mutases
{Escherichia coli}
EYRSLKFETERHEFPNFQGNAVINFTDANVPYTRIIEHKHFDYVETKHTVVTKEYPLEWKVGDEP
YYPV
>d1cf3a2 d.16.1.4 (A:325-520) Glucose oxidase {Aspergillus niger}
NLQDQTTATVRSRITSAGAGQGQAAWFATFNETFGDYSEKAHELLNTKLEQWAEEAVARGGFHNT
TALLIQYENYRDWIVNHNVAYSELFLDTAGVASFDVWDLLPFTRGYVHILDKDPYLHHFAYDPQY
FLNELDLLGQAAATQLARNISNSGAMQTYFAGETIPGDNLAYDADLSAWTEYIPYHFRPNYHGVG
T
>d1gpea2 d.16.1.4 (A:329-524) Glucose oxidase {Penicillium
amagasakiense}
NMQDQTTTTVSSRASSAGAGQGQAVFFANFTETFGDYAPQARDLLNTKLDQWAEETVARGGFHNV
TALKVQYENYRNWLLDEDVAFAELFMDTEGKINFDLWDLIPFTRGSVHILSSDPYLWQFANDPKF
FLNEFDLLGQAAASKLARDLTSQGAMKEYFAGETLPGYNLVQNATLSQWSDYVLQNFRPNWHAVS
S
>d1b5qa2 d.16.1.5 (A:294-405) Polyamine oxidase {Maize (Zea mays)}
DMAVYTKIFLKFPRKFWPEGKGREFFLYASSRRGYYGVWQEFEKQYPDANVLLVTVTDEESRRIE
QQSDEQTKAEIMQVLRKMFPGKDVPDATDILVPRWWSDRFYKGTFSN
>d1f8ra2 d.16.1.5 (A:320-432) L-amino acid oxidase {Malayan pit viper
(Calloselasma rhodostoma)}
HYRSGTKIFLTCTTKFWEDDGIHGGKSTTDLPSRFIYYPNHNFTNGVGVIIAYGIGDDANFFQAL
DFKDCADIVFNDLSLIHQLPKKDIQSFCYPSVIQKWSLDKYAMGGITT
>d1gosa2 d.16.1.5 (A:290-401) Monoamine oxidase B {Human (Homo
sapiens)}
PLGSVIKCIVYYKEPFWRKKDYCGTMIIDGEEAPVAYTLDDTKPEGNYAAIMGFILAHKARKLAR
LTKEERLKKLCELYAKVLGSLEALEPVHYEEKNWCEEQYSGGCYTTY
>d1d5ta2 d.16.1.6 (A:292-388) Guanine nucleotide dissosiation
inhibitor, GDI {Cow (Bos taurus)}
RKAGQVIRIICILSHPIKNTNDANSCQIIIPQNQVNRKSDIYVCMISYAHNVAAQGKYIAIASTT
VETTDPEKEVEPALGLLEPIDQKFVAISDLYE
>d1mola_ d.17.1.1 (A:) Monellin, B & A chains together {Serendipity
berry (Dioscoreophyllum cumminsii)}
GEWEIIDIGPFTQNLGKFAVDEENKIGQYGRLTFNKVIRPCMKKTIYENEREIKGYEYQLYVYAS
DKLFRADISEDYKTRGRKLLRFNGPVPPP
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>d1eqka_ d.17.1.2 (A:) Phytocystatin {Japanese rice (Oryza sativa),
subsp. japonica, oryzacystatin-I}
MSSDGGPVLGGVEPVGNENDLHLVDLARFAVTEHNKKANSLLEFEKLVSVKQQVVAGTLYYFTIE
VKEGDAKKLYEAKVWEKPWMDFKELQEFKPVDASANA
>d1cewi_ d.17.1.2 (I:) Cystatin {Chicken (Gallus gallus)}
GAPVPVDENDEGLQRALQFAMAEYNRASNDKYSSRVVRVISAKRQLVSGIKYILQVEIGRTTCPK
SSGDLQSCEFHDEPEMAKYTTCTFVVYSIPWLNQIKLLESKCQ
>d1dvd__ d.17.1.2 (-) Cystatin A (stefin A) {Human (Homo sapiens)}
MIPGGLSEAKPATPEIQEIVDKVKPQLEEKTNETYGKLEAVQYKTQVVAGTNYYIKVRAGDNKYM
HLKVFKSLPGQNEDLVLTGYQVDKNKDDELTGF
>d1stfi_ d.17.1.2 (I:) Cystatin B (stefin B) {Human (Homo sapiens)}
MMSGAPSATQPATAETQHIADQVRSQLEEKYNKKFPVFKAVSFKSQVVAGTNYFIKVHVGDEDFV
HLRVFQSLPHENKPLTLSNYQTNKAKHDELTYF
>d1g96a_ d.17.1.2 (A:) Cystatin C {Human (Homo sapiens)}
VGGPMDASVEEEGVRRALDFAVGEYNKASNDMYHSRALQVVRARKQIVAGVNYFLDVELGRTTCT
KTQPNLDNCPFHDQPHLKRKAFCSFQIYAVPWQGTMTLSKSTCQDA
>d1oaca2 d.17.2.1 (A:91-185) Copper amine oxidase, domains 1 and 2
{Escherichia coli}
KRPHPLNALTADEIKQAVEIVKASADFKPNTRFTEISLLPPDKEAVWAFALENKPVDQPRKADVI
MLDGKHIIEAVVDLQNNKLLSWQPIKDAHG
>d1oaca3 d.17.2.1 (A:186-300) Copper amine oxidase, domains 1 and 2
{Escherichia coli}
MVLLDDFASVQNIINNSEEFAAAVKKRGITDAKKVITTPLTVGYFDGKDGLKQDARLLKVISYLD
VGDGNYWAHPIENLVAVVDLEQKKIVKIEEGPVVPVPMTARPFDGRDRVA
>d1ksia2 d.17.2.1 (A:6-98) Copper amine oxidase, domains 1 and 2 {Pea
seedling (Pisum sativum)}
VQHPLDPLTKEEFLAVQTIVQNKYPISNNRLAFHYIGLDDPEKDHVLRYETHPTLVSIPRKIFVV
AIINSQTHEILINLRIRSIVSDNIHNGY
>d1ksia3 d.17.2.1 (A:99-206) Copper amine oxidase, domains 1 and 2
{Pea seedling (Pisum sativum)}
GFPILSVDEQSLAIKLPLKYPPFIDSVKKRGLNLSEIVCSSFTMGWFGEEKNVRTVRLDCFMKES
TVNIYVRPITGITIVADLDLMKIVEYHDRDIEAVPTAENTEYQ
>d1av4_2 d.17.2.1 (9-96) Copper amine oxidase, domains 1 and 2
{Arthrobacter globiformis}
ASPFRLASAGEISEVQGILRTAGLLGPEKRIAYLGVLDPARGAGSEAEDRRFRVFIHDVSGARPQ
EVTVSVTNGTVISAVELDTAATG
>d1av4_3 d.17.2.1 (97-211) Copper amine oxidase, domains 1 and 2
{Arthrobacter globiformis}
ELPVLEEEFEVVEQLLATDERWLKALAARNLDVSKVRVAPLSAGVFEYAEERGRRILRGLAFVQD
FPEDSAWAHPVDGLVAYVDVVSKEVTRVIDTGVFPVPAEHGNYTDPELTG
>d1a2va2 d.17.2.1 (A:18-115) Copper amine oxidase, domains 1 and 2
{Yeast (Hansenula polymorpha)}
PARPAHPLDPLSTAEIKAATNTVKSYFAGKKISFNTVTLREPARKAYIQWKEQGGPLPPRLAYYV
ILEAGKPGVKEGLVDLASLSVIETRALETVQPI
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>d1a2va3 d.17.2.1 (A:116-236) Copper amine oxidase, domains 1 and 2 {Yeast (Hansenula polymorpha)}
LTVEDLCSTEEVIRNDPAVIEQCVLSGIPANEMHKVYCDPWTIGYDERWGTGKRLQQALVYYRSD
EDDSQYSHPLDFCPIVDTEEKKVIFIDIPNRRRKVSKHKHANFYPKHMIEKVGAMR
>d1eeja2 d.17.3.1 (A:1-60) Disulfide bond isomerase, DsbC, N-terminal domain {Escherichia coli}
DDAAIQQTLAKMGIKSSDIQPAPVAGMKTVLTNSGVLYITDDGKHIIQGPMYDVSGTAPV
>d3stda_ d.17.4.1 (A:) Scytalone dehydratase {Fungus (Magnaporthe grisea)}
GEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGMVSSK
QVLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKI
DGVWKFAGLKPDIRWGEFDFDRIFEDGRETFG
>d1ouna_ d.17.4.2 (A:) Nuclear transport factor-2 (NTF2) {Rat (Rattus norvegicus)}
GDKPIWEQIGSSFIQHYYQLFDNDRTQLGAIYIDASCLTWEGQQFQGKAAIVEKLSSLPFQKIQH
SITAQDHQPTPDSCIISMVVGQLKADEDPIMGFHQMFLLKNINDAWVCTNDMFRLALHNF
>d1jkga_ d.17.4.2 (A:) NTF2-related export protein 1 (p15) {Human (Homo sapiens)}
ASVDFKTYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLP
SSEFQISVVDCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNTVWKIASD
CFRFQDWAS
>d1jkgb_ d.17.4.2 (B:) NTF2-like domain of Tip associating protein, TAP {Human (Homo sapiens)}
APPCKGSYFGTENLKSLVLHFLQQYYAIYDSGDRQGLLDAYHDGACCSLSIPFIPQNPARSSLAE
YFKDSRNVKKLKDPTLRFRLLKHTRLNVVAFLNELPKTQHDVNSFVVDISAQTSTLLCFSVNGVF
KEVDGKSRDSLRAFTRTFIAVPASNSGLCIVNDELFVRNASSEEIQRAFAMPAPTP
>d1qjga_ d.17.4.3 (A:) Delta-5-3-ketosteroid isomerase, steroid delta-isomerase, KSI {Comamonas testosteroni and Pseudomonas testosteroni}
MNTPEHMTAVVQRYVAALNAGDLDGIVALFADDATVENPVGSEPRSGTAAIREFYANSLKLPLAV
ELTQEVRAVANEAAFAFIVSFEYQGRKTVVAPIDHFRFNGAGKVVSMRALFGEKNIHAGA
>d1ea2a_ d.17.4.3 (A:) Delta-5-3-ketosteroid isomerase, steroid delta-isomerase, KSI {Pseudomonas putida}
NLPTAQEVQGLMARFIELVDVGDIEAIVQMYADDATVEDPFGQPPIHGREQIAAFYRQGLGGGKV
RACLTGPVRASHNGCGAMPFRVEMVWNGQPCALDVIDVMRFDEHGRIQTMQAYWSEVNLSV
>d1eg9b_ d.17.4.4 (B:) Naphthalene 1,2-dioxygenase beta subunit {Pseudomonas putida}
MINIQEDKLVSAHDAEEILRFFNCHDSALQQEATTLLTQEAHLLDIQAYRAWLEHCVGSEVQYQV
ISRELRAASERRYKLNEAMNVYNENFQQLKVRVEHQLDPQNWGNSPKLRFTRFITNVQAAMDVND
KELLHIRSNVILHRARRGNQVDVFYAAREDKWKRGEGGVRKLVQRFVDYPERILQTHNLMVFL
>d1euic_ d.17.5.1 (C:) Uracil-DNA glycosylase inhibitor protein {Bacteriophage pbs2}
QLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGEN
KIKML
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>d1ugia_ d.17.5.1 (A:) Uracil-DNA glycosylase inhibitor protein
{Bacteriophage pbs2}
TNLSDIIEKETGKQLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYK
PWALVIQDSNGENKIKML
>d1pcfa_ d.18.1.1 (A:) Transcriptional coactivator PC4 C-terminal
domain {Human (Homo sapiens)}
AMFQIGKMRYVSVRDFKGKVLIDIREYWMDPEGEMKPGRKGISLNPEQWSQLKEQISDIDDAVRK
L
>d1jb0d_ d.187.1.1 (D:) Photosystem I subunit PsaD {Synechococcus
elongatus}
TTLTGQPPLYGGSTGGLLSAADTEEKYAITWTSPKEQVFEMPTAGAAVMREGENLVYFARKEQCL
ALAAQQLRPRKINDYKIYRIFPDGETVLIHPKDGVFPEKVNKGREAVNSVPRSIGQNPNPSQLKF
TGKKPYDP
>d3frua2 d.19.1.1 (A:1-178) Fc (IgG) receptor, alpha-1 and alpha-2
domains {Rat (Rattus norvegicus)}
AEPRLPLMYHLAAVSDLSTGLPSFWATGWLGAQQYLTYNNLRQEADPCGAWIWENQVSWYWEKET
TDLKSKEQLFLEAIRTLENQINGTFTLQGLLGCELAPDNSSLPTAVFALNGEEFMRFNPRTGNWS
GEWPETDIVGNLWMKQPEAARKESEFLLTSCPERLLGHLERGRQNLEW
>d1cd1a2 d.19.1.1 (A:7-185) CD1, alpha-1 and alpha-2 domains {Mouse
(Mus musculus)}
NYTFRCLQMSSFANRSWSRTDSVVWLGDLQTHRWSNDSATISFTKPWSQGKLSNQQWEKLQHMFQ
VYRVSFTRDIQELVKMMSPKEDYPIEIQLSAGCEMYPGNASESFLHVAFQGKYVVRFWGTSWQTV
PGAPSWLDLPIKVLNADQGTSATVQMLLNDTCPLFVRGLLEAGKSDLEK
>d1hdma2 d.19.1.1 (A:13-93) MHC class II, N-terminal domains of alpha
and beta chains {Human (Homo sapiens), HLA-DM}
LQNHTFLHTVYCQDGSPSVGLSEAYDEDQLFFFDFSQNTRVPRLPEFADWAQEQGDAILFDKEFC
EWMIQQIPKLDGKIPV
>d1hdmb2 d.19.1.1 (B:3-87) MHC class II, N-terminal domains of alpha
and beta chains {Human (Homo sapiens), HLA-DM}
FVAHVESTCLLDDAGTPKDFTYCISFNKDLLTCWDPEENKMAPCNSLANVLSQHLNQKDTLMQRL
NGLQNCATHTQPFWGSLTNR
>d1aqdb2 d.19.1.1 (B:4-92) MHC class II, N-terminal domains of alpha
and beta chains {Human (Homo sapiens), HLA-DR1}
RPRFLWQLKFECHFFNGTERVRLLERCIYNQEESVRFDSDVGEYRAVTELGRPDAEYWNSQKDLL
EQRRAAVDTYCRHNYGVGESFTVQ
>d1bx2b2 d.19.1.1 (B:3-92) MHC class II, N-terminal domains of alpha
and beta chains {Human (Homo sapiens), HLA-DR2}
TRPRFLWQPKRECHFFNGTERVRFLDRYFYNQEESVRFDSDVGEFRAVTELGRPDAEYWNSQKDI
LEQARAAVDTYCRHNYGVVESFTVQ
>d1fv1a2 d.19.1.1 (A:3-81) MHC class II, N-terminal domains of alpha
and beta chains {Human (Homo sapiens), HLA-DR2}
EEHVIIQAEFYLNPDQSGEFMFDFDGDEIFHVDMAKKETVWRLEEFGRFASFEAQGALANIAVDK
ANLEIMTKRSNYTP
>d1fv1b2 d.19.1.1 (B:1-92) MHC class II, N-terminal domains of alpha
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and beta chains {Human (Homo sapiens), HLA-DR2}
GDTRPRFLQQDKYECHFFNGTERVRFLHRDIYNQEEDLRFDSDVGEYRAVTELGRPDAEYWNSQK
DFLEDRRAAVDTYCRHNYGVGESFTVQ
>d1a6ab2 d.19.1.1 (B:5-92) MHC class II, N-terminal domains of alpha
and beta chains {Human (Homo sapiens), HLA-DR3}
PRFLEYSTSECHFFNGTERVRYLDRYFHNQEENVRFDSDVGEFRAVTELGRPDAEYWNSQKDLLE
QKRGRVDNYCRHNYGVVESFTVQ
>d1d5zb2 d.19.1.1 (B:1-92) MHC class II, N-terminal domains of alpha
and beta chains {Human (Homo sapiens), HLA-DR4}
GDTRPRFLEQVKHECHFFNGTERVRFLDRYFYHQEEYVRFDSDVGEYRAVTELGRPDAEYWNSQK
DLLEQKRAAVDTYCRHNYGVGESFTVQ
>d1jk8a2 d.19.1.1 (A:2-84) MHC class II, N-terminal domains of alpha
and beta chains {Human (Homo sapiens), HLA-DQ8}
VADHVASYGVNLYQSYGPSGQYSHEFDGDEEFYVDLERKETVWQLPLFRRFRRFDPQFALTNIAV
LKHNLNIVIKRSNSTAATN
>d1jk8b2 d.19.1.1 (B:3-94) MHC class II, N-terminal domains of alpha
and beta chains {Human (Homo sapiens), HLA-DQ8}
SPEDFVYQFKGMCYFTNGTERVRLVTRYIYNREEYARFDSDVGVYRAVTPLGPPAAEYWNSQKEV
LERTRAELDTVCRHNYQLELRTTLQRR
>d1iaka2 d.19.1.1 (A:1-81) MHC class II, N-terminal domains of alpha
and beta chains {Mouse (Mus musculus), I-AK}
IEADHVGSYGITVYQSPGDIGQYTFEFDGDELFYVDLDKKETVWMLPEFAQLRRFEPQGGLQNIA
TGKHNLEILTKRSNSTP
>d1iakb2 d.19.1.1 (B:5-92) MHC class II, N-terminal domains of alpha
and beta chains {Mouse (Mus musculus), I-AK}
GSFVHQFQPFCYFTNGTQRIRLVIRYIYNREEYVRFDSDVGEYRAVTELGRPDAEYWNKQYLERT
RAELDTVCRHNYEKTETPTSLR
>d1fnga2 d.19.1.1 (A:1-81) MHC class II, N-terminal domains of alpha
and beta chains {Mouse (Mus musculus), I-EK}
IKEEHTIIQAEFYLLPDKRGEFMFDFDGDEIFHVDIEKSETIWRLEEFAKFASFEAQGALANIAV
DKANLDVMKERSNNTP
>d1fngb2 d.19.1.1 (B:4-92) MHC class II, N-terminal domains of alpha
and beta chains {Mouse (Mus musculus), I-EK}
RPWFLEYCKSECHFYNGTQRVRLLVRYFYNLEENLRFDSDVGEFRAVTELGRPDAENWNSQPEFL
EQKRAEVDTVCRHNYEIFDNFLVP
>d1i3rb2 d.19.1.1 (B:1-120) MHC class II, N-terminal domains of alpha
and beta chains {Mouse (Mus musculus), I-EK}
GKKVITAFNEGLKGGGGSLVGGGSGGGGSRPWFLEYCKSECHFYNGTQRVRLLVRYFYNLEENLR
FDSDVGEFRAVTELGRPDAENWNSQPEFLEQKRAEVDTVCRHNYEIFDNFLVPRR
>d2iadb2 d.19.1.1 (B:5-93) MHC class II, N-terminal domains of alpha
and beta chains {Mouse (Mus musculus), I-AD}
RHFVVQFKGECYYTNGTQRIRLVTRYIYNREEYVRYDSDVGEYRAVTELGRPDAEYWNSQPEILE
RTRAEVDTACRHNYEGPETSTSLR
>d1es0a2 d.19.1.1 (A:1B-82) MHC class II, N-terminal domains of alpha
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and beta chains {Mouse (Mus musculus), I-A(G7)}
DIEADHVGFYGTTVYQSPGDIGQYTHEFDGDELFYVDLDKKKTVWRLPEFGQLILFEPQGGLQNI
AAEKHNLGILTKRSNFTPA
>d1es0b2 d.19.1.1 (B:5-93) MHC class II, N-terminal domains of alpha
and beta chains {Mouse (Mus musculus), I-A(G7)}
RHFVHQFKGECYFTNGTQRIRLVTRYIYNREEYLRFDSDVGEYRAVTELGRHSAEYYNKQYLERT
RAELDTACRHNYEETEVPTSLR
>d1k8ia2 d.19.1.1 (A:11-92) MHC class II, N-terminal domains of alpha
and beta chains {Mouse (Mus musculus), H2-DM}
QNHTFRHTLFCQDGIPNIGLSETYDEDELFSFDFSQNTRVPRLPDFAEWAQGQGDASAIAFDKSF
CEMLMREVSPKLEGQIP
>d1k8ib2 d.19.1.1 (B:1-94) MHC class II, N-terminal domains of alpha
and beta chains {Mouse (Mus musculus), H2-DM}
GFVAHVESTCVLNDAGTPQDFTYCVSFNKDLLACWDPDVGKIVPCEFGVLSRLAEIISNILNEQE
SLIHRLQNGLQDCATHTQPFWDVLTHRTR
>d1i4fa2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains
{Human (Homo sapiens), HLA-A2.1}
GSHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYWDGETR
KVKAHSQTHRVDLGTLRGYYNQSEAGSHTVQRMYGCDVGSDWRFLRGYHQYAYDGKDYIALKEDL
RSWTAADMAAQTTKHKWEAAHVAEQLRAYLEGTCVEWLRRYLENGKETLQR
>d1hsaa2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains
{Human (Homo sapiens), HLA-B2705}
GSHSMRYFHTSVSRPGRGEPRFITVGYVDDTLFVRFDSDAASPREEPRAPWIEQEGPEYWDRETQ
ICKAKAQTDREDLRTLLRYYNQSEAGSHTLQNMYGCDVGPDGRLLRGYHQDAYDGKDYIALNEDL
SSWTAADTAAQITQRKWEAARVAEQLRAYLEGECVEWLRRYLENGKETLQR
>d1hsba2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains
{Human (Homo sapiens), HLA-AW68}
GSHSMRYFYTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYWDRNTR
NVKAQSQTDRVDLGTLRGYYNQSEAGSHTIQMMYGCDVGSDGRFLRGYRQDAYDGKDYIALKEDL
RSWTAADMAAQTTKHKWEAAHVAEQWRAYLEGTCVEWLRRYLENGKETLQR
>d1agda2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains
{Human (Homo sapiens), HLA-B0801}
GSHSMRYFDTAMSRPGRGEPRFISVGYVDDTQFVRFDSDAASPREEPRAPWIEQEGPEYWDRNTQ
IFKTNTQTDRESLRNLRGYYNQSEAGSHTLQSMYGCDVGPDGRLLRGHNQYAYDGKDYIALNEDL
RSWTAADTAAQITQRKWEAARVAEQDRAYLEGTCVEWLRRYLENGKDTLER
>d1a1na2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains
{Human (Homo sapiens), HLA-B*3501}
GSHSMRYFYTAMSRPGRGEPRFIAVGYVDDTQFVRFDSDAASPRTEPRPPWIEQEGPEYWDRNTQ
IFKTNTQTYRESLRNLRGYYNQSEAGSHIIQRMYGCDLGPDGRLLRGHDQSAYDGKDYIALNEDL
SSWTAADTAAQITQRKWEAARVAEQLRAYLEGLCVEWLRRYLENGKETLQR
>d1e27a2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains
{Human (Homo sapiens), HLA-B*5101}
GSHSMRYFYTAMSRPGRGEPRFIAVGYVDDTQFVRFDSDAASPRTEPRAPWIEQEGPEYWDRNTQ
IFKTNTQTYRENLRIALRYYNQSEAGSHTWQTMYGCDVGPDGRLLRGHNQYAYDGKDYIALNEDL
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SSWTAADTAAQITQRKWEAAREAEQLRAYLEGLCVEWLRRHLENGKETLQR
>d1efxa2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains
{Human (Homo sapiens), HLA-CW3}
GSHSMRYFYTAVSRPGRGEPHFIAVGYVDDTQFVRFDSDAASPRGEPRAPWVEQEGPEYWDRETQ
KYKRQAQTDRVSLRNLRGYYNQSEAGSHIIQRMYGCDVGPDGRLLRGYDQYAYDGKDYIALNEDL
RSWTAADTAAQITQRKWEAAREAEQLRAYLEGLCVEWLRRYLKNGKETLQR
>d1qqda2 d.19.1.1 (A:2-181) MHC class I, alpha-1 and alpha-2 domains
{Human (Homo sapiens), HLA-CW4}
SHSMRYFSTSVSWPGRGEPRFIAVGYVDDTQFVRFDSDAASPRGEPREPWVEQEGPEYWDRETQK
YKRQAQADRVNLRKLRGYYNQSEDGSHTLQRMFGCDLGPDGRLLRGYNQFAYDGKDYIALNEDLR
SWTAADTAAQITQRKWEAAREAEQRRAYLEGTCVEWLRRYLENGKETLQR
>d1mhea2 d.19.1.1 (A:2-181) MHC class I, alpha-1 and alpha-2 domains
{Human (Homo sapiens), HLA-E}
SHSLKYFHTSVSRPGRGEPRFISVGYVDDTQFVRFDNDAASPRMVPRAPWMEQEGSEYWDRETRS
ARDTAQIFRVNLRTLRGYYNQSEAGSHTLQWMHGCELGPDRRFLRGYEQFAYDGKDYLTLNEDLR
SWTAVDTAAQISEQKSNDASEAEHQRAYLEDTCVEWLHKYLEKGKETLLH
>d1de4a2 d.19.1.1 (A:4-181) MHC class I, alpha-1 and alpha-2 domains
{Human (Homo sapiens), hemochromatosis protein Hfe}
RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWLQLSQS
LKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDHLEFCPDTLDW
RAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVLD
>d1fzka2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains
{Mouse (Mus musculus), H-2KB}
GPHSLRYFVTAVSRPGLGEPRYMEVGYVDDTEFVRFDSDAENPRYEPRARWMEQEGPEYWERETQ
KAKGNEQSFRVDLRTLLGYYNQSKGGSHTIQVISGCEVGSDGRLLRGYQQYAYDGCDYIALNEDL
KTWTAADMAALITKHKWEQAGAAEYYRAYLEGTCVEWLRRYLKNGNATLLR
>d1jpfa2 d.19.1.1 (A:2-181) MHC class I, alpha-1 and alpha-2 domains
{Mouse (Mus musculus), H-2DB}
PHSMRYFETAVSRPGLEEPRYISVGYVDNKEFVRFDSDAENPRYEPRAPWMEQEGPEYWERETQK
AKGQEQWFRVSLRNLLGYYNQSAGGSHTLQQMSGCDLGSDWRLLRGYLQFAYEGRDYIALNEDLK
TWTAADMAAQITRRKWEQSGAAEHYKAYLEGECVEWLHRYLKNGNATLLR
>d1mhca2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains
{Mouse (Mus musculus), H-2M3}
GSHSLRYFHTAVSRPGRGEPQYISVGYVDDVQFQRCDSIEEIPRMEPRAPWMEKERPEYWKELKL
KVKNIAQSARANLRTLLRYYNQSEGGSHILQWMVSCEVGPDMRLLGAHYQAAYDGSDYITLNEDL
SSWTAVDMVSQITKSRLESAGTAEYFRAYVEGECLELLHRFLRNGKEILQR
>d1ld9a2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains
{Mouse (Mus musculus), H-2LD}
GPHSMRYFETAVSRPGLGEPRYISVGYVDNKEFVRFDSDAENPRYEPQAPWMEQEGPEYWERITQ
IAKGQEQWFRVNLRTLLGYYNQSAGGTHTLQWMYGCDVGSDGRLLRGYEQFAYDGCDYIALNEDL
KTWTAADMAAQITRRKWEQAGAAEYYRAYLEGECVEWLHRYLKNGNATLLR
>d1qo3a2 d.19.1.1 (A:2-181) MHC class I, alpha-1 and alpha-2 domains
{Mouse (Mus musculus), H-2DD}
SHSLRYFVTAVSRPGFGEPRYMEVGYVDNTEFVRFDSDAENPRYEPRARWIEQEGPEYWERETRR
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AKGNEQSFRVDLRTALRYYNQSAGGSHTLQWMAGCDVESDGRLLRGYWQFAYDGCDYIALNEDLK
TWTAADMAAQITRRKWEQAGAAERDRAYLEGECVEWLRRYLKNGNATLLR
>d1k8da2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains
{Mouse (Mus musculus), IB QA-2}
GQHSLQYFHTAVSRPGLGEPWFISVGYVDDTQFVRFDSDAENPRMEPRARWMEQEGPEYWERETQ
IAKGHEQSFRGSLRTAQSYYNQSKGGSHTLQWMYGCDMGSDGRLLRGYLQFAYEGRDYIALNEDL
KTWTAVDMAAQITRRKWEQAGIAEKDQAYLEGTCMQSLRRYLELGKETLLR
>d1ed3a2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains
{Rat (Rattus norvegicus), RT1-AA}
GSHSLRYFYTAVSRPGLGEPRFIAVGYVDDTEFVRFDSDAENPRMEPRARWMEREGPEYWEQQTR
IAKEWEQIYRVDLRTLRGYYNQSEGGSHTIQEMYGCDVGSDGSLLRGYRQDAYDGRDYIALNEDL
KTWTAADFAAQITRNKWERARYAERLRAYLEGTCVEWLSRYLELGKETLLR
>d1zaga2 d.19.1.1 (A:5-183) Zinc-alpha-2-glycoprotein, ZAG {Human
(Homo sapiens)}
DGRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNSKDRKSQPMGLWRQVEGMEDWKQDSQL
QKAREDIFMETLKDIVEYYNDSNGSHVLQGRFGCEIENNRSSGAFWKYYYDGKDYIEFNKEIPAW
VPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYSKNILDR
>d1hyrc2 d.19.1.1 (C:0-180) MHC I homolog {Human (Homo sapiens), Mic-a}
MEPHSLRYNLTVLSWDGSVQSGFLTEVHLDGQPFLRCDRQKCRAKPQGQWAEDVLGNKTWDRETR
DLTGNGKDLRMTLAHIKDQKEGLHSLQEIRVCEIHEDNSTRSSQHFYYDGELFLSQNLETKEWTM
PQSSRAQTLAMNVRNFLKEDAMKTKTHYHAMHADCLQELRRYLKSGVVLRR
>d1c16a2 d.19.1.1 (A:1-180) MHC I homolog {Mouse (Mus musculus), t22}
GSHSLRYFYTAVSRPGLGEPWFIIVGYVDDMQVLRFSSKEETPRMAPWLEQEEADNWEQQTRIVT
IQGQLSERNLMTLVHFYNKSMDDSHTLQWLQGCDVEPDRHLCLWYNQLAYDSEDLPTLNENPSSC
TVGNSTVPHISQDLKSHCSDLLQKYLEKGKERLL
>d1exua2 d.19.1.1 (A:4-176) Class I MHC-related Fc receptor {Human
(Homo sapiens)}
HLSLLYHLTAVSSPAPGTPAFWVSGWLGPQQYLSYNSLRGEAEPCGAWVWENQVSWYWEKETTDL
RIKEKLFLEAFKALGGKGPYTLQGLLGCELGPDNTSVPTAKFALNGEEFMNFDLKQGTWGGDWPE
ALAISQRWQQQDKAANKELTFLLFSCPHRLREHLERGRGNLEW
>d1kcgc_ d.19.1.1 (C:) Class I MHC-related molecule Ulbp3 {Human (Homo
sapiens)}
DAHSLWYNFTIIHLPRHGQQWCEVQSQVDQKNFLSYDCGSDKVLSMGHLEEQLYATDAWGKQLEM
LREVGQRLRLELADTELEDFTPSGPLTLQVRMSCECEADGYIRGSWQFSFDGRKFLLFDSNNRKW
TVVHAGARRMKEKWEKDSGLTTFFKMVSMRDCKSWLRDFLMHRKKRLE
>d1jfma_ d.19.1.1 (A:) NK cell ligand RAE-1 beta {Mouse (Mus musculus)}
DAHSLRCNLTIKDPTPADPLWYEAKCFVGEILILHLSNINKTMTSGDPGETANATEVKKCLTQPL
KNLCQKLRNKVSNTKVDTHKTNGYPHLQVTMIYPQSQGRTPSATWEFNISDSYFFTFYTENMSWR
SANDESGVIMNKWKDDGEFVKQLKFLIHECSQKMDEFLKQSKEK
>d2aak__ d.20.1.1 (-) Ubiquitin conjugating enzyme {Arabidopsis
thaliana}
MSTPARKRLMRDFKRLQQDPPAGISGAPQDNNIMLWNAVIFGPDDTPWDGGTFKLSLQFSEDYPN
KPPTVRFVSRMFHPNIYADGSICLDILQNQWSPIYDVAAILTSIQSLLCDPNPNSPANSEAARMY
SESKREYNRRVRDVVEQSWT
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>d1fzya_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Baker's yeast
(Saccharomyces cerevisiae), ubc1}
SRAKRIMKEIQAVKDDPAAHITLEFVSESDIHHLKGTFLGPPGTPYEGGKFVVDIEVPMEYPFKP
PKMQFDTKVYHPNISSVTGAICLDILKNAWSPVITLKSALISLQALLQSPEPNDPQDAEVAQHYL
RDRESFNKTAALWTRLYAS
>d1ayza_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Baker's yeast
(Saccharomyces cerevisiae), ubc2 (RAD6)}
STPARRRLMRDFKRMKEDAPPGVSASPLPDNVMVWNAMIIGPADTPYEDGTFRLLLEFDEEYPNK
PPHVKFLSEMFHPNVYANGEICLDILQNRWTPTYDVASILTSIQSLFNDPNPASPANVEAATLFK
DHKSQYVKRVKETVEKSWEDDMD
>d1qcqa_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Baker's yeast
(Saccharomyces cerevisiae), ubc4}
MSSSKRIAKELSDLERDPPTSCSAGPVGDDLYHWQASIMGPADSPYAGGVFFLSIHFPTDYPFKP
PKISFTTKIYHPNINANGNICLDILKDQWSPALTLSKVLLSICSLLTDANPDDPLVPEIAHIYKT
DRPKYEATAREWTKKYAV
>d2ucz__ d.20.1.1 (-) Ubiquitin conjugating enzyme {Baker's yeast
(Saccharomyces cerevisiae), ubc7}
SKTAQKRLLKELQQLIKDSPPGIVAGPKSENNIFIWDCLIQGPPDTPYADGVFNAKLEFPKDYPL
SPPKLTFTPSILHPNIYPNGEVCISILHSPGDDPNMYELAEERWSPVQSVEKILLSVMSMLSEPN
IESGANIDACILWRDNRPEFERQVKLSILKSLGF
>d1jata_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Baker's yeast
(Saccharomyces cerevisiae), ubc13}
AASLPKRIIKETEKLVSDPVPGITAEPHDDNLRYFQVTIEGPEQSPYEDGIFELELYLPDDYPME
APKVRFLTKIYHPNIDRLGRICLDVLKTNWSPALQIRTVLLSIQALLASPNPNDPLANDVAEDWI
KNEQGAKAKAREWTKLYAKKKP
>d1j7db_ d.20.1.1 (B:) Ubiquitin conjugating enzyme {Human (Homo
sapiens), ubc13}
AGLPRRIIKETQRLLAEPVPGIKAEPDESNARYFHVVIAGPQDSPFEGGTFKLELFLPEEYPMAA
PKVRFMTKIYHPNVDKLGRICLDILKDKWSPALQIRTVLLSIQALLSAPNPDDPLANDVAEQWKT
NEAQAIETARAWTRLYAMN
>d1jatb_ d.20.1.1 (B:) Ubiquitin conjugating enzyme {Baker's yeast
(Saccharomyces cerevisiae), mms2}
SKVPRNFRLLEELEKGEKGFGPESCSYGLADSDDITMTKWNGTILGPPHSNHENRIYSLSIDCGP
NYPDSPPKVTFISKINLPCVNPTTGEVQTDFHTLRDWKRAYTMETLLLDLRKEMATPANKKLRQP
KEGETF
>d1j7da_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Human (Homo
sapiens), mms2}
GVKVPRNFRLLEELEEGQKGVGDGTVSWGLEDDEDMTLTRWTGMIIGPPRTNYENRIYSLKVECG
PKYPEAPPSVRFVTKINMNGINNSSGMVDARSIPVLAKWQNSYSIKVVLQELRRLMMSKENMKLP
QPPEGQTYNN
>d1c4zd_ d.20.1.1 (D:) Ubiquitin conjugating enzyme {Human (Homo
sapiens), ubch7}
SRRLMKELEEIRKCGMKNFRNIQVDEANLLTWQGLIVPDNPPYDKGAFRIEINFPAEYPFKPPKI
TFKTKIYHPNIDEKGQVCLPVISAENWKPATKTDQVIQSLIALVNDPQPEHPLRADLAEEYSKDR
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KKFCKNAEEFTKKY
>d1u9aa_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Human (Homo
sapiens), ubc9}
LNMSGIALSRLAQERKAWRKDHPFGFVAVPTKNPDGTMNLMNWECAIPGKKGTPWEGGLFKLRML
FKDDYPSSPPKCKFEPPLFHPNVYPSGTVCLSILEEDKDWRPAITIKQILLGIQELLNEPNIQDP
AQAEAYTIYCQNRVEYEKRVRAQAKKFAPS
>d1i7ka_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Human (Homo
sapiens), ubch10}
PVGKRLQQELMTLMMSGDKGISAFPESDNLFKWVGTIHGAAGTVYEDLRYKLSLEFPSGYPYNAP
TVKFLTPCYHPNVDTQGNISLDILKEKWSALYDVRTILLSIQSLLGEPNIDSPLNTHAAELWKNP
TAFKKYLQETYSKQVT
>d2e2c__ d.20.1.1 (-) Ubiquitin conjugating enzyme {Clam (Spisula
solidissima), E-2C}
MTTSKERHSVSKRLQQELRTLLMSGDPGITAFPDGDNLFKWVATLDGPKDTVYESLKYKLTLEFP
SDYPYKPPVVKFTTPCWHPNVDQSGNICLDILKENWTASYDVRTILLSLQSLLGEPNNASPLNAQ
AADMWSNQTEYKKVLHEKYKTAQSDK
>d1bwza1 d.21.1.1 (A:1-130) Diaminopimelate epimerase {Haemophilus
influenzae}
MQFSKMHGLGNDFVVVDGVTQNVFFTPETIRRLANRHCGIGFDQLLIVEAPYDPELDFHYRIFNA
DGSEVSQCGNGARCFARFVTLKGLTNKKDISVSTQKGNMVLTVKDMNQIRVNMGEPIWEPAKIPF
>d1bwza2 d.21.1.1 (A:131-274) Diaminopimelate epimerase {Haemophilus
influenzae}
TANKFEKNYILRTDIQTVLCGAVSMGNPHCVVQVDDIQTANVEQLGPLLESHERFPERVNAGFMQ
IINKEHIKLRVYERGAGETQACGSGACAAVAVGIMQGLLNNNVQVDLPGGSLMIEWNGVGHPLYM
TGEATHIYDGFITL
>d1h6ra_ d.22.1.1 (A:) Green fluorescent protein, GFP {Jellyfish
(Aequorea victoria)}
SKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFIVTTGKLPVPWPTLVTTFAY
GLQCFARYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFK
EDGNILGHKLEYNYNSHCVYIVADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLP
DNHYLCYQSALSKDPNEKRDHMVLLEFVTAAGITH
>d2emd__ d.22.1.1 (-) Green fluorescent protein, GFP {Jellyfish
(Aequorea victoria)}
ELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLSYGVQC
FSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGN
ILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHY
LSTQSALSKDPNEKRDHMVLLEFVTAAGIT
>d1ggxa_ d.22.1.1 (A:) Red fluorescent protein (fp583 or
dsred(clontech)) {Coral (Discosoma sp.)}
VIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDILSPQFQYGSKV
YVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIYKVKFIGVNFPSDGPVM
QKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSIYMAKKPVQLPGYYYVDSKLDI
TSHNEDYTIVEQYERTEGRHHLFL
>d1gl4a1 d.22.1.2 (A:399-631) Domain G2 of nidogen-1 {Mouse (Mus
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musculus)}
GSPQRVNGKVKGRIFVGSSQVPVVFENTDLHSYVVMNHGRSYTAISTIPETVGYSLLPLAPIGGI
IGWMFAVEQDGFKNGFSITGGEFTRQAEVTFLGHPGKLVLKQQFSGIDEHGHLTISTELEGRVPQ
IPYGASVHIEPYTELYHYSSSVITSSSTREYTVMEPDQDGAAPSHTHIYQWRQTITFQECAHDDA
RPALPSTQQLSVDSVFVLYNKEERILRYALSNSIGPVR
>d1c8za_ d.23.1.1 (A:) Transcriptional factor tubby, C-terminal
domain {Mouse (Mus musculus)}
GSVDIEVQDLEEFALRPAPQGITIKCRITRDKKGMDRGMFPTYFLHLDREDGKKVFLLAGRKRKK
SKTSNYLISVDPTDLSRGGDSYIGKLRSNLMGTKFTVYDNGVNPQKASSSTLESGTLRQELAAVC
YETNVLGFKGPRKMSVIVPGMNMVHERVCIRPRNEHETLLARWQNKNTESIIELQNKTPVWNDDT
QSYVLNFHGRVTQASVKNFQIIHGNDPDYIVMQFGRVAEDVFTMDYNYPLCALQAFAIALSSFDS
KLACE
>d2pil__ d.24.1.1 (-) Pilin {Gc (Neisseria gonorrhoeae)}
FTLIELMIVIAIVGILAAVALPAYQDYTARAQVSEAILLAEGQKSAVTEYYLNHGKWPENNTSAG
VASPPSDIKGKYVKEVEVKNGVVTATMLSSGVNNEIKGKKLSLWARRENGSVKWFCGQPVTRTDD
DTVADAKDGKEIDTKHLPSTCRDNFDAK
>d1hpwa_ d.24.1.1 (A:) Pilin {Pseudomonas aeruginosa}
ALEGTEFARAQLSEAMTLASGLKTKVSDIFSQDGSCPANTAATAGIEKDTDINGKYVAKVTTGGT
AAASGGCTIVATMKASDVATPLRGKTLTLTLGNADKGSYTWACTSNADNKYLPKTCQTATTTTP
>d1dzoa_ d.24.1.1 (A:) Pilin {Pseudomonas aeruginosa, type IV pilin,
pak pilin}
GTEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKLGTIALKP
DPADGTADITLTFTMGGAGPKNKGKIITLTRTAADGLWKCTSDQDEQFIPKGCSR
>d1p32a_ d.25.1.1 (A:) Acidic mitochondrial matrix protein p32 {Human
(Homo sapiens)}
MHTDGDKAFVDFLSDEIKEERKIQKHKTLPKMSGGWELELNGTEAKLVRKVAGEKITVTFNINNS
IPPTFDGEEEPSQGQKVEEQEPELTSTPNFVVEVIKNDDGKKALVLDCHYPEDEVGQEDEAESDI
FSIREVSFQSTGESEWKDTNYTLNTDSLDWALYDHLMDFLADRGVDNTFADELVELSTALEHQEY
ITFLEDLKSFVKSQ
>d1bkf__ d.26.1.1 (-) FK-506 binding protein (FKBP12), an immunophilin
{Human (Homo sapiens)}
GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDKNKPFKFMLGKQEVIRGWEEGVAQ
MSVGQRAKLTISPDYAYGATGVPGIIPPHATLVFDVELLKLE
>d1c9ha_ d.26.1.1 (A:) Calcineurin (FKBP12.6) {Human (Homo sapiens)}
GVEIETISPGDGRTFPKKGQTCVVHYTGMLQNGKKFDSSRDRNKPFKFRIGKQEVIKGFEEGAAQ
MSLGQRAKLTCTPDVAYGATGHPGVIPPNATLIFDVELLNLE
>d1yat__ d.26.1.1 (-) Calcineurin (FKBP12.6) {Baker's yeast
(Saccharomyces cerevisiae)}
SEVIEGNVKIDRISPGDGATFPKTGDLVTIHYTGTLENGQKFDSSVDRGSPFQCNIGVGQVIKGW
DVGIPKLSVGEKARLTIPGPYAYGPRGFPGLIPPNSTLVFDVELLKVN
>d1pbk__ d.26.1.1 (-) FKBP25 {Human (Homo sapiens)}
PKYTKSVLKKGDKTNFPKKGDVVHCWYTGTLQDGTVFDTNIQTSAKKKKNAKPLSFKVGVGKVIR
GWDEALLTMSKGEKARLEIEPEWAYGKKGQPDAKIPPNAKLTFEVELVDID
>d1rot__ d.26.1.1 (-) FKBP59-I, N-terminal domain {Rabbit
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(Oryctolagus cuniculus)}
GVDISPKQDEGVLKVIKREGTGTETPMIGDRVFVHYTGWLLDGTKFDSSLDRKDKFSFDLGKGEV
IKAWDIAVATMKVGELCRITCKPEYAYGSAGSPPKIPPNATLVFEVELFEFKG
>d1pina2 d.26.1.1 (A:45-163) Mitotic rotamase PIN1, domain 2 {Human
(Homo sapiens)}
GKNGQGEPARVRCSHLLVKHSQSRRPSSWRQEKITRTKEEALELINGYIQKIKSGEEDFESLASQ
FSDCSSAKARGDLGAFSRGQMQKPFEDASFALRTGEMSGPVFTDSGIHIILRTE
>d1eq3a_ d.26.1.1 (A:) Parvulin {Human (Homo sapiens), hpar14}
NAVKVRHILCEKHGKIMEAMEKLKSGMRFNEVAAQYSEDKARQGGDLGWMTRGSMVGPFQEAAFA
LPVSGMDKPVFTDPPVKTKFGYHIIMVEGRK
>d1fd9a_ d.26.1.1 (A:) Macrophage infectivity potentiator protein
(MIP) {Legionella pneumophila}
TDKDKLSYSIGADLGKNFKNQGIDVNPEAMAKGMQDAMSGAQLALTEQQMKDVLNKFQKDLMAKR
TAEFNKKADENKVKGEAFLTENKNKPGVVVLPSGLQYKVINSGNGVKPGKSDTVTVEYTGRLIDG
TVFDSTEKTGKPATFQVSQVIPGWTEALQLMPAGSTWEIYVPSGLAYGPRSVGGPIGPNETLIFK
IHLISVKKS
>d1grj_2 d.26.1.2 (80-158) GreA transcript cleavage factor,
C-terminal domain {Escherichia coli}
MPNNGRVIFGATVTVLNLDSDEEQTYRIVGDDEADFKQNLISVNSPIARGLIGKEEDDVVVIKTP
GGEVEFEVIKVEYL
>d3eipa_ d.26.2.1 (A:) Colicin E3 immunity protein {Escherichia coli}
GLKLDLTWFDKSTEDFKGEEYSKDFGDDGSVMESLGVPFKDNVNNGCFDVIAEWVPLLQPYFNHQ
IDISDNEYFVSFDYRDGDW
>d1edqa3 d.26.3.1 (A:444-516) Chitinase A {Serratia marcescens}
YGRGWTGVNGYQNNIPFTGTATGPVKGTWENGIVDYRQIAGQFMSGEWQYTYDATAEAPYVFKPS
TGDLITFD
>d1goia3 d.26.3.1 (A:292-379) Chitinase B {Serratia marcescens}
YGRAFKGVSGGNGGQYSSHSTPGEDPYPSTDYWLVGCEECVRDKDPRIASYRQLEQMLQGNYGYQ
RLWNDKTKTPYLYHAQNGLFVTY
>d1d2ka2 d.26.3.1 (A:293-354) Chitinase 1 {Fungus (Coccidioides
immitis)}
YGRAFASTDGIGTSFNGVGGGSWENGVWDYKDMPQQGAQVTELEDIAASYSYDKNKRYLISY
>d1e9la2 d.26.3.1 (A:267-336) Chitinase-like lectin ym1 {Mouse (Mus
musculus)}
YGHTFILSDPSKTGIGAPTISTGPPGKYTDESGLLAYYEVCTFLNEGATEVWDAPQEVPYAYQGN
EWVGY
>d1fjgp_ d.27.1.1 (P:) Ribosomal protein S16 {Thermus thermophilus}
MVKIRLARFGSKHNPHYRIVVTDARRKRDGKYIEKIGYYDPRKTTPDWLKVDVERARYWLSVGAQ
PTDTARRLLRQAGVFRQE
>d1fjgs_ d.28.1.1 (S:) Ribosomal protein S19 {Thermus thermophilus}
PRSLKKGVFVDDHLLEKVLELNAKGEKRLIKTWSRRSTIVPEMVGHTIAVYNGKQHVPVYITENM
VGHKLGEFAPTRTYRGHGK
>d1qkha_ d.28.1.1 (A:) Ribosomal protein S19 {Thermus thermophilus}
GVFVDDHLLEKVLELNAKGEKRLIKTWSRRSTIVPEMVGHTIAVYNGKQHVPVYITENMVGHKLG
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EFAPTRTY
>d1jj2w_ d.29.1.1 (W:) Ribosomal protein L31e {Archaeon Haloarcula
marismortui}
ERVVTIPLRDARAEPNHKRADKAMILIREHLAKHFSVDEDAVRLDPSINEAAWARGRANTPSKIR
VRAARFEEEGEAIVEAE
>d1b33n_ d.30.1.1 (N:) Allophycocyanin linker chain (domain)
{Mastigocladus laminosus}
GRLFKITACVPSQTRIRTQRELQNTYFTKLVPYENWFREQQRIQKMGGKIVKVELATGKQGINTG
LA
>d1qcsa2 d.31.1.1 (A:86-201) C-terminal domain of NSF-N, NSF-Nc
{Hamster (Cricetulus griseus)}
DKAKQCIGTMTIEIDFLQKKNIDSNPYDTDKMAAEFIQQFNNQAFSVGQQLVFSFNDKLFGLLVK
DIEAMDPSILKGEPASGKRQKIEVGLVVGNSQVAFEKAENSSLNLIGKAKT
>d1cr5a2 d.31.1.1 (A:108-210) C-terminal domain of NSF-N, NSF-Nc
{Baker's yeast (Saccharomyces cerevisiae), sec18p}
SGKQSYLGSIDIDISFRARGKAVSTVFDQDELAKQFVRCYESQIFSPTQYLIMEFQGHFFDLKIR
NVQAIDLGDIEPTSAVATGIETKGILTKQTQINFFKGR
>d1cz4a2 d.31.1.1 (A:92-185) C-terminal domain of VAT-N, VAT-Nc
{Archaeon Thermoplasma acidophilum}
TEIAKKVTLAPIIRKDQRLKFGEGIEEYVQRALIRRPMLEQDNISVPGLTLAGQTGLLFKVVKTL
PSKVPVEIGEETKIEIREEPASEVLEEGG
>d1e32a3 d.31.1.1 (A:107-200) Membrane fusion atpase p97 domain 2,
P97-Nc {Mouse (Mus musculus)}
DVKYGKRIHVLPIDDTVEGITGNLFEVYLKPYFLEAYRPIRKGDIFLVRGGMRAVEFKVVETDPS
PYCIVAPDTVIHCEGEPIKREDEEESLNE
>d1qipa_ d.32.1.1 (A:) Glyoxalase I (lactoylglutathione lyase) {Human
(Homo sapiens)}
GGLTDEAALSCCSDADPSTKDFLLQQTMLRVKDPKKSLDFYTRVLGMTLIQKCDFPIMKFSLYFL
AYEDKNDIPKEKDEKIAWALSRKATLELTHNWGTEDDETQSYHNGNSDPRGFGHIGIAVPDVYSA
CKRFEELGVKFVKKPDDGKMKGLAFIQDPDGYWIEILNPNKMATLM
>d1f9za_ d.32.1.1 (A:) Glyoxalase I (lactoylglutathione lyase)
{Escherichia coli}
MRLLHTMLRVGDLQRSIDFYTKVLGMKLLRTSENPEYKYSLAFVGYGPETEEAVIELTYNWGVDK
YELGTAYGHIALSVDNAAEACEKIRQNGGNVTREAGPVKGGTTVIAFVEDPDGYKIELIEEKDAG
RGLGN
>d1qtoa_ d.32.1.2 (A:) Bleomycin resistance protein, BRP
{Streptomyces verticillus}
MVKFLGAVPVLTAVDVPANVSFWVDTLGFEKDFGDRDFAGVRRGDIRLHISRTEHQIVADNTSAW
IEVTDPDALHEEWARAVSTDYADTSGPAMTPVGESPAGREFAVRDPAGNCVHFTAGE
>d1byla_ d.32.1.2 (A:) Bleomycin resistance protein, BRP
{Streptoalloteichus hindustanus}
FMAKLTSAVPVLTARDVAGAVEFWTDRLGFSRDFVEDDFAGVVRDDVTLFISAVQDQVVPDNTLA
WVWVRGLDELYAEWSEVVSTNFRDASGPAMTEIGEQPWGREFALRDPAGNCVHFVAE
>d1ecsa_ d.32.1.2 (A:) Bleomycin resistance protein, BRP {Klebsiella
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pneumoniae}
TDQATPNLPSRDFDSTAAFYERLGFGIVFRDAGWMILQRGDLMLEFFAHPGLDPLASWFSCCLRL
DDLAEFYRQCKSVGIQETSSGYPRIHAPELQGWGGTMAALVDPDGTLLRLIQNEL
>d1jc4a_ d.32.1.4 (A:) Methylmalonyl-CoA epimerase
{Propionibacterium shermanii}
NEDLFICIDHVAYACPDADEASKYYQETFGWHELHREENPEQGVVEIMMAPAAKLTEHMTQVQVM
APLNDESTVAKWLAKHNGRAGLHHMAWRVDDIDAVSATLRERGVQLLYDEPKLGTGGNRINFMHP
KSGKGVLIELTQYPK
>d1gdga1 d.32.1.3 (A:1-132) 2,3-Dihydroxybiphenyl dioxygenase (DHBD,
BPHC enzyme) {Pseudomonas sp.}
SIERLGYLGFAVKDVPAWDHFLTKSVGLMAAGSAGDAALYRADQRAWRIAVQPGELDDLAYAGLE
VDDAAALERMADKLRQAGVAFTRGDEALMQQRKVMGLLCLQDPFGLPLEIYYGPAEIFHEPFLPS
AP
>d1gdga2 d.32.1.3 (A:133-288) 2,3-Dihydroxybiphenyl dioxygenase
(DHBD, BPHC enzyme) {Pseudomonas sp.}
VSGFVTGDQGIGHFVRCVPDTAKAMAFYTEVLGFVLSDIIDIQMGPETSVPAHFLHCNGRHHTIA
LAAFPIPKRIHHFMLQANTIDDVGYAFDRLDAAGRITSLLGRHTNDQTLSFYADTPSPMIEVEFG
WGPRTVDSSWTVARHSRTAMWGHKSV
>d1han_1 d.32.1.3 (2-132) 2,3-Dihydroxybiphenyl dioxygenase (DHBD,
BPHC enzyme) {Burkholderia cepacia (formerly Pseudomonas cepacia)}
SIRSLGYMGFAVSDVAAWRSFLTQKLGLMEAGTTDNGDLFRIDSRAWRIAVQQGEVDDLAFAGYE
VADAAGLAQMADKLKQAGIAVTTGDASLARRRGVTGLITFADPFGLPLEIYYGASEVFEKPFLPG
A
>d1han_2 d.32.1.3 (133-289) 2,3-Dihydroxybiphenyl dioxygenase (DHBD,
BPHC enzyme) {Burkholderia cepacia (formerly Pseudomonas cepacia)}
AVSGFLTGEQGLGHFVRCVPDSDKALAFYTDVLGFQLSDVIDMKMGPDVTVPAYFLHCNERHHTL
AIAAFPLPKRIHHFMLEVASLDDVGFAFDRVDADGLITSTLGRHTNDHMVSFYASTPSGVEVEYG
WSARTVDRSWVVVRHDSPSMWGHKSVR
>d1mpya1 d.32.1.3 (A:1-145) Catechol 2,3-dioxygenase
(metapyrocatechase) {Pseudomonas putida, mt2}
MNKGVMRPGHVQLRVLDMSKALEHYVELLGLIEMDRDDQGRVYLKAWTEVDKFSLVLREADEPGM
DFMGFKVVDEDALRQLERDLMAYGCAVEQLPAGELNSCGRRVRFQAPSGHHFELYADKEYTGKWG
LNDVNPEAWPRDLKG
>d1mpya2 d.32.1.3 (A:146-307) Catechol 2,3-dioxygenase
(metapyrocatechase) {Pseudomonas putida, mt2}
MAAVRFDHALMYGDELPATYDLFTKVLGFYLAEQVLDENGTRVAQFLSLSTKAHDVAFIHHPEKG
RLHHVSFHLETWEDLLRAADLISMTDTSIDIGPTRHGLTHGKTIYFFDPSGNRNEVFCGGDYNYP
DHKPVTWTTDQLGKAIFYHDRILNERFMTVLT
>d1cjxa1 d.32.1.3 (A:4-153) 4-hydroxyphenylpyruvate dioxygenase,
HppD {Pseudomonas fluorescens}
YENPMGLMGFEFIEFASPTPGTLEPIFEIMGFTKVATHRSKNVHLYRQGEINLILNNEPNSIASY
FAAEHGPSVCGMAFRVKDSQKAYNRALELGAQPIHIDTGPMELNLPAIKGIGGAPLYLIDRFGEG
SSIYDIDFVYLEGVERNPVG
>d1cjxa2 d.32.1.3 (A:154-356) 4-hydroxyphenylpyruvate dioxygenase,
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HppD {Pseudomonas fluorescens}
AGLKVIDHLTHNVYRGRMVYWANFYEKLFNFREARYFDIKGEYTGLTSKAMSAPDGMIRIPLNEE
SSKGAGQIEEFLMQFNGEGIQHVAFLTDDLVKTWDALKKIGMRFMTAPPDTYYEMLEGRLPDHGE
PVDQLQARGILLDGSSVEGDKRLLLQIFSETLMGPVFFEFIQRKGDDGFGEGNFKALFESIERDQ
VRRGVLAT
>d1fx3a_ d.33.1.1 (A:) Bacterial protein-export protein SecB
{Haemophilus influenzae}
QPVLQIQRIYVKDVSFEAPNLPHIFQQEWKPKLGFDLSTETTQVGDDLYEVVLNISVETTLEDSG
DVAFICEVKQAGVFTISGLEDVQMAHCLTSQCPNMLFPYARELVSNLVNRGTFPALNLSPVNFDA
LFVEYMNRQQAEN
>d1bm8__ d.34.1.1 (-) DNA-binding domain of Mlu1-box binding protein
MBP1 {Baker's yeast (Saccharomyces cerevisiae)}
QIYSARYSGVDVYEFIHSTGSIMKRKKDDWVNATHILKAANFAKAKRTRILEKEVLKETHEKVQG
GFGKYQGTWVPLNIAKQLAEKFSVYDQLKPLFDF
>d1dk0a_ d.35.1.1 (A:) Heme-binding protein A (HasA) {Serratia
marcescens}
AFSVNYDSSFGGYSIHDYLGQWASTFGDVNHTNGNVTDANSGGFYGGSLSGSQYAISSTANQVTA
FVAGGNLTYTLFNEPAHTLYGQLDSLSFGDGLSGGDTSPYSIQVPDVSFGGLNLSSLQAQGHDGV
VHQVVYGLMSGDTGALETALNGILDDYGLSVNSTFDQVAAATA
>d1eyqa_ d.36.1.1 (A:) Chalcone isomerase {Alfalfa (Medicago sativa)}
SITAITVENLEYPAVVTSPVTGKSYFLGGAGERGLTIEGNFIKFTAIGVYLEDIAVASLAAKWKG
KSSEELLETLDFYRDIISGPFEKLIRGSKIRELSGPEYSRKVMENCVAHLKSVGTYGDAEAEAMQ
KFAEAFKPVNFPPGASVFYRQSPDGILGLSFSPDTSIPEKEAALIENKAVSSAVLETMIGEHAVS
PDLKRCLAARLPALLNE
>d1b3ob2 d.37.1.1 (B:112-159) Type II inosine monophosphate
dehydrogenase {Human (Homo sapiens)}
QGFITDPVVLSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRLVGIIS
>d1jr1a2 d.37.1.1 (A:113-155) Type II inosine monophosphate
dehydrogenase {Chinese hamster (Cricetulus griseus)}
GFITDPVVLSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRLV
>d1jr1a3 d.37.1.1 (A:178-232) Type II inosine monophosphate
dehydrogenase {Chinese hamster (Cricetulus griseus)}
IMTKREDLVVAPAGITLKEANEILQRSKKGKLPIVNENDELVAIIARTDLKKNRD
>d1zfja2 d.37.1.1 (A:95-158) Type II inosine monophosphate
dehydrogenase {Streptococcus pyogenes}
NGVIIDPFFLTPEHKVSEAEELMQRYRISGVPIVETLANRKLVGIITNRDMRFISDYNAPISEH
>d1zfja3 d.37.1.1 (A:159-220) Type II inosine monophosphate
dehydrogenase {Streptococcus pyogenes}
MTSEHLVTAAVGTDLETAERILHEHRIEKLPLVDNSGRLSGLITIKDIEKVIEFPHAAKDEF
>d1bvqa_ d.38.1.1 (A:) 4-hydroxybenzoyl-CoA thioesterase
{Pseudomonas sp., CBS-3}
ARSITMQQRIEFGDCDPAGIVWYPNYHRWLDAASRNYFIKCGLPPWRQTVVERGIVGTPIVSCNA
SFVCTASYDDVLTIETCIKEWRRKSFVQRHSVSRTTPGGDVQLVMRADEIRVFAMNDGERLRAIE
VPADYIELC
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>d1mkaa_ d.38.1.2 (A:) beta-Hydroxydecanol thiol ester dehydrase {Escherichia coli}
VDKRESYTKEDLLASGRGELFGAKGPQLPAPNMLMMDRVVKMTETGGNFDKGYVEAELDINPDLW
FFGCHFIGDPVMPGCLGLDAMWQLVGFYLGWLGGEGKGRALGVGEVKFTGQVLPTAKKVTYRIHF
KRIVNRRLIMGLADGEVLVDGRLIYTASDLKVGLFQDTSAF
>d1c8ua1 d.38.1.3 (A:2-115) Thioesterase II (TesB) {Escherichia coli}
SQALKNLLTLLNLEKIEEGLFRGQSEDLGLRQVFGGQVVGQALYAAKETVPEERLVHSFHSYFLR
PGDSKKPIIYDVETLRDGNSFSARRVAAIQNGKPIFYMTASFQAPEAGF
>d1c8ua2 d.38.1.3 (A:116-286) Thioesterase II (TesB) {Escherichia coli}
EHQKTMPSAPAPDGLPSETQIAQSLAHLLPPVLKDKFICDRPLEVRPVEFHNPLKGHVAEPHRQV
WIRANGSVPDDLRVHQYLLGYASDLNFLPVALQPHGIGFLEPGIQIATIDHSMWFHRPFNLNEWL
LYSVESTSASSARGFVRGEFYTQDGVLVASTVQEGVMRNHN
>d1cmia_ d.39.1.1 (A:) Dynein light chain 8 (DLC8) {Human (Homo sapiens)}
KAVIKNADMSEEMQQDSVECATQALEKYNIEKDIAAHIKKEFDKKYNPTWHCIVGRNFGSYVTHE
TKHFIYFYLGQVAILLFKSG
>d1csei_ d.40.1.1 (I:) Eglin C {Leech (Hirudo medicinalis)}
KSFPEVVGKTVDQAREYFTLHYPQYNVYFLPEGSPVTLDLRYNRVRVFYNPGTNVVNHVPHVG
>d1egl__ d.40.1.1 (-) Eglin C {Leech (Hirudo medicinalis)}
TEFGSELKSFPEVVGKTVDQAREYFTLHYPQYDVYFLPEGSPVTLDLRYNRVRVFYNPGTNVVNH
VPHVG
>d1ypci_ d.40.1.1 (I:) Chymotrypsin inhibitor CI-2 {Barley (Hordeum vulgare)}
MKTEWPELVGKSVAAAKKVILQDKPEAQIIVLPVGTIVTMEYRIDRVRLFVDKLDNIAQVPRVG
>d2snii_ d.40.1.1 (I:) Chymotrypsin inhibitor CI-2 {Barley (Hordeum vulgare)}
LKTEWPELVGKSVEEAKKVILQDKPEAQIIVLPVGTIVTMEYRIDRVRLFVDKLDNIAEVPRVG
>g1cq4.1 d.40.1.1 (A:,B:) Chymotrypsin inhibitor CI-2 {Barley (Hordeum vulgare)}
KTEWPELVGKSVEEAKKVILQDKPEAQIIVLPVGTIVXYRIDRVRLFVDKLDNIAQVPRVG
>d1tin__ d.40.1.1 (-) Trypsin inhibitor V {Pumpkin (Cucurbita maxima)}
SSCPGKSSWPHLVGVGGSVAKAIIERQNPNVKAVILEEGTPVTKDFRCNRVRIWVNKRGLVVSPP
RIG
>d1dwma_ d.40.1.1 (A:) Trypsin inhibitor LUTI {Flax (Linum usitatissimum)}
SRRCPGKNAWPELVGKSGNMAAATVERENRNVHAIVLKEGSAMTKDFRCDRVWVIVNDHGVVTSV
PHIT
>d1jv2b3 d.200.1.1 (B:606-690) Integrin beta tail domain {Human (Homo sapiens)}
DACTFKKECVECKKFDREPYMTENTCNRYCRDEIESVKELKDTGKDAVNCTYKNEDDCVVRFQYY
EDSSGKSILYVVEEPECPKG
>d1hlra3 d.41.1.1 (A:194-310) Aldehyde oxidoreductase, domain 3 {Desulfovibrio gigas}

DYGADLGLKMPAGTLHLAMVQAKVSHANIKGIDTSEALTMPGVHSVITHKDVKGKNRITGLITFP
TNKGDGWDRPILCDEKVFQYGDCIALVCADSEANARAAAEKVKVDLEELPAY
>d1dgja3 d.41.1.1 (A:194-310) Aldehyde oxidoreductase, domain 3 {Desulfovibrio desulfuricans}
EFGADAALRMPENTLHLALAQAKVSHALIKGIDTSEAEKMPGVYKVLTHKDVKGKNRITGLITFP
TNKGDGWERPILNDSKIFQYGDALAIVCADSEANARAAAEKVKFDLELLPEY
>d1fiqc1 d.41.1.1 (C:571-694) Xanthine oxidase, domain 5 (?) {Cow (Bos taurus)}
DTVGRPLPHLAAAMQASGEAVYCDDIPRYENELFLRLVTSTRAHAKIKSIDVSEAQKVPGFVCFL
SADDIPGSNETGLFNDETVFAKDTVTCVGHIIGAVVADTPEHAERAAHVVKVTYEDLPA
>d1fo4a3 d.41.1.1 (A:537-694) Xanthine oxidase, domain 5 (?) {Cow (Bos taurus)}
KLDPTYTSATLLFQKHPPANIQLFQEVPNGQSKEDTVGRPLPHLAAAMQASGEAVYCDDIPRYEN
ELFLRLVTSTRAHAKIKSIDVSEAQKVPGFVCFLSADDIPGSNETGLFNDETVFAKDTVTCVGHI
IGAVVADTPEHAERAAHVVKVTYEDLPA
>d1jrob1 d.41.1.1 (B:2-123) Xanthine dehydrogenase chain B, N-terminal domain {Rhodobacter capsulatus}
SVGKPLPHDSARAHVTGQARYLDDLPCPANTLHLAFGLSTEASAAITGLDLEPVRESPGVIAVFT
AADLPHDNDASPAPSPEPVLATGEVHFVGQPIFLVAATSHRAARIAARKARITYAPR
>d1qj2b1 d.41.1.1 (B:10-146) Carbon monoxide (CO) dehydrogenase molybdoprotein, N-domain {Pseudomonas carboxydovorans}
TSAERAEKLQGMGCKRKRVEDIRFTQGKGNYVDDVKLPGMLFGDFVRSSHAHARIKSIDTSKAKA
LPGVFAVLTAADLKPLNLHYMPTLAGDVQAVLADEKVLFQNQEVAFVVAKDRYVAADAIELVEVD
YEPLPVL
>d1ffvb1 d.41.1.1 (B:7-146) Carbon monoxide (CO) dehydrogenase molybdoprotein, N-domain {Hydrogenophaga pseudoflava}
DAEARELALAGMGASRLRKEDARFIQGKGNYVDDIKMPGMLHMDIVRAPIAHGRIKKIHKDAALA
MPGVHAVLTAEDLKPLKLHWMPTLAGDVAAVLADEKVHFQMQEVAIVIADDRYIAADAVEAVKVE
YDELPVVIDP
>d1qapa2 d.41.2.1 (A:8-129) Quinolinic acid phosphoribosyltransferase, N-terminal domain {Salmonella typhimurium}
DDRRDALLERINLDIPAAVAQALREDLGGEVDAGNDITAQLLPADTQAHATVITREDGVFCGKRW
VEEVFIQLAGDDVRLTWHVDDGDAIHANQTVFELQGPARVLLTGERTALNFVQTLSG
>d1qpoa2 d.41.2.1 (A:2-116) Quinolinic acid phosphoribosyltransferase, N-terminal domain {Mycobacterium tuberculosis}
GLSDWELAAARAAIARGLDEDLRYGPDVTTLATVPASATTTASLVTREAGVVAGLDVALLTLNEV
LGTNGYRVLDRVEDGARVPPGEALMTLEAQTRGLLTAERTMLNLVGHLSG
>d2tpt_3 d.41.3.1 (336-440) Thymidine phosphorylase {Escherichia coli}
TAMLTKAVYADTEGFVSEMDTRALGMAVVAMGGGRRQASDTIDYSVGFTDMARLGDQVDGQRPLA
VIHAKDENNWQEAAKAVKAAIKLADKAPESTPTVYRRISE
>d1brwa3 d.41.3.1 (A:331-433) Pyrimidine nucleoside phosphorylase

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{Bacillus stearothermophilus}
KAAYTSTVTAAADGYVAEMAADDIGTAAMWLGAGRAKKEDVIDLAVGIVLHKKIGDRVQKGEALA
TIHSNRPDVLDVKEKIEAAIRLSPQPVARPPLIYETIV
>d1ffkf_ d.41.4.1 (F:) Ribosomal protein L10e {Archaeon Haloarcula
marismortui}
KPGAHFRNSIKPAYTRREYISGIPGKGIAQFKMGNNGAGPTYPAQVENVVEKPVQIRHNALEAAR
NAANRFVQNSGAAANYKFRIRKFPFHVIREQDGDGMRAPFGKSVGTAARSHGANHDFIAWVNPDP
AVEFAWRRAYMKVTPTVNIDSSPAGNA
>d1jj2h_ d.41.4.1 (H:) Ribosomal protein L10e {Archaeon Haloarcula
marismortui}
KPGAMYRNSSKPAYTRREYISGIPGKKIAQFDMGNNGAGPTYPAQVELVVEKPVQIRHNALEAAR
VAANRYVQNSGAAANYKFRIRKFPFHVIRENKAAAAAAAAAAADGMRAPFGKPVGTAARVHGANH
IFIAWVNPDPNVEEAWRRAKMKVTPTINIDSSPAGNA
>d1fm0e_ d.41.5.1 (E:) Molybdopterin synthase subunit MoaE
{Escherichia coli}
AETKIVVGPQPFSVGEEYPWLAERDEDGAVVTFTGKVRNHNLGDSVNALTLEHYPGMTEKALAEI
VDEARNRWPLGRVTVIHRIGELWPGDEIVFVGVTSAHRSSAFEAGQFIMDYLKTRAPFWKREATP
EGDRWVEARESDQQAAKRW
>d1buoa_ d.42.1.1 (A:) Promyelocytic leukemia zinc finger (PLZF)
protein BTB domain {Human (Homo sapiens)}
MGMIQLQNPSHPTGLLCKANQMRLAGTLCDVVIMVDSQEFHAHRTVLACTSKMFEILFHRNSQHY
TLDFLSPKTFQQILEYAYTATLQAKAEDLDDLLYAAEILEIEYLEEQCLKMLETIQ
>d1vcbb_ d.42.1.1 (B:) Elongin C {Human (Homo sapiens)}
MYVKLISSDGHEFIVKREHALTSGTIKAMLSGPGQFAENETNEVNFREIPSHVLSKVCMYFTYKV
RYTNSSTEIPEFPIAPEIALELLMAANFLDC
>d1hv2a_ d.42.1.1 (A:) Elongin C {Baker's yeast (Saccharomyces
cerevisiae)}
MSQDFVTLVSKDDKEYEISRSAAMISPTLKAMIEGPFRESKGRIELKQFDSHILEKAVEYLNYNL
KYSGVSEDDDEIPEFEIPTEMSLELLLAADYLSI
>d1a68__ d.42.1.2 (-) Shaker potassium channel {California sea hare
(Aplysia californica)}
ERVVINVSGLRFETQLKTLNQFPDTLLGNPQKRNRYYDPLRNEYFFDRNRPSFDAILYFYQSGGR
LRRPVNVPLDVFSEEIKFYELG
>d1t1da_ d.42.1.2 (A:) Shaker potassium channel {California sea hare
(Aplysia californica)}
ERVVINVSGLRFETQLKTLNQFPDTLLGNPQKRNRYYDPLRNEYFFDRNRPSFDAILYFYQSGGR
LRRPVNVPLDVFSEEIKFYELGENAFERYREDEGF
>d3kvt__ d.42.1.2 (-) akv3.1 voltage-gated potassium channel
{California sea hare (Aplysia californica)}
ENRVIINVGGIRHETYKATLKKIPATRLSRLTEGMLNYDPVLNEYFFDRHPGVFAQIINYYRSGK
LHYPTDVCGPLFEEELEFWGLDSNQVEPCCWMTYTAHR
>d1exbe_ d.42.1.2 (E:) KV1.1 {Rat (Rattus norvegicus)}
CERVVINISGLRFETQLKTLAQFPNTLLGNPKKRMRYFDPLRNEYFFDRNRPSFDAILYYYQSGG
RLRRPVNVPLDMFSEEIKFYELGEEA
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>d1dsxa_ d.42.1.2 (A:) Kv1.2 {Rat (Rattus norvegicus)}
ERVVINISGLRFEVQLKTLAQFPETLLGDPKKRMRYFDPLRNEYFFDRNRPSFDAILYYYQSGGR
LRRPVNVPLDIFSEEIRFYELG
>d1qdva_ d.42.1.2 (A:) Kv1.2 {Rat (Rattus norvegicus)}
ERVVINISGLRFETQLKTLAQFPETLLGDPKKRMRYFDPLRNEYFFDRNRPSFDAILYYYQSGGR
LRRPVNVPLDIFSEEIRFYELGEEAMEMFREDEG
>d1fs1b2 d.42.1.2 (B:2-68) Cyclin A/CDK2-associated p45, Skp1 {Human (Homo sapiens)}
PSIKLQSSDGEIFEVDVEIAKQSVTIKTMLEDLGMDPVPLPNVNAAILKKVIQWCTHHKDD
>d1efub2 d.43.1.1 (B:140-282) Elongation factor Ts (EF-Ts), dimerisation domain {Escherichia coli}
DVLGSYQHGARIGVLVAAKGADEELVKHIAMHVAASKPEFIKPEDVSAEVVEKEYQVQLDIAMQS
GKPKEIAEKMVEGRMKKFTGEVSLTGQPFVMEPSKTVGQLLKEHNAEVTGFIRFEVGEGIEKVET
DFAAEVAAMSKQS
>d1efub4 d.43.1.1 (B:55-139) Elongation factor Ts (EF-Ts), dimerisation domain {Escherichia coli}
VAADGVIKTKIDGNYGIILEVNCQTDFVAKDAGFQAFADKVLDAAVAGKITDVEVLKAQFEEERV
ALVAKIGENINIRRVAALEG
>d1tfe__ d.43.1.1 (-) Elongation factor Ts (EF-Ts), dimerisation domain {Thermus thermophilus}
AREGIIGHYIHHNQRVGVLVELNCETDFVARNELFQNLAKDLAMHIAMMNPRYVSAEEIPAEELE
KERQIYIQAALNEGKPQQIAEKIAEGRLKKYLEEVVLLEQPFVKDDKVKVKELIQQAIAKIGENI
VVRRFCRFELGA
>d1i0ha2 d.44.1.1 (A:91-205) Mn superoxide dismutase (MnSOD) {Escherichia coli}
GTTLQGDLKAAIERDFGSVDNFKAEFEKAAASRFGSGWAWLVLKGDKLAVVSTANQDSPLMGEAI
SGASGFPIMGLDVWEHAYFLKFQNRRPDYIKEFWNVVNWDEAAARFAAKK
>d1mnga2 d.44.1.1 (A:93-203) Mn superoxide dismutase (MnSOD) {Thermus thermophilus}
GGAKEPVGELKKAIDEQFGGFQALKEKLTQAAMGRFGSGWAWLVKDPFGKLHVLSTPNQDNPVME
GFTPIVGIDVWEHAYYLKYQNRRADYLQAIWNVLNWDVAEEFFKKA
>d1ap6a2 d.44.1.1 (A:84-198) Mn superoxide dismutase (MnSOD) {Human (Homo sapiens)}
NGGGEPKGELLEAIKRDFGSFDKFKEKLTAASVGVQGSGWGWLGFNKERGHLQIAACPNQDPLQG
TTGLIPLLGIDVWEHAYYLQYKNVRPDYLKAIWNVINWENVTERYMACKK
>d1kkca2 d.44.1.1 (A:98-213) Mn superoxide dismutase (MnSOD) {Aspergillus fumigatus}
EKSGGGKIDQAPVLKAAIEQRWGSFDKFKDAFNTTLLGIQGSGWGWLVTDGPKGKLDITTTHDQD
PVTGAAPVFGVDMWEHAYYLQYLNDKASYAKGIWNVINWAEAENRYIAGDK
>d1dt0a2 d.44.1.1 (A:84-197) Fe superoxide dismutase (FeSOD) {Pseudomonas ovalis}
AGGQPTGALADAINAAFGSFDKFKEEFTKTSVGTFGSGWGWLVKKADGSLALASTIGAGCPLTIG
DTPLLTCDVWEHAYYIDYRNLRPKYVEAFWNLVNWAFVAEQFEGKTYKV
>d3sdpa2 d.44.1.1 (A:84-190) Fe superoxide dismutase (FeSOD)
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{Pseudomonas ovalis}
DAGGQPTGALADAINAAFGSFDKFKEEFTKTSVGTFGSGWAWLVKADGSLALCSTIGAGAPLTSG
DTPLLTCDVWEHAYYIDYRNLRPKYVEAFWNLVNWAFVAEEG
>d1isaa2 d.44.1.1 (A:83-192) Fe superoxide dismutase (FeSOD)
{Escherichia coli}
NAGGEPTGKVAEAIAASFGSFADFKAQFTDAAIKNFGSGWTWLVKNSDGKLAIVSTSNAGTPLTT
DATPLLTVDVWEHAYYIDYRNARPGYLEHFWALVNWEFVAKNLAA
>d1idsa2 d.44.1.1 (A:86-199) Fe superoxide dismutase (FeSOD)
{Mycobacterium tuberculosis}
NGGDKPTGELAAAIADAFGSFDKFRAQFHAAATTVQGSGWAALGWDTLGNKLLIFQVYDHQTNFP
LGIVPLLLLDMWEHAFYLQYKNVKVDFAKAFWNVVNWADVQSRYAAATS
>d1coja2 d.44.1.1 (A:91-212) Fe superoxide dismutase (FeSOD) {Aquifex
pyrophilus}
GGKGEPSEALKKKIEEDIGGLDACTNELKAAAMAFRGWAILGLDIFSGRLVVNGLDAHNVYNLTG
LIPLIVIDTYEHAYYVDYKNKRPPYIDAFFKNINWDVVNERFEKAMKAYEALKDFIK
>d1sssa2 d.44.1.1 (A:93-208) Fe superoxide dismutase (FeSOD)
{Archaeon Sulfolobus solfataricus}
PSGKGGGKPGGALADLINKQYGSFDRFKQVFTETANSLPGTGWAVLYYDTESGNLQIMTFENHFQ
NHIAEIPIILILDEFEHAYYLQYKNKRADYVNAWWNVVNWDAAEKKLQKYL
>d1b06a2 d.44.1.1 (A:93-210) Fe superoxide dismutase (FeSOD)
{Archaeon Sulfolobus acidocaldarius}
PAGKGGGKPGGALADLIDKQYGSFDRFKQVFSESANSLPGSGWTVLYYDNESGNLQIMTVENHFM
NHIAELPVILIVDEFEHAYYLQYKNKRGDYLNAWWNVVNWDDAEKRLQKYLNK
>d1bsma2 d.44.1.1 (A:87-201) Cambialistic superoxide dismutase
{Propionibacterium shermanii}
SAPERPTDELGAAIDEFFGSFDNMKAQFTAAATGIQGSGWASLVWDPLGKRINTLQFYDHQNNLP
AGSIPLLQLDMWEHAFYLQYKNVKGDYVKSWWNVVNWDDVALRFSEARVA
>d1qnna2 d.44.1.1 (A:85-191) Cambialistic superoxide dismutase
{Porphyromonas gingivalis}
KGGAPKGKLGEAIDKQFGSFEKFKEEFNTAGTTLFGSGWVWLASDANGKLSIEKEPNAGNPVRKG
LNPLLGFDVWEHAYYLTYQNRRADHLKDLWSIVDWDIVESRY
>d1ctf__ d.45.1.1 (-) Ribosomal protein L7/12, C-terminal domain
{Escherichia coli}
EFDVILKAAGANKVAVIKAVRGATGLGLKEAKDLVESAPAALKEGVSKDDAEALKKALEEAGAEV
EVK
>d1dd3a2 d.45.1.1 (A:58-128) Ribosomal protein L7/12, C-terminal
domain {Thermotoga maritima}
EFDVVLKSFGQNKIQVIKVVREITGLGLKEAKDLVEKAGSPDAVIKSGVSKEEAEEIKKKLEEAG
AEVELK
>d1ekta_ d.46.1.1 (A:) Transcription-state regulator AbrB, the
N-terminal DNA recognition domain {Bacillus subtilis}
MKSTGIVRKVDELGRVVIPIELRRTLGIAEKDALEIYVDDEKIILKKYKPNMT
>d1mmsa2 d.47.1.1 (A:8-70) Ribosomal protein L11, N-terminal domain
{Thermotoga maritima}
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QIKLQLPAGKATPAPPVGPALGQHGVNIMEFCKRFNAETADKAGMILPVVITVYEDKSFTFII
>d2reb_2 d.48.1.1 (269-328) RecA protein, C-terminal domain
{Escherichia coli}
NFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQGKANATAWLKDNPETAKEIEKKVRELLL
>d1g19a2 d.48.1.1 (A:270-329) RecA protein, C-terminal domain
{Mycobacterium tuberculosis}
SREGSLIDMGVDQGLIRKSGAWFTYEGEQLGQGKENARNFLVENADVADEIEKKIKEKLG
>d1e8oa_ d.49.1.1 (A:) Signal recognition particle alu RNA binding
heterodimer, SRP9/14 {Human (Homo sapiens)}
PQYQTWEEFSRAAEKLYLADPMKARVVLKYRHSDGNLCVKVTDDLVCLVYKTDQAQDVKKIEKFH
SQLMRLMVA
>d1e8ob_ d.49.1.1 (B:) Signal recognition particle alu RNA binding
heterodimer, SRP9/14 {Human (Homo sapiens)}
VLLESEQFLTELTRLFQKCRTSGSVYITLKKYDGRTKPIPKKGTVEGFEPADNKCLLRATDGKKK
ISTVVSSKEVNKFQMAYSNLLRANMDGLK
>d1914__ d.49.1.1 (-) Signal recognition particle alu RNA binding
heterodimer, SRP9/14 {Mouse (Mus musculus)}
MVLLESEQFLTELTRLFQKCRSSGSVFITLKKYDGRTKPIPRKSSVEGLEPAENKCLLRATDGKR
KISTVVSSKEVNKFQMAYSNLLRANMDGLKKRDKKNKSKKSKPAQGGEQKLISEEDDSAGSPMPQ
FQTWEEFSRAAEKLYLADPMKVRVVLKYRHVDGNLCIKVTDDLVCLVYRTDQAQDVKKIEKFHSQ
LMRLMVAKESRNV
>d1di2a_ d.50.1.1 (A:) Double-stranded RNA-binding protein A, second
dsRBD {Xenopus laevis}
MPVGSLQELAVQKGWRLPEYTVAQESGPPHKREFTITCRVETFVETGSGTSKQVAKRVAAEKLLT
KFKT
>d1ekza_ d.50.1.1 (A:) Staufen, domain III {Fruit fly (Drosophila
melanogaster)}
MDEGDKKSPISQVHEIGIKRNMTVHFKVLREEGPAHMKNFITACIVGSIVTEGEGNGKKVSKKRA
AEKMLVELQKL
>d1stu__ d.50.1.1 (-) Staufen, domain III {Fruit fly (Drosophila
melanogaster)}
PISQVHEIGIKRNMTVHFKVLREEGPAHMKNFITACIVGSIVTEGEGNGKKVSKKRAAEKMLVEL
QKL
>d1qu6a1 d.50.1.1 (A:1-90) dsRNA-dependent protein kinase pkr {Human
(Homo sapiens)}
GSHMEMAGDLSAGFFMEELNTYRQKQGVVLKYQELPNSGPPHDRRFTFQVIIDGREFPEGEGRSK
KEAKNAAAKLAVEILNKEKKAVSPL
>d1qu6a2 d.50.1.1 (A:91-179) dsRNA-dependent protein kinase pkr
{Human (Homo sapiens)}
LLTTTNSSEGLSMGNYIGLINRIAQKKRLTVNYEQCASGVHGPEGFHYKCKMGQKEYSIGTGSTK
QEAKQLAAKLAYLQILSEETGSGC
>d1pkp_2 d.50.1.2 (4-77) Ribosomal S5 protein, N-terminal domain
{Bacillus stearothermophilus}
INPNKLELEERVVAVNRVAKVVKGGRRLRFSALVVVGDKNGHVGFGTGKAQEVPEAIRKAIEDAK
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KNLIEVPIV
>d1fjge2 d.50.1.2 (E:5-73) Ribosomal S5 protein, N-terminal domain
{Thermus thermophilus}
DFEEKMILIRRTARMQAGGRRFRFGALVVVGDRQGRVGLGFGKAPEVPLAVQKAGYYARRNMVEV
PLQN
>d1ah5_2 d.50.2.1 (220-313) Porphobilinogen deaminase
(hydroxymethylbilane synthase), C-terminal domain {Escherichia coli}
NHHETALRVTAERAMNTRLEGGCQVPIGSYAELIDGEIWLRALVGAPDGSQIIRGERRGAPQDAE
QMGISLAEELLNNGAREILAEVYNGDAPA
>d1pda_2 d.50.2.1 (220-307) Porphobilinogen deaminase
(hydroxymethylbilane synthase), C-terminal domain {Escherichia coli}
NHHETALRVTAERAMNTRLEGACQVPIGSYAELIDGEIWLRGLVGAPDGSQIIRGERRGAPQDAE
QMGISLAEELLNNGAREILAEVY
>d1dq3a2 d.50.3.1 (A:336-414) PI-Pfui intein middle domain {Archaeon
Pyrococcus furiosus}
GNFGLPLNFNAFKEWASEYGVEFKTNGSQTIAIINDERISLGQWHTRNRVSKAVLVKMLRKLYEA
TKDEEVKRMLHLIE
>d1jida_ d.201.1.1 (A:) SRP19 {Human (Homo sapiens)}
AARSPADQDRFICIYPAYLNNKKTIAEGRRIPISKAVENPTATEIQDVCSAVGLNVFLEKNKMYS
REWNRDVQYRGRVRVQLKQEDGSLCLVQFPSRKSVMLYAAEMIPKLKTR
>d1dt4a_ d.51.1.1 (A:) Neuro-oncological ventral antigen 1, nova-1,
KH3 {Human (Homo sapiens)}
MKDVVEIAVPENLVGAILGKGGKTLVEYQELTGCRIQISKKGEFLPGTRNRKVTITGTPAATQAA
QYLITQRI
>d1dtja_ d.51.1.1 (A:) Neuro-oncological ventral antigen 2, nova-2,
KH3 {Human (Homo sapiens)}
MKELVEMAVPENLVGAILGKGGKTLVEYQELTGARIQISKKGEFLPGTRNRRVTITGSPAATQAA
QYLISQRVT
>d1ec6a_ d.51.1.1 (A:) Neuro-oncological ventral antigen 2, nova-2,
KH3 {Human (Homo sapiens)}
MKELVEIAVPENLVGAILGKGGKTLVEYQELTGARIQISKKGEFLPGTRNRRVTITGSPAATQAA
QYLISQRVTYEQGVRASNPQKV
>d1vig__ d.51.1.1 (-) Vigilin, KH6 {Human (Homo sapiens)}
INRMDYVEINIDHKFHRHLIGKSGANINRIKDQYKVSVRIPPDSEKSNLIRIEGDPQGVQQAKRE
LLELAS
>d2fmr__ d.51.1.1 (-) Fragile X protein, KH1 {Human (Homo sapiens)}
ASRFHEQFIVREDLMGLAIGTHGANIQQARKVPGVTAIDLDEDTCTFHIYGEDQDAVKKARSFLE
>d1khma_ d.51.1.1 (A:) HnRNP K, KH3 {Human (Homo sapiens)}
GSPNSYGDLGGPIITTQVTIPKDLARSIIGKGGQRIKQIRHESGASIKIDEPLEGSEDRIITITG
TQDQIQNAQYLLQNSVKQYSGKFF
>d1k1ga_ d.51.1.1 (A:) RNA splicing factor 1 {Human (Homo sapiens)}
TRVSDKVMIPQDEYPEINFVGLLIGPRGNTLKNIEKECNAKIMIRGKGSVKEGKVGRKDGQMLPG
EDEPLHALVTANTMENVKKAVEQIRNILKQGIETPEDQNDLRKMQLRELARLNGTLR
>d2proc1 d.52.1.1 (C:18-85) Alpha-lytic protease prodomain
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{Lysobacter enzymogenes}
IFPTQLPQYLQTEKLARTQAAAIEREFGAQFAGSWIERNEDGSFKLVAATSGARKSSTLGGVEVR
NVR
>d3proc1 d.52.1.1 (C:6-85) Alpha-lytic protease prodomain {Lysobacter
enzymogenes}
PQLKFAMQRDLGIFPTQLPQYLQTEKLARTQAAAIEREFGAQFAGSWIERNEDGSFKLVAATSGA
RKSSTLGGVEVRNVR
>d3proc2 d.52.1.1 (C:86-163) Alpha-lytic protease prodomain
{Lysobacter enzymogenes}
YSLKQLQSAMEQLDAGANARVKGVSKPLDGVQSWYVDPRSNAVVVKVDDGATDAGVDFVALSGAD
SAQVRIESSPGKL
>d1gpma3 d.52.2.1 (A:405-525) GMP synthetase, C-terminal,
dimerisation domain {Escherichia coli}
GPGLGVRVLGEVKKEYCDLLRRADAIFIEELRKADLYDKVSQAFTVFLPVRSVGVMGDGRKYDWV
VSLRAVETIDFMTAHWAHLPYDFLGRVSNRIINEVNGISRVVYDISGKPPATIEWE
>d1fjgc1 d.52.3.1 (C:2-106) Ribosomal protein S3 N-terminal domain
{Thermus thermophilus}
GNKIHPIGFRLGITRDWESRWYAGKKQYRHLLLEDQRIRGLLEKELYSAGLARVDIERAADNVAV
TVHVAKPGVVIGRGGERIRVLREELAKLTGKNVALNVQEV
>d1egaa2 d.52.3.1 (A:183-295) GTPase Era C-terminal domain
{Escherichia coli}
DYITDRSQRFMASEIIREKLMRFLGAELPYSVTVEIERFVSNERGGYDINGLILVEREGQKKMVI
GNKGAKIKTIGIEARKDMQEMFEAPVHLELWVKVKSGWADDERALRSL
>d1hh2p2 d.52.3.1 (P:199-276) Transcription factor NusA, C-terminal
domains {Thermotoga maritima}
RVPEFVIGLMKLEIPEVENGIVEIKAIAREPGVRTKVAVASNDPNVDPIGACIGEGGSRIAAILK
ELKGEKLDVLKWS
>d1hh2p3 d.52.3.1 (P:277-344) Transcription factor NusA, C-terminal
domains {Thermotoga maritima}
DDPKQLIANALAPATVIEVEILDKENKAARVLVPPTQLSLAIGKGGQNARLAAKLTGWKIDIKPI
MNL
>d1k0ra2 d.52.3.1 (A:184-262) Transcription factor NusA, C-terminal
domains {Mycobacterium tuberculosis}
THPNLVRKLFSLEVPEIADGSVEIVAVAREAGHRSKIAVRSNVAGLNAKGACIGPMGQRVRNVMS
ELSGEKIDIIDYDD
>d1k0ra3 d.52.3.1 (A:263-329) Transcription factor NusA, C-terminal
domains {Mycobacterium tuberculosis}
DPARFVANALSPAKVVSVSVIDQTARAARVVVPDFQLSLAIGKEGQNARLAARLTGWRIDIRGDA
PP
>d1e3ha4 d.52.3.1 (A:579-632) Polynucleotide phosphorylase/guanosine
pentaphosphate synthase (PNPase/GPSI), domain 6 {Streptomyces
antibioticus}
APRIITVKIPVDKIGEVIGPKRQMINQIQEDTGAEITIEDDGTIYIGAADGPAA
>d1fjgc2 d.53.1.1 (C:107-207) Ribosomal protein S3 C-terminal domain
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{Thermus thermophilus}
QNPNLSAPLVAQRVAEQIERRFAVRRAIKQAVQRVMESGAKGAKVIVSGRIGGAEQARTEWAAQG
RVPLHTLRANIDYGFALARTTYGVLGVKAYIFLGEV
>d1hh2p4 d.202.1.1 (P:1-126) Transcription factor NusA, N-terminal
domain {Thermotoga maritima}
MNIGLLEALDQLEEEKGISKEEVIPILEKALVSAYRKNFGNSKNVEVVIDRNTGNIKVYQLLEVV
EEVEDPATQISLEEAKKIDPLAEVGSIVKKELNVKNFGRIAAQTAKQVLIQRIRELEKEKQ
>d1k0ra4 d.202.1.1 (A:-4-99) Transcription factor NusA, N-terminal
domain {Mycobacterium tuberculosis}
VSRRHMNIDMAALHAIEVDRGISVNELLETIKSALLTAYRHTQGHQTDARIEIDRKTGVVRVIAR
ETDEAGNLISEWDDTPEGFGRIAATTARQVMLQRFRDAE
>d1onea2 d.54.1.1 (A:1-141) Enolase {Baker's yeast (Saccharomyces
cerevisiae)}
AVSKVYARSVYDSRGNPTVEVELTTEKGVFRSIVPSGASTGVHEALEMRDGDKSKWMGKGVLHAV
KNVNDVIAPAFVKANIDVKDQKAVDDFLISLDGTANKSKLGANAILGVSLAASRAAAAEKNVPLY
KHLADLSKSKT
>d1pdz_2 d.54.1.1 (1-139) Enolase {Lobster (Homarus vulgaris)}
SITKVFARTIFDSRGNPTVEVDLYTSKGLFRAAVPSGASTGVHEALEMRDGDKSKYHGKSVFNAV
KNVNDVIVPEIIKSGLKVTQQKECDEFMCKLDGTENKSSLGANAILGVSLAICKAGAAELGIPLY
RHIANLANY
>d1e9ia2 d.54.1.1 (A:1-139) Enolase {Escherichia coli}
SKIVKIIGREIIDSRGNPTVEAEVHLEGGFVGMAAAPSGASTGSREALELRDGDKSRFLGKGVTK
AVAAVNGPIAQALIGKDAKDQAGIDKIMIDLDGTENKSKFGANAILAVSLANAKAAAAAKGMPLY
EHIAELNGT
>d1bqg_2 d.54.1.1 (12-143) D-glucarate dehydratase {Pseudomonas
putida}
GAPVITDLKVVPVAGHDSMLLNLSGAHGPLFTRNILILTDSSGHVGVGEVPGGEGIRKTLEDARH
LLINQSIGNYQSLLNKVRNAFADRDVGGRGLQTFDLRIAVHAVTAVESALLDLLGQHLQVPVAAL
LG
>d1ec7a2 d.54.1.1 (A:5-137) D-glucarate dehydratase {Escherichia
coli}
FTTPVVTEMQVIPVAGHDSMLMNLSGAHAPFFTRNIVIIKDNSGHTGVGEIPGGEKIRKTLEDAI
PLVVGKTLGEYKNVLTLVRNTFADRDAGGRGLQTFDLRTTIHVVTGIEAAMLDLLGQHLGVNVAS
LLG
>d1fhua2 d.54.1.1 (A:1-99) O-succinylbenzoate synthase {Escherichia
coli}
MRSAQVYRWQIPMDAGVVLRDRRLKTRDGLYVCLREGEREGWGEISPLPGFSQETWEEAQSVLLA
WVNNWLAGDCELPQMPSVAFGVSCALAELTDTLP
>d1muca2 d.54.1.1 (A:4-130) Muconate-lactonizing enzyme (cis muconate
cycloisomerase) {Pseudomonas putida}
ALIERIDAIIVDLPTIRPHKLAMHTMQQQTLVVLRVRCSDGVEGIGEATTIGGLAYGYESPEGIK
ANIDAHLAPALIGLAADNINAAMLKLDKLAKGNTFAKSGIESALLDAQGKRLGLPVSELLGG
>d2mnr_2 d.54.1.1 (3-132) Mandelate racemase {Pseudomonas putida}
EVLITGLRTRAVNVPLAYPVHTAVGTVGTAPLVLIDLATSAGVVGHSYLFAYTPVALKSLKQLLD
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DMAAMIVNEPLAPVSLEAMLAKRFCLAGYTGLIRMAAAGIDMAAWDALGKVHETPLVKLLGANAR
>d2chr_2 d.54.1.1 (1-126) Chlormuconate cycloisomerase {Alcaligenes eutrophus}
MKIDAIEAVIVDVPTKRPIQMSITTVHQQSYVIVRVYSEGLVGVGEGGSVGGPVWSAECAETIKI
IVERYLAPHLLGTDAFNVSGALQTMARAVTGNASAKAAVEMALLDLKARALGVSIAELLGG
>d1jpdx2 d.54.1.1 (X:-2-113) L-Ala-D/L-Glu epimerase {Escherichia coli}
GSHMRTVKVFEEAWPLHTPFVIARGSRSEARVVVVELEEEGIKGTGECTPYPRYGESDASVMAQI
MSVVPQLEKGLTREELQKILPAGAARNALDCALWDLAARRQQQSLADLIGI
>d1jpma2 d.54.1.1 (A:1-125) L-Ala-D/L-Glu epimerase {Bacillus subtilis}
MKIIRIETSRIAVPLTKPFKTALRTVYTAESVIVRITYDSGAVGWGEAPPTLVITGDSMDSIESA
IHHVLKPALLGKSLAGYEAILHDIQHLLTGNMSAKAAVEMALYDGWAQMCGLPLYQMLGG
>d1kcza2 d.54.1.1 (A:1-160) beta-Methylaspartase {Clostridium tetanomorphum}
MKIVDVLCTPGLTGFYFDDQRAIKKGAGHDGFTYTGSTVTEGFTQVRQKGESISVLLVLEDGQVA
HGDCAAVQYSGAGGRDPLFLAKDFIPVIEKEIAPKLIGREITNFKPMAEEFDKMTVNGNRLHTAI
RYGITQAILDAVAKTRKVTMAEVIRDEYNP
>d1kkoa2 d.54.1.1 (A:1-160) beta-Methylaspartase {Citrobacter amalonaticus}
MKIKQALFTAGYSSFYFDDQQAIKNGAGHDGFIYTGDPVTPGFTSVRQAGECVSVQLILENGAVA
VGDCAAVQYSGAGGRDPLFLAEHFIPFLNDHIKPLLEGRDVDAFLPNARFFDKLRIDGNLLHTAV
RYGLSQALLDATALASGRLKTEVVCDEWQL
>d1bxea_ d.55.1.1 (A:) Ribosomal protein L22 {Thermus aquaticus, subsp. Thermus thermophilus}
MEAKAIARYVRISPRKVRLVVDLIRGKSLEEARNILRYTNKRGAYFVAKVLESAAANAVNNHDML
EDRLYVKAAYVDEGPALKRVLPRARGRADIIKKRTSHITVILGEK
>d1jj2q_ d.55.1.1 (Q:) Ribosomal protein L22 {Archaeon Haloarcula marismortui}
GISYSVEADPDTTAKAMLRERQMSFKHSKAIAREIKGKTAGEAVDYLEAVIEGDQPVPFKQHNSG
VGHKSKVDGWDAGRYPEKASKAFLDLLENAVGNADHQGFDGEAMTIKHVAAHKVGEQQGRKPRAM
GRASAWNSPQVDVELILEEP
>d1gd8a_ d.188.1.1 (A:) Prokaryotic ribosomal protein L17 {Thermus thermophilus}
SSHRLALYRNQAKSLLTHGRITTTVPKAKELRGFVDHLIHLAKRGDLHARRLVLRDLQDVKLVRK
LFDEIAPRYRDRQGGYTRVLKLAERRRGDGAPLALVELVE
>d1oela3 d.56.1.1 (A:137-190,A:367-409) GroEL {Escherichia coli}
PCSDSKAIAQVGTISANSDETVGKLIAEAMDKVGKEGVITVEDGTGLQDELDVVXERVAKLAGGV
AVIKVGAATEVEMKEKKARVEDALHATRAAVEE
>d1ioka3 d.56.1.1 (A:137-190,A:367-409) GroEL {Paracoccus denitrificans}
PVNDSSEVAQVGTISANGESFIGQQIAEAMQRVGNEGVITVEENKGMETEVEVVXERVAKLAGGV
AVIRVGGMTEIEVKERKDRVDDALNATRAAVQE
>d1a6da3 d.56.1.2 (A:146-214,A:368-403) Thermosome {Archaeon

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Thermoplasma acidophilum}
TDDATLRKIALTALSGKNTGLSNDFLADLVVKAVNAVAEVRDGKTIVDTANIKVDKKNGGSVNDT
QFISXAVSILIRGGTDHVVSEVERALNDAIRVVAITKEDGK
>d1a6db3 d.56.1.2 (B:145-215,B:368-403) Thermosome {Archaeon
Thermoplasma acidophilum}
GADEKALLLKMAQTSLNSKSASVAKDKLAEISYEAVKSVAELRDGKYYVDFDNIQVVKKQGGAID
DTQLINXKAVSILVRGETEHVVDEMERSITDSLHVVASALEDG
>d1h6ha_ d.189.1.1 (A:) p40phox NADPH oxidase {Human (Homo sapiens)}
AVAQQLRAESDFEQLPDDVAISANIADIEEKRGFTSHFVFVIEVKTKGGSKYLIYRRYRQFHALQ
SKLEERFGPDSKSSALACTLPTLPAKVYVGVKQEIAEMRIPALNAYMKSLLSLPVWVLMDEDVRI
FFYQSPYDSEQVP
>d1gd5a_ d.189.1.1 (A:) p47phox NADPH oxidase {Human (Homo sapiens)}
GSMGDTFIRHIALLGFEKRFVPSQHYVYMFLVKWQDLSEKVVYRRFTEIYEFHKTLKEMFPIEAG
AINPENRIIPHLPAPKWFDGQRAAENRQGTLTEYCSTLMSLPTKISRCPHLLDFFKVRPDDLKLP
>d1ji8a_ d.203.1.1 (A:) DsrC, the gamma subunit of dissimilatory
sulfite reductase {Archaeon Pyrobaculum aerophilum}
MPVKCPGEYQVDGKKVILDEDCFMQNPEDWDEKVAEWLARELEGIQKMTEEHWKLVKYLREYWET
FGTCPPIKMVTKETGFSLEKIYQLFPSGPAHGACKVAGAPKPTGCV
>d1ghha_ d.57.1.1 (A:) DNA damage-inducible protein DinI {Escherichia
coli}
MRIEVTIAKTSPLPAGAIDALAGELSRRIQYAFPDNEGHVSVRYAAANNLSVIGATKEDKQRISE
ILQETWESADDWFVSE
>d1fxd__ d.58.1.1 (-) Ferredoxin II {Desulfovibrio gigas}
PIEVNDDCMACEACVEICPDVFEMNEEGDKAVVINPDSDLDCVEEAIDSCPAEAIVRS
>d1dura_ d.58.1.1 (A:) Ferredoxin II {Peptostreptococcus
asaccharolyticus}
AYVINDSCIACGACKPECPVNCIQEGSIYAIDADSCIDCGSCASVCPVGAPNPED
>d1fca__ d.58.1.1 (-) Ferredoxin II {Clostridium acidi-urici}
AYVINEACISCGACEPECPVDAISQGGSRYVIDADTCIDCGACAGVCPVDAPVQA
>d2fdn__ d.58.1.1 (-) Ferredoxin II {Clostridium acidi-urici}
AYVINEACISCGACEPECPVNAISSGDDRYVIDADTCIDCGACAGVCPVDAPVQA
>d1clf__ d.58.1.1 (-) Ferredoxin II {Clostridium pasteurianum}
AYKIADSCVSCGACASECPVNAISQGDSIFVIDADTCIDCGNCANVCPVGAPVQE
>d1blu__ d.58.1.1 (-) Ferredoxin II {Chromatium vinosum}
ALMITDECINCDVCEPECPNGAISQGDETYVIEPSLCTECVGHYETSQCVEVCPVDCIIKDPSHE
ETEDELRAKYERITG
>d7fd1a_ d.58.1.2 (A:) Ferredoxin {Azotobacter vinelandii}
AFVVTDNCIKCKYTDCVEVCPVDCFYEGPNFLVIHPDECIDCALCEPECPAQAIFSEDEVPEDMQ
EFIQLNAELAEVWPNITEKKDPLPDAEDWDGVKGKLQHLER
>d1bc6__ d.58.1.2 (-) Ferredoxin {Bacillus schlegelii}
AYVITEPCIGTKDASCVEVCPVDCIHEGEDQYYIDPDVCIDCGACEAVCPVSAIYHEDFVPEEWK
SYIQKNRDFFKK
>d1h98a_ d.58.1.2 (A:) Ferredoxin {Thermus thermophilus}
PHVICEPCIGVKDQSCVEVCPVECIYDGGDQFYIHPEECIDCGACVPACPVNAIYPEEDVPEQWK
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SYIEKNRKLAGL
>d1xer__ d.58.1.3 (-) Ferredoxin {Archaeon Sulfolobus sp.}
GIDPNYRTNRQVVGEHSGHKVYGPVEPPKVLGIHGTIVGVDFDLCIADGSCINACPVNVFQWYDT
PGHPASEKKADPVNEQACIFCMACVNVCPVAAIDVKPP
>d1vjw__ d.58.1.4 (-) Ferredoxin {Thermotoga maritima}
MKVRVDADACIGCGVCENLCPDVFQLGDDGKAKVLQPETDLPCAKDAADSCPTGAISVE
>d1fxra_ d.58.1.4 (A:) Ferredoxin I {Sulfate-reducing bacteria
(Desulfovibrio africanus)}
ARKFYVDQDECIACESCVEIAPGAFAMDPEIEKAYVKDVEGASQEEVEEAMDTCPVQCIHWEDE
>d1iqza_ d.58.1.4 (A:) Ferredoxin {Bacillus thermoproteolyticus}
PKYTIVDKETCIACGACGAAAPDIYDYDEDGIAYVTLDDNQGIVEVPDILIDDMMDAFEGCPTDS
IKVADEPFDGDPNKFE
>d1jb0c_ d.58.1.4 (C:) Photosystem I iron-sulfur protein PsaC
{Synechococcus elongatus}
AHTVKIYDTCIGCTQCVRACPTDVLEMVPWDGCKAGQIASSPRTEDCVGCKRCETACPTDFLSIR
VYLGAETTRSMGLAY
>d1feha3 d.58.1.5 (A:127-209) Fe-only hydrogenase, second domain
{Clostridium pasteurianum}
KDKTEYVDERSKSLTVDRTKCLLCGRCVNACGKNTETYAMKFLNKNGKTIIGAEDEKCFDDTNCL
LCGQCIIACPVAALSEKS
>d1hfel2 d.58.1.5 (L:2-86) Fe-only hydrogenase larger subunit,
N-domain {Desulfovibrio desulfuricans}
SRTVMERIEYEMHTPDPKADPDKLHFVQIDEAKCIGCDTCSQYCPTAAIFGEMGEPHSIPHIEAC
INCGQCLTHCPENAIYEAQS
>d1keka5 d.58.1.5 (A:669-785) Pyruvate-ferredoxin oxidoreductase,
PFOR, domain V {Desulfovibrio africanus}
TSQFEKRGVAINVPQWVPENCIQCNQCAFVCPHSAILPVLAKEEELVGAPANFTALEAKGKELKG
YKFRIQINTLDCMGCGNCADICPPKEKALVMQPLDTQRDAQVPNLEYAARIP
>d1h7wa5 d.58.1.5 (A:845-1017) Dihydropyrimidine dehydrogenase,
C-terminal domain {Pig (Sus scrofa)}
ELQGWDGQSPGTESHQKGKPVPRIAELMGKKLPNFGPYLEQRKKIIAEEKMRLKEQNAAFPPLER
KPFIPKKPIPAIKDVIGKALQYLGTFGELSNIEQVVAVIDEEMCINCGKCYMTCNDSGYQAIQFD
PETHLPTVTDTCTGCTLCLSVCPIIDCIRMVSRTTPYEPKRGL
>d1jnrb_ d.58.1.5 (B:) Adenylylsulfate reductase B subunit {Archaeon
Archaeoglobus fulgidus}
PSFVNPEKCDGCKALERTACEYICPNDLMTLDKEKMKAYNREPDMCWECYSCVKMCPQGAIDVRG
YVDYSPLGGACVPMRGTSDIMWTVKYRNGKVLRFKFAIRTTPWGSIQPFEGFPEPTEEALKSELL
AGEPEIIGTSEFPQVKKKA
>d1d09b1 d.58.2.1 (B:1-100) Aspartate carbamoyltransferase
{Escherichia coli}
MTHDNKLQVEAIKRGTVIDHIPAQIGFKLLSLFKLTETDQRITIGLNLPSGEMGRKDLIKIENTF
LSEDQVDQLALYAPQATVNRIDNYEVVGKSRPSLP
>d2atcb1 d.58.2.1 (B:1-100) Aspartate carbamoyltransferase
{Escherichia coli}
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MTHNDKLQVAEIKRGTVINHIPAEIGFKLLSLFKLTETQDRITIGLNLPSGEMGRKDLIKIENTF
LSEDEVDELALYAPQATVNRINDYEVVGKSRPSLP
>d1pca_2 d.58.3.1 (4A-99A) Procarboxypeptidase A {Pig (Sus scrofa)}
KEDFVGHQVLRISVDDEAQVQKVKELEDLEHLQLDFWRGPARPGFPIDVRVPFPSIQAVKVFLEA
HGIRYTIMIEDVQLLLDEEQEQMFASQGR
>d1pyta_ d.58.3.1 (A:) Procarboxypeptidase A {Cow (Bos taurus)}
KEDFVGHQVLRITAADEAEVQTVKELEDLEHLQLDFWRGPGQPGSPIDVRVPFPSLQAVKVFLEA
HGIRYRIMIEDVQSLLDEEQEQMFASQSR
>d1aye_2 d.58.3.1 (4A-99A) Procarboxypeptidase A {Human (Homo sapiens)}
LETFVGDQVLEIVPSNEEQIKNLLQLEAQEHLQLDFWKSPTTPGETAHVRVPFVNVQAVKVFLES
QGIAYSIMIEDVQVLLDKENEEMLFNRRR
>d1nsa_2 d.58.3.1 (7A-95A) Procarboxypeptidase B {Pig (Sus scrofa)}
FEGEKVFRVNVEDENDISELHELASTRQIDFWKPDSVTQIKPHSTVDFRVKAEDILAVEDFLEQN
ELQYEVLINNLRSVLEAQFDSVSR
>d1pba__ d.58.3.1 (-) Procarboxypeptidase B {Pig (Sus scrofa)}
HHSGEHFEGEKVFRVNVEDENDISELHELASTRQIDFWKPDSVTQIKPHSTVDFRVKAEDILAVE
DFLEQNELQYEVLINN
>d1spbp_ d.58.3.2 (P:) Subtilisin prosegment {Bacillus amyloliquefaciens}
EKKYIVGFKQTMSTMSAAKKKDVISEKGGKVQKQFKYVDAASATLNEKAVKELKKDPSVAYVEED
HVAHAY
>d1scjb_ d.58.3.2 (B:) Subtilisin prosegment {Bacillus subtilis}
EKKYIVGFKQTMSAMSSAKKKDVISQKGGKVEKQFKYVNAAAATLDEKAVKELKKDPSVAYVEED
HIAHEY
>d1itpa_ d.58.3.2 (A:) Proteinase A inhibitor 1, POIA1 {Oyster mushroom (Pleurotus ostreatus)}
GSAGKFIVIFKNDVSEDKIRETKDEVIAEGGTITNEYNMPGMKGFAGELTPQSLTKFQGLQGDLI
DSIEEDGIVTTQ
>d1mli__ d.58.4.1 (-) Muconalactone isomerase {Pseudomonas putida}
MLFHVKMTVKLPVDMDPAKATQLKADEKELAQRLQREGTWRHLWRIAGHYANYSVFDVPSVEALH
DTLMQLPLFPYMDIEVDGLCRHPSSIHSDDR
>d2pii__ d.58.5.1 (-) PII (product of glnB) {Escherichia coli}
MKKIDAIIKPFKLDDVREALAEVGITGMTVTEVKGFGRQKGHTELYRGAEYMVDFLPKVKIEIVV
PDDIVDTCVDTIIRTAQTGKIGDGKIFVFDVARVIRIRTGEEDDAAI
>d1gnka_ d.58.5.1 (A:) PII-homolog GlnK {Escherichia coli}
MKLVTVIIKPFKLEDVREALSSIGIQGLTVTEVKGFGRQKGHAELYRGAEYSVNFLPKVKIDVAI
ADDQLDEVIDIVSKAAYTGKIGDGKIFVAELQRVIRIRTGEADEAAL
>d1nuea_ d.58.6.1 (A:) Nucleoside diphosphate kinases {Human (Homo sapiens)}
ANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFFPGLVK
YMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSDSVKSAEKEIS
LWFKPEELVDYKSCAHDWVYE
>d1ehwa_ d.58.6.1 (A:) Nucleoside diphosphate kinases {Human (Homo
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sapiens), NDK4}
HMGTRERTLVAVKPDGVQRRLVGDVIQRFERRGFTLVGMKMLQAPESVLAEHYQDLRRKPFYPAL
IRYMSSGPVVAMVWEGYNVVRASRAMIGHTDSAEAAPGTIRGDFSVHISRNVIHASDSVEGAQRE
IQLWFQSSELVSW
>d1be4a_ d.58.6.1 (A:) Nucleoside diphosphate kinases {Cow (Bos taurus)}
ANSERTFIAIKPDGVQRGLMGEIIKRFEQKGFRLVAMKFMRASEDLLKEHYIDLKDRPFFAGLVK
YMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSDSVESAEKEIA
LWFRPEELVNYKSCAQNWIYE
>d1hlwa_ d.58.6.1 (A:) Nucleoside diphosphate kinases {Dictyostelium discoideum}
VNKERTFLAVKPDGVARGLVGEIIARYEKKGFVLVGLKQLVPTKDLAESHYAEHKERPFFGGLVS
FITSGPVVAMVFEGKGVVASARLMIGVTNPLASAPGSIRGDFGVDVGRNIIAGSDSVESANREIA
LWFKPEELLTEVKPNPNLYE
>d1nsqa_ d.58.6.1 (A:) Nucleoside diphosphate kinases {Drosophila melanogaster}
AANKERTFIMVKPDGVQRGLVGKIIERFEQKGFKLVALKFTWASKELLEKHYADLSARPFFPGLV
NYMNSGPVVPMVWEGLNVVKTGRQMLGATNPADSLPGTIRGDFCIQVGRNIIHGSDAVESAEKEI
ALWFNEKELVTWTPAAKDWIYE
>d1nhkl_ d.58.6.1 (L:) Nucleoside diphosphate kinases {Myxococcus xanthus}
AIERTLSIIKPDGLEKGVIGKIISRFEEKGLKPVAIRLQHLSQAQAEGFYAVHKARPFFKDLVQF
MISGPVVLMVLEGENAVLANRDIMGATNPAQAAEGTIRKDFATSIDKNTVHGSDSLENAKIEIAY
FFRETEIHSYPYQ
>d1ha1_1 d.58.7.1 (8-92) Nuclear ribonucleoprotein A1, RNP A1, UP1 {Human (Homo sapiens)}
EPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCVVMRDPNTKRSRGFGFVTYATVEEVDAAMN
ARPHKVDGRVVEPKRAVSRE
>d1ha1_2 d.58.7.1 (99-180) Nuclear ribonucleoprotein A1, RNP A1, UP1 {Human (Homo sapiens)}
AHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRGSGKKRGFAFVTFDDHDSVDKIVI
QKYHTVNGHNCEVRKAL
>d2up1a2 d.58.7.1 (A:99-190) Nuclear ribonucleoprotein A1, RNP A1, UP1 {Human (Homo sapiens)}
GAHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRGSGKKRGFAFVTFDDHDSVDKIV
IQKYHTVNGHNCEVRKALSKQEMASAS
>d1fht__ d.58.7.1 (-) Splicesomal U1A protein {Human (Homo sapiens)}
AVPETRPNHTIYINNLNEKIKKDELKKSLYAIFSQFGQILDILVSRSLKMRGQAFVIFKEVSSAT
NALRSMQGFPFYDKPMRIQYAKTDSDIIAKMKGTFVERDRKREKRKPKSQE
>d1nrca_ d.58.7.1 (A:) Splicesomal U1A protein {Human (Homo sapiens)}
TRPNHTIYINNLNEKIKKDELKKSLYAIFSQFGQILDILVSRSLKMRGQAFVIFKEVSSATNALR
SMQGFPFYDKPMRICYAKTD
>d1urna_ d.58.7.1 (A:) Splicesomal U1A protein {Human (Homo sapiens)}
AVPETRPNHTIYINNLNEKIKKDELKKSLHAIFSRFGQILDILVSRSLKMRGQAFVIFKEVSSAT

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NALRSMQGFPFYDKPMRIQYAKTDSDIIAKM
>d2u1a__ d.58.7.1 (-) Splicesomal U1A protein {Human (Homo sapiens)}
MAPAQPLSENPPNHILFLTNLPEETNELMLSMLFNQFPGFKEVRLVPGRHDIAFVEFDNEVQAGA
ARDALQGFKITQNNAMKISFAKK
>d1a9nb_ d.58.7.1 (B:) Splicing factor U2B'' {Human (Homo sapiens)}
IRPNHTIYINNMNDKIKKEELKRSLYALFSQFGHVVDIVALKTMKMRGQAFVIFKELGSSTNALR
QLQGFPFYGKPMRIQYAKTDSDIISKMRG
>d1u2fa_ d.58.7.1 (A:) Splicing factor U2AF 65 KDa subunit {Human (Homo sapiens)}
ARRLYVGNIPFGITEEAMMDFFNAQMRLGGLTQAPGNPVLAVQINQDKNFAFLEFRSVDETTQAM
AFDGIIFQGQSLKIRRPHDYQPLPG
>d2u2fa_ d.58.7.1 (A:) Splicing factor U2AF 65 KDa subunit {Human (Homo sapiens)}
AHKLFIGGLPNYLNDDQVKELLTSFGPLKAFNLVKDSATGLSKGYAFCEYVDINVTDQAIAGLNG
MQLGDKKLLVQRASVGAKNA
>d1b7fa1 d.58.7.1 (A:123-204) Sex-lethal protein {Drosophila melanogaster}
SNTNLIVNYLPQDMTDRELYALFRAIGPINTCRIMRDYKTGYSYGYAFVDFTSEMDSQRAIKVLN
GITVRNKRLKVSYARPG
>d1b7fa2 d.58.7.1 (A:205-289) Sex-lethal protein {Drosophila melanogaster}
GESIKDTNLYVTNLPRTITDDQLDTIFGKYGSIVQKNILRDKLTGRPRGVAFVRYNKREEAQEAI
SALNNVIPEGGSQPLSVRLA
>d1sxl__ d.58.7.1 (-) Sex-lethal protein {Drosophila melanogaster}
MSYARPGGESIKDTNLYVTNLPRTITDDQLDTIFGKYGSIVQKNILRDKLTGRPRGVAFVRYNKR
EEAQEAISALNNVIPEGGSQPLSVRLAEEHGK
>d1d8za_ d.58.7.1 (A:) Hu antigen C (Huc) {Mouse (Mus musculus)}
MDSKTNLIVNYLPQNMTQDEFKSLFGSIGDIESCKLVRDKITGQSLGYGFVNYSDPNDADKAINT
LNGLKLQTKTIKVSYARPSSASIR
>d1d9aa_ d.58.7.1 (A:) Hu antigen C (Huc) {Mouse (Mus musculus)}
DANLYVSGLPKTMSQKEMEQLFSQYGRIITSRILLDQATGVSRGVGFIRFDKRIEAEEAIKGLNG
QKPLGAAEPITVKFANNPSQ
>d1fxla1 d.58.7.1 (A:37-118) Hu antigen D (Hud) {Human (Homo sapiens)}
SKTNLIVNYLPQNMTQEEFRSLFGSIGEIESCKLVRDKITGQSLGYGFVNYIDPKDAEKAINTLN
GLRLQTKTIKVSYARPS
>d1fxla2 d.58.7.1 (A:119-203) Hu antigen D (Hud) {Human (Homo sapiens)}
SASIRDANLYVSGLPKTMTQKELEQLFSQYGRIITSRILVDQVTGVSRGVGFIRFDKRIEAEEAI
KGLNGQKPSGATEPITVKFA
>d1hd1a_ d.58.7.1 (A:) Heterogeneous nuclear ribonucleoprotein d0 {Human (Homo sapiens)}
KMFIGGLSWDTTKKDLKDYFSKFGEVVDCTLKLDPITGRSRGFGFVLFKESESVDKVMDQKEHKL
NGKVIDPKRA
>d2msta_ d.58.7.1 (A:) Neural RNA-binding protein Musashi-1 {Mouse (Mus musculus)}
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KIFVGGLSVNTTVEDVKHYFEQFGKVDDAMLMFDKTTNRHRGFGFVTFESEDIVEKVCEIHFHEI
NNKMVECKKA
>d1cvja1 d.58.7.1 (A:11-90) Poly(A)-binding protein {Human (Homo
sapiens)}
ASLYVGDLHPDVTEAMLYEKFSPAGPILSIRVCRDMITRRSLGYAYVNFQQPADAERALDTMNFD
VIKGKPVRIMWSQRD
>d1cvja2 d.58.7.1 (A:91-179) Poly(A)-binding protein {Human (Homo
sapiens)}
PSLRKSGVGNIFIKNLDKSIDNKALYDTFSAFGNILSCKVVCDENGSKGYGFVHFETQEAAERAI
EKMNGMLLNDRKVFVGRFKSRKER
>d1qm9a1 d.58.7.1 (A:1-110) Polypyrimidine tract-binding protein
{Human (Homo sapiens)}
MGNSVLLVSNLNPERVTPQSLFILFGVYGDVQRVKILFNKKENALVQMADGNQAQLAMSHLNGHK
LHGKPIRITLSKHQNVQLPREGQEDQGLTKDYGNSPLHRFKKPGS
>d1qm9a2 d.58.7.1 (A:111-198) Polypyrimidine tract-binding protein
{Human (Homo sapiens)}
KNFQNIFPPSATLHLSNIPPSVSEEDLKVLFSSNGGVVKGFKFFQKDRKMALIQMGSVEEAVQAL
IDLHNHDLGENHHLRVSFSKSTI
>d1fj7a_ d.58.7.1 (A:) Nucleolin {Golden hamster (Mesocricetus
auratus)}
GSHMLEDPVEGSESTTPFNLFIGNLNPNKSVAELKVAISELFAKNDLAVVDVRTGTNRKFGYVDF
ESAEDLEKALELTGLKVFGNEIKLEKPKGRDGTRGC
>d1fjca_ d.58.7.1 (A:) Nucleolin {Golden hamster (Mesocricetus
auratus)}
SHMLEDPCTSKKVRAARTLLAKNLSFNITEDELKEVFEDALEIRLVSQDGKSKGIAYIEFKSEAD
AEKNLEEKQGAEIDGRSVSLYYTGEKGGTRG
>d1fjeb1 d.58.7.1 (B:1-91) Nucleolin {Golden hamster (Mesocricetus
auratus)}
GSHMVEGSESTTPFNLFIGNLNPNKSVAELKVAISELFAKNDLAVVDVRTGTNRKFGYVDFESAE
DLEKALELTGLKVFGNEIKLEKPKGR
>d1fjeb2 d.58.7.1 (B:92-175) Nucleolin {Golden hamster (Mesocricetus
auratus)}
DSKKVRAARTLLAKNLSFNITEDELKEVFEDALEIRLVSQDGKSKGIAYIEFKSEADAEKNLEEK
QGAEIDGRSVSLYYTGEKG
>d1h6kx_ d.58.7.1 (X:) CBP20, 20KDa nuclear cap-binding protein {Human
(Homo sapiens)}
KSCTLYVGNLSFYTTEEQIYELFSKSGDIKKIIMGLDKMTACGFCFVEYYSRADAENAMRYINGT
RLDDRIIRTDWDAG
>d1fo1a2 d.58.7.2 (A:123-191) mRNA export factor tap {Human (Homo
sapiens)}
TIPYGRKYDKAWLLSMIQSKCSVPFTPIEFHYENTRAQFFVEDASTASALKAVNYKILDRENRRI
SIII
>d1ft8a2 d.58.7.2 (A:118-199) mRNA export factor tap {Human (Homo
sapiens)}
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NWFKITIPYGRKYDKAWLLSMIQSKCSVPFTPIEFHYENTRAQFFVEDASTASALKAVNYKILDR
ENRRISIIINSSAPPHT
>d1ft8e1 d.58.7.2 (E:) mRNA export factor tap {Human (Homo sapiens)}
WFKITIPYGRKYDKAWLLSMIQSKCSVPFTPIEFHYENTRAQFFVEDASTASALKAV
>d1koha2 d.58.7.2 (A:105-200) mRNA export factor tap {Human (Homo sapiens)}
RGGAGTSQDGTSKNWFKITIPYGRKYDKAWLLSMIQSKSSVPFTPIEFHYENTRAQFFVEDASTA
SALKAVNYKILDRENRRISIIINSSAPPHTI
>d1jmta_ d.58.7.3 (A:) U2AF35 (35 KDa subunit) {Human (Homo sapiens)}
SQTIALLNIYRNPQNSSQSADGLRSAVSDVEMQEHYDEFFEEVFTEMEEKYGEVEEMNVCDNLGD
HLVGNVYVKFRREEDAEKAVIDLNNRWFNGQPIHAELSP
>d1dbda_ d.58.8.1 (A:) Papillomavirus-1 E2 protein {Bovine papillomavirus type 1}
RRTTNDGFHLLKAGGSCFALISGTANQVKCYRFRVKKNHRHRYENCTTTWFTVADNGAERQGQAQ
ILITFGSPSQRQDFLKHVPLPPGMNISGFTASLDF
>d2bopa_ d.58.8.1 (A:) Papillomavirus-1 E2 protein {Bovine papillomavirus type 1}
SCFALISGTANQVKCYRFRVKKNHRHRYENCTTTWFTVADNGAERQGQAQILITFGSPSQRQDFL
KHVPLPPGMNISGFTASLDF
>d1a7ge_ d.58.8.1 (E:) Papillomavirus-1 E2 protein {Human papillomavirus type 31}
ATTPIIHLKGDANILKCLRYRLSKYKQLYEQVSSTWHWTCTDGKHKNAIVTLTYISTSQRDDFLN
TVVIPNTVSVSTGYMTI
>d1by9__ d.58.8.1 (-) Papillomavirus-1 E2 protein {Human papillomavirus type 16}
TTPIVHLKGDANTLKCLRYRFKKHCTLYTAVSSTWHWTGHNVKHKSAIVTLTYDSEWQRDQFLSQ
VKIPKTITVSTGFMS
>d1f9fa_ d.58.8.1 (A:) Papillomavirus-1 E2 protein {Human papillomavirus type 18}
HMTPIIHLKGDRNSLKCLRYRLRKHSDHYRDISSTWHWTGAGNEKTGILTVTYHSETQRTKFLNT
VAIPDSVQILVGYMTM
>d1b3ta_ d.58.8.1 (A:) Epstein barr virus nuclear antigen-1 (ebna1) {Epstein-Barr virus}
KGGWFGKHRGQGGSNPKFENIAEGLRALLARSHVERTTDEGTWVAGVFVYGGSKTSLYNLRRGTA
LAIPQCRLTPLSRLPFGMAPGPGPQPGPLRESIVCYFMVFLQTHIFAEVLKDAIKDLVMTKPAPT
CNIRVTVCSFDDGVDLP
>d1vhib_ d.58.8.1 (B:) Epstein barr virus nuclear antigen-1 (ebna1) {Epstein-Barr virus}
PKFENIAEGLRALLARSHVERTTDEGTWVAGVFVYGGSKTSLYNLRRGTALAIPQCRLTPLSRLP
FGMAPGPGPQPGPLRESIVCYFMVFLQTHIFAEVLKDAIKDLVMTKPAPTCNIRVTVCSFDDGVD
LP
>d3rubl2 d.58.9.1 (L:22-147) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Tobacco (Nicotiana tabacum), variant turkish samsun}

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LTYYTPEYQTKDTDILAAFRVTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDRYKGRCYR
IERVVGEKDQYIAYVAYPLDLFEEGSVTNMFTSIVGNVFGFKALRALRLEDLRIPPAYVKT
>d1bura2 d.58.9.1 (A:12-147) Ribulose 1,5-bisphosphate
carboxylase-oxygenase {Spinach (Spinacia oleracea)}
EFKAGVKDYKLTYYTPEYETLDTDILAAFRVSPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTN
LDRYKGRCYHIEPVAGEENQYICYVAYPLDLFEEGSVTNMFTSIVGNVFGFKALRALRLEDLRIP
VAYVKT
>d1bwva2 d.58.9.1 (A:7-149) Ribulose 1,5-bisphosphate
carboxylase-oxygenase {Galdieria partita}
RIKNSRYESGVIPYAKMGYWNPDYQVKDTDVLALFRVTPQPGVDPIEAAAAVAGESSTATWTVVW
TDLLTAADLYRAKAYKVDQVPNNPEQYFAYIAYELDLFEEGSIANLTASIIGNVFGFKAVKALRL
EDMRLPLAYLKTFQ
>d1gk8a2 d.58.9.1 (A:7-149) Ribulose 1,5-bisphosphate
carboxylase-oxygenase {Chlamydomonas reinhardtii}
TKAGAGFKAGVKDYRLTYYTPDYVVRDTDILAAFRMTPQPGVPPEECGAAVAAESSTGTWTTVWT
DGLTSLDRYKGRCYDIEPVPGEDNQYIAYVAYPIDLFEEGSVTNMFTSIVGNVFGFKALRALRLE
DLRIPPAYVKTFV
>d1bxna2 d.58.9.1 (A:22-150) Ribulose 1,5-bisphosphate
carboxylase-oxygenase {Alcaligenes eutrophus}
YKMGYWDGDYVPKDTDLLALFRITPQDGVDPVEAAAAVAGESSTATWTVVWTDRLTACDMYRAKA
YRVDPVPNNPEQFFCYVAYDLSLFEEGSIANLTASIIGNVFSFKPIKAARLEDMRFPVAYVKT
>d1rbla2 d.58.9.1 (A:9-147) Ribulose 1,5-bisphosphate
carboxylase-oxygenase {Synechococcus sp., strain pcc 6301}
SAAGYKAGVKDYKLTYYTPDYTPKDTDLLAAFRFSPQPGVPADEAGAAIAAESSTGTWTTVWTDL
LTDMDRYKGKCYHIEPVAGEENSYFAFIAYPLDLFEEGSVTNILTSIVGNVFGFKAIRSLRLEDI
RFPVALVKT
>d5ruba2 d.58.9.1 (A:2-137) Ribulose 1,5-bisphosphate
carboxylase-oxygenase {Rhodospirillum rubrum}
DQSSRYVNLALKEEDLIAGGEHVLCAYIMKPKAGYGYVATAAHFAAESSTGTNVEVCTTDDFTRG
VDALVYEVDEARELTKIAYPVALFDRNITDGKAMIASFLTLTMGNNQGMGDVEYAKMHDFYVPEA
YRALFD
>d1geha2 d.58.9.1 (A:12-136) Ribulose 1,5-bisphosphate
carboxylase-oxygenase {Archaeon Thermococcus kodakaraensis}
YVDKGYEPSKKRDIIAVFRVTPAEGYTIEQAAGAVAAESSTGTWTTLYPWYEQERWADLSAKAYD
FHDMGDGSWIVRIAYPFHAFEEANLPGLLASIAGNIFGMKRVKGLRLEDLYFPEKLIREF
>d2acy__ d.58.10.1 (-) Acylphosphatase {Cow (Bos taurus)}
AEGDTLISVDYEIFGKVQGVFFRKYTQAEGKKLGLVGWVQNTDQGTVQGQLQGPASKVRHMQEWL
ETKGSPKSHIDRASFHNEKVIVKLDYTDFQIVK
>d1aps__ d.58.10.1 (-) Acylphosphatase {Horse (Equus caballus)}
STARPLKSVDYEVFGRVQGVCFRMYAEDEARKIGVVGWVKNTSKGTVTGQVQGPEEKVNSMKSWL
SKVGSPSSRIDRTNFSNEKTISKLEYSNFSVRY
>d1i1ga2 d.58.37.1 (A:62-141) LprA {Archaeon Pyrococcus furiosus}
YSLVTITGVDTKPEKLFEVAEKLKEYDFVKELYLSSGDHMIMAVIWAKDGEDLAEIISNKIGKIE
GVTKVCPAIILEKLK
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>d1dar_4 d.58.11.1 (600-689) Elongation factor G (EF-G), domains III and V {Thermus thermophilus}
VILEPIMRVEVTTPEEYMGDVIGDLNARRGQILGMEPRGNAQVIRAFVPLAEMFGYATDLRSKTQ
GRGSFVMFFDHYQEVPKQVQEKLIK
>d1fnma4 d.58.11.1 (A:404-482) Elongation factor G (EF-G), domains III and V {Thermus thermophilus}
VPEPVIDVAIEPKTKADQEKLSQALARLAEEDPTFRVSTHPETGQTIISGMGELHLEIIVDRLKR
EFKVDANVGKPQVA
>d1b64__ d.58.12.1 (-) Guanine nucleotide exchange factor (GEF) domain from elongation factor-1 beta {Human (Homo sapiens)}
MLVAKSSILLDVKPWDDETDMAKLEECVRSIQADGLVWGSSKLVPVGYGIKKLQIQCVVEDDKVG
TDMLEEQITAFEDYVQSMDVAAFNKI
>d1f60b_ d.58.12.1 (B:) Guanine nucleotide exchange factor (GEF) domain from elongation factor-1 beta {Baker's yeast (Saccharomyces cerevisiae)}
PAAKSIVTLDVKPWDDETNLEEMVANVKAIEMEGLTWGAHQFIPIGFGIKKLQINCVVEDDKVSL
DDLQQSIEEDEDHVQSTDIAAMQKL
>d1gh8a_ d.58.12.1 (A:) aEF-1beta {Archaeon Methanobacterium thermoautotrophicum}
MGDVVATIKVMPESPDVDLEALKKEIQERIPEGTELHKIDEEPIAFGLVALNVMVVVGDAEGGTE
AAEESLSGIEGVSNIEVTDVRRLM
>d1b7yb4 d.58.13.1 (B:682-775) Phenylalanyl-tRNA synthetase {Thermus thermophilus (Thermus aquaticus)}
LAFQDPSRHPAAFRDLAVVVPAPTPYGEVEALVREAAGPYLESLALFDLYQGPPLPEGHKSLAFH
LRFRHPKRTLRDEEVEEAVSRVAEALRAR
>d1jjcb4 d.58.13.1 (B:682-785) Phenylalanyl-tRNA synthetase {Thermus thermophilus (Thermus aquaticus)}
LAFQDPSRHPAAFRDLAVVVPAPTPYGEVEALVREAAGPYLESLALFDLYQGPPLPEGHKSLAFH
LRFRHPKRTLRDEEVEEAVSRVAEALRARGFGLRGLDTP
>d1loua_ d.58.14.1 (A:) Ribosomal protein S6 {Thermus thermophilus}
MRRYEVNIVLNPNLDQSQLALEKEIIQRAAENYGARVEKVEELGLRRLAYPIAKDPQGYFLWYQV
EMPEDRVNDLARELRIRDNVRRVMVVKSQEPF
>d1qjha_ d.58.14.1 (A:) Ribosomal protein S6 {Thermus thermophilus}
MRRYEVNIVLNPNLDQSQLALEKEIIQRALENYGARVEKVAILGLMVLAYPIAKDPQGYFLWYQV
EMPEDRVNDLARELRIRDNVRRVMVVKS
>d1fjgj_ d.58.15.1 (J:) Ribosomal protein S10 {Thermus thermophilus}
KIRIKLRGFDHKTLDASAQKIVEAARRSGAQVSGPIPLPTRVRRFTVIRGPFKHKDSREHFELRT
HNRLVDIINPNRKTIEQLMTLDLPTGVEIEIKT
>d1fa0a1 d.58.16.1 (A:352-523) Poly(A) polymerase, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
NDFFFRYKFYLEITAYTRGSDEQHLKWSGLVESKVRLLVMKLEVLAGIKIAHPFTKPFESSYCCP
TEDDYEMIQDKYGSHKTETALNALKLVTDENKEEESIKDAPKAYLSTMYIGLDFNIENKKEKVDI
HIPCTEFVNLCRSFNEDYGDHKVFNLALRFVKGYDLPDEVFD
>d1f5aa1 d.58.16.1 (A:365-498) Poly(A) polymerase, C-terminal domain
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{Cow (Bos taurus)}
PNFFQKYKHYIVLLASAPTEKQRLEWVGLVESKIRILVGSLEKNEFITLAHVNPQSFPAPKENPD
KEEFRTMWVIGLVFKKTENSENLSVDLTYDIQSFTDTVYRQAINSKMFEVDMKIAAMHVKRKQLH
QLLP
>d1afj__ d.58.17.1 (-) Mercuric ion binding protein MerP {Shigella
flexneri}
ATQTVTLAVPGMTCAACPITVKKALSKVEGVSKVDVGFEKREAVVTFDDTKASVQKLTKATADAG
YPSSVKQ
>d1fvqa_ d.58.17.1 (A:) Copper transporter domain ccc2a {Baker's yeast
(Saccharomyces cerevisiae)}
AREVILAVHGMTCSACTNTINTQLRALKGVTKCDISLVTNECQVTYDNEVTADSIKEIIEDCGFD
CEILRDS
>d1aw0__ d.58.17.1 (-) Menkes copper-transporting ATPase {Human (Homo
sapiens)}
LTQETVINIDGMTCNSCVQSIEGVISKKPGVKSIRVSLANSNGTVEYDPLLTSPETLRGAIEDMG
FDATLSD
>d1cc8a_ d.58.17.1 (A:) ATX1 metallochaperone protein (ATOX1)
{Baker's yeast (Saccharomyces cerevisiae)}
AEIKHYQFNVVMTCSGCSGAVNKVLTKLEPDVSKIDISLEKQLVDVYTTLPYDFILEKIKKTGKE
VRSGKQL
>d1fe0a_ d.58.17.1 (A:) ATX1 metallochaperone protein (ATOX1) {Human
(Homo sapiens), HAH1}
PKHEFSVDMTCGGCAEAVSRVLNKLGGVKYDIDLPNKKVCIESEHSMDTLLATLKKTGKTVSYLG
L
>d1cpza_ d.58.17.1 (A:) Copper chaperone {Enterococcus hirae}
AQEFSVKGMSCNHCVARIEEAVGRISGVKKVKVQLKKEKAVVKFDEANVQATEICQAINELGYQA
EVI
>d1k0va_ d.58.17.1 (A:) Copper chaperone {Bacillus subtilis, CopZ}
MEQKTLQVEGMSCQHCVKAVETSVGELDGVSAVHVNLEAGKVDVSFDADKVSVKDIADAIEDQGY
DVAKIEGR
>d1qupa2 d.58.17.1 (A:2-73) Copper chaperone for superoxide dismutase,
N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
TTNDTYEATYAIPMHCENCVNDIKACLKNVPGINSLNFDIEQQIMSVESSVAPSTIINTLRNCGK
DAIIRGA
>d1gmua2 d.58.38.1 (A:71-138) Urease metallochaperone UreE,
C-terminal domain {Klebsiella aerogenes}
DEEVSVVRCDDPFMLAKACYALGNRHVPLQIMPGELRYHHDHVLDDMLRQFGLTVTFGQLPFEPE
AGA
>d1eara2 d.58.38.1 (A:75-142) Urease metallochaperone UreE,
C-terminal domain {Bacillus pasteurii}
LEKVYVIKPQTMQEMGKMAFEIGNRHTMCIIEDDEILVRYDKTLEKLIDEVGVSYEQSERRFKEP
FKY
>d1psda3 d.58.18.1 (A:327-410) Phosphoglycerate dehydrogenase,
regulatory (C-terminal) domain {Escherichia coli}
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FPEVSLPLHGGRRLMHIHENRPGVLTALNKIFAEQGVNIAAQYLQTSAQMGYVVIDIEADEDVAE
KALQAMKAIPGTIRARLLY
>d1tdj_2 d.58.18.2 (336-423) Allosteric threonine deaminase
C-terminal domain {Escherichia coli}
QREALLAVTIPEEKGSFLKFCQLLGGRSVTEFNYRFADAKNACIFVGVRLSRGLEERKEILQMLN
DGGYSVVDLSDDEMAKLHVRYMV
>d1tdj_3 d.58.18.2 (424-514) Allosteric threonine deaminase
C-terminal domain {Escherichia coli}
GGRPSHPLQERLYSFEFPESPGALLRFLNTLGTYWNISLFHYRSHGTDYGRVLAAFELGDHEPDF
ETRLNELGYDCHDETNNPAFRFFLAG
>d1phza1 d.58.18.3 (A:19-115) Phenylalanine hydroxylase N-terminal
domain {Rat (Rattus norvegicus)}
GQETSYIEDNSNQNGAISLIFSLKEEVGALAKVLRLFEENDINLTHIESRPSRLNKDEYEFFTYL
DKRTKPVLGSIIKSLRNDIGATVHELSRDKEK
>d1cg2a2 d.58.19.1 (A:214-326) Carboxypeptidase G2, dimerisation
domain {Pseudomonas sp., strain rs-16}
SGIAYVQVNITGKASHAGAAPELGVNALVEASDLVLRTMNIDDKAKNLRFNWTIAKAGNVSNIIP
ASATLNADVRYARNEDFDAAMKTLEERAQQKKLPEADVKVIVTRGRPA
>d1dqaa1 d.58.20.1 (A:587-703) NAD-binding domain of HMG-CoA
reductase {Human (Homo sapiens)}
GMTRGPVVRLPRACDSAEVKAWLETSEGFAVIKEAFDSTSRFARLQKLHTSIAGRNLYIRFQSRS
GDAMGMNMISKGTEKALSKLHEYFPEMQILAVSGNYCTDKKPAAINWIEGRG
>d1qaxa1 d.58.20.1 (A:111-220) NAD-binding domain of HMG-CoA
reductase {Pseudomonas mevalonii}
LMHAQVQIVGIQDPLNARLSLLRRKDEIIELANRKDQLLNSLGGGCRDIEVHTFADTPRGPMLVA
HLIVDVRDAMGANTVNTMAEAVAPLMEAITGGQVRLRILSNLADL
>d1ekra_ d.58.21.1 (A:) Molybdenum cofactor biosynthesis protein C,
MoaC {Escherichia coli}
GEAHMVDVSAKAETVREARAEAFVTMRSETLAMIIDGRHHKGDVFATARIAGIQAAKRTWDLIPL
CHPLMLSKVEVNLQAEPEHNRVRIETLCRLTGKTGVEMEALTAASVAALTIYDMCKAVQKDMVIG
PVRLLAKSGGKSGDFK
>d1f3va_ d.58.22.1 (A:) TRADD, N-terminal domain {Human (Homo
sapiens)}
HEEWVGSAYLFVESSLDKVVLSDAYAHPQQKVAVYRALQAALAESGGSPDVLQMLKIHRSDPQLI
VQLRFCGRQPCGRFLRAYREGALRAALQRSLAAALAQHSVPLQLELRAGAERLDALLADEERCLS
CILAQQPDRLRDEELAELEDALRNLKCG
>d1mla_2 d.58.23.1 (128-197) Probable ACP-binding domain of
malonyl-CoA ACP transacylase {Escherichia coli}
GTGAMAAIIGLDDASIAKACEEAAEGQVVSPVNFNSPGQVVIAGHKEAVERAGAACKAAGAKRAL
PLPVS
>d1ffgb_ d.58.24.1 (B:) CheY-binding domain of CheA {Escherichia coli}
PRRIILSRLKAGEVDLLEEELGHLTTLTDVVKGADSLSAILPGDIAEDDITAVLCFVIEADQITF
ETV
>d1kp6a_ d.58.25.1 (A:) Killer toxin KP6 alpha-subunit {Smut fungus
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(Ustilago maydis)}
NNAFCAGFGLSCKWECWCTAHGTGNELRYATAAGCGDHLSKSYYDARAGHCLFSDDLRNQFYSHC
SSLNNNMSCRSLSK
>d1h72c2 d.58.26.1 (C:168-300) Homoserine kinase, C-terminal domain
{Archaeon Methanococcus jannaschii}
FKLDILIAIPNISINTKEAREILPKAVGLKDLVNNVGKACGMVYALYNKDKSLFGRYMMSDKVIE
PVRGKLIPNYFKIKEEVKDKVYGITISGSGPSIIAFPKEEFIDEVENILRDYYENTIRTEVGKGV
EVV
>d1fi4a2 d.58.26.2 (A:191-393) Mevalonate 5-diphosphate
decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}
QMKACVLVVSDIKKDVSSTQGMQLTVATSELFKERIEHVVPKRFEVMRKAIVEKDFATFAKETMM
DSNSFHATCLDSFPPIFYMNDTSKRIISWCHTINQFYGETIVAYTFDAGPNAVLYYLAENESKLF
AFIYKLFGSVPGWDKKFTTEQLEAFNHQFESSNFTARELDLELQKDVARVILTQVGSGPQETNES
LIDAKTGL
>d1regx_ d.58.27.1 (X:) Translational regulator protein regA
{Bacteriophage T4}
MIEITLKKPEDFLKVKETLTRMGIANNKDKVLYQSCHILQKKGLYYIVHFKEMLRMDGRQVEMTE
EDEVRRDSIAWLLEDWGLIEIVPGQRTFMKDLTNNFRVISFKQKHEWKLVPKYTIGN
>d1fvga_ d.58.28.1 (A:) Peptide methionine sulfoxide reductase {Cow
(Bos taurus)}
KIVSPQEALPGRKEPLVVAAKHHVNGNRTVEPFPEGTQMAVFGMGCFWGAERKFWTLKGVYSTQV
GFAGGYTPNPTYKEVCSGKTGHAEVVRVVFQPEHISFEELLKVFWENHDPTQGMRQGNDHGSQYR
SAIYPTSAEHVGAALKSKEDYQKVLSEHGFGLITTDIREGQTFYYAEDYHQQYLSKDPDGYC
>d1ff3a_ d.58.28.1 (A:) Peptide methionine sulfoxide reductase
{Escherichia coli}
SLFDKKHLVSPADALPGRNTPMPVATLHAVNGHSMTNVPDGMEIAIFAMGCFWGVERLFWQLPGV
YSTAAGYTGGYTPNPTYREVCSGDTGHAEAVRIVYDPSVISYEQLLQVFWENHDPAQGMRQGNDH
GTQYRSAIYPLTPEQDAAARASLERFQAAMLAADDDRHITTEIANATPFYYAEDDHQQYLHKNPY
GYCGIGGIGVCLPPEA
>d1ff3c_ d.58.28.1 (C:) Peptide methionine sulfoxide reductase
{Escherichia coli}
LVSPADALPGRNTPMPVATLHAVNGHSMTNVPDGMEIAIFAMGCFWGVERLFWQLPGVYSTAAGY
TGGYTPNPTYREVCSGDTGHAEAVRIVYDPSVISYEQLLQVFWENHDPAQGMRQGNDHGTQYRSA
IYPLTPEQDAAARASLERFQAAMLAADDDRHITTEIANATPFYYAEDDHQQYLHK
>d1azsa_ d.58.29.1 (A:) Adenylyl cyclase VC1, domain C1a {Dog (Canis
familiaris)}
DMMFHKIYIQKHDNVSILFADIEGFTSLASQCTAQELVMTLNELFARFDKLAAENHCLRIKILGD
CYYCVSGLPEARADHAHCCVEMGMDMIEAISLVREMTGVNVNMRVGIHSGRVHCGVLGLRKWQFD
VWSNDVTLANHMEAGGKAGRIHITKATLSYLNGDYEVEPGCGGERNAYLKEHSIETFLIL
>d1azsb_ d.58.29.1 (B:) Adenylyl cyclase IIC1, domain C2a {Rat (Rattus
norvegicus)}
HQSYDCVCVMFASIPDFKEFYTESDVNKEGLECLRLLNEIIADFDDLLSKPKFSGVEKIKTIGST
YMAATGLSAIPSQEHAQEPERQYMHIGTMVEFAYALVGKLDAINKHSFNDFKLRVGINHGPVIAG
VIGAQKPQYDIWGNTVNVASRMDSTGVLDKIQVTEETSLILQTLGYTCTCRGIINVKGKGDLKTY
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FVNT
>d1fx2a_ d.58.29.1 (A:) Receptor-type monomeric adenylyl cyclase {Trypanosome (Trypanosoma brucei), different isoform}
NNNRAPKEPTDPVTLIFTDIESSTALWAAHPDLMPDAVAAHHRMVRSLIGRYKCYEVKTVGDSFM
IASKSPFAAVQLAQELQLCFLHHDWGTNALDDSYREFEEQRAEGECEYTPPTAHMDPEVYSRLWN
GLRVRVGIHTGLCDIRHDEVTKGYDYYGRTPNMAARTESVANGGQVLMTHAAYMSLSAEDRKQID
VTALGDVALRGVSDPVKMYQLNTVPSRNFAALRLDREYFD
>d1fx4a_ d.58.29.1 (A:) Receptor-type monomeric adenylyl cyclase {Trypanosome (Trypanosoma brucei), different isoform}
DNDSAPKEPTGPVTLIFTDIESSTALWAAHPDLMPDAVATHHRLIRSLITRYECYEVKTVGDSFM
IASKSPFAAVQLAQELQLCFLRLDWETNAVDESYREFEEQRAEGECEYTPPTASLDPEVYSRLWN
GLRVRVGIHTGLCDIRYDEVTKGYDYYGRTSNMAARTESVANGGQVLMTHAAYMSLSGEDRNQLD
VTTLGATVLRGVPEPVRMYQLNAVPGRNFAALRLDR
>d1eqoa_ d.58.30.1 (A:) 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK {Escherichia coli}
TVAYIAIGSNLASPLEQVNAALKALGDIPESHILTVSSFYRTPPLGPQDQPDYLNAAVALETSLA
PEELLNHTQRIELQQGRVRKAERWGPRTLDLDIMLFGNEVINTERLTVPHYDMKNRGFMLWPLFE
IAPELVFPDGEMLRQILHTRAFDKLNKW
>d1cbka_ d.58.30.1 (A:) 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK {Haemophilus influenzae}
MITAYIALGSNLNTPVEQLHAALKAISQLSNTHLVTTSSFYKSKPLGPQDQPDYVNAVAKIETEL
SPLKLLDELQRIENEQGRVRLRRWGERTLDLDILLYGNEIIQNERLTIPHYDMHNREFVIVPLFE
IASDLVLPNSQIITELVKQFADHKMIKLNP
>d1gpja3 d.58.39.1 (A:1-143) Glutamyl tRNA-reductase catalytic, N-terminal domain {Archaeon Methanopyrus kandleri}
MEDLVSVGITHKEAEVEELEKARFESDEAVRDIVESFGLSGSVLLQTSNRVEVYASGARDRAEEL
GDLIHDDAWVKRGSEAVRHLFRVASGLESMMVGEQEILRQVKKAYDRAARLGTLDEALKIVFRRA
INLGKRAREETRI
>d1hbnc_ d.58.31.1 (C:) Methyl-coenzyme M reductase gamma chain {Archaeon Methanobacterium thermoautotrophicum}
AQYYPGTTKVAQNRRNFCNPEYELEKLREISDEDVVKILGHRAPGEEYPSVHPPLEEMDEPEDAI
REMVEPIDGAKAGDRVRYIQFTDSMYFAPAQPYVVRSRAYLCRYRGADAGTLSGRQIIETRERDLE
KISKELLETEFFDPARSGVRGKSVHGHSLRLDEDGMMFDMLRRQIYNKDTGRVEMVKNQIGDELD
EPVDLGEPLDEETLMEKTTIYRVDGEAYRDDVEAVEIMQRIHVLRSQGGFNL
>d1e6vc_ d.58.31.1 (C:) Methyl-coenzyme M reductase gamma chain {Archaeon Methanopyrus kandleri}
FYYPGETDVAENRRKYMNPNYELKKLREIPDEDIVRLMGHREPGEEYPSVHPPLEEMEEPECPIR
ELVEPTEGAKAGDRIRYIQFTDSVYFAPIHPYIRARMYMWRYRGVDTGSLSGRQIIEVRERDLEK
IAKELLETEIFDPARSGVRGATVHGHALRLDENGLMLHALRRYRLNEETGEVEYVKDQVGIELDE
PIPVGAPADEDDLKERTTIYRIDGTPYREDEELLQVVQRIHELRTLAGYRPEE
>d1e6yc_ d.58.31.1 (C:) Methyl-coenzyme M reductase gamma chain {Archaeon Methanosarcina barkeri}
AYERQYYPGATSVAANRRKHMSGKLEKLREISDEDLTAVLGHRAPGSDYPSTHPPLAEMGEPACS
TRENVAATPGAAAGDRVRYIQFADSMYNAPATPYFRSYFAAINFRGVDPGTLSGRQIVEARERDM
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EQCAKVQMETEITDHALAGVRGATVHGHSVRLQEDGVMFDMLDRRRLENGTIIMDKDQVAIPLDR
KVDLGKPMSSEEAAKRTTIYRVDNVAFRDDAEVVEWVHRIFDQRTKFGFQPK
>d1hbna2 d.58.31.2 (A:2-269) Alpha chain {Archaeon Methanobacterium
thermoautotrophicum}
ADKLFINALKKKFEESPEEKKTTFYTLGGWKQSERKTEFVNAGKEVAAKRGIPQYNPDIGTPLGQ
RVLMPYQVSTTDTYVEGDDLHFVNNAAMQQMWDDIRRTVIVGLNHAHAVIEKRLGKEVTPETITH
YLETVNHAMPGAAVVQEHMVETHPALVADSYVKVFTGNDEIADEIDPAFVIDINKQFPEDQAETL
KAEVGDGIWQVVRIPTIVSRTCDGATTSRWSAMQIGMSMISAYKQAAGEAATGDFAYAAKHAEVI
HMGTYLPV
>d1e6va2 d.58.31.2 (A:8-272) Alpha chain {Archaeon Methanopyrus
kandleri}
LFMKALKEKFEESPEEKYTKFYIFGGWKQSERKKEFKEWADKIVEERGVPHYNPDIGVPLGQRKL
MSYQVSGTDVFVEGDDLTFVNNAAMQQMWDDIRRTVIVGMDTAHRVLERRLGKEVTPETINEYME
TLNHALPGGAVVQEHMVEIHPGLTWDCYAKIITGDLELADEIDDKFLIDIEKLFPEEQAEQLIKA
IGNRTYQVCRMPTIVGHVCDGATMYRWAAMQIAMSFICAYKIAAGEAAVSDFAFASKHAEVINMG
EMLPA
>d1e6ya2 d.58.31.2 (A:1002-1283) Alpha chain {Archaeon Methanosarcina
barkeri}
AADIFSKFKKDMEVKFAQEFGSNKQTGGDITDKTAKFLRLGPEQDPRKVEMIKAGKEIAEKRGIA
FYNPMMHSGAPLGQRAITPYTISGTDIVCEPDDLHYVNNAAMQQMWDDIRRTCIVGLDMAHETLE
KRLGKEVTPETINHYLEVLNHAMPGAAVVQEMMVETHPALVDDCYVKVFTGDDALADEIDKQFLI
DINKEFSEEQAAQIKASIGKTSWQAIHIPTIVSRTTDGAQTSRWAAMQIGMSFISAYAMCAGEAA
VADLSFAAKHAALVSMGEMLPA
>d1hbnb2 d.58.31.2 (B:2-188) Beta chain {Archaeon Methanobacterium
thermoautotrophicum}
AKFEDKVDLYDDRGNLVEEQVPLEALSPLRNPAIKSIVQGIKRTVAVNLEGIENALKTAKVGGPA
CKIMGRELDLDIVGNAESIAAAAKEMIQVTEDDDTNVELLGGGKRALVQVPSARFDVAAEYSAAP
LVTATAFVQAIINEFDVSMYDANMVKAAVLGRYPQSVEYMGANIATMLDIPQKLEGP
>d1e6vb2 d.58.31.2 (B:7-189) Beta chain {Archaeon Methanopyrus
kandleri}
DTVDLYDDRGNCVAEEVPIEVLSPMRNEAIQSIVNDIKRTVAVDLEGIENALQNATVGGKGMKIP
GREMDVDIVDNAEAIADEIEKMIRVYQDDDTNVEPMYDGKRLLVQLPSERVKVMADPYSGTLQAG
MAVVHAIIDVCEVDMWDANMVKAAVFGRYPQTIDYFGGNVASMLDVPMKQEGV
>d1e6yb2 d.58.31.2 (B:2002-2185) Beta chain {Archaeon Methanosarcina
barkeri}
SDTVDIYDDRGKLLESNVDIMSLAPTRNAAIQSIIMDTKRSVAVNLAGIQGALASGKMGGKGRQI
LGRGLNYDIVGNADAIAENVKKLVQVDEGDDTNVIKVKGGKSLLIQSPKSRIIAGADFMSATTVG
AAAVTQTIMDMFGTDPYDAPIVKSAVWGSYPQTMDLMGGQVQGILSIPQNNEGL
>d1e8ga1 d.58.32.1 (A:274-560) Vanillyl-alcohol oxidase {Fungus
(Penicillium simplicissimum)}
GGYQSYLITLPKDGDLKQAVDIIRPLRLGMALQNVPTIRHILLDAAVLGDKRSYSSRTEPLSDEE
LDKIAKQLNLGRWNFYGALYGPEPIRRVLWETIKDAFSAIPGVKFYFPEDTPENSVLRVRDKTMQ
GIPTYDELKWIDWLPNGAHLFFSPIAKVSGEDAMMQYAVTKKRCQEAGLDFIGTFTVGMREMHHI
VCIVFNKKDLIQKRKVQWLMRTLIDDCAANGWGEYRTHLAFMDQIMETYNWNNSSFLRFNEVLKN
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AVDPNGIIAPGKSGVWPSQYSHVTWKL
>d1diqa1 d.58.32.1 (A:243-521) Flavoprotein subunit of p-cresol methylhydroxylase {Pseudomonas putida}
PVFKPFEVIFEDEADIVEIVDALRPLRMSNTIPNSVVIASTLWEAGSAHLTRAQYTTEPGHTPDS
VIKQMQKDTGMGAWNLYAALYGTQEQVDVNWKIVTDVFKKLGKGRIVTQEEAGDTQPFKYRAQLM
SGVPNLQEFGLYNWRGGGGSMWFAPVSEARGSECKKQAAMAKRVLHKYGLDYVAEFIVAPRDMHH
VIDVLYDRTNPEETKRADACFNELLDEFEKEGYAVYRVNTRFQDRVAQSYGPVKRKLEHAIKRAV
DPNNILAPGRSGIDLNNDF
>d1f0xa1 d.58.32.2 (A:274-567) D-lactate dehydrogenase {Escherichia coli}
KNQQVFYIGTNQPEVLTEIRRHILANFENLPVAGEYMHRDIYDIAEKYGKDTFLMIDKLGTDKMP
FFFNLKGRTDAMLEKVKFFRPHFTDRAMQKFGHLFPSHLPPRMKNWRDKYEHHLLLKMAGDGVGE
AKSWLVDYFKQAEGDFFVCTPEEGSKAFLHRFAAAGAAIRYQAVHSDEVEDILALDIALRRNDTE
WYEHLPPEIDSQLVHKLYYGHFMCYVFHQDYIVKKGVDVHALKEQMLELLQQRGAQYPAEHNVGH
LYKAPETLQKFYRENDPTNSMNPGIGKTSKRKNW
>d1i19a1 d.58.32.3 (A:274-613) Cholesterol oxidase {Brevibacterium sterolicum}
FRQRCQSYTDIPWRELFAPKGADGRTFEKFVAESGGAEAIWYPFTEKPWMKVWTVSPTKPDSSNE
VGSLGSAGSLVGKPPQAREVSGPYNYIFSDNLPEPITDMIGAINAGNPGIAPLFGPAMYEITKLG
LAATNANDIWGWSKDVQFYIKATTLRLTEGGGAVVTSRANIATVINDFTEWFHERIEFYRAKGEF
PLNGPVEIRCCGLDQAADVKVPSVGPPTISATRPRPDHPDWDVAIWLNVLGVPGTPGMFEFYREM
EQWMRSHYNNDDATFRPEWSKGWAFGPDPYTDNDIVTNKMRATYIEGVPTTENWDTARARYNQID
PHRVFTNGFMDKLLP
>d1ftra1 d.58.33.1 (A:1-148) Formylmethanofuran:tetrahydromethanopterin formyltransferase {Archaeon Methanopyrus kandleri}
MEINGVEIEDTFAEAFEAKMARVLITAASHKWAMIAVKEATGFGTSVIMCPAEAGIDCGYVPPEE
TPDGRPGVTIMIGHNDEDELKEQLLDRIGQCVMTAPTASAFDAMPEAEKEDEDRVGYKLSFFGDG
YQEEDELDGRKVWKIPVV
>d1ftra2 d.58.33.1 (A:149-296) Formylmethanofuran:tetrahydromethanopterin formyltransferase {Archaeon Methanopyrus kandleri}
EGEFIVEDSFGITTGVAGGNFYIMAESQPAGLQAAEAAVDAIKGVEGAYAPFPGGIVASASKVGS
KQYDFLPASTNDAYCPTVEDNELPEGVKCVYEIVINGLNEEAVKEAMRVGIEAACQQPGVVKISA
GNFGGKLGQYEIHLHDLF
>d1qd1a1 d.58.34.1 (A:2-180) Formiminotransferase domain of formiminotransferase-cyclodeaminase. {Pig (Sus scrofa)}
SQLVECVPNFSEGKNQEVIDAISRAVAQTPGCVLLDVDSGPSTNRTVYTFVGRPEDVVEGALNAA
RAAYQLIDMSRHHGEHPRMGALDVCPFIPVRGVTMDECVRCAQAFGQRLAEELGVPVYLYGEAAR
TAGRQSLPALRAGEYEALPEKLKQAEWAPDFGPSAFVPSWGATVAGARK
>d1qd1a2 d.58.34.1 (A:181-326) Formiminotransferase domain of formiminotransferase-cyclodeaminase. {Pig (Sus scrofa)}
FLLAFNINLLSTREQAHRIALDLREQGRGKDQPGRLKKVQAIGWYLDEKNLAQVSTNLLDFEVTG
LHTVFEETCREAQELSLPVVGSQLVGLVPLKALLDAAAFYCEKENLFLLQDEHRIRLVVNRLGLD

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SLAPFKPKERIIEYLV
>d1dj0a1 d.58.35.1 (A:7-114) Pseudouridine synthase I {Escherichia coli}
PPVYKIALGIEYDGSKYYGWQRQNEVRSVQEKLEKALSQVANEPITVFCAGRTDAGVHGTGQVVH
FETTALRKDAAWTLGVNANLPGDIAVRWVKTVPDDFHARFSAT
>d1dj0a2 d.58.35.1 (A:115-270) Pseudouridine synthase I {Escherichia coli}
ARRYRYIIYNHRLRPAVLSKGVTHFYEPLDAERMHRAAQCLLGENDFTSFRAVQCQSRTPWRNVM
HINVTRHGPYVVVDIKANAFVHHMVRNIVGSLMEVGAHNQPESWIAELLAAKDRTLAAATAKAEG
LYLVAVDYPDRYDLPKPPMGPLFLAD
>d1k8wa1 d.58.35.2 (A:9-73) Pseudouridine synthase II TruB {Escherichia coli}
MDINGVLLLDKPQGMSSNDALQKVKRIYNANRAGHTGALDPLATGMLPICLGEATKFSQYLLDSD
>d1k8wa2 d.58.35.2 (A:74-312) Pseudouridine synthase II TruB {Escherichia coli}
KRYRVIARLGQRTDTSDADGQIVEERPVTFSAEQLAAALDTFRGDIEQIPSMYSALKYQGKKLYE
YARQGIEVPREARPITVYELLFIRHEGNELELEIHCSKGTYIRTIIDDLGEKLGCGAHVIYLRRL
AVSKYPVERMVTLEHLRELVEQAEQQDIPAAELLDPLLMPMDSPASDYPVVNLPLTSSVYFKNGN
PVRTSGAPLEGLVRVTEGENGKFIGMGEIDDEGRVAPRRLVVEY
>d1aop_1 d.58.36.1 (81-145) Sulfite reductase, domains 1 and 3 {Escherichia coli}
LLRCRLPGGVITTKQWQAIDKFAGENTIYGSIRLTNRQTFQFHGILKKNVKPVHQMLHSVGLDAL
>d1aop_2 d.58.36.1 (346-425) Sulfite reductase, domains 1 and 3 {Escherichia coli}
IGWVKGIDDNWHLTLFIENGRILDYPARPLKTGLLEIAKIHKGDFRITANQNLIIAGVPESEKAK
IEKIAKESGLMNAVT
>d1bxya_ d.59.1.1 (A:) Prokaryotic ribosomal protein L30 {Thermus thermophilus}
MPRLKVKLVKSPIGYPKDQKAALKALGLRRLQQERVLEDTPAIRGNVEKVAHLVRVEVVE
>d1jj2v_ d.59.1.1 (V:) Archaeal L30 (L30a) {Archaeon Haloarcula marismortui}
MHALVQLRGEVNMHTDIQDTLEMLNIHHVNHCTLVPETDAYRGMVAKVNDFVAFGEPSQETLETV
LATRAEPLEGDADVDDEWVAEHTDYDDISGLAFALLSEETTLREQGLSPTLRLHPPRGGHDGVKH
PVKEGGQLGKHDTEGIDDLLEAMR
>d1fw9a_ d.190.1.1 (A:) Chorismate lyase {Escherichia coli}
SHPALTQLRALRYSKEIPALDPQLLDWLLLEDSMTKRFEQQGKTVSVTMIREGFVEQNEIPEELP
LLPKESRYWLREILLSADGEPWLAGRTVVPVSTLSGPELALQKLGKTPLGRYLFTSSTLTRDFIE
IGRDAGLWGRRSRLRLSGKPLLLTELFLPASPLY
>d1bowa_ d.60.1.1 (A:) Multidrug-binding domain of transcription activator BmrR {Bacillus subtilis}
RLGEVFVLDEEEIRIIQTEAEGIGPENVLNASYSKLKKFIESADGFTNNSYGATFSFQPYTSIDE
MTYRHIFTPVLTNKQISSITPDMEITTIPKGRYACIAYNFSPEHYFLNLQKLIKYIADRQLTVVS
DVYELIIPIHYSPKKQEEYRVEMKIRIL
>d1d5ya3 d.60.1.2 (A:122-294) Rob transcription factor, C-terminal
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domain {Escherichia coli}
EFTMPEHKFVTLEDTPLIGVTQSYSCSLEQISDFRHEMRYQFWHDFLGNAPTIPPVLYGLNETRP
SQDKDDEQEVFYTTALAQDQADGYVLTGHPVMLQGGEYVMFTYEGLGTGVQEFILTVYGTCMPML
NLTRRKGQDIERYYPAEDAKAGDRPINLRCELLIPIRRKLAAA
>d1jh6a_ d.61.1.1 (A:) tRNA splicing product Appr>p cyclic nucleotide
phosphodiesterase {Thale cress (Arabidopsis thaliana)}
MEEVKKDVYSVWALPDEESEPRFKKLMEALRSEFTGPRFVPHVTVAVSAYLTADEAKKMFESACD
GLKAYTATVDRVSTGTFFFQCVFLLLQTTPEVMEAGEHCKNHFNCSTTTPYMPHLSLLYAELTEE
EKKNAQEKAYTLDSSLDGLSFRLNRLALCKTDTEDKTLETWETVAVCNLNP
>d1f32a_ d.62.1.1 (A:) Pepsin inhibitor-3 {Pig roundworm (Ascaris
suum)}
FLFSMSTGPFICTVKDNQVFVANLPWTMLEGDDIQVGKEFAARVEDCTNVKHDMAPTCTKPPPFC
GPQDMKMFNFVGCSVLGNKLFIDQKYVRDLTAKDHAEVQTFREKIAAFEEQQENQPPSSGMPHGA
VPAGGLSPPPPPSFCTV
>d1d8ia_ d.63.1.1 (A:) mRNA triphosphatase CET1 {Baker's yeast
(Saccharomyces cerevisiae)}
HMYRNVPIWAQKWKPTIKALQSINVKDLKIDPSFLNIIPDDDLTKSVQDWVYATIYSIAPELRSF
IELEMKFGVIIDAKGPDRVNPPVSSQCVFTELDAHLTPNIDASLFKELSKYIRGISEVTENTGKF
SIIESQTRDSVYRVGLSTQRPRFLRMSTDIKTGRVGQFIEKRHVAQLLLYSPKDSYDVKISLNLE
LPVPDNDPPEKYKSQSPISERTKDRVSYIHNDSCTRIDITKVENHNQNSKSRQSETTHEVELEIN
TPALLNAFDNITNDSKEYASLIRTFLNNGTIIRRKLSSLSY
>d2if1__ d.64.1.1 (-) Eukaryotic translation initiation factor eIF-1
(SUI1) {Human (Homo sapiens)}
MRGSHHHHHHTDPMSAIQNLHSFDPFADASKGDDLLPAGTEDYIHIRIQQRNGRKTLTTVQGIAD
DYDKKKLVKAFKKKFACNGTVIEHPEYGEVIQLQGDQRKNICQFLVEIGLAKDDQLKVHGF
>d1d1ra_ d.64.1.1 (A:) YciH {Escherichia coli}
KGDGVVRIQRQTSGRKGKGVCLITGVDLDDAELTKLAAELKKKCGCGGAVKDGVIEIQGDKRDLL
KSLLEAKGMKVKLAGGLE
>d1lbu_2 d.65.1.1 (84-213) Zn2+ DD-carboxypeptidase, C-terminal,
catalytic domain {Streptomyces albus G}
VNFTYAELNRCNSDWSGGKVSAATARANALVTMWKLQAMRHAMGDKPITVNGGFRSVTCNSNVGG
ASNSRHMYGHAADLGAGSQGFCALAQAARNHGFTEILGPGYPGHNDHTHVAGGDGRFWSAPSCGI
>d1vhh__ d.65.1.2 (-) Sonic hedgehog {Mouse (Mus musculus)}
KLTPLAYKQFIPNVAEKTLGASGRYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRC
KDKLNALAISVMNQWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVE
AGFDWVYYESKAHIHCSVKAENSVAAK
>d1qf6a2 d.66.1.1 (A:2-62) Threonyl-tRNA synthetase (ThrRS),
N-terminal 'additional' domain {Escherichia coli}
PVITLPDGSQRHYDHAVSPMDVALDIGPGLAKACIAGRVNGELVDACDLIENDAQLSIITA
>d1fjgd_ d.66.1.2 (D:) Ribosomal protein S4 {Thermus thermophilus}
GRYIGPVCRLCRREGVKLYLKGERCYSPKCAMERRPYPPGQHGQKRARRPSDYAVRLREKQKLRR
IYGISERQFRNLFEEASKKKGVTGSVFLGLLESRLDNVVYRLGFAVSRRQARQLVRHGHITVNGR
RVDLPSYRVRPGDEIAVAEKSRNLELIRQNLEAMKGRKVGPWLSLDVEGMKGKFLRLPDREDLAL
PVQENLVIEFYSR
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>d1c06a_ d.66.1.2 (A:) Ribosomal protein S4 {Bacillus stearothermophilus}
MKLSEYGLQLQEKQKLRHMYGVNERQFRKTFEEAGKMPGKHGENFMILLESRLDNLVYRLGLART
RRQARQLVTHGHILVDGSRVNIPSYRVKPGQTIAVREKSRNLQVIKEALEANNYIPDYLSFDPEK
MEGTYTRLPERSELPAEINEALIVEFYSR
>d1dm9a_ d.66.1.3 (A:) Heat shock protein 15 kD {Escherichia coli}
PAVEVRLDKWLWAARFYKTRALAREMIEGGKVHYNGQRSKPSKIVELNATLTLRQGNDERTVIVK
AITEQRRPASEAALLYEETAESVEKREKMALARKLNALT
>d1qf6a3 d.67.1.1 (A:63-241) Threonyl-tRNA synthetase (ThrRS), second 'additional' domain {Escherichia coli}
KDEEGLEIIRHSCAHLLGHAIKQLWPHTKMAIGPVIDNGFYYDVDLDRTLTQEDVEALEKRMHEL
AEKNYDVIKKKVSWHEARETFANRGESYKVSILDENIAHDDKPGLYFHEEYVDMCRGPHVPNMRF
CHHFKLMKTAGAYWRGDSNNKMLQRIYGTAWADKKALNAYLQRLEEAAK
>d1f7ua3 d.67.2.1 (A:2-135) Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain {Baker's yeast (Saccharomyces cerevisiae)}
ASTANMISQLKKLSIAEPAVAKDSHPDVNIVDLMRNYISQELSKISGVDSSLIFPALEWTNTMER
GDLLIPIPRLRIKGANPKDLAVQWAEKFPCGDFLEKVEANGPFIQFFFNPQFLAKLVIPDILTRK
EDYG
>d1iq0a3 d.67.2.1 (A:1-96) Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain {Thermus thermophilus}
MLRRALEEAIAQALKEMGVPVRLKVARAPKDKPGDYGVPLFALAKELRKPPQAIAQELKDRLPLP
EFVEEAVPVGGYLNFRLRTEALLREALRPKA
>d1dd5a_ d.67.3.1 (A:) Ribosome recycling factor, RRF {Thermotoga maritima}
VNPFIKEAKEKMKRTLEKIEDELRKMRTGKPSPAILEEIKVDYYGVPTPVNQLATISISEERTLV
IKPWDKSVLSLIEKAINASDLGLNPINDGNVIRLVFPSPTTEQREKWVKKAKEIVEEGKIAIRNI
RREILKKIKEDQKEGLIPEDDAKRLENEIQKLTDEFIEKLDEVFEIKKEEIMEF
>d1eh1a_ d.67.3.1 (A:) Ribosome recycling factor, RRF {Thermus thermophilus}
MTLKELYAETRSHMQKSLEVLEHNLAGLRTGRANPALLLHLKVEYYGAHVPLNQIATVTAPDPRT
LVVQSWDQNALKAIEKAIRDSDLGLNPSNKGDALYINIPPLTEERRKDLVRAVRQYAEEGRVAIR
NIRREALDKLKKLAKELHLSEDETKRAEAEIQKITDEFIAKADQLAEKKEQEILG
>d1ek8a_ d.67.3.1 (A:) Ribosome recycling factor, RRF {Escherichia coli}
MISDIRKDAEVRMDKCVEAFKTQISKIRTGRASPSLLDGIVVEYYGTPTPLRQLASVTVEDSRTL
KINVFDRSMSPAVEKAIMASDLGLNPNSAGSDIRVPLPPLTEERRKDLTKIVRGEAEQARVAVRN
VRRDANDKVKALLKDKEISEDDDRRSQDDVQKLTDAAIKKIEAALADKEAELMQF
>d1ge9a_ d.67.3.1 (A:) Ribosome recycling factor, RRF {Aquifex aeolicus}
MIKELEDIFKEAEKDMKKAVEYYKNEIAGLRTSRASTALVEEIKVEYYGSKVPIKQLGTISVPEH
NQIVIQVWDQNAVPAIEKAIREELNLNPTVQGNVIRVTLPPLTEERRRELVRLLHKITEEARVRV
RNVRREAKEMIEELEGISEDEKKRALERLQKLTDKYIDEINKLMEAKEKEIMSV
>d1j98a_ d.185.1.2 (A:) Autoinducer-2 production protein LuxS
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{Bacillus subtilis}
VESFELDHNAVVAPYVRHCGVHKVGTDGVVNKFDIRFCQPNKQAMKPDTIHTLEHLLAFTIRSHA
EKYDHFDIIDISPMGCQTGYYLVVSGETTSAEIVDLLEDTMKEAVEITEIPAANEKQCGQAKLHD
LEGAKRLMRFWLSQDKEELLKVFG
>d1inna_ d.185.1.2 (A:) Autoinducer-2 production protein LuxS
{Deinococcus radiodurans}
NVESFDLDHTKVKAPYVRLAGVKTTPKGDQISKYDLRFLQPNQGAIDPAAIHTLEHLLAGYMRDH
LEGVVDVSPMGCRTGMYMAVIGEPDEQGVMKAFEAALKDTAGHDQPIPGVSELECGNYRDHDLAA
ARQHARDVLDQGLKVQETILL
>d1j6wa_ d.185.1.2 (A:) Autoinducer-2 production protein LuxS
{Haemophilus influenzae}
LLDSFKVDHTKMNAPAVRIAKTMLTPKGDNITVFDLRFCIPNKEILSPKGIHTLEHLFAGFMRDH
LNGDSIEIIDISPMGCRTGFYMSLIGTPNEQKVSEAWLASMQDVLGVQDQASIPELNIYQCGSYT
EHSLEDAHEIAKNVIARGIGVNKNEDLSLDN
>d1j6xa_ d.185.1.2 (A:) Autoinducer-2 production protein LuxS
{Helicobacter pylori}
MKMNVESFNLDHTKVKAPYVRIADRKKGVNGDLIVKYDVRFKQPNRDHMDMPSLHSLEHLVAEII
RNHANYVVDWSPMGCQTGFYLTVLNHDNYTEILEVLEKTMQDVLKAKEVPASNEKQCGWAANHTL
EGAQNLARAFLDKRAEWSEVG
>d1hr6b1 d.185.1.1 (B:24-245) Mitochondrial processing peptidase (MPP)
beta chain {Baker's yeast (Saccharomyces cerevisiae)}
PGTRTSKLPNGLTIATEYIPNTSSATVGIFVDAGSRAENVKNNGTAHFLEHLAFKGTQNRPQQGI
ELEIENIGSHLNAYTSRENTVYYAKSLQEDIPKAVDILSDILTKSVLDNSAIERERDVIIRESEE
VDKMYDEVVFDHLHEITYKDQPLGRTILGPIKNIKSITRTDLKDYITKNYKGDRMVLAGAGAVDH
EKLVQYAQKYFGHVPKSESPVPLGSPR
>d1hr6b2 d.185.1.1 (B:246-462) Mitochondrial processing peptidase
(MPP) beta chain {Baker's yeast (Saccharomyces cerevisiae)}
GPLPVFCRGERFIKENTLPTTHIAIALEGVSWSAPDYFVALATQAIVGNWDRAIGTGTNSPSPLA
VAASQNGSLANSYMSFSTSYADSGLWGMYIVTDSNEHNVRLIVNEILKEWKRIKSGKISDAEVNR
AKAQLKAALLLSLDGSTAIVEDIGRQVVTTGKRLSPEEVFEQVDKITKDDIIMWANYRLQNKPVS
MVALGNTSTVPNVSYIEEKLNQ
>d1hr6a1 d.185.1.1 (A:14-233) Mitochondrial processing peptidase (MPP)
alpha chain {Baker's yeast (Saccharomyces cerevisiae)}
ARTDNFKLSSLANGLKVATSNTPGHFSALGLYIDAGSRFEGRNLKGCTHILDRLAFKSTEHVEGR
AMAETLELLGGNYQCTSSRENLMYQASVFNQDVGKMLQLMSETVRFPKITEQELQEQKLSAEYEI
DEVWMKPELVLPELLHTAAYSGETLGSPLICPRGLIPSISKYYLLDYRNKFYTPENTVAAFVGVP
HEKALELTGKYLGDWQSTHPPITKK
>d1hr6a2 d.185.1.1 (A:234-470) Mitochondrial processing peptidase
(MPP) alpha chain {Baker's yeast (Saccharomyces cerevisiae)}
VAQYTGGESCIPPAPVFGNLPELFHIQIGFEGLPIDHPDIYALATLQTLLGGGGSFSAGGPGKGM
YSRLYTHVLNQYYFVENCVAFNHSYSDSGIFGISLSCIPQAAPQAVEVIAQQMYNTFANKDLRLT
EDEVSRAKNQLKSSLLMNLESKLVELEDMGRQVLMHGRKIPVNEMISKIEDLKPDDISRVAEMIF
TGNVNNAGNGKGRATVVMQGDRGSFGDVENVLKAYGLGNSSS
>d1be3a1 d.185.1.1 (A:1-233) Cytochrome bc1 core subunit 1 {Cow (Bos
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taurus)}
TATYAQALQSVPETQVSQLDNGLRVASEQSSQPTCTVGVWIDAGSRYESEKNNGAGYFVEHLAFK
GTKNRPGNALEKEVESMGAHLNAYSTREHTAYYIKALSKDLPKAVELLADIVQNCSLEDSQIEKE
RDVILQELQENDTSMRDVVFNYLHATAFQGTPLAQSVEGPSENVRKLSRADLTEYLSRHYKAPRM
VLAAAGGLEHRQLLDLAQKHFSGLSGTYDEDAVPTLSP
>d1be3a2 d.185.1.1 (A:234-446) Cytochrome bc1 core subunit 1 {Cow (Bos taurus)}
CRFTGSQICHREDGLPLAHVAIAVEGPGWAHPDNVALQVANAIIGHYDCTYGGGAHLSSPLASIA
ATNKLCQSFQTFNICYADTGLLGAHFVCDHMSIDDMMFVLQGQWMRLCTSATESEVLRGKNLLRN
ALVSHLDGTTPVCEDIGRSLLTYGRRIPLAEWESRIAEVDARVVREVCSKYFYDQCPAVAGFGPI
EQLPDYNRIRSGMFWLRF
>d1bcca1 d.185.1.1 (A:4-232) Cytochrome bc1 core subunit 1 {Chicken (Gallus gallus)}
YAQALQSVPETQVSQLDNGVRVASEQSSQPTCTVGVWIDAGSRYESEKNNGAGYFLEHLAFKGTK
NRPQNALEKEVESMGAHLNAYSSREHTAYYIKALSKDVPKAVELLADIVQNCSLEDSQIEKERDV
IVRELQENDTSMREVVFNYLHATAFQGTGLAQSVEGPSENIRKLSRADLTEYLSTHYTAPRMVLA
AAGGVEHQQLLELAQKHFGGVPFTYDDDAVPTLS
>d1bcca2 d.185.1.1 (A:233-445) Cytochrome bc1 core subunit 1 {Chicken (Gallus gallus)}
KCRFTGSQIRHREDGLPLAHVAIAVEGPGWAHPDLVALQVANAIIGHYDRTYGGGLHSSSPLASI
AVTNKLCQSFQTFSICYSETGLFGFYFVCDRMSIDDMMFVLQGQWMRLCTSISESEVLRGKNFLR
NALVSHLDGTTPVCEDIGRELLTYGRRIPLEEWEERLAEVDARMVREVCSKYIYDQCPAVAGPGP
IEQLPDYNRIRSGMFWLR
>d1ezva1 d.185.1.1 (A:27-239) Cytochrome bc1 core subunit 1 {Baker's yeast (Saccharomyces cerevisiae)}
AEVTQLSNGIVVATEHNPAHTASVGVVFGSGAANENPYNNGVSNLWKNIFLSKENSAVAAKEGLA
LSSNISRDFQSYIVSSLPGSTDKSLDFLNQSFIQQKANLLSSSNFEATKKSVLKQVQDFEDNDHP
NRVLEHLHSTAFQNTPLSLPTRGTLESLENLVVADLESFANNHFLNSNAVVVGTGNIKHEDLVNS
IESKNLSLQTGTKPVLKK
>d1ezva2 d.185.1.1 (A:240-456) Cytochrome bc1 core subunit 1 {Baker's yeast (Saccharomyces cerevisiae)}
KAAFLGSEVRLRDDTLPKAWISLAVEGEPVNSPNYFVAKLAAQIFGSYNAFEPASRLQGIKLLDN
IQEYQLCDNFNHFSLSYKDSGLWGFSTATRNVTMIDDLIHFTLKQWNRLTISVTDTEVERAKSLL
KLQLGQLYESGNPVNDANLLGAEVLIKGSKLSLGEAFKKIDAITVKDVKAWAGKRLWDQDIAIAG
TGQIEGLLDYMRIRSDMSMMRW
>d1be3b1 d.185.1.1 (B:21-235) Cytochrome bc1 core subunit 2 {Cow (Bos taurus)}
PQDLEFTRLPNGLVIASLENYAPASRIGLFIKAGSRYENSNNLGTSHLLRLASSLTTKGASSFKI
TRGIEAVGGKLSVTSTRENMAYTVECLRDDVDILMEFLLNVTTAPEFRRWEVAALQPQLRIDKAV
ALQNPQAHVIENLHAAAYRNALANSLYCPDYRIGKVTPVELHDYVQNHFTSARMALIGLGVSHPV
LKQVAEQFLNIRGGLGLSGA
>d1be3b2 d.185.1.1 (B:236-439) Cytochrome bc1 core subunit 2 {Cow (Bos taurus)}
KAKYHGGEIREQNGDSLVHAALVAESAAIGSAEANAFSVLQHVLGAGPHVKRGSNATSSLYQAVA

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KGVHQPFDVSAFNASYSDSGLFGFYTISQAASAGDVIKAAYNQVKTIAQGNLSNPDVQAAKNKLK
AGYLMSVESSEGFLDEVGSQALAAGSYTPPSTVLQQIDAVADADVINAAKKFVSGRKSMAASGNL
GHTPFIDEL
>d1bccb1 d.185.1.1 (B:18-235) Cytochrome bc1 core subunit 2 {Chicken
(Gallus gallus)}
PPHPQDLEITKLPNGLVIASLENYSPGSTIGVFIKAGSRYENSSNLGTSHLLRLASSLTTKGASS
FKITRGIEAVGGKLSVESTRENMAYTVECLRDDVEILMEFLLNVTTAPEFRPWEVADLQPQLKID
KAVAFQNPQTHVIENLHAAAYRNALADSLYCPDYRIGKVTSVELHDFVQNHFTSARMALVGLGVS
HPVLKNVAEQLLNIRGGLGLSGA
>d1bccb2 d.185.1.1 (B:236-439) Cytochrome bc1 core subunit 2 {Chicken
(Gallus gallus)}
KAKYRGGEIREQNGDSLVHAAIVAESAAIGGAEANAFSVLQHVLGANPHVKRGLNATSSLYQAVA
KGVHQPFDVSAFNASYSDSGLFGFYTISQAAYAGQVIKAAYNQVKTIAQGNVSNENVQAAKNKLK
AKYLMSVESSEGFLEEVGSQALAAGSYNPPSTVLQQIDAVADADVIKAAKKFVSRQKSMAASGNL
GHTPFVDEL
>d1ezvb1 d.185.1.1 (B:17-218) Cytochrome bc1 core subunit 2 {Baker's
yeast (Saccharomyces cerevisiae)}
LTVSARDAPTKISTLAVKVHGGSRYATKDGVAHLLNRFNFQNTNTRSALKLVRESELLGGTFKST
LDREYITLKATFLKDDLPYYVNALADVLYKTAFKPHELTESVLPAARYDYAVAEQCPVKSAEDQL
YAITFRKGLGNPLLYDGVERVSLQDIKDFADKVYTKENLEVSGENVVEADLKRFVDESLLSTLPA
GKSLVSK
>d1ezvb2 d.185.1.1 (B:219-368) Cytochrome bc1 core subunit 2 {Baker's
yeast (Saccharomyces cerevisiae)}
SEPKFFLGEENRVRFIGDSVAAIGIPVNKASLAQYEVLANYLTSALSELSGLISSAKLDKFTDGG
LFTLFVRDQDSAVVSSNIKKIVADLKKGKDLSPAINYTKLKNAVQNESVSSPIELNFDAVKDFKL
GKFNYVAVGDVSNLPYLDEL
>d1tig__ d.68.1.1 (-) Translation initiation factor IF3, C-terminal
domain {Bacillus stearothermophilus}
INVKEVRLSPTIEEHDFNTKLRNARKFLEKGDKVKATIRFKGRAITHKEIGQRVLDRLSEACADI
AVVETAPKMDGRNMFLVLAPKND
>d2ifea_ d.68.1.1 (A:) Translation initiation factor IF3, C-terminal
domain {Escherichia coli}
VIQVKEIKFRPGTDEGDYQVKLRSLIRFLEEGDKAKITLRFRGREMAHQQIGMEVLNRVKDDLQE
LAVVESFPTKIEGRQMIMVLAPKKKQ
>d1i96v_ d.68.1.1 (V:) Translation initiation factor IF3, C-terminal
domain {Thermus thermophilus}
EVKSIKFRVKIDEHDYQTKLGHIKRFLQEGHKVKVTIMFRGREVAHPELGERILNRVTEDLKDLA
VVEMKPEMLGRDMNMLLAPVK
>d1dcja_ d.68.3.1 (A:) SirA {Escherichia coli}
MTDLFSSPDHTLDALGLRCPEPVMMVRKTVRNMQPGETLLIIADDPATTRDIPGFCTFMEHELVA
KETDGLPYRYLIRKGG
>d1jdqa_ d.68.3.2 (A:) Hypothetical protein TM0983 {Thermotoga
maritima}
GSSHHHHHHSSGLVPRGSHMAKYQVTKTLDVRGEVCPVPDVETKRALQNMKPGEILEVWIDYPMS
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KERIPETVKKLGHEVLEIEEVGPSEWKIYIKVK
>d1qmha2 d.68.2.1 (A:5-184,A:280-338) RNA 3'-terminal phosphate
cyclase, RPTC {Escherichia coli}
MIALDGAQGEGGGQILRSALSLSMITGQPFTITSIRAGRAKPGLLRQHLTAVKAATEICGATVEG
AELGSQRLLFRPGTVRGGDYRFAIGSAGSCTLVLQTVLPALWFADGPSRVEVSGGTDNPSAPPAD
FIRRVLEPLLAKIGIHQQTTLLRHGFYPAGGGVVATEVSPVASFNTLQLGXAVGEYLADQLVLPM
ALAGAGEFTVAHPSCHLLTNIAVVERFLPVRFSLIETDGVTRVSI
>d1uae__ d.68.2.2 (-) UDP-N-acetylglucosamine enolpyruvyl
transferase (EPT, MurA, MurZ) {Escherichia coli}
MDKFRVQGPTKLQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDVDTSMKLLSQLGAKVE
RNGSVHIDARDVNVFCAPYDLVKTMRASIWALGPLVARFGQGQVSLPGGCTIGARPVDLHISGLE
QLGATIKLEEGYVKASVDGRLKGAHIVMDKVSVGATVTIMCAATLAEGTTIIENAAREPEIVDTA
NFLITLGAKISGQGTDRIVIEGVERLGGGVYRVLPDRIETGTFLVAAAISRGKIICRNAQPDTLD
AVLAKLRDAGADIEVGEDWISLDMHGKRPKAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGFITE
TVFENRFMHVPELSRMGAHAEIESNTVICHGVEKLSGAQVMATDLRASASLVLAGCIAEGTTVVD
RIYHIDRGYERIEDKLRALGANIERVKG
>d1ejda_ d.68.2.2 (A:) UDP-N-acetylglucosamine enolpyruvyl
transferase (EPT, MurA, MurZ) {Enterobacter cloacae}
MDKFRVQGPTRLQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDIDTTMKLLTQLGTKVE
RXGSVWIDASNVNNFSAPYDLVKTMRASIWALGPLVARFGQGQVSLPGGCAIGARPVDLHIFGLE
KLGAEIKLEEGYVKASVNGRLKGAHIVMDKVSVGATVTIMSAATLAEGTTIIENAAREPEIVDTA
NFLVALGAKISGQGTDRITIEGVERLGGGVYRVLPDRIETGTFLVAAAISGGKIVCRNAQPDTLD
AVLAKLREAGADIETGEDWISLDMHGKRPKAVTVRTAPHPAFPTDMQAQFTLLNLVAEGTGVITE
TIFENRFMHVPELIRMGAHAEIESNTVICHGVEKLSGAQVMATDLRASASLVLAGCIAEGTTVVD
RIYHIDRGYERIEDKLRALGANIERVKGE
>d1g6sa_ d.68.2.2 (A:) 5-enol-pyruvyl shikimate-3-phosphate(EPSP)
synthase {Escherichia coli}
MESLTLQPIARVDGTINLPGSKSVSNRALLLAALAHGKTVLTNLLDSDDVRHMLNALTALGVSYT
LSADRTRCEIIGNGGPLHAEGALELFLGNAGTAMRPLAAALCLGSNDIVLTGEPRMKERPIGHLV
DALRLGGAKITYLEQENYPPLRLQGGFTGGNVDVDGSVSSQFLTALLMTAPLAPEDTVIRIKGDL
VSKPYIDITLNLMKTFGVEIENQHYQQFVVKGGQSYQSPGTYLVEGDASSASYFLAAAAIKGGTV
KVTGIGRNSMQGDIRFADVLEKMGATICWGDDYISCTRGELNAIDMDMNHIPDAAMTIATAALFA
KGTTTLRNIYNWRVKETDRLFAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMC
FSLVALSDTPVTILDPKCTAKTFPDYFEQLARISQAA
>d1imua_ d.204.1.1 (A:) Ribosome binding protein Y (HI0257, YfiA
homologue) {Haemophilus influenzae}
MTLNITSKQMDITPAIREHLEERLAKLGKWQTQLISPHFVLNKVPNGFSVEASIGTPLGNLLASA
TSDDMYKAINEVEEKLERQLNKLQHKSESRRADERLKDSFEN
>d1tola2 d.69.1.1 (A:125-216) C-terminal domain of TolA {Escherichia
coli}
SGADINNYAGQIKSAIESKFYDASSYAGKTCTLRIKLAPDGMLLDIKPEGGDPALCQAALAAAKL
AKIPKPPSQAVYEVFKNAPLDFKPAAA
>d1kpta_ d.70.1.1 (A:) Virally encoded KP4 toxin {Ustilago maydis,
P4 strain}
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LGINCRGSSQCGLSGGNLMVRIRDQACGNQGQTWCPGERRAKVCGTGNSISAYVQSTNNCISGTE
ACRHLTNLVNHGCRVCGSDPLYAGNDVSRGQLTVNYVNSC
>g1kve.1 d.70.1.2 (A:,B:) SMK toxin {Halotolerant yeast (Pichia farinosa)}
WSLRWRMQKSTTIAAIAGCSGAATFGGLAGGIVGCIAAGILAILQGFEVNWHNGGGGDRSNPVXG
EATTIWGVGADEAIDKGTPSKNDLQNMSADLAKNGFKGHQGVACSTVKDGNKDVYMIKFSLAGGS
NDPGGSPCSDD
>d1ev0a_ d.71.1.1 (A:) Cell division protein MinE topological specificity domain {Escherichia coli}
RSDAEPHYLPQLRKDILEVICKYVQIDPEMVTVQLEQKDGDISILELNVTLPEAEELK
>d1dw9a2 d.72.1.1 (A:87-156) Cyanase C-terminal domain {Escherichia coli}
RIPTDPTMYRFYEMLQVYGTTLKALVHEKFGDGIISAINFKLDVKKVADPEGGERAVITLDGKYL
PTKPF
>d3rubs_ d.73.1.1 (S:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Tobacco (Nicotiana tabacum), variant turkish samsun}
MQVWPPINKKKYETLSYLPDLSQEQLLSEVEYLLKNGWVPCLEFETEHGFVYRENNKSPGYYDGR
YWTMWKLPMFGCTDATQVLAEVEEAKKAYPQAWIRIIGFDNVRQVQCISFIAYKPEGY
>d1burs_ d.73.1.1 (S:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Spinach (Spinacia oleracea)}
MQVWPILGMKKYETLSYLPPLTTEQLLAEVNYLLVNNWIPCLEFEVKDGFVYREHLKSPGYYDGR
YWTMWKLPMFGCTDPAQVLNELEECKKAYPDAFIRIIGFDNKRQVQCISFIAYKPAGY
>d8ruci_ d.73.1.1 (I:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Spinach (Spinacia oleracea)}
MQVWPILNLKKYETLSYLPPLTTDQLARQVDYLLNNKWVPCLEFETDHGFVYREHHNSPGYYDGR
YWTMWKLPMFGCTDPAQVLNELEECKKEYPNAFIRIIGFDSNREVQCISFIAYKPAGY
>d1bwvs_ d.73.1.1 (S:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Galdieria partita}
VRITQGTFSFLPDLTDEQIKKQIDYMISKKLAIGIEYTNDIHPRNAYWEIWGLPLFDVTDPAAVL
FEINACRKARSNFYIKVVGFSSVRGIESTIISFIVNRPKHEPGFNLMRQEDKSRSIKYTIHSYES
YKPEDERY
>d1gk8i_ d.73.1.1 (I:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Chlamydomonas reinhardtii}
MVWTPVNNKMFETFSYLPPLTDEQIAAQVDYIVANGWIPCLEFAEADKAYVSNESAIRFGSVSCL
YYDNRYWTMWKLPMFGCRDPMQVLREIVACTKAFPDAYVRLVAFDNQKQVQIMGFLVQRP
>d1bxni_ d.73.1.1 (I:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Alcaligenes eutrophus}
MRITQGTFSFLPELTDEQITKQLEYCLNQGWAVGLEYTDDPHPRNTYWEMFGLPMFDLRDAAGIL
MEINNARNTFPNHYIRVTAFDSTHTVESVVMSFIVNRPADEPGFRLVRQEEPGRTLRYSIESYA
>d1rblm_ d.73.1.1 (M:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Synechococcus sp., strain pcc 6301}
SMKTLPKERRFETFSYLPPLSDRQIAAQIEYMIEQGFHPLIEFNEHSNPEEFYWTMWKLPLFACA
APQQVLDEVRECRSEYGDCYIRVAGFDNIKECQTSSFIVHRPGR
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>d1dcpa_ d.74.1.1 (A:) Pterin-4a-carbinolamine dehydratase (PCD)/dimerization cofactor of HNF1 (DCoH) {Rat (Rattus norvegicus)}
HRLSAEERDQLLPNLRAVGWNELEGRDAIFKQFHFKDFNRAFGFMTRVALQAEKLDHHPEWFNVY
NKVHITLSTHECAGLSERDINLASFIEQVAVSMT
>d1xxaa_ d.74.2.1 (A:) C-terminal domain of arginine repressor {Escherichia coli}
LKNLVLDIDYNDAVVVIHTSPGAAQLIARLLDSLGKAEGILGTIAGDDTIFTTPANGFTVKDLYE
AILELF
>d1b4ba_ d.74.2.1 (A:) C-terminal domain of arginine repressor {Bacillus stearothermophilus}
ALVDVFIKLDGTGNLLVLRTLPGNAHAIGVLLDNLDWDEIVGTICGDDTCLIICRTPKDAKKVSN
QLLSML
>d1f9na2 d.74.2.1 (A:79-149) C-terminal domain of arginine repressor {Bacillus subtilis}
ALMDAFVKIDSASHMIVLKTMPGNAQAIGALMDNLDWDEMMGTICGDDTILIICRTPEDTEGVKN
RLLELL
>d1i50k_ d.74.3.2 (K:) RPB11 {Baker's yeast (Saccharomyces cerevisiae)}
MNAPDRFELFLLGEGESKLKIDPDTKAPNAVVITFEKEDHTLGNLIRAELLNDRKVLFAAYKVEH
PFFARFKLRIQTTEGYDPKDALKNACNSIINKLGALKTNFETEWNLQTL
>d1bdfa1 d.74.3.1 (A:2-52,A:179-232) RNA polymerase alpha {Escherichia coli}
QGSVTEFLKPRLVDIEQVSSTHAKVTLEPLERGFGHTLGNALRAILLSSMPXPVERIAYNVEAAR
VEQRTDLDKLVIEMETNGTIDPEEAIRRAATILAEQLEAFV
>d1i6va1 d.74.3.1 (A:6-49,A:173-229) RNA polymerase alpha {Thermus aquaticus}
LKAPVFTATTQGDHYGEFVLEPLERGFGVTLGNPLRRILLSSIPXPVRRVAFQVEDTRLGQRTDL
DKLTLRIWTDGSVTPLEALNQAVAILKEHLNYFANPE
>d1i50c1 d.74.3.1 (C:3-41,C:173-268) RPB3 {Baker's yeast (Saccharomyces cerevisiae)}
EEGPQVKIREASKDNVDFILSNVDLAMANSLRRVMIAEIXAAAIEFEYDPWNKLKHTDYWYEQDS
AKEWPQSKNCEYEDPPNEGDPFDYKAQADTFYMNVESVGSIPVDQVVVRGIDTLQKKVASILLAL
TQMDQD
>d1c0aa2 d.74.4.1 (A:288-420) Prokaryotic AspRS, insert domain {Escherichia coli}
NPMELTDVADLLKSVEFAVFAGPANDPKGRVAALRVPGGASLTRKQIDEYGNFVKIYGAKGLAYI
KVNERAKGLEGINSPVAKFLNAEIIEDILDRTAAQDGDMIFFGADNKKIVADAMGALRLKVGKDL
GLT
>d1g51a2 d.74.4.1 (A:295-414) Prokaryotic AspRS, insert domain {Thermus thermophilus}
FGLELKEVGPLFRQSGFRVFQEAESVKALALPKALSRKEVAELEEVAKRHKAQGLAWARVEEGGF
SGGVAKFLEPVREALLQATEARPGDTLLFVAGPRKVAATALGAVRLRAADLLGLK
>d1a79a2 d.75.1.1 (A:9-82) tRNA splicing endonuclease EdnA, N-terminal domain {Archaeon Methanococcus jannaschii}
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KITGLLDGDRVIVFDKNGISKLSARHYGNVEGNFLSLSLVEALYLINLGWLEVKYKDNKPLSFEE
LYEYARNVE
>d1ewqa4 d.75.2.1 (A:1-120) DNA repair protein MutS, domain I {Thermus aquaticus}
MEGMLKGEGPGPLPPLLQQYVELRDQYPDYLLLFQVGDFYECFGEDAERLARALGLVLTHKTSKD
FTTPMAGIPLRAFEAYAERLLKMGFRLAVADQVEPAEEAEGLVRREVTQLLTPGT
>d1e3ma4 d.75.2.1 (A:2-116) DNA repair protein MutS, domain I {Escherichia coli}
SAIENFDAHTPMMQQYLRLKAQHPEILLFYRMGDFYELFYDDAKRASQLLDISLTKRGASAGEPI
PMAGIPYHAVENYLAKLVNQGESVAICEQIGDPATSKGPVERKVVRIVTP
>d1e3mb4 d.75.2.1 (B:14-116) DNA repair protein MutS, domain I {Escherichia coli}
MQQYLRLKAQHPEILLFYRMGDFYELFYDDAKRASQLLDISLTKRGASAGEPIPMAGIPYHAVEN
YLAKLVNQGESVAICEQIGDPATSKGPVERKVVRIVTP
>d1gyfa_ d.76.1.1 (A:) GYF domain from cd2bp2 protein {Human (Homo sapiens)}
DVMWEYKWENTGDAELYGPFTSAQMQTWVSEGYFPDGVYCRKLDPPGGQFYNSKRIDFDLYT
>d1jg5a_ d.205.1.1 (A:) GTP cyclohydrolase I feedback regulatory protein, GFRP {Rat (Rattus norvegicus)}
PYLLISTQIRMEVGPTMVGDEHSDPELMQQLGASKRRVLGNNFYEYYVNDPPRIVLDKLECRGFR
VLSMTGVGQTLVWCLHKE
>d1iq4a_ d.77.1.1 (A:) Ribosomal protein L5 {Bacillus stearothermophilus}
MNRLKEKYLNEVVPALMSKFNYKSIMQVPKIEKIVINMGVGDAVQNPKALDSAVEELTLIAGQRP
VVTRAKKSIAGFRLRQGMPIGAKVTLRGERMYEFLDKLISVSLPRARDFRGVSKKSFDGRGNYTL
GIKEQLIFPEIDYDKVNKVRGMDIVIVTTANTDEEARELLALLGMPFQK
>d1jj2d_ d.77.1.1 (D:) Ribosomal protein L5 {Archaeon Haloarcula marismortui}
FHEMREPRIEKVVVHMGIGHGGRDLANAEDILGEITGQMPVRTKAKRTVGEFDIREGDPIGAKVT
LRDEMAEEFLQTALPLAELATSQFDDTGNFSFGVEEHTEFPSQEYDPSIGIYGLDVTVNLVRPGY
RVAKRDKASRSIPTKHRLNPADAVAFIESTYDVEV
>d1eika_ d.78.1.1 (A:) RNA polymerase subunit RBP5 (RNA polymerase subunit H) {Archaeon Methanobacterium thermoautotrophicum}
MKREILKHQLVPEHVILNESEAKRVLKELDAHPEQLPKIKTTDPVAKAIGAKRGDIVKIIRKSPT
AEEFVTYRLVQD
>d1hmja_ d.78.1.1 (A:) RNA polymerase subunit RBP5 (RNA polymerase subunit H) {Archaeon Methanococcus jannaschii}
PKHEIVPKEEVEEILKRYNIKIQQLPKIYEDDPVIQEIGAKEGDVVRVIRKSPTAGVSIAYRLVI
KRI
>d1dzfa2 d.78.1.1 (A:144-215) Eukaryotic RPB5 C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
ITHHELVPKHIRLSSDEKRELLKRYRLKESQLPRIQRADPVALYLGLKRGEVVKIIRKSETSGRY
ASYRICM
>d1qkla_ d.78.1.2 (A:) RPB6 {Human (Homo sapiens)}
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MSDNEDNFDGDDFDDVEEDEGLDDLENAEEEGQENVEILPSGERPQANQKRITTPYMTKYERARV
LGTRALQIAMCAPVMVELEGETDPLLIAMKELKARKIPIIIRRYLPDGSYEDWGVDELIITD
>d1i50f_ d.78.1.2 (F:) RPB6 {Baker's yeast (Saccharomyces cerevisiae)}
KAIPKDQRATTPYMTKYERARILGTRALQISMNAPVFVDLEGETDPLRIAMKELAEKKIPLVIRR
YLPDGSFEDWSVEELIVDL
>d1qu9a_ d.79.1.1 (A:) Conserved 'hypothetical' protein YjgF {Escherichia coli}
SKTIATENAPAAIGPYVQGVDLGNMIITSGQIPVNPKTGEVPADVAAQARQSLDNVKAIVEAAGL
KVGDIVKTTVFVKDLNDFATVNATYEAFFTEHNATFPARSCVEVARLPKDVKIEIEAIAVRR
>d1qd9a_ d.79.1.1 (A:) Purine regulatory protein YabJ {Bacillus subtilis}
TKAVHTKHAPAAIGPYSQGIIVNNMFYSSGQIPLTPSGEMVNGDIKEQTHQVFSNLKAVLEEAGA
SFETVVKATVFIADMEQFAEVNEVYGQYFDTHKPARSCVEVARLPKDALVEIEVIALVK
>d1jd1a_ d.79.1.1 (A:) Highdosage growth inhibitor YER057cp (YEO7_YEAST) {Baker's yeast (Saccharomyces cerevisiae)}
TTLTPVICESAPAAAASYSHAMKVNNLIFLSGQIPVTPDNKLVEGSIADKAEQVIQNIKNVLEAS
NSSLDRVVKVNIFLADINHFAEFNSVYAKYFNTHKPARSCVAVAALPLGVDMEMEAIAAER
>d1dbfa_ d.79.1.2 (A:) Chorismate mutase {Bacillus subtilis}
MMIRGIRGATTVERDTEEEILQKTKQLLEKIIEENHTKPEDVVQMLLSATPDLHAVFPAKAVREL
SGWQYVPVTCMQEMDVTGGLKKCIRVMMTVQTDVPQDQIRHVYLEKAVVLRPDLSLTKNTEL
>d1fnja_ d.79.1.2 (A:) Chorismate mutase {Bacillus subtilis}
MIRGIRGATTVERDTEEEILQKTKQLLEKIIEENHTKPEDVVQMLLSATPDLHAVFPAKAVRELS
GWQYVPVTCMQEMDVTGGLKKSIKVMMTVQTDVPQDQIRHVYLEKAVVLR
>d1jy8a_ d.79.5.1 (A:) 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase IspF {Escherichia coli}
MRIGHGFDVHAFGGEGPIIIGGVRIPYEKGLLAHSDGDVALHALTDALLGAAALGDIGKLFPDTD
PAFKGADSRELLREAWRRIQAKGYTLGNVDVTIIAQAPKMLPHIPQMRVFIAEDLGCHMDDVNVK
ATTTEKLGFTGRGEGIACEAVALLI
>d1fsz_2 d.79.2.1 (232-356) Cell-division protein FtsZ {Archaeon Methanococcus jannaschii}
INVDFADVKAVMNNGGLAMIGIGESDSEKRAKEAVSMALNSPLLDVDIDGATGALIHVMGPEDLT
LEEAREVVATVSSRLDPNATIIWGATIDENLENTVRVLLVITGVQSRIEFTDTGLKRKKL
>d1tuba2 d.79.2.1 (A:246-440) Tubulin alpha-subunit {Pig (Sus scrofa)}
GALNVDLTEFQTNLVPYPRGHFPLATYAPVISAEKAYHEQLSVAEITNACFEPANQMVKCDPRHG
KYMACCLLYRGDVVPKDVNAAIATIKTKRTIQFVDWCPTGFKVGINYEPPTVVPGGDLAKVQRAV
CMLSNTTAIAEAWARLDHKFDLMYAKRAFVHWYVGEGMEEGEFSEAREDMAALEKDYEEVGVDSV
>d1tubb2 d.79.2.1 (B:246-437) Tubulin beta-subunit {Pig (Sus scrofa)}
GQLNADLRKLAVNMVPFPRLHFFMPGFAPLTSRGSQQYRALTVPELTQQMFDAKNMMAACDPRHG
RYLTVAAVFRGRMSMKEVDEQMLNVQNKNSSYFVEWIPNNVKTAVCDIPPRGLKMSATFIGNSTA
IQELFKRISEQFTAMFRRKAFLHWYTGEGMDEMEFTEAESNMNDLVSEYQQYQD
>d1ck9a_ d.79.3.1 (A:) Eukaryotic ribosomal protein L30 (L30e) {Baker's yeast (Saccharomyces cerevisiae)}
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APVKSQESINQKLALVIKSGKYTLGYKSTVKSLRQGKSKLIIIAANTPVLRKSELEYYAMLSKTK
VYYFQGGNNELGTAVGKLFRVGVVSILEAGDSDILTTLA
>d1jj2f_ d.79.3.1 (F:) Ribosomal protein L7ae {Archaeon Haloarcula
marismortui}
PVYVDFDVPADLEDDALEALEVARDTGAVKKGTNETTKSIERGSAELVFVAEDVQPEEIVMHIPE
LADEKGVPFIFVEQQDDLGHAAGLEVGSAAAAVTDAGAAATVLEEIADKVEELR
>d1e7ka_ d.79.3.1 (A:) Spliceosomal 15.5kd protein {Human (Homo
sapiens)}
ADVNPKAYPLADAHLTKKLLDLVQQSCNYKQLRKGANEATKTLNRGISEFIVMAADAEPLEIILH
LPLLCEDKNVPYVFVRSKQALGRACGVSRPVIACSVTIKEGSQLKQQIQSIQQSIERLLV
>d1dt9a2 d.79.3.2 (A:277-422) C-terminal domain of eukaryotic peptide
chain release factor subunit 1, ERF1 {Human (Homo sapiens)}
NVKFIQEKKLIGRYFDEISQDTGKYCFGVEDTLKALEMGAVEILIVYENLDIMRYVLHCQGTEEE
KILYLTPEQEKDKSHFTDKETGQEHELIESMPLLEWFANNYKKFGATLEIVTDKSQEGSQFVKGF
GGIGGILRYRVDFQGM
>d1clia1 d.79.4.1 (A:5-170) Aminoimidazole ribonucleotide synthetase
(PurM) N-terminal domain {Escherichia coli}
TSLSYKDAGVDIDAGNALVGRIKGVVKKTRRPEVMGGLGGFGALCALPQKYREPVLVSGTDGVGT
KLRLAMDLKRHDTIGIDLVAMCVNDLVVQGAEPLFFLDYYATGKLDVDTASAVISGIAEGCLQSG
CSLVGGETAEMPGMYHGEDYDVAGFCVGVVEKSEII
>d1clib1 d.79.4.1 (B:1021-1170) Aminoimidazole ribonucleotide
synthetase (PurM) N-terminal domain {Escherichia coli}
ALVGRIKGVVKKTRRPEVMGGLGGFGALCALPQKYREPVLVSGTDGVGTKLRLAMDLKRHDTIGI
DLVAMCVNDLVVQGAEPLFFLDYYATGKLDVDTASAVISGIAEGCLQSGCSLVGGETAEMPGMYH
GEDYDVAGFCVGVVEKSEII
>d1otfa_ d.80.1.1 (A:) 4-oxalocrotonate tautomerase {Pseudomonas sp.,
DmpI}
PIAQLYIIEGRTDEQKETLIRQVSEAMANSLDAPLERVRVLITEMPKNHFGIGGEPASK
>d1bjpa_ d.80.1.1 (A:) 4-oxalocrotonate tautomerase {Pseudomonas
putida, XylH}
PIAQIHILEGRSDEQKETLIREVSEAISRSLDAPLTSVRVIITEMAKGHFGIGGELASKVRR
>d1otga_ d.80.1.2 (A:) 5-carboxymethyl-2-hydroxymuconate isomerase
(CHMI) {Escherichia coli}
PHFIVECSDNIREEADLPGLFAKVNPTLAATGIFPLAGIRSRVHWVDTWQMADGQHDYAFVHMTL
KIGAGRSLESRQQAGEMLFELIKTHFAALMESRLLALSFEIEELHPTLNFKQNNVHALFK
>d1gd0a_ d.80.1.3 (A:) Microphage migration inhibition factor (MIF)
{Human (Homo sapiens)}
PMFIVNTNVPRASVPDGFLSELTQQLAQATGKPPQYIAVHVVPDQLMAFGGSSEPCALCSLHSIG
KIGGAQNRSYSKLLCGLLAERLRISPDRVYINYYDMNAANVGWNNSTFALEHH
>d1fim__ d.80.1.3 (-) Microphage migration inhibition factor (MIF)
{Rat (Rattus norvegicus)}
PAFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAVHVVPDQLMTFSGTSDPCALCSLHSIG
KIGGAQNRNYSKLLCGLLSDRLHISPDRVYINYYDANA
>d1mfia_ d.80.1.3 (A:) Microphage migration inhibition factor (MIF)
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{Mouse (Mus musculus)}
PMFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAVHVVPDQLMTFSGTNDPCALCSLHSIG
KIGGAQNRNYSKLLCGLLSDRLHISPDRVYINYYDMNAANVGWNGSTFA
>d1hfoa_ d.80.1.3 (A:) Microphage migration inhibition factor (MIF)
{Trichina (Trichinella spiralis)}
PIFTLNTNIKATDVPSDFLSSTSALVGNILSKPGSYVAVHINTDQQLSFGGSTNPAAFGTLMSIG
GIEPSRNRDHSAKLFDHLNTKLGIPKNRMYIHFVNLNGDDVGWNGTTF
>d1dpta_ d.80.1.3 (A:) D-dopachrome tautomerase {Human (Homo
sapiens)}
PFLELDTNLPANRVPAGLEKRLCAAAASILGKPADRVNVTVRPGLAMALSGSTEPCAQLSISSIG
VVGTAEDNRSHSAHFFEFLTKELALGQDRILIRFFPLESWQIGKIGTVMTFL
>d1gado2 d.81.1.1 (O:149-312) Glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) {Escherichia coli}
CTTNCLAPLAKVINDNFGIIEGLMTTVHATTATQKTVDGPSHKDWRGGRGASQNIIPSSTGAAKA
VGKVLPELNGKLTGMAFRVPTPNVSVVDLTVRLEKAATYEQIKAAVKAAAEGEMKGVLGYTEDDV
VSTDFNGEVCTSVFDAKAGIALNDNFVKLVSWYD
>d1gd1o2 d.81.1.1 (O:149-312) Glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) {Bacillus stearothermophilus, nca 1503}
CTTNCLAPFAKVLHEQFGIVRGMMTTVHSYTNDQRILDLPHKDLRRARAAAESIIPTTTGAAKAV
ALVLPELKGKLNGMAMRVPTPNVSVVDLVAELEKEVTVEEVNAALKAAAEGELKGILAYSEEPLV
SRDYNGSTVSSTIDALSTMVIDGKMVKVVSWYD
>d1cero2 d.81.1.1 (O:149-312) Glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) {Thermus aquaticus}
CTTNSLAPVMKVLEEAFGVEKALMTTVHSYTNDQRLLDLPHKDLRRARAAAINIIPTTTGAAKAT
ALVLPSLKGRFDGMALRVPTATGSISDITALLKREVTAEEVNAALKAAAEGPLKGILAYTEDEIV
LQDIVMDPHSSIVDAKLTKALGNMVKVFAWYD
>d1hdgo2 d.81.1.1 (O:149-312) Glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) {Thermotoga maritima}
CTTNSIAPIVKVLHEKFGIVSGMLTTVHSYTNDQRVLDLPHKDLRRARAAAVNIIPTTTGAAKAV
ALVVPEVKGKLDGMAIRVPTPDGSITDLTVLVEKETTVEEVNAVMKEATEGRLKGIIGYNDEPIV
SSDIIGTTFSGIFDATITNVIGGKLVKVASWYD
>d1b7go2 d.81.1.1 (O:139-300) Glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) {Archaeon Sulfolobus solfataricus}
CNTTALLRTICTVNKVSKVEKVRATIVRRAADQKEVKKGPINSLVPDPATVPSHHAKDVNSVIRN
LDIATMAVIAPTTLMHMHFINITLKDKVEKKDILSVLENTPRIVLISSKYDAEATAELVEVARDL
KRDRNDIPEVMIFSDSIYVKDDEVMLMYAVHQ
>d1cf2o2 d.81.1.1 (O:139-303) Glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) {Archaeon Methanothermus fervidus}
SCNTTGLCRTLKPLHDSFGIKKVRAVIVRRGADPAQVSKGPINAIIPNPPKLPSHHGPDVKTVLD
INIDTMAVIVPTTLMHQHNVMVEVEETPTVDDIIDVFEDTPRVILISAEDGLTSTAEIMEYAKEL
GRSRNDLFEIPVWRESITVVDNEIYYMQAVHQESD
>d1ggaa2 d.81.1.1 (A:165-333) Glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) {Trypanosoma brucei brucei, glycosome}
CTTNCLAPLVHVLVKEGFGISTGLMTTVHSYTATQKTVDGVSVKDWRGGRAAALNIIPSTTGAAK
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AVGMVIPSTQGKLTGMAFRVPTADVSVVDLTFIATRDTSIKEIDAALKRASKTYMKNILGYTDEE
LVSADFISDSRSSIYDSKATLQNNLPNERRFFKIVSWYD
>d1i32a2 d.81.1.1 (A:166-334) Glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) {Leishmania mexicana}
CTTNCLAPIVHVLTKENFGIETGLMTTIHSYTATQKTVDGVSLKDWRGGRAAAVNIIPSTTGAAK
AVGMVIPSTKGKLTGMSFRVPTPDVSVVDLTFRATRDTSIQEIDKAIKKAAQTYMKGILGFTDEE
LVSADFINDNRSSVYDSKATLQNNLPGEKRFFKVVSWYD
>d1dssg2 d.81.1.1 (G:149-312) Glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) {Lobster (Palinurus versicolor)}
CTTNCLAPVAKVLHENFEIVEGLMTTVHAVTATQKTVDGPSAKDWRGGRGAAQNIIPSSTGAAKA
VGKVIPELDGKLTGMAFRVPTPNVSVVDLTVRLGKECSYDDIKAAMKAASEGPLQGVLGYTEDDV
VSCDFTGDNRSSIFDAKAGIQLSKTFVKVVSWYD
>d3gpdg2 d.81.1.1 (G:151-314) Glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) {Human (Homo sapiens)}
CTTNCLAPLAKVIHDHFGIVEGLMTTVHAITATQKTVDSPSGKLWRGGRGAAQNLIPASTGAAKA
VGKVIPELDGKLTGMAFRVPTANVSVLDLTCRLEKPAKYDDIKKVVKEASEGPLKGILGYTEDEV
VSDDFNGSNHSSIFDAGAGIELNDTFVKLVSWYD
>d1jn0a2 d.81.1.1 (A:149-312) Glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) {Spinach (Spinacia oleracea)}
CTTNCLAPFVKVLDQKFGIIKGTMTTTHSYTGDQRLLDASHRDLRRARAACLNIVPTSTGAAKAV
ALVLPQLKGKLNGIALRVPTPNVSVVDLVVQVSKKTFAEEVNAAFRESADQELKGILSVCDEPLV
SIDFRCTDVSSTIDSSLTMVMGDDMVKVIAWYD
>d1gl3a2 d.81.1.1 (A:134-354) Aspartate beta-semialdehyde
dehydrogenase {Escherichia coli}
NCTVSLMLMSLGGLFANDLVDWVSVATYQAASGGGARHMRELLTQMGHLYGHVADELATPSSAIL
DIERKVTTLTRSGELPVDNFGVPLAGSLIPWIDKQLDNGQSREEWKGQAETNKILNTSSVIPVDG
LCVRVGALRCHSQAFTIKLKKDVSIPTVEELLAAHNPWAKVVPNDREITMRELTPAAVTGTLTTP
VGRLRKLNMGPEFLSAFTVGDQLLWG
>d1ebfa2 d.81.1.2 (A:151-340) Homoserine dehydrogenase {Baker's yeast
(Saccharomyces cerevisiae)}
PIISFLREIIQTGDEVEKIEGIFSGTLSYIFNEFSTSQANDVKFSDVVKVAKKLGYTEPDPRDDL
NGLDVARKVTIVGRISGVEVESPTSFPVQSLIPKPLESVKSADEFLEKLSDYDKDLTQLKKEAAT
ENKVLRFIGKVDVATKSVSVGIEKYDYSHPFASLKGSDNVISIKTKRYTNPVVIQGAGAG
>d1e5qa2 d.81.1.2 (A:125-391) Saccharopine reductase {Rice blast
fungus (Magnaporthe grisea)}
LDPGIDHLYAIKTIEEVHAAGGKIKTFLSYCGGLPAPESSDNPLGYKFSWSSRGVLLALRNAASF
YKDGKVTNVAGPELMATAKPYFIYPGFAFVAYPNRDSTPYKERYQIPEADNIVRGTLRYQGFPQF
IKVLVDIGFLSDEEQPFLKEAIPWKEATQKIVKASSASEQDIVSTIVSNATFESTEEQKRIVAGL
KWLGIFSDKKITPRGNALDTLCATLEEKMQFEEGERDLVMLQHKFEIENKDGSRETRTSSLCEYG
APIGSGG
>d1f06a2 d.81.1.3 (A:119-268) Diaminopimelic acid dehydrogenase
(DAPDH) {Corynebacterium glutamicum}
WDPGMFSINRVYAAAVLAEHQQHTFWGPGLSQGHSDALRRIPGVQKAVQYTLPSEDALEKARRGE
AGDLTGKQTHKRQCFVVADAADHERIENDIRTMPDYFVGYEVEVNFIDEATFDSEHTGMPHGGHV
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ITTGDTGGFNHTVEYILKLD
>d1dih_2 d.81.1.3 (131-240) Dihydrodipicolinate reductase
{Escherichia coli}
VGVNVMLKLLEKAAKVMGDYTDIEIIEAHHRHKVDAPSGTALAMGEAIAHALDKDLKDCAVYSRE
GHTGERVPGTIGFATVRAGDIVGEHTAMFADIGERLEITHKASSR
>d1k5ha3 d.81.1.3 (A:126-274) 1-deoxy-D-xylulose-5-phosphate
reductoisomerase {Escherichia coli}
ESLVTCGRLFMDAVKQSKAQLLPVDSEHNAIFQSLPQPIQHNLGYADLEQNGVVSILLTGSGGPF
RETPLRDLATMTPDQACRHPNWSMGRKISVDSATMMNKGLEYIEARWLFNASASQMEVLIHPQSV
IHSMVRYQDGSVLAQLGEP
>d1gcua2 d.81.1.4 (A:129-246) Biliverdin reductase {Rat (Rattus
norvegicus)}
MEEFEFLRREVLGKELLKGSLRFTASPLEEERFGFPAFSGISRLTWLVSLFGELSLISATLEERK
EDQYMKMTVQLETQNKGLLSWIEEKGPGLKRNRYVNFQFTSGSLEEVPSVGVN
>d1h6da2 d.81.1.5 (A:213-374) Glucose-fructose oxidoreductase
{Zymomonas mobilis}
DPMNRAAVKLIRENQLGKLGMVTTDNSDVMDQNDPAQQWRLRRELAGGGSLMDIGIYGLNGTRYL
LGEEPIEVRAYTYSDPNDERFVEVEDRIIWQMRFRSGALSHGASSYSTTTTSRFSVQGDKAVLLM
DPATGYYQNLISVQTPGHANQSMMPQFIMPAN
>d1dpga2 d.81.1.5 (A:182-412,A:427-485) Glucose 6-phosphate
dehydrogenase {Leuconostoc mesenteroides}
KEMVQNIAALRFGNPIFDAAWNKDYIKNVQVTLSEVLGVEERAGYYDTAGALLDMIQNHTMQIVG
WLAMEKPESFTDKDIRAAKNAAFNALKIYDEAEVNKYFVRAQYGAGDSADFKPYLEELDVPADSK
NNTFIAGELQFDLPRWEGVPFYVRSGKRLAAKQTRVDIVFKAGTFNFGSEQEAQEAVLSIIIDPK
GAIELKLNAKSVEDAFNTRTIDLGWTVSDEDKKNTPXGSNFADWNGVSIAWKFVDAISAVYTADK
APLETYKSGSMGPEASDKLLAANGDAWVFKG
>d1qkia2 d.81.1.5 (A:200-434,A:450-511) Glucose 6-phosphate
dehydrogenase {Human (Homo sapiens)}
DHYLGKEMVQNLMVLRFANRIFGPIWNRDNIACVILTFKEPFGTEGRGGYFDEFGIIRDVMQNHL
LQMLCLVAMEKPASTNSDDVRDEKVKVLKCISEVQANNVVLGQYVGNPDGEGEATKGYLDDPTVP
RGSTTATFAAVVLYVENERWDGVPFILRCGKALNERKAEVRLQFHDVAGDIFHQQCKRNELVIRV
QPNEAVYTKMMTKKPGMFFNPEESELDLTYGNRYKNVKLPXMHFVRSDELLEAWRIFTPLLHQIE
LEKPKPIPYIYGSRGPTEADELMKRVGFQYEGTYKWVN
>d1oaca4 d.82.1.1 (A:5-90) Copper amine oxidase, domain N {Escherichia
coli}
AHMVPMDKTLKEFGADVQWDDYAQLFTLIKDGAYVKVKPGAQTAIVNGQPLALQVPVVMKDNKAW
VSDTFINDVFQSGLDQTFQVE
>d1ekga_ d.82.2.1 (A:) C-terminal domain of frataxin {Human (Homo
sapiens)}
LDETTYERLAEETLDSLAEFFEDLADKPYTFEDYDVSFGSGVLTVKLGGDLGTYVINKQTPNKQI
WLSSPSSGPKRYDWTGKNWVYSHDGVSLHELLAAELTKALKTKLDLSSLAYSGK
>d1ew4a_ d.82.2.1 (A:) CyaY {Escherichia coli}
MNDSEFHRLADQLWLTIEERLDDWDGDSDIDCEINGGVLTITFENGSKIIINRQEPLHQVWLATK
QGGYHFDLKGDEWICDRSGETFWDLLEQAATQQAGETVSFR
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>d1ewfa1 d.83.1.1 (A:1-217) Bactericidal permeability-increasing
protein, BPI {Human (Homo sapiens)}
VNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPS
SQISMVPNVGLKFSISNANIKISGKWKAQKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTI
TCSSCSSHINSVHVHISKSKVGWLIQLFHKKIESALRNKMNSQVCEKVTNSVSSELQPYFQTLPV
MTKIDSVAGINYGLVAPPATTA
>d1ewfa2 d.83.1.1 (A:218-456) Bactericidal permeability-increasing
protein, BPI {Human (Homo sapiens)}
ETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLVYQEAGVLKMTLRD
DMIPKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQPTGLTFYPAVDVQAFAVL
PNSALASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELKHSNIGPFPVELLQDIMNYIVPIL
VLPRVNEKLQKGFPLPTPARVQLYNVVLQPHQNFLLFGADVVYK
>d1ihra_ d.191.1.1 (A:) Dimeric C-terminal domain of membrane protein
TonB {Escherichia coli}
ARAQALRIEGQVKVKFDVTPDGRVDNVQILSAKPANMFEREVKNAMRRWRYEPGKPGSGIVVNIL
FKINGTTE
>d2sici_ d.84.1.1 (I:) Subtilisin inhibitor {Streptomyces
albogriseolus, s-3253}
YAPSALVLTVGKGVSATTAAPERAVTLTCAPGPSGTHPAAGSACADLAAVGGDLNALTRGEDVMC
PMVYDPVLLTVDGVWQGKRVSYERVFSNECEMNAHGSSVFAF
>d1e6ta_ d.85.1.1 (A:) MS2 virus coat protein {Bacteriophage MS2}
ASNFTQFVLVDNGGTGDVTVAPSNFANGVAEWISSNSRSQAYKVTCSVRQSSAQNRKYTIKVEVP
KVATQTVGGVELPVAAWRSYLNMELTIPIFATNSDCELIVKAMQGLLKDGNPIPSAIAANSGIY
>d1unaa_ d.85.1.1 (A:) GA coat protein {Bacteriophage GA}
ATLHSFVLVDNGGTGNVTVVPVSNANGVAEWLSNNSRSQAYRVTASYRASGADKRKYTIKLEVPK
IVTQVVNGVELPVSAWKAYASIDLTIPIFAATDDVTVISKSLTGLFKVGNPIAEAISSQSGFYA
>d1frsa_ d.85.1.1 (A:) fr coat protein {Bacteriophage FR}
ASNFEEFVLVDNGGTGDVKVAPSNFANGVAEWISSNSRSQAYKVTCSVRQSSANNRKYTVKVEVP
KVATQVQGGVELPVAAWRSYMNMELTIPVFATNDDCALIVKALQGTFKTGNPIATAIAANSGIY
>d1qbea_ d.85.1.1 (A:) Qbeta coat protein {Bacteriophage Qbeta}
AKLETVTLGNIGKDGKQTLVLNPRGVNPTNGVASLSQAGAVPALEKRVTVSVSQPSRNRKNYKVQ
VKIQNPTACTANGSCDPSVTRQAYADVTFSFTQYSTDEERAFVRTELAALLASPLLIDAIDQLNP
AY
>d1dwna_ d.85.1.1 (A:) PP7 coat protein {Bacteriophage PP7}
SKTIVLSVGEATRTLTEIQSTADRQIFEEKVGPLVGRLRLTASLRQNGAKTAYRVNLKLDQADVV
DCSTSVCGELPKVRYTQVWSHDVTIVANSTEASRKSLYDLTKSLVATSQVEDLVVNLVPLGR
>d1ej1a_ d.86.1.1 (A:) Translation initiation factor eIF4e {Mouse (Mus
musculus)}
KHPLQNRWALWFFKNDKSKTWQANLRLISKFDTVEDFWALYNHIQLSSNLMPGCDYSLFKDGIEP
MWEDEKNKRGGRWLITLNKQQRRSDLDRFWLETLLCLIGESFDDYSDDVCGAVVNVRAKGDKIAI
WTTECENRDAVTHIGRVYKERLGLPPKIVIGYQSHADTATKSGSTTKNRFVV
>d1ap8__ d.86.1.1 (-) Translation initiation factor eIF4e {Baker's
yeast (Saccharomyces cerevisiae)}
MSVEEVSKKFEENVSVDDTTATPKTVLSDSAHFDVKHPLNTKWTLWYTKPAVDKSESWSDLLRPV
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TSFQTVEEFWAIIQNIPEPHELPLKSDYHVFRNDVRPEWEDEANAKGGKWSFQLRGKGADIDELW
LRTLLAVIGETIDEDDSQINGVVLSIRKGGNKFALWTKSEDKEPLLRIGGKFKQVLKLTDDGHLE
FFPHSSANGRHPQPSITL
>d3grs_3 d.87.1.1 (364-478) Glutathione reductase {Human (Homo
sapiens)}
YNNIPTVVFSHPPIGTVGLTEDEAIHKYGIENVKTYSTSFTPMYHAVTKRKTKCVMKMVCANKEE
KVVGIHMQGLGCDEMLQGFAVAVKMGATKADFDNTVAIHPTSSEELVTLR
>d1gesa3 d.87.1.1 (A:336-450) Glutathione reductase {Escherichia
coli}
YSNIPTVVFSHPPIGTVGLTEPQAREQYGDDQVKVYKSSFTAMYTAVTTHRQPCRMKLVCVGSEE
KIVGIHGIGFGMDEMLQGFAVALKMGATKKDFDNTVAIHPTAAEEFVTMR
>d1feca3 d.87.1.1 (A:358-485) Trypanothione reductase {Crithidia
fasciculata}
HTKVACAVFSIPPMGVCGYVEEDAAKKYDQVAVYESSFTPLMHNISGSTYKKFMVRIVTNHADGE
VLGVHMLGDSSPEIIQSVAICLKMGAKISDFYNTIGVHPTSAEELCSMRTPAYFYEKGKRVEK
>d1aoga3 d.87.1.1 (A:358-487) Trypanothione reductase {Trypanosoma
cruzi}
DHTRVASAVFSIPPIGTCGLIEEVASKRYEVVAVYLSSFTPLMHKVSGSKYKTFVAKIITNHSDG
TVLGVHLLGDNAPEIIQGIGICLKLNAKISDFYNTIGVHPTSAEELCSMRTPSYYYVKGEKMEKP
>d1h6va3 d.87.1.1 (A:367-499) Mammalian thioredoxin reductase {Rat
(Rattus norvegicus)}
YDNVPTTVFTPLEYGCCGLSEEKAVEKFGEENIEVYHSFFWPLEWTVPSRDNNKCYAKVICNLKD
NERVVGFHVLGPNAGEVTQGFAAALKCGLTKQQLDSTIGIHPVCAEIFTTLSVTKRSGGDILQSG
CCG
>d1nhp_3 d.87.1.1 (322-447) NADH peroxidase {Enterococcus faecalis}
GVQGSSGLAVFDYKFASTGINEVMAQKLGKETKAVTVVEDYLMDFNPDKQKAWFKLVYDPETTQI
LGAQLMSKADLTANINAISLAIQAKMTIEDLAYADFFFQPAFDKPWNIINTAALEAVKQER
>d1d7ya3 d.87.1.1 (A:309-405) NADH-dependent ferredoxin reductase,
BphA4 {Pseudomonas sp., KKS102}
TAPGYAELPWYWSDQGALRIQVAGLASGDEEIVRGEVSLDAPKFTLIELQKGRIVGATCVNNARD
FAPLRRLLAVGAKPDRAALADPATDLRKLAAA
>d1lvl_3 d.87.1.1 (336-458) Dihydrolipoamide dehydrogenase
{Pseudomonas putida}
PAAIAAVCFTDPEVVVVGKTPEQASQQGLDCIVAQFPFAANGRAMSLESKSGFVRVVARRDNHLI
LGWQAVGVAVSELSTAFAQSLEMGACLEDVAGTIHAHPTLGEAVQEAALRALGHALHI
>d1lpfa3 d.87.1.1 (A:349-472) Dihydrolipoamide dehydrogenase
{Pseudomonas fluorescens}
YDLIPSVIYTHPEIAWVGKTEQTLKAEGVEVNVGTFPFAASGRAMAANDTTGLVKVIADAKTDRV
LGVHVIGPSAAELVQQGAIGMEFGTSAEDLGMMVFSHPTLSEALHEAALAVNGHAIHIA
>d3lada3 d.87.1.1 (A:349-472) Dihydrolipoamide dehydrogenase
{Azotobacter vinelandii}
YDLIPAVIYTHPEIAGVGKTEQALKAEGVAINVGVFPFAASGRAMAANDTAGFVKVIADAKTDRV
LGVHVIGPSAAELVQQGAIAMEFGTSAEDLGMMVFAHPALSEALHEAALAVSGHAIHVA
>d1ebda3 d.87.1.1 (A:347-461) Dihydrolipoamide dehydrogenase
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{Bacillus stearothermophilus}
AIPAVVFSDPECASVGYFEQQAKDEGIDVIAAKFPFAANGRALALNDTDGFLKLVVRKEDGVIIG
AQIIGPNASDMIAELGLAIEAGMTAEDIALTIHAHPTLGEIAMEAAEVAL
>d1ojt_3 d.87.1.1 (471-598) Dihydrolipoamide dehydrogenase
{Neisseria meningitidis}
ARVIPGVAYTSPEVAWVGETELSAKASARKITKANFPWAASGRAIANGCDKPFTKLIFDAETGRI
IGGGIVGPNGGDMIGEVCLAIEMGCDAADIGKTIHPHPTLGESIGMAAEVALGTCTDLPPQKK
>d1jeha3 d.87.1.1 (A:356-478) Dihydrolipoamide dehydrogenase
{Baker's yeast (Saccharomyces cerevisiae)}
YNNIPSVMYSHPEVAWVGKTEEQLKEAGIDYKIGKFPFAANSRAKTNQDTEGFVKILIDSKTERI
LGAHIIGPNAGEMIAEAGLALEYGASAEDVARVCHAHPTLSEAFKEANMAAYDKAIHC
>d1dxla3 d.87.1.1 (A:348-470) Dihydrolipoamide dehydrogenase {Garden
pea (Pisum sativum)}
YDKVPGVVYTNPEVASVGKTEEQVKETGVEYRVGKFPFMANSRAKAIDNAEGLVKIIAEKETDKI
LGVHIMAPNAGELIHEAAIALQYDASSEDIARVCHAHPTMSEAIKEAAMATYDKPIHI
>d1fcda3 d.87.1.1 (A:328-401) Flavocytochrome c sulfide dehydrogenase,
FCSD, flavin-binding subunit {Purple phototrophic bacterium
(Chromatium vinosum)}
PGTPSYLNTCYSILAPAYGISVAAIYRPNADGSAIESVPDSGGVTPVDAPDWVLEREVQYAYSWY
NNIVHDTFG
>d1qj2c1 d.87.2.1 (C:178-285) Carbon monoxide (CO) dehydrogenase
flavoprotein, C-terminal domain {Pseudomonas carboxydovorans}
GHGYAYEKLKRKIGDYATAAAAVVLTMSGGKCVTASIGLTNVANTPLWAEEAGKVLVGTALDKPA
LDKAVALAEAITAPASDGRGPAEYRTKMAGVMLRRAVERAKAR
>d1ffvc1 d.87.2.1 (C:178-287) Carbon monoxide (CO) dehydrogenase
flavoprotein, C-terminal domain {Hydrogenophaga pseudoflava}
GTGWAYEKLKRKTGDWATAGCAVVMRKSGNTVSHIRIALTNVAPTALRAEAAEAALLGKAFTKEA
VQAAADAAIAICEPAEDLRGDADYKTAMAGQMVKRALNAAWARCA
>d1fo4a4 d.87.2.1 (A:415-531) Xanthine oxidase, domain 4 (?) {Cow (Bos
taurus)}
DEFFSAFKQASRREDDIAKVTCGMRVLFQPGSMQVKELALCYGGMADRTISALKTTQKQLSKFWN
EKLLQDVCAGLAEELSLSPDAPGGMIEFRRTLTLSFFFKFYLTVLKKLGKDS
>d1jroa3 d.87.2.1 (A:346-462) Xanthine dehydrogenase chain A, domain
4 {Rhodobacter capsulatus}
PGLRCYKLSKRFDQDISAVCGCLNLTLKGSKIETARIAFGGMAGVPKRAAAFEAALIGQDFREDT
IAAALPLLAQDFTPLSDMRASAAYRMNAAQAMALRYVRELSGEAVAVLEVMP
>d1srsa_ d.88.1.1 (A:) Serum response factor (SRF) core {Human (Homo
sapiens)}
TRGRVKIKMEFIDNKLRRYTTFSKRKTGIMKKAYELSTLTGTQVLLLVASETGHVYTFATRKLQP
MITSETGKALIQTCLNSPD
>d1mnma_ d.88.1.1 (A:) MCM1 transcriptional regulator {Baker's yeast
(Saccharomyces cerevisiae)}
QKERRKIEIKFIENKTRRHVTFSKRKHGIMKKAFELSVLTGTQVLLLVVSETGLVYTFSTPKFEP
IVTQQEGRNLIQACLNAPDD
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>d1egwa_ d.88.1.1 (A:) Mef2a core {Human (Homo sapiens)}
GRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVL
LKYTEY
>d1tbd__ d.89.1.1 (-) The origin DNA-binding domain of SV40 T-antigen
{Simian virus 40}
GSKVEDPKDFPSELLSFLSHAVFSNRTLACFAIYTTKEKAALLYKKIMEKYSVTFISRHNSYNHN
ILFFLTPHRHRVSAINNYAQKLCTFSFLICKGVNKEYLMYSALTRDPFSVIEESLPGGLKEHDFN
PESS
>d1f08a_ d.89.1.2 (A:) Replication initiation protein E1 {Bovine
papillomavirus}
GSRATVFKLGLFKSLFLCSFHDITRLFKNDKTTNQQWVLAVFGLAEVFFEASFELLKKQCSFLQM
QKRSHEGGTCAVYLICFNTAKSRETVRNLMANMLNVREECLMLQPPKIRGLSAALFWFKSSLSPA
TLKHGALPEWIRAQTTLN
>d1nox__ d.90.1.1 (-) NADH oxidase {Thermus thermophilus, HB8}
PVLDAKTAALKRRSIRRYRKDPVPEGLLREILEAALRAPSAWNLQPWRIVVVRDPATKRALREAA
FGQAHVEEAPVVLVLYADLEDALAHLDEVIHPGVQGERREAQKQAIQRAFAAMGQEARKAWASGQ
SYILLGYLLLLLEAYGLGSVPMLGFDPERVRAILGLPSRAAIPALVALGYPAEEGYPSHRLPLER
VVLWR
>d1bkja_ d.90.1.1 (A:) Flavin reductase P (NADPH:FMN oxidoreductase)
{Vibrio harveyi}
NNTIETILAHRSIRKFTAVPITDEQRQTIIQAGLAASSSSMLQVVSIVRVTDSEKRNELAQFAGN
QAYVESAAEFLVFCIDYQRHATINPDVQADFTELTLIGAVDSGIMAQNCLLAAESMGLGGVYIGG
LRNSAAQVDELLGLPENSAVLFGMCLGHPDQNPEVKPRLPAHVVVHENQYQELNLDDIQSYDQTM
QAYYASRTSNQKLSTWSQEVTGKLAGESRPHILPYLNSKGLAKR
>d1vfra_ d.90.1.1 (A:) Flavin reductase P (NADPH:FMN oxidoreductase)
{Vibrio fischeri}
THPIIHDLENRYTSKKYDPSKKVSQEDLAVLLEALRLSASSINSQPWKFIVIESDAAKQRMHDSF
ANMHQFNQPHIKACSHVILFANKLSYTRDDYDVVLSKAVADKRITEEQKEAAFASFKFVELNCDE
NGEHKAWTKPQAYLALGNALHTLARLNIDSTTMEGIDPELLSEIFADELKGYECHVALAIGYHHP
SEDYNASLPKSRKAFEDVITIL
>d1kqba_ d.90.1.1 (A:) Nitroreductase {Enterobacter cloacae}
DIISVALKRHSTKAFDASKKLTAEEAEKIKTLLQYSPSSTNSQPWHFIVASTEEGKARVAKSAAG
TYVFNERKMLDASHVVVFCAKTAMDDAWLERVVDQEEADGRFNTPEAKAANHKGRTYFADMHRVD
LKDDDQWMAKQVYLNVGNFLLGVGAMGLDAVPIEGFDAAILDEEFGLKEKGFTSLVVVPVGHHSV
EDFNATLPKSRLPLSTIVTEC
>d1icra_ d.90.1.1 (A:) Nitroreductase {Escherichia coli, minor form}
DIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVAKSAAG
NYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKGRKFFADMHRKD
LHDDAEWMAKQVYLNVGNFLLGVAALGLDAVPIEGFDAAILDAEFGLKEKGYTSLVVVPVGHHSV
EDFNATLPKSRLPQNITLTEV
>d1f5va_ d.90.1.1 (A:) Nitroreductase {Escherichia coli,
oxygen-insensitive form}
MTPTIELICGHRSIRHFTDEPISEAQREAIINSARATSSSSFLQCSSIIRITDKALREELVTLTG
GQKHVAQAAEFWVFCADFNRHLQICPDAQLGLAEQLLLGVVDTAMMAQNALIAAESLGLGGVYIG
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GLRNNIEAVTKLLKLPQHVLPLFGLCLGWPADNPDLKPRLPASILVHENSYQPLDKGALAQYDEQ
LAEYYLTRGSNNRRDTWSDHIRRTIIKESRPFILDYLHKQGWATR
>d1dt9a3 d.91.1.1 (A:5-142) N-terminal domain of eukaryotic peptide
chain release factor subunit 1, ERF1 {Human (Homo sapiens)}
PSAADRNVEIWKIKKLIKSLEAARGNGTSMISLIIPPKDQISRVAKMLADEFGTASNIKSRVNRL
SVLGAITSVQQRLKLYNKVPPNGLVVYCGTIVTEEGKEKKVNIDFEPFKPINTSLYLCDNKFHTE
ALTALLSD
>d1c7ka_ d.92.1.1 (A:) Zinc protease {Streptomyces caespitosus}
TVTVTYDPSNAPSFQQEIANAAQIWNSSVRNVQLRAGGNADFSYYEGNDSRGSYAQTDGHGRGYI
FLDYQQNQQYDSTRVTAHETGHVLGLPDHYQGPCSELMSGGGPGPSCTNPYPNAQERSRVNALWA
NG
>d1g12a_ d.92.1.12 (A:) Fungal zinc peptidase {Grifola frondosa}
TYNGCSSSEQSALAAAASAAQSYVAESLSYLQTHTAATPRYTTWFGSYISSRHSTVLQHYTDMNS
NDFSSYSFDCTCTAAGTFAYVYPNRFGTVYLCGAFWKAPTTGTDSQAGTLVHESSHFTRNGGTKD
YAYGQAAAKSLATMDPDKAVMNADNHEYFSENNPAQS
>d1eb6a_ d.92.1.12 (A:) Fungal zinc peptidase {Aspergillus oryzae,
deuterolysin}
TEVTDCKGDAESSLTTALSNAAKLANQAAEAAESGDESKFEEYFKTTDQQTRTTVAERLRAVAKE
AGSTSGGSTTYHCNDPYGYCEPNVLAYTLPSKNEIANCDIYYSELPPLAQKCHAQDQATTTLHEF
THAPGVYQPGTEDLGYGYDAATQLSAQDALNNADSYALYANAIELKC
>d1ezm__ d.92.1.2 (-) Elastase {Pseudomonas aeruginosa}
AEAGGPGGNQKIGKYTYGSDYGPLIVNDRCEMDDGNVITVDMNSSTDDSKTTPFRFACPTNTYKQ
VNGAYSPLNDAHFFGGVVFKLYRDWFGTSPLTHKLYMKVHYGRSVENAYWDGTAMLFGDGATMFY
PLVSLDVAAHEVSHGFTEQNSGLIYRGQSGGMNEAFSDMAGEAAEFYMRGKNDFLIGYDIKKGSG
ALRYMDQPSRDGRSIDNASQYYNGIDVHHSSGVYNRAFYLLANSPGWDTRKAFEVFVDANRYYWT
ATSNYNSGACGVIRSAQNRNYSAADVTRAFSTVGVTCP
>d8tlne_ d.92.1.2 (E:) Thermolysin {Bacillus thermoproteolyticus}
ITGTSTVGVGRGVLGDQKNINTTYSTYYYLQDNTRGDGIFTYDAKYRTTLPGSLWADADNQFFAS
YDAPAVDAHYYAGVTYDYYKNVHNRLSYDGNNAAIRSSVHYSQGYNNAFWNGSEMVYGDGDGQTF
IPLSGGIDVVAHELTHAVTDYTAGLIYQNESGAINEAISDIFGTLVEFYANKNPDWEIGEDVYTP
GISGDSLRSMSDPAKYGDPDHYSKRYTGTQDNGGVHINSGIINKAAYLISQGGTHYGVSVVGIGR
DKLGKIFYRALTQYLTPTSNFSQLRAAAVQSATDLYGSTSQEVASVKQAFDAVGVK
>d1npc__ d.92.1.2 (-) Neutral protease {Bacillus cereus, strain dsm
3101}
VTGTNKVGTGKGVLGDTKSLNTTLSGSSYYLQDNTRGATIFTYDAKNRSTLPGTLWADADNVFNA
AYDAAAVDAHYYAGKTYDYYKATFNRNSINDAGAPLKSTVHYGSNYNNAFWNGSQMVYGDGDGVT
FTSLSGGIDVIGHELTHAVTENSSNLIYQNESGALNEAISDIFGTLVEFYDNRNPDWEIGEDIYT
PGKAGDALRSMSDPTKYGDPDHYSKRYTGSSDNGGVHTNSGIINKQAYLLANGGTHYGVTVTGIG
KDKLGAIYYRANTQYFTQSTTFSQARAGAVQAAADLYGANSAEVAAVKQSFSAVGVN
>d1bqba_ d.92.1.2 (A:) Aureolysin {Staphylococcus aureus}
AAATGTGKGVLGDTKDININSIDGGFSLEDLTHQGKLSAYNFNDQTGQATLITNEDENFVKDDQR
AGVDANYYAKQTYDYYKNTFGRESYDNHGSPIVSLTHVNHYGGQDNRNNAAWIGDKMIYGDGDGR
TFTNLSGANDVVAHEITHGVTQQTANLEYKDQSGALNESFSDVFGYFVDDEDFLMGEDVYTPGKE
GDALRSMSNPEQFGQPSHMKDYVYTEKDNGGVHTNSGIPNKAAYNVIQAIGKSKSEQIYYRALTE
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YLTSNSNFKDLKDALYQAAKDLYEQQTAEQVYEAWNEVGVE
>d1hs6a3 d.92.1.13 (A:209-460) Leukotriene A4 hydrolase catalytic domain {Human (Homo sapiens)}
LESRQIGPRTLVWSEKEQVEKSAYEFSETESMLKIAEDLGGPYVWGQYDLLVLPPSFPYGGMENP
CLTFVTPTLLAGDKSLSNVIAHEISHSWTGNLVTNKTWDHFWLNEGHTVYLERHICGRLFGEKFR
HFNALGGWGELQNSVKTFGETHPFTKLVVDLTDIDPDVAYSSVPYEKGFALLFYLEQLLGGPEIF
LGFLKAYVEKFSYKSITTDDWKDFLYSYFKDKVDVLNQVDWNAWLYSPGLPPIKPNY
>d1dmta_ d.92.1.4 (A:) Neutral endopeptidase (neprilysin) {Human (Homo sapiens)}
GICKSSDCIKSAARLIQNMDATTEPCTDFFKYACGGWLKRNVIPETSSRYGNFDILRDELEVVLK
DVLQEPKTEDIVAVQKAKALYRSCINESAIDSRGGEPLLKLLPDIYGWPVATENWEQKYGASWTA
EKAIAQLNSKYGKKVLINLFVGTDDKNSVNHVIHIDQPRLGLPSRDYYECTGIYKEACTAYVDFM
ISVARLIRQEERLPIDENQLALEMNKVMELEKEIANATAKPEDRNDPMLLYNKMTLAQIQNNFSL
EINGKPFSWLNFTNEIMSTVNISITNEEDVVVYAPEYLTKLKPILTKYSARDLQNLMSWRFIMDL
VSSLSRTYKESRNAFRKALYGTTSETATWRRCANYVNGNMENAVGRLYVEAAFAGESKHVVEDLI
AQIREVFIQTLDDLTWMDAETKKRAEEKALAIKERIGYPDDIVSNDNKLNNEYLELNYKEDEYFE
NIIQNLKFSQSKQLKKLREKVDKDEWISGAAVVNAFYSSGRNQIVFPAGILQPPFFSAQQSNSLN
YGGIGMVIGHEITHGFDDNGRNFNKDGDLVDWWTQQSASNFKEQSQCMVYQYGNFSWDLAGGQHL
NGINTLGENIADNGGLGQAYRAYQNYIKKNGEEKLLPGLDLNHKQLFFLNFAQVWCGTYRPEYAV
NSIKTDVHSPGNFRIIGTLQNSAEFSEAFHCRKNSYMNPEKKCRVW
>d1i1ip_ d.92.1.5 (P:) Neurolysin (endopeptidase 24.16) {Rat (Rattus norvegicus)}
MSSYTAAGRNVLRWDLSPEQIKTRTEQLIAQTKQVYDTVGTIALKEVTYENCLQVLADIEVTYIV
ERTMLDFPQHVSSDREVRAASTEADKKLSRFDIEMSMREDVFQRIVHLQETCDLEKIKPEARRYL
EKSIKMGKRNGLHLSEHIRNEIKSMKKRMSELCIDFNKNLNEDDTSLVFSKAELGALPDDFIDSL
EKTDEDKYKVTLKYPHYFPVMKKCCVPETRRKMEMAFHTRCKQENTAILQQLLPLRAQVAKLLGY
NTHADFVLELNTAKSTSRVAAFLDDLSQKLKPLGEAEREFILSLKKKECEERGFEYDGKINAWDL
HYYMTQTEELKYSVDQESLKEYFPIEVVTEGLLSIYQELLGLSFEQVPDAHVWNKSVSLYTVKDK
ATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSRMMSVAALVVNFSQPVAGRPSLLRHDE
VRTYFHEFGHVMHQICAQTDFARFSGTNVETDFVEVPSQMLENWVWDVDSLRKLSKHYKDGHPIT
DELLEKLVASRLVNTGLLTLRQIVLSKVDQSLHTNATLDAASEYAKYCTEILGVAATPGTNMPAT
FGHLAGGYDGQYYGYLWSEVFSMDMFHSCFKKEGIMNPEVGMKYRNLILKPGGSLDGMDMLQNFL
QREPNQKAFLMSRGL
>d1j7na1 d.92.1.14 (A:27-263) Anthrax toxin lethal factor, N- and C-terminal domains {Bacillus anthracis}
ERNKTQEEHLKEIMKHIVKIEVKGEEAVKKEAAEKLLEKVPSDVLEMYKAIGGKIYIVDGDITKH
ISLEALSEDKKKIKDIYGKDALLHEHYVYAKEGYEPVLVIQSSEDYVENTEKALNVYYEIGKILS
RDILSKINQPYQKFLDVLNTIKNASDSDGQDLLFTNQLKEHPTDFSVEFLEQNSNEVQEVFAKAF
AYYIEPQHRDVLQLYAPEAFNYMDKFNEQEINLSLEELKDQR
>d1j7na2 d.92.1.14 (A:551-773) Anthrax toxin lethal factor, N- and C-terminal domains {Bacillus anthracis}
PKSKIDTKIQEAQLNINQEWNKALGLPKYTKLITFNVHNRYASNIVESAYLILNEWKNNIQSDLI
KKVTNYLVDGNGRFVFTDITLPNIAEQYTHQDEIYEQVHSKGLYVPESRSILLHGPSKGVELRND
SEGFIHEFGHAVDDYAGYLLDKNQSDLVTNSKKFIDIFKEEGSNLTSYGRTNEAEFFAEAFRLMH

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STDHAERLKVQKNAPKTFQFINDQIKFI
>d1lml__ d.92.1.3 (-) Leishmanolysin {Leishmania major}
VVRDVNWGALRIAVSTEDLTDPAYHCARVGQHVKDHAGAIVTCTAEDILTNEKRDILVKHLIPQA
VQLHTERLKVQQVQGKWKVTDMVGDICGDFKVPQAHITEGFSNTDFVMYVASVPSEEGVLAWATT
CQTFSDGHPAVGVINIPAANIASRYDQLVTRVVTHEMAHALGFSGPFFEDARIVANVPNVRGKNF
DVPVINSSTAVAKAREQYGCDTLEYLEVEDQGGAGSAGSHIKMRNAQDELMAPAAAAGYYTALTM
AIFQDLGFYQADFSKAEVMPWGQNAGCAFLTNKCMEQSVTQWPAMFCNESEDAIRCPTSRLSLGA
CGVTRHPGLPPYWQYFTDPSLAGVSAFMDYCPVVVPYSDGSCTQRASEAHASLLPFNVFSDAARC
IDGAFRPKATDGIVKSYAGLCANVQCDTATRTYSVQVHGSNDYTNCTPGLRVELSTVSNAFEGGG
YITCPPYVEVCQGNVQAAKD
>d1kapp2 d.92.1.6 (P:1-246) Metallo protease, catalytic (N-terminal)
domain {Pseudomonas aeruginosa, alkaline protease}
GRSDAYTQVDNFLHAYARGGDELVNGHPSYTVDQAAEQILREQASWQKAPGDSVLTLSYSFLTKP
NDFFNTPWKYVSDIYSLGKFSAFSAQQQAQAKLSLQSWSDVTNIHFVDAGQGDQGDLTFGNFSSS
VGGAAFAFLPDVPDALKGQSWYLINSSYSANVNPANGNYGRQTLTHEIGHTLGLSHPGDYNAGEG
DPTYADATYAEDTRAYSVMSYWEEQNTGQDFKGAYSSAPLLDDIAAIQKLY
>d1sat_2 d.92.1.6 (4-246) Metallo protease, catalytic (N-terminal)
domain {Serratia marcescens}
TGYDAVDDLLHYHERGNGIQINGKDSFSNEQAGLFITRENQTWNGYKVFGQPVKLTFSFPDYKFS
STNVAGDTGLSKFSAEQQQQAKLSLQSWADVANITFTEVAAGQKANITFGNYSQDRPGHYDYGTQ
AYAFLPNTIWQGQDLGGQTWYNVNQSNVKHPATEDYGRQTFTHEIGHALGLSHPGDYNAGEGDPT
YADVTYAEDTRQFSLMSYWSETNTGGDNGGHYAAAPLLDDIAAIQHLY
>d3btaa3 d.92.1.7 (A:1-546) Botulinum neurotoxin {Clostridium
botulinum, serotype A}
PFVNKQFNYKDPVNGVDIAYIKIPNVGQMQPVKAFKIHNKIWVIPERDTFTNPEEGDLNPPPEAK
QVPVSYYDSTYLSTDNEKDNYLKGVTKLFERIYSTDLGRMLLTSIVRGIPFWGGSTIDTELKVID
TNCINVIQPDGSYRSEELNLVIIGPSADIIQFECKSFGHEVLNLTRNGYGSTQYIRFSPDFTFGF
EESLEVDTNPLLGAGKFATDPAVTLAHELIHAGHRLYGIAINPNRVFKVNTNAYYEMSGLEVSFE
ELRTFGGHDAKFIDSLQENEFRLYYYNKFKDIASTLNKAKSIVGTTASLQYMKNVFKEKYLLSED
TSGKFSVDKLKFDKLYKMLTEIYTEDNFVKFFKVLNRKTYLNFDKAVFKINIVPKVNYTIYDGFN
LRNTNLAANFNGQNTEINNMNFTKLKNFTGLFEFYKLLCVRGIITSKTKSLDKGYNKALNDLCIK
VNNWDLFFSPSEDNFTNDLNKGEEITSDTNIEAAEENISLDLIQQYYLTFNFDNEPENISIENLS
SDIIGQLELMPNIERFPNGKKYELDK
>d1epwa3 d.92.1.7 (A:1-533) Botulinum neurotoxin {Clostridium
botulinum, serotype B}
PVTINNFNYNDPIDNNNIIMMEPPFARGTGRYYKAFKITDRIWIIPERYTFGYKPEDFNKSSGIF
NRDVCEYYDPDYLNTNDKKNIFLQTMIKLFNRIKSKPLGEKLLEMIINGIPYLGDRRVPLEEFNT
NIASVTVNKLISNPGEVERKKGIFANLIIFGPGPVLNENETIDIGIQNHFASREGFGGIMQMKFC
PEYVSVFNNVQENKGASIFNRRGYFSDPALILMHELIHVLHGLYGIKVDDLPIVPNEKKFFMQST
DAIQAEELYTFGGQDPSIITPSTDKSIYDKVLQNFRGIVDRLNKVLVCISDPNININIYKNKFKD
KYKFVEDSEGKYSIDVESFDKLYKSLMFGFTETNIAENYKIKTRASYFSDSLPPVKIKNLLDNEI
YTIEEGFNISDKDMEKEYRGQNKAINKQAYEEISKEHLAVYKIQMCKSVKAPGICIDVDNEDLFF
IADKNSFSDDLSKNERIEYNTQSNYIENDFPINELILDTDLISKIELPSENTESLTDFNVDVPVY
EKQPAIKKIFTDE
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>d1f83a_ d.92.1.7 (A:) Botulinum neurotoxin {Clostridium botulinum, serotype B}
PVTINNFNYNDPIDNNNIIMMEPPFARGTGRYYKAFKITDRIWIIPERYTFGYKPEDFNKSSGIF
NRDVCEYYDPDYLNTNDKKNIFLQTMIKLFNRIKSKPLGEKLLEMIINGIPYLGDRRVPLEEFNT
NIASVTVNKLISNPGEVERKKGIFANLIIFGPGPVLNENETIDIGIQNHFASREGFGGIMQMKFC
PEYVSVFNNVQENKGASIFNRRGYFSDPALILMHELIHVLHGLYGIKVDDLPIVPNEKKFFMQST
DAIQAEELYTFGGQDPSIITPSTDKSIYDKVLQNFRGIVDRLNKVLVCISDPNININIYKNKFKD
KYKFVEDSEGKYSIDVESFDKLYKSLMFGFTETNIAENYKIKTRASYFSDSLPPVKIKNLLDNEI
YTIEEGFNISDKDMEKEYRGQNKAINKQAYEEISK
>d1ast__ d.92.1.8 (-) Astacin {European fresh water crayfish (Astacus astacus)}
AAILGDEYLWSGGVIPYTFAGVSGADQSAILSGMQELEEKTCIRFVPRTTESDYVEIFTSGSGCW
SYVGRISGAQQVSLQANGCVYHGTIIHELMHAIGFYHEHTRMDRDNYVTINYQNVDPSMTSNFDI
DTYSRYVGEDYQYYSIMHYGKYSFSIQWGVLETIVPLQNGIDLTDPYDKAHMLQTDANQINNLYT
NECSL
>d4aig__ d.92.1.9 (-) Snake venom metalloprotease {Eastern diamondback rattlesnake (Crotalus adamanteus), adamalysin II}
NLPQRYIELVVVADRRVFMKYNSDLNIIRTRVHEIVNIINEFYRSLNIRVSLTDLEIWSGQDFIT
IQSSSSNTLNSFGEWRERVLLTRKRHDNAQLLTAINFEGKIIGKAYTSSMCNPRSSVGIVKDHSP
INLLVAVTMAHELGHNLGMEHDGKDCLRGASLCIMRPGLTPGRSYEFSDDSMGYYQKFLNQYKPQ
CILNKP
>d1atla_ d.92.1.9 (A:) Snake venom metalloprotease {Western diamonback rattlesnake (Crotalus atrox), atrolysin C}
LPQRYIELVVVADHRVFMKYNSDLNTIRTRVHEIVNFINGFYRSLNIHVSLTDLEIWSNEDQINI
QSASSDTLNAFAEWRETDLLNRKSHDNAQLLTAIELDEETLGLAPLGTMCDPKLSIGIVQDHSPI
NLLMGVTMAHELGHNLGMEHDGKDCLRGASLCIMRPGLTKGRSYEFSDDSMHYYERFLKQYKPQC
ILNKP
>d1buda_ d.92.1.9 (A:) Snake venom metalloprotease {Five-pace snake (Agkistrodon acutus), acutolysin A}
FQRYMEIVIVVDHSMVKKYNGDSDSIKAWVYEMINTITESYSYLKIDISLSGLEIWSGKDLIDVE
ASAGNTLKSFGEWRAKDLIHRISHDNAQLLTATDFDGATIGLAYVASMCNPKRSVGVIQDHSSVN
RLVAITLAHEMAHNLGVSHDEGSCSCGGKSCIMSPSISDETIKYFSDCSYIQCRDYISKENPPCI
LN
>d1quaa_ d.92.1.9 (A:) Snake venom metalloprotease {Chinese five-pace snake (Agkistrodon acutus), acutolysin C}
PAPQTSIELFLIVDHSMYAKYNSNSSKITTTLKARVNIMNAIYSSLNLVITLSGIEMWSAADLIT
VQSSSRNTLKLFASWRETDLLKRTSNDNAQLLTATNFNGNTVGLAYLKTMCNSKYSVGLIQDHSA
IPLLMAVTMAHELGHNLGMNHDGAGCSCATCIMAPVLSSGPAKSFSDCSKHDYQSFLTIHKPQCL
LN
>d1bkca_ d.92.1.10 (A:) TNF-alpha converting enzyme, TACE, catalytic domain {Human (Homo sapiens)}
DPMKNTCKLLVVADHRFYRYMGRGEESTTTNYLIELIDRVDDIYRNTAWDNAGFKGYGIQIEQIR
ILKSPQEVKPGEKHYNMAKSYPNEEKDAWDVKMLLEQFSFDIAEEASKVCLAHLFTYQDFDMGTL
GLAYVGSPRANSHGGVCPKAYYSPVGKKNIYLNSGLTSTKNYGKTILTKEADLVTTHELGHNFGA
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EHDPDGLAECAPNEDQGGKYVMYPIAVSGDHENNKMFSQCSKQSIYKTIESKAQECFQER
>d1cgla_ d.92.1.11 (A:) Fibroblast collagenase (MMP-1) {Human (Homo
sapiens)}
VLTEGNPRWEQTHLRYRIENYTPDLPRADVDHAIEKAFQLWSDVTPLTFTKVSEGQADIMISFVR
GDHRDNSPFDGPGGNLAHAFDPGPGIGGDAHFDEDERWTNNFREYNLHRVAAHELGHSLGLSHST
DIGALMYPSYTFSGDVQLAQDDIDGIQAIYGRSQNPVQ
>d1hfc__ d.92.1.11 (-) Fibroblast collagenase (MMP-1) {Human (Homo
sapiens)}
PRWEQTHLTYRIENYTPDLPRADVDHAIEKAFQLWSNVTPLTFTKVSEGQADIMISFVRGDHRDN
SPFDGPGGNLAHAFQPGPGIGGDAHFDEDERWTNNFREYNLHRVAAHELGHSLGLSHSTDIGALM
YPSYTFSGDVQLAQDDIDGIQAIYGRS
>d1fbl_2 d.92.1.11 (100-271) Fibroblast collagenase (MMP-1) {Pig (Sus
scrofa)}
FVLTPGNPRWENTHLTYRIENYTPDLSREDVDRAIEKAFQLWSNVSPLTFTKVSEGQADIMISFV
RGDHRDNSPFDGPGGNLAHAFQPGPGIGGDAHFDEDERWTKNFRDYNLYRVAAHELGHSLGLSHS
TDIGALMYPNYIYTGDVQLSQDDIDGIQAIYGPSENPVQPSG
>d1hova_ d.92.1.11 (A:) MMP-2 {Human (Homo sapiens)}
MYNFFPRKPKWDKNQITYRIIGYTPDLDPETVDDAFARAFQVWSDVTPLRFSRIHDGEADIMINF
GRWEHGDGYPFDGKDGLLAHAFAPGTGVGGDSHFDDDELWTNTSANYSLFLVAAHEFGHAMGLEH
SQDPGALMAPIYTYTKNFRLSQDDIKGIQELYG
>d1i76a_ d.92.1.11 (A:) Neutrophil collagenase (MMP-8) {Human (Homo
sapiens)}
MLTPGNPKWERTNLTYRIRNYTPQLSEAEVERAIKDAFELWSVASPLIFTRISQGEADINIAFYQ
RDHGDNSPFDGPNGILAHAFQPGQGIGGDAHFDAEETWTNTSANYNLFLVAAHEFGHSLGLAHSS
DPGALMYPNYAFRETSNYSLPQDDIDGIQAIYG
>d1qiba_ d.92.1.11 (A:) Gelatinase A {Human (Homo sapiens)}
RKPKWDKNQITYRIIGYTPDLDPETVDDAFARAFQVWSDVTPLRFSRIHDGEADIMINFGRWEHG
DGYPFDGKDGLLAHAFAPGTGVGGDSHFDDDELWSLGKGVGYSLFLVAAHEFGHAMGLEHSQDPG
ALMAPIYTYTKNFRLSQDDIKGIQELYGASP
>d1hy7a_ d.92.1.11 (A:) Stromelysin-1 (MMP-3) {Human (Homo sapiens),
fibroblast}
FRTFPGIPKWRKTHLTYRIVNYTPDLPKDAVDSAVEKALKVWEEVTPLTFSRLYEGEADIMISFA
VREHGDFYPFDGPGNVLAHAYAPGPGINGDAHFDDDEQWTKDTTGTNLFLVAAHEIGHSLGLFHS
ANTEALMYPLYHSLTDLTRFRLSQDDINGIQSLYGPPP
>d1mmq__ d.92.1.11 (-) Matrilysin (MMP-9) {Human (Homo sapiens)}
YSLFPNSPKWTSKVVTYRIVSYTRDLPHITVDRLVSKALNMWGKEIPLHFRKVVWGTADIMIGFA
RGAHGDSYPFDGPGNTLAHAFAPGTGLGGDAHFDEDERWTDGSSLGINFLYAATHELGHSLGMGH
SSDPNAVMYPTYGNGDPQNFKLSQDDIKGIQKLYGK
>d1hv5a_ d.92.1.11 (A:) Stromelysin-3 (MMP-11) {Mouse (Mus musculus)}
MFVLSGGRWEKTDLTYRILRFPWQLVREQVRQTVAEALQVWSEVTPLTFTEVHEGRADIMIDFAR
YWHGDNLPFDGPGGILAHAFFPKTHREGDVHFDYDETWTIGDNQGTDLLQVAAHEFGHVLGLQHT
TAAKALMSPFYTFRYPLSLSPDDRRGIQHLYG
>d1jk3a_ d.92.1.11 (A:) Macrophage elastase (MMP-12) {Human (Homo
sapiens)}
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GPVWRKHYITYRINNYTPDMNREDVDYAIRKAFQVWSNVTPLKFSKINTGMADILVVFARGAHGD
FHAFDGKGGILAHAFGPGSGIGGDAHFDEDEFWTTHSGGTNLFLTAVHAIGHSLGLGHSSDPKAV
MFPTYKYVDINTFRLSADDIRGIQSLYG
>d830ca_ d.92.1.11 (A:) Collagenase-3 (MMP-13) {Human (Homo sapiens)}
YNVFPRTLKWSKMNLTYRIVNYTPDMTHSEVEKAFKKAFKVWSDVTPLNFTRLHDGIADIMISFG
IKEHGDFYPFDGPSGLLAHAFPPGPNYGGDAHFDDDETWTSSSKGYNLFLVAAHEFGHSLGLDHS
KDPGALMFPIYTYTGKSHFMLPDDDVQGIQSLYGPGDE
>d1cxva_ d.92.1.11 (A:) Collagenase-3 (MMP-13) {Mouse (Mus musculus)}
YNVFPRTLKWSQTNLTYRIVNYTPDMSHSEVEKAFRKAFKVWSDVTPLNFTRIYDGTADIMISFG
TKEHGDFYPFDGPSGLLAHAFPPGPNYGGDAHFDDDETWTSSSKGYNLFIVAAHELGHSLGLDHS
KDPGALMFPIYTYTGKSHFMLPDDDVQGIQFLYG
>d1bqqm_ d.92.1.11 (M:) Membrane-type matrix metalloproteinase
(CDMT1-MMP) {Human (Homo sapiens)}
IQGLKWQHNEITFCIQNYTPKVGEYATYEAIRKAFRVWESATPLRFREVPYAYIREGHEKQADIM
IFFAEGFHGDSTPFDGEGGFLAHAYFPGPNIGGDTHFDSAEPWTVRNEDLNGNDIFLVAVHELGH
ALGLEHSSDPSAIMAPFYQWMDTENFVLPDDDRRGIQQLYGGES
>d1qba_4 d.92.2.1 (201-337) Bacterial chitobiase, Domain 2 {Serratia
marcescens}
SNADLQTLPAGALRGKIVPTPMQVKVHAQDADLRKGVALDLSTLVKPAADVVSQRFALLGVPVQT
NGYPIKTDIQPGKFKGAMAVSGAYELKIGKKEAQVIGFDQAGVFYGLQSILSLVPSDGSGKIATL
DASDAPR
>d1jaka2 d.92.2.1 (A:8-150) beta-N-acetylhexosaminidase, N-terminal
domain {Streptomyces plicatus}
DRKAPVRPTPLDRVIPAPASVDPGGAPYRITRGTHIRVDDSREARRVGDYLADLLRPATGYRLPV
TAHGHGGIRLRLAGGPYGDEGYRLDSGPAGVTITARKAAGLFHGVQTLRQLLPPAVEKDSAQPGP
WLVAGGTIEDTPR
>d1cwdl_ d.93.1.1 (L:) p56-lck tyrosine kinase {Human (Homo sapiens)}
GSWFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNQGEVVKHYKIRNLDNG
GFYISPRITFPGLHELVRHYTNASDGLCTRLSR
>d1lkka_ d.93.1.1 (A:) p56-lck tyrosine kinase {Human (Homo sapiens)}
LEPEPWFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNQGEVVKHYKIRNL
DNGGFYISPRITFPGLHELVRHYTNASDGLCTRLSRPCQT
>d1bkl__ d.93.1.1 (-) v-src tyrosine kinase {Rous sarcoma virus,
Schmidt-ruppin strain a}
EEWYFGKITRRESESLLLNPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKIRKLDSG
GFYITSRTQFSSLQQLVAYYSKHADGLCHRLTNVCPTSKEFIVTD
>d1shaa_ d.93.1.1 (A:) v-src tyrosine kinase {Rous sarcoma virus,
Schmidt-ruppin strain a}
AEEWYFGKITRRESERLLLNPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKIRKLDS
GGFYITSRTQFSSLQQLVAYYSKHADGLCHRLTNVCPT
>d1a09a_ d.93.1.1 (A:) c-src tyrosine kinase {Human (Homo sapiens)}
DSIQAEEWYFGKITRRESERLLLNAENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKIR
KLDSGGFYITSRTQFNSLQQLVAYYSKHADGLCHRLTTVCP
>d1g83a2 d.93.1.1 (A:142-245) Tyrosine kinase Fyn {Human (Homo
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sapiens)}
DSIQAEEWYFGKLGRKDAERQLLSFGNPRGTFLIRESETTKGAYSLSIRDWDDMKGDHVKHYKIR
KLDNGGYYITTRAQFETLQQLVQHYSERAAGLSSRLVVP
>d1ayaa_ d.93.1.1 (A:) Tyrosine phosphatase Syp {Mouse (Mus musculus)}
MRRWFHPNITGVEAENLLLTRGVDGSFLARPSKSNPGDFTLSVRRNGAVTHIKIQNTGDYYDLYG
GEKFATLAELVQYYMEHHGQLKEKNGDVIELKYPLN
>d1fhs__ d.93.1.1 (-) Growth factor receptor-bound protein 2 (GRB2)
{Human (Homo sapiens)}
GIEMKPHPWFFGKIPRAKAEEMLSKQRHDGAFLIRESESAPGDFSLSVKFGNDVQHFKVLRDGAG
KYFLWVVKFNSLNELVDYHRSTSVSRNQQIFLRDIEQVPQQPTYVQA
>d1zfpe_ d.93.1.1 (E:) Growth factor receptor-bound protein 2 (GRB2)
{Human (Homo sapiens)}
KPHPWFFGKIPRAKAEEMLSKQRHDGAFLIRESESAPGDFSLSVKFGNDVQHFKVLRDGAGKYFL
WVVKFNSLNELVDYHRSTSVSRNQQIFLRDIEQ
>d1qcfa2 d.93.1.1 (A:146-248) Hemopoetic cell kinase Hck {Human (Homo
sapiens)}
EEWFFKGISRKDAERQLLAPGNMLGSFMIRDSETTKGSYSLSVRDYDPRQGDTVKHYKIRTLDNG
GFYISPRSTFSTLQELVDHYKKGNDGLCQKLSVPCMSS
>d1mil__ d.93.1.1 (-) Shc adaptor protein {Human (Homo sapiens)}
GSQLRGEPWFHGKLSRREAEALLQLNGDFLVRESTTTPGQYVLTGLQSGQPKHLLLVDPEGVVRT
KDHRFESVSHLISYHMDNHLPIISAGSELCLQQPVERKL
>d1qada_ d.93.1.1 (A:) Phosphatidylinositol 3-kinase, p85-alpha
subunit {Cow (Bos taurus)}
EDLPHHDEKTWNVGSSNRNKAENLLRGKRDGTFLVRESSKQGCYACSVVVDGEVKHCVINKTATG
YGFAEPYNLYSSLKELVLHYQHTSLVQHNDSLNVTLAYPVYA
>d1pica_ d.93.1.1 (A:) Phosphatidylinositol 3-kinase, p85-alpha
subunit {Human (Homo sapiens)}
GSPIPHHDEKTWNVGSSNRNKAENLLRGKRDGTFLVRESSKQGCYACSVVVDGEVKHCVINKTAT
GYGFAEPYNLYSSLKELVLHYQHTSLVQHNDSLNVTLAYPVYAQQRR
>d1fu6a_ d.93.1.1 (A:) Phosphatidylinositol 3-kinase, p85-alpha
subunit {Rat (Rattus norvegicus)}
GMNNNMSLQDAEWYWGDISREEVNEKLRDTADGTFLVRDASTKMHGDYTLTLRKGGNNKSIKIFH
RDGKYGFSDPLTFNSVVELINHYRNESLAQYNPKLDVKLLYPVSKY
>d1ab2__ d.93.1.1 (-) Proto-oncogen tyrosine kinase {Human (Homo
sapiens)}
GSGNSLEKHSWYHGPVSRNAAEYLLSSGINGSFLVRESESSPGQRSISLRYEGRVYHYRINTASD
GKLYVSSESRFNTLAELVHHHSTVADGLITTLHYPAPKRGIHRD
>d1a81a1 d.93.1.1 (A:9-137) Syk tyrosine kinase {Human (Homo sapiens)}
SANHLPFFFGNITREEAEDYLVQGGMSDGLYLLRQSRNYLGGFALSVAHGRKAHHYTIERELNGT
YAIAGGRTHASPADLCHYHSQESDGLVCLLKKPFNRPQGVQPKTGPFEDLKENLIREYVKQTWN
>d1a81a2 d.93.1.1 (A:138-262) Syk tyrosine kinase {Human (Homo
sapiens)}
LQGQALEQAIISQKPQLEKLIATTAHEKMPWFHGKISREESEQIVLIGSKTNGKFLIRARDNNGS
YALCLLHEGKVLHYRIDKDKTGKLSIPEGKKFDTLWQLVEHYSYKADGLLRVLTVPCQKI
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>d1a81e1 d.93.1.1 (E:9-117) Syk tyrosine kinase {Human (Homo sapiens)}
SANHLPFFFGNITREEAEDYLVQGGMSDGLYLLRQSRNYLGGFALSVAHGRKAHHYTIERELNGT
YAIAGGRTHASPADLCHYHSQESDGLVCLLKKPFNRPQGVQPKT
>d1a81e2 d.93.1.1 (E:152-262) Syk tyrosine kinase {Human (Homo
sapiens)}
PQLEKLIATTAHEKMPWFHGKISREESEQIVLIGSKTNGKFLIRARDNNGSYALCLLHEGKVLHY
RIDKDKTGKLSIPEGKKFDTLWQLVEHYSYKADGLLRVLTVPCQKI
>d1csya_ d.93.1.1 (A:) Syk tyrosine kinase {Human (Homo sapiens)}
GSRRASVGSHEKMPWFHGKISREESEQIVLIGSKTNGKFLIRARDNNGSYALCLLHEGKVLHYRI
DKDKTGKLSIPEGKKFDTLWQLVEHYSYKADGLLRVLTVPCQKIGTQ
>d2plda_ d.93.1.1 (A:) Phospholipase C-gamma-1 {Cow (Bos taurus)}
GSPGIHESKEWYHASLTRAQAEHMLMRVPRDGAFLVRKRNEPNSYAISFRAEGKIKHCRVQQEGQ
TVMLGNSEFDSLVDLISYYEKHPLYRKMKLRYPINEENSS
>d1blk__ d.93.1.1 (-) P55 Blk protein tyrosine kinase {Mouse (Mus
musculus)}
GSVAPVETLEVEKWFFRTISRKDAERQLLAPMNKAGSFLIRESESNKGAFSLSVKDITTQGEVVK
HYKIRSLDNGGYYISPRITFPTLQALVQHYSKKGDGLCQKLTLPCVNLA
>d2abl_2 d.93.1.1 (140-237) Abl tyrosine kinase {Human (Homo sapiens)}
SLEKHSWYHGPVSRNAAEYLLSSGINGSFLVRESESSPGQRSISLRYEGRVYHYRINTASDGKLY
VSSESRFNTLAELVHHHSTVADGLITTLHYPAP
>d1jwoa_ d.93.1.1 (A:) Csk homologous kinase Chk {Human (Homo sapiens)}
LSLMPWFHGKISGQEAVQQLQPPEDGLFLVRESARHPGDYVLCVSFGRDVIHYRVLHRDGHLTID
EAVFFCNLMDMVEHYSKDKGAICTKLVRPKRK
>d1bf5a3 d.93.1.1 (A:569-710) STAT-1 {Human (Homo sapiens)}
LLPLWNDGCIMGFISKERERALLKDQQPGTFLLRFSESSREGAITFTWVERSQNGGEPDFHAVEP
YTKKELSAVTFPDIIRNYKVMAAENIPENPLKYLYPNIDKDHAFGKYYSRGYIKTELISVS
>d1bg1a3 d.93.1.1 (A:576-716) STAT3b {Mouse (Mus musculus)}
ILALWNEGYIMGFISKERERAILSTKPPGTFLLRFSESSKEGGVTFTWVEKDISGSTQIQSVEPY
TKQQLNNMSFAEIIMGYKIMDATNILVSPLVYLYPDIPKEEAFGKYCRPESQEHPEADPGSAAPY
LKTKFICVTPF
>d2cbla3 d.93.1.1 (A:264-351) Cbl {Human (Homo sapiens)}
THPGYMAFLTYDEVKARLQKFIHKPGSYIFRLSCTRLGQWAIGYVTADGNILQTIPHNKPLFQAL
IDGFREGFYLFPDGRNQNPDLTG
>d2shpa2 d.93.1.1 (A:2-110) Tyrosine phoshatase shp-2 {Human (Homo
sapiens)}
KSRRWFHPNITGVEAENLLLTRGVDGSFLARPSKSNPGDLTLSVRRNGAVTHIKIQNTGDYYDLY
GGEKFATLAELVQYYMEHHGQLKEKNGDVIELKYPLNCADPTSE
>d2shpa3 d.93.1.1 (A:111-218) Tyrosine phoshatase shp-2 {Human (Homo
sapiens)}
RWFHGHLSGKEAEKLLTEKGKHGSFLVRESQSHPGDFVLSVRTGDDKGESNDGKSKVTHVMIRCQ
ELKYDVGGGERFDSLTDLVEHYKKNPMVETLGTVLQLKQPLNT
>d1d4ta_ d.93.1.1 (A:) The Xlp protein Sap {Human (Homo sapiens)}
MDAVAVYHGKISRETGEKLLLATGLDGSYLLRDSESVPGVYCLCVLYHGYIYTYRVSQTETGSWS
AETAPGVHKRYFRKIKNLISAFQKPDQGIVIPLQYPVEK
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>d1spha_ d.94.1.1 (A:) Histidine-containing phosphocarrier protein
(HPr) {Bacillus subtilis}
AQKTFKVTADSGIHARPATVLVQTASKYDADVNLEYNGKTVNLKDIMGVMSLGIAKGAEITISAS
GADENDALNALEETMKSEGLGE
>d1ptf__ d.94.1.1 (-) Histidine-containing phosphocarrier protein
(HPr) {Enterococcus faecalis}
MEKKEFHIVAETGIHARPATLLVQTASKFNSDINLEYKGKSVNLKSIMGVMSLGVGQGSDVTITV
DGADEAEGMAAIVETLQKEGLA
>d1opd__ d.94.1.1 (-) Histidine-containing phosphocarrier protein
(HPr) {Escherichia coli}
MFEQEVTITAPNGLHTRPAAQFVKEAKGFTSEITVTSNGKSASAKDLFKLQTLGLTQGTVVTISA
EGEDEQKAVEHLVKLMAELE
>d1pch__ d.94.1.1 (-) Histidine-containing phosphocarrier protein
(HPr) {Mycoplasma capricolum}
AKFSAIITDKVGLHARPASVLAKEASKFSSNITIIANEKQGNLKSIMNVMAMAIKTGTEITIQAD
GNDADQAIQAIKQTMIDTALIQG
>d1zer__ d.94.1.1 (-) Histidine-containing phosphocarrier protein
(HPr) {Staphylococcus aureus}
MEQNSYVIIDETGIHARPATMLVQTASKFDSDIQLEYNGKKVNLKSIMGVMSLGVGKDAEITIYA
DGSDESDAIQAISDVLSKEGLT
>d1qr5a_ d.94.1.1 (A:) Histidine-containing phosphocarrier protein
(HPr) {Staphylococcus carnosus}
MEQQSYTIIDETGIHARPATMLVQTASKFDSDIQLEYNGKKVNLKSIMGVMSLGVGKDAEITIYA
DGSDEADAIQAITDVLSKEGLTE
>d1k1ca_ d.94.1.1 (A:) Crh, catabolite repression HPr-like protein
{Bacillus subtilis}
VQQKVEVRLKTGLQARPAALFVQEANRFTSDVFLEKDGKKVNAKSIMGLMSLAVSTGTEVTLIAQ
GEDEQEALEKLAAYVQEEV
>d1jrma_ d.206.1.1 (A:) Hypothetical protein MTH637 {Archaeon
Methanobacterium thermoautotrophicum}
VITMDCLREVGDDLLVNIEVSPASGKFGIPSYNEWRKRIEVKIHSPPQKGKANREIIKEFSETFG
RDVEIVSGQKSRQKTIRIQGMGRDLFLKLVSEKFGLEIP
>d1iba__ d.95.1.1 (-) Glucose permease domain IIB {Escherichia coli}
MAPALVAAFGGKENITNLDACITRLRVSVADVSKVDQAGLKKLGAAGVVVAGSGVQAIFGTKSDN
LKTEMDEYIRNFG
>d1af5__ d.95.2.1 (-) DNA endonuclease I-CreI {Chlamydomonas
reinhardtii}
KYNKEFLLYLAGFVDGDGSIIAQIKPNQSYKFKHQLSLTFQVTQKTQRRWFLGKLVDEIGVGYVR
DRGSVSDYILSEIKPLHNFLTQLQPFLKLKQKQANLVLKIIEQLPLEVCTWVDQIAALNDS
>d1g9za_ d.95.2.1 (A:) DNA endonuclease I-CreI {Chlamydomonas
reinhardtii}
NTKYNKEFLLYLAGFVDGDGSIIAQIKPNQSYKFKHQLSLTFQVTQKTQRRWFLDKLVDEIGVGY
VRDRGSVSDYILSEIKPLHNFLTQLQPFLKLKQKQANLVLKIIEQLPSAKESPDKFLEVCTWVDQ
IAALNDSKTRKTTSETVRAVLD
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>d1b24a1 d.95.2.1 (A:7-99) I-dmoI {Archaeon Desulfurococcus mobilis}
VSGISAYLLGLIIGDGGLYKLKYKGNRSEYRVVITQKSENLIKQHIAPLMQFLIDELNVKSKIQI
VKGDTRYELRVSSKKLYYYFANMLERIR
>d1b24a2 d.95.2.1 (A:100-179) I-dmoI {Archaeon Desulfurococcus
mobilis}
LFNMREQIAFIKGLYVAEGDKTLKRLRIWNKNKALLEIVSRWLNNLGVRNTIHLDDHRHGVYVLN
ISLRDRIKFVHTILS
>d1dfaa2 d.95.2.2 (A:181-298) PI-SceI {Baker's yeast (Saccharomyces
cerevisiae)}
PILYENDHFFDYMQKSKFHLTIEGPKVLAYLLGLWIGDGLSDRATFSVDSRDTSLMERVTEYAEK
LNLCAEYKDRKEPQVAKTVNLYSKVVRGNGIRNNLNTENPLWDAIVGLGFLKD
>d1dfaa3 d.95.2.2 (A:299-415) PI-SceI {Baker's yeast (Saccharomyces
cerevisiae)}
GVKNIPSFLSTDNIGTRETFLAGLIDSDGYVTDEHGIKATIKTIHTSVRDGLVSLARSLGLVVSV
NAEPAKVDMNGTKHKISYAIYMSGGDVLLNVLSKCAGSKKFRPAPAAAFARE
>d1dq3a3 d.95.2.2 (A:129-226) PI-Pfui intein {Archaeon Pyrococcus
furiosus}
PDGEDYKFIFDYWLAGFIAGDGCFDKYHSHVKGHEYIYDRLRIYDYRIETFEIINDYLEKTFGRK
YSIQKDRNIYYIDIKARNITSHYLKLLEGIDNG
>d1dq3a4 d.95.2.2 (A:227-335) PI-Pfui intein {Archaeon Pyrococcus
furiosus}
IPPQILKEGKNAVLSFIAGLFDAEGHVSNKPGIELGMVNKRLIEDVTHYLNALGIKARIREKLRK
DGIDYVLHVEEYSSLLRFYELIGKNLQNEEKREKLEKVLSNHKG
>d1a8ra_ d.96.1.1 (A:) GTP cyclohydrolase I {Escherichia coli}
PSLSKEAALVHEALVARGLETPLRPPVHEMDNETRKSLIAGHMTEIMQLLNLDLADDSLMETPHR
IAKMYVDEIFSGLDYANFPKITLIENKMKVDEMVTVRDITLTSTCESHFVTIDGKATVAYIPKDS
VIGLSKINRIVQFFAQRPQVQERLTQQILIALQTLLGTNNVAVSIDAVHYCVKARGIRDATSATT
TTSLGGLFKSSQNTRHEFLRAVRHHN
>d1is8a_ d.96.1.1 (A:) GTP cyclohydrolase I {Rat (Rattus norvegicus)}
RPRSEEDNELNLPNLAAAYSSILRSLGEDPQRQGLLKTPWRAATAMQFFTKGYQETISDVLNDAI
FDEDHDEMVIVKDIDMFSMCEHHLVPFVGRVHIGYLPNKQVLGLSKLARIVEIYSRRLQVQERLT
KQIAVAITEALQPAGVGVVIEATHMCMVMRGVQKMNSKTVTSTMLGVFREDPKTREEFLTLIRS
>d1b66a_ d.96.1.2 (A:) 6-pyruvoyl tetrahydropterin synthase {Rat
(Rattus norvegicus)}
LRRRARLSRLVSFSASHRLHSPSLSAEENLKVFGKCNNPNGHGHNYKVVVTIHGEIDPVTGMVMN
LTDLKEYMEEAIMKPLDHKNLDLDVPYFADVVSTTENVAVYIWENLQRLLPVGALYKVKVYETDN
NIVVYKGE
>d1dhn__ d.96.1.3 (-) 7,8-dihidroneopterin aldolase {Staphylococcus
aureus}
MQDTIFLKGMRFYGYHGALSAENEIGQIFKVDVTLKVDLSEAGRTDNVIDTVHYGEVFEEVKSIM
EGKAVNLLEHLAERIANRINSQYNRVMETKVRITKENPPIPGHYDGVGIEIVRENK
>d1b9la_ d.96.1.3 (A:) 7,8-dihydroneopterin triphosphate epimerase
{Escherichia coli}
AQPAAIIRIKNLRLRTFIGIKEEEINNRQDIVINVTIHYPADKARTSEDINDALNYRTVTKNIIQ
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HVENNRFSLLEKLTQDVLDIAREHHWVTYAEVEIDKLHALRYADSVSMTLSWQR

>d1uox_1 d.96.1.4 (1-136) Urate oxidase (uricase) {Aspergillus flavus}

SAVKAARYGKDNVRVYKVHKDEKTGVQTVYEMTVCVLLEGEIETSYTKADNSVIVATDSIKNTIYITAKQNPVTPPELFGSILGTHFIEKYNHIHAAHVNIVCHRWTRMDIDGKPHPHSFIRDSEEKRNVQVDVVE

>d1uox_2 d.96.1.4 (137-295) Urate oxidase (uricase) {Aspergillus flavus}

GKGIDIKSSLSGLTVLKSTNSQFWGFLRDEYTTLKETWDRILSTDVDATWQWKNFSGLQEVRSHVPKFDATWATAREVTLKTFAEDNSASVQATMYKMAEQILARQQLIETVEYSLPNKHYFEIDLSWHKGLQNTGKNAEVFAPQSDPNGLIKCTVGRS

>d1puc__ d.97.1.1 (-) suc1 {Fission yeast (Schizosaccharomyces pombe)}

SKSGVPRLLTASERERLEPFIDQIHYSPRYADDEYEYRHVMLPKAMLKAIPTDYFNPETGTLRILQEEEWRGLGITQSLGWEMYEVHVPEPHILLFKREKD

>d1qb3a_ d.97.1.1 (A:) cks1 {Baker's yeast (Saccharomyces cerevisiae)}

HAFQGRKLTDQERARVLEFQDSIHYSPRYSDDNYEYRHVMLPKAMLKVIPSDYFNSEVGTLRILTEDEWRGLGITQSLGWEHYECHAPEPHILLFKRPLNYEAELRAATAAAQ

>d1cksa_ d.97.1.1 (A:) CksHs2 {Human (Homo sapiens)}

AHKQIYYSDKYFDEHYEYRHVMLPRELSKQVPKTHLMSEEEWRRLGVQQSLGWVHYMIHEPEPHILLFRRPLPK

>d1buhb_ d.97.1.1 (B:) CksHs1 {Human (Homo sapiens)}

QIYYSDKYDDEEFEYRHVMLPKDIAKLVPKTHLMSESEWRNLGVQQSQGWVHYMIHEPEPHILLFRRPLP

>d1jtgb_ d.98.1.1 (B:) beta-lactamase-inhibitor protein, BLIP {Streptomyces clavuligerus}

AGVMTGAKFTQIQFGMTRQQVLDIAGAENCETGGSFGDSIHCRGHAAGDYYAYATFGFTSAAADAKVDSKSQEKLLAPSAPTLTLAKFNQVTVGMTRAQVLATVGQGSCTTWSEYYPAYPSTAGVTLSLSCFDVDGYSSTGFYRGSAHLWFTDGVLQGKRQWDLV

>d1div_1 d.99.1.1 (56-149) Ribosomal protein L9 C-domain {Bacillus stearothermophilus}

RQAAEELANAKKLKEQLEKLTVTIPAKAGEGGRLFGSITSKQIAESLQAQHGLKLDKRKIELADAIRALGYTNVPVKLHPEVTATLKVHVTEQK

>d1div_2 d.100.1.1 (1-55) Ribosomal protein L9 N-domain {Bacillus stearothermophilus}

MKVIFLKDVKGKGKKGEIKNVADGYANNFLFKQGLAIEATPANLKALEAQKQKEQ

>d1qhka_ d.100.1.2 (A:) N-terminal domain of RNase HI {Baker's yeast (Saccharomyces cerevisiae)}

GNFYAVRKGRETGIYNTWNECKNQVDGYGGAIYKKFNSYEQAKSFLG

>d1e3ha5 d.101.1.1 (A:152-262) Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domains 2 and 5 {Streptomyces antibioticus}

FSGPIGGVRVALIRGQWVAFPTHTELEDAVFDMVVAGRVLEDGDVAIMMVEAEATEKTIQLVKDG

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AEAPTEEVVAAGLDAAKPFIKVLCKAQADLAAKAAKPTGEFPVFLD
>d1e3ha6 d.101.1.1 (A:483-578) Polynucleotide
phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI),
domains 2 and 5 {Streptomyces antibioticus}
APVAGIAMGLISQEINGETHYVALTDILGAEDAFGDMDFKVAGTKEFVTALQLDTKLDGIPASVL
AAALKQARDARLHILDVMMEAIDTPDEMSPN
>d1efnb_ d.102.1.1 (B:) Regulatory factor Nef {Human immunodeficiency
virus type 1}
RPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQNYTPGPGVRY
PLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREVLEWRFDSRLAFHHVARELHP
EYF
>d2nef__ d.102.1.1 (-) Regulatory factor Nef {Human immunodeficiency
virus type 1}
AWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
FPDWQNYTPGPGIRYPLTFGWCYKLVPVEPEKLEEANKDDPEREVLEWRFDSRLAFHHMARELHP
EYFKNA
>d1cby__ d.103.1.1 (-) Mosquitocidal delta-endotoxin CytB {Bacillus
thuringiensis, strain Kyushuensis}
CSAPIIRKPFKHIVLTVPSSDLDNFNTVFYVQPQYINQALHLANAFQGAIDPLNLNFNFEKALQI
ANGIPNSAIVKTLNQSVIQQTVEISVMVEQLKKIIQEVLGLVINSTSFWNSVEATIKGTFTNLDT
QIDEAWIFWHSLSAHNTSYYYNILFSIQNEDTGAVMAVLPLAFEVSVDVEKQKVLFFTIKDSARY
EVKMKALTLVQALHSSNAPIVDIFNVNNYNLY
>d1seta2 d.104.1.1 (A:111-421) Seryl-tRNA synthetase (SerRS) {Thermus
thermophilus, strain hb27}
VGGEEANREIKRVGGPPEFSFPPLDHVALMEKNGWWEPRISQVSGSRSYALKGDLALYELALLRF
AMDFMARRGFLPMTLPSYAREKAFLGTGHFPAYRDQVWAIAETDLYLTGTAEVVLNALHSGEILP
YEALPLRYAGYAPAFRSEAGSFGKDVRGLMRVHQFHKVEQYVLTEASLEASDRAFQELLENAEEI
LRLLELPYRLVEVATGDMGPGKWRQVDIEVYLPSEGRYRETHSCSALLDWQARRANLRYRDPEGR
VRYAYTLNNTALATPRILAMLLENHQLQDGRVRVPQALIPYMGKEVLEPCG
>d1e1oa2 d.104.1.1 (A:161-502) Lysyl-tRNA synthetase (LysRS)
{Escherichia coli, gene lysU}
DQEVRYRQRYLDLIANDKSRQTFVVRSKILAAIRQFMVARGFMEVETPMMQVIPGGASARPFITH
HNALDLDMYLRIAPELYLKRLVVGGFERVFEINRNFRNEGISVRHNPEFTMMELYMAYADYHDLI
ELTESLFRTLAQEVLGTTKVTYGEHVFDFGKPFEKLTMREAIKKYRPETDMADLDNFDAAKALAE
SIGITVEKSWGLGRIVTEIFDEVAEAHLIQPTFITEYPAEVSPLARRNDVNPEITDRFEFFIGGR
EIGNGFSELNDAEDQAERFQEQVNAKAAGDDEAMFYDEDYVTALEYGLPPTAGLGIGIDRMIMLF
TNSHTIRDVILFPAMRP
>d1bbua2 d.104.1.1 (A:161-502) Lysyl-tRNA synthetase (LysRS)
{Escherichia coli, gene lysS}
DQEARYRQRYLDLISNDESRNTFKVRSQILSGIRQFMVNRGFMEVETPMMQVIPGGAAARPFITH
HNALDLDMYLRIAPELYLKRLVVGGFERVFEINRNFRNEGISVRHNPEFTMMELYMAYADYKDLI
ELTESLFRTLAQDILGKTEVTYGDVTLDFGKPFEKLTMREAIKKYRPETDMADLDNFDSAKAIAE
SIGIHVEKSWGLGRIVTEIFEEVAEAHLIQPTFITEYPAEVSPLARRNDVNPEITDRFEFFIGGR
EIGNGFSELNDAEDQAQRFLDQVAAKDAGDDEAMFYDEDYVTALEHGLPPTAGLGIGIDRMVMLF
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TNSHTIRDVILFPAMRP
>d1kmma2 d.104.1.1 (A:4-325) Histidyl-tRNA synthetase (HisRS)
{Escherichia coli}
NIQAIRGMNDYLPGETAIWQRIEGTLKNVLGSYGYSEIRLPIVEQTPLFKRAIGEVTDVVEKEMY
TFEDRNGDSLTLRPEGTAGCVRAGIEHGLLYNQEQRLWYIGPMFRHERPQKGRYRQFHQLGCEVF
GLQGPDIDAELIMLTARWWRALGISEHVTLELNSIGSLEARANYRDALVAFLEQHKEKLDEDCKR
RMYTNPLRVLDSKNPEVQALLNDAPALGDYLDEESREHFAGLCKLLESAGIAYTVNQRLVRGLDY
YNRTVFEWVTNSLGSQGTVCAGGRYDGLVEQLGGRATPAVGFAMGLERLVLLVQAVNPEFKA
>d1qe0a2 d.104.1.1 (A:1-325) Histidyl-tRNA synthetase (HisRS)
{Staphylococcus aureus}
MIKIPRGTQDILPEDSKKWRYIENQLDELMTFYNYKEIRTPIFESTDLFARGVGDSTDVVQKEMY
TFKDKGDRSITLRPEGTAAVVRSYIEHKMQGNPNQPIKLYYNGPMFRYERKQKGRYRQFNQFGVE
AIGAENPSVDAEVLAMVMHIYQSFGLKHLKLVINSVGDMASRKEYNEALVKHFEPVIHEFCSDCQ
SRLHTDPMRILDCKVDRDKEAIKTAPRITDFLNEESKAYYEQVKAYLDDLGIPYTEDPNLVRGLD
YYTHTAFELMMDNPNYDGAITTLCGGGRYNGLLELLDGPSETGIGFALSIERLLLALEEEGIELD
>d1h4vb2 d.104.1.1 (B:2-325) Histidyl-tRNA synthetase (HisRS)
{Thermus thermophilus}
TARAVRGTKDLFGKELRMHQRIVATARKVLEAAGALELVTPIFEETQVFEKGVGAATDIVRKEMF
TFQDRGGRSLTLRPEGTAAMVRAYLEHGMKVWPQPVRLWMAGPMFRAERPQKGRYRQFHQVNYEA
LGSENPILDAEAVVLLYECLKELGLRRLKVKLSSVGDPEDRARYNAYLREVLSPHREALSEDSKE
RLEENPMRILDSKSERDQALLKELGVRPMLDFLGEEARAHLKEVERHLERLSVPYELEPALVRGL
DYYVRTAFEVHHEEIGAQSALGGGGRYDGLSELLGGPRVPGVGFAFGVERVALALEAEGFGLPE
>d1atia2 d.104.1.1 (A:1-394) Glycyl-tRNA synthetase (GlyRS) {Thermus
thermophilus}
AASSLDELVALCKRRGFIFQSSEIYGGLQGVYDYGPLGVELKNNLKQAWWRRNVYERDDMEGLDA
SVLTHRLVLHYSGHEATFADPMVDNRITKKRYRLDHLLKEQPEEVLKRLYRAMEVEEENLHALVQ
AMMQAPERAGGAMTAAGVLDPASGEPGDWTPPRYFNMMFQDLRGPRGGRGLLAYLRPETAQGIFV
NFKNVLDATSRKLGFGIAQIGKAFRNEITPRNFIFRVREFEQMEIEYFVRPGEDEYWHRYWVEER
LKWWQEMGLSRENLVPYQQPPESSAHYAKATVDILYRFPHGSLELEGIAQRTDFDLGSHTKDQEA
LGITARVLRNEHSTQRLAYRDPETGKWFVPYVIEPSAGVDRGVLALLAEAFTREELPNGEERIVL
KLKP
>d1b76a2 d.104.1.1 (A:1-394) Glycyl-tRNA synthetase (GlyRS) {Thermus
thermophilus}
AASSLDELVALCKRRGFIFQSSEIYGGLQGVYDYGPLGVELKNNLKQAWWRRNVYERDDMEGLDA
SVLTHRLVLHYSGHEATFADPMVDNAKARYWTPPRYFNMMFQDLRGPRGGRGLLAYLRPETAQGI
FVNFKNVLDATSRKLGFGIAQIGKAFRNEITPRNFIFRVREFEQMEIEYFVRPGEDEYWHRYWVE
ERLKWWQEMGLSRENLVPYQQPPESSAHYAKATVDILYRFPHGSLELEGIAQRTDFDLGSHTKDQ
EALGITARVLRNEHSTQRLAYRDPETGKWFVPYVIEPSAGVDRGVLALLAEAFTREELPNGEERI
VLKLKP
>d1qf6a4 d.104.1.1 (A:242-532) Threonyl-tRNA synthetase (ThrRS)
{Escherichia coli}
RDHRKIGKQLDLYHMQEEAPGMVFWHNDGWTIFRELEVFVRSKLKEYQYQEVKGPFMMDRVLWEK
TGHWDNYKDAMFTTSSENREYCIKPMNCPGHVQIFNQGLKSYRDLPLRMAEFGSCHRNEPSGSLH
GLMRVRGFTQDDAHIFCTEEQIRDEVNGCIRLVYDMYSTFGFEKIVVKLSTRPEKRIGSDEMWDR
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AEADLAVALEENNIPFEYQLGEGAFYGPKIEFTLYDCLDRAWQCGTVQLDFSLPSRLSASYVGED
NERKVPVMIHRAILGSMERFIGILTEEFAGF
>d1eova2 d.104.1.1 (A:205-557) Aspartyl-tRNA synthetase (AspRS)
{Baker's yeast (Saccharomyces cerevisiae)}
PILLEDASRSEAEAEAAGLPVVNLDTRLDYRVIDLRTVTNQAIFRIQAGVCELFREYLATKKFTE
VHTPKLLGAPSEGGSSVFEVTYFKGKAYLAQSPQFNKQQLIVADFERVYEIGPVFRAENSNTHRH
MTEFTGLDMEMAFEEHYHEVLDTLSELFVFIFSELPKRFAHEIELVRKQYPVEEFKLPKDGKMVR
LTYKEGIEMLRAAGKEIGDFEDLSTENEKFLGKLVRDKYDTDFYILDKFPLEIRPFYTMPDPANP
KYSNSYDFFMRGEEILSGAQRIHDHALLQERMKAHGLSPEDPGLKDYCDGFSYGCPPHAGGGIGL
ERVVMFYLDLKNIRRASLFPRDPKRLRP
>d1b8aa2 d.104.1.1 (A:104-438) Aspartyl-tRNA synthetase (AspRS)
{Archaeon Pyrococcus kodakaraensis}
PLPLDPTGKVKAELDTRLNNRFMDLRRPEVMAIFKIRSSVFKAVRDFFHENGFIEIHTPKIIATA
TEGGTELFPMKYFEEDAFLAESPQLYKEIMMASGLDRVYEIAPIFRAEEHNTTRHLNEAWSIDSE
MAFIEDEEEVMSFLERLVAHAINYVREHNAKELDILNFELEEPKLPFPRVSYDKALEILGDLGKE
IPWGEDIDTEGERLLGKYMMENENAPLYFLYQYPSEAKPFYIMKYDNKPEICRAFDLEYRGVEIS
SGGQREHRHDILVEQIKEKGLNPESFEFYLKAFRYGMPPHGGFGLGAERLIKQMLDLPNIREVIL
FPRDRRRLTP
>d1c0aa3 d.104.1.1 (A:107-287,A:421-585) Aspartyl-tRNA synthetase
(AspRS) {Escherichia coli}
VLPLDSNHVNTEEARLKYRYLDLRRPEMAQRLKTRAKITSLVRRFMDDHGFLDIETPMLTKATPE
GARDYLVPSRVHKGKFYALPQSPQLFKQLLMMSGFDRYYQIVKCFRDEDLRADRQPEFTQIDVET
SFMTAPQVREVMEALVRHLWLEVKGVDLGDFPVMTFAEAERRYGSDKPDLRXDESKWAPLWVIDF
PMFEDDGEGGLTAMHHPFTSPKDMTAAELKAAPENAVANAYDMVINGYEVGGGSVRIHNGDMQQT
VFGILGINEEEQREKFGFLLDALKYGTPPHAGLAFGLDRLTMLLTGTDNIRDVIAFPKTTAAACL
MTEAPSFANPTALAELSIQVVK
>d1g51a3 d.104.1.1 (A:105-294,A:415-580) Aspartyl-tRNA synthetase
(AspRS) {Thermus thermophilus}
TPPFPVDAGWRGEEEKEASEELRLKYRYLDLRRRRMQENLRLRHRVIKAIWDFLDREGFVQVETP
FLTKSTPEGARDFLVPYRHEPGLFYALPQSPQLFKQMLMVAGLDRYFQIARCFRDEDLRADRQPD
FTQLDLEMSFVEVEDVLELNERLMAHVFREALGVELPLPFPRLSYEEAMERYGSDKPDLRXREGF
RFLWVVDFPLLEWDEEEEAWTYMHHPFTSPHPEDLPLLEKDPGRVRALAYDLVLNGVEVGGGSIR
IHDPRLQARVFRLLGIGEEEQREKFGFFLEALEYGAPPHGGIAWGLDRLLALMTGSPSIREVIAF
PKNKEGKDPLTGAPSPVPEEQLRELGLMVVRP
>d1jjca_ d.104.1.1 (A:) Phenyl-tRNA synthetase (PheRS) alpha subunit,
PheS {Thermus thermophilus and (Thermus aquaticus)}
RVDVSLPGASLFSGGLHPITLMERELVEIFRALGYQAVEGPEVESEFFNFDALNIPEHHPARDMW
DTFWLTGEGFRLEGPLGEEVEGRLLLRTHTSPMQVRYMVAHTPPFRIVVPGRVFRFEQTDATHEA
VFHQLEGLVVGEGIAMAHLKGAIYELAQALFGPDSKVRFQPVYFPFVEPGAQFAVWWPEGGKWLE
LGGAGMVHPKVFQAVDAYRERLGLPPAYRGVTGFAFGLGVERLAMLRYGIPDIRYFFGGRLKFLE
QFKGVL
>d1jjcb5 d.104.1.1 (B:475-681) Phenyl-tRNA synthetase (PheRS) beta
subunit, PheT, central domain {Thermus thermophilus (Thermus
aquaticus)}
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ALPAFFPAPDNRGVEAPYRKEQRLREVLSGLGFQEVYTYSFMDPEDARRFRLDPPRLLLLNPLAP
EKAALRTHLFPGLVRVLKENLDLDRPERALLFEVGRVFREREETHLAGLLFGEGVGLPWAKERLS
GYFLLKGYLEALFARLGLAFRVEAQAFPFLHPGVSGRVLVEGEEVGFLGALHPEIAQELELPPVH
LFELRLPLPDKP
>d1hc7a2 d.104.1.1 (A:5-276) Prolyl-tRNA synthetase (ProRS) {Thermus
thermophilus}
KGLTPQSQDFSEWYLEVIQKAELADYGPVRGTIVVRPYGYAIWENIQQVLDRMFKETGHQNAYFP
LFIPMSFLRKEAEHVEGFSPELAVVTHAGGEELEEPLAVRPTSETVIGYMWSKWIRSWRDLPQLL
NQWGNVVRWEMRTRPFLRTSEFLWQEGHTAHATREEAEEEVRRMLSIYARLAREYAAIPVIEGLK
TEKEKFAGAVYTTTIEALMKDGKALQAGTSHYLGENFARAFDIKFQDRDLQVKYVHTTSWGLSWR
FIGAIIMTHGDD
>d1g5ha2 d.104.1.1 (A:41-330) The aaRS-like accessory subunit of
mitochondrial polymerase gamma, N-terminal domain {Mouse (Mus
musculus)}
EALVDLCRRRHFLSGTPQQLSTAALLSGCHARFGPLGVELRKNLASQWWSSMVVFREQVFAVDSL
HQEPGSSQPRDSAFRLVSPESIREILQDREPSKEQLVAFLENLLKTSGKLRATLLHGALEHYVNC
LDLVNRKLPFGLAQIGVCFHPVSNSNQTPSSVTRVGEKTEASLVWFTPTRTSSQWLDFWLRHRLL
WWRKFAMSPSNFSSADCQDELGRKGSKLYYSFPWGKEPIETLWNLGDQELLHTYPGNVSTIQGRD
GRKNVVPCVLSVSGDVDLGTLAYLYDSFQL
>d12asa_ d.104.1.1 (A:) Asparagine synthetase {Escherichia coli}
AYIAKQRQISFVKSHFSRQLEERLGLIEVQAPILSRVGDGTQDNLSGAEKAVQVKVKALPDAQFE
VVHSLAKWKRQTLGQHDFSAGEGLYTHMKALRPDEDRLSPLHSVYVDQWDWERVMGDGERQFSTL
KSTVEAIWAGIKATEAAVSEEFGLAPFLPDQIHFVHSQELLSRYPDLDAKGRERAIAKDLGAVFL
VGIGGKLSDGHRHDVRAPDYDDWSTPSELGHAGLNGDILVWNPVLEDAFELSSMGIRVDADTLKH
QLALTGDEDRLELEWHQALLRGEMPQTIGGGIGQSRLTMLLLQLPHIGQVQAGVWPAAVRESVPS
LL
>d1bia_3 d.104.1.2 (64-270) Biotin repressor/biotin holoenzyme
synthetase, catalytic (central) domain {Escherichia coli}
IQLLNAKQILGQLDGGSVAVLPVIDSTNQYLLDRIGELKSGDACIAEYQQAGRGRRGRKWFSPFG
ANLYLSMFWRLEQGPAAAIGLSLVIGIVMAEVLRKLGADKVRVKWPNDLYLQDRKLAGILVELTG
KTGDAAQIVIGAGINMAMRRVEESVVNQGWITLQEAGINLDRNTLAAMLIRELRAALELFEQEGL
APYLSRWEKLDN
>d1qtsa2 d.105.1.1 (A:825-938) Alpa-adaptin AP2, C-terminal subdomain
{Mouse (Mus musculus)}
FFQPTEMASQDFFQRWKQLSNPQQEVQNIFKAKHPMDTEITKAKIIGFGSALLEEVDPNPANFVG
AGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKDTVSQRLCELLSEQF
>d1e42a2 d.105.1.1 (A:825-937) Beta2-adaptin AP2, C-terminal
subdomain {Human (Homo sapiens)}
LFVEDGKMERQVFLATWKDIPNENELQFQIKECHLNADTVSSKLQNNNVYTIAKRNVEGQDMLYQ
SLKLTNGIWILAELRIQPGNPNYTLSLKCRAPEVSQYIYQVYDSILKN
>d1c44a_ d.106.1.1 (A:) Sterol carrier protein 2 (SCP2) {Rabbit
(Oryctolagus cuniculus)}
SSAGDGFKANLVFKEIEKKLEEEGEQFVKKIGGIFAFKVKDGPGGKEATWVVDVKNGKGSVLPNS
DKKADCTITMADSDLLALMTGKMNPQSAFFQGKLKITGNMGLAMKLQNLQLQPGKAKL
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>d1ikta_ d.106.1.1 (A:) SCP2-like domain of MFE-2 {Human (Homo sapiens)}
LQSTFVFEEIGRRLKDIGPEVVKKVNAVFEWHITKGGNIGAKWTIDLKSGSGKVYQGPAKGAADT
TIILSDEDFMEVVLGKLDPQKAFFSGRLKARGNIMLSQKLQMILKDYAKL
>d1eq6a_ d.107.1.1 (A:) Ran-binding protein mog1p {Baker's yeast (Saccharomyces cerevisiae)}
SMNNKEVELYGGAITTVVPPGFIDASTLREVPDTQEVYVNSRRDEEEFEDGLATNESIIVDLLET
VDKSDLKEAWQFHVEDLTELNGTTKWEALQEDTVQQGTKFTGLVMEVANKWGKPDLAQTVVIGVA
LIRLTQFDTDVVISINVPLTKEEASQASNKELPARCHAVYQLLQEMVRKFHVVDTSLFA
>d1b87a_ d.108.1.1 (A:) Aminoglycoside 6'-N-acetyltransferase {Enterococcus faecium}
MIISEFDRNNPVLKDQLSDLLRLTWPEEYGDSSAEEVEEMMNPERIAVAAVDQDELVGFIGAIPQ
YGITGWELHPLVVESSRRKNQIGTRLVNYLEKEVASRGGITIYLGTDDLDHGTTLSQTDLYEHTF
DKVASIQNLREHPYEFYEKLGYKIVGVLPNANGWDKPDIWMAKTIIPRPDS
>d1bo4a_ d.108.1.1 (A:) Aminoglycoside 3-N-acetyltransferase {Serratia marcescens}
GIIRTCRLGPDQVKSMRAALDLFGREFGDVATYSQHQPDSDYLGNLLRSKTFIALAAFDQEAVVG
ALAAYVLPKFEQPRSEIYIYDLAVSGEHRRQGIATALINLLKHEANALGAYVIYVQADYGDDPAV
ALYTKLG
>d1cm0a_ d.108.1.1 (A:) Histone acetyltransferase domain of P300/CBP associating factor, PCAF {Human (Homo sapiens)}
KVIEFHVVGNSLNQKPNKKILMWLVGLQNVFSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIG
GICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHDILNFLTYADEYAIGYFKKQG
FSKEIKIPKTKYVGYIKDYEGATLMGCELNPRI
>d1ygha_ d.108.1.1 (A:) Catalytic domain of GCN5 histone acetyltransferase {Baker's yeast (Saccharomyces cerevisiae)}
KIEFRVVNNDNTKENMMVLTGLKNIFQKQLPKMPKEYIARLVYDRSHLSMAVIRKPLTVVGGITY
RPFDKREFAEIVFCAISSTEQVRGYGAHLMNHLKDYVRNTSNIKYFLTYADNYAIGYFKKQGFTK
EITLDKSIWMGYIKDYEGGTLMQCSMLPRIRYLD
>d1qsta_ d.108.1.1 (A:) Catalytic domain of GCN5 histone acetyltransferase {Tetrahymena thermophila}
LDFDILTNDGTHRNMKLLIDLKNIFSRQLPKMPKEYIVKLVFDRHHESMVILKNKQKVIGGICFR
QYKPQRFAEVAFLAVTANEQVRGYGTRLMNKFKDHMQKQNIEYLLTYADNFAIGYFKKQGFTKEH
RMPQEKWKGYIKDYDGGTLMECYIHPYVDY
>d1qsma_ d.108.1.1 (A:) Histone acetyltransferase HPA2 {Baker's yeast (Saccharomyces cerevisiae)}
DNITVRFVTENDKEGWQRLWKSYQDFYEVSFPDDLDDFNFGRFLDPNIKMWAAVAVESSSEKIIG
MINFFNHMTTWDFKDKIYINDLYVDENSRVKGAGGKLIQFVYDEADKLGTPSVYWCTDESNHRAQ
LLYVKVGYKAPKILYKRKGY
>d1bob__ d.108.1.1 (-) Histone acetyltransferase HAT1 {Baker's yeast (Saccharomyces cerevisiae)}
FKPETWTSSANEALRVSIVGENAVQFSPLFTYPIYGDSEKIYGYKDLIIHLAFDSVTFKPYVNVK
YSAKLGDDNIVDVEKKLLSFLPKDDVIVRDEAKWVDCFAEERKTHNLSDVFEKVSEYSLNGEEFV
VYKSSLVDDFARRMHRRVQIFSLLFIEAANYIDETDPSWQIYWLLNKKTKELIGFVTTYKYWHYL
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GAKSFDEDIDKKFRAKISQFLIFPPYQNKGHGSCLYEAIIQSWLEDKSITEITVEDPNEAFDDLR
DRNDIQRLRKLGYDAVFQKHSDLSDEFLESSRKSLKLEERQFNRLVEMLLLLNNS
>d1fy7a_ d.108.1.1 (A:) Histone acetyltransferase ESA1 {Baker's yeast
(Saccharomyces cerevisiae)}
ARVRNLNRIIMGKYEIEPWYFSPYPIELTDEDFIYIDDFTLQYFGSKKQYERYRKKCTLRHPPGN
EIYRDDYVSFFEIDGRKQRTWCRNLCLLSKLFLDHKTLYYDVDPFLFYCMTRRDELGHHLVGYFS
KEKESADGYNVACILTLPQYQRMGYGKLLIEFSYELSKKENKVGSPEKPLSDLGLLSYRAYWSDT
LITLLVEHQKEITIDEISSMTSMTTTDILHTAKTLNILRYYKGQHIIFLNEDILDRYNRLKAKKR
RTIDPNRLIWKPP
>d1cjwa_ d.108.1.1 (A:) Serotonin N-acetyltranferase {Sheep (Ovis
aries)}
HTLPANEFRCLTPEDAAGVFEIEREAFISVSGNCPLNLDEVQHFLTLCPELSLGWFVEGRLVAFI
IGSLWDEERLTQESLALHRPRGHSAHLHALAVHRSFRQQGKGSVLLWRYLHHVGAQPAVRRAVLM
CEDALVPFYQRFGFHPAGPCAIVVGSLTFTEMHCSL
>d1i12a_ d.108.1.1 (A:) Glucosamine-phoshate N-acetyltransferase
GNA1 {Baker's yeast (Saccharomyces cerevisiae)}
LPDGFYIRRMEEGDLEQVTETLKVLTTVGTITPESFCKLIKYWNEATVWNDNEDKKIMQYNPMVI
VDKRTETVAATGNIIIERKIIHELGLCGHIEDIAVNSKYQGQGLGKLLIDQLVTIGFDYGCYKII
LDCDEKNVKFYEKCGFSNAGVEMQIRK
>d1iica1 d.108.1.2 (A:34-218) N-myristoyl transferase, NMT {Baker's
yeast (Saccharomyces cerevisiae)}
AMKDHKFWRTQPVKDFDEKVVEEGPIDKPKTPEDISDKPLPLLSSFEWCSIDVDNKKQLEDVFVL
LNENYVEDRDAGFRFNYTKEFFNWALKSPGWKKDWHIGVRVKETQKLVAFISAIPVTLGVRGKQV
PSVEINFLCVHKQLRSKRLTPVLIKEITRRVNKCDIWHALYTAGIVLPAPVSTCR
>d1iica2 d.108.1.2 (A:219-455) N-myristoyl transferase, NMT {Baker's
yeast (Saccharomyces cerevisiae)}
YTHRPLNWKKLYEVDFTGLPDGHTEEDMIAENALPAKTKTAGLRKLKKEDIDQVFELFKRYQSRF
ELIQIFTKEEFEHNFIGEESLPLDKQVIFSYVVEQPDGKITDFFSFYSLPFTILNNTKYKDLGIG
YLYYYATDADFQFKDRFDPKATKALKTRLCELIYDACILAKNANMDVFNALTSQDNTLFLDDLKF
GPGDGFLNFYLFNYRAKPITGGLNPDNSNDIKRRSNVGVVML
>d1nmta1 d.108.1.2 (A:60-224) N-myristoyl transferase, NMT {Yeast
(Candida albicans)}
EGPIDKLKTPEDVPNDPLPLISDFEWSTLDIDDNLQLDELYKLLYDNYVEDIDATFRFKYSHEFF
QWALKPPGWRKDWHVGVRVKSTGKLVAFIAATPVTFKLNKSNKVIDSVEINFLCIHKKLRNKRLA
PVLIKEITRRVNKQNIWQALYTGGSILPTPLTTCR
>d1nmta2 d.108.1.2 (A:225-451) N-myristoyl transferase, NMT {Yeast
(Candida albicans)}
YQHRPINWSKLHDVGFSHLPPNQTKSSMVASYTLPNNPKLKGLRPMTGKDVSTVLSLLYKYQERF
DIVQLFTEEEFKHWMLGHDENSDSNVVKSYVVEDENGIITDYFSYYLLPFTVLDNAQHDELGIAY
LFYYASDSFEKPNYKKRLNELITDALITSKKFGVDVFNCLTCQDNTYFLKDCKFGSGDGFLNYYL
FNYRTFPMDGGIDKKTKEVVEDQTSGIGVVLL
>d2vik__ d.109.1.1 (-) Villin, domain 1 (res. 1-126) {Chicken (Gallus
gallus)}
VELSKKVTGKLDKTTPGIQIWRIENMEMVPVPTKSYGNFYEGDCYVLLSTRKTGSGFSYNIHYWL
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GKNSSQDEQGAAAIYTTQMDEYLGSVAVQHREVQGHESETFRAYFKQGLIYKQGGVASGMK
>d1svy__ d.109.1.1 (-) Severin, domain 2 {Dictyostelium discoideum}
EYKPRLLHISGDKNAKVAEVPLATSSLNSGDCFLLDAGLTIYQFNGSKSSPQEKNKAAEVARAID
AERKGLPKVEVFCETDSDIPAEFWKLLGGKGAIAAKH
>d1d0na2 d.109.1.1 (A:153-262) Gelsolin {Horse (Equus caballus)}
VPNEVVVQRLLQVKGRRVVRATEVPVSWESFNNGDCFILDLGNNIYQWCGSKSNRFERLKATQVS
KGIRDNERSGRAQVSVFEEGAEPEAMLQVLGPKPTLPEATEDTVK
>d1d0na3 d.109.1.1 (A:263-383) Gelsolin {Horse (Equus caballus)}
EDAANRKLAKLYKVSNGAGPMVVSLVADENPFAQGALRSEDCFILDHGKDGKIFVWKGKQANMEE
RKAALKTASDFISKMDYPKQTQVSVLPEGGETPLFRQFFKNWRDPDQTEGLGLAYL
>d1d0na4 d.109.1.1 (A:384-532) Gelsolin {Horse (Equus caballus)}
SSHIAHVERVPFDAATLHTSTAMAAQHGMDDDGTGQKQIWRVEGSNKVPVDPATYGQFYGGDSYI
ILYNYRHGSRQGQIIYNWQGAQSTQDEVAASAILTAQLDEELGGTPVQSRVVQGKEPAHLMSLFG
GKPMIVYKGGTSREGGQTA
>d1d0na5 d.109.1.1 (A:533-628) Gelsolin {Horse (Equus caballus)}
PASTRLFQVRASSSGATRAVEIIPKAGALNSNDAFVLKTPSAAYLWVGAGASEAEKTGAQELLRV
LRAQPVQVAEGSEPDSFWEALGGKATYRTSP
>d1d0na6 d.109.1.1 (A:629-755) Gelsolin {Horse (Equus caballus)}
RLKDKKMDAHPPRLFACSNKIGRFVIEEVPGEFMQEDLATDDVMLLDTWDQVFVWVGKDSQDEEK
TEALTSAKRYIDTDPAHRDRRTPITVVKQGFEPPSFVGWFLGWDDSYWSVDPLDRALAELAA
>d1d4xg_ d.109.1.1 (G:) Gelsolin {Human (Homo sapiens)}
VEHPEFLKAGKEPGLQIWRVEKFDLVPVPTNLYGDFFTGDAYVILKTVQLRNGNLQYDLHYWLGN
ECSQDESGAAAIFTVQLDDYLNGRAVQHREVQGFESATFLGYFKSGLKYKKGGVASGFK
>d1db0b1 d.109.1.1 (B:412-532) Gelsolin {Human (Homo sapiens)}
MDDDGTGQKQIWRIEGSNKVPVDPATYGQFYGGDSYIILYNYRHGGRQGQIIYNWQGAQSTQDEV
AASAILTAQLDEELGGTPVQSRVVQGKEPAHLMSLFGGKPMIIYKGGTSREGGQTA
>d1db0b3 d.109.1.1 (B:629-742) Gelsolin {Human (Homo sapiens)}
RLKDKKMDAHPPRLFACSNKIGRFVIEEVPGELMQEDLATDDVMLLDTWDQVFVWVGKDSQDEEK
TEALTSAKRYIETDPANRDRRTPITVVKQGFEPPSFVGWFLGWDDSYWS
>d1kcqa_ d.109.1.1 (A:) Gelsolin {Human (Homo sapiens)}
VVQRLFQVKGRRVVRATEVPVSWESFNNGDCFILDLGNNIHQWCGSNSNRYERLKATQVSKGIRD
NERSGRARVHVSEEGTEPEAMLQVLGPKPALPAGTEDTA
>d1f7sa_ d.109.1.2 (A:) Cofilin (actin depolymerizing factor, ADF)
{Plant (Arabidopsis thaliana), ADF1}
ASGMAVHDDCKLRFLELKAKRTHRFIVYKIEEKQKQVVVEKVGQPIQTYEEFAACLPADECRYAI
YDFDFVTAENCQKSKIFFIAWCPDIAKVRSKMIYASSKDRFKRELDGIQVELQATDPTE
>d1cfya_ d.109.1.2 (A:) Cofilin (actin depolymerizing factor, ADF)
{Baker's yeast (Saccharomyces cerevisiae)}
VAVADESLTAFNDLKLGKKYKFILFGLNDAKTEIVVKETSTDPSYDAFLEKLPENDCLYAIYDFE
YEINGNEGKRSKIVFFTWSPDTAPVRSKMVYASSKDALRRALNGVSTDVQGTDFSEVSYDSVLER
VSR
>d1cnua_ d.109.1.2 (A:) Cofilin (actin depolymerizing factor, ADF)
{Amoeba (Acanthamoeba castellanii), actophorin}
GIAVSDDCVQKFNELKLGHQHRYVTFKMNASNTEVVVEHVGGPNATYEDFKSQLPERDCRYAIFD
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YEFQVDGGQRNKITFILWAPDSAPIKSKMMYTSTKDSIKKKLVGIQVEVQATDAAEISEDAVSER
AKKD
>d1hqz1_ d.109.1.2 (1:) Cofilin-like domain of actin-binding protein
abp1p {Baker's yeast (Saccharomyces cerevisiae)}
LEPIDYTTHSREIDAEYLKIVRGSDPDTTWLIISPNAKKEYEPESTGSSFHDFLQLFDETKVQYG
LARVSPPGSDVEKIIIIGWCPDSAPLKTRASFAANFAAVANNLFKGYHVQVTARDEDDLDENELL
MKISNAAGA
>d1ak7__ d.109.1.2 (-) Destrin {Human and pig (Homo sapiens) and (Sus
scrofa)}
TMITPSSGNSASGVQVADEVCRIFYDMKVRKCSTPEEIKKRKKAVIFCLSADKKCIIVEEGKEIL
VGDVGVTITDPFKHFVGMLPEKDCRYALYDASFETKESRKEELMFFLWAPELAPLKSKMIYASSK
DAIKKKFQGIKHECQANGPEDLNRACIAEKLGGSLIVAFEGCPV
>d1pne__ d.110.1.1 (-) Profilin (actin-binding protein) {Cow (Bos
taurus)}
AGWNAYIDNLMADGTCQDAAIVGYKDSPSVWAAVPGKTFVNITPAEVGILVGKDRSSFFVNGLTL
GGQKCSVIRDSLLQDGEFTMDLRTKSTGGAPTFNITVTMTAKTLVLLMGKEGVHGGMINKKCYEM
ASHLRRSQY
>d1fil__ d.110.1.1 (-) Profilin (actin-binding protein) {Human (Homo
sapiens), isoform I}
AGWNAYIDNLMADGTCQDAAIVGYKDSPSVWAAVPGKTFVNITPAEVGVLVGKDRSSFYVNGLTL
GGQKCSVIRDSLLQDGEFSMDLRTKSTGGAPTFNVTVTKTDKTLVLLMGKEGVHGGLINKKCYEM
ASHLRRSQY
>d1d1ja_ d.110.1.1 (A:) Profilin (actin-binding protein) {Human (Homo
sapiens), isoform II}
AGWQSYVDNLMCDGCCQEAAIVGYCDAKYVWAATAGGVFQSITPIEIDMIVGKDREGFFTNGLTL
GAKKCSVIRDSLYVDGDCTMDIRTKSQGGEPTYNVAVGRAGRALVIVMGKEGVHGGTLNKKAYEL
ALYLRRSD
>d1acf__ d.110.1.1 (-) Profilin (actin-binding protein) {Acanthamoeba
castellanii}
SWQTYVDTNLVGTGAVTQAAILGLDGNTWATSAGFAVTPAQGTTLAGAFNNADAIRAGGFDLAGV
HYVTLRADDRSIYGKKGSSGVITVKTSKAILVGVYNEKIQPGTAANVVEKLADYLIGQGF
>d1f2ka_ d.110.1.1 (A:) Profilin (actin-binding protein)
{Acanthamoeba castellanii}
SWQTYVDTNLVGTGAVTQAAIIGHDGNTWATSAGFAVSPANGAALANAFKDATAIRSNGFELAGT
RYVTIRADDRSVYGKKGSAGVITVKTSKAILIGVYNEKIQPGTAANVVEKLADYLIGQGF
>d1ypra_ d.110.1.1 (A:) Profilin (actin-binding protein) {Baker's
yeast (Saccharomyces cerevisiae)}
SWQAYTDNLIGTGKVDKAVIYSRAGDAVWATSGGLSLQPNEIGEIVQGFDNPAGLQSNGLHIQGQ
KFMLLRADDRSIYGRHDAEGVVCVRTKQTVIIAHYPPTVQAGEATKIVEQLADYLIGVQY
>d1cqa__ d.110.1.1 (-) Profilin (actin-binding protein) {Birch
(Betula verrucosa)}
SWQTYVDEHLMCDIDGQGEELAASAIVGHDGSVWAQSSSFPQFKPQEITGIMKDFEEPGHLAPTG
LHLGGIKYMVIQGEAGAVIRGKKGSGGITIKKTGQALVFGIYEEPVTPGQCNMVVERLGDYLIDQ
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>d3nul__ d.110.1.1 (-) Profilin (actin-binding protein) {Mouse-ear cress (Arabidopsis thaliana)}
SWQSYVDDHLMCDVEGNHLTAAAILGQDGSVWAQSAKFPQLKPQEIDGIKKDFEEPGFLAPTGLF
LGGEKYMVIQGEQGAVIRGKKGPGGVTIKKTNQALVFGFYDEPMTGGQCNLVVERLGDYLIESEL
>d1g5ua_ d.110.1.1 (A:) Profilin (actin-binding protein) {Para rubber tree (Hevea brasiliensis), hevb8}
SWQTYVDDHLMCDIDGHRLTAAAIIGHDGSVWAQSSSFPQFKSDEVAAVMKDFDEPGSLAPTGLH
LGGTKYMVIQGEPGAVIRGKKGSGGITVKRTGQALIIGIYDEPLTPGQCNMIVERLGDYLLDQGL
>d1f5ma_ d.110.2.1 (A:) Hypothetical protein ykl069wp {Baker's yeast (Saccharomyces cerevisiae)}
STGFHHADHVNYSSNLNKEEILEQLLLSYEGLSDGQVNWVCNLSNASSLIWHAYKSLAVDINWAG
FYVTQASEENTLILGPFQGKVACQMIQFGKGVCGTAASTKETQIVPDVNKYPGHIACDGETKSEI
VVPIISNDGKTLGVIDIDCLDYEGFDHVDKEFLEKLAKLINKSCVF
>d3pyp__ d.110.3.1 (-) Photoactive yellow protein, PYP {Ectothiorhodospira halophila}
MEHVAFGSEDIENTLAKMDDGQLDGLAFGAIQLDGDGNILQYNAAEGDITGRDPKQVIGKNFFKD
VAPCTDSPEFYGKFKEGVASGNLNTMFEYTFDYQMTPTKVKVHMKKALSGDSYWVFVKRV
>d1ew0a_ d.110.3.2 (A:) Histidine kinase FixL heme domain {Rhizobium meliloti}
GSHMLETEDVVRARDAHLRSILDTVPDATVVSATDGTIVSFNAAAVRQFGYAEEEVIGQNLRILM
PEPYRHEHDGYLQRYMATGEKRIIGIDRVVSGQRKDGSTFPMKLAVGEMRSGGERFFTGFIRDLT
>d1dp6a_ d.110.3.2 (A:) Histidine kinase FixL heme domain {Bradyrhizobium japonicum}
DAMIVIDGHGIIQLFSTAAERLFGWSELEAIGQNVNILMPEPDRSRHDSYISRYRTTSDPHIIGI
GRIVTGKRRDGTTFPMHLSIGEMQSGGEPYFTGFVRDLTEHQQTQARLQEL
>d1bywa_ d.110.3.3 (A:) Erg potassium channel, N-terminal domain {Human (Homo sapiens)}
SRKFIIANARVENCAVIYCNDGFCELCGYSRAEVMQRPCTCDFLHGPCTQRRAAAQIAQALLGAE
ERKVEIAFYRKDGSCFLCLVDVVPVKNEDGAVIMFILNFEVVMEK
>d1g28a_ d.110.3.4 (A:) Photoreceptor phy3 flavin-binding domain, lov2 {Maidenhair fern (Adiantum capillus-veneris)}
KSFVITDPRLPDNPIIFASDRFLELTEYTREEVLGNNCRFLQGRGTDRKAVQLIRDAVKEQRDVT
VQVLNYTKGGRAFWNLFHLQVMRDENGDVQYFIGVQQEM
>d1ifqa_ d.110.4.1 (A:) Sec22b {Mouse (Mus musculus)}
SVLLTMIARVADGLPLAASMQEDEQSGRDLQQYQSQAKQLFRKLNEQSPTRCTLEAGAMTFHYII
EQGVCYLVLCEAAFPKKLAFAYLEDLHSEFDEQHGKKVPTVSRPYSFIEFDTFIQKTKKLYI
>d1h8ma_ d.110.4.1 (A:) Synaptobrevin homolog 1 ykt6 {Baker's yeast (Saccharomyces cerevisiae)}
MRIYYIGVFRSGGEKALELSEVKDLSQFGFFERSSVGQFMTFFAETVASRTGAGERQSIEEGNYI
GHVYARSEGICGVLITDKQYPVRPAYTLLNKILDEYLVAHPKEEWADVTETNDALKMKQLDTYIS
KYQDPSQADA
>d1cfe__ d.111.1.1 (-) Pathogenesis-related protein 1 (PR1) {Tomato (Lycopersicon esculentum), P14a}
QNSPQDYLAVHNDARAQVGVGPMSWDANLASRAQNYANSRAGDCNLIHSGAGENLAKGGGDFTGR

AAVQLWVSERPSYNYATNQCVGGKKCRHYTQVVWRNSVRLGCGRARCNNGWWFISCNYDPVGNWI
GQRPY
>d1qnxa_ d.111.1.1 (A:) Insect allergen 5 (AG5) {Yellow jacket (Vespula vulgaris), Ves v 5}
AEAEFNNYCKIKCLKGGVHTACKYGSLKPNCGNKVVVSYGLTKQEKQDILKEHNDFRQKIARGLE
TRGNPGPQPPAKNMKNLVWNDELAYVAQVWANQCQYGHDTCRDVAKYQVGQNVALTGSTAAKYDD
PVKLVKMWEDEVKDYNPKKKFSGNDFLKTGHYTQMVWANTKEVGCGSIKYIQEKWHKHYLVCNYG
PSGNFKNEELYQTK
>d1a6ja_ d.112.1.1 (A:) Nitrogen regulatory bacterial protein IIa-ntr {Escherichia coli}
LQLSSVLNRECTRSRVHCQSKKRALEIISELAAKQLSLPPQVVFEAILTREKMGSTGIGNGIAIP
HGKLEEDTLRAVGVFVQLETPIAFDAIDNQPVDLLFALLVPADQTKTHLHTLSLVAKRLADKTIC
RRLRAAQSDEELYQIITDTE
>d1a3aa_ d.112.1.1 (A:) Phosphotransferase IIa-mannitol {Escherichia coli}
LFKLGAENIFLGRKAATKEEAIRFAGEQLVKGGYVEPEYVQAMLDREKLTPTYLGESIAVPHGTV
EAKDRVLKTGVVFCQYPEGVRFGEEEDDIARLVIGIAARNNEHIQVITSLTNALDDESVIERLAH
TTSVDEVLELLAGRK
>d1hynp_ d.112.1.2 (P:) Erythrocite membrane Band 3 {Human (Homo sapiens)}
KVYVELQELVMDEKNQELRWMEAARWVQLEENLGENGAWGRPHLSHLTFWSLLELRRVFTKGTVL
LDLQETSLAGVANQLLDRFIFEDQIRPQDREELLRALLLKHSHAGELEALGGVKPAVLTRSGDPS
QPLLPQHSSLETQLFCEQGDGGTEGHSPSGILEKIPPDSEATLVLVGRADFLEQPVLGFVRLQEA
AELEAVELPVPIRFLFVLLGPEAPHIDYTQLGRAAATLMSERVFRIDAYMAQSRGELLHSLEGFL
DCSLVLPPTDAPSEQALLSLVPVQRELLRRRYQ
>d1mut__ d.113.1.1 (-) Nucleoside triphosphate pyrophosphorylase (MutT) {Escherichia coli}
MKKLQIAVGIIRNENNEIFITRRAADAHMANKLEFPGGKIEMGETPEQAVVRELQEEVGITPQHF
SLFEKLEYEFPDRHITLWFWLVERWEGEPWGKEGQPGEWMSLVGLNADDFPPANEPVIAKLKRL
>d1g0sa_ d.113.1.1 (A:) ADP-ribose pyrophosphatase {Escherichia coli}
MLKPDNLPVTFGKNDVEIIARETLYRGFFSLDLYRFRHRLFNGQMSHEVRREIFERGHAAVLLPF
DPVRDEVVLIEQIRIAAYDTSETPWLLEMVAGMIEEGESVEDVARREAIEEAGLIVKRTKPVLSF
LASPGGTSERSSIMVGEVDATTASGIHGLADENEDIRVHVVSREQAYQWVEEGKIDNAASVIALQ
WLQLHHQALKNEWA
>d1jkna_ d.113.1.1 (A:) Diadenosine tetraphosphate hydrolase {Narrow-leaved blue lupine (Lupinus angustifolius)}
GPLGSMDSPPEGYRRNVGICLMNNDKKIFAASRLDIPDAWQMPQGGIDEGEDPRNAAIRELREET
GVTSAEVIAEVPYWLTYDFPPKVREKLNIQWGSDWKGQAQKWFLFKFTGQDQEINLLGDGSEKPE
FGEWSWVTPEQLIDLTVEFKKPVYKEVLSVFAPHL
>d1hx3a_ d.113.1.2 (A:) Isopentenyl diphosphate isomerase {Escherichia coli}
EHVILLNAQGVPTGTLEKYAAHTADTRLHLAFSSWLFNAKGQLLVTRRALSKKAWPGVWTNSVAG
HPQLGESNEDAVIRRCRYELGVEITPPESIYPDFRYRATDPSGIVENEVCPVFAARTTSALQIND
DEVMDYQWCDLADVLHGIDATPWAFSPWMVMQATNREARKRLSAFT

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>d1hzta_ d.113.1.2 (A:) Isopentenyl diphosphate isomerase
{Escherichia coli}
LHLAFSSWLFNAKGQLLVTRRALSKKAWPGVWTNSVCGHPQLGESNEDAVIRRCRYELGVEITPP
ESIYPDFRYRATDPSGIVENEVCPVFAARTTSALQINDDEVMDYQWCDLADVLHGIDATPWAFSP
WMVMQATNREARKRLSAFTQLKL
>d1ush_1 d.114.1.1 (363-550) 5'-nucleotidase (syn. UDP-sugar
hydrolase), C-terminal domain {Escherichia coli}
KIGETNGRLEGDRDKVRFVQTNMGRLILAAQMDRTGADFAVMSGGGIRDSIEAGDISYKNVLKVQ
PFGNVVVYADMTGKEVIDYLTAVAQMKPDSGAYPQFANVSFVAKDGKLNDLKIKGEPVDPAKTYR
MATLNFNATGGDGYPRLDNKPGYVNTGFIDAEVLKAYIQKSSPLDVSVYEPKGEVSWQ
>d1hrua_ d.115.1.1 (A:) Hypothetical protein YrdC {Escherichia coli}
NNLQRDAIAAAIDVLNEERVIAYPTEAVFGVGCDPDSETAVMRLLELKQRPVDKGLILIAANYEQ
LKPYIDDTMLTDVQRETIFSRWPGPVTFVFPAPATTPRWLTGRFDSLAVRVTDHPLVVALCQAYG
KPLVSTSANLSGLPPCRTVDEVRAQFGAAFPVVPGETGGRLNPSEIRDALTGELFR
>d1g57a_ d.115.1.2 (A:) 3,4-dihydroxy-2-butanone 4-phosphate
synthase, DHBP synthase, RibB {Escherichia coli}
LLSSFGTPFERVENALAALREGRGVMVLDDEDRENEGDMIFPAETMTVEQMALTIRHGSGIVCLC
ITEDRRKQLDLPMMVENNTSAYGTGFTVTIEAAEGVTTGVSAADRITTVRAAIADGAKPSDLNRP
GHVFPLRAQAGGVLTRGGHTEATIDLMTLAGFKPAGVLCELTNDDGTMARAPECIEFANKHNMAL
VTIEDLVAYRQAHE
>d1dbxa_ d.116.1.1 (A:) Hypothetical protein HI1434 (YbaK homologue)
{Haemophilus influenzae}
TPAIDLLKKQKIPFILHTYDHDPNNQHFGDEAAEKLGIDPNRSFKTLLVAENGDQKKLACFVLAT
ANMLNLKKAAKSIGVKKVEMADKDAAQKSTGYLVGGISPLGQKKRVKTVINSTALEFETIYVSGG
KRGLSVEIAPQDLAKVLGAEFTDIVDE
>d1qqqa_ d.117.1.1 (A:) Thymidylate synthase {Escherichia coli}
MKQYLELMQKVLDEGTQKNDRTGTGTLSIFGHQMRFNLQDGFPLVTTKRCHLRSIIHELLWFLQG
DTNIAYLHENNVTIWDEWADENGDLGPVYGKQWRAWPTPDGRHIDQITTVLNQLKNDPDSRRIIV
SAWNVGELDKMALAPCHAFFQFYVADGKLSCQLYQRSCDVFLGLPFNIASYALLVHMMAQQCDLE
VGDFVWTGGDTHLYSNHMDQTHLQLSREPRPLPKLIIKRKPESIFDYRFEDFEIEGYDSHPGIKA
PVAI
>d1tsy__ d.117.1.1 (-) Thymidylate synthase {Lactobacillus casei}
MLEQPYLDLAKKVLDEGHFKPDRTHTGTYSIFGHQMRFDLSKGFPLLTTKKVPFGLIKSELLWFL
HGDTNIRFLLQHRNHIWDEWAFEKWVKSDEYHGPDMTDFGHRSQKDPEFAAVYHEEMAKFDDRVL
HDDAFAAKYGDLGLVYGSQWRAWHTSKGDTIDQLGDVIEQIKTHPYSRKLIVSAWNPEDVPTMAL
PPCHTLYQFYVNDGKLSLQLYQRSADIFLGVPFNIASYALLTHLVAHECGLEVGEFIHTFGDAHL
YVNHLDQIKEQLSRTPRPAPTLQLNPDKHDIFDFDMKDIKLLNYDPYPAIKAPVAV
>d1bkpa_ d.117.1.1 (A:) Thymidylate synthase {Bacillus subtilis}
TQFDKQYNSIIKDIINNGISDEEFDVRTKWDSDGTPAHTLSVISKQMRFDNSEVPILTTKKVAWK
TAIKELLWIWQLKSNDVNDLNMMGVHIWDQWKQEDGTIGHAYGFQLGKKNRSLNGEKVDQVDYLL
HQLKNNPSSRRHITMLWNPDELDAMALTPCVYETQWYVKHGKLHLEVRARSNDMALGNPFNVFQY
NVLQRMIAQVTGYELGEYIFNIGDCHVYTRHIDNLKIQMEREQFEAPELWINPEVKDFYDFTIDD
FKLINYKHGDKLLFEVAV
>d1tis__ d.117.1.1 (-) Thymidylate synthase {Bacteriophage T4}
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MKQYQDLIKDIFENGYETDDRTGTGTIALFGSKLRWDLTKGFPAVTTKKLAWKACIAELIWFLSG
STNVNDLRLIQHDSLIQGKTVWDENYENQAKDLGYHSGELGPIYGKQWRDFGGVDQIIEVIDRIK
KLPNDRRQIVSAWNPAELKYMALPPCHMFYQFNVRNGYLDLQWYQRSVDVFLGLPFNIASYATLV
HIVAKMCNLIPGDLIFSGGNTHIYMNHVEQCKEILRREPKELCELVISGLPYKFRYLSTKEQLKY
VLKLRPKDFVLNNYVSHPPIKGKMAV
>d1f28a_ d.117.1.1 (A:) Thymidylate synthase {Pneumocystis carinii}
NAEEQQYLNLVQYIINHGEDRPDRTGTGTLSVFAPSPLKFSLRNKTFPLLTTKRVFIRGVIEELL
WFIRGETDSLKLREKNIHIWDANGSREYLDSIGLTKRQEGDLGPIYGFQWRHFGAEYIDCKTNYI
GQGVDQLANIIQKIRTSPYDRRLILSAWNPADLEKMALPPCHMFCQFYVHIPSNNHRPELSCQLY
QRSCDMGLGVPFNIASYALLTCMIAHVCDLDPGDFIHVMGDCHIYKDHIEALQQQLTRSPRPFPT
LSLNRSITDIEDFTLDDFNIQNYHPYETIKMKMSI
>d2tsra_ d.117.1.1 (A:) Thymidylate synthase {Rat (Rattus norvegicus)}
QHGELQYLRQVEHIMRCGFKKEDRTGTGTLSVFGMQARYSLRDEFPLLTTKRVFWKGVLEELLWF
IKGSTNAKELSSKGVRIWDANGSRDFLDSLGFSARQEGDLGPVYGFQWRHFGADYKDMDSDYSGQ
GVDQLQKVIDTIKTNPDDRRIIMCAWNPKDLPLMALPPCHALCQFYVVNGELSCQLYQRSGDMGL
GVPFNIASYALLTYMIAHITGLQPGDFVHTLGDAHIYLNHIEPLKIQLQREPRPFPKLRILRKVE
TIDDFKVEDFQIEGYNPHPTI
>d1hvya_ d.117.1.1 (A:) Thymidylate synthase {Human (Homo sapiens)}
PPHGELQYLGQIQHILRCGVRKDDRTGTGTLSVFGMQARYSLRDEFPLLTTKRVFWKGVLEELLW
FIKGSTNAKELSSKGVKIWDANGSRDFLDSLGFSTREEGDLGPVYGFQWRHFGAEYRDMESDYSG
QGVDQLQRVIDTIKTNPDDRRIIMCAWNPRDLPLMALPPCHALCQFYVVNSELSCQLYQRSGDMG
LGVPFNIASYALLTYMIAHITGLKPGDFIHTLGDAHIYLNHIEPLKIQLQREPRPFPKLRILRKV
EKIDDFKAEDFQIEGYNPHPTIKMEMAV
>d1b5ea_ d.117.1.1 (A:) dCMP hydroxymethylase {Bacteriophage T4}
MISDSMTVEEIRLHLGLALKEKDFVVDKTGVKTIEIIGASFVADEPFIFGALNDEYIQRELEWYK
SKSLFVKDIPGETPKIWQQVASSKGEINSNYGWAIWSEDNYAQYDMCLAELGQNPDSRRGIMIYT
RPSMQFDYNKDGMSDFMCTNTVQYLIRDKKINAVVNMRSNDVVFGFRNDYAWQKYVLDKLVSDLN
AGDSTRQYKAGSIIWNVGSLHVYSRHFYLVDHWWKTGETHISKKDY
>d1kq4a_ d.207.1.1 (A:) Thy1 homologue {Thermotoga maritima, TM0449}
HMKIDILDKGFVELVDVMGNDLSAVRAARVSFDMGLKDEERDRHLIEYLMKHGHETPFEHIVFTF
HVKAPIFVARQWFRHRIASYNELSGRYSKLSYEFYIPSPERLEGYKTTIPPERVTEKISEIVDKA
YRTYLELIESGVPREVARIVLPLNLYTRFFWTVNARSLMNFLNLRADSHAQWEIQQYALAIARIF
KEKCPWTFEAFLKYAYKGDIL
>d1lba__ d.118.1.1 (-) Bacteriophage T7 lysozyme (Zn amidase) {Bacteriophage T7}
AKQRESTDAIFVHCSATKPSQNVGVREIRQWHKEQGWLDVGYHFIIKRDGTVEAGRDEMAVGSHA
KGYNHNSIGVCLVGGIDDKGKFDANFTPAQMQSLRSLLVTLLAKYEGAVLRAHHEVAPKACPSFD
LKRWWEKNELVTSDRG
>d1cyo__ d.120.1.1 (-) Cytochrome b5 {Cow (Bos taurus)}
SKAVKYYTLEEIQKHNNSKSTWLILHYKVYDLTKFLEEHPGGEEVLREQAGGDATENFEDVGHST
DARELSKTFIIGELHPDDRSKIT
>d1f03a_ d.120.1.1 (A:) Cytochrome b5 {Cow (Bos taurus)}
AVKYYTLEEIQKHNNSKSTWLILHYKVYDLTKFLEEHPGGEAVLRAQAGGDATANFEAVGHSTDA
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RELSKTFIIGELHPDDR
>d1aqa__ d.120.1.1 (-) Cytochrome b5 {Rat (Rattus norvegicus)}
KYYTLEEIQKHKDSKSTWVILHHKVYDLTKFLEEHPGGEEVLREQAGGDATENFEDVGHSTDARE
LSKTYIIGELHPDDRSKIA
>d1axx__ d.120.1.1 (-) Cytochrome b5 {Rat (Rattus norvegicus)}
DKDVKYYTLEEIQKHKDSKSTWVILHHKVYDLTKFLEEHPGGEEVLREQAGGDATENFEDVGHST
DARELSKTYIIGELHPDDRSKIAKPSETL
>d1euea_ d.120.1.1 (A:) Cytochrome b5 {Rat (Rattus norvegicus)}
DPAVTYYRLEEVAKRNTAEETWMVIHGRVYDITRFLSEHPGGEEILLEQAGADATESFEDIGHSP
DAREMLKQYYIGDVHPNDLKP
>d1icca_ d.120.1.1 (A:) Cytochrome b5 {Rat (Rattus norvegicus)}
DPAVTYYRLEEVAKRNTSEETWMVIHGRVYDLTRFLSEHPGGEEVLREQAGADATESFEDVGHSP
DAREMLKQYYIGDVHPNDLKPK
>d1do9a_ d.120.1.1 (A:) Cytochrome b5 {Rabbit (Oryctolagus cuniculus)}
DKDVKYYTLEEIKKHNHSKSTWLILHHKVYDLTKFLEEHPGGEEVLREQAGGDATENFEDVGHST
DARELSKTFIIGELHPDDRSKLSKPMETL
>d1cxya_ d.120.1.1 (A:) Cytochrome b558 {Ectothiorhodospira vacuolata}
TLPVFTLEQVAEHHSPDDCWMAIHGKVYDLTPYVPNHPGPAGMMLVWCGQESTEAWETKSYGEPH
SSLAARLLQRYLIGTL
>d1ltda2 d.120.1.1 (A:10-97) Flavocytochrome b2, N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
KISPAEVAKHNKPDDCWVVINGYVYDLTRFLPNHPGGQDVIKFNAGKDVTAIFEPLHAPNVIDKY
IAPEKKLGPLQGSMPPELVCPPY
>d1soxa2 d.120.1.1 (A:3-93) Sulfite oxidase, N-terminal domain {Chicken (Gallus gallus)}
SYPEYTREEVGRHRSPEERVWVTHGTDVFDVTDFVELHPGGPDKILLAAGGALEPFWALYAVHGE
PHVLELLQQYKVGELSPDEAPAAPDA
>d1vcc__ d.121.1.1 (-) Vaccinia DNA topoisomerase I, 9 kDa N-terminal fragment {Vaccinia virus, strain WR}
MRALFYKDGKLFTDNNFLNPVSDDNPAYEVLQHVKIPTHLTDVVVYEQTWEEALTRLIFVGSDSK
GRRQYFYGKMHV
>d1amw__ d.122.1.1 (-) HSP90 {Baker's yeast (Saccharomyces cerevisiae)}
ASETFEFQAEITQLMSLIINTVYSNKEIFLRELISNASDALDKIRYKSLSDPKQLETEPDLFIRI
TPKPEQKVLEIRDSGIGMTKAELINNLGTIAKSGTKAFMEALSAGADVSMIGQFGVGFYSLFLVA
DRVQVISKSNDDEQYIWESNAGGSFTVTLDEVNERIGRGTILRLFLKDDQLEYLEEKRIKEVIKR
HSEFVAYPIQLVVTKEVE
>d1byqa_ d.122.1.1 (A:) HSP90 {Human (Homo sapiens)}
PMEEEEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISNSSDALDKIRYETLTDPSKLDSGKE
LHINLIPNKQDRTLTIVDTGIGMTKADLINNLGTIAKSGTKAFMEALQAGADISMIGQFGVGFYS
AYLVAEKVTVITKHNDDEQYAWESSAGGSFTVRTDTGEPMGRGTKVILHLKEDQTEYLEERRIKE
IVKKHSQFIGYPITLFVE
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>d1ei1a2 d.122.1.2 (A:2-220) DNA gyrase B {Escherichia coli}
SNSSDSSSIKVLKGLDAVRKRPGMYIGDTDDGTGLHHMVFEVVDNAIDEALAGHCKEIIVTIHAD
NSVSVQDDGRGIPTGIHPEEGVSAAEVIMTVLHAGGKFDDNSYKVSGGLHGVGVSVVNALSQKLE
LVIQREGKIHRQIYEHGVPQAPLAVTGETEKTGTMVRFWPSLETFTNVTEFEYEILAKRLRELSF
LDSGVSIRLRDKRDGKEDHFHYEG
>d1b63a2 d.122.1.2 (A:-2-216) DNA mismatch repair protein MutL {Escherichia coli}
SHMPIQVLPPQLANQIAAGEVVERPASVVKELVENSLDAGATRIDIDIERGGAKLIRIRDNGCGI
KKDELALALARHATSKIASLDDLEAIISLGFRGEALASISSVSRLTLTSRTAEQQEAWQAYAEGR
DMNVTVKPAAHPVGTTLEVLDLFYNTPARRKFLRTEKTEFNHIDEIIRRIALARFDVTINLSHNG
KIVRQYRAVPEGGQKERRLGAIC
>d1bkna2 d.122.1.2 (A:20-216) DNA mismatch repair protein MutL {Escherichia coli}
VERPASVVKELVENSLDAGATRIDIDIERGGAKLIRIRDNGCGIKKDELALALARHATSKIASLD
DLEAIISLGFRGEALASISSVSRLTLTSRTAEQQEAWQAYAEGRDMNVTVKPAAHPVGTTLEVLD
LFYNTPARRKFLRTEKTEFNHIDEIIRRIALARFDVTINLSHNGKIVRQYRAVPEGGQKERRLGA
IC
>d1h7sa2 d.122.1.2 (A:29-231) DNA mismatch repair protein PMS2 {Human (Homo sapiens)}
GQVVLSLSTAVKELVENSLDAGATNIDLKLKDYGVDLIEVSDNGCGVEEENFEGLTLKHHTSKIQ
EFADLTQVETFGFRGEALSSLCALSDVTISTCHASAKVGTRLMFDHNGKIIQKTPYPRPRGTTVS
VQQLFSTLPVRHKEFQRNIKKEYAKMVQVLHAYCIISAGIRVSCTNQLGQGKRQPVVCTGGSPSI
KENIGSVF
>d1bxda_ d.122.1.3 (A:) Histidine kinase domain of the osmosensor EnvZ {Escherichia coli}
TGQEMPMEMADLNAVLGEVIAAESGYEREIETALYPGSIEVKMHPLSIKRAVANMVVNAARYGNG
WIKVSSGTEPNRAWFQVEDDGPGIAPEQRKHLFQPFVRGDSARTISGTGLGLAIVQRIVDNHNGM
LELGTSERGGLSIRAWLPVPVTRAQGTTKEG
>d1i58a_ d.122.1.3 (A:) Histidine kinase CheA {Thermotoga maritima}
GSHMVPISFVFNRFPRMVRDLAKKMNKEVNFIMRGEDTELDRTFVEEIGEPLLHLLRNAIDHGIE
PKEERIAKGKPPIGTLILSARHEGNNVVIEVEDDGRGIDKEKIIRKAIEKGLIDESKAATLSDQE
ILNFLFVPGFSTKEKVSEVSGRGVGMDVVKNVVESLNGSISIESEKDKGTKVTIRLPLT
>d1id0a_ d.122.1.3 (A:) Histidine kinase PhoQ domain {Escherichia coli}
RELHPVAPLLDNLTSALNKVYQRKGVNISLDISPEISFVGEQNDFVEVMGNVLDNACKYCLEFVE
ISARQTDEHLYIVVEDDGPGIPLSKREVIFDRGQRVDTLRPGQGVGLAVAREITEQYEGKIVAGE
SMLGGARMEVIFGRQH
>d1gkza2 d.122.1.4 (A:186-378) Branched-chain alpha-ketoacid dehydrogenase kinase (BCK) {Rat (Rattus norvegicus)}
DFVGIICTRLSPKKIIEKWVDFARRLCEHKYGNAPRVRINGHVAARFPFIPMPLDYILPELLKNA
MRATMESHLDTPYNVPDVVITIANNDVDLIIRISDRGGGIAHKDLDRVMDYHFTTAEASTQDPRI
SPLFGHLDMHSGGQSGPMHGFGFGLPTSRAYAEYLGGSLQLQSLQGIGTDVYLRLRHIDGREE
>d1jm6a2 d.122.1.4 (A:1177-1366) Pyruvate dehydrogenase kinase {Rat (Rattus norvegicus), isozyme 2}

PKHIGSIDPNCSVSDVVKDAYDMAKLLCDKYYMASPDLEIQEVNATNATQPIHMVYVPSHLYHML
FELFKNAMRATVESHESSLTLPPIKIMVALGEEDLSIKMSDRGGGVPLRKIERLFSYMYSTAPTP
QPGTGGTPLAGFGYGLPISRLYAKYFQGDLQLFSMEGFGTDAVIYLKALSTDSVERLPVY
>d1ixma_ d.123.1.1 (A:) Sporulation responce regulatory protein Spo0B {Bacillus subtilis}
SDTALTNELIHLLGHSRHDWMNKLQLIKGNLSLQKYDRVFEMIEEMVIDAKHESKLSNLKTPHLA
FDFLTFNWKTHYMTLEYEVLGEIKDLSAYDQKLAKLMRKLFHLFDQAVSRESENHLTVSLQTDHP
DRQLILYLDFHGAFADPSAFDDIRQNGYEDVDIMRFEITSHECLIEIGL
>d1bola_ d.124.1.1 (A:) Ribonuclease Rh {Rhizopus niveus}
SSCSSTALSCSNSANSDTCCSPEYGLVVLNMQWAPGYGPDNAFTLHGLWPDKCSGAYAPSGGCDS
NRASSSIASVIKSKDSSLYNSMLTYWPSNQGNNNVFWSHEWSKHGTCVSTYDPDCYDNYEEGEDI
VDYFQKAMDLRSQYNVYKAFSSNGITPGGTYTATEMQSAIESYFGAKAKIDCSSGTLSDVALYFY
VRGRDTYVITDALSTGSCSGDVEYPTK
>d1bk7a_ d.124.1.1 (A:) Ribonuclease MC1 {Bitter gourd (Momordica charantia)}
FDSFWFVQQWPPAVCSFQKSGSCPGSGLRTFTIHGLWPQQSGTSLTNCPGSPFDITKISHLQSQL
NTLWPNVLRANNQQFWSHEWTKHGTCSESTFNQAAYFKLAVDMRNNYDIIGALRPHAAGPNGRTK
SRQAIKGFLKAKFGKFPGLRCRTDPQTKVSYLVQVVACFAQDGSTLIDCTRDTCGANFIF
>d1dixa_ d.124.1.1 (A:) RNase LE {Tomatoes (Lycopersicon esculentum)}
ASGSKDFDFFYFVQQWPGSYCDTKQSCCYPTTGKPAADFGIHGLWPNNNDGTYPSNCDPNSPYDQ
SQISDLISSMQQNWPTLACPSGSGSTFWSHEWEKHGTCAESVLTNQHAYFKKALDLKNQIDLLSI
LQGADIHPDGESYDLVNIRNAIKSAIGYTPWIQCNVDQSGNSQLYQVYICVDGSGSSLIECPIFP
GGKCGTSIEFPTF
>d1iqqa_ d.124.1.1 (A:) S3-RNase {Japanese pear (Pyrus pyrifolia)}
YDYFQFTQQYQLAVCNSNRTLCKDPPDKLFTVHGLWPSNMVGPDPSKCPIKNIRKREKLLEHQLE
IIWPNVFDRTKNNLFWDKEWMKHGSCGYPTIDNENHYFETVIKMYISKKQNVSRILSKAKIEPDG
KKRALLDIENAIRNGADNKKPKLKCQKKGTTTELVEITLCSDKSGEHFIDCPHPFEPISPHYCPT
NNIKY
>d1g2ra_ d.192.1.1 (A:) Hypothetical cytosolic protein SP0554 {Streptococcus pneumoniae}
RKIPLRKSVVSNEVIDKRDLLRIVKNKEGQVFIDPTGKANGRGAYIKLDNAEALEAKKKKVFNRS
FSMEVEESFYDELIAYVDHKVKRRELGLE
>d1c4ka3 d.125.1.1 (A:570-730) Ornithine decarboxylase C-terminal domain {Lactobacillus sp., strain 30a}
APLKQVLPSIYAANEERYNGYTIRELCQELHDFYKNNNTFTYQKRLFLREFFPEQGMLPYEARQE
FIRNHNKLVPLNKIEGEIALEGALPYPPGVFCVAPGEKWSETAVKYFTILQDGINNFPGFAPEIQ
GVYFKQEGDKVVAYGEVYDAEVAKNDDRYNN
>d1g61a_ d.126.1.1 (A:) Ribosome anti-association factor eIF6 (aIF6) {Archaeon Methanococcus jannaschii}
MIIRKYFSGIPTIGVLALTTEEITLLPIFLDKDDVNEVSEVLETKCLQTNIGGSSLVGSLSVANK
YGLLLPKIVEDEELDRIKNFLKENNLDLNVEIIKSKNTALGNLILTNDKGALISPELKDFKKDIE
DSLNVEVEIGTIAELPTVGSNAVVTNKGCLTHPLVEDDELEFLKSLFKVEYIGKGTANKGTTSVG
ACIIANSKGAVVGGDTTGPELLIIEDALGL
>d1g62a_ d.126.1.1 (A:) Ribosome anti-association factor eIF6 (aIF6)

{Baker's yeast (Saccharomyces cerevisiae)}
MATRTQFENSNEIGVFSKLTNTYCLVAVGGSENFYSAFEAELGDAIPIVHTTIAGTRIIGRMTAG
NRRGLLVPTQTTDQELQHLRNSLPDSVKIQRVEERLSALGNVICCNDYVALVHPDIDRETEELIS
DVLGVEVFRQTISGNILVGSYCSLSNQGGLVHPQTSVQDQEELSSLLQVPLVAGTVNRGSSVVGA
GMVVNDYLAVTGLDTTAPELSVIESIFRL
>d1jdw__ d.126.1.2 (-) L-arginine: glycine amidinotransferase {Human (Homo sapiens)}
CPVSSYNEWDPLEEVIVGRAENACVPPFTIEVKANTYEKYWPFYQKQGGHYFPKDHLKKAVAEIE
EMCNILKTEGVTVRRPDPIDWSLKYKTPDFESTGLYSAMPRDILIVVGNEIIEAPMAWRSRFFEY
RAYRSIIKDYFHRGAKWTTAPKPTMADELYNQDYPIHSVEDRHKLAAQGKFVTTEFEPCFDAADF
IRAGRDIFAQRSQVTNYLGIEWMRRHLAPDYRVHIISFKDPNPMHIDATFNIIGPGIVLSNPDRP
CHQIDLFKKAGWTIITPPTPIIPDDHPLWMSSKWLSMNVLMLDEKRVMVDANEVPIQKMFEKLGI
TTIKVNIRNANSLGGGFHCWTCDVRRRGTLQSYLD
>d1bwda_ d.126.1.2 (A:) L-arginine: inosamine-phosphate amidinotransferase {Streptomyces griseus}
RSLVSVHNEWDPLEEVIVGTAVGARVPTADRSVFAVEYAGDYESQEQIPSGAYPDRVLKETEEEL
HVLAAELTKLGVTVRRPGPRDHSALIKTPDWETDGFHDYCPRDGLLSVGQTIIETPMALRSRFLE
SLAYKDLLLEYFASGSRWLSAPKPRLTDDSYAPQAPAGERLTDEEPVFDAANVLRFGTDLLYLVS
DSGNELGAKWLQSAVGDTYTVHPCRKLYASTHVDSTIVPLRPGLVLTNPSRVNDENMPDFLRSWE
NITCPELVDIGFTGDKPHCSVWIGMNLLVVRPDLAVVDRRQTALIRLLEKHGMNVLPLQLTHSRT
LGGGFHCATLDVRRTGALETYQF
>d1h70a_ d.126.1.3 (A:) Dimethylarginine dimethylaminohydrolase DDAH {Pseudomonas aeruginosa}
FMFKHIIARTPARSLVDGLTSSHLGKPDYAKALEQHNAYIRALQTCDVDITLLPPDERFPDSVFV
EDPVLCTSRCAIITRPGAESRRGETEIIEETVQRFYPGKVERIEAPGTVEAGDIMMVGDHFYIGE
SARTNAEGARQMIAILEKHGLSGSVVRLEKVLHLKTGLAYLEHNNLLAAGEFVSKPEFQDFNIIE
IPEEESYAANCIWVNERVIMPAGYPRTREKIARLGYRVIEVDTSEYRKIDGGVSSMSLRF
>d1chma2 d.127.1.1 (A:157-402) Creatinase, catalytic (C-terminal) domain {Pseudomonas putida}
MIKSAEEHVMIRHGARIADIGGAAVVEALGDQVPEYEVALHATQAMVRAIADTFEDVELMDTWTW
FQSGINTDGAHNPVTTRKVNKGDILSLNCFPMIAGYYTALERTLFLDHCSDDHLRLWQVNVEVHE
AGLKLIKPGARCSDIARELNEIFLKHDVLQYRTFGYGHSFGTLSHYYGREAGLELREDIDTVLEP
GMVVSMEPMIMLPEGLPGAGGYREHDILIVNENGAENITKFPYGPEKNIIR
>d1c22a_ d.127.1.1 (A:) Methionine aminopeptidase {Escherichia coli}
AISIKTPEDIEKMRVAGRLAAEVLEMIEPYVKPGVSTGELDRICNDYIVNEQHAVSACLGYHGYP
KSVCISINEVVCHGIPDDAKLLKDGDIVNIDVTVIKDGFHGDTSKMFIVGKPTIMGERLCRITQE
SLYLALRMVKPGINLREIGAAIQKFVEAEGFSVVREYCGHGIGQGFHEEPQVLHYDSRETNVVLK
PGMTFTIEPMVNAGKKEIRTMKDGWTVKTKDRSLSAQYEHTIVVTDNGCEILTLRKDDTIPAIIS
HD
>d1xgsa2 d.127.1.1 (A:1-194,A:272-295) Methionine aminopeptidase {Archaeon Pyrococcus furiosus}
MDTEKLMKAGEIAKKVREKAIKLARPGMLLLELAESIEKMIMELGGKPAFPVNLSINEIAAHYTP
YKGDTTVLKEGDYLKIDVGVHIDGFIADTAVTVRVGMEEDELMEAAKEALNAAISVARAGVEIKE
LGKAIENEIRKRGFKPIVNLSGHKIERYKLHAGISIPNIYRPHDNYVLKEGDVFAIEPFATIGAX

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RNGIVAQFEHTIIVEKDSVIVTTE
>d1b6a_2  d.127.1.1  (110-374,449-478)  Methionine  aminopeptidase
{Human (Homo sapiens)}
KVQTDPPSVPICDLYPNGVFPKGQECEYPPTQDGRTAAWRTTSEEKKALDQASEEIWNDFREAAE
AHRQVRKYVMSWIKPGMTMIEICEKLEDCSRKLIKENGLNAGLAFPTGCSLNNCAAHYTPNAGDT
TVLQYDDICKIDFGTHISGRIIDCAFTVTFNPKYDTLLKAVKDATNTGIKCAGIDVRLCDVGEAI
QEVMESYEVEIDGKTYQVKPIRNLNGHSIGQYRIHAGKTVPIVKGGEATRMEEGEVYAIETFGST
GKGVVXDIKGSYTAQFEHTILLRPTCKEVVSRGDDY
>d1az9_2 d.127.1.1 (177-440) Aminopeptidase P, C-terminal domain
{Escherichia coli}
SPEEIAVLRRAGEITAMAHTRAMEKCRPGMFEYHLEGEIHHEFNRHGARYPSYNTIVGSGENGCI
LHYTENECEMRDGDLVLIDAGCEYKGYAGDITRTFPVNGKFTQAQREIYDIVLESLETSLRLYRP
GTSILEVTGEVVRIMVSGLVKLGILKGDVDELIAQNAHRPFFMHGLSHWLGLDVHDVGVYGQDRS
RILEPGMVLTVEPGLYIAPDAEVPEQYRGIGIRIEDDIVITETGNENLTASVVKKPEEIEALMVA
ARKQ
>d1f52a2  d.128.1.1  (A:101-468)  Glutamine  synthetase,  C-terminal
domain {Salmonella typhimurium}
DRDPRSIAKRAEDYLRATGIADTVLFGPEPEFFLFDDIRFGASISGSHVAIDDIEGAWNSSTKYE
GGNKGHRPGVKGGYFPVPPVDSAQDIRSEMCLVMEQMGLVVEAHHHEVATAGQNEVATRFNTMTK
KADEIQIYKYVVHNVAHRFGKTATFMPKPMFGDNGSGMHCHMSLAKNGTNLFSGDKYAGLSEQAL
YYIGGVIKHAKAINALANPTTNSYKRLVPGYEAPVMLAYSARNRSASIRIPVVASPKARRIEVRF
PDPAANPYLCFAALLMAGLDGIKNKIHPGEPMDKNLYDLPPEEAKEIPQVAGSLEEALNALDLDR
EFLKAGGVFTDEAIDAYIALRREEDDRVRMTPHPVEFELYYSV
>d1crka2 d.128.1.2 (A:99-380) Creatine kinase, C-terminal domain
{Chicken (Gallus gallus), mitochondria}
TMKHHTDLDASKITHGQFDERYVLSSRVRTGRSIRGLSLPPACSRAERREVENVVVTALAGLKGD
LSGKYYSLTNMSERDQQQLIDDHFLFDKPVSPLLTCAGMARDWPDARGIWHNNDKTFLVWINEED
HTRVISMEKGGNMKRVFERFCRGLKEVERLIKERGWEFMWNERLGYVLTCPSNLGTGLRAGVHVK
LPRLSKDPRFPKILENLRLQKRGTGGVDTAAVADVYDISNLDRMGRSEVELVQIVIDGVNYLVDC
EKKLEKGQDIKVPPPLPQFGRK
>d1qh4a2 d.128.1.2 (A:103-381) Creatine kinase, C-terminal domain
{Chicken (Gallus gallus), brain-type}
TDEHKTDLNADNLQGGDDLDPNYVLSSRVRTGRSIRGFCLPPHCSRGERRAIEKLSVEALGSLGG
DLKGKYYALRNMTDAEQQQLIDDHFLFDKPVSPLLLASGMARDWPDARGIWHNDNKTFLVWINEE
DHLRVISMQKGGNMKEVFTRFCTGLTQIETLFKSKNYEFMWNPHLGYILTCPSNLGTGLRAGVHI
KLPNLGKHEKFGEVLKRLRLQKRGTGGVDTAAVGGVFDVSNADRLGFSEVELVQMVVDGVKLLIE
MEKRLEKGQSIDDLMPAQK
>d1qk1a2 d.128.1.2 (A:103-379) Creatine kinase, C-terminal domain
{Human (Homo sapiens), mitochondria}
TTDLDASKIRSGYFDERYVLSSRVRTGRSIRGLSLPPACTRAERREVERVVVDALSGLKGDLAGR
YYRLSEMTEAEQQQLIDDHFLFDKPVSPLLTAAGMARDWPDARGIWHNNEKSFLIWVNEEDHTRV
ISMEKGGNMKRVFERFCRGLKEVERLIQERGWEFMWNERLGYILTCPSNLGTGLRAGVHIKLPLL
SKDSRFPKILENLRLQKRGTGGVDTAATGGVFDISNLDRLGKSEVELVQLVIDGVNYLIDCERRL
ERGQDIRIPTPVIHTKH
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>d2crka2 d.128.1.2 (A:103-381) Creatine kinase, C-terminal domain
{Rabbit (Oryctolagus cuniculus)}
TDKHKTDLNHENLKGGDDLDPHYVLSSRVRTGRSIKGYTLPPHCSRGERRAVEKLSVEALNSLTG
EFKGKYYPLKSMTEQEQQQLIDDHFLFDKPVSPLLLASGMARDWPDARGIWHNDNKSFLVWVNEE
DHLRVISMEKGGNMKEVFRRFCVGLQKIEEIFKKAGHPFMWNEHLGYVLTCPSNLGTGLRGGVHV
KLAHLSKHPKFEEILTRLRLQKRGTSVFDTAAVGSVFDISNADRLGSSEVEQVQLVVDGVKLMVE
MEKKLEKGQSIDDMIPAQK
>d1g0wa2 d.128.1.2 (A:103-381) Creatine kinase, C-terminal domain
{Cow (Bos taurus), retinal isoform}
TDEHKTDLNPDNLQGGDDLDPNYVLSSRVRTGRSIRGFCLPPHCSRGERRAIEKLAVEALSSLDG
DLAGRYYALKSMTEAEQQQLIDDHFLFDKPVSPLLLASGMARDWPDARGIWHNDNKTFLVWINEE
DHLRVISMQKGGNMKEVFTRFCNGLTQIETLFKSKNYEFMWNPHLGYILTCPSNLGTGLRAGVHI
KLPHLGKHEKFSEVLKRLRLQKRGTGGVDTAAVGGVFDVSNADRLGFSEVELVQMVVDGVKLLIE
MEQRLEQGQAIDDLMPAQK
>d1bg0_2 d.128.1.2 (96-357) Arginine kinase {Horseshoe crab (Limulus
polyphemus)}
TDKHPPKQWGDINTLVGLDPAGQFIISTRVRCGRSLQGYPFNPCLTAEQYKEMEEKVSSTLSSME
DELKGTYYPLTGMSKATQQQLIDDHFLFKEGDRFLQTANACRYWPTGRGIFHNDAKTFLVWVNEE
DHLRIISMQKGGDLKTVYKRLVTAVDNIESKLPFSHDDRFGFLTFCPTNLGTTMRASVHIQLPKL
AKDRKVLEDIASKFNLQVRGTRGEHTESEGGVYDISNKRRLGLTEYQAVREMQDGILEMIKMEKA
AA
>d1cdwa1 d.129.1.1 (A:155-252) TATA-box binding protein (TBP),
C-terminal domain {Human (Homo sapiens)}
SGIVPQLQNIVSTVNLGCKLDLKTIALRARNAEYNPKRFAAVIMRIREPRTTALIFSSGKMVCTG
AKSEENSRLAARKYARVVQKLGFPAKFLDFKIQ
>d1cdwa2 d.129.1.1 (A:253-333) TATA-box binding protein (TBP),
C-terminal domain {Human (Homo sapiens)}
NMVGSCDVKFPIRLEGLVLTHQQFSSYEPELFPGLIYRMIKPRIVLLIFVSGKVVLTGAKVRAEI
YEAFENIYPILKGFRK
>d1qnaa1 d.129.1.1 (A:17-115) TATA-box binding protein (TBP),
C-terminal domain {Arabidopsis thaliana}
HPSGIVPTLQNIVSTVNLDCKLDLKAIALQARNAEYNPKRFAAVIMRIREPKTTALIFASGKMVC
TGAKSEDFSKMAARKYARIVQKLGFPAKFKDFKI
>d1qnaa2 d.129.1.1 (A:116-198) TATA-box binding protein (TBP),
C-terminal domain {Arabidopsis thaliana}
QNIVGSCDVKFPIRLEGLAYSHAAFSSYEPELFPGLIYRMKVPKIVLLIFVSGKIVITGAKMRDE
TYKAFENIYPVLSEFRKI
>d1ytba1 d.129.1.1 (A:61-155) TATA-box binding protein (TBP),
C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
SGIVPTLQNIVATVTLGCRLDLKTVALHARNAEYNPKRFAAVIMRIREPKTTALIFASGKMVVTG
AKSEDDSKLASRKYARIIQKIGFAAKFTDF
>d1ytba2 d.129.1.1 (A:156-240) TATA-box binding protein (TBP),
C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
KIQNIVGSCDVKFPIRLEGLAFSHGTFSSYEPELFPGLIYRMVKPKIVLLIFVSGKIVLTGAKQR
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EEIYQAFEAIYPVLSEFRKM
>d1aisa1 d.129.1.1 (A:1-92) TATA-box binding protein (TBP), C-terminal domain {Archaeon Pyrococcus woesei}
MVDMSKVKLRIENIVASVDLFAQLDLEKVLDLCPNSKYNPEEFPGIICHLDDPKVALLIFSSGKL
VVTGAKSVQDIERAVAKLAQKLKSIGV
>d1aisa2 d.129.1.1 (A:93-181) TATA-box binding protein (TBP), C-terminal domain {Archaeon Pyrococcus woesei}
KFKRAPQIDVQNMVFSGDIGREFNLDVVALTLPNCEYEPEQFPGVIYRVKEPKSVILLFSSGKIV
CSGAKSEADAWEAVRKLLRELDKY
>d1mpga2 d.129.1.2 (A:1-99) 3-Methyladenine DNA glycosylase II (gene alkA or aidA) {Escherichia coli}
MYTLNWQPPYDWSWMLGFLAARAVSSVETVADSYYARSLAVGEYRGVVTAIPDIARHTLHINLSA
GLEPVAAECLAKMSRLFDLQCNPQIVNGALGRLG
>d1ko9a2 d.129.1.2 (A:12-135) 8-oxoguanine glycosylase {Human (Homo sapiens)}
GHRTLASTPALWASIPCPRSELRLDLVLPSGQSFRWREQSPAHWSGVLADQVWTLTQTEEQLHCT
VYRGDKSQASRPTPDELEAVRKYFQLDVTLAQLYHHWGSVDSHFQEVAQKFQGVRLLRQ
>d1f46a_ d.129.4.1 (A:) Cell-division protein ZipA, C-terminal domain {Escherichia coli}
RKEAVIIMNVAAHHGSELNGELLLNSIQQAGFIFGDMNIYHRHLSPDGSGPALFSLANMVKPGTF
DPEMKDFTTPGVTIFMQVPSYGDELQLFKLMLQSAQHIADEVGGVVLDDQRRMMTPQKLREYQDI
IREVKDANA
>d3pmga4 d.129.2.1 (A:421-561) Phosphoglucomutase {Rabbit (Oryctolagus cuniculus)}
RNFFTRYDYEEVEAEGATKMMKDLEALMFDRSFVGKQFSANDKVYTVEKADNFEYHDPVDGSVSK
NQGLRLIFADGSRIIFRLSGTGSAGATIRLYIDSYEKDNAKINQDPQVMLAPLISIALKVSQLQE
RTGRTAPTVIT
>d1kfia4 d.129.2.1 (A:444-572) Exocytosis-sensitive phosphoprotein, pp63/parafusin {Paramecium tetraurelia}
RNYYSRYDYEQVDSAGANKMMEHLKTKFQYFEQLKQGNKADIYDYVDPVDQSVSKNQGVRFVFGD
GSRIIFRLSGTGSVGATIRIYFEQFEQQQIQHETATALANIIKLGLEISDIAQFTGRNEPTVIT
>d1bv1__ d.129.3.1 (-) Major tree pollen allergen {White birch (Betula verrucosa), Bet v 1}
GVFNYETETTSVIPAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFPEGLPFK
YVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNKYHTKGDHEVKA
EQVKASKEMGETLLRAVESYLLAHSDAYN
>d1e09a_ d.129.3.1 (A:) Major tree pollen allergen {Sweet cherry (Prunus avium), pru av 1}
GVFTYESEFTSEIPPPRLFKAFVLDADNLVPKIAPQAIKHSEILEGDGGPGTIKKITFGEGSQYG
YVKHKIDSIDKENYSYSYTLIEGDALGDTLEKISYETKLVASPSGGSIIKSTSHYHTKGNVEIKE
EHVKAGKEKASNLFKLIETYLKGHPDAYN
>d1em2a_ d.129.3.2 (A:) Lipid transport domain of Mln64 {Human (Homo sapiens)}
SFSAQEREYIRQGKEATAVVDQILAQEENWKFEKNNEYGDTVYTIEVPFHGKTFILKTFLPCPAE
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LVYQEVILQPERMVLWNKTVTACQILQRVEDNTLISYDVSAGAAGGVVSPRDFVNVRRIERRRDR
YLSSGIATSHSAKPPTHKYVRGENGPGGMIVLKSASNPRVCTFVWILNTDLKGRLPRYLIHQSLA
ATMFEFAFHLRQRISELGA
>d1fvza_ d.129.3.4 (A:) Phoshatidylinositol transfer protein, PITP
{Rat (Rattus norvegicus)}
VLLKEYRVILPVSVDEYQVGQLYSVAEASKNETGGGEGVEVLVNEPYEKDDGEKGQYTHKIYHLQ
SKVPTFVRMLAPEGALNIHEKAWNAYPYCRTVITNEYMKEDFLIKIETWHKPDLGTQENVHKLEP
EAWKHVEVIYIDIADRSQVLSKDYKAEEDPAKFKSIKTGRGPLGPNWKQELVNQKDCPYMCAYKL
VTVKFKWWGLQNKVENFIHKQEKRLFTNFHRQLFCWLDKWVDLTMDDIRRMEEETKRQLDEMRQK
DPVKGMTAD
>d1eg9a2 d.129.3.3 (A:155-447) Naphthalene 1,2-dioxygenase alpha
subunit, C-domain {Pseudomonas putida}
EAPPLMDYLGDAAWYLEPMFKHSGGLELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRS
GESIFSSLAGNAALPPEGAGLQMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEI
GDVRARIYRSHLNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQ
RTFGPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYR
GFYRAYQAHVSSSNWAEFEHASSTWHTELTKTT
>d1mxa_1 d.130.1.1 (1-102) S-adenosylmethionine synthetase
{Escherichia coli}
AKHLFTSESVSEGHPDKIADQISDAVLDAILEQDPKARVACETYVKTGMVLVGGEITTSAWVDIE
EITRNTVREIGYVHSDMGFDANSCAVLSAIGKQSPDI
>d1mxa_2 d.130.1.1 (108-231) S-adenosylmethionine synthetase
{Escherichia coli}
RADPLEQGAGDQGLMFGYATNETDVLMPAPITYAHRLVQRQAEVRKNGTLPWLRPDAKSQVTFQY
DDGKIVGIDAVVLSTQHSEEIDQKSLQEAVMEEIIKPILPAEWLTSATKFFINPTGRFV
>d1mxa_3 d.130.1.1 (232-383) S-adenosylmethionine synthetase
{Escherichia coli}
IGGPMGDCGLTGRKIIVDTYGGMARHGGGAFSGKDPSKVDRSAAYAARYVAKNIVAAGLADRCEI
QVSYAIGVAEPTSIMVETFGTEKVPSEQLTLLVREFFDLRPYGLIQMLDLLHPIYKETAAYGHFG
REHFPWEKTDKAQLLRDAAGLK
>d1qm4a1 d.130.1.1 (A:17-116) S-adenosylmethionine synthetase {Rat
(Rattus norvegicus)}
GAFMFTSESVGEGHPDKICDQISDAVLDAHLKQDPNAKVACETVCKTGMVLLCGEITSMAMIDYQ
RVVRDTIKHIGYDDSAKGFDFKTCNVLVALEQQSP
>d1qm4a2 d.130.1.1 (A:129-252) S-adenosylmethionine synthetase {Rat
(Rattus norvegicus)}
EDVGAGDQGLMFGYATDETEECMPLTIVLAHKLNTRMADLRRSGVLPWLRPDSKTQVTVQYVQDN
GAVIPVRVHTIVISVQHNEDITLEAMREALKEQVIKAVVPAKYLDEDTIYHLQPSGRFV
>d1qm4a3 d.130.1.1 (A:253-396) S-adenosylmethionine synthetase {Rat
(Rattus norvegicus)}
IGGPQGDAGVTGRKIIVDTYGGWGAHGGGAFSGKDYTKVDRSAAYAARWVAKSLVKAGLCRRVLV
QVSYAIGVAEPLSISIFTYGTSKKTERELLEVVNKNFDLRPGVIVRDLDLKKPIYQKTACYGHFG
RSEFPWEVPKKLVF
>d2pola1 d.131.1.1 (A:1-122) DNA polymerase III, beta subunit
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{Escherichia coli}
MKFTVEREHLLKPLQQVSGPLGGRPTLPILGNLLLQVADGTLSLTGTDLEMEMVARVALVQPHEP
GATTVPARKFFDICRGLPEGAEIAVQLEGERMLVRSGRSRFSLSTLPAADFPNLDDW
>d2pola2 d.131.1.1 (A:123-244) DNA polymerase III, beta subunit
{Escherichia coli}
QSEVEFTLPQATMKRLIEATQFSMAHQDVRYYLNGMLFETEGEELRTVATDGHRLAVCSMPIGQS
LPSHSVIVPRKGVIELMRMLDGGDNPLRVQIGSNNIRAHVGDFIFTSKLVDGRFPDY
>d2pola3 d.131.1.1 (A:245-366) DNA polymerase III, beta subunit
{Escherichia coli}
RRVLPKNPDKHLEAGCDLLKQAFARAAILSNEKFRGVRLYVSENQLKITANNPEQEEAEEILDVT
YSGAEMEIGFNVSYVLDVLNALKCENVRMMLTDSVSSVQIEDAASQSAAYVVMPMRL
>d1b77a1 d.131.1.2 (A:1-110) gp45 sliding clamp {Bacteriophage RB69}
MKLSKDTIAILKNFASINSGILLSQGKFIMTRAVNGTTYAEANISDEIDFDVALYDLNSFLSILS
LVSDDAEISMHTDGNIKIADTRSTVYWPAADKSTIVFPNKPIQFP
>d1b77a2 d.131.1.2 (A:111-228) gp45 sliding clamp {Bacteriophage
RB69}
VASVITEIKAEDLQQLLRVSRGLQIDTIAITNKDGKIVINGYNKVEDSGLTRPKYSLTLTDYDGS
NNFNFVINMANMKIQPGNYKVMLWGAGDKVAAKFESSQVSYVIAMEADSTHDF
>d1czda1 d.131.1.2 (A:1001-1110) gp45 sliding clamp {Bacteriophage
T4}
MKLSKDTTALLKNFATINSGIMLKSGQFIMTRAVNGTTYAEANISDVIDFDVAIYDLNGFLGILS
LVNDDAEISQSEDGNIKIADARSTIFWPAADPSTVVAPNKPIPFP
>d1czda2 d.131.1.2 (A:1111-1228) gp45 sliding clamp {Bacteriophage
T4}
VASAVTEIKAEDLQQLLRVSRGLQIDTIAITVKEGKIVINGFNKVEDSALTRVKYSLTLGDYDGE
NTFNFIINMANMKMQPGNYKLLLWAKGKQGAAKFEGEHANYVVALEADSTHDF
>d1dmla1 d.131.1.2 (A:29-169) UL42 {Human herpes virus type 1}
APCQVVLQGAELNGILQAFAPLRTSLLDSLLVMGDRGILIHNTIFGEQVFLPLEHSQFSRYRWRG
PTAAFLSLVDQKRSLLSVFRANQYPDLRRVELAITGQAPFRTLVQRIWTTTSDGEAVELASETLM
KRELTSFVVLV
>d1dmla2 d.131.1.2 (A:170-319) UL42 {Human herpes virus type 1}
PQGTPDVQLRLTRPQLTKVLNATGADSATPTTFELGVNGKFSVFTTSTCVTFAAREEGVSSSTST
QVQILSNALTKAGQAAANAKTVYGENTHRTFSVVVDDCSMRAVLRRLQVGGGTLKFFLTTPVPSL
CVTATGPNAVSAVFLLKPQK
>d1plq_1 d.131.1.2 (1-126) Prolifirating cell nuclear antigen (PCNA)
{Baker's yeast (Saccharomyces cerevisiae)}
MLEAKFEEASLFKRIIDGFKDCVQLVNFQCKEDGIIAQAVDDSRVLLVSLEIGVEAFQEYRCDHP
VTLGMDLTSLSKILRCGNNTDTLTLIADNTPDSIILLFEDTKKDRIAEYSLKLMDIDADFL
>d1plq_2 d.131.1.2 (127-258) Prolifirating cell nuclear antigen (PCNA)
{Baker's yeast (Saccharomyces cerevisiae)}
KIEELQYDSTLSLPSSEFSKIVRDLSQLSDSINIMITKETIKFVADGDIGSGSVIIKPFVDMEHP
ETSIKLEMDQPVDLTFGAKYLLDIIKGSSLSDRVGIRLSSEAPALFQFDLKSGFLQFFLAPKFND
EE
>d1axca1 d.131.1.2 (A:1-126) Prolifirating cell nuclear antigen (PCNA)
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{Human (Homo sapiens)}
MFEARLVQGSILKKVLEALKDLINEACWDISSSGVNLQSMDSSHVSLVQLTLRSEGFDTYRCDRN
LAMGVNLTSMSKILKCAGNEDIITLRAEDNADTLALVFEAPNQEKVSDYEMKLMDLDVEQL
>d1axca2 d.131.1.2 (A:127-255) Prolifirating cell nuclear antigen (PCNA) {Human (Homo sapiens)}
GIPEQEYSCVVKMPSGEFARICRDLSHIGDAVVISCAKDGVKFSASGELGNGNIKLSQTSNVDKE
EEAVTIEMNEPVQLTFALRYLNFFTKATPLSSTVTLSMSADVPLVVEYKIADMGHLKYYLAPKI
>d1ge8a1 d.131.1.2 (A:2-117) Prolifirating cell nuclear antigen (PCNA) {Archaeon Pyrococcus furiosus}
PFEIVFEGAKEFAQLIDTASKLIDEAAFKVTEDGISMRAMDPSRVVLIDLNLPSSIFSKYEVVEP
ETIGVNLDHLKKILKRGKAKDTLILKKGEENFLEITIQGTATRTFRVPLID
>d1ge8a2 d.131.1.2 (A:126-247) Prolifirating cell nuclear antigen (PCNA) {Archaeon Pyrococcus furiosus}
PELPFTAKVVVLGEVLKDAVKDASLVSDSIKFIARENEFIMKAEGETQEVEIKLTLEDEGLLDIE
VQEETKSAYGVSYLSDMVKGLGKADEVTIKFGNEMPMQMEYYIRDEGRLTFLLAPRV
>d1hlra4 d.133.1.1 (A:311-907) Aldehyde oxidoreductase {Desulfovibrio gigas}
MSGPAAAAEDAIEIHPGTPNVYFEQPIVKGEDTGPIFASADVTVEGDFYVGRQPHMPIEPDVAFA
YMGDDGKCYIHSKSIGVHLHLYMIAPGVGLEPDQLVLVANPMGGTFGYKFSPTSEALVAVAAMAT
GRPVHLRYNYQQQQQYTGKRSPWEMNVKFAAKKDGTLLAMESDWLVDHGPYSEFGDLLTLRGAQF
IGAGYNIPNIRGLGRTVATNHVWGSAFRGYGAPQSMFASECLMDMLAEKLGMDPLELRYKNAYRP
GDTNPTGQEPEVFSLPDMIDQLRPKYQAALEKAQKESTATHKKGVGISIGVYGSGLDGPDASEAW
AELNADGTITVHTAWEDHGQGADIGCVGTAHEALRPMGVAPEKIKFTWPNTATTPNSGPSGGSRE
QVMTGNAIRVACENLLKACEKPGGGYYTYDELKAADKPTKITGNWTASGATHCDAVTGLGKPFVV
YMYGVFMAEVTVDVATGQTTVDGMTLMADLGSLCNQLATDGQIYGGLAQGIGLALSEDFEDIKKH
ATLVGAGFPFIKQIPDKLDIVYVNHPRPDGPFGASGVGELPLTSPHAAIINAIKSATGVRIYRLP
AYPEKVLEALKA
>d1dgja4 d.133.1.1 (A:311-906) Aldehyde oxidoreductase {Desulfovibrio desulfuricans}
MSAPEAMAPDAIEIHPGTPNVYYDQLEEKGEDTVPFFNDPANVVAEGSYYTQRQPHLPIEPDVGY
GYINEQGQVVIHSKSVAIHLHALMIAPGLGLEFPKDLVLVQNTTGGTFGYKFSPTMEALVGVAVM
ATGRPCHLRYNYEQQQNYTGKRSPFWTTMRYAADRQGKILAMETDWSVDHGPYSEFGDLLTLRGA
QYIGAGYGIANIRGTGRTVATNHCWGAAFRGYGAPESEFPSEVLMDELAEKLGMDPFELRALNCY
REGDTTSSGQIPEVMSLPEMFDKMRPYYEESKKRVKERSTAEIKRGVGVALGVYGAGLDGPDTSE
AWVELNDDGSVTLGNSWEDHGQGADAGSLGTAHEALRPLGITPENIHLVMNDTSKTPNSGPAGGS
RSQVVTGNAIRVACEMLIEGMRKPGGGFFTPAEMKAEGRPMRYDGKWTAPAKDCDAKGQGSPFAC
YMYGLFLTEVAVEVATGKATVEKMVCVADIGKICNKLVVDGQIYGGLAQGVGLALSEDYEDLKKH
STMGGAGIPSIKMIPDDIEIVYVETPRKDGPFGASGVGEMPLTAPHAAIINGIYNACGARVRHLP
ARPEKVLEAMP
>d1fo4a5 d.133.1.1 (A:695-1332) Xanthine oxidase, C-terminal domain {Cow (Bos taurus)}
IITIEDAIKNNSFYGSELKIEKGDLKKGFSEADNVVSGELYIGGQDHFYLETHCTIAIPKGEEGE
MELFVSTQNAMKTQSFVAKMLGVPVNRILVRVKRMGGGFGGKETRSTLVSVAVALAAYKTGHPVR
CMLDRNEDMLITGGRHPFLARYKVGFMKTGTIVALEVDHYSNAGNSRDLSHSIMERALFHMDNCY

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KIPNIRGTGRLCKTNLSSNTAFRGFGGPQALFIAENWMSEVAVTCGLPAEEVRWKNMYKEGDLTH
FNQRLEGFSVPRCWDECLKSSQYYARKSEVDKFNKENCWKKRGLCIIPTKFGISFTVPFLNQAGA
LIHVYTDGSVLVSHGGTEMGQGLHTKMVQVASKALKIPISKIYISETSTNTVPNSSPTAASVSTD
IYGQAVYEACQTILKRLEPFKKKNPDGSWEDWVMAAYQDRVSLSTTGFYRTPNLGYSFETNSGNA
FHYFTYGVACSEVEIDCLTGDHKNLRTDIVMDVGSSLNPAIDIGQVEGAFVQGLGLFTLEELHYS
PEGSLHTRGPSTYKIPAFGSIPTEFRVSLLRDCPNKKAIYASKAVGEPPLFLGASVFFAIKDAIR
AARAQHTNNNTKELFRLDSPATPEKIRNACVDKFTTLCVTGAPGNCKPWSLRV
>d1jrob2  d.133.1.1  (B:124-777)  Xanthine  dehydrogenase  chain  B,
C-terminal domain {Rhodobacter capsulatus}
PAILTLDQALAADSRFEGGPVIWARGDVETALAGAAHLAEGCFEIGGQEHFYLEGQAALALPAEG
GVVIHCSSQHPSEIQHKVAHALGLAFHDVRVEMRRMGGGFGGKESQGNHLAIACAVAARATGRPC
KMRYDRDDDMVITGKRHDFRIRYRIGADASGKLLGADFVHLARCGWSADLSLPVCDRAMLHADGS
YFVPALRIESHRLRTNTQSNTAFRGFGGPQGALGMERAIEHLARGMGRDPAELRALNFYDPPERG
GLSAPPSPPEPIATKKTQTTHYGQEVADCVLGELVTRLQKSANFTTRRAEIAAWNSTNRTLARGI
ALSPVKFGISFTLTHLNQAGALVQIYTDGSVALNHGGTEMGQGLHAKMVQVAAAVLGIDPVQVRI
TATDTSKVPNTSATAASSGADMNGMAVKDACETLRGRLAGFVAAREGCAARDVIFDAGQVQASGK
SWRFAEIVAAAYMARISLSATGFYATPKLSWDRLRGQGRPFLYFAYGAAITEVVIDRLTGENRIL
RTDILHDAGASLNPALDIGQIEGAYVQGAGWLTTEELVWDHCGRLMTHAPSTYKIPAFSDRPRIF
NVALWDQPNREETIFRSKAVGEPPFLLGISAFLALHDACAACGPHWPDLQAPATPEAVLAAVRRA
EGRA
>d1qj2b2 d.133.1.1 (B:147-809) Carbon monoxide (CO) dehydrogenase
molybdoprotein {Pseudomonas carboxydovorans}
VDPFKAMEPDAPLLREDIKDKMTGAHGARKHHNHIFRWEIGDKEGTDATFAKAEVVSKDMFTYHR
VHPSPLETCQCVASMDKIKGELTLWGTFQAPHVIRTVVSLISGLPEHKIHVIAPDIGGGFGNKVG
AYSGYVCAVVASIVLGVPVKWVEDRMENLSTTSFARDYHMTTELAATKDGKILAMRCHVLADHGA
FDACADPSKWPAGFMNICTGSYDMPVAHLAVDGVYTNKASGGVAYRXSFRVTEAVYAIERAIETL
AQRLEMDSADLRIKNFIQPEQFPYMAPLGWEYDSGNYPLAMKKAMDTVGYHQLRAEQKAKQEAFK
RGETREIMGIGISFFTEIVGAGPSKNCDILGVSMFDSAEIRIHPTGSVIARMGTKSQGQGHETTY
AQIIATELGIPADDIMIEEGNTDTAPYGLGTYGSRSTPTAGAATAVAARKIKAKAQMIAAHMLEV
HEGDLEWDVDRFRVKGLPEKFKTMKELAWASYNSPPPNLEPGLEAVNYYDPPNMTYPFGAYFCIM
DIDIDTGVAKTRRFYALDDCGTRINPMIIEGQVHGGLTEAFAVAMGQEIRYDEQGNVLGASFMDF
FLPTAVETPKWETDYTVTPSPHHPIGAKGVGESPHVGGVPCFSNAVNDAYAFLNAGHIQMPHDAW
RLWKVGEQLGLHV
>d1ffvb2 d.133.1.1 (B:147-803) Carbon monoxide (CO) dehydrogenase
molybdoprotein {Hydrogenophaga pseudoflava}
IDALKPDAPVLREDLAGKTSGAHGPREHHNHIFTWGAGDKAATDAVFANAPVTVSQHMYYPRVHP
CPLETCGCVASFDPIKGDLTTYITSQAPHVVRTVVSMLSGIPESKVRIVSPDIGGGFGNKVGIYP
GYVCAIVASIVLGRPVKWVEDRVENISTTAFARDYHMDGELAATPDGKILGLRVNVVADHGAFDA
CADPTKFPAGLFHICSGSYDIPRAHCSVKGVYTNKAPGGVAYRCSFRVTEAVYLIERMVDVLAQK
LNMDKAEIRAKNFIRKEQFPYTTQFGFEYDSGDYHTALKKVLDAVDYPALRAEQAARRADPNSPT
LMGIGLVTFTEVVGAGPSKMCDILGVGMFDSCEIRIHPTGSAIARMGTITQGQGHQTTYAQIIAT
ELGIPSEVIQVEEGDTSTAPYGLGTYGSRSTPVAGAAIALAARKIHAKARKIAAHMLEVNENDLD
WEVDRFKVKGDDSKFKTMADIAWQAYHQPPAGLEPGLEAVHYYDPPNFTYPFGIYLCVVDIDRAT
GETKVRRFYALDDCGTRINPMIIEGQIHGGLTEGYAVAMGQQMPFDAQGNLLGNTLMDYFLPTAV
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ETPHWETDHTVTPSPHHPIGAKGVAESPHVGSIPTFTAAVVDAFAHVGVTHLDMPHTSYRVWKSL
KEHNLAL
>d1aop_3 d.134.1.1 (149-345) Sulfite reductase hemoprotein (SiRHP),
domains 2 and 4 {Escherichia coli}
NDMNRNVLCTSNPYESQLHAEAYEWAKKISEHLLPRTRAYAEIWLDQEKVATTDEEPILGQTYLP
RKFKTTVVIPPQNDIDLHANDMNFVAIAENGKLVGFNLLVGGGLSIEHGNKKTYARTASEFGYLP
LEHTLAVAEAVVTTQRDWGNRTDRKNAKTKYTLERVGVETFKAEVERRAGIKFEPIRPYEFTGRG
DR
>d1aop_4 d.134.1.1 (426-570) Sulfite reductase hemoprotein (SiRHP),
domains 2 and 4 {Escherichia coli}
PQRENSMACVSFPTCPLAMAEAERFLPSFIDNIDNLMAKHGVSDEHIVMRVTGCPNGCGRAMLAE
VGLVGKAPGRYNLHLGGNRIGTRIPRMYKENITEPEILASLDELIGRWAKEREAGEGFGDFTVRA
GIIRPVLDPARDLWD
>d1klqa_ d.135.1.1 (A:) The spindle assembly checkpoint protein mad2
{Human (Homo sapiens)}
GSITLRGSAEIVAEFFSFGINSILYQRGIYPSETFTRVQKYGLTLLVTTDLELIKYLNNVVEQLK
DWLYKCSVQKLVVVISNIESGEVLERWQFDIECDKTAKDDSAPREKSQKAIQDEIRSVIRQITAT
VTFLPLLEVSCSFDLLIYTDKDLVVPEKWEESGPQFITNSEEVRLRSFTTTIHKVNSMVAYKIPV
ND
>d1byra_ d.136.1.1 (A:) Nuclease Nuc {Salmonella typhimurium}
EPSVQVGYSPEGSARVLVLSAIDSAKTSIRMMAYSFTAPDIMKALVAAKKRGVDVKIVIDERGNT
GRASIAAMNYIANSGIPLRTDSNFPIQHDKVIIVDNVTVETGSFNFTKAAETKNSENAVVIWNMP
KLAESFLEHWQDRWNQGRDYRS
>d1f0ia1 d.136.1.2 (A:6-263) Phospholipase D {Streptomyces sp.}
AATPHLDAVEQTLRQVSPGLEGDVWERTSGNKLDGSAADPSDWLLQTPGCWGDDKCADRVGTKRL
LAKMTENIGNATRTVDISTLAPFPNGAFQDAIVAGLKESAAKGNSLKVRILVGAAPVYHMNGIPS
KYRDKLTAKLGKAAENITLNVASMTTSKTAFSWNHSKILVVDGQSALTGGINSWKDDYLDTTHPV
SDVDLALTGPAAGSAGRYLDTLWTWTCKNKSNIASVWFAASGNAGCMPTMHKDTNPKASPATG
>d1f0ia2 d.136.1.2 (A:264-514) Phospholipase D {Streptomyces sp.}
NVPVIAVGGLGVGIKDVDPKSTFRPDLPTASDTKCVVGLHDNTNADRDYDTVNPEESALRALVAS
AKGHIEISQQDLNATCPPLPRYDIRLYDALAAKMAAGVKVRIVVSDPANRGAVGSGGYSQIKSLS
EISDTLRNRLANITGGQQAAKTAMCSNLQLATFRSSPNGKWADGHPYAQHHKLVSVDSSTFYIGS
KNLYPSWLQDFGYIVESPEAAKQLDAKLLDPQWKYSQETATVDYARGICGA
>d1jy1a1 d.136.1.3 (A:145-350) Tyrosyl-DNA phosphodiesterase TDP1
{Human (Homo sapiens)}
LEDPGEGQDIWDMLDKGNPFQFYLTRVSGVKPKYNSGALHIKDILSPLFGTLVSSAQFNYCFDVD
WLVKQYPPEFRKKPILLVHGDKREAKAHLHAQAKPYENISLCQAKLDIAFGTHHTKMMLLLYEEG
LRVVIHTSNLIHADWHQKTQGIWLSPLYPRIADGTHKSGESPTHFKANLISYLTAYNAPSLKEWI
DVIHKHDLSET
>d1jy1a2 d.136.1.3 (A:351-608) Tyrosyl-DNA phosphodiesterase TDP1
{Human (Homo sapiens)}
NVYLIGSTPGRFQGSQKDNWGHFRLKKLLKDHASSMPNAESWPVVGQFSSVGSLGADESKWLCSE
FKESMLTLGKESKTPGKSSVPLYLIYPSVENVRTSLEGYPAGGSLPYSIQTAEKQNWLHSYFHKW
SAETSGRSNAMPHIKTYMRPSPDFSKIAWFLVTSANLSKAAWGALEKNGTQLMIRSYELGVLFLP
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SALGLDSFKVKQKFFAGSQEPMATFPVPYDLPPELYGSKDRPWIWNIPYVKAPDTHGNMWVPS
>d1ckv__ d.137.1.1 (-) Soluble methane monooxygenase regulatory
protein B {Escherichia coli}
MSVNSNAYDAGIMGLKGKDFADQFFADENQVVHESDTVVLVLKKSDEINTFIEEILLTDYKKNVN
PTVNVEDRAGYWWIKANGKIEVDCDEISELLGRQFNVYDFLVDVSSTIGRAYTLGNKFTITSELM
GLDRKLEDYHA
>d2moba_ d.137.1.1 (A:) Soluble methane monooxygenase regulatory
protein B {Methylosinus trichosporium}
SNAVVLVLMKSDEIDAIIEDIVLKGGKAKNPSIVVEDKAGFWWIKADGAIEIDAAEAGELLGKPF
SVYDLLINVSSTVGRAYTLGTKFTITSEL
>d1g10a_ d.137.1.1 (A:) Toluene-4-monooxygenase catalytic effector
protein {Pseudomonas mendocina}
STLADQALHNNNVGPIIRAGDLVEPVIETAEIDNPGKEITVEDRRAYVRIAAEGELILTRKTLEE
QLGRPFNMQELEINLASFAGQIQADEDQIRFYFDKTM
>d1hqi__ d.137.1.1 (-) Phenol hydroxylase P2 protein {Pseudomonas sp.,
CF600}
MSSLVYIAFQDNDNARYVVEAIIQDNPHAVVQHHPAMIRIEAEKRLEIRRETVEENLGRAWDVQE
MLVDVITIGGNVDEDDDRFVLEWKN
>d1jjcb6 d.138.1.1 (B:191-399) B3/B4 domain of PheRS, PheT {Thermus
thermophilus (Thermus aquaticus)}
LKAEALPLPFALKVEDPEGAPHFTLGYAFGLRVAPSPLWMQRALFAAGMRPINNVVDVTNYVMLE
RAQPMHAFDLRFVGEGIAVRRAREGERLKTLDGVERTLHPEDLVIAGWRGEESFPLGLAGVMGGA
ESEVREDTEAIALEVACFDPVSIRKTARRHGLRTEASHRFERGVDPLGQVPAQRRALSLLQALAG
ARVAEALLEAGSPK
>d1clia2 d.139.1.1 (A:171-345) Aminoimidazole ribonucleotide
synthetase (PurM) C-terminal domain {Escherichia coli}
DGSKVSDGDVLIALGSSGPHSNGYSLVRKILEVSGCDPQTTELDGKPLADHLLAPTRIYVKSVLE
LIEKVDVHAIAHLTGGGFWENIPRVLPDNTQAVIDESSWQWPEVFNWLQTAGNVEHHEMYRTFNC
GVGMIIALPAPEVDKALALLNANGENAWKIGIIKASDSEQRVVIE
>d1hw7a_ d.193.1.1 (A:) Heat shock protein 33, Hsp33 {Escherichia coli}
HDQLHRYLFENFAVRGELVTVSETLQQILENHDYPQPVKNVLAELLVATSLLTATLKFDGDITVQ
LQGDGPMNLAVINGNNNQQMRGVARVQGEIPENADLKTLVGNGYVVITITPSEGERYQGVVGLEG
DTLAACLEDYFMRSEQLPTRLFIRTGDVDGKPAAGGMLLQVMPAQNAQQDDFDHLATLTETIKTE
ELLTLPANEVLWRLYHEEEVTVYDPQDVEFKCTC
>d1jw3a_ d.208.1.1 (A:) Hypothetical protein MTH1598 {Archaeon
Methanobacterium thermoautotrophicum}
MKGFEFFDVTADAGFWAYGHDLEEVFENAALAMFEVMTDTSLVEAAEERRVEITSEDRVSLLYDW
LDELLFIHDTEFILFSKFKVKIDEKDDGLHLTGTAMGEEIKEGHERRDEVKAVTFHMMEILDEDG
LIKARVILDL
>d1dl5a2 d.197.1.1 (A:214-317) Protein-L-isoaspartyl
O-methyltransferase, C-terminal domain {Thermotoga maritima}
NLLERNRKLLREFPFNREILLVRSHIFVELVDLLTRRLTEIDGTFYYAGPNGVVEFLDDRMRIYG
DAPEIENLLTQWESCGYRSFEYLMLHVGYNAFSHISCSI
>d1seia_ d.140.1.1 (A:) Ribosomal protein S8 {Bacillus
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stearothermophilus}
VMTDPIADMLTAIRNANMVRHEKLEVPASKIKREIAEILKREGFIRDYEYIEDNKQGILRIFLKY
GPNERVITGLKRISKPGLRVYVKAHEVPRVLNGLGIAILSTSQGVLTDKEARQKGTGGEIIAYVI
>d1an7a_ d.140.1.1 (A:) Ribosomal protein S8 {Thermus thermophilus}
TDPIADMLTRIRNATRVYKESTDVPASRFKEEILRILAREGFIKGYERVDVDGKPYLRVYLKYGP
RRQGPDPRPEQVIHHIRRISKPGRRVYVGVKEIPRVRRGLGIAILSTSKGVLTDREARKLGVGGE
LICEVW
>d1i94h_ d.140.1.1 (H:) Ribosomal protein S8 {Thermus thermophilus}
MLTDPIADMLTRIRNATRVYKESTEVPASRFKEEILKILAREGFIKGYERVEVDGKPYLRIHLKY
GPRRQGPDPRPEQVIKHIRRISRPGRRVYVGVKEIPRVRRGLGIAILSTPKGVLTDREARKLGVG
GELICEVW
>d1i6ua_ d.140.1.1 (A:) Ribosomal protein S8 {Archaeon Methanococcus
jannaschii}
SLMDPLANALNHISNCERVGKKVVYIKPASKLIGRVLKVMQDNGYIGEFEFIEDGRAGIFKVELI
GKINKCGAIKPRFPVKKFGYEKFEKRYLPARDFGILIVSTTQGVMSHEEAKKRGLGGRLLAYVY
>d1rl6a1 d.141.1.1 (A:7-81) Ribosomal protein L6 {Bacillus
stearothermophilus}
PIEIPAGVTVTVNGNTVTVKGPKGELTRTFHPDMTITVEGNVITVTRPSDEKHHRALHGTTRSLL
ANMVEGVSKG
>d1rl6a2 d.141.1.1 (A:82-170) Ribosomal protein L6 {Bacillus
stearothermophilus}
YEKALELVGVGYRASKQGKKLVLSVGYSHPVEIEPEEGLEIEVPSQTKIIVKGADKQRVGELAAN
IRAVRPPEPYKGKGIRYEGELVRL
>d1jj2e1 d.141.1.1 (E:1-79) Ribosomal protein L6 {Archaeon Haloarcula
marismortui}
PRVELEIPEDVDAEQDHLDITVEGDNGSVTRRLWYPDIDVSVDGDTVVIESDEDNAKTMSTIGTF
QSHIENMFHGVTEG
>d1jj2e2 d.141.1.1 (E:80-172) Ribosomal protein L6 {Archaeon
Haloarcula marismortui}
WEYGMEVFYSHFPMQVNVEGDEVVIENFLGEKAPRRTTIHGDTDVEIDGEELTVSGPDIEAVGQT
AADIEQLTRINDKDVRVFQDGVYITRKP
>d1gsa_2 d.142.1.1 (123-314) Glutathione synthetase {Escherichia
coli}
NEKLFTAWFSDLTPETLVTRNKAQLKAFWEKHSDIILKPLDGMGGASIFRVKEGDPNLGVIAETL
TEHGTRYCMAQNYLPAIKDGDKRVLVVDGEPVPYCLARIPQGGETRGNLAAGGRGEPRPLTESDW
KIARQIGPTLKEKGLIFVGLDIIGDRLTEINVTSPTCIREIEAEFPVSITGMLMDAIEARLQ
>d1iow_2 d.142.1.1 (97-306) D-ala-D-ala ligase {Escherichia coli,
gene ddlB}
KLRSKLLWQGAGLPVAPWVALTRAEFEKGLSDKQLAEISALGLPVIVKPSREGSSVGMSKVVAEN
ALQDALRLAFQHDEEVLIEKWLSGPEFTVAILGEEILPSIRIQPSGTFYDYEAKFLSDETQYFCP
AGLEASQEANLQALVLKAWTTLGCKGWGRIDVMLDSDGQFYLLEANTSPGMTSHSLVPMAARQAG
MSFSQLVVRILELAD
>d1ehia2 d.142.1.1 (A:135-362) D-alanine:D-lactate ligase, VanA
{Leuconostoc mesenteroides, Ddl2}
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DKALTKELLTVNGIRNTKYIVVDPESANNWSWDKIVAELGNIVFVKAANQGSSVGISRVTNAEEY
TEALSDSFQYDYKVLIEEAVNGARELEVGVIGNDQPLVSEIGAHTVPNQGSGDGWYDYNNKFVDN
SAVHFQIPAQLSPEVTKEVKQMALDAYKVLNLRGEARMDFLLDENNVPYLGEPNTLPGFTNMSLF
KRLWDYSDINNAKLVDMLIDYGFEDFAQNKKLS

>d1e4ea2 d.142.1.1 (A:132-342) D-alanine:D-lactate ligase, VanA {Enterococcus faecium}
DKSLTYIVAKNAGIATPAFWVINKDDRPVAATFTYPVFVKPARSGSSFGVKKVNSADELDYAIES
ARQYDSKILIEQAVSGCEVGCAVLGNSAALVVGEVDQIRLQYGIFRIHQEVEPEKGSENAVITVP
ADLSAEERGRIQETVKKIYKTLGCRGLARVDMFLQDNGRIVLNEVNTLPGFTSYSRYPRMMAAAG
ISLPELIDRLIVLALK

>d1dv1a3 d.142.1.2 (A:115-330) Biotin carboxylase subunit of acetyl-CoA carboxylase {Escherichia coli}
DKVSAIAAMKKAGVPCVPGSDGPLGDDMDKNRAIAKRIGYPVIIKASGGGGGRGMRVVRGDAELA
QSISMTRAEAKAAFSNDMVYMEKYLENPRHVEIQVLADGQGNAIYLAERDCSMQRRHQKVVEEAP
APGITPELRRYIGERCAKACVDIGYRGAGTFEFLFENGEFYFIEMNTRIQVEHPVTEMITGVDLI
KEQLRIAAGQPLSIKQEEVHV

>d1gsoa3 d.142.1.2 (A:104-327) Glycinamide ribonucleotide synthetase (GAR-syn) {Escherichia coli}
SKAFTKDFLARHKIPTAEYQNFTEVEPALAYLREKGAPIVIKADGLAAGKGVIVAMTLEEAEAAV
HDMLAGNAFGDAGHRIVIEEFLDGEEASFIVMVDGEHVLPMATSQDHKRVGDKDTGPNTGGMGAY
SPAPVVTDDVHQRTMERIIWPTVKGMAAEGNTYTGFLYAGLMIDKQGNPKVIEFNCRFGDLETQP
IMLRMKSDLVELCLAACESKLDEKTSEWD

>d1b6ra3 d.142.1.2 (A:79-276) N5-carboxyaminoimidazole ribonucleotide synthetase, AIRC, PurK {Escherichia coli}
DRLTQKQLFDKLHLPTAPWQLLAERSEWPAVFDRLGELAIVKRRTGGYDGRGQWRLRANETEQLP
AECYGECIVEQGINFSGEVSLVGARGFDGSTVFYPLTHNLHQDGILRTSVAFPQANAQQQARAEE
MLSAIMQELGYVGVMAMECFVTPQGLLINELAPRVHNSGHWTQNGASISQFELHLRAITDLPLPQ
PVV

>d1eyza3 d.142.1.2 (A:113-318) Glycinamide ribonucleotide transformylase PurT {Escherichia coli}
NREGIRRLAAEELQLPTSTYRFADSESLFREAVADIGYPCIVKPVMSSSGKGQTFIRSAEQLAQA
WKYAQQGGRAGAGRVIVEGVVKFDFEITLLTVSAVDGVHFCAPVGHRQEDGDYRESWQPQQMSPL
ALERAQEIARKVVLALGGYGLFGVELFVCGDEVIFSEVSPRPHDTGMVTLISQDLSEFALHVRAF
LGLPVGGIRQY

>d1a9xa5 d.142.1.2 (A:128-402) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia coli}
DRRRFDVAMKKIGLETARSGIAHTMEEALAVAADVGFPCIIRPSFTMGGSGGGIAYNREEFEEIC
ARGLDLSPTKELLIDESLIGWKEYEMEVVRDKNDNCIIVCSIENFDAMGIHTGDSITVAPAQTLT
DKEYQIMRNASMAVLREIGVETGGSNVQFAVNPKNGRLIVIEMNPRVSRSSALASKATGFPIAKV
AAKLAVGYTLDELMNDITGGRTPASFEPSIDYVVTKIPRFNFEKFAGANDRLTTQMKSVGEVMAI
GRTQQESLQKALRGL

>d1a9xa6 d.142.1.2 (A:677-935) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia coli}
RFQHAVERLKLKQPANATVTAIEMAVEKAKEIGYPLVVRAAMEIVYDEADLRRYFQTAVLLDHFL

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DDAVEVDVDAICDGEMVLIGGIMEHIEQAGVHSGDSACSLPAYTLSQEIQDVMRQQVQKLAFELQ
VRGLMNVQFAVKNNEVYLIEVNPRAARTVPFVSKATGVPLAKVAARVMAGKSLAEQGVTKEVIPP
YYSVKEVVLPFNKFPGVDPLLGPEMRSTGEVMGVGRTFAEAFAKAQLGS
>d1auva2 d.142.1.3 (A:214-417) Synapsin Ia, C-terminal domain {Cow
(Bos taurus)}
NSLHSVYNFCDKPWVFAQMVRLHKKLGTEEFPLINQTFYPNHKEMLSSTTYPVVVKMGHAHSGMG
KVKVDNQHDFQDIASVVALTKTYATTEPFIDAKYDVRIQKIGQNYKAYMRTSVSGNWKTNTGSAM
LEQIAMSDRYKLWVDTCSEIFGGLDICAVEALHGKDGRDHIIEVVGSSMPLIGDHQDEDKQLIVE
LVVNKMAQA
>d1jkjb2 d.142.1.4 (B:1-238) Succinyl-CoA synthetase, beta-chain,
N-terminal domain {Escherichia coli}
MNLHEYQAKQLFARYGLPAPVGYACTTPREAEEAASKIGAGPWVVKCQVHAGGRGKAGGVKVVNS
KEDIRAFAENWLGKRLVTYQTDANGQPVNQILVEAATDIAKELYLGAVVDRSSRRVVFMASTEGG
VEIEKVAEETPHLIHKVALDPLTGPMPYQGRELAFKLGLEGKLVQQFTKIFMGLATIFLERDLAL
IEINPLVITKQGDLICLDGKLGADGNALFRQPDLREMRDQSQE
>d1eucb2 d.142.1.4 (B:0-245) Succinyl-CoA synthetase, beta-chain,
N-terminal domain {Pig (Sus scrofa)}
MVNLQEYQSKKLMSDNGVKVQRFFVADTANEALEAAKRLNAKEIVLKAQILAGGRGKGVFSSGLK
GGVHLTKDPEVVGQLAKQMIGYNLATKQTPKEGVKVNKVMVAEALDISRETYLAILMDRSCNGPV
LVGSPQGGVDIEEVAASNPELIFKEQIDIIEGIKDSQAQRMAENLGFLGPLQNQAADQIKKLYNL
FLKIDATQVEVNPFGETPEGQVVCFDAKINFDDNAEFRQKDIFAMDDKSEN
>d1kbla3 d.142.1.5 (A:2-376) Pyruvate phosphate dikinase, N-terminal
domain {Clostridium symbiosum}
AKWVYKFEEGNASMRNLLGGKGCNLAEMTILGMPIPQGFTVTTEACTEYYNSGKQITQEIQDQIF
EAITWLEELNGKKFGDTEDPLLVSVRSGARASMPGMMDTILNLGLNDVAVEGFAKKTGNPRFAYD
SYRRFIQMYSDVVMEVPKSHFEKIIDAMKEEKGVHFDTDLTADDLKELAEKFKAVYKEAMNGEEF
PQEPKDQLMGAVKAVFRSWDNPRAIVYRRMNDIPGDWGTAVNVQTMVFGNKGETSGTGVAFTRNP
STGEKGIYGEYLINAQGEDVVAGVRTPQPITQLENDMPDCYKQFMDLAMKLEKHFRDMQDMEFTI
EEGKLYFLQTRNGKRTAPAALQIACDLVDEGMITEEEAVVRIEAKSLDQL
>d2hgsa2 d.142.1.6 (A:304-474) Eukaryotic glutathione synthetase
{Human (Homo sapiens)}
TKKVQQELSRPGMLEMLLPGQPEAVARLRATFAGLYSLDVGEEGDQAIAEALAAPSRFVLKPQRE
GGGNNLYGEEMVQALKQLKDSEERASYILMEKIEPEPFENCLLRPGSPARVVQCISELGIFGVYV
RQEKTLVMNKHVGHLLRTKAIEHADGGVAAGVAVLDNPYPV
>d2hgsa3 d.142.1.6 (A:3-201) Eukaryotic glutathione synthetase {Human
(Homo sapiens)}
TNWGSLLQDKQQLEELARQAVDRALAEGVLLRTSQEPTSSEVVSYAPFTLFPSLVPSALLEQAYA
VQMDFNLLVDAVSQNAAFLEQTLSSTIKQDDFTARLFDIHKQVLKEGIAQTVFLGLNRSDYMFQR
SADGSPALKQIEINTISASFGGLASRTPAVHRHVLSVLSKTKEAGKILSNNPSKGLALGIAKAWE
LYGS
>d1a0i_2 d.142.2.1 (2-240) ATP-dependent DNA ligase, N-terminal
domain {Bacteriophage T7}
VNIKTNPFKAVSFVESAIKKALDNAGYLIAEIKYDGVRGNICVDNTANSYWLSRVSKTIPALEHL
NGFDVRWKRLLNDDRCFYKDGFMLDGELMVKGVDFNTGSGLLRTKWTDTKNQEFHEELFVEPIRK
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KDKVPFKLHTGHLHIKLYAILPLHIVESGEDCDVMTLLMQEHVKNMLPLLQEYFPEIEWQAAESY
EVYDMVELQQLYEQKRAEGHEGLIVKDPMCIYKRGKKSGWWKMK
>d1fvia2 d.142.2.1 (A:2-189) ATP-dependent DNA ligase, N-terminal domain {Chlorella virus, PBCV-1}
AITKPLLAATLENIEDVQFPCLATPKIAGIRSVKQTQMLSRTFKPIRNSVMNRLLTELLPEGSDG
EISIEGATFQDTTSAVMTGHKMYNAKFSYYWFDYVTDDPLKKYIDRVEDMKNYITVHPHILEHAQ
VKIIPLIPVEINNITELLQYERDVLSKGFEGVMIRKPDGKYKFGRSTLKEGILLKMKQ
>d1b04a_ d.142.2.2 (A:) Adenylation domain of NAD+-dependent DNA ligase {Bacillus stearothermophilus}
DRQQAERRAAELRELLNRYGYEYYVLDRPSVPDAEYDRLMQELIAIEEQYPELKTSDSPTQRIGG
PPLEAFRKVAHRVPMMSLANAFGEGDLRDFDRRVRQEVGEAAYVCELAIDGLAVSVRYEDGYFVQ
GATRGDGTTGEDITENLKTIRSLPLRLKEPVSLEARGEAFMPKASFLRLNEERKARGEELFANPR
NAAAGSLRQLDPKVAASRQLDLFVYGLADAEALGIASHSEALDYLQALGFKVNPERRRCANIDEV
IAFVSEWHDKRPQLPYEIDGIVIKVDSFAQQRALGATAKSPRWAIAYKFPAE
>d1dgsa3 d.142.2.2 (A:1-314) Adenylation domain of NAD+-dependent DNA ligase {Thermus filiformis}
MTREEARRRINELRDLIRYHNYRYYVLADPEISDAEYDRLLRELKELEERFPEFKSPDSPTEQVG
ARPLEPTFRPVRHPTRMYSLDNAFTYEEVLAFEERLEREAEAPSLYTVEHKVDGLSVLYYEEGVW
STGSGDGEVGEEVTQNLLTIPTIPRRLKGVPDRLEVRGEVYMPIEAFLRLNEELEERGEKVFKNP
RNAAAGSLRQKDPRVTAKRGLRATFYALGLGLGLEESGLKSQYELLLWLKEKGFPVEHCYEKALG
AEGVEEVYRRGLAQRHALPFEADGVVLKLDDLTLWGELGYTARAPRFALAYKFP
>d1ckma2 d.142.2.3 (A:11-238) RNA guanylyltransferase (mRNA capping enzyme), N-terminal domain {Chlorella virus, PBCV-1}
NITTERAVLTLNGLQIKLHKVVGESRDDIVAKMKDLAMDDHKFPRLPGPNPVSIERKDFEKLKQN
KYVVSEKTDGIRFMMFFTRVFGFKVCTIIDRAMTVYLLPFKNIPRVLFQGSIFDGELCVDIVEKK
FAFVLFDAVVVSGVTVSQMDLASRFFAMKRSLKEFKNVPEDPAILRYKEWIPLEHPTIIKDHLKK
ANAIYHTDGLIIMSVDEPVIYGRNFNLFKLKPG
>d1a48__ d.143.1.1 (-) SAICAR synthase {Baker's yeast (Saccharomyces cerevisiae)}
SITKTELDGILPLVARGKVRDIYEVDAGTLLFVATDRISAYDVIMENSIPEKGILLTKLSEFWFK
FLSNDVRNHLVDIAPGKTIFDYLPAKLSEPKYKTQLEDRSLLVHKHKLIPLEVIVRGYITGSAWK
EYVKTGTVHGLKQPQGLKESQEFPEPIFTPSTKAEQGEHDENISPAQAAELVGEDLSRRVAELAV
KLYSKCKDYAKEKGIIIADTKFEFGIDEKTNEIILVDEVLTPDSSRFWNGASYKVGESQDSYDKQ
FLRDWLTANKLNGVNGVKMPQDIVDRTRAKYIEAYETLTGSKWSH
>d1bo1a_ d.143.1.2 (A:) Phosphatidylinositol phosphate kinase IIbeta, PIPK IIbeta {Human (Homo sapiens)}
KLFRASEPILSVLMWGVNHTINELSNVPVPVMLMPDDFKAYSKIKVDNHLFNKENLPSRFKFKEY
CPMVFRNLRERFGIDDQDYQNSVTRSAPINSDSQGRCGTRFLTTYDRRFVIKTVSSEDVAEMHNI
LKKYHQFIVECHGNTLLPQFLGMYRLTVDGVETYMVVTRNVFSHRLTVHRKYDLKGSTVAREASD
KEKAKDLPTFKDNDFLNEGQKLHVGEESKKNFLEKLKRDVEFLAQLKIMDYSLLVGIHDVDRAEQ
EEMEVEERAEDEECENDGVGGNLLCSYGTPPDSPGNLLSFPRFFGPGEFDPSVDVYAMKSHESSP
KKEVYFMAIIDILTPYDTKKKAAHAAKTVKHGAGAEISTVNPEQYSKRFNEFMSNILT
>d1blxa_ d.144.1.1 (A:) Cyclin-dependent PK (CDK, different isozymes) {Human (Homo sapiens)}
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GLCRADQQYECVAEIGEGAYGKVFKARDLKNGGRFVALKRVRVQTGEEGMPLSTIREVAVLRHLE
TFEHPNVVRLFDVCTVSRTDRETKLTLVFEHVDQDLTTYLDKVPEPGVPTETIKDMMFQLLRGLD
FLHSHRVVHRDLKPQNILVTSSGQIKLADFGLARIYSFQMALTSVVVTLWYRAPEVLLQSSYATP
VDLWSVGCIFAEMFRRKPLFRGSSDVDQLGKILDVIGLPGEEDWPRDVALPRQAFHSKSAQPIEK
FVTDIDELGKDLLLKCLTFNPAKRISAYSALSHPYFQDLERCKEN
>d1jvpp_ d.144.1.1 (P:) Cyclin-dependent PK (CDK, different isozymes) {Human (Homo sapiens)}
MENFQKVEKIGEGTYGVVYKARNKLTGEVVALKKIRLDTETEGVPSTAIREISLLKELNHPNIVK
LLDVIHTENKLYLVFEFLHQDLKKFMDASALTGIPLPLIKSYLFQLLQGLAFCHSHRVLHRDLKP
QNLLINTEGAIKLADFGLARAFGVPVRTYTHEVVTLWYRAPEILLGCKYYSTAVDIWSLGCIFAE
MVTRRALFPGDSEIDQLFRIFRTLGTPDEVVWPGVTSMPDYKPSFPKWARQDFSKVVPPLDEDGR
SLLSQMLHYDPNKRISAKAALAHPFFQDVTKPVPHLRL
>d1apme_ d.144.1.1 (E:) cAMP-dependent PK, catalytic subunit {Mouse (Mus musculus)}
SEQESVKEFLAKAKEDFLKKWETPSQNTAQLDQFDRIKTLGTGSFGRVMLVKHKESGNHYAMKIL
DKQKVVKLKQIEHTLNEKRILQAVNFPFLVKLEFSFKDNSNLYMVMEYVAGGEMFSHLRRIGRFA
EPHARFYAAQIVLTFEYLHSLDLIYRDLKPENLLIDQQGYIQVTDFGFAKRVKGRTWTLCGTPEY
LAPEIILSKGYNKAVDWWALGVLIYEMAAGYPPFFADQPIQIYEKIVSGKVRFPSHFSSDLKDLL
RNLLQVDLTKRFGNLKNGVNDIKNHKWFATTDWIAIYQRKVEAPFIPKFKGPGDTSNFDDYEEEE
IRVSINEKCGKEFTEF
>d1fota_ d.144.1.1 (A:) cAMP-dependent PK, catalytic subunit {Baker's yeast (Saccharomyces cerevisiae)}
YSLQDFQILRTLGTGSFGRVHLIRSRHNGRYYAMKVLKKEIVVRLKQVEHTNDERLMLSIVTHPF
IIRMWGTFQDAQQIFMIMDYIEGGELFSLLRKSQRFPNPVAKFYAAEVCLALEYLHSKDIIYRDL
KPENILLDKNGHIKITDFGFAKYVPDVTYTLCGTPDYIAPEVVSTKPYNKSIDWWSFGILIYEML
AGYTPFYDSNTMKTYEKILNAELRFPPFFNEDVKDLLSRLITRDLSQRLGNLQNGTEDVKNHPWF
KEVVWEKLLSRNIETPYEPPIQQGQGDTSQFDKYPEEDINYGVQGEDPYADLFRDF
>d1a06__ d.144.1.1 (-) Calmodulin-dependent protein kinase {Rat (Rattus norvegicus)}
WKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKKALEGKEGSMENEIAVLHKIK
HPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQVLDAVKYLHDLGIVH
RDLKPENLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPEVLAQKPYSKAVDCWSI
GVIAYILLCGYPPFYDENDAKLFEQILKAEYEFDSPYWDDISDSAKDFIRHLMEKDPEKRFTCEQ
ALQHPWIAGDTALDKNIHQSVSEQIKKNFAKSKWKQAFNATAVVRHM
>d1ia8a_ d.144.1.1 (A:) Cell cycle checkpoint kinase chk1 {Human (Homo sapiens)}
AVPFVEDWDLVQTLGEGAYGEVQLAVNRVTEEAVAVKIVDMKRAVDCPENIKKEICINKMLNHEN
VVKFYGHRREGNIQYLFLEYCSGGELFDRIEPDIGMPEPDAQRFFHQLMAGVVYLHGIGITHRDI
KPENLLLDERDNLKISDFGLATVFRYNNRERLLNKMCGTLPYVAPELLKRREFHAEPVDVWSCGI
VLTAMLAGELPWDQPSDSCQEYSDWKEKKTYLNPWKKIDSAPLALLHKILVENPSARITIPDIKK
DRWYNKPLKKGAKRP
>d1phk__ d.144.1.1 (-) gamma-subunit of glycogen phosphorylase kinase (Phk) {Rabbit (Oryctolagus cuniculus)}
FYENYEPKEILGRGVSSVVRRCIHKPTCKEYAVKIIDVTGGGSFSAEEVQELREATLKEVDILRK

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VSGHPNIIQLKDTYETNTFFFLVFDLMKKGELFDYLTEKVTLSEKETRKIMRALLEVICALHKLN
IVHRDLKPENILLDDDMNIKLTDFGFSCQLDPGEKLREVCGTPSYLAPEIIECSMNDNHPGYGKE
VDMWSTGVIMYTLLAGSPPFWHRKQMLMLRMIMSGNYQFGSPEWDDYSDTVKDLVSRFLVVQPQK
RYTAEEALAHPFFQQYV
>d1h8fa_ d.144.1.1 (A:) Glycogen synthase kinase-3 beta (Gsk3b) {Human
(Homo sapiens)}
SKVTTVVATPGQGPDRPQEVSYTDTKVIGNGSFGVVYQAKLCDSGELVAIKKVLQGKAFKNRELQ
IMRKLDHCNIVRLRYFFYSSGEKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYQ
LFRSLAYIHSFGICHRDIKPQNLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIF
GATDYTSSIDVWSAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFAFP
QIKAHPWTKVFRPRTPPEAIALCSRLLEYTPTARLTPLEACAHSFFDELRDPNVKLPNGRDTPAL
FNFTTQELSSNPPLATILIPPHARIQA
>d1tkia_ d.144.1.1 (A:) Titin, kinase domain {Human (Homo sapiens)}
KELYEKYMIAEDLGRGEFGIVHRCVETSSKKTYMAKFVKVKGTDQVLVKKEISILNIARHRNILH
LHESFESMEELVMIFEFISGLDIFERINTSAFELNEREIVSYVHQVCEALQFLHSHNIGHFDIRP
ENIIYQTRRSSTIKIIEFGQARQLKPGDNFRLLFTAPEYYAPEVHQHDVVSTATDMWSLGTLVYV
LLSGINPFLAETNQQIIENIMNAEYTFDEEAFKEISIEAMDFVDRLLVKERKSRMTASEALQHPW
LKQKIERVSTKVIRTLKHRRYYHTLIKKDLNMVVSAARISCGGAIRSQKGVSVAKVKVASI
>d1koba_ d.144.1.1 (A:) Twitchin, kinase domain {California sea hare
(Aplysia californica), twk43}
INDYDKFYEDIWKKYVPQPVEVKQGSVYDYYDILEELGSGAFGVVHRCVEKATGRVFVAKFINTP
YPLDKYTVKNEISIMNQLHHPKLINLHDAFEDKYEMVLILEFLSGGELFDRIAAEDYKMSEAEVI
NYMRQACEGLKHMHEHSIVHLDIKPENIMCETKKASSVKIIDFGLATKLNPDEIVKVTTATAEFA
APEIVDREPVGFYTDMWAIGVLGYVLLSGLSPFAGEDDLETLQNVKRCDWEFDEDAFSSVSPEAK
DFIKNLLQKEPRKRLTVHDALEHPWLKGDHSNLTSRIPSSRYNKIRQKIKEKYADWPAPQPAIGR
IANFSSLRKHRPQEYQIYDSYFDRKEAV
>d1koa_2 d.144.1.1 (5915-6264) Twitchin, kinase domain
{Caenorhabditis elegans, pjk4}
YDNYVFDIWKQYYPQPVEIKHDHVLDHYDIHEELGTGAFGVVHRVTERATGNNFAAKFVMTPHES
DKETVRKEIQTMSVLRHPTLVNLHDAFEDDNEMVMIYEFMSGGELFEKVADEHNKMSEDEAVEYM
RQVCKGLCHMHENNYVHLDLKPENIMFTTKRSNELKLIDFGLTAHLDPKQSVKVTTGTAEFAAPE
VAEGKPVGYYTDMWSVGVLSYILLSGLSPFGGENDDETLRNVKSCDWNMDDSAFSGISEDGKDFI
RKLLLADPNTRMTIHQALEHPWLTPGNAPGRDSQIPSSRYTKIRDSIKTKYDAWPEPLPPLGRIS
NYSSLRKHRPQEYSIRDAFWDRSEA
>d1p38__ d.144.1.1 (-) MAP kinase p38 {Mouse (Mus musculus)}
ERPTFYRQELNKTIWEVPERYQNLSPVGSGAYGSVCAAFDTKTGHRVAVKKLSRPFQSIIHAKRT
YRELRLLKHMKHENVIGLLDVFTPARSLEEFNDVYLVTHLMGADLNNIVKCQKLTDDHVQFLIYQ
ILRGLKYIHSADIIHRDLKPSNLAVNEDCELKILDFGLARHTDDEMTGYVATRWYRAPEIMLNWM
HYNQTVDIWSVGCIMAELLTGRTLFPGTDHIDQLKLILRLVGTPGAELLKKISSESARNYIQSLA
QMPKMNFANVFIGANPLAVDLLEKMLVLDSDKRITAAQALAHAYFAQYHDPDDEPVADPYDQSFE
SRDLLIDEWKSLTYDEVISFVPPPLD
>d1cm8a_ d.144.1.1 (A:) MAP kinase p38-gamma {Human (Homo sapiens)}
RSGFYRQEVTKTAWEVRAVYRDLQPVGSGAYGAVCSAVDGRTGAKVAIKKLYRPFQSELFAKRAY
RELRLLKHMRHENVIGLLDVFTPDETLDDFTDFYLVMPFMGTDLGKLMKHEKLGEDRIQFLVYQM
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LKGLRYIHAAGIIHRDLKPGNLAVNEDCELKILDFGLARQADSEMTGYVVTRWYRAPEVILNWMR
YTQTVDIWSVGCIMAEMITGKTLFKGSDHLDQLKEIMKVTGTPPAEFVQRLQSDEAKNYMKGLPE
LEKKDFASILTNASPLAVNLLEKMLVLDAEQRVTAGEALAHPYFESLHDTEDEPQVQKYDDSFDD
VDRTLDEWKRVTYKEVLSFKP
>d1pme__ d.144.1.1 (-) MAP kinase Erk2 {Human (Homo sapiens)}
GQVFDVGPRYTNLSYIGEGAYGMVCSAYDNVNKVRVAIKKISPFEHQTYCQRTLREIKILLRFRH
ENIIGINDIIRAPTIEQMKDVYLVTHLMGADLYKLLKTQHLSNDHICYFLYQILRGLKYIHSANV
LHRDLKPSNLLLNTTCDLKICDFGLARVADPDHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSID
IWSVGCILAEMLSNRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINLKARNYLLSLPHKNKVPW
NRLFPNADSKALDLLDKMLTFNPHKRIEVEQALAHPYLEQYYDPSDEPIAEAPFKFDMELDDLPK
EKLKELIFEETARFQPGYRS
>d1jnk__ d.144.1.1 (-) c-jun N-terminal kinase (jnk3s) {Human (Homo
sapiens)}
DNQFYSVEVGDSTFTVLKRYQNLKPIGSGAQGIVCAAYDAVLDRNVAIKKLSRPFQNQTHAKRAY
RELVLMKCVNHKNIISLLNVFTPQKTLEEFQDVYLVMELMDANLCQVIQMELDHERMSYLLYQML
CGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLARTAGTSFMMTPYVVTRYYRAPEVILGMG
YKENVDIWSVGCIMGEMVRHKILFPGRDYIDQWNKVIEQLGTPCPEFMKKLQPTVRNYVENRPKY
AGLTFPKLFPDSLFPADSEHNKLKASQARDLLSKMLVIDPAKRISVDDALQHPYINVWYDPAEVE
APPPQIYDKQLDEREHTIEEWKELIYKEVMN
>d1ckia_ d.144.1.1 (A:) Casein kinase-1, CK1 {Rat (Rattus norvegicus)}
MELRVGNRYRLGRKIGSGSFGDIYLGTDIAAGEEVAIKLECVKTKHPQLHIESKIYKMMQGGVGI
PTIRWCGAEGDYNVMVMELLGPSLEDLFNFCSRKFSLKTVLLLADQMISRIEYIHSKNFIHRDVK
PDNFLMGLGKKGNLVYIIDFGLAKKYRDARTHQHIPYRENKNLTGTARYASINTHLGIEQSRRDD
LESLGYVLMYFNLGSLPWQGLKAATKRQKYERISEKKMSTPIEVLCKGYPSEFATYLNFCRSLRF
DDKPDYSYLRQLFRNLFHRQGFSYDYVFDWNMLKFGASR
>d1csn__ d.144.1.1 (-) Casein kinase-1, CK1 {Fission yeast
(Schizosaccharomyces pombe)}
NVVGVHYKVGRRIGEGSFGVIFEGTNLLNNQQVAIKFEPRRSDAPQLRDEYRTYKLLAGCTGIPN
VYYFGQEGLHNVLVIDLLGPSLEDLLDLCGRKFSVKTVAMAAKQMLARVQSIHEKSLVYRDIKPD
NFLIGRPNSKNANMIYVVDFGMVKFYRDPVTKQHIPYREKKNLSGTARYMSINTHLGREQSRRDD
LEALGHVFMYFLRGSLPWQGLKAATNKQKYERIGEKKQSTPLRELCAGFPEEFYKYMHYARNLAF
DATPDYDYLQGLFSKVLERLNTTEDENFDWNLL
>d1a6o__ d.144.1.1 (-) Protein kinase CK2, alpha subunit {Maize (Zea
mays)}
SKARVYADVNVLRPKEYWDYEALTVQWGEQDDYEVVRKVGRGKYSEVFEGINVNNNEKCIIKILK
PVKKKKIKREIKILQNLCGGPNIVKLLDIVRDQHSKTPSLIFEYVNNTDFKVLYPTLTDYDIRYY
IYELLKALDYCHSQGIMHRDVKPHNVMIDHELRKLRLIDWGLAEFYHPGKEYNVRVASRYFKGPE
LLVDLQDYDYSLDMWSLGCMFAGMIFRKEPFFYGHDNHDQLVKIAKVLGTDGLNVYLNKYRIELD
PQLEALVGRHSRKPWLKFMNADNQHLVSPEAIDFLDKLLRYDHQERLTALEAMTHPYFQQVRAAE
NS
>d1b6cb_ d.144.1.1 (B:) Type I TGF-beta receptor R4 {Human (Homo
sapiens)}
TTLKDLIYDMTTSGSGSGLPLLVQRTIARTIVLQESIGKGRFGEVWRGKWRGEEVAVKIFSSREE
RSWFREAEIYQTVMLRHENILGFIAADNKDNGTWTQLWLVSDYHEHGSLFDYLNRYTVTVEGMIK
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LALSTASGLAHLHMEIVGTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAVRHDSATDTIDIAP
NHRVGTKRYMAPEVLDDSINMKHFESFKRADIYAMGLVFWEIARRCSIGGIHEDYQLPYYDLVPS
DPSVEEMRKVVCEQKLRPNIPNRWQSCEALRVMAKIMRECWYANGAARLTALRIKKTLSQLSQQE
G
>d1f3mc_ d.144.1.1 (C:) pak1 {Human (Homo sapiens)}
SDEEILEKLRSIVSVGDPKKKYTRFEKIGQGASGTVYTAMDVATGQEVAIRQMNLQQQPKKELII
NEILVMRENKNPNIVNYLDSYLVGDELWVVMEYLAGGSLTDVVTETCMDEGQIAAVCRECLQALE
FLHSNQVIHRDIKSDNILLGMDGSVKLTDFGFCAQITPEQSKRSTMVGTPYWMAPEVVTRKAYGP
KVDIWSLGIMAIEMIEGEPPYLNENPLRALYLIATNGTPELQNPEKLSAIFRDFLNRCLDMDVEK
RGSAKELLQHQFLKIAKPLSSLTPLIAAAKEATK
>d1howa_ d.144.1.1 (A:) Sky1p {Baker's yeast (Saccharomyces cerevisiae)}
FHPAFKGEPYKDARYILVRKLGWGHFSTVWLAKDMVNNTHVAMKIVRGDKVYTEAAEDEIKLLQR
VNDADNTKEDSMGANHILKLLDHFNHKGPNGVHVVMVFEVLGENLLALIKKYEHRGIPLIYVKQI
SKQLLLGLDYMHRRCGIIHTDIKPENVLMEIVDSPENLIQIKIADLGNACWYDEHYTNSIQTREY
RSPEVLLGAPWGCGADIWSTACLIFELITGDFLFEPDEGHSYTKDDDHIAQIIELLGELPSYLLR
NGKYTRTFFNSRGLLRNISKLKFWPLEDVLTEKYKFSKDEAKEISDFLSPMLQLDPRKRADAGGL
VNHPWLKDTLGMEEIRVPDRELYGSGSDIPGWFEEVR
>d1qcfa3 d.144.1.2 (A:249-531) Haemopoetic cell kinase Hck {Human (Homo sapiens)}
KPQKPWEKDAWEIPRESLKLEKKLGAGQFGEVWMATYNKHTKVAVKTMKPGSMSVEAFLAEANVM
KTLQHDKLVKLHAVVTKEPIYIITEFMAKGSLLDFLKSDEGSKQPLPKLIDFSAQIAEGMAFIEQ
RNYIHRDLRAANILVSASLVCKIADFGLARVIEDNEYTAREGAKFPIKWTAPEAINFGSFTIKSD
VWSFGILLMEIVTYGRIPYPGMSNPEVIRALERGYRMPRPENCPEELYNIMMRCWKNRPEERPTF
EYIQSVLDDFYTATESQYEEIP
>d1qpca_ d.144.1.2 (A:) Lymphocyte kinase (lck) {Human (Homo sapiens)}
KPWWEDEWEVPRETLKLVERLGAGQFGEVWMGYYNGHTKVAVKSLKQGSMSPDAFLAEANLMKQL
QHQRLVRLYAVVTQEPIYIITEYMENGSLVDFLKTPSGIKLTINKLLDMAAQIAEGMAFIEERNY
IHRDLRAANILVSDTLSCKIADFGLARLIEDNEYTAREGAKFPIKWTAPEAINYGTFTIKSDVWS
FGILLTEIVTHGRIPYPGMTNPEVIQNLERGYRMVRPDNCPEELYQLMRLCWKERPEDRPTFDYL
RSVLEDFFTATE
>d1fmk_3 d.144.1.2 (249-533) c-src tyrosine kinase {Human (Homo sapiens)}
KPQTQGLAKDAWEIPRESLRLEVKLGQGCFGEVWMGTWNGTTRVAIKTLKPGTMSPEAFLQEAQV
MKKLRHEKLVQLYAVVSEEPIYIVTEYMSKGSLLDFLKGETGKYLRLPQLVDMAAQIASGMAYVE
RMNYVHRDLRAANILVGENLVCKVADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKS
DVWSFGILLTELTTKGRVPYPGMVNREVLDQVERGYRMPCPPECPESLHDLMCQCWRKEPEERPT
FEYLQAFLEDYFTSTEPQYQPGENL
>d1fgka_ d.144.1.2 (A:) Fibroblast growth factor receptor 1 {Human (Homo sapiens)}
ELPEDPRWELPRDRLVLGKPLGEGAFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDL
ISEMEMMKMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYSYNPSHNPEE
QLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGLARDIHHIDYYKKTT
NGRLPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELFKLLKEGHRMDKPS
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NCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRIVALTS
>d1vr2a_ d.144.1.2 (A:) Vascular endothelial growth factor receptor
2 (kdr) {Human (Homo sapiens)}
LPYDASKWEFPRDRLKLGKPLGRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMS
ELKILIHIGHHLNVVNLLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKVAPEDLYKDF
LTLEHLICYSFQVAKGMEFLASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGD
ARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPD
YTTPEMYQTMLDCWHGEPSQRPTFSELVEHLGNLLQANA
>d1ir3a_ d.144.1.2 (A:) Insulin receptor {Human (Homo sapiens)}
SSVFVPDEWEVSREKITLLRELGQGSFGMVYEGNARDIIKGEAETRVAVKTVNESASLRERIEFL
NEASVMKGFTCHHVVRLLGVVSKGQPTLVVMELMAHGDLKSYLRSLRPEAENNPGRPPPTLQEMI
QMAAEIADGMAYLNAKKFVHRDLAARNCMVAHDFTVKIGDFGMTRDIYETDYYRKGGKGLLPVRW
MAPESLKDGVFTTSSDMWSFGVVLWEITSLAEQPYQGLSNEQVLKFVMDGGYLDQPDNCPERVTD
LMRMCWQFNPKMRPTFLEIVNLLKDDLHPSFPEVSFFHSEENK
>d1k3aa_ d.144.1.2 (A:) Insulin-like growth factor 1 receptor {Human
(Homo sapiens)}
VPDEWEVAREKITMSRELGQGSFGMVYEGVAKGVVKDEPETRVAIKTVNEAASMRERIEFLNEAS
VMKEFNCHHVVRLLGVVSQGQPTLVIMELMTRGDLKSYLRSLRPEMENNPVLAPPSLSKMIQMAG
EIADGMAYLNANKFVHRDLAARNCMVAEDFTVKIGDFGMTRDIYETDYYRKGGKGLLPVRWMSPE
SLKDGVFTTYSDVWSFGVVLWEIATLAEQPYQGLSNEQVLRFVMEGGLLDKPDNCPDMLLELMRM
CWQYNPKMRPSFLEIISSIKEEMEPGFREVSFYYSEENK
>d1byga_ d.144.1.2 (A:) C-terminal src kinase (csk) {Human (Homo
sapiens)}
GWALNMKELKLLQTIGKGEFGDVMLGDYRGNKVAVKCIKNDATAQAFLAEASVMTQLRHSNLVQL
LGVIVEEKGGLYIVTEYMAKGSLVDYLRSRGRSVLGGDCLLKFSLDVCEAMEYLEGNNFVHRDLA
ARNVLVSEDNVAKVSDFGLTKEASSTQDTGKLPVKWTAPEALREKKFSTKSDVWSFGILLWEIYS
FGRVPYPRIPLKDVVPRVEKGYKMDAPDGCPPAVYEVMKNCWHLDAAMRPSFLQLREQLEHIKTH
EL
>d1iepa_ d.144.1.2 (A:) Abelsone tyrosine kinase (abl) {Mouse (Mus
musculus)}
MDPSSPNYDKWEMERTDITMKHKLGGGQYGEVYEGVWKKYSLTVAVKTLKEDTMEVEEFLKEAAV
MKEIKHPNLVQLLGVCTREPPFYIITEFMTYGNLLDYLRECNRQEVSAVVLLYMATQISSAMEYL
EKKNFIHRDLAARNCLVGENHLVKVADFGLSRLMTGDTYTAHAGAKFPIKWTAPESLAYNKFSIK
SDVWAFGVLLWEIATYGMSPYPGIDLSQVYELLEKDYRMERPEGCPEKVYELMRACWQWNPSDRP
SFAEIHQAFETMFQ
>d1jpaa_ d.144.1.2 (A:) ephb2 receptor tyrosine kinase {Mouse (Mus
musculus)}
KIFIDPFTFEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGKREIFVAIKTLKSG
YTEKQRRDFLSEASIMGQFDHPNVIHLEGVVTKSTPVMIITEFMENGSLDSFLRQNDGQFTVIQL
VGMLRGIAAGMKYLADMNYVHRDLAARNILVNSNLVCKVSDFGLSRFLEDDTSDPTYTSALGGKI
PIRWTAPEAIQYRKFTSASDVWSYGIVMWEVMSYGERPYWDMTNQDVINAIEQDYRLPPPMDCPS
ALHQLMLDCWQKDRNHRPKFGQIVNTLDKMIRNPNSLKA
>d1fvra_ d.144.1.2 (A:) Tie2 kinase {Human (Homo sapiens)}
PTIYPVLDWNDIKFQDVIGEGNFGQVLKARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLC
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KLGHHPNIINLLGACEHRGYLYLAIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLL
HFAADVARGMDYLSQKQFIHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAI
ESLNYSVYTTNSDVWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMR
QCWREKPYERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAE
>d1cjaa_ d.144.1.3 (A:) Actin-fragmin kinase, catalytic domain {Slime mold (Physarum polycephalum)}
AGALWEIEKELFTKLPAPSSAINSHLQPAKPKVPQKKPSKWDPPAEFKVDLSTAVSYNDIGDINW
KNLQQFKGIERSEKGTEGLFFVETESGVFIVKRSTNIESETFCSLLCMRLGLHAPKVRVVSSNSE
EGTNMLECLAAIDKSFRVITTLANQANILLMELVRGITLNKLTTTSAPEVLTKSTMQQLGSLMAL
DVIVNNSDRLPIAWTNEGNLDNIMLSERGATVVPIDSKIIPLDASHPHGERVRELLRTLIAHPGH
ESSQFHSIRDIITLYTGYDVGTEGSISMQEGFLATVRECASFDLDAFERELLSWQESLQKCHNLS
ISPQAIPFILRMLRIFH
>d1ia9a_ d.144.1.5 (A:) Trp Ca-channel kinase domain {Mouse (Mus musculus)}
YYYSAVERNNLMRLSQSIPFVPVPPRGEPVTVYRLEESSPSILNNSMSSWSQLGLCAKIEFLSKE
EMGGGLRRAVKVLCTWSEHDILKSGHLYIIKSFLPEVINTWSSIYKEDTVLHLCLREIQQQRAAQ
KLTFAFNQMKPKSIPYSPRFLEVFLLYCHSAGQWFAVEECMTGEFRKYNNNNGDEIIPTNTLEEI
MLAFSHWTYEYTRGELLVLDLQGVGENLTDPSVIKAEEKRSCDMVFGPANLGEDAIKNFRAKHHC
NSCCRKLKLPDLKRNDYT
>d1e8xa4 d.144.1.4 (A:726-1092) Phoshoinositide 3-kinase (PI3K), catalytic domain {Pig (Sus scrofa)}
TAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLPQSFRVPYDPG
LKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQDMLILQILRIMESIW
ETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLSHWLKEKCPIEEK
FQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSFLGINKERVPF
VLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLALRHHTNLLIILFSMMLMTGMPQLTSKEDIEY
IRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLHLVL
>d1j7la_ d.144.1.6 (A:) Type IIIa 3',5"-aminoglycoside phosphotransferase {Enterococcus faecalis}
AKMRISPELKKLIEKYRCVKDTEGMSPAKVYKLVGENENLYLKMTDSRYKGTTYDVEREKDMMLW
LEGKLPVPKVLHFERHDGWSNLLMSEADGVLCSEEYEDEQSPEKIIELYAECIRLFHSIDISDCP
YTNSLDSRLAELDYLLNNDLADVDCENWEEDTPFKDPRELYDFLKTEKPEEELVFSHGDLGDSNI
FVKDGKVSGFIDLGRSGRADKWYDIAFCVRSIREDIGEEQYVELFFDLLGIKPDWEKIKYYILLD
ELF
>d1e8ga2 d.145.1.1 (A:6-273) Vanillyl-alcohol oxidase {Fungus (Penicillium simplicissimum)}
EFRPLTLPPKLSLSDFNEFIQDIIRIVGSENVEVISSKDQIVDGSYMKPTHTHDPTHVMDQDYFL
ASAIVAPRNVADVQSIVGLANKFSFPLWPISIGRNSGYGGAAPRVSGSVVLDMGKNMNRVLEVNV
EGAYCVVEPGVTYHDLHNYLEANNLRDKLWLDVPDLGGGSVLGNAVERGVGYTPYGDHWMMHSGM
EVVLANGELLRTGMGALPDPKRPETMGLKPEDQPWSKIAHLFPYGFGPYIDGLFSQSNMGIVTKI
GIWLMPNP
>d1diqa2 d.145.1.1 (A:7-242) Flavoprotein subunit of p-cresol methylhydroxylase {Pseudomonas putida}
AVLPKGVTQGEFNKAVQKFRALLGDDNVLVESDQLVPYNKIMMPVENAAHAPSAAVTATTVEQVQ

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GVVKICNEHKIPIWTISTGRNFGYGSAAPVQRGQVILDLKKMNKIIKIDPEMCYALVEPGVTFGQ
MYDYIQENNLPVMLSFSAPSAIAGPVGNTMDRGVGYTPYGEHFMMQCGMEVVLANGDVYRTGMGG
VPGSNTWQIFKWGYGPTLDGMFTQANYGICTKMGFWLMPKP
>d1f0xa2 d.145.1.1 (A:9-273) D-lactate dehydrogenase {Escherichia
coli}
NKAFLNELARLVGSSHLLTDPAKTARYRKGFRSGQGDALAVVFPGSLLELWRVLKACVTADKIIL
MQAANTGLTEGSTPNGNDYDRDVVIISTLRLDKLHVLGKGEQVLAYPGTTLYSLEKALKPLGREP
HSVIGSSCIGASVIGGICNNSGGSLVQRGPAYTEMSLFARINEDGKLTLVNHLGIDLGETPEQIL
SKLDDDRIKDDDVRHDGRHAHDYDYVHRVRDIEADTPARYNADPDRLFESSGCAGKLAVFAVRLD
TFEAE
>d1i19a2 d.145.1.1 (A:57-273) Cholesterol oxidase {Brevibacterium
sterolicum}
VAPLPTPPNFPNDIALFQQAYQNWSKEIMLDATWVCSPKTPQDVVRLANWAHEHDYKIRPRGAMH
GWTPLTVEKGANVEKVILADTMTHLNGITVNTGGPVATVTAGAGASIEAIVTELQKHDLGWANLP
APGVLSIGGALAVNAHGAALPAVGQTTLPGHTYGSLSNLVTELTAVVWNGTTYALETYQRNDPRI
TPLLTNLGRCFLTSVTMQAGPN
>d1uxy_1 d.145.1.2 (3-200) Uridine
diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB),
N-terminal domain {Escherichia coli}
HSLKPWNTFGIDHNAQHIVCAEDEQQLLNAWQYATAEGQPVLILGEGSNVLFLEDYRGTVIINRI
KGIEIHDEPDAWYLHVGAGENWHRLVKYTLQEGMPGLENLALIPGCVGSSPIQNIGAYGVELQRV
CAYVDSVELATGKQVRLTAKECRFGYRDSIFKHEYQDRFAIVAVGLRLPKEWQPVLTYGDLTRLD
PTT
>d1hska1 d.145.1.2 (A:15-208) Uridine
diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB),
N-terminal domain {Staphylococcus aureus}
NKDIYQALQQLIPNEKIKVDEPLKRYTYTKTGGNADFYITPTKNEEVQAVVKYAYQNEIPVTYLG
NGSNIIIREGGIRGIVISLLSLDHIEVSDDAIIAGSGAAIIDVSRVARDYALTGLEFACGIPGSI
GGAVYMNAGAYGGEVKDCIDYALCVNEQGSLIKLTTKELELDYRNSIIQKEHLVVLEAAFTLAP
>d1qj2c2 d.145.1.3 (C:1-177) Carbon monoxide (CO) dehydrogenase
flavoprotein, N-terminal domain {Pseudomonas carboxydovorans}
MIPGSFDYHRPKSIADAVALLTKLGEDARPLAGGHSLIPIMKTRLATPEHLVDLRDIGDLVGIRE
EGTDVVIGAMTTQHALIGSDFLAAKLPIIRETSLLIADPQIRYMGTIGGNAANGDPGNDMPALMQ
CLGAAYELTGPEGARIVAARDYYQGAYFTAIEPGELLTAIRIPVPPT
>d1ffvc2 d.145.1.3 (C:1-177) Carbon monoxide (CO) dehydrogenase
flavoprotein, N-terminal domain {Hydrogenophaga pseudoflava}
MIPPRFEYHAPKSVGEAVALLGQLGSDAKLLAGGHSLLPMMKLRFAQPEHLIDINRIPELRGIRE
EGSTVVIGAMTVENDLISSPIVQARLPLLAEAAKLIADPQVRNRGTIGGDIAHGDPGNDHPALSI
AVEAHFVLEGPNGRRTVPADGFFLGTYMTLLEENEVMVEIRVPAFAQ
>d1fiqb2 d.145.1.3 (B:224-414) Xanthine oxidase, domain 3 (?) {Cow
(Bos taurus)}
PKQLRFEGERVTWIQASTLKELLDLKAQHPEAKLVVGNTEIGIEMKFKNQLFPMIICPAWIPELN
AVEHGPEGISFGAACALSSVEKTLLEAVAKLPTQKTEVFRGVLEQLRWFAGKQVKSVASLGGNII
TASPISDLNPVFMASGTKLTIVSRGTRRTVPMDHTFFPSYRKTLLGPEEILLSIEIPYSRE
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>d1fo4a6 d.145.1.3 (A:192-414) Xanthine oxidase, domain 3 (?) {Cow (Bos taurus)}
SPSLFNPEEFMPLDPTQEPIFPPELLRLKDVPPKQLRFEGERVTWIQASTLKELLDLKAQHPEAK
LVVGNTEIGIEMKFKNQLFPMIICPAWIPELNAVEHGPEGISFGAACALSSVEKTLLEAVAKLPT
QKTEVFRGVLEQLRWFAGKQVKSVASLGGNIITASPISDLNPVFMASGTKLTIVSRGTRRTVPMD
HTFFPSYRKTLLGPEEILLSIEIPYSRE
>d1jroa4 d.145.1.3 (A:179-345) Xanthine dehydrogenase chain A, domain 3 {Rhodobacter capsulatus}
PAFLPETSDALADWYLAHPEATLIAGGTDVSLWVTKALRDLPEVAFLSHCKDLAQIRETPDGYGI
GAGVTIAALRAFAEGPHPALAGLLRRFASEQVRQVATIGGNIANGSPIGDGPPALIAMGASLTLR
RGQERRRMPLEDFFLEYRKQDRRPGEFVESVTLPKSA
>d1uxy_2 d.146.1.1 (201-342) Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain {Escherichia coli}
VTPQQVFNAVCHMRTTKLPDPKVNGNAGAFFKNPVVSAETAKALLSQFPTAPNYPQADGSVKLAA
GWLIDQCQLKGMQIGGAAVHRQQALVLINEDNAKSEDVVQLAHHVRQKVGEKFNVWLEPEVRFIG
ASGEVSAVETIS
>d1hska2 d.146.1.1 (A:209-317) Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain {Staphylococcus aureus}
GKMTEIQAKMDDLTERRESKQPLEYPSCGSVFQRPPGHFAGKLIQDSNLQGHRIGGVEVSTKHAG
FMVNVDNGTATDYENLIHYVQKTVKEKFGIELNREVRIIGEHPK
>d1qlma_ d.147.1.1 (A:) Methenyltetrahydromethanopterin cyclohydrolase {Archaeon Methanopyrus kandleri}
MVSVNENALPLVERMIERAELLNVEVQELENGTTVIDCGVEAAGGFEAGLLFSEVCMGGLATVEL
TEFEHDGLCLPAVQVTTDHPAVSTLAAQKAGWQVQVGDYFAMGSGPARALALKPKETYEEIDYED
DADVAILCLESSELPDEDVAEHVADECGVDPENLYLLVAPTASIVGSVQVSARVVETGLYKLLEV
LEYDVTRVKYATGTAPIAPVADDDGEAMGRTNDCILYGGTVVYLYVEGDDELPEVVEELPSEASED
YGKPFMKIFEEADYDFYKIDPGVFAPARVVVNDLSTGKTYTAGEINVDVLKESFSL
>d1c4za_ d.148.1.1 (A:) Ubiquitin-protein ligase E3a, Hect catalytic domain (E6ap) {Human (Homo sapiens)}
NPYLRLKVRRDHIIDDALVRLEMIAMENPADLKKQLYVEFEGEQGVDEGGVSKEFFQLVVEEIFN
PDIGMFTYDESTKLFWFNPSSFETEGQFTLIGIVLGLAIYNNCILDVHFPMVVYRKLMGKKGTFR
DLGDSHPVLYQSLKDLLEYEGNVEDDMMITFQISQTDLFGNPMMYDLKENGDKIPITNENRKEFV
NLYSDYILNKSVEKQFKAFRRGFHMVTNESPLKYLFRPEEIELLICGSRNLDFQALEETTEYDGG
YTRDSVLIREFWEIVHSFTDEQKRLFLQFTTGTDRAPVGGLGKLKMIIAKNGPDTERLPTSHTCF
NVLLLPEYSSKEKLKERLLKAITYA
>d2ahja_ d.149.1.1 (A:) Nitrile hydratase alpha chain {Rhodococcus erythropolis}
IDHTTENAAPAQAPVSDRAWALFRALDGKGLVPDGYVEGWKKTFEEDFSPRRGAELVARAWTDPE
FRQLLLTDGTAAVAQYGYLGPQGEYIVAVEDTPTLKNVIVCSLASCTAWPILGLPPTWYKSFEYR
ARVVREPRKVLSEMGTEIASDIEIRVYDTTAETRYMVLPQRPAGTEGWSQEQLQEIVTKDCLIGV
AIPQV
>d1f7la_ d.150.1.2 (A:) Holo-(acyl carrier protein) synthase ACPS
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{Bacillus subtilis}
GIYGIGLDITELKRIASMAGRQKRFAERILTRSELDQYYELSEKRKNEFLAGRFAAKEAFSKAFG
TGIGRQLSFQDIEIRKDQNGKPYIICTKLSPAAVHVSITHTKEYAAAQVVIER
>d1ftha_ d.150.1.2 (A:) Holo-(acyl carrier protein) synthase ACPS
{Streptococcus pneumoniae}
MIVGHGIDIEELASIESAVTRHEGFAKRVLTALEMERFTSLKGRRQIEYLAGRWSAKEAFSKAMG
TGISKLGFQDLEVLNNERGAPYFSQAPFSGKIWLSISHTDQFVTASVILEEN
>d1qr0a1 d.150.1.1 (A:1-101) 4'-Phosphopantetheinyl transferase SFP
{Bacillus subtilis}
MKIYGIYMDRPLSQEENERFMTFISPEKREKCRRFYHKEDAHRTLLGDVLVRSVISRQYQLDKSD
IRFSTQEYGKPCIPDLPDAHFNISHSGRWVIGAFDS
>d1qr0a2 d.150.1.1 (A:102-228) 4'-Phosphopantetheinyl transferase
SFP {Bacillus subtilis}
QPIGIDIEKTKPISLEIAKRFFSKTEYSDLLAKDKDEQTDYFYHLWSMKESFIKQEGKGLSLPLD
SFSVRLHQDGQVSIELPDSHSPCYIKTYEVDPGYKMAVCAAHPDFPEDITMVSYEELLRAAA
>d1ako__ d.151.1.1 (-) DNA-repair enzyme exonuclease III {Escherichia
coli}
MKFVSFNINGLRARPHQLEAIVEKHQPDVIGLQETKVHDDMFPLEEVAKLGYNVFYHGQKGHYGV
ALLTKETPIAVRRGFPGDDEEAQRRIIMAEIPSLLGNVTVINGYFPQGESRDHPIKFPAKAQFYQ
NLQNYLETELKRDNPVLIMGDMNISPTDLDIGIGEENRKRWLRTGKCSFLPEEREWMDRLMSWGL
VDTFRHANPQTADRFSWFDYRSKGFDDNRGLRIDLLLASQPLAECCVETGIDYEIRSMEKPSDHA
PVWATFRR
>d1hd7a_ d.151.1.1 (A:) DNA repair endonuclease Hap1 {Human (Homo
sapiens)}
LYEDPPDQKTSPSGKPATLKICSWNVDGLRAWIKKKGLDWVKEEAPDILCLQETKCSENKLPAEL
QELPGLSHQYWSAPSDKEGYSGVGLLSRQCPLKVSYGIGDEEHDQEGRVIVAEFDSFVLVTAYVP
NAGRGLVRLEYRQRWDEAFRKFLKGLASRKPLVLCGDLNVAHEEIDLRNPKGNKKNAGFTPQERQ
GFGELLQAVPLADSFRHLYPNTPYAYTFWTYMMNARSKNVGWRLDYFLLSHSLLPALCDSKIRSK
ALGSDHCPITLYLAL
>d2dnja_ d.151.1.1 (A:) Deoxyribonuclease I {Cow (Bos taurus)}
LKIAAFNIRTFGETKMSNATLASYIVRIVRRYDIVLIQEVRDSHLVAVGKLLDYLNQDDPNTYHY
VVSEPLGRNSYKERYLFLFRPNKVSVLDTYQYDDGCESCGNDSFSREPAVVKFSSHSTKVKEFAI
VALHSAPSDAVAEINSLYDVYLDVQQKWHLNDVMLMGDFNADCSYVTSSQWSSIRLRTSSTFQWL
IPDSADTTATSTNCAYDRIVVAGSLLQSSVVPGSAAPFDFQAAYGLSNEMALAISDHYPVEVTLT
>d1i9za_ d.151.1.2 (A:) Synaptojanin, IPP5C domain {Yeast
(Schizosaccharomyces pombe)}
YDPIHEYVNHELRKRENEFSEHKNVKIFVASYNLNGCSATTKLENWLFPENTPLADIYVVGFQEI
VQLTPQQVISADPAKRREWESCVKRLLNGKCTSGPGYVQLRSGQLVGTALMIFCKESCLPSIKNV
EGTVKKTGLGGVSGNKGAVAIRFDYEDTGLCFITSHLAAGYTNYDERDHDYRTIASGLRFRRGRS
IFNHDYVVWFGDFNYRISLTYEEVVPCIAQGKLSYLFEYDQLNKQMLTGKVFPFFSELPITFPPT
YKFDIGTDIYDTSDKHRVPAWTDRILYRGELVPHSYQSVPLYYSDHRPIYATYEANIVKVDREKK
KILFEELYNQRKQEVRDASQ
>d1aora2 d.152.1.1 (A:1-210) Aldehyde ferredoxin oxidoreductase
{Archaeon Pyrococcus furiosus}
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MYGNWGRFIRVNLSTGDIKVEEYDEELAKKWLGSRGLAIYLLLKEMDPTVDPLSPENKLIIAAGP
LTGTSAPTGGRYNVVTKSPLTGFITMANSGGYFGAELKFAGYDAIVVEGKAEKPVYIYIKDEHIE
IRDASHIWGKKVSETEATIRKEVGSEKVKIASIGPAGENLVKFAAIMNDGHRAAGRGGVGAVMGS
KNLKAIAVEGSKTVP
>d1b25a2 d.152.1.1 (A:1-210) Formaldehyde ferredoxin oxidoreductase {Archaeon Pyrococcus furiosus}
MYGWWGRILRVNLTTGEVKVQEYPEEVAKKFIGGRGLAAWILWNEARGVEPLSPENKLIFAAGPF
NGLPTPSGGKLVVAAKSPLTGGYGDGNLGTMASVHLRRAGYDALVVEGKAKKPVYIYIEDDNVSI
LSAEGLWGKTTFETERELKEIHGKNVGVLTIGPAGENLVKYAVVISQEGRAAGRPGMGAVMGSKK
LKAVVIRGTKEIPVA
>d1gdoa_ d.153.1.1 (A:) Glucosamine 6-phosphate synthase, N-terminal domain {Escherichia coli}
CGIVGAIAQRDVAEILLEGLRRLEYRGYDSAGLAVVDAEGHMTRLRRLGKVQMLAQAAEEHPLHG
GTGIAHTRWATHGEPSEVNAHPHVSEHIVVVHNGIIENHEPLREELKARGYTFVSETDTEVIAHL
VNWELKQGGTLREAVLRAIPQLRGAYGTVIMDSRHPDTLLAARSGSPLVIGLGMGENFIASDQLA
LLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKRQDIESNL
>d1gph12 d.153.1.1 (1:1-234) Glutamine PRPP amidotransferase, N-terminal domain {Bacillus subtilis}
CGVFGIWGHEEAPQITYYGLHSLQHRGQEGAGIVATDGEKLTAHKGQGLITEVFQNGELSKVKGK
GAIGHVRYATAGGGGYENVQPLLFRSQNNGSLALAHNGNLVNATQLKQQLENQGSIFQTSSDTEV
LAHLIKRSGHFTLKDQIKNSLSMLKGAYAFLIMTETEMIVALDPNGLRPLSIGMMGDAYVVASET
CAFDVVGATYLREVEPGEMLIINDEGMKSERFSMNINRS
>d1ecfa2 d.153.1.1 (A:1-249) Glutamine PRPP amidotransferase, N-terminal domain {Escherichia coli}
CGIVGIAGVMPVNQSIYDALTVLQHRGQDAAGIITIDANNCFRLRKANGLVSDVFEARHMQRLQG
NMGIGHVRYPTAGSSSASEAQPFYVNSPYGITLAHNGNLTNAHELRKKLFEEKRRHINTTSDSEI
LLNIFASELDNFRHYPLEADNIFAAIAATNRLIRGAYACVAMIIGHGMVAFRDPNGIRPLVLGKR
DIDENRTEYMVASESVALDTLGFDFLRDVAPGEAIYITEEGQLFTRQCADNPVS
>d1ct9a2 d.153.1.1 (A:1-192) Asparagine synthetase B, N-terminal domain {Escherichia coli}
ASIFGVFDIKTDAVELRKKALELSRLMRHRGPDWSGIYASDNAILAHERLSIVDVNAGAQPLYNQ
QKTHVLAVNGEIYNHQALRAEYGDRYQFQTGSDCEVILALYQEKGPEFLDDLQGMFAFALYDSEK
DAYLIGRDHLGIIPLYMGYDEHGQLYVASEMKALVPVCRTIKEFPAGSYLWSQDGEIRSYYH
>d1jgta2 d.153.1.1 (A:4-209) beta-Lactam synthetase {Streptomyces clavuligerus}
PVLPAAFGFLASARTGGGRAPGPVFATRGSHTDIDTPQGERSLAATLVHAPSVAPDRAVARSLTG
APTTAVLAGEIYNRDELLSVLPAGPAPEGDAELVLRLLERYDLHAFRLVNGRFATVVRTGDRVLL
ATDHAGSVPLYTCVAPGEVRASTEAKALAAHRDPKGFPLADARRVAGLTGVYQVPAGAVMDIDLG
SGTAVTHRTWT
>d1ea0a3 d.153.1.1 (A:1-422) Alpha subunit of glutamate synthase, N-terminal domain {Azospirillum brasilense}
CGVGFIAAIDGKPRRSVVEKGIEALKAVWHRGAVDADGKTGDGAGIHVAVPQKFFKDHVKVIGHR
APDNKLAVGQVFLPRISLDAQEACRCIVETEILAFGYYIYGWRQVPINVDIIGEKANATRPEIEQ
IIVGNNKGVSDEQFELDLYIIRRRIEKAVKGEQINDFYICSLSARSIIYKGMFLAEQLTTFYPDL
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LDERFESDFAIYHQRYSTNTFPTWPLAQPFRMLAHNGEINTVKGNVNWMKAHETRMEHPAFGTHM
QDLKPVIGVGLSDSGSLDTVFEVMVRAGRTAPMVKMMLVPQALTSSQTTPDNHKALIQYCNSVME
PWDGPAALAMTDGRWVVGGMDRNGLRPMRYTITTDGLIIGGSETGMVKIDETQVIEKGRLGPGEM
IAVDLQSGKLYRDRELKDHLATLKPWDKWVQN
>g1gk9.1 d.153.1.2 (A:,B:) Penicillin acylase {Escherichia coli}
QSSSEIKIVRDEYGMPHIYANDTWHLFYGYGYVVAQDRLFQMEMARRSTQGTVAEVLGKDFVKFD
KDIRRNYWPDAIRAQIAALSPEDMSILQGYADGMNAWIDKVNTNPETLLPKQFNTFGFTPKRWEP
FDVAMIFVGTMANRFSDSTSEIDNLALLTALKDKYGVSQGMAVFNQLKWLVNPSAPTTIAVQESN
YPLKFNQQNSQTAXSNMWVIGKSKAQDAKAIMVNGPQFGWYAPAYTYGIGLHGAGYDVTGNTPFA
YPGLVFGHNGVISWGSTAGFGDDVDIFAERLSAEKPGYYLHNGKWVKMLSREETITVKNGQAETF
TVWRTVHGNILQTDQTTQTAYAKSRAWDGKEVASLLAWTHQMKAKNWQEWTQQAAKQALTINWYY
ADVNGNIGYVHTGAYPDRQSGHDPRLPVPGTGKWDWKGLLPFEMNPKVYNPQSGYIANWNNSPQK
DYPASDLFAFLWGGADRVTEIDRLLEQKPRLTADQAWDVIRQTSRQDLNLRLFLPTLQAATSGLT
QSDPRRQLVETLTRWDGINLLNDDGKTWQQPGSAILNVWLTSMLKRTVVAAVPMPFDKWYSASGY
ETTQDGPTGSLNISVGAKILYEAVQGDKSPIPQAVDLFAGKPQQEVVLAALEDTWETLSKRYGNN
VSNWKTPAMALTFRANNFFGVPQAAAEETRHQAEYQNRGTENDMIVFSPTTSDRPVLAWDVVAPG
QSGFIAPDGTVDKHYEDQLKMYENFGRKSLWLTKQDVEAHKESQEVLHVQR
>g1cp9.1 d.153.1.2 (A:,B:) Penicillin acylase {Providencia rettgeri}
ESTQIKIERDNYGVPHIYANDTYSLFYGYGYAVAQDRLFQMEMAKRSTQGTVSEVFGKDYISFDK
EIRNNYWPDSIHKQINQLPSQEQDILRGYADGMNAWIKQINTKPDDLMPKQFIDYDFLPSQWTSF
DVAMIMVGTLANRFSDMNSEIDNLALLTALKDKYGEQLGVEFFNQINWLNNPNAPTTISSEEFTY
SDXSNVWLVGKTKASGAKAILLNGPQFGWFNPAYTYGIGLHGAGFNIVGNTPFAYPAILFGHNGH
VSWGSTAGFGDGVDIFAEQVSPEDPNSYLHQGQWKKMLSRQETLNVKGEQPITFEIYRTVHGNVV
KRDKTTHTAYSKARAWDGKELTSLMAWVKQGQAQNWQQWLDQAQNQALTINWYYADKDGNIGYVH
TGHYPDRQINHDPRLPVSGTGEWDWKGIQPFANNPKVYNPKSGYIANWNNSPAKNYPASDLFAFL
WGSADRVKEIDNRIEAYDKLTADDMWAILQQTSRVDLNHRLFTPFLTQATQGLPSNDNSVKLVSM
LQQWDGINQLSSDGKHYIHPGSAILDIWLKEMLKATLGQTVPAPFDKWYLASGYETTQEGPTGSL
NISTGAKLLYESLLEDKSPISQSIDLFSGQPQNDVIRKTLNTTYQKMIEKYGDNPANWQTPATAL
TFRENNFFGIPQALPQENFHQNEYHNRGTENDLIVFTEEGVSAWDVVAPGQSGFISPQGKPSPHY
QDQLSLYQQFGKKPLWLNSEDVAPYIESTETLIIER
>g1fm2.1 d.153.1.2 (A:,B:) Cephalosporin acylase {Brevundimonas diminuta}
QAPIAAYKPRSNEILWDGYGVPHIYGVDAPSAFYGYGWAQARSHGDNILRLYGEARGKGAEYWGP
DYEQTTVWLLTNGVPERAQQWYAQQSPDFRANLDAFAAGINAYAQQNPDDISPEVRQVLPVSGAD
VVAHAHRLMNFLYVASPGRTLGXSNSWAVAPGKTANGNALLLQNPHLSWTTDYFTYYEAHLVTPD
FEIYGATQIGLPVIRFAFNQRMGITNTVNGMVGATNYRLTLQDGGYLYDGQVRPFERRQASYRLR
QADGSTVDKPLEIRSSVHGPVFERADGTAVAVRVAGLDRPGMLEQYFDMITAHSFDDYEAAMARM
QVPTFNIVYADREGTINYSFNGVAPKRAEGDIAFWQGNVPGDSSRYLWTETHPLDDLPRVTNPPG
GFVQNSNDPPWTPTWPVTYCPANHPSYLAPQTPHSLRAQQSVRLMSENDDLTLERFMALQFSHRA
VMADRTLPDLIPAALIDPDPEVQAAARLLAAWDRDFTSDSRAALLFEEWARLFAGQNFAGQAAFA
TPWSLDKPVSTPYGVRDPKAAVDQLRTAIANTKRKYGAIDRPFGDASRMILNDVNVPGAAGYGNL
GSFRVFTWSDPDENGIRTPVHGETWVAMIEFSTPVRAYGLMSYGNSRQPGTTHYSDQIERVSRAD
FRELLLRREQVEAAVQERTPFNF
>d2pvaa_ d.153.1.3 (A:) Penicillin V acylase {Bacillus sphaericus}
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CSSLSIRTTDDKSLFARTMDFTMEPDSKVIIVPRNYGIRLLEKENVVINNSYAFVGMGSTDITSP
VLYDGVNEKTYADEPKKGTGLMGAMLYYATFATYADEPKKGTTGINPVYVISQVLGNCVTVDDVI
EKLTSYTLLNEANIILGFAPPLHYTFTDASGESIVIEPDKTGITIHRKTIGVMTNSPGYEWHQTN
LRAYIGVTPNPPQDIMMGDLDLTPFGQGAGGLGLPGDFTPSARFLRVAYWKKYTEKAKNETEGVT
NLFHILSSVNIPKGVVLTNEGKTDYTIYTSAMCAQSKNYYFKLYDNSRISAVSLMAENLNSQDLI
TFEWDRKQDIKQLNQVN
>d1pma1_ d.153.1.4 (1:) Proteasome beta subunit (catalytic) {Archaeon
Thermoplasma acidophilum}
TTTVGITLKDAVIMATERRVTMENFIMHKNGKKLFQIDTYTGMTIAGLVGDAQVLVRYMKAELEL
YRLQRRVNMPIEAVATLLSNMLNQVKYMPYMVQLLVGGIDTAPHVFSIDAAGGSVEDIYASTGSG
SPFVYGVLESQYSEKMTVDEGVDLVIRAISAAKQRDSASGGMIDVAVITRKDGYVQLPTDQIESR
IRKLGLIL
>d1ryp1_ d.153.1.4 (1:) Proteasome beta subunit (catalytic) {Baker's
yeast (Saccharomyces cerevisiae)}
QFNPYGDNGGTILGIAGEDFAVLAGDTRNITDYSINSRYEPKVFDCGDNIVMSANGFAADGDALV
KRFKNSVKWYHFDHNDKKLSINSAARNIQHLLYGKRFFPYYVHTIIAGLDEDGKGAVYSFDPVGS
YEREQCRAGGAAASLIMPFLDNQVNFKNQYEPGTNGKVKKPLKYLSVEEVIKLVRDSFTSATERH
IQVGDGLEILIVTKDGVRKEFYELKRD
>d1ryp2_ d.153.1.4 (2:) Proteasome beta subunit (catalytic) {Baker's
yeast (Saccharomyces cerevisiae)}
TQQPIVTGTSVISMKYDNGVIIAADNLGSYGSLLRFNGVERLIPVGDNTVVGISGDISDMQHIER
LLKDLVTENAYDNPLADAEEALEPSYIFEYLATVMYQRRSKMNPLWNAIIVAGVQSNGDQFLRYV
NLLGVTYSSPTLATGFGAHMANPLLRKVVDRESDIPKTTVQVAEEAIVNAMRVLYYRDARSSRNF
SLAIIDKNTGLTFKKNLQVENMKWDFAKDIKGYGTQKI
>d1ryph_ d.153.1.4 (H:) Proteasome beta subunit (catalytic) {Baker's
yeast (Saccharomyces cerevisiae)}
LKKGEVSLGASIMAVTFKDGVILGADSRTTTGAYIANRVTDKLTRVHDKIWCCRSGSAADTQAIA
DIVQYHLELYTSQYGTPSTETAASVFKELCYENKDNLTAGIIVAGYDDKNKGEVYTIPLGGSVHK
LPYAIAGSGSTFIYGYCDKNFRENMSKEETVDFIKHSLSQAIKWDGSSGGVIRMVVLTAAGVERL
IFYPDEYEQL
>d1rypi_ d.153.1.4 (I:) Proteasome beta subunit (catalytic) {Baker's
yeast (Saccharomyces cerevisiae)}
TTIVGVKFNNGVVIAADTRSTQGPIVADKNCAKLHRISPKIWCAGAGTAADTEAVTQLIGSNIEL
HSLYTSREPRVVSALQMLKQHLFKYQGHIGAYLIVAGVDPTGSHLFSIHAHGSTDVGYYLSLGSG
SLAAMAVLESHWKQDLTKEEAIKLASDAIQAGIWNDLGSGSNVDVCVMEIGKDAEYLRNYLTPNV
REEKQKSYKFPRGTTAVLKESIVNICD
>d1rypj_ d.153.1.4 (J:) Proteasome beta subunit (catalytic) {Baker's
yeast (Saccharomyces cerevisiae)}
SDPSSINGGIVVAMTGKDCVAIACDLRLGSQSLGVSNKFEKIFHYGHVFLGITGLATDVTTLNEM
FRYKTNLYKLKEERAIEPETFTQLVSSSLYERRFGPYFVGPVVAGINSKSGKPFIAGFDLIGCID
EAKDFIVSGTASDQLFGMCESLYEPNLEPEDLFETISQALLNAADRDALSGWGAVVYIIKKDEVV
KRYLKMRQD
>d1rypk_ d.153.1.4 (K:) Proteasome beta subunit (catalytic) {Baker's
yeast (Saccharomyces cerevisiae)}
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MDIILGIRVQDSVILASSKAVTRGISVLKDSDDKTRQLSPHTLMSFAGEAGDTVQFAEYIQANIQ
LYSIREDYELSPQAVSSFVRQELAKSIRSRRPYQVNVLIGGYDKKKNKPELYQIDYLGTKVELPY
GAHGYSGFYTFSLLDHHYRPDMTTEEGLDLLKLCVQELEKRMPMDFKGVIVKIVDKDGIRQVDDF
QAQ
>d1rypl_ d.153.1.4 (L:) Proteasome beta subunit (catalytic) {Baker's
yeast (Saccharomyces cerevisiae)}
TTTLAFRFQGGIIVAVDSRATAGNWVASQTVKRVIEINPFLLGTMAGGAADCQFWETWLGSQCRL
HELREKERISVAAASKILSNLVYQYKGAGLSMGTMICGYTRKEGPTIYYVDSDGTRLKGDIFCVG
SGQTFAYGVLDSNYKWDLSVEDALYLGKRSILAAAHRDAYSGGSVNLYHVTEDGWIYHGNHDVGE
LFWKVKEEEGSFNNVIG
>d1pmaa_ d.153.1.4 (A:) Proteasome alpha subunit (non-catalytic)
{Archaeon Thermoplasma acidophilum}
TVFSPDGRLFQVEYAREAVKKGSTALGMKFANGVLLISDKKVRSRLIEQNSIEKIQLIDDYVAAV
TSGLVADARVLVDFARISAQQEKVTYGSLVNIENLVKRVADQMQQYTQYGGVRPYGVSLIFAGID
QIGPRLFDCDPAGTINEYKATAIGSGKDAVVSFLEREYKENLPEKEAVTLGIKALKSSLEEGEEL
KAPEIASITVGNKYRIYDQEEVKKFL
>d1rypa_ d.153.1.4 (A:) Proteasome alpha subunit (non-catalytic)
{Baker's yeast (Saccharomyces cerevisiae)}
AGYDRHITIFSPEGRLYQVEYAFKATNQTNINSLAVRGKDCTVVISQKKVPDKLLDPTTVSYIFC
ISRTIGMVVNGPIPDARNAALRAKAEAAEFRYKYGYDMPCDVLAKRMANLSQIYTQRAYMRPLGV
ILTFVSVDEELGPSIYKTDPAGYYVGYKATATGPKQQEITTNLENHFKKSKIDHINEESWEKVVE
FAITHMIDALGTEFSKNDLEVGVATKDKFFTLSAENIEERLVAIAEQD
>d1rypb_ d.153.1.4 (B:) Proteasome alpha subunit (non-catalytic)
{Baker's yeast (Saccharomyces cerevisiae)}
MTDRYSFSLTTFSPSGKLGQIDYALTAVKQGVTSLGIKATNGVVIATEKKSSSPLAMSETLSKVS
LLTPDIGAVYSGMGPDYRVLVDKSRKVAHTSYKRIYGEYPPTKLLVSEVAKIMQEATQSGGVRPF
GVSLLIAGHDEFNGFSLYQVDPSGSYFPWKATAIGKGSVAAKTFLEKRWNDELELEDAIHIALLT
LKESVEGEFNGDTIELAIIGDENPDLLGYTGIPTDKGPRFRKLTSQEINDRLEAL
>d1rypc_ d.153.1.4 (C:) Proteasome alpha subunit (non-catalytic)
{Baker's yeast (Saccharomyces cerevisiae)}
GSRRYDSRTTIFSPEGRLYQVEYALESISHAGTAIGIMASDGIVLAAERKVTSTLLEQDTSTEKL
YKLNDKIAVAVAGLTADAEILINTARIHAQNYLKTYNEDIPVEILVRRLSDIKQGYTQHGGLRPF
GVSFIYAGYDDRYGYQLYTSNPSGNYTGWKAISVGANTSAAQTLLQMDYKDDMKVDDAIELALKT
LSKTTDSSALTYDRLEFATIRKGANDGEVYQKIFKPQEIKDILVKTGIT
>d1rypd_ d.153.1.4 (D:) Proteasome alpha subunit (non-catalytic)
{Baker's yeast (Saccharomyces cerevisiae)}
GYDRALSIFSPDGHIFQVEYALEAVKRGTCAVGVKGKNCVVLGCERRSTLKLQDTRITPSKVSKI
DSHVVLSFSGLNADSRILIEKARVEAQSHRLTLEDPVTVEYLTRYVAGVQQRYTQSGGVRPFGVS
TLIAGFDPRDDEPKLYQTEPSGIYSSWSAQTIGRNSKTVREFLEKNYDRKEPPATVEECVKLTVR
SLLEVVQTGAKNIEITVVKPDSDIVALSSEEINQYVTQIEQEKQEQ
>d1rype_ d.153.1.4 (E:) Proteasome alpha subunit (non-catalytic)
{Baker's yeast (Saccharomyces cerevisiae)}
DRGVSTFSPEGRLFQVEYSLEAIKLGSTAIGIATKEGVVLGVEKRATSPLLESDSIEKIVEIDRH
IGCAMSGLTADARSMIEHARTAAVTHNLYYDEDINVESLTQSVCDLALRFGEGASGEERLMSRPF
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GVALLIAGHDADDGYQLFHAEPSGTFYRYNAKAIGSGSEGAQAELLNEWHSSLTLKEAELLVLKI
LKQVMEEKLDENNAQLSCITKQDGFKIYDNEKTAELIKELKEKEAAE
>d1rypf_ d.153.1.4 (F:) Proteasome alpha subunit (non-catalytic)
{Baker's yeast (Saccharomyces cerevisiae)}
FRNNYDGDTVTFSPTGRLFQVEYALEAIKQGSVTVGLRSNTHAVLVALKRNADELSSYQKKIIKC
DEHMGLSLAGLAPDARVLSNYLRQQCNYSSLVFNRKLAVERAGHLLCDKAQKNTQSYGGRPYGVG
LLIIGYDKSGAHLLEFQPSGNVTELYGTAIGARSQGAKTYLERTLDTFIKIDGNPDELIKAGVEA
ISQSLRDESLTVDNLSIAIVGKDTPFTIYDGEAVAKYI
>d1rypg_ d.153.1.4 (G:) Proteasome alpha subunit (non-catalytic)
{Baker's yeast (Saccharomyces cerevisiae)}
GTGYDLSNSVFSPDGRNFQVEYAVKAVENGTTSIGIKCNDGVVFAVEKLITSKLLVPQKNVKIQV
VDRHIGCVYSGLIPDGRHLVNRGREEAASFKKLYKTPIPIPAFADRLGQYVQAHTLYNSVRPFGV
STIFGGVDKNGAHLYMLEPSGSYWGYKGAATGKGRQSAKAELEKLVDHHPEGLSAREAVKQAAKI
IYLAHEDNKEKDFELEISWCSLSETNGLHKFVKGDLLQEAIDFAQKEIN
>d1ht1a_ d.153.1.4 (A:) HslV (ClpQ) protease {Escherichia coli}
TTIVSVRRNGHVVIAGDGQATLGNTVMKGNVKKVRRLYNDKVIAGFAGGTADAFTLFELFERKLE
MHQGHLVKAAVELAKDWRTDRMLRKLEALLAVADETASLIITGNGDVVQPENDLIAIGSGGPYAQ
AAARALLENTELSAREIAEKALDIAGDICIYTNHFHTIEELSYK
>d1jjwa_ d.153.1.4 (A:) HslV (ClpQ) protease {Haemophilus influenzae}
TTIVSVRRNGQVVVGGDGQVSLGNTVMKGNARKVRRLYNGKVLAGFAGGTADAFTLFELFERKLE
MHQGHLLKSAVELAKDWRTDRALRKLEAMLIVADEKESLIITGIGDVVQPEEDQILAIGSGGNYA
LSAARALVENTELSAHEIVEKSLRIAGDICVFTNTNFTIEELP
>g1apy.1 d.153.1.5 (A:,B:) Glycosylasparaginase
(aspartylglucosaminidase, AGA) {Human (Homo sapiens)}
SPLPLVVNTWPFKNATEAAWRALASGGSALDAVESGCAMCEREQCDGSVGFGGSPDELGETTLDA
MIMDGTTMDVGAVGDLRRIKNAIGVARKVLEHTTHTLLVGESATTFAQSMGFINEDLSTSASQAL
HSDWLARNCQPNYWRNVIPDPSKYCGPYKPPXTIGMVVIHKTGHIAAGTSTNGIKFKIHGRVGDS
PIPGAGAYADDTAGAAAATGNGDILMRFLPSYQAVEYMRRGEDPTIACQKVISRIQKHFPEFFGA
VICANVTGSYGAACNKLSTFTQFSFMVYNSEKNQPTEEKVDCI
>g2gac.1 d.153.1.5 (A:,B:) Glycosylasparaginase
(aspartylglucosaminidase, AGA) {Flavobacterium meningosepticum}
NKPIVLSTWNFGLHANVEAWKVLSKGGKALDAVEKGVRLVEDDPTERSVGYGGRPDRDGRVTLDA
CIMDENYNIGSVACMEHIKNPISVARAVMEKTPHVMLVGDGALEFALSQGFKKENLLTAESEKEW
KEWLKTXCIGMIALDAQGNLSGACTTSGMAYKMHGRVGDSPIIGAGLFVDNEIGAATATGHGEEV
IRTVGTHLVVELMNQGRTPQQACKEAVERIVKIVNRRGKNLKDIQVGFIALNKKGEYGAYCIQDG
FNFAVHDQKGNRLETP
>d1b65a_ d.154.1.1 (A:) L-aminopeptidase D-Ala-esterase/amidase
{Ochrobactrum anthropi}
KPRARDLGLPFTGVTGPYNAITDVDGVGVGFQTIIENEPRPGRKRPARSGVTAILPHMQSETPVP
VYAGVHRFNGNGEMTGTHWIEDGGYFLGPVVITNTHGIGMAHHATVRWMVDRYASTYQTDDFLWI
MPVVAETYDGALNDINGFPVTEADVRKALDNVASGPVQEGNCGGGTGMITYGFKGGTGTASRVVE
FGGRSFTIGALVQANHGQRDWLTIAGVPVGQHMRDGTPQSQLQERGSIIVVLATDLPLMPHQLKR
LARRASIGIGRNGTPGGNNSGDIFIAFSTANQRPMQHRSAPFLDVEMVNDEPLDTVYLAAVDSVE
EAVVNAMIAAEDMGGTPFDRLLVQAIDHERLRAVLRQYGRLA
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>g1pya.1 d.155.1.1 (A:,B:) Histidine decarboxylase {Lactobacillus sp.,
strain 30a}
SELDAKLNKLGVDRIAISPYKQWTRGYMEPGNIGNGYVTGLKVDAGVRDKSDDDVLDGIVSYDRA
ETKNAYIGQINMTTASXFTGVQGRVIGYDILRSPEVDKAKPLFTETQWDGSELPIYDAKPLQDAL
VEYFGTEQDRRHYPAPGSFIVCANKGVTAERPKNDADMKPGQGYGVWSAIAISFAKDPTKDSSMF
VEDAGVWETPNEDELLEYLEGRRKAMAKSIAECGQDAHASFESSWIGFAYTMMEPGQIGNAITVA
PYVSLPIDSIPGGSILTPDKDMEIMENLTMPEWLEKMGYKSLSANNALKY
>d1jl0a_ d.156.1.1 (A:) S-adenosylmethionine decarboxylase {Human
(Homo sapiens)}
HFFEGTEKLLEVWFSRQQPDANQGSGDLRTIPRSEWDILLKDVQCSIISVTKTDKQEAYVLSESS
MFVSKRRFILKTCGTTLLLKALVPLLKLARDYSGFDSIQSFFYSRKNFMKPSHQGYPHRNFQEEI
EFLNAIFPNGAGYCMGRMNSDCWYLYTLDFPESRVISQPDQTLEILMSELDPAVMDQFYMKDGVT
AKDVTRESGIRDLIPGSVIDATMFNPCGYSMNGMKSDGTYWTIAITPEPEFSYVSFETNLSQTSY
DDLIRKVVEVFKPGKFVTTLFVNQSSKCRTVLASPQKIEGFKRLDCQSAMFNDYNFVFTSFAKKQ
>d2bc2a_ d.157.1.1 (A:) Zn metallo-beta-lactamase {Bacillus cereus}
TVIKNETGTISISQLNKNVWVHTELGSFNGEAVPSNGLVLNTSKGLVLVDSSWDDKLTKELIEMV
EKKFQKRVTDVIITHAHADRIGGIKTLKERGIKAHSTALTAELAKKNGYEEPLGDLQTVTNLKFG
NMKVETFYPGKGHTEDNIVVWLPQYNILVGGALVKSTSAKDLGNVADAYVNEWSTSIENVLKRYR
NINAVVPGHGEVGDKGLLLHTLDLLK
>d1a7ta_ d.157.1.1 (A:) Zn metallo-beta-lactamase {Bacteroides
fragilis}
SVKISDDISITQLSDKVYTYVSLAEIEGWGMVPSNGMIVINNHQAALLDTPINDAQTEMLVNWVT
DSLHAKVTTFIPNHWHGDCIGGLGYLQRKGVQSYANQMTIDLAKEKGLPVPEHGFTDSLTVSLDG
MPLQCYYLGGGHATDNIVVWLPTENILFGGCMLKDNQTTSIGNISDADVTAWPKTLDKVKAKFPS
ARYVVPGHGNYGGTELIEHTKQIVNQYIESTS
>d1smla_ d.157.1.1 (A:) Zn metallo-beta-lactamase {Xanthomonas
maltophilia}
EVPLPQLRAYTVDASWLQPMAPLQIADHTWQIGTEDLTALLVQTPDGAVLLDGGMPQMASHLLDN
MKARGVTPRDLRLILLSHAHADHAGPVAELKRRTGAKVAANAESAVLLARGGSDDLHFGDGITYP
PANADRIVMDGEVITVGGIVFTAHFMAGHTPGSTAWTWTDTRNGKPVRIAYADSLSAPGYQLQGN
PRYPHLIEDYRRSFATVRALPCDVLLTPHPGASNWDYAAGARAGAKALTCKAYADAAEQKFDGQL
AKETAG
>d1jjea_ d.157.1.1 (A:) Zn metallo-beta-lactamase {Pseudomonas
aeruginosa, IMP-1}
SLPDLKIEKLDEGVYVHTSFEEVNGWGVVPKHGLVVLVNAEAYLIDTPFTAKDTEKLVTWFVERG
YKIKGSISSHFHSDSTGGIEWLNSRSIPTYASELTNELLKKDGKVQATNSFSGVNYWLVKNKIEV
FYPGPGHTPDNVVVWLPERKILFGGCFIKPYGLGNLGDANIEAWPKSAKLLKSKYGKAKLVVPSH
SEVGDASLLKLTLEQAVKGLNESKK
>d1qh5a_ d.157.1.2 (A:) Glyoxalase II (hydroxyacylglutathione
hydrolase) {Human (Homo sapiens)}
MKVEVLPALTDNYMYLVIDDETKEAAIVDPVQPQKVVDAARKHGVKLTTVLTTHHHWDHAGGNEK
LVKLESGLKVYGGDDRIGALTHKITHLSTLQVGSLNVKCLATPCHTSGHICYFVSKPGGSEPPAV
FTGDTLFVAGCGKFYEGTADEMCKALLEVLGRLPPDTRVYCGHEYTINNLKFARHVEPGNAAIRE
KLAWAKEKYSIGEPTVPSTLAEEFTYNPFMRVREKTVQQHAGETDPVTTMRAVRREKDQFKMPRD
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>d1e5da2 d.157.1.3 (A:2-250) Rubredoxin oxygen:oxidoreductase (ROO), N-terminal domain {Desulfovibrio gigas}
QATKIIDGFHLVGAIDWNSRDFHGYTLSPMGTTYNAYLVEDEKTTLFDTVKAEYKGELLCGIASV
IDPKKIDYLVIQHLELDHAGALPALIEACQPEKIFTSSLGQKAMESHFHYKDWPVQVVKHGETLS
LGKRTVTFYETRMLHWPDSMVSWFADEKVLISNDIFGQNIAASERFSDQIPVHTLERAMREYYAN
IVNPYAPQTLKAIETLVGAGVAPEFICPDHGVIFRGADQCTFAVQKYVEYAEQK
>d1a6q__ d.158.1.1 (-) Protein serine/threonine phosphatase 2C {Human (Homo sapiens)}
GAFLDKPKMEKHNAQGQGNGLRYGLSSMQGWRVEMEDAHTAVIGLPSGLESWSFFAVYDGHAGSQ
VAKYCCEHLLDHITNNQDFKGSAGAPSVENVKNGIRTGFLEIDEHMRVMSEKKHGADRSGSTAVG
VLISPQHTYFINCGDSRGLLCRNRKVHFFTQDHKPSNPLEKERIQNAGGSVMIQRVNGSLAVSRA
LGDFDYKCVHGKGPTEQLVSPEPEVHDIERSEEDDQFIILACDGIWDVMGNEELCDFVRSRLEVT
DDLEKVCNEVVDTCLYKGSRDNMSVILICFPNAPKVSPEAVKKEAELDKYLECRVEEIIKKQGEG
VPDLVHVMRTLASENIPSLPPGGELASKRNVIEAVYNRLNPY
>d4kbpa2 d.159.1.1 (A:121-432) Plant purple acid phosphatase, catalytic domain {Kidney bean (Phaseolus vulgaris)}
QTGLDVPYTFGLIGDLGQSFDSNTTLSHYELSPKKGQTVLFVGDLSYADRYPNHDNVRWDTWGRF
TERSVAYQPWIWTAGNHEIEFAPEINETEPFKPFSYRYHVPYEASQSTSPFWYSIKRASAHIIVL
SSYSAYGRGTPQYTWLKKELRKVKRSETPWLIVLMHSPLYNSYNHHFMEGEAMRTKFEAWFVKYK
VDVVFAGHVHAYERSERVSNIAYKITDGLCTPVKDQSAPVYITIGDAGNYGVIDSNMIQPQPEYS
AFREASFGHGMFDIKNRTHAHFSWNRNQDGVAVEADSVWFFNRHWYPVDDST
>d1qhwa_ d.159.1.1 (A:) Mammalian purple acid phosphatase {Rat (Rattus norvegicus)}
STLRFVAVGDWGGVPNAPFHTAREMANAKEIARTVQIMGADFIMSLGDNFYFTGVHDANDKRFQE
TFEDVFSDRALRNIPWYVLAGNHDHLGNVSAQIAYSKISKRWNFPSPYYRLRFKVPRSNITVAIF
MLDTVMLCGNSDDFVSQQPEMPRDLGVARTQLSWLKKQLAAAKEDYVLVAGHYPIWSIAEHGPTR
CLVKNLRPLLAAYGVTAYLCGHDHNLQYLQDENGVGYVLSGAGNFMDPSVRHQRKVPNGYLRFHY
GSEDSLGGFTYVEIGSKEMSITYVEASGKSLFKTSLPRRP
>d1utea_ d.159.1.1 (A:) Mammalian purple acid phosphatase {Pig (Sus scrofa)}
PTPILRFVAVGDWGGVPNAPFHTAREMANAKAIATTVKTLGADFILSLGDNFYFTGVHDAKDKRF
QETFEDVFSDPSLRNVPWHVLAGNHDHLGNVSAQIAYSKISKRWNFPSPYYRLRFKIPRSNVSVA
IFMLDTVTLCGNSDDFVSQQPERPRNLALARTQLAWIKKQLAAAKEDYVLVAGHYPVWSIAEHGP
THCLVKQLLPLLTTHKVTAYLCGHDHNLQYLQDENGLGFVLSGAGNFMDPSKKHLRKVPNGYLRF
HFGAENSLGGFAYVEITPKEMSVTYIEASGKSLFKTKLPRRA
>d1ii7a_ d.159.1.4 (A:) Mre11 {Archaeon Pyrococcus furiosus}
MKFAHLADIHLGYEQFHKPQREEEFAEAFKNALEIAVQENVDFILIAGDLFHSSRPSPGTLKKAI
ALLQIPKEHSIPVFAIEGNHDRTQRGPSVLNLLEDFGLVYVIGMRKEKVENEYLTSERLGNGEYL
VKGVYKDLEIHGMKYMSSAWFEANKEILKRLFRPTDNAILMLHQGVREVSEARGEDYFEIGLGDL
PEGYLYYALGHIHKRYETSYSGSPVVYPGSLERWDFGDYEVRYEWDGIKFKERYGVNKGFYIVED
FKPRFVEIKVRPFIDVKIKGSEEEIRKAIKRLIPLIPKNAYVRLNIGWRKPFDLTEIKELLNVEY
LKIDTWRI
>d1ush_2 d.159.1.2 (26-362) 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain {Escherichia coli}

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YEQDKTYKITVLHTNDHHGHFWRNEYGEYGLAAQKTLVDGIRKEVAAEGGSVLLLSGGDINTGVP
ESDLQDAEPDFRGMNLVGYDAMAIGNHEFDNPLTVLRQQEKWAKFPLLSANIYQKSTGERLFKPW
ALFKRQDLKIAVIGLTTDDTAKIGNPEYFTDIEFRKPADEAKLVIQELQQTEKPDIIIAATHMGH
YDNGEHGSNAPGDVEMARALPAGSLAMIVGGHSQDPVCMAAENKKQVDYVPGTPCKPDQQNGIWI
VQAHEWGKYVGRADFEFRNGEMKMVNYQLIPVNLKKKVTWEDGKSERVLYTPEIAENQQMISLLS
PFQNKGKAQLEV
>d1jk7a_ d.159.1.3 (A:) Protein phosphatase-1 (PP-1) {Human (Homo
sapiens)}
KLNIDSIIQRLLEVRGSKPGKNVQLQENEIRGLCLKSREIFLSQPILLELEAPLKICGDIHGQYY
DLLRLFEYGGFPPESNYLFLGDYVDRGKQSLETICLLLAYKIKYPENFFLLRGNHECASINRIYG
FYDECKRRYNIKLWKTFTDCFNCLPIAAIVDEKIFCCHGGLSPDLQSMEQIRRIMRPTDVPDQGL
LCDLLWSDPDKDVLGWGENDRGVSFTFGAEVVAKFLHKHDLDLICRAHQVVEDGYEFFAKRQLVT
LFSAPNYCGEFDNAGAMMSVDETLMCSFQILKPA
>d1tcoa_ d.159.1.3 (A:) Protein phosphatase-2B (PP-2B, calcineurin
A subunit) {Cow (Bos taurus)}
VPFPPSHRLTAKEVFDNDGKPRVDILKAHLMKEGRLEETVALRIITEGASILRQEKNLLDIDAPV
TVCGDIHGQFFDLMKLFEVGGSPANTRYLFLGDYVDRGYFSIECVLYLWALKILYPKTLFLLRGN
HECRHLTEYFTFKQECKIKYSERVYDACMDAFDCLPLAALMNQQFLCVHGGLSPEINTLDDIRKL
DRFKEPPAYGPMCDILWSDPLEDFGNEKTQEHFTHNTVRGCSYFYSYPAVCEFLQHNNLLSILRA
HEAQDAGYRMYRKSQTTGFPSLITIFSAPNYLDVYNNKAAVLKYENNVMNIRQFNCSPHPYWLPN
FMDVFTWSLPFVGEKVTEMLVNVLNIC
>d1auia_ d.159.1.3 (A:) Protein phosphatase-2B (PP-2B, calcineurin
A subunit) {Human (Homo sapiens)}
TDRVVKAVPFPPSHRLTAKEVFDNDGKPRVDILKAHLMKEGRLEESVALRIITEGASILRQEKNL
LDIDAPVTVCGDIHGQFFDLMKLFEVGGSPANTRYLFLGDYVDRGYFSIECVLYLWALKILYPKT
LFLLRGNHECRHLTEYFTFKQECKIKYSERVYDACMDAFDCLPLAALMNQQFLCVHGGLSPEINT
LDDIRKLDRFKEPPAYGPMCDILWSDPLEDFGNEKTQEHFTHNTVRGCSYFYSYPAVCEFLQHNN
LLSILRAHEAQDAGYRMYRKSQTTGFPSLITIFSAPNYLDVYNNKAAVLKYENNVMNIRQFNCSP
HPYWLPNFMDVFTWSLPFVGEKVTEMLVNVLNICSDDELGSEEDGFDGATAAARKEVIRNKIRAI
GKMARVFSVLREESESVLTLKGLTPTGMLPSGVLSGGKQTLQSATVEAIEADEAIKGFSPQHKIT
SFEEAKGLDRINERMPPR
>d1g5ba_ d.159.1.3 (A:) lambda ser/thr protein phosphatase
{Bacteriophage lambda}
MRYYEKIDGSKYRNIWVVGDLHGCYTNLMNKLDTIGFDNKKDLLISVGDLVDRGAENVECLELIT
FPWFRAVRGNHEQMMIDGLSERGNVNHWLLNGGGWFFNLDYDKEILAKALAHKADELPLIIELVS
KDKKYVICHADYPFDEYEFGKPVDHQQVIWNRERISNSQNGIVKEIKGADTFIFGHTPAVKPLKF
ANQMYIDTGAVFCGNLTLIQVQGA
>d1emsa2 d.160.1.1 (A:10-280) NIT-FHIT fusion protein, N-terminal
domain {Nematode (Caenorhabditis elegans)}
MATGRHFIAVCQMTSDNDLEKNFQAAKNMIERAGEKKCEMVFLPECFDFIGLNKNEQIDLAMATD
CEYMEKYRELARKHNIWLSLGGLHHKDPSDAAHPWNTHLIIDSDGVTRAEYNKLHLFDLEIPGKV
RLMESEFSKAGTEMIPPVDTPIGRLGLSICYDVRFPELSLWNRKRGAQLLSFPSAFTLNTGLAHW
ETLLRARAIENQCYVVAAAQTGAHNPKRQSYGHSMVVDPWGAVVAQCSERVDMCFAEIDLSYVDT
LREMQPVFSHR
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>d1f89a_ d.160.1.1 (A:) hypothetical protein yl85 {Baker's yeast
(Saccharomyces cerevisiae)}
SASKILSQKIKVALVQLSGSSPDKMANLQRAATFIERAMKEQPDTKLVVLPECFNSPYSTDQFRK
YSEVINPKEPSTSVQFLSNLANKFKIILVGGTIPELDPKTDKIYNTSIIFNEDGKLIDKHRKVHL
FDVDIPNGISFHESETLSPGEKSTTIDTKYGKFGVGICYDMRFPELAMLSARKGAFAMIYPSAFN
TVTGPLHWHLLARSRAVDNQVYVMLCSPARNLQSSYHAYGHSIVVDPRGKIVAEAGEGEEIIYAE
LDPEVIESFRQAVPLTKQRRF
>d1erza_ d.160.1.2 (A:) N-carbamoyl-D-aminoacid amidohydrolase
{Agrobacterium sp.}
TRQMILAVGQQGPIARAETREQVVVRLLDMLTKAASRGANFIVFPELALTTFFPRWHFTDEAELD
SFYETEMPGPVVRPLFEKAAELGIGFNLGYAELVVEGGVKRRFNTSILVDKSGKIVGKYRKIHLP
GHKEYEAYRPFQHLEKRYFEPGDLGFPVYDVDAAKMGMFICNDRRWPEAWRVMGLRGAEIICGGY
NTPTHNPPVPQHDHLTSFHHLLSMQAGSYQNGAWSAAAGKVGMEENCMLLGHSCIVAPTGEIVAL
TTTLEDEVITAAVDLDRCRELREHIFNFKQHRQPQHYGLIAEL
>d1hq0a_ d.194.1.1 (A:) Type 1 cytotoxic necrotizing factor, catalytic
domain {Escherichia coli}
SIESTSKSNFQKLSRGNIDVLKGRGSISSTRQRAIYPYFEAANADEQQPLFFYIKKDRFDNHGYD
QYFYDNTVGPNGIPTLNTYTGEIPSDSSSLGSTYWKKYNLTNETSIIRVSNSARGANGIKIALEE
VQEGKPVIITSGNLSGCTTIVARKEGYIYKVHTGTTKSLAGFTSTTGVKKAVEVLELLTKEPIPR
VEGIMSNDFLVDYLSENFEDSLITYSSSEKKPDSQITIIRDNVSVFPYFLDNIPEHGFGTSATVL
VRVDGNVVVRSLSESYSLNADASEISVLKVFSKKF
>d1qdla_ d.161.1.1 (A:) Anthranilate synthase
aminodeoxyisochorismate synthase/lyase subunit, TrpE {Archaeon
Sulfolobus solfataricus}
AMEVHPISEFASPFEVFKCIERDFKVAGLLESIGGPQYKARYSVIAWSTNGYLKIHDDPVNILNG
YLKDLKLADIPGLFKGGMIGYISYDAVRFWEKIRDLKPAAEDWPYAEFFTPDNIIIYDHNEGKVY
VNADLSSVGGCGDIGEFKVSFYDESLNKNSYERIVSESLEYIRSGYIFQVVLSRFYRYIFSGDPL
RIYYNLRRINPSPYMFYLKFDEKYLIGSSPELLFRVQDNIVETYPIAGTRPRGADQEEDLKLELE
LMNSEKDKAEHLMLVDLARNDLGKVCVPGTVKVPELMYVEKYSHVQHIVSKVIGTLKKKYNALNV
LSATFPAGTVSGAPKPMAMNIIETLEEYKRGPYAGAVGFISADGNAEFAIAIRTAFLNKELLRIH
AGAGIVYDSNPESEYFETEHKLKALKTAIGVR
>d1i1qa_ d.161.1.1 (A:) Anthranilate synthase
aminodeoxyisochorismate synthase/lyase subunit, TrpE {Salmonella
typhimurium}
KPTLELLTCDAAYRENPTALFHQVCGDRPATLLLESADIDSKDDLKSLLLVDSALRITALGDTVT
IQALSDNGASLLPLLDTALPAGVENDVLPAGRVLRFPPVSPLLDENARLCSLSVFDAFRLLQGVV
NIPTQEREAMFFGGLFAYDLVAGFEALPHLEAGNNCPDYCFYLAETLMVIDHQKKSTRIQASLFT
ASDREKQRLNARLAYLSQQLTQPAPPLPVTPVPDMRCECNQSDDAFGAVVRQLQKAIRAGEIFQV
VPSRRFSLPCPSPLAAYYVLKKSNPSPYMFFMQDNDFTLFGASPESSLKYDAASRQIEIYPIAGT
RPRGRRADGTLDRDLDSRIELDMRTDHKELSEHLMLVDLARNDLARICTPGSRYVADLTKVDRYS
YVMHLVSRVVGELRHDLDALHAYRACMNMGTLSGAPKVRAMQLIADAEGQRRGSYGGAVGYFTAH
GDLDTCIVIRSALVENGIATVQAGAGIVLDSVPQSEADETRNKARAVLRAIATAHHA
>d1i7qa_ d.161.1.1 (A:) Anthranilate synthase
aminodeoxyisochorismate synthase/lyase subunit, TrpE {Serratia
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marcescens}
TKPQLTLLKVQASYRGDPTTLFHQLCGARPATLLLESAEINDKQNLQSLLVIDSALRITALGHTV
SVQALTANGPALLPLLDEALPPEVRNQARPNGRELTFPAIDAVQDEDARLRSLSVFDALRTILTL
VDSPADEREAVMLGGLFAYDLVAGFENLPALRQDQRCPDFCFYLAETLLVLDHQRGSARLQASVF
SEQASEAQRLQHRLEQLQAELQQPPQPIPHQKLENMQLSCNQSDEEYGAVVSELQEAIRQGEIFQ
VVPSRRFSLPCPAPLGPYQTLKDNNPSPYMFFMQDDDFTLFGASPESALKYDAGNRQIEIYPIAG
TRPRGRRADGSLDLDLDSRIELEMRTDHKELAEHLMLVDLARNDLARICQAGSRYVADLTKVDRY
SFVMHLVSRVVGTLRADLDVLHAYQACMNMGTLSGAPKVRAMQLIAALRSTRRGSYGGRVGYFTA
VRNLDTCIVIRSAYVEDGHRTVQAGAGVVQDSIPEREADETRNKARAVLRAIATAHHAKEVF
>d1k0ga_ d.161.1.1 (A:) P-aminobenzoate synthase component I
{Escherichia coli}
MKTLSPAVITLLWRQDAAEFYFSRLSHLPWAMLLHSGYADHPYSRFDIVVAEPICTLTTFGKETV
VSESEKRTTTTDDPLQVLQQVLDRADIRPTHNEDLPFQGGALGLFGYDLGRRFESLPEIAEQDIV
LPDMAVGIYDWALIVDHQRHTVSLLSHNDVNARRAWLESQQFSPQEDFTLTSDWQSNMTREQYGE
KFRQVQEYLHSGDCYQVNLAQRFHATYSGDEWQAFLQLNQANRAPFSAFLRLEQGAILSLSPERF
ILCDNSEIQTRPIKGTLPRLPDPQEDSKQAVKLANSAKDRAENLMIVDLMRNDIGRVAVAGSVKV
PELFVVEPFPAVHHLVSTITAQLPEQLHASDLLRAAFPGGSITGAPKVRAMEIIDELEPQRRNAW
CGSIGYLSFCGNMDTSITIRTLTAINGQIFCSAGGGIVADSQEEAEYQETFDKVNRILKQLEK
>d1mlda2 d.162.1.1 (A:145-313) Malate dehydrogenase {Pig (Sus
scrofa)}
VTTLDIVRANAFVAELKGLDPARVSVPVIGGHAGKTIIPLISQCTPKVDFPQDQLSTLTGRIQEA
GTEVVKAKAGAGSATLSMAYAGARFVFSLVDAMNGKEGVVECSFVKSQETDCPYFSTPLLLGKKG
IEKNLGIGKISPFEEKMIAEAIPELKASIKKGEEFVKNM
>d5mdha2 d.162.1.1 (A:155-333) Malate dehydrogenase {Pig (Sus
scrofa)}
TRLDHNRAKAQIALKLGVTSDDVKNVIIWGNHSSTQYPDVNHAKVKLQAKEVGVYEAVKDDSWLK
GEFITTVQQRGAAVIKARKLSSAMSAAKAICDHVRDIWFGTPEGEFVSMGIISDGNSYGVPDDLL
YSFPVTIKDKTWKIVEGLPINDFSREKMDLTAKELAEEKETAFEFLSSA
>d7mdha2 d.162.1.1 (A:198-385) Malate dehydrogenase {Sorghum (Sorghum
vulgare), chloroplast}
TRLDENRAKCQLALKAGVFYDKVSNVTIWGNHSTTQVPDFLNAKIDGRPVKEVIKRTKWLEEEFT
ITVQKRGGALIQKWGRSSAASTAVSIADAIKSLVTPTPEGDWFSTGVYTTGNPYGIAEDIVFSMP
CRSKGDGDYELATDVSNDDFLWERIKKSEAELLAEKKCVAHLTGEGNAYCDVPEDTML
>d1civa2 d.162.1.1 (A:194-385) Malate dehydrogenase {Flaveria
bidentis, chloroplast}
TRLDENRAKCQLALKAGVFYDKVSNVTIWGNHSTTQVPDFLNAKIHGIPVTEVIRDRKWLEDEFT
NMVQTRGGVLIKKWGRSSAASTAVSIVDAIRSLVTPTPEGDWFSTGVYTNGNPYGIAEDIVFSMP
CRSKGDGDYEFVKDVIFDDYLSKKIKKSEDELLAEKKCVAHLTGEGIAVCDLPEDTMLPGEM
>d2cmd_2 d.162.1.1 (146-312) Malate dehydrogenase {Escherichia coli}
VTTLDIIRSNTFVAELKGKQPGEVEVPVIGGHSGVTILPLLSQVPGVSFTEQEVADLTKRIQNAG
TEVVEAKAGGGSATLSMGQAAARFGLSLVRALQGEQGVVECAYVEGDGQYARFFSQPLLLGKNGV
EERKSIGTLSAFEQNALEGMLDTLKKDIALGQEFVNK
>d1bdma2 d.162.1.1 (A:155-332) Malate dehydrogenase {Thermus flavus}
TRLDHNRAKAQLAKKTGTGVDRIRRMTVWGNHSSIMFPDLFHAEVDGRPALELVDMEWYEKVFIP
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TVAQRGAAIIQARGASSAASAANAAIEHIRDWALGTPEGDWVSMAVPSQGEYGIPEGIVYSFPVT
AKDGAYRVVEGLEINEFARKRMEITAQELLDEMEQVKALGLI
>d2hlpa2 d.162.1.1 (A:163-330) Malate dehydrogenase {Archaeon
Haloarcula marismortui}
FGGRLDSARFRYVLSEEFDAPVQNVEGTILGEHGDAQVPVFSKVRVDGTDPEFSGDEKEQLLGDL
QESAMDVIERKGATEWGPARGVAHMVEAILHDTGRVLPASVKLEGEFGHEDTAFGVPVRLGSNGV
EEIVEWDLDDYEQDLMADAAEKLSDQYDKIS
>d1b8pa2 d.162.1.1 (A:159-329) Malate dehydrogenase {Aquaspirillum
arcticum}
LRLDHNRALSQIAAKTGKPVSSIEKLFVWGNHSPTMYADYRYAQIDGASVKDMINDDAWNRDTFL
PTVGKRGAAIIDARGVSSAASAANAAIDHIHDWVLGTAGKWTTMGIPSDGSYGIPEGVIFGFPVT
TENGEYKIVQGLSIDAFSQERINVTLNELLEEQNGVQHLLG
>d1guya2 d.162.1.1 (A:144-306) Malate dehydrogenase {Chloroflexus
aurantiacus}
AGVLDAARYRTFIAMEAGVSVEDVQAMLMGGHGDEMVPLPRFSTISGIPVSEFIAPDRLAQIVER
TRKGGGEIVNLLKTGSAYYAPAAATAQMVEAVLKDKKRVMPVAAYLTGQYGLNDIYFGVPVILGA
GGVEKILELPLNEEEMALLNASAKAVRATLDTL
>d1gv0a2 d.162.1.1 (A:143-305) Malate dehydrogenase {Chlorobium
tepidum}
AGVLDSARFRSFIAMELGVSMQDVTACVLGGHGDAMVPVVKYTTVAGIPVADLISAERIAELVER
TRTGGAEIVNHLKQGSAFYSPATSVVEMVESIVLDRKRVLTCAVSLDGQYGIDGTFVGVPVKLGK
NGVEHIYEIKLDQSDLDLLQKSAKIVDENCKML
>d1guza2 d.162.1.1 (A:143-305) Malate dehydrogenase {Chlorobium
vibrioforme}
AGVLDAARFRSFIAMELGVSMQDINACVLGGHGDAMVPVVKYTTVAGIPISDLLPAETIDKLVER
TRNGGAEIVEHLKQGSAFYAPASSVVEMVESIVLDRKRVLPCAVGLEGQYGIDKTFVGVPVKLGR
NGVEQIYEINLDQADLDLLQKSAKIVDENCKML
>d1hyha2 d.162.1.1 (A:167-329) L-2-hydroxyisocapronate dehydrogenase,
L-HICDH {Lactobacillus confusus}
GTLLDTARMQRAVGEAFDLDPRSVSGYNLGEHGNSQFVAWSTVRVMGQPIVTLADAGDIDLAAIE
EEARKGGFTVLNGKGYTSYGVATSAIRIAKAVMADAHAELVVSNRRDDMGMYLSYPAIIGRDGVL
AETTLDLTTDEQEKLLQSRDYIQQRFDEIVDTL
>d9ldta2 d.162.1.1 (A:163-331) Lactate dehydrogenase {Pig (Sus
scrofa)}
SGCNLDSARFRYLMGERLGVHPLSCHGWILGEHGDSSVPVWSGVNVAGVSLKNLHPELGTDADKE
HWKAVHKEVVDSAYEVIKLKGYTSWAIGLSVADLAESIMKNLRRVHPISTMIKGLYGIKENVFLS
VPCILGQNGISDVVKVTLTPEEEAHLKKSADTLWGIQKELQF
>d1i0za2 d.162.1.1 (A:161-332) Lactate dehydrogenase {Human (Homo
sapiens), heart isoform (H chain)}
SGCNLDSARFRYLMAEKLGIHPSSCHGWILGEHGDSSVAVWSGVNVAGVSLQELNPEMGTDNDSE
NWKEVHKMVVESAYEVIKLKGYTNWAIGLSVADLIESMLKNLSRIHPVSTMVKGMYGIENEVFLS
LPCILNARGLTSVINQKLKDDEVAQLKKSADTLWDIQKDLKD
>d1i10a2 d.162.1.1 (A:160-331) Lactate dehydrogenase {Human (Homo
sapiens), muscle isoform (M chain)}
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SGCNLDSARFRYLMGERLGVHPLSCHGWVLGEHGDSSVPVWSGMNVAGVSLKTLHPDLGTDKDKE
QWKEVHKQVVESAYEVIKLKGYTSWAIGLSVADLAESIMKNLRRVHPVSTMIKGLYGIKDDVFLS
VPCILGQNGISDLVKVTLTSEEEARLKKSADTLWGIQKELQF
>d2ldx_2 d.162.1.1 (160-331) Lactate dehydrogenase {Mouse (Mus musculus)}
SGCNLDSARFRYLIGEKLGVNPTSCHGWVLGEHGDSSVPIWSGVNVAGVTLKSLNPAIGTDKNKQ
HWKNVHKQVVEGGYEVLDMKGYTSWAIGLSVTDLARSILKNLKRVHPVTTLVKGFHGIKEEVFLS
IPCVLGESGITDFVKVNMTAEEEGLLKKSADTLWNMQKNLEL
>d1ldm_2 d.162.1.1 (161-329) Lactate dehydrogenase {Dogfish (Squalus acanthias)}
SGCNLDSARFRYLMGERLGVHSCSCHGWVIGEHGDSVPSVWSGMNVASIKLHPLDGTNKDKQDWK
KLHKDVVDSAYEVIKLKGYTSWAIGLSVADLAETIMKNLCRVHPVSTMVKDFYGIKDNVFLSLPC
VLNDHGISNIVKMKLKPNEEQQLQKSATTLWDIQKDLKF
>d1ceqa2 d.162.1.1 (A:164-329) Lactate dehydrogenase {Malaria parasite (Plasmodium falciparum)}
GGVLDTSRLKYYISQKLNVCPRDVNAHIVGAHGNKMVLLKRYITVGGIPLQEFINNKLISDAELE
AIFDRTVNTALEIVNLHASPYVAPAAAIIEMAESYLKDLKKVLICSTLLEGQYGHSDIFGGTPVV
LGANGVEQVIELQLNSEEKAKFDEAIAETKRMKALA
>d1ldna2 d.162.1.1 (A:163-330) Lactate dehydrogenase {Bacillus stearothermophilus}
TILDTARFRFLLGEYFSVAPQNVHAYIIGEHGDTELPVWSQAYIGVMPIRKLVESKGEEAQKDLE
RIFVNVRDAAYQIIEKKGATYYGIAMGLARVTRAILHNENAILTVSAYLDGLYGERDVYIGVPAV
INRNGIREVIEIELNDDEKNRFHHSAATLKSVLARAFT
>d1llc_2 d.162.1.1 (165-334) Lactate dehydrogenase {Lactobacillus casei}
TSLDTARFRQSIAEMVNVDARSVHAYIMGEHGDTEFPVWSHANIGGVTIAEWVKAHPEIKEDKLV
KMFEDVRDAAYEIIKLKGATFYGIATALARISKAILNDENAVLPLSVYMDGQYGINDLYIGTPAV
INRNGIQNILEIPLTDHEEESMQKSASQLKKVLTDAFAKNDI
>d1ez4a2 d.162.1.1 (A:163-334) Lactate dehydrogenase {Lactobacillus pentosus}
TSLDSSRLRVALGKQFNVDPRSVDAYIMGEHGDSEFAAYSTATIGTRPVRDVAKEQGVSDDDLAK
LEDGVRNKAYDIINLKGATFYGIGTALMRISKAILRDENAVLPVGAYMDGQYGLNDIYIGTPAII
GGTGLKQIIESPLSADELKKMQDSAATLKKVLNDGLAELEN
>d1llda2 d.162.1.1 (A:150-319) Lactate dehydrogenase {Bifidobacterium longum, strain am101-2}
TNLDSARLRFLIAQQTGVNVKNVHAYIAGEHGDSEVPLWESATIGGVPMSDWTPLPGHDPLDADK
REEIHQEVKNAAYKIINGKGATNYAIGMSGVDIIEAVLHDTNRILPVSSMLKDFHGISDICMSVP
TLLNRQGVNNTINTPVSDKELAALKRSAETLKETAAQFGF
>d1a5z_2 d.162.1.1 (164-333) Lactate dehydrogenase {Thermotoga maritima}
GTVLDTARLRTLIAQHCGFSPRSVHVYVIGEHGDSEVPVWSGAMIGGIPLQNMCQVCQKCDSKIL
ENFAEKTKRAAYEIIERKGATHYAIALAVADIVESIFFDEKRVLTLSVYLEDYLGVKDLCISVPV
TLGKHGVERILELNLNEEELEAFRKSASILKNAINEITAEEN
>d1hyea2 d.162.1.1 (A:146-313) MJ0490, lactate/malate dehydrogenase
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{Archaeon Methanococcus jannaschii}
LGTHLDSLRFKVAIAKFFGVHIDEVRTRIIGEHGDSMVPLLSATSIGGIPIQKFERFKELPIDEI
IEDVKTKGEQIIRLKGGSEFGPAAAILNVVRCIVNNEKRLLTLSAYVDGEFDGIRDVCIGVPVKI
GRDGIEEVVSIELDKDEIIAFRKSAEIIKKYCEEVKNL
>d1aiha_ d.163.1.1 (A:) Integrase {Bacteriophage HP1}
ETELAFLYERDIYRLLAECDNSRNPDLGLIVRICLATGARWSEAETLTQSQVMPYKITFTNTKSK
KNRTVPISDELFDMLPKKRGRLFNDAYESFENAVLRAEIELPKGQLTHVLRHTFASHFMMNGGNI
LVLKEILGHSTIEMTMRYAHFAPSHLESAVKFNPLSNPAQ
>d1ae9a_ d.163.1.1 (A:) Integrase (Int) {Bacteriophage lambda}
RSRLTADEYLKIYQAAESSPCWLRLAMELAVVTGQRVGDLCEMKWSDIVDGYLYVEQSKTGVKIA
IPTALHIDALGISMKETLDKCKEILGGETIIASTRREPLSSGTVSRYFMRARKASGLSFEGDPPT
FHELRSLSARLYEKQISDKFAQHLLGHKSDTMASQFRDDRGREWDKIEI
>d1f44a2 d.163.1.1 (A:130-343) Cre recombinase {Bacteriophage P1}
RAKQALAFERTDFDQVRSLMENSDRCQDIRNLAFLGIAYNTLLRIAEIARIRVKDISRTDGGRML
IHIGRTKTLVSTAGVEKALSLGVTKLVERWISVSGVADDPNNYLFCRVRKNGVAAPSATSQLSTR
ALEGIFEATHRLIYGAKDDSGQRYLAWSGHSARVGAARDMARAGVSIPEIMQAGGWTNVNIVMNF
IRNLDSETGAMVRLLEDGD
>d5crxb2 d.163.1.1 (B:130-314) Cre recombinase {Bacteriophage P1}
RAKQALAFERTDFDQVRSLMENSDRCQDIRNLAFLGIAYNTLLRIAEIARIRVKDISRTDGGRML
IHIGRTKTLVSTAGVEKALSLGVTKLVERWISVSGVADDPNNYLFCRVRKNGVAAPSATSQLSTR
ALEGIFEATHRLIYGAKDDSGQRYLAWSGHSARVGAARDMARAGVSIPEIMQAGG
>d1a0p_2 d.163.1.1 (111-292) Recombinase XerD {Escherichia coli}
KDLSEAQVERLLQAPLIDQPLELRDKAMLEVLYATGLRVSELVGLTMSDISLRQGVVRVIGKGNK
ERLVPLGEEAVYWLETYLEHGRPWLLNGVSIDVLFPSQRAQQMTRQTFWHRIKHYAVLAGIDSEK
LSPHVLRHAFATHLLNHGADLRVVQMLLGHSDLSTTQIYTHVATERLRQLHQ
>d1floa2 d.163.1.1 (A:135-423) Flp recombinase {Baker's yeast
(Saccharomyces cerevisiae)}
KGNSHSKKMLKALLSEGESIWEITEKILNSFEYTSRFTKTKTLYQFLFLATFINCGRFSDIKNVD
PKSFKLVQNKYLGVIIQCLVTETKTSVSRHIYFFSARGRIDPLVYLDEFLRNSEPVLKRVNRTGN
SSSNKQEYQLLKDNLVRSYNKALKKNAPYSIFAIKNGPKSHIGRHLMTSFLSMKGLTELTNVVGN
WSDKRASAVARTTYTHQITAIPDHYFALVSRYYAYDPISKEMIALKDETNPIEEWQHIEQLKGSA
EGSIRYPAWNGIISQEVLDYLSSYINRRI
>d1a31a1 d.163.1.2 (A:431-626,A:720-765) Eukaryotic DNA
topoisomerase I, catalytic core {Human (Homo sapiens)}
PSSRIKGEKDWQKYETARRLKKCVDKIRNQYREDWKSKEMKVRQRAVALYFIDKLALRAGNEKEE
GETADTVGCCSLRVEHINLHPELDGQEYVVEFDFLGKDSIRYYNKVPVEKRVFKNLQLFMENKQP
EDDLFDRLNTGILNKHLQDLMEGLTAKVFRTYNASITLQQQLKELTAPDENIPAKILSYNRANRA
VXKLNYLDPRITVAWCKKWGVPIEKIYNKTQREKFAWAIDMADEDYEF
>d1a41__ d.163.1.2 (-) Eukaryotic DNA topoisomerase I, catalytic core
{Vaccinia virus}
NAKRDRIFVRVYNVMKRINCFINKNIKKSSTDSNYQLAVFMLMETMFFIRFGKMKYLKENETVGL
LTLKNKHIEISPDEIVIKFVGKDKVSHEFVVHKSNRLYKPLLKLTDDSSPEEFLFNKLSERKVYE
CIKQFGIRIKDLRTYGVNYTFLYNFWTNVKSISPLPSPKKLIALTIKQTAEVVGHTPSISKRAYM
ATTILEMVKDKNFLDVVSKTTFDEFLSIVVDHVKS
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>d1mhda_ d.164.1.1 (A:) SMAD MH1 domain {Human (Homo sapiens)}
PIVKRLLGWKKGEQNGQEEKWCEKAVKSLVKKLKKTGQLDELEKAITTQNVNTKCITIPRSLDGR
LQVSHRKGLPHVIYCRLWRWPDLHSHHELRAMELCEFAFNMKKDEVCVNPYHYQRVET
>d1hufa_ d.195.1.1 (A:) YopH tyrosine phosphatase N-terminal domain {Yersinia pestis}
LSLSDLHRQVSRLVQQESGDCTGKLRGNVAANKETTFQGLTIASGARESEKVFAQTVLSHVANVV
LTQEDTAKLLQSTVKHNLNNYDLRSVGNGNSVLVSLRSDQMTLQDAKVLLEAALRQES
>d1mrj__ d.165.1.1 (-) alpha-Trichosanthin {Mongolian snake gourd (Trichosanthes kirilowii maxim)}
DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETISVAID
VTNVYIMGYRAGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAAGKIRENIPLGLP
ALDSAITTLFYYNANSAASALMVLIQSTSEAARYKFIEQQIGKRVDKTFLPSLAIISLENSWSAL
SKQIQIASTNNGQFESPVVLINAQNQRVTITNVDAGVVTSNIALLLNRNNMA
>d1bryy_ d.165.1.1 (Y:) Bryodin {Red briony (Bryonia dioica)}
DVSFRLSGATTTSYGVFIKNLREALPYERKVYNIPLLRSSISGSGRYTLLHLTNYADETISVAVD
VTNVYIMGYLAGDVSYFFNEASATEAAKFVFKDAKKKVTLPYSGNYERLQTAAGKIRENIPLGLP
ALDSAITTLYYYTASSAASALLVLIQSTAESARYKFIEQQIGKRVDKTFLPSLATISLENNWSAL
SKQIQIASTNNGQFESPVVLIDGNNQRVSITNASARVVTSNIALLLNRNNIA
>d1mrg__ d.165.1.1 (-) alpha-Momorcharin (momordin) {Bitter gourd (Momordica charantia)}
DVSFRLSGADPRSYGMFIKDLRNALPFREKVYNIPLLLPSVSGAGRYLLMHLFNRDGKTITVAVD
VTNIYIMGYLADTTSYFFNEPAAELASQYVFRDARRKITLPYSGDYERLQIAAGKPREKIPIGLP
ALDSAISTLLHYDSTAAAGALLVLIQTTAEAARFKYIEQQIQERAYRDEVPSLATISLENSWSGL
SKQIQLAQGNNGIFRTPIVLVDNKGNRVQITNVTSKVVTSNIQLLLNTRNI
>d1cf5a_ d.165.1.1 (A:) Beta-momorcharin {Bitter gourd (Momordica charantia)}
DVNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLNLTSYAYETISVAID
VTNVYVVAYRTRDVSYFFKESPPEAYNILFKGTRKITLPYTGNYENLQTAAHKIRENIDLGLPAL
SSAITTLFYYNAQSAPSALLVLIQTTAEAARFKYIERHVAKYVATNFKPNLAIISLENQWSALSK
QIFLAQNQGGKFRNPVDLIKPTGQRFQVTNVDSDVVKGNIKLLLNSRASTADEN
>d1ce7a_ d.165.1.1 (A:) Mistletoe lectin I A-chain {European mistletoe (Viscum album)}
YERGDLDVTAQTTGAGYFSFITLLRDYVSSGSFSNAIPLLSQSGGGGEAGRFVLVELTNSGGDGI
TVAIDVTNLYVVAYQAGSQSYFLSGPGGRHGFTGTTRSSLPFNGSYPDLEQYGGQRKQIPLGIDQ
LIQSVTALKFPGSTRTGARSILILIQMISEAARFNPILWRARQYINSGASFLPDVYMLELETSWG
QQSTQVQHSTDGVFNNPIALADPGGGVTLTNVRDVIASLAIMLFVC
>d1abra_ d.165.1.1 (A:) Abrin A-chain {Abrus precatorius}
EDRPIKFSTEGATSQSYKQFIEALRERLRGGLIHDIPVLPDPTTLQERNRYITVELSNSDTESIE
VGIDVTNAYVVAYRAGTQSYFLRDAPSSASDYLFTGTDQHSLPFYGTYGDLERWAHQSRQQIPLG
LQALTHGISFFRSGGNDNEEKARTLIVIIQMVAEAARFRYISNRVRVSIQTGTAFQPDAAMISLE
NNWDNLSRGVQESVQDTFPNQVTLTNIRNEPVIVDSLSHPTVAVLALMLFVCNPPN
>d1apa__ d.165.1.1 (-) Pokeweed antiviral protein alpha {Pokeweed (Phytolacca americana)}
INTITFDVGNATINKYATFMKSIHNQAKDPTLKCYGIPMLPNTNLTPKYLLVTLQDSSLKTITLM
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LKRNNLYVMGYADTYNGKCRYHIFKDISNTTERNDVMTTLCPNPSSRVGKNINYDSSYPALEKKV
GRPRSQVQLGIQILNSGIGKIYGVDSFTEKTEAEFLLVAIQMVSEAARFKYIENQVKTNFNRAFY
PNAKVLNLEESWGKISTAIHNAKNGALTSPLELKNANGSKWIVLRVDDIEPDVGLLKYVNGTCQA
T
>d1d6aa_ d.165.1.1 (A:) Pokeweed antiviral protein alpha {Pokeweed
(Phytolacca americana)}
VNTIIYNVGSTTISKYATFLNDLRNEAKDPSLKCYGIPMLPNTNTNPKYVLVELQGSNKKTITLM
LRRNNLYVMGYSDPFETNKCRYHIFNDISGTERQDVETTLCPNANSRVSKNINFDSRYPTLESKA
GVKSRSQVQLGIQILDSNIGKISGVMSFTEKTEAEFLLVAIQMVSEAARFKYIENQVKTNFNRAF
NPNPKVLNLQETWGKISTAIHDAKNGVLPKPLELVDASGAKWIVLRVDEIKPDVALLNYVGGSCQ
TT
>d1qi7a_ d.165.1.1 (A:) Saporin So6 {Common soapwort (Saponaria
officinalis)}
VTSITLDLVNPTAGQYSSFVDKIRNNVKDPNLKYGGTDIAVIGPPSKEKFLRINFQSSRGTVSLG
LKRDNLYVVAYLAMDNTNVNRAYYFKSEITSAELTALFPEATTANQKALEYTEDYQSIEKNAQIT
QGDKSRKELGLGIDLLLTFMEAVNKKARVVKNEARFLLIAIQMTAEVARFRYIQNLVTKNFPNKF
DSDNKVIQFEVSWRKISTAIYGDAKNGVFNKDYDFGFGKVRQVKDLQMGLLMYLGKPK
>d1ift__ d.165.1.1 (-) Ricin A-chain {Castor bean (Ricinus communis)}
YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSV
TLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRE
NIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAP
DPSVITLENSWGRLSTAIQESNQGAFASPIQLQRRNGSKFSVYDVSILIPIIALMVYRCAPPP
>d1hwma_ d.165.1.1 (A:) Ebulin A-chain {Sambucus ebulus}
IDYPSVSFNLAGAKSTTYRDFLKNLRDRVATGTYEVNGLPVLRRESEVQVKNRFVLVRLTNYNGD
TVTSAVDVTNLYLVAFSANGNSYFFKDATELQKSNLFLGTTQHTLSFTGNYDNLETAAGTRRESI
ELGPNPLDGAITSLWYDGGVARSLLVLIQMVPEAARFRYIEQEVRRSLQQLTSFTPNALMLSMEN
NWSSMSLEVQLSGDNVSPFSGTVQLQNYDHTPRLVDNFEELYKITGIAILLFRCVA
>d1dm0a_ d.165.1.2 (A:) Shiga toxin, A-chain {Shigella dysenteriae}
KEFTLDFSTAKTYVDSLNVIRSAIGTPLQTISSGGTSLLMIDSGTGDNLFAVDVRGIDPEEGRFN
NLRLIVERNNLYVTGFVNRTNNVFYRFADFSHVTFPGTTAVTLSGDSSYTTLQRVAGISRTGMQI
NRHSLTTSYLDLMSHSGTSLTQSVARAMLRFVTVTAEALRFRQIQRGFRTTLDDLSGRSYVMTAE
DVDLTLNWGRLSSVLPDYHGQDSVRVGRISFGSINAILGSVALILNCHHHASRVARMASDEFPSM
CPADGRVRGITHNKILWDSSTLGAILM
>g1lts.1 d.166.1.1 (A:,C:) Heat-labile toxin, A-chain {Escherichia
coli, type IB}
RLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSLSLRS
AHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIPYSQIYGWYRVNFG
VIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAPQGCGXGDTCNEETQ
NLSTIYLREYQSKVKRQIFSDYQSEVDIYNRI
>g1tii.1 d.166.1.1 (A:,C:) Heat-labile toxin, A-chain {Escherichia
coli, type IIB}
NDYFRADSRTPDEVRRSGGLIPRGQDEAYERGTPININLYDHARGTATGNTRYNDGYVSTTTTLR
QAHLLGQNMLGGYNEYYIYVVAAAPNLFDVNGVLGRYSPYPSENEYAALGGIPLSQIIGWYRVSF
GAIEGGMHRNRDYRRDLFRGLSAAPNEDGYRIAGFPDGFPAWEEVPWREFAPNSCLPXTTCASLT
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NKLSQHDLADFKKYIKRKFTLMTLLSINN
>d1f0la2 d.166.1.1 (A:1-187) Diphtheria toxin, N-terminal domain {Corynebacterium diphtheriae}
GADDVVDSSKSFVMENFSSYHGTKPGYVDSIQKGIQKPKSGTQGNYDDDWKGFYSTDNKYDAAGY
SVDNENPLSGKAGGVVKVTYPGLTKVLALKVDNAETIKKELGLSLTEPLMEQVGTEEFIKRFGDG
ASRVVLSLPFAEGSSSVEYINNWEQAKALSVELEINFETRGKRGQDAMYEYMAQACA
>d1ikpa2 d.166.1.1 (A:395-606) Exotoxin A, C-terminal domain {Pseudomonas aeruginosa}
PTGAEFLGDGGDVSFSTRGTQNWTVERLLQAHRQLEERGYVFVGYHGTFLEAAQSIVFGGVRARS
QDLDAIWRGFYIAGDPALAYGYAQDQEPDARGRIRNGALLRVYVPRSSLPGFYRTSLTLAAPEAA
GEVERLIGHPLPLRLDAITGPEEEGGRLETILGWPLAERTVVIPSAIPTDPRNVGGDLDPSSIPD
KEQAISALPDYASQPGK
>d1prta_ d.166.1.1 (A:) Pertussis toxin, S1 subunit {Bordetella pertussis}
DPPATVYRYDSRPPEDVFQNGFTAWGNNDNVLEHLTGRSCQVGSSNSAFVSTSSSRRYTEVYLEH
RMQEAVEAERAGRGTGHFIGYIYEVRADNNFYGAASSYFEYVDTYGDNAGRILAGALATYQSEYL
AHRRIPPENIRRVTRVYHNGITGETTTTEYSNARYVSQQTRANPNPYTSRRSVASIVGTLVRMAP
VVGACMARQAESSEAMAAWSERAGEAMVLVYYESIAYSF
>g1xtc.1 d.166.1.1 (A:,C:) Cholera toxin {Vibrio cholerae}
NDDKLYRADSRPPDEIKQSGGLMPRGQSEYFDRGTQMNINLYDHARGTQTGFVRHDDGYVSTSIS
LRSAHLVGQTILSGHSTYYLYVLATAPNMFNVNDVLGAYSPHPDEQEVSALGGIPYSQIYGWYRV
HFGVLDEQLHRNRGYRDRYYSNLDIAPAADGYGLAGFPPEHRAWREEPWIHHAPPGCGNAPRXSN
TCDEKTQSLGVKFLDEYQSKVKRQIFSGYQSDIDTHNRIKDEL
>d1qs1a1 d.166.1.1 (A:60-264) Vegetative insecticidal protein 2 (VIP2) {Bacillus cereus}
TDKVEDFKEDKEKAKEWGKEKEKEWKLTATEKGKMNNFLDNKNDIKTNYKEITFSMAGSFEDEIK
DLKEIDKMFDKTNLSNSIITYKNVEPTTIGFNKSLTEGNTINSDAMAQFKEQFLDRDIKFDSYLD
THLTAQQVSSKERVILKVTVPSGKGSTTPTKAGVILNNSEYKMLIDNGYMVHVDKVSKVVKKGVE
CLQIEGTLKK
>d1qs1a2 d.166.1.1 (A:265-461) Vegetative insecticidal protein 2 (VIP2) {Bacillus cereus}
SLDFKNDINAEAHSWGMKNYEEWAKDLTDSQREALDGYARQDYKEINNYLRNQGGSGNEKLDAQI
KNISDALGKKPIPENITVYRWCGMPEFGYQISDPLPSLKDFEEQFLNTIKEDKGYMSTSLSSERL
AAFGSRKIILRLQVPKGSTGAYLSAIGGFASEKEILLDKDSKYHIDKVTEVIIKGVKRYVVDATL
LT
>d1g24a_ d.166.1.1 (A:) Exoenzyme c3 {Clostridium botulinum}
AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGFPSNLI
KQVELLDKSFNKMKTPENIMLFRGDDPAYLGTEFQNTLLNSNGTINKTAFEKAKAKFLNKDRLEY
GYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFAGQLEMLLPRHSTYHIDDMRLSSDGK
QIIITATMMGTAINPK
>d1j7na3 d.166.1.1 (A:264-550) Anthrax toxin lethal factor, middle domain {Bacillus anthracis}
MLSRYEKWEKIKQHYQHWSDSLSEEGRGLLKKLQIPIEPKKDDIIHSLSQEEKELLKRIQIDSSD
FLSTEEKEFLKKLQIDIRDSLSEEEKELLNRIQVDSSNPLSEKEKEFLKKLKLDIQPYDINQRLQ
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DTGGLIDSPSINLDVRKQYKRDIQNIDALLHQSIGSTLYNKIYLYENMNINNLTATLGADLVDST
DNTKINRGIFNEFKKNFKYSISSNYMIVDINERPALDNERLKWRIQLSPDTRAGYLENGKLILQR
NIGLEIKDVQIIKQSEKEYIRIDAKVV
>d1a26_2 d.166.1.2 (797-1012) Poly(ADP-ribose) polymerase,
C-terminal domain {Chicken (Gallus gallus)}
LRTDIKVVDKDSEEAKIIKQYVKNTHAATHNAYDLKVVEIFRIEREGESQRYKPFKQLHNRQLLW
HGSRTTNFAGILSQGLRIAPPEAPVTGYMFGKGIYFADMVSKSANYCHTSQADPIGLILLGEVAL
GNMYELKNASHITKLPKGKHSVKGLGKTAPDPTATTTLDGVEVPLGNGISTGINDTCLLYNEYIV
YDVAQVNLKYLLKLKFNYKTS
>d1g2aa_ d.167.1.1 (A:) Peptide deformylase {Escherichia coli}
SVLQVLHIPDERLRKVAKPVEEVNAEIQRIVDDMFETMYAEEGIGLAATQVDIHQRIIVIDVSEN
RDERLVLINPELLEKSGETGIEEGCLSIPEQRALVPRAEKVKIRALDRDGKPFELEADGLLAICI
QHEMDHLVGKLFMDYLSPLKQQRIRQKVEKLDRL
>d2def__ d.167.1.1 (-) Peptide deformylase {Escherichia coli}
VLQVLHIPDERLRKVAKPVEEVNAEIQRIVDDMFETMYAEEGIGLAATQVDIHQRIIVIDVSENR
DERLVLINPELLEKSGETGIEEGCLSIPEQRALVPRAEKVKIRALDRDGKPFELEADGLLAICIQ
HEMDHLVGKLFMDYLS
>d1jbia_ d.209.1.1 (A:) Cochlin {Human (Homo sapiens)}
TAPIAITCFTRGLDIRKEKADVLCPGGCPLEEFSVYGNIVYASVSSICGAAVHRGVISNSGGPVR
VYSLPGRENYSSVDANGIQSQMLSRWSASFTVTLE
>d1chua3 d.168.1.1 (A:238-353) L-aspartate oxidase {Escherichia coli}
LEFNQFHPTALYHPQARNFLLTEALRGEGAYLKRPDGTRFMPDFDERGELAPRDIVARAIDHEMK
RLGADCMFLDISHKPADFIRQHFPMIYEKLLGLGIDLTQEPVPIVPAAHYT
>d1fuma3 d.168.1.1 (A:226-357) Fumarate reductase flavoprotein
subunit {Escherichia coli}
MEFVQYHPTGLPGSGILMTEGCRGEGGILVNKNGYRYLQDYGMGPETPLGEPKNKYMELGPRDKV
SQAFWHEWRKGNTISTPRGDVVYLDLRHLGEKKLHERLPFICELAKAYVGVDPVKEPIPVRPTAH
YT
>d1qlaa3 d.168.1.1 (A:251-371) Fumarate reductase flavoprotein
subunit {Wolinella succinogenes}
MEAVQFHPTPLFPSGILLTEGCRGDGGILRDVDGHRFMPDYEPEKKELASRDVVSRRMIEHIRKG
KGVQSPYGQHLWLDISILGRKHIETNLRDVQEICEYFAGIDPAEKWAPVLPMQHYS
>d1e39a3 d.168.1.1 (A:360-505) Flavocytochrome c3 (respiratory
fumarate reductase) {Shewanella frigidimarina}
QYIQAAPTLSVKGGVMVTEAVRGNGAILVNREGKRFVNEITTRDKASAAILAQTGKSAYLIFDDS
VRKSLSKIDKYIGLGVAPTADSLVKLGKMEGIDGKALTETVARYNSLVSSGKDTDFERPNLPRAL
NEGNYYAIEVTPGVHH
>d1qo8a3 d.168.1.1 (A:360-505) Flavocytochrome c3 (respiratory
fumarate reductase) {Shewanella frigidimarina}
HPTVGKDSRILISETVRGVGAVMVNKDGNRFISELTTRDKASDAILKQPGQFAWIIFDNQLYKKA
KMVRGYDHLEMLYKGDTVEQLAKSTGMKVADLAKTVSDYNGYVASGKDTAFGRADMPLNMTQSPY
YAVKVAPGIHHTMGGV
>d1d4ca3 d.168.1.1 (A:360-505) Flavocytochrome c3 (respiratory
fumarate reductase) {Shewanella putrefaciens}
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YIQAHPTYSPAGGVMITEAVRGNGAIVVNREGNRFMNEITTRDKASAAILQQKGESAYLVFDDSI
RKSLKAIEGYVHLNIVKEGKTIEELAKQIDVPAAELAKTVTAYNGFVKSGKDAQFERPDLPRELV
VAPFYALEIAPAVHHT
>d1jnra3 d.168.1.1 (A:257-401) Adenylylsulfate reductase A subunit
{Archaeon Archaeoglobus fulgidus}
FEHRFIPFRFKDGYGPVGAWFLFFKCKAKNAYGEEYIKTRAAELEKYKPYGAAQPIPTPLRNHQV
MLEIMDGNQPIYMHTEEALAELAGGDKKKLKHIYEEAFEDFLDMTVSQALLWACQNIDPQEQPSE
AAPAEPYIMGSHSGE
>d1lit__ d.169.1.1 (-) Lithostathine, inhibitor of stone formation
{Human (Homo sapiens)}
CPEGTNAYRSYCYYFNEDRETWVDADLYCQNMNSGNLVSVLTQAEGAFVASLIKESGTDDFNVWI
GLHDPKKNRRWHWSSGSLVSYKSWGIGAPSSVNPGYCVSLTSSTGFQKWKDVPCEDKFSFVCKFK
N
>d1qdda_ d.169.1.1 (A:) Lithostathine, inhibitor of stone formation
{Human (Homo sapiens)}
QEAQTELPQARISCPEGTNAYRSYCYYFNEDRETWVDADLYCQNMNSGNLVSVLTQAEGAFVASL
IKESGTDDFNVWIGLHDPKKNRAWHWSSGSLVSYKSWGIGAPSSVNPGYCVSLTSSTGFQKWKDV
PCEDKFSFVCKFKN
>d1b6e__ d.169.1.1 (-) CD94 {Human (Homo sapiens)}
CSCQEKWVGYRCNCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSSSQQFYWIGLSYSE
EHTAWLWENGSALSQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQQLI
>d1e87a_ d.169.1.1 (A:) CD69 {Human (Homo sapiens)}
SSCSEDWVGYQRKCYFISTVKRSWTSAQNACSEHGATLAVIDSEKDMNFLKRYAGREEHWVGLKK
EPGHPWKWSNGKEFNNWFNVTGSDKCVFLKNTEVSSMECEKNLYWICNKPYK
>d1hq8a_ d.169.1.1 (A:) NK cell-activating receptor nkg2d {Mouse (Mus
musculus)}
GYCGPCPNNWICHRNNCYQFFNEEKTWNQSQASCLSQNSSLLKIYSKEEQDFLKLVKSYHWMGLV
QIPANGSWQWEDGSSLSYNQLTLVEIPKGSCAVYGSSFKAYTEDCANLNTYICMKRAV
>d1hyra_ d.169.1.1 (A:) NK cell-activating receptor nkg2d {Human (Homo
sapiens)}
ESYCGPCPKNWICYKNNCYQFFDESKNWYESQASCMSQNASLLKVYSKEDQDLLKLVKSYHWMGL
VHIPTNGSWQWEDGSILSPNLLTIIEMQKGDCALYASSFKGYIENCSTPNTYICMQRTV
>d1egia_ d.169.1.1 (A:) Macrophage mannose receptor, CRD4 {Human (Homo
sapiens)}
CPEDWGASSRTSLCFKLYAKGKHEKKTWFESRDFCRALGGDLASINNKEEQQTIWRLITASGSYH
KLFWLGLTYGSPSEGFTWSDGSPVSYENWAYGEPNNYQNVEYCGELKGDPTMSWNDINCEHLNNW
ICQIQ
>d1bj3a_ d.169.1.1 (A:) Snake coagglutinin {Habu snake (Trimeresurus
flavoviridis)}
DCPSGWSSYEGHCYKPFKLYKTWDDAERFCTEQAKGGHLVSIESAGEADFVAQLVTENIQNTKSY
VWIGLRVQGKEKQCSSEWSDGSSVSYENWIEAESKTCLGLEKETGFRKWVNIYCGQQNPFVCEA
>d1ixxa_ d.169.1.1 (A:) Snake coagglutinin {Habu snake (Trimeresurus
flavoviridis)}
DCLSGWSSYEGHCYKAFEKYKTWEDAERVCTEQAKGAHLVSIESSGEADFVAQLVTQNMKRLDFY
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IWIGLRVQGKVKQCNSEWSDGSSVSYENWIEAESKTCLGLEKETDFRKWVNIYCGQQNPFVCEA
>d1ixxb_ d.169.1.1 (B:) Snake coagglutinin {Habu snake (Trimeresurus
flavoviridis)}
DCPSDWSSYEGHCYKPFSEPKNWADAENFCTQQHAGGHLVSFQSSEEADFVVKLAFQTFGHSIFW
MGLSNVWNQCNWQWSNAAMLRYKAWAEESYCVYFKSTNNKWRSRACRMMAQFVCEFQA
>d1c3aa_ d.169.1.1 (A:) Snake coagglutinin {Habu snake (Trimeresurus
flavoviridis), flavocetin-A}
DFDCIPGWSAYDRYCYQAFSKPKNWEDAESFCEEGVKTSHLVSIESSGEGDFVAQLVAEKIKTSF
QYVWIGLRIQNKEQQCRSEWSDASSVNYENLVKQFSKKCYALKKGTELRTWFNVYCGTENPEVCK
YTPEC
>d1c3ab_ d.169.1.1 (B:) Snake coagglutinin {Habu snake (Trimeresurus
flavoviridis), flavocetin-A}
GFCCPLGWSSYDEHCYQVFQQKMNWEDAEKFCTQQHKGSHLVSFHSSEEVDFVTSKTFPILKYDF
VWIGLSNVWNECTKEWSDGTKLDYKAWSGGSDCIVSKTTDNQWLSMDCSSKYYVVCKFQA
>d1fvua_ d.169.1.1 (A:) Snake coagglutinin {Snake (Bothrops jararaca),
botrocetin}
DCPSGWSSYEGNCYKFFQQKMNWADAERFCSEQAKGGHLVSIKIYSKEKDFVGDLVTKNIQSSDL
YAWIGLRVENKEKQCSSEWSDGSSVSYENVVERTVKKCFALEKDLGFVLWINLYCAQKNPFVCKS
PPP
>d1fvub_ d.169.1.1 (B:) Snake coagglutinin {Snake (Bothrops jararaca),
botrocetin}
DCPPDWSSYEGHCYRFFKEWMHWDDAEEFCTEQQTGAHLVSFQSKEEADFVRSLTSEMLKGDVVW
IGLSDVWNKCRFEWTDGMEFDYDDYYLIAEYECVASKPTNNKWWIIPCTRFKNFVCEFQA
>d1ioda_ d.169.1.1 (A:) Snake coagglutinin {Sharp-nosed viper
(Deinagkistrodon acutus)}
DCSSGWSSYEGHCYKVFKQSKTWADAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIKSAKIH
VWIGLRAQNKEKQCSIEWSDGSSISYENWIEEESKKCLGVHIETGFHKWENFYCEQQDPFVCEA
>d1iodb_ d.169.1.1 (B:) Snake coagglutinin {Sharp-nosed viper
(Deinagkistrodon acutus)}
DCPSDWSSYEGHCYKPFNEPKNWADAENFCTQQHTGSHLVSFQSTEEADFVVKLAFQTFDYGIFW
MGLSKIWNQCNWQWSNAAMLKYTDWAEESYCVYFKSTNNKWRSITCRMIANFVCEFQA
>d1jwia_ d.169.1.1 (A:) Snake coagglutinin {Puff adder (Bitis
arientans), bitiscetin}
CLPDWSSYKGHCYKVFKKVGTWEDAEKFCVENSGHLASIDSKEEADFVTKLASQTLTKFVYDAWI
GLRDESKTQQCSPQWTDGSSVVYENVDEPTKCFGLDVHTEYRTWTDLPCGEKNPFICKS
>d1jwib_ d.169.1.1 (B:) Snake coagglutinin {Puff adder (Bitis
arientans), bitiscetin}
GCLPDWSSYKGHCYKVFKVEKTWADAEKFCKELVNGGHLMSVNSREEGEFISKLALEKMRIVLVW
IGLSHFWRICPLRWTDGARLDYRALSDEPICFVAESFHNKWIQWTCNRKKSFVCKYRV
>d2afpa_ d.169.1.1 (A:) Type II antifreeze protein {Sea raven
(Hemitripterus americanus)}
QRAGPNCPAGWQPLGDRCIYYETTAMTWALAETNCMKLGGHLASIHSQEEHSFIQTLNAGVVWIG
GSACLQAGAWTWSDGTPMNFRSWCSTKPDDVLAACCMQMTAAADQCWDDLPCPASHKSVCAMTF
>d1h8ua_ d.169.1.1 (A:) Eosinophil major basic protein {Human (Homo
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sapiens)}
RYLLVRSLQTFSQAWFTCRRCYRGNLVSIHNFNINYRIQCSVSALNQGQVWIGGRITGSGRCRRF
QWVDGSRWNFAYWAAHQPWSRGGHCVALCTRGGYWRRAHCLRRLPFICSY
>d1qo3c_ d.169.1.1 (C:) NK cell receptor ly49a {Mouse (Mus musculus)}
STVLDSLQHTGRGDKVYWFCYGMKCYYFVMDRKTWSGCKQTCQSSSLSLLKIDDEDELKFLQLVV
PSDSCWVGLSYDNKKKDWAWIDNRPSKLALNTRKYNIRDGGCMLLSKTRLDNGNCDQVFICICGK
RLD
>d1qo3d_ d.169.1.1 (D:) NK cell receptor ly49a {Mouse (Mus musculus)}
DKVYWFCYGMKCYYFVMDRKTWSGCKQTCQSSSLSLLKIDDEDELKFLQLVVPSDSCWVGLSYDN
KKKDWAWIDNRPSKLALNTRKYNIRDGGCMLLSKTRLDNGNCDQVFICICGKRLDK
>d1dv8a_ d.169.1.1 (A:) H1 subunit of the asialoglycoprotein receptor
{Human (Homo sapiens)}
CPVNWVEHERSCYWFSRSGKAWADADNYCRLEDAHLVVVTSWEEQKFVQHHIGPVNTWMGLHDQN
GPWKWVDGTDYETGFKNWRPEQPDDWYGHGLGGGEDCAHFTDDGRWNDDVCQRPYRWVCETEL
>d1k9ia_ d.169.1.1 (A:) DC-SIGN (dendritic cell-specific ICAM-3
grabbing nonintegrin) {Human (Homo sapiens)}
PCPWEWTFFQGNCYFMSNSQRNWHDSITACKEVGAQLVVIKSAEEQNFLQLQSSRSNRFTWMGLS
DLNQEGTWQWVDGSPLLPSFKQYWNRGEPNNVGEEDCAEFSGNGWNDDKCNLAKFWICKKSAA
>d1k9ja_ d.169.1.1 (A:) DC-SIGNR (DC-SIGN related receptor) {Human
(Homo sapiens)}
CRHCPKDWTFFQGNCYFMSNSQRNWHDSVTACQEVRAQLVVIKTAEEQNFLQLQTSRSNRFSWMG
LSDLNQEGTWQWVDGSPLSPSFQRYWNSGEPNNSGNEDCAEFSGSGWNDNRCDVDNYWICKKPAA
>d1g1sa1 d.169.1.1 (A:1-118) E-selectin {Human (Homo sapiens)}
WTYHYSTKAYSWNISRKYCQNRYTDLVAIQNKNEIDYLNKVLPYYSSYYWIGIRKNNKTWTWVGT
KKALTNEAENWADNEPNNKRNNEDCVEIYIKSPSAPGKWNDEHCLKKKHALCY
>d1g1ta1 d.169.1.1 (A:1-118) E-selectin {Human (Homo sapiens)}
WSYNTSTEAMTYDEASAYCQQRYTHLVAIQNKEEIEYLNSILSYSPSYYWIGIRKVNNVWVWVGT
QKPLTEEAKNWAPGEPNNRQKDEDCVEIYIKREKDVGMWNDERCSKKKLALCY
>d1hup_1 d.169.1.1 (112-228) Mannose-binding protein A, lectin domain
{Human (Homo sapiens)}
KQVGNKFFLTNGEIMTFEKVKALCVKFQASVATPRNAAENGAIQNLIKEEAFLGITDEKTEGQFV
DLTGNRLTYTNWNEGEPNNAGSDEDCVLLLKNGQWNDVPCSTSHLAVCEFPI
>d1fifa1 d.169.1.1 (A:105-226) Mannose-binding protein A, lectin
domain {Rat (Rattus norvegicus)}
KKSGKKFFVTNHERMPFSKVKALCSELRGTVAIPRNAEENKAIQEVAKTSAFLGITDEVTEGQFM
YVTGGRLTYSNWKKDQPDDWYGHGLGGGEDCVHIVDNGLWNDDSCQRPYTAVCEFPA
>d1rdl1_ d.169.1.1 (1:) Mannose-binding protein A, lectin domain {Rat
(Rattus norvegicus)}
KYFMSSVRRMPLNRAKALCSELQGTVATPRNAEENRAIQNVAKDVAFLGITDQRTENVFEDLTGN
RVRYTNWNEGEPNNVGSGENCVVLLTNGKWNDVPCSDSFLVVCEFS
>d2msba_ d.169.1.1 (A:) Mannose-binding protein A, lectin domain {Rat
(Rattus norvegicus)}
KKFFVTNHERMPFSKVKALCSELRGTVAIPRNAEENKAIQEVAKTSAFLGITDEVTEGQFMYVTG
GRLTYSNWKKDEPNDHGSGEDCVTIVDNGLWNDISCQASHTAVCEFP
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>d1b08a1 d.169.1.1 (A:235-355) Surfactant protein, lectin domain {Human (Homo sapiens), SP-D}
PNGQSVGEKIFKTAGFVKPFTEAQLLCTQAGGQLASPRSAAENAALQQLVVAKNEAAFLSMTDSK
TEGKFTYPTGESLVYSNWAPGEPNDDGGSEDCVEIFTNGKWNDRACGEKRLVVCEF
>d1byfa_ d.169.1.1 (A:) Lectin TC14 {Tunicate (Polyandrocarpa misakiensis)}
DYEILFSDETMNYADAGTYCQSRGMALVSSAMRDSTMVKAILAFTEVKGHDYWVGADNLQDGAYN
FLWNDGVSLPTDSDLWSPNEPSNPQSWQLCVQIWSKYNLLDDVGCGGARRVICEKELD
>d1tn3__ d.169.1.1 (-) Tetranectin {Human (Homo sapiens)}
ALQTVCLKGTKVHMKCFLAFTQTKTFHEASEDCISRGGTLSTPQTGSENDALYEYLRQSVGNEAE
IWLGLNDMAAEGTWVDMTGARIAYKNWETEITAQPDGGKTENCAVLSGAANGKWFDKRCRDQLPY
ICQFGIV
>d1prtb2 d.169.1.2 (B:4-89) Pertussis toxin, S2/S3 subunits, N-terminal domain {Bordetella pertussis}
GIVIPPQEQITQHGSPYGRCANKTRALTVAELRGSGDLQEYLRHVTRGWSIFALYDGTYLGGEYG
GVIKDGTPGGAFDLKTTFCIM
>d1prtc2 d.169.1.2 (C:4-89) Pertussis toxin, S2/S3 subunits, N-terminal domain {Bordetella pertussis}
GIVIPPKALFTQQGGAYGRCPNGTRALTVAELRGNAELQTYLRQITPGWSIYGLYDGTYLGQAYG
GIIKDAPPGAGFIYRETFCIT
>d1prea1 d.169.1.2 (A:2-84) Proaerolysin, N-terminal domain {Aeromonas hydrophila}
EPVYPDQLRLFSLGQGVCGDKYRPVNREEAQSVKSNIVGMMGQWQISGLANGWVIMGPGYNGEIK
PGTASNTWCYPTNPVTGE
>d1f00i3 d.169.1.3 (I:842-939) Intimin {Escherichia coli}
LIVPNMSKRVTYNDAVNTCKNFGGKLPSSQNELENVFKAWGAANKYEYYKSSQTIISWVQQTAQD
AKSGVASTYDLVKQNPLNNIKASESNAYATCVK
>d1cwva5 d.169.1.3 (A:887-986) Invasin {Yersinia pseudotuberculosis}
NRWIYDGGRSLVSSLEASRQCQGSDMSAVLESSRATNGTRAPDGTLWGEWGSLTAYSSDWQSGEY
WVKKTSTDFETMNMDTGALQPGPAYLAFPLCALSI
>d1tsg__ d.169.1.4 (-) TSG-6, Link module {Human (Homo sapiens)}
GVYHREARSGKYKLTYAEAKAVCEFEGGHLATYKQLEAARKIGFHVCAAGWMAKGRVGYPIVKPG
PNCGFGKTGIIDYGIRLNRSERWDAYCYNPHAK
>d1bnla_ d.169.1.5 (A:) Endostatin {Human (Homo sapiens)}
HSHRDFQPVLHLVALNAPLSGGMRGIRGADFQCFQQARAVGLAGTFRAFLSSRLQDLYSIVRRAD
RAAVPIVNLKDELLFPSWEALFSGSEGPLKPGARIFSFDGKDVLRHPTWPQKSVWHGSDPNGRRL
TESYCETWRTEAPSATGQASSLLGGRLLGQSAASCHHAYIVLCIENSF
>d1koe__ d.169.1.5 (-) Endostatin {Mouse (Mus musculus)}
QPVLHLVALNTPLSGGMRGIRGADFQCFQQARAVGLSGTFRAFLSSRLQDLYSIVRRADRGSVPI
VNLKDEVLSPSWDSLFSGSQGQLQPGARIFSFDGRDVLRHPAWPQKSVWHGSDPSGRRLMESYCE
TWRTETTGATGQASSLLSGRLLEQKAASCHNSYIVLCIENSF
>d1dy2a_ d.169.1.5 (A:) Endostatin domain of collagen alpha1(xv) {Mouse (Mus musculus)}
RPVLHLVALNTPVAGDIRADFQCFQQARAAGLLSTFRAFLSSHLQDLSTVVRKAERFGLPIVNLK
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GQVLFNNWDSIFSGDGGQFNTHIPIYSFDGRDVMTDPSWPQKVVWHGSNPHGVRLVDKYCEAWRT
TDMAVTGFASPLSTGKILDQKAYSCANRLIVLCIENSF
>d1by2__ d.170.1.1 (-) M2BP {Human (Homo sapiens)}
AVNDGDMRLADGGATNQGRVEIFYRGQWGTVCDNLWDLTDASVVCRALGFENATQALGRAAFGQG
SGPIMLDEVQCTGTEASLADCKSLGWLKSNCRHERDAGVVCTNETRSTHTL
>d1mwpa_ d.170.2.1 (A:) N-terminal domain of the amyloid precursor
protein {Human (Homo sapiens)}
LLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPV
TIQNWCKRGRKQCKTHPHFVIPYRCLVGEFV
>d1fid__ d.171.1.1 (-) Fibrinogen C-terminal domains {Human (Homo
sapiens), gamma}
QIHDITGKDCQDIANKGAKQSGLYFIKPLKANQQFLVYCEIDGSGNGWTVFQKRLDGSVDFKKNW
IQYKEGFGHLSPTGTTEFWLGNEKIHLISTQSAIPYALRVELEDWNGRTSTADYAMFKVGPEADK
YRLTYAYFAGGDAGDAFDGFDFGDDPSDKFFTSHNGMQFSTWDNDNDKFEGNCAEQDGSGWWMNK
CHAGHLNGVYYQGGTYSKASTPNGYDNGIIWATWKTRWYSMKKTTMKIIPFNRLTIGEGQQHHL
>d1fzcb1 d.171.1.1 (B:200-458) Fibrinogen C-terminal domains {Human
(Homo sapiens), beta}
SCNIPVVSGKECEEIIRKGGETSEMYLIQPDSSVKPYRVYCDMNTENGGWTVIQNRQDGSVDFGR
KWDPYKQGFGNVATNTDGKNYCGLPGEYWLGNDKISQLTRMGPTELLIEMEDWKGDKVKAHYGGF
TVQNEANKYQISVNKYRGTAGNALMDGASQLMGENRTMTIHNGMFFSTYDRDNDGWLTSDPRKQC
SKEDGGGWWYNRCHAANPNGRYYWGGQYTWDMAKHGTDDGVVWMNWKGSWYSMRKMSMKIRPFF
>d1fzda_ d.171.1.1 (A:) Fibrinogen C-terminal domains {Human (Homo
sapiens), fibrinogen-420, alpha-E}
GGWLLIQQRMDGSLNFNRTWQDYKRGFGSLNDEGEGEFWLGNDYLHLLTQRGSVLRVELEDWAGN
EAYAEYHFRVGSEAEGYALQVSSYEGTAGDALIEGSVEEGAEYTSHNNMQFSTFDRDADQWEENC
AEVYGGGWWYNNCQAANLNGIYYPGGSYDPRNNSPYEIENGVVWVSFRGADYSLRAVRMKIRPLV
TQ
>d1jfec1 d.171.1.1 (C:142-393) Fibrinogen C-terminal domains {Chicken
(Gallus gallus), gamma}
TAEIQETTGRDCQDIANKGARKSGLYFIKPQKAKQSFLVYCEIDTYGNGWTVLQRRLDGSEDFRR
NWVQYKEGFGHLSPDDTTEFWLGNEKIHLITTQSTLPYALRIELEDWSGKKGTADYAVFKVGTEE
DKYRLTYAYFIGGEAGDAFDGFNFGDDPSDKSYTYHNGMRFSTFDNDNDNFEGNCAEQDGSGWWM
NRCHAGHLNGPYYIGGVYSRDTGTNSYDNGIIWATWRDRWYSMKKTTMKIIPFNRLS
>d1jfeb1 d.171.1.1 (B:200-464) Fibrinogen C-terminal domains {Chicken
(Gallus gallus), beta}
SPCVASCNIPVVSGRECEDIYRKGGETSEMYIIQPDPFTTPYRVYCDMETDNGGWTLIQNRQDGS
VNFGRAWDEYKRGFGNIAKSGGKKYCDTPGEYWLGNDKISQLTKIGPTKVLIEMEDWNGDKVSAL
YGGFTIHNEGNKYQLSVSNYKGNAGNALMEGASQLYGENRTMTIHNGMYFSTYDRDNDGWLTTDP
RKQCSKEDGGGWWYNRCHAANPNGRYYWGGTYSWDMAKHGTDDGIVWMNWKGSWYSMKKMSMKIK
PYFPD
>d1jc9a_ d.171.1.1 (A:) Tachylectin 5a {Japanese horseshoe crab
(Tachypleus tridentatus)}
DPTDCADILLNGYRSSGGYRIWPKSWMTVGTLNVYCDMETDGGGWTVIQRRGNYGNPSDYFYKPW
KNYKLGFGNIEKDFWLGNDRIFALTNQRNYMIRFDLKDKENDTRYAIYQDFWIENEDYLYCLHIG
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NYSGDAGNSFGRHNGHNFSTIDKDHDTHETHCAQTYKGGWWYDRCHESNLNGLYLNGEHNSYADG
IEWRAWKGYHYSLPQVEMKIRPVEF
>d1g9mg_ d.172.1.1 (G:) gp120 core {Human immunodeficiency virus type
1}
EVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPCVKLTPLCVGAGSCNTSVITQACPKVSFE
PIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSVN
FTDNAKTIIVQLNTSVEINCTGAGHCNISRAKWNNTLKQIASKLREQFGNNKTIIFKQSSGGDPE
IVTHSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTITLPCRIKQIINMWQKVGKAMY
APPISGQIRCSSNITGLLLTRDGGNSNNESEIFRPGGGDMRDNWRSELYKYKVVKIE
>d1g9ng_ d.172.1.1 (G:) gp120 core {Human immunodeficiency virus type
1}
LENVTENFNMWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVGAGSCNTSVITQACPKVSFEPIP
IHYCAPAGFAILKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEEIVIRSENFTN
NAKTIIVQLNESVVINCTGAGHCNLSKTQWENTLEQIAIKLKEQFGNNKTIIFNPSSGGDPEIVT
HSFNCGGEFFYCNSTQLFTWNDTRKLNNTGRNITLPCRIKQIINMWQEVGKAMYAPPIRGQIRCS
SNITGLLLTRDGGKDTNGTEIFRPGGGDMRDNWRSELYKYKVVKIE
>d1msk__  d.173.1.1  (-)  Methionine  synthase  (activation  domain)
{Escherichia coli}
TPPVTLEAARDNDFAFDWQAYTPPVAHRLGVQEVEASIETLRNYIDWTPFFMTWSLAGKYPRILE
DEVVGVEAQRLFKDANDMLDKLSAEKTLNPRGVVGLFPANRVGDDIEIYRDETRTHVINVSHHLR
QQTEKTGFANYCLADFVAPKLSGKADYIGAFAVTGGLEEDALADAFEAQHDDYNKIMVKALADRL
AEAFAEYLHERVRKVYWGYAPNENLSNEELIRENYQGIRPAPGYPACPEHTEKATIWELLEVEKH
TGMKLTESFAMWPGASVSGWYFSHPDSKYYAVAQIQRDQVEDYARRKGMSVTEVERWLAPNLGYD
AD
>d1jwka_ d.174.1.1 (A:) Nitric oxide (NO) synthase oxygenase domain
{Mouse (Mus musculus)}
QYVRIKNWGSGEILHDTLHHKATSCDFTCKSKSCLGSIMNPKSLTRGPRDKPTPLEELLPHAIEF
INQYYGSFKEAKIEEHLARLEAVTKEIETTGTYQLTLDELIFATKMAWRNAPRCIGRIQWSNLQV
FDARNCSTAQEMFQHICRHILYATNNGNIRSAITVFPQRSDGKHDFRLWNSQLIRYAGYQMPDGT
IRGDAATLEFTQLCIDLGWKPRYGRFDVLPLVLQADGQDPEVFEIPPDLVLEVTMEHPKYEWFQE
LGLKWYALPAVANMLLEVGGLEFPACPFNGWYMGTEIGVRDFCDTQRYNILEEVGRRMGLETHTL
ASLWKDRAVTEINVAVLHSFQKQNVTIMDHHTASESFMKHMQNEYRARGGCPADWIALVPPVSGS
ITPVFHQEMLNYVLSPFYYYQIEPWKTHIWQN
>d1nos__ d.174.1.1 (-) Nitric oxide (NO) synthase oxygenase domain
{Mouse (Mus musculus)}
NPKSLTRGPRDKPTPLEELLPHAIEFINQYYGSFKEAKIEEHLARLEAVTKEIETTGTYQLTLDE
LIFATKMAWRNAPRCIGRIQWSNLQVFDARNCSTAQEMFQHICRHILYATNNGNIRSAITVFPQR
SDGKHDFRLWNSQLIRYAGYQMPDGTIRGDAATLEFTQLCIDLGWKPRYGRFDVLPLVLQADGQD
PEVFEIPPDLVLEVTMEHPKYEWFQELGLKWYALPAVANMLLEVGGLEFPACPFNGWYMGTEIGV
RDFCDTQRYNILEEVGRRMGLETHTLASLWKDRAVTEINVAVLHSFQKQNVTIMDHHTASESFMK
HMQNEYRARGGCPADWIWLVPPVSGSITPVFHQEMLNYVLSPFYYYQIEPWKTHIWQNEHHHH
>d3nosa_ d.174.1.1 (A:) Nitric oxide (NO) synthase oxygenase domain
{Human (Homo sapiens)}
KFPRVKNWEVGSITYDTLSAQAQQDGPCTPRRCLGSLVFPRKLQGRPSPGPPAPEQLLSQARDFI
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NQYYSSIKRSGSQAHEQRLQEVEAEVAATGTYQLRESELVFGAKQAWRNAPRCVGRIQWGKLQVF
DARDCRSAQEMFTYICNHIKYATNRGNLRSAITVFPQRCPGRGDFRIWNSQLVRYAGYRQQDGSV
RGDPANVEITELCIQHGWTPGNGRFDVLPLLLQAPDEPPELFLLPPELVLEVPLEHPTLEWFAAL
GLRWYALPAVSNMLLEIGGLEFPAAPFSGWYMSTEIGTRNLCDPHRYNILEDVAVCMDLDTRTTS
SLWKDKAAVEINVAVLHSYQLAKVTIVDHHAATASFMKHLENEQKARGGCPADWAWIVPPISGSL
TPVFHQEMVNYFLSPAFRYQPDPW
>d4nosa_ d.174.1.1 (A:) Nitric oxide (NO) synthase oxygenase domain {Human (Homo sapiens)}
RHVRIKNWGSGMTFQDTLHHKAKGILTCRSKSCLGSIMTPKSLTRGPRDKPTPPDELLPQAIEFV
NQYYGSFKEAKIEEHLARVEAVTKEIETTGTYQLTGDELIFATKQAWRNAPRCIGRIQWSNLQVF
DARSCSTAREMFEHICRHVRYSTNNGNIRSAITVFPQRSDGKHDFRVWNAQLIRYAGYQMPDGSI
RGDPANVEFTQLCIDLGWKPKYGRFDVVPLVLQANGRDPELFEIPPDLVLEVAMEHPKYEWFREL
ELKWYALPAVANMLLEVGGLEFPGCPFNGWYMGTEIGVRDFCDVQRYNILEEVGRRMGLETHKLA
SLWKDQAVVEINIAVIHSFQKQNVTIMDHHSAAESFMKYMQNEYRSRGGCPADWIWLVPPMSGSI
TPVFHQEMLNYVLSPFYYYQVEAWKTHVWQD
>d1d0ca_ d.174.1.1 (A:) Nitric oxide (NO) synthase oxygenase domain {Cow (Bos taurus)}
GPKFPRVKNWELGSITYDTLCAQSQQDGPCTPRRCLGSLVLPRKLQTRPSPGPPPAEQLLSQARD
FINQYYSSIKRSGSQAHEERLQEVEAEVASTGTYHLRESELVFGAKQAWRNAPRCVGRIQWGKLQ
VFDARDCSSAQEMFTYICNHIKYATNRGNLRSAITVFPQRAPGRGDFRIWNSQLVRYAGYRQQDG
SVRGDPANVEITELCIQHGWTPGNGRFDVLPLLLQAPDEAPELFVLPPELVLEVPLEHPTLEWFA
ALGLRWYALPAVSNMLLEIGGLEFSAAPFSGWYMSTEIGTRNLCDPHRYNILEDVAVCMDLDTRT
TSSLWKDKAAVEINLAVLHSFQLAKVTIVDHHAATVSFMKHLDNEQKARGGCPADWAWIVPPISG
SLTPVFHQEMVNYILSPAFRYQPDPW
>d1k25a3 d.175.1.1 (A:67-263) Penicillin-binding protein 2x (pbp-2x), N-terminal domain {Streptococcus pneumoniae}
QITRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDKKYKSATGKILYVEDAQFNKVAEVFHKYLD
MEESYVREQLSQPNLKQVSFGSKGNGITYANMMAIKKELETAEVKGIDFTTSPNRSYPNGQFASS
FIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRVGNIVPGTELVSQQTVDGKDV
YT
>d1qmea3 d.175.1.1 (A:71-263) Penicillin-binding protein 2x (pbp-2x), N-terminal domain {Streptococcus pneumoniae}
TVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEES
YVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGL
AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYT
>d1soxa3 d.176.1.1 (A:94-343) Sulfite oxidase, middle catalytic domain {Chicken (Gallus gallus)}
QDPFAGDPPRHPGLRVNSQKPFNAEPPAELLAERFLTPNELFFTRNHLPVPAVEPSSYRLRVDGP
GGGTLSLSLAELRSRFPKHEVTATLQCAGNRRSEMSRVRPVKGLPWDIGAISTARWGGARLRDVL
LHAGFPEELQGEWHVCFEGLDADPGGAPYGASIPYGRALSPAADVLLAYEMNGTELPRDHGFPVR
VVVPGVVGARSVKWLRRVAVSPDESPSHWQQNDYKGFSPCVDWDTVDYRTAPAIQ
>d1hyoa2 d.177.1.1 (A:119-416) Fumarylacetoacetate hydrolase, FAH, C-terminal domain {Mouse (Mus musculus)}
ATIGDYTDFYSSRQHATNVGIMFRGKENALLPNWLHLPVGYHGRASSIVVSGTPIRRPMGQMRPD

NSKPPVYGACRLLDMELEMAFFVGPGNRFGEPIPISKAHEHIFGMVLMNDWSARDIQQWEYVPLG
PFLGKSFGTTISPWVVPMDALMPFVVPNPKQDPKPLPYLCHSQPYTFDINLSVSLKGEGMSQAAT
ICRSNFKHMYWTMLQQLTHHSVNGCNLRPGDLLASGTISGSDPESFGSMLELSWKGTKAIDVGQG
QTRTFLLDGDEVIITGHCQGDGYRVGFGQCAGKVLPAL
>d1i7oa1 d.177.1.1 (A:1-213) 4-hydroxyphenylacetate degradation
bifunctional isomerase/decarboxylase HpcE {Escherichia coli}
MKGTIFAVALNHRSQLDAWQEAFQQSPYKAPPKTAVWFIKPRNTVIGCGEPIPFPQGEKVLSGAT
VALIVGKTATKVREEDAAEYIAGYALANDVSLPEESFYRPAIKAKCRDGFCPIGETVALSNVDNL
TIYTEINGRPADHWNTADLQRNAAQLLSALSEFATLNPGDAILLGTPQARVEIQPGDRVRVLAEG
FPPLENPVVDEREVTTRK
>d1i7oa2 d.177.1.1 (A:214-429) 4-hydroxyphenylacetate degradation
bifunctional isomerase/decarboxylase HpcE {Escherichia coli}
SFPTLPHPHGTLFALGLNYADHASELEFKPPEEPLVFLKAPNTLTGDNQTSVRPNNIEYMHYEAE
LVVVIGKQARNVSEADAMDYVAGYTVCNDYAIRDYLENYYRPNLRVKSRDGLTPMLSTIVPKEAI
PDPHNLTLRTFVNGELRQQGTTADLIFSVPFLIAYLSEFMTLNPGDMIATGTPKGLSDVVPGDEV
VVEVEGVGRLVNRIVSEETAK
>d1toh__ d.178.1.1 (-) Tyrosine hydroxylase {Rat (Rattus norvegicus)}
KVPWFPRKVSELDKCHHLVTKFDPDLDLDHPGFSDQVYRQRRKLIAEIAFQYKHGEPIPHVEYTA
EEIATWKEVYVTLKGLYATHACREHLEGFQLLERYCGYREDSIPQLEDVSRFLKERTGFQLRPVA
GLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLGHVPMLADRTFAQFSQDIGLASL
GASDEEIEKLSTVYWFTVEFGLCKQNGELKAYGAGLLSSYGELLHSLSEEPEVRAFDPDTAAVQP
YQDQTYQPVYFVSESFNDAKDKLRNYASRIQRPFSVKFDPYTLAIDVLDSPHTIQRSLEGVQDEL
HTLAHALSAIS
>d3pah__ d.178.1.1 (-) Phenylalanine hydroxylase {Human (Homo
sapiens)}
TVPWFPRTIQELDRFANQILSYGAELDADHPGFKDPVYRARRKQFADIAYNYRHGQPIPRVEYME
EEKKTWGTVFKTLKSLYKTHACYEYNHIFPLLEKYCGFHEDNIPQLEDVSQFLQTCTGFRLRPVA
GLLSSRDFLGGLAFRVFHCTQYIRHGSKPMYTPEPDICHELLGHVPLFSDRSFAQFSQEIGLASL
GAPDEYIEKLATIYWFTVEFGLCKQGDSIKAYGAGLLSSFGELQYCLSEKPKLLPLELEKTAIQN
YTVTEFQPLYYVAESFNDAKEKVRNFAATIPRPFSVRYDPYTQRIEVL
>d1phza2 d.178.1.1 (A:116-427) Phenylalanine hydroxylase {Rat (Rattus
norvegicus)}
NTVPWFPRTIQELDRFANQILSYGAELDADHPGFKDPVYRARRKQFADIAYNYRHGQPIPRVEYT
EEEKQTWGTVFRTLKALYKTHACYEHNHIFPLLEKYCGFREDNIPQLEDVSQFLQTCTGFRLRPV
AGLLSSRDFLGGLAFRVFHCTQYIRHGSKPMYTPEPDICHELLGHVPLFSDRSFAQFSQEIGLAS
LGAPDEYIEKLATIYWFTVEFGLCKEGDSIKAYGAGLLSSFGELQYCLSDKPKLLPLELEKTACQ
EYSVTEFQPLYYVAESFSDAKEKVRTFAATIPRPFSVRYDPYTQRVEVLDNT
>d1dqaa4 d.179.1.1 (A:462-586,A:704-870) Substrate-binding domain of
HMG-CoA reductase {Human (Homo sapiens)}
LSDAEIIQLVNAKHIPAYKLETLIETHERGVSIRRQLLSKKLSEPSSLQYLPYRDYNYSLVMGAC
CENVIGYMPIPVGVAGPLCLDEKEFQVPMATTEGCLVASTNRGCRAIGLGGGASSRVLADXKSVV
CEAVIPAKVVREVLKTTTEAMIEVNINKNLVGSAMAGSIGGYNAHAANIVTAIYIACGQDAAQNV
GSSNCITLMEASGPTNEDLYISCTMPSIEIGTVGGGTNLLPQQACLQMLGVQGACKDNPGENARQ
LARIVCGTVMAGELSLMAALAAGHLVKSHMIHN

>d1hw8a2 d.179.1.1 (A:441-586,A:704-861) Substrate-binding domain of HMG-CoA reductase {Human (Homo sapiens)}
EPRPNEECLQILGNAEKGAKFLSDAEIIQLVNAKHIPAYKLETLIETHERGVSIRRQLLSKKLSE
PSSLQYLPYRDYNYSLVMGACCENVIGYMPIPVGVAGPLCLDEKEFQVPMATTEGCLVASTNRGC
RAIGLGGGASSRVLADXKSVVCEAVIPAKVVREVLKTTTEAMIEVNINKNLVGSAMAGSIGGYNA
HAANIVTAIYIACGQDAAQNVGSSNCITLMEASGPTNEDLYISCTMPSIEIGTVGGGTNLLPQQA
CLQMLGVQGACKDNPGENARQLARIVCGTVMAGELSLMAALAAGH
>d1hw8c2 d.179.1.1 (C:488-586,C:704-860) Substrate-binding domain of HMG-CoA reductase {Human (Homo sapiens)}
HERGVSIRRQLLSKKLSEPSSLQYLPYRDYNYSLVMGACCENVIGYMPIPVGVAGPLCLDEKEFQ
VPMATTEGCLVASTNRGCRAIGLGGGASSRVLADXKSVVCEAVIPAKVVREVLKTTTEAMIEVNI
NKNLVGSAMAGSIGGYNAHAANIVTAIYIACGQDAAQNVGSSNCITLMEASGPTNEDLYISCTMP
SIEIGTVGGGTNLLPQQACLQMLGVQGACKDNPGENARQLARIVCGTVMAGELSLMAALAAG
>d1qaxa2 d.179.1.1 (A:4-110,A:221-428) Substrate-binding domain of HMG-CoA reductase {Pseudomonas mevalonii}
DSRLPAFRNLSPAARLDHIGQLLGLSHDDVSLLANAGALPMDIANGMIENVIGTFELPYAVASNF
QINGRDVLVPLVVEEPSIVAAASYMAKLARANGGFTTSSSAPXRLARAQVRITPQQLETAEFSGE
AVIEGILDAYAFAAVDPYRAATHNKGIMNGIDPLIVATGNDWRAVEAGAHAYACRSGHYGSLTTW
EKDNNGHLVGTLEMPMPVGLVGGATKTHPLAQLSLRILGVKTAQALAEIAVAVGLAQNLGAMRAL
ATEGIQRGHMALHARNIAVVAGARGDEVDWVARQLVEYHDVRADRAVALLKQKRGQ
>d1qaxb2 d.179.1.1 (B:504-610,B:721-875) Substrate-binding domain of HMG-CoA reductase {Pseudomonas mevalonii}
DSRLPAFRNLSPAARLDHIGQLLGLSHDDVSLLANAGALPMDIANGMIENVIGTFELPYAVASNF
QINGRDVLVPLVVEEPSIVAAASYMAKLARANGGFTTSSSAPXRLARAQVRITPQQLETAEFSGE
AVIEGILDAYAFAAVDPYRAATHNKGIMNGIDPLIVATGNDWRAVEAGAHAYACRSGHYGSLTTW
EKDNNGHLVGTLEMPMPVGLVGGATKTHPLAQLSLRILGVKTAQALAEIAVAVGLAQNLGAMRAL
ATE
>d1k92a2 d.210.1.1 (A:189-444) Argininosuccinate synthetase, C-terminal domain {Escherichia coli}
AYSTDSNMLGATHEAKDLEYLNSSVKIVNPIMGVKFWDESVKIPAEEVTVRFEQGHPVALNGKTF
SDDVEMMLEANRIGGRHGLGMSDQIENRIIEAKSRGIYEAPGMALLHIAYERLLTGIHNEDTIEQ
YHAHGRQLGRLLYQGRWFDSQALMLRDSLQRWVASQITGEVTLELRRGNDYSILNTVSENLTYKP
ERLTMEKGDSVFSPDDRIGQLTMRNLDITDTREKLFGYAKTGLLSSSAASGVPQVENLENK
>d16vpa_ d.180.1.1 (A:) Conserved core of transcriptional regulatory protein vp16 {Herpes simplex virus type 1}
SRMPSPPMPVPPAALFNRLLDDLGFSAGPALCTMLDTWNEDLFSALPTNADLYRECKFLSTLPSD
VVEWGDAYVPERTQIDIRAHGDVAFPTLPATRDGLGLYYEALSRFFHAELRAREESYRTVLANFC
SALYRYLRASVRQLHRQAHMRGRDRDLGEMLRATIADRYYRETARLARVLFLHLYLFLTREILWA
AYAEQMMRPDLFDCLCCDLESWRQLAGLFQPFMFVNGALTVRGVPIEARRLRELNHIREHLNLPL
VRSAATEEPGAPLTTPPTLHGNQARASGYFMVLIRAKLDSYSSFTTSPSEAVMREHAYSRAPTKN
NYGSTIEGLLDLPDDDAPEEAGLAAPRLSFL
>d1bdfa2 d.181.1.1 (A:53-178) RNA polymerase alpha subunit {Escherichia coli}
GCAVTEVEIDGVLHEYSTKEGVQEDILEILLNLKGLAVRVQGKDEVILTLNKSGIGPVTAADITH

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DGDVEIVKPQHVICHLTDENASISMRIKVQRGRGYVPASTRIHSEEDERPIGRLLVDACYS
>d1i6va2 d.181.1.1 (A:50-172) RNA polymerase alpha subunit {Thermus
aquaticus}
GTAVTSVYIEDVLHEFSTIPGVKEDVVEIILNLKELVVRFLDPKMASTTLILRAEGPKEVRAVDF
TPSADVEIMNPDLHIATLEEGGKLYMEVRVDRGVGYVPAERHGIKDRINAIPVDAIFS
>d1i50c2 d.181.1.1 (C:42-172) RPB3 {Baker's yeast (Saccharomyces
cerevisiae)}
PTLAIDSVEVETNTTVLADEFIAHRLGLIPLQSMDIEQLEYSRDCFCEDHCDKCSVVLTLQAFGE
SESTTNVYSKDLVIVSNLMGRNIGHPIIQDKEGNGVLICKLRKGQELKLTCVAKKGIAKEHAKWG
P
>d1el6a_ d.182.1.1 (A:) Baseplate structural protein gp11
{Bacteriophage T4}
SRLADFLGFRPKTGDIDVMNRQSVGSVTISQLAKGFYEPNIESAINDVHNFSIKDVGTIITNKTG
VSPEGVSQTDYWAFSGTVTDDSLPPGSPITVLVFGLPVSATTGMTAIEFVAKVRVALQEAIASFT
AINSYKDHPTDGSKLEVTYLDNQKHVLSTYSTYGITISQEIISESKPGYGTWNLLGAQTVTLDNQ
QTPTVFYHFERTA
>d1fh6a_ d.183.1.1 (A:) Major capsid protein gp5 {Bacteriophage HK97}
SLGSDADSAGSLIQPMQIPGIIMPGLRRLTIRDLLAQGRTSSNALEYVREEVFTNNADVVAEKAL
KPESDITFSKQTANVKTIAHWVQASRQVMDDAPMLQSYINNRLMYGLALKEEGQLLNGDGTGDNL
EGLNKVATAYDTSLNATGDTRADIIAHAIYQVTESEFSASGIVLNPRDWHNIALLKDNEGRYIFG
GPQAFTSNIMWGLPVVPTKAQAAGTFTVGGFDMASQVWDRMDATVEVSREDRDNFVKNMLTILCE
ERLALAHYRPTAIIKGTFSS
>d1fn9a_ d.196.1.1 (A:) Outer capsid protein sigma 3 {Reovirus}
MEVCLPNGHQVVDLINNAFEGRVSIYSAQEGWDKTISAQPDMMVCGGAVVCMHCLGVVGSLQRKL
KHLPHHRCNQQIRHQDYVDVQFADRVTAHWKRGMLSFVAQMHEMMNDVSPDDLDRVRTEGGSLVE
LNWLQVDPNSMFRSIHSSWTDPLQVVDDLDTKLDQYWTALNLMIDSSDLIPNFMMRDPSHAFNGV
KLGGDARQTQFSRTFDSRSSLEWGVMVYDYSELEHDPSKGRAYRKELVTPARDFGHFGLSHYSRA
TTPILGKMPAVFSGMLTGNCKMYPFIKGTAKLKTVRKLVEAVNHAWGVEKIRYALGPGGMTGWYN
RTMQQAPIVLTPAALTMFPDTIKFGDLNYPVMIGDPMILG
>d1qgwa_ d.184.1.1 (A:) Phycoerythrin 545 alpha-subunits {Cryptophyte
(Rhodomonas sp.), cs24}
AMDKSAKAPQITIFDHRGCSRAPKESTGGKAGGQDDEMMVKVASTKVTVSESDAAKKLQEFITFE
KGIDGPFTSKN
>d1qgwb_ d.184.1.1 (B:) Phycoerythrin 545 alpha-subunits {Cryptophyte
(Rhodomonas sp.), cs24}
AMDKSAKAPVITIFDHRGCSRAPKEYTGAKAGGKDDEMMVKAQSVKIEVSTGTAEGVLATSLAKM
TK
>d1jyoe_ d.184.1.2 (E:) Virulence effector SptP domain {Salmonella
typhimurium}
DKAYVAPEKFSSKVLTWLGKMPLFKNTEVVQKHTENIRVQDQKILQTFLHALTEKYGETAVNDAL
LMSRINMNKPLTQRLAVQITECVKAADEGFINLIKSK
>g1hle.1 e.1.1.1 (A:,B:) Elastase inhibitor {Horse (Equus caballus)}
MEQLSTANTHFAVDLFRALNESDPTGNIFISPLSISSALAMIFLGTRGNTAAQVSKALYFDTVED
IHSRFQSLNADINKPGAPYILKLANRLYGEKTYNFLADFLASTQKMYGAELASVDFQQAPEDARK
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EINEWVKGQTEGKIPELLVKGMVDNMTKLVLVNAIYFKGNWQQKFMKEATRDAPFRLNKKDTKTV
KMMYQKKKFPYNYIEDLKCRVLELPYQGKELSMIILLPDDIEDESTGLEKIEKQLTLDKLREWTK
PENLYLAEVNVHLPRFKLEESYDLTSHLARLGVQDLFNRGKADLSGMSGARDLFVSKIIHKSFVD
LNEEGTEAAAATAGTILLAXEENFNADHPFIFFIRHNPSANILFLGRFSSP
>d1ovaa_ e.1.1.1 (A:) Ovalbumin {Hen (Gallus gallus)}
GSIGAASMEFCFDVFKELKVHHANENIFYCPIAIMSALAMVYLGAKDSTRTQINKVVRFDKLPGF
GDSIEAQCGTSVNVHSSLRDILNQITKPNDVYSFSLASRLYAEERYPILPEYLQCVKELYRGGLE
PINFQTAADQARELINSWVESQTNGIIRNVLQPSSVDSQTAMVLVNAIVFKGLWEKAFKDEDTQA
MPFRVTEQESKPVQMMYQIGLFRVASMASEKMKILELPFASGTMSMLVLLPDEVSGLEQLESIIN
FEKLTEWTSSNVMEERKIKVYLPRMKMEEKYNLTSVLMAMGITDVFSSSANLSGISSAESLKISQ
AVHAAHAEINEAGREVVGSAEAGVDAASVSEEFRADHPFLFCIKHIATNAVLFFGRCVSP
>g1as4.1 e.1.1.1 (A:,B:) Antichymotrypsin, alpha-1 {Human (Homo
sapiens)}
GLASANVDFAFSLYKQLVLKAPDKNVIFSPLSISTALAFLSLGAHNTTLTEILKGLKFNLTETSE
AEIHQSFQHLLRTLNQSSDELQLSMGNAMFVKEQLSLLDRFTEDAKRLYGSEAFATDFQDSAAAK
KLINDYVKNGTRGKITDLIKDLDSQTMMVLVNYIFFKAKWEMPFDPQDTHQSRFYLSKKKWVMVP
MMSLHHLTIPYFRDEELSCTVVELKYTGNASALFILPDQDKMEEVEAMLLPETLKRWRDSLEFRE
IGELYLPKFSISRDYNLNDILLQLGIEEAFTSKADLSGITGARNLAVSQVVHKAVLDVFEEGTEA
SRATAVKITLLXGTIVRFNRPFLMIIVPTDTQNIFFMSKVTNPKQ
>d1qlpa_ e.1.1.1 (A:) Antitrypsin, alpha-1 {Human (Homo sapiens)}
FNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEI
PEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEE
AKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVK
VPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRR
SASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEA
AGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK
>d1atta_ e.1.1.1 (A:) Antithrombin {Cow (Bos taurus)}
VEDVCTAKPRDIPVNPMCIYRATEGQGSEQKIPGATNRRVWELSKANSHFATAFYQHLADSKNNN
DNIFLSPLSISTAFAMTKLGACNNTLTQLMEVFKFDTISEKTSDQIHFFFAKLNCRLYRKANKSS
ELVSANRLFGDKSITFNETYQDISEVVYGAKLQPLDFKGNAEQSRLTINQWISNKTEGRITDVIP
PQAINEFTVLVLVNTIYFKGLWKSKFSPENTRKELFYKADGESCSVLMMYQESKFRYRRVAESTQ
VLELPFKGDDITMVLILPKLEKTLAKVEQELTPDMLQEWLDELTETLLVVHMPRFRIEDSFSVKE
QLQDMGLEDLFSPEKSRLPGIVAEGRSDLYVSDAFHKAFLEVNEEGSEAAASTVISIAGRSLRVT
FKANRPFLVLIREVALNTIIFMGRVANPCVD
>d1e05i_ e.1.1.1 (I:) Antithrombin {Human (Homo sapiens)}
SPVDICTAKPRDIPMNPMCIYRSPEKKATEDEGSEQKIPEATNRRVWELSKANSRFATTFYQHLA
DSKNDNDNIFLSPLSISTAFAMTKLGACNDTLQQLMEVFKFDTISEKTSDQIHFFFAKLNCRLYR
KANKSSKLVSANRLFGDKSLTFNETYQDISELVYGAKLQPLDFKENAEQSRAAINKWVSNKTEGR
ITDVIPSEAINELTVLVLVNTIYFKGLWKSKFSPENTRKELFYKADGESCSASMMYQEGKFRYRR
VAEGTQVLELPFKGDDITMVLILPKPEKSLAKVEKELTPEVLQEWLDELEEMMLVVHMPRFRIED
GFSLKEQLQDMGLVDLFSPEKSKLPGIVAEGRDDLYVSDAFHKAFLEVNEEGSEAAASTAVVIAG
RSLNPNRVTFKANRPFLVFIREVPLNTIIFMGRVANPCV
>d1a7ca_ e.1.1.1 (A:) Plasminogen activator inhibitor-1 {Human (Homo
sapiens)}
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HHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPYGVASVLAMLQLTTGGETQQQIQAAMGFKI
DDKGMAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFMPHFFRLFRSTVKQVDFSEVER
ARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNGQWKTPFPDSSTHRRLFHKSDGST
VSVPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISH
WKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKI
EVNESGTVESSSTAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP
>d1by7a_ e.1.1.1 (A:) Plasminogen activator inhibitor-2 {Human (Homo
sapiens)}
EDLCVANTLFALNLFKHLAKASPTQNLFLSPWSISSTMAMVYMGSRGSTEDQMAKVLQFNEVGAA
ADKIHSSFRSLSSAINASTGNYLLESVNKLFGEKSASFREEYIRLCQKYYSSEPQAVDFLECAEE
ARKKINSWVKTQTKGKIPNLLPEGSVDGDTRMVLVNAVYFKGKWKTPFEKKLNGLYPFRVNSAQR
TPVQMMYLREKLNIGYIEDLKAQILELPYAGDVSMFLLLPDEIADVSTGLELLESEITYDKLNKW
TSKDKMAEDEVEVYIPQFKLEEHYELRSILRSMGMEDAFNKGRANFSGMSERNDLFLSEVFHQAM
VDVNEEGTEAAAGTGGVMTGRTGHGGPQFVADHPFLFLIMHKITNCILFFGRFSSP
>g1jjo.1 e.1.1.1 (A:,C:,E:) Neuroserpin {Mouse (Mus musculus)}
TITEWSVNMYNHLRGTGEDENILFSPLSIALAMGMMELGAXENQYVMKLANSLFVQNGFHVNEEF
LQMLKMYFNAEVNHVDFSQNVAVANSINKWVENYTNSLLKDLVSPEDFDGVTNLALINAVYFKGN
WKSQFRPENTRTFSFTKDDESEVQIPMMYQQGEFYYGEFSDGSNEAGGIYQVLEIPYEGDEISMM
LALSRQEVPLATLEPLLKAQLIEEWANSVKKQKVEVYLPRFTVEQEIDLKDILKALGVTEIFIKD
ANLTAMSDKKELFLSKAVHKSCIEVNEEGSEAAAASGMIAISXYPQVIVDHPFLYLIRNRKSGII
LFMGRVMNPHH
>d1sek__ e.1.1.1 (-) Serpin K {Tobacco hawkmoth (Manduca sexta)}
GETDLQKILRESNDQFTAQMFSEVVKANPGQNVVLSAFSVLPPLGQLALASVGESHDELLRALAL
PNDNVTKDVFADLNRGVRAVKGVDLKMASKIYVAKGLELNDDFAAVSRDVFGSEVQNVDFVKSVE
AAGAINKWVEDQTNNRIKNLVDPDALDETTRSVLVNAIYFKGSWKDKFNKERTMDRDFHVSKDKT
IKVPTMIGKKDVRYADVPELDAKMIEMSYEGDQASMIIILPNQVDGITALEQKLKDPKALSRAEE
RLYNTEVEIYLPKFKIETTTDLKEVLSNMNIKKLFTPGAARLENLLKTKESLYVDAAIQKAFIEV
NEEGAEAAAANAFKITTYSFHFVPKVEINKPFFFSLKYNRNSMFSGVCVQP
>d1k9oi_ e.1.1.1 (I:) Alaserpin (serpin 1) {Tobacco hornworm (Manduca
sexta)}
GETDLQKILRESNDQFTAQMFSEVVKANPGQNVVLSAFSVLPPLGQLALASVGESHDELLRALAL
PNDNVTKDVFADLNRGVRAVKGVDLKMASKIYVAKGLELNDDFAAVSRDVFGSEVQNVDFVKSVE
AAGAINKWVEDQTNNRIKNLVDPDALDETTRSVLVNAIYFKGSWKDKFVKERTMDRDFHVSKDKT
IKVPTMIGKKDVRYADVPELDAKMIEMSYEGDQASMIIILPNQVDGITALEQKLKDPKALSRAEE
RLYNTEVEITLPKFKIETTTDLKEVLSNMNIKKLFTPGAARLENLLKTKESLTVDAAIQKAFIEV
NEEGAEAAAANAFGIVPKSLILYPEVHIDRPFYFELKIDGIPMFNGKVIEP
>g1f0c.1 e.1.1.1 (A:,B:) Viral serpin crmA (cytokine response modifier
protein) {Cowpox virus}
MDIFREIASSMKGENVFISPPSISSVLTILYYGANGSTAEQLSKYVEKEADKNKDDISFKSMNKV
YGRYSAVFKDSFLRKIGDNFQTVDFTDCRTVDAINKCVDIFTEGKINPLLDEPLSPDTCLLAISA
VYFKAKWLMPFEKEFTSDYPFYVSPTEMVDVSMMSMYGEAFNHASVKESFGNFSIIELPYVGDTS
MVVILPDNIDGLESIEQNLTDTNFKKWCDSMDAMFIDVHIPKFKVTGSYNLVDALVKLGLTEVFG
STGDYSNMCNSDVSVDAMIHKTYIDVNEEYTEAAAATCALVADCAXSTVTNEFCADHPFIYVIRH
VDGKILFVGRYCSPTTN
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>d1imva_ e.1.1.1 (A:) Rigment epithelium-derived factor, PEDF {Human (Homo sapiens)}
TGALVEEEDPFFKVPVNKLAAAVSNFGYDLYRVRSSMSPTTNVLLSPLSVATALSALSLGADERT
ESIIHRALYYDLISSPDIHGTYKELLDTVTAPQKNLKSASRIVFEKKLRIKSSFVAPLEKSYGTR
PRVLTGNPRLDLQEINNWVQAQMKGKLARSTKEIPDEISILLLGVAHFKGQWVTKFDSRKTSLED
FYLDEERTVRVPMMSDPKAVLRYGLDSDLSCKIAQLPLTGSMSIIFFLPLKVTQNLTLIEESLTS
EFIHDIDRELKTVQAVLTVPKLKLSYEGEVTKSLQEMKLQSLFDSPDFSKITGKPIKLTQVEHRA
GFEWNEDGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRDTDTGALLFIGKILDPRGP
>d1ecra_ e.2.1.1 (A:) Replication terminator protein (Tus) {Escherichia coli}
DLVDRLNTTFRQMEQELAIFAAHLEQHKLLVARVFSLPEVKKEDEHNPLNRIEVKQHLGNDAQSL
ALRHFRHLFIQQQSENRSSKAAVRLPGVLCYQVDNLSQAALVSHIQHINKLKTTFEHIVTVESEL
PTAARFEWVHRHLPGLITLNAYRTLTVLHDPATLRFGWANKHIIKNLHRDEVLAQLEKSLKSPRS
VAPWTREEWQRKLEREYQDIAALPQNAKLKIKRPVKVQPIARVWYKGDQKQVQHACPTPLIALIN
RDNGAGVPDVGELLNYDADNVQHRYKPQAQPLRLIIPRLHLYVAD
>d1es5a_ e.3.1.1 (A:) D-ala carboxypeptidase/transpeptidase {Streptomyces sp., K15}
KPTIAAVGGYAMNNGTGTTLYTKAADTRRSTGSTTKIMTAKVVLAQSNLNLDAKVTIQKAYSDYV
VANNASQAHLIVGDKVTVRQLLYGLMLPSGCDAAYALADKYGSGSTRAARVKSFIGKMNTAATNL
GLHNTHFDSFDGIGNGANYSTPRDLTKIASSAMKNSTFRTVVKTKAYTAKTVTKTGSIRTMDTWK
NTNGLLSSYSGAIGVKTGAGPEAKYCLVFAATRGGKTVIGTVLASTSIPARESDATKIMNYGFAL
>d1hvba_ e.3.1.1 (A:) D-ala carboxypeptidase/transpeptidase {Streptomyces sp., R61}
DLPAPDDTGLQAVLHTALSQGAPGAMVRVDDNGTIHQLSEGVADRATGRAITTTDRFRVGSVTKS
FSAVVLLQLVDEGKLDLDASVNTYLPGLLPDDRITVRQVMSHRSGLYDYTNDMFAQTVPGFESVR
NKVFSYQDLITLSLKHGVTNAPGAAYSYSNTNFVVAGMLIEKLTGHSVATEYQNRIFTPLNLTDT
FYVHPDTVIPGTHANGYLTPDEAGGALVDSTEQTVSWAQSAGAVISSTQDLDTFFSALMSGQLMS
AAQLAQMQQWTTVNSTQGYGLGLRRRDLSCGISVYGHTGTVQGYYTYAFASKDGKRSVTALANTS
NNVNVLNTMARTLESAFCGKP
>d1ci9a_ e.3.1.1 (A:) Esterase EstB {Burkholderia gladioli}
AASLAARLDAVFDQALRERRLVGAVAIVARHGEILYRRAQGLADREAGRPMREDTLFRLASVTKP
IVALAVLRLVARGELALDAPVTRWLPEFRPRLADGSEPLVTIHHLLTHTSGLGYWLLEGAGSVYD
RLGISDGIDLRDFDLDENLRRLASAPLSFAPGSGWQYSLALDVLGAVVERATGQPLAAAVDALVA
QPLGMRDCGFVSAEPERFAVPYHDGQPEPVRMRDGIEVPLPEGHGAAVRFAPSRVFEPGAYPSGG
AGMYGSADDVLRALEAIRANPGFLPETLADAARRDQAGVGAETRGPGWGFGYLSAVLDDPAAAGT
PQHAGTLQWGGVYGHSWFVDRALGLSVLLLTNTAYEGMSGPLTIALRDAVYA
>d1btl__ e.3.1.1 (-) beta-Lactamase, class A {Escherichia coli, TEM-1}
HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRIDAGQEQ
LGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNM
GDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPL
LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIAEIGASLI
KHW
>d1bza__ e.3.1.1 (-) beta-Lactamase, class A {Escherichia coli, TOHO-1}
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SVQQQLEALEKSSGGRLGVALINTADNSQILYRADERFAMCSTSKVMAAAAVLKQSESDKHLLNQ
RVEIKKSDLVNYNPIAEKHVNGTMTLAELGAAALQYSDNTAMNKLIAHLGGPDKVTAFARSLGDE
TFRLDRTAPTLNTAIPGDPRDTTTPLAMAQTLKNLTLGKALAETQRAQLVTWLKGNTTGSASIRA
GLPKSWVVGDKTGSGDYGTTNDIAVIWPENHAPLVLVTYFTQPEQKAERRRDILAAAAKIVT
>d1g56a_ e.3.1.1 (A:) beta-Lactamase, class A {Klebsiella pneumoniae,
SHV-1}
SPQPLEQIKLSESQLSGRVGMIEMDLASGRTLTAWRADERFPMMSTFKVVLCGAVLARVDAGDEQ
LERKIHYRQQDLVDYSPVSEKHLADGMTVGELCAAAITMSDNSAANLLLATVGGPAGLTAFLRQI
GDNVTRLDRWETELNEALPGDARDTTTPASMAATLRKLLTSQRLSARSQRQLLQWMVDDRVAGPL
IRSVLPAGWFIADKTGAGERGARGIVALLGPNNKAERIVVIYLRDTPASMAERNQQIAGIGAALI
EHWQR
>d1g6aa_ e.3.1.1 (A:) beta-Lactamase, class A {Pseudomonas aeruginosa,
PSE-4 carbenicillinase}
SKFQQVEQDVKAIEVSLSARIGVSVLDTQNGEYWDYNGNQRFPLTSTFKTIACAKLLYDAEQGKV
NPNSTVEIKKADLVTYSPVIEKQVGQAITLDDACFATMTTSDNTAANIILSAVGGPKGVTDFLRQ
IGDKETRLDRIEPDLNEGKLGDLRDTTTPKAIASTLNKFLFGSALSEMNQKKLESWMVNNQVTGN
LLRSVLPAGWNIADKSGAGGFGARSITAVVWSEHQAPIIVSIYLAQTQASMEERNDAIVKIGHSI
FDVYTS
>d1alq__ e.3.1.1 (-) beta-Lactamase, class A {Staphylococcus aureus}
SEPIVLVIFTNKDNKSDKPNDKLISETAKSVMKEFAAGSKNAAKELNDLEKKYNAHIGVYALDTK
SGKEVKFNSDKRFAYASTSKAINSAILLEQVPYNKLNKKVHINKDDIVAYSPILEKYVGKDITLK
ALIEASMTYSDNTANNKIIKEIGGIKKVKQRLKELGDKVTNPVRYEIELNYYSPKSKKDTSTPAA
FGKTLNKLIANGKLSKENKKFLLDLMLNNKSGDTLIKDGVPKDYKVADKSGQAITYASRNDVAFV
YPK
>d1ghpa_ e.3.1.1 (A:) beta-Lactamase, class A {Staphylococcus aureus}
KELNDLEKKYNAHIGVYALDTKSGKEVKFNSDKRFAYASTSKAINSAILLEQVPYNKLNKKVHIN
KDDIVAYSPILEKYVGKDITLKALIEASMTYSDNTANNKIIKEIGGIKKVKQRLKELGDKVTNPV
RYDIELQYYSPKSKKDTSTPAAFGKTLNKLIANGKLSKENKKFLLDLMLNNKSGDTLIKDGVPKD
YKVADKSGQAITYASRNDVAFVYPKGQSEPIVLVIFTNKDNKSDKPNDKLISETAKSVMKEF
>d4blma_ e.3.1.1 (A:) beta-Lactamase, class A {Bacillus
licheniformis}
DDFAKLEEQFDAKLGIFALDTGTNRTVAYRPDERFAFASTIKALTVGVLLQQKSIEDLNQRITYT
RDDLVNYNPITEKHVDTGMTLKELADASLRYSDNAAQNLILKQIGGPESLKKELRKIGDEVTNPE
RFEPELNEVNPGETQDTSTARALVTSLRAFALEDKLPSEKRELLIDWMKRNTTGDALIRAGVPDG
WEVADKTGAASYGTRNDIAIIWPPKGDPVVLAVLSSRDKKDAKYDDKLIAEATKVVMKALN
>d1buea_ e.3.1.1 (A:) beta-Lactamase, class A {Enterobacter cloacae,
NMC-A carbapenemase}
NTKGIDEIKNLETDFNGRIGVYALDTGSGKSFSYRANERFPLCSSFKGFLAAAVLKGSQDNRLNL
NQIVNYNTRSLEFHSPITTKYKDNGMSLGDMAAAALQYSDNGATNIILERYIGGPEGMTKFMRSI
GDEDFRLDRWELDLNTAIPGDERDTSTPAAVAKSLKTLALGNILSEHEKETYQTWLKGNTTGAAR
IRASVPSDWVVGDKTGSCGAYGTANDYAVVWPKNRAPLIISVYTTKNEKEAKHEDKVIAEASRIA
IDNLK
>d1bsg__ e.3.1.1 (-) beta-Lactamase, class A {Streptomyces albus G}
SDAERRLAGLERASGARLGVYAYDTGSGRTVAYRADELFPMCSVFKTLSSAAVLRDLDRNGEFLS
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RRILYTQDDVEQADGAPETGKPQNLANGMTVEELCEVSITASDNCAANLMLRELGGPAAVTRFVR
SLGDRVTRLDRWEPELNSAEPGRVTDTTSPRAITRTYGRLVLGDALNPRDRRLLTSWLLANTTSG
DRFRAGLPDDWTLGDKTGAGRYGTNNDAGVTWPPGRAPIVLTVLTAKTEQDAARDDGLVADAARV
LAETLG
>d1mfoa_ e.3.1.1 (A:) beta-Lactamase, class A {Mycobacterium
fortuitum}
APIDDQLAELERRDNVLIGLYAANLQSGRRITHRPDEMFAMCSTFKGYVAARVLQMAEHGEISLD
NRVFVDADALVPNSPVTEARAGAEMTLAELCQAALQRSDNTAANLLLKTIGGPAAVTAFARSVGD
ERTRLDRWEVELNSAIPGDPRDTSTPAALAVGYRAILAGDALSPPQRGLLEDWMRANQTSSMRAG
LPEGWTTADKTGSGDYGSTNDAGIAFGPDGQRLLLVMMTRSQAHDPKAENLRPLIGELTALVLPS
LL
>d1e25a_ e.3.1.1 (A:) beta-Lactamase, class A {Pseudomonas aeruginosa,
PER-1}
SPLLKEQIESIVIGKKATVGVAVWGPDDLEPLLINPFEKFPMQSVFKLHLAMLVLHQVDQGKLDL
NQTVIVNRAKVLQNTWAPIMKAYQGDEFSVPVQQLLQYSVSHSDNVACDLLFELVGGPAALHDYI
QSMGIKETAVVANEAQMHADDQVQYQNWTSMKGAAEILKKFEQKTQLSETSQALLWKWMVETTTG
PERLKGLLPAGTVVAHKTGTSQIKAGKTAATNDLGIILLPDGRPLLVAVFVKDSAESSRTNEAII
AQVAQTAYQFELKKLSAL
>d1dy6a_ e.3.1.1 (A:) beta-Lactamase, class A {Serratia marcescens,
Sme-1}
NKSDAAAKQIKKLEEDFDGRIGVFAIDTGSGNTFGYRSDERFPLCSSFKGFLAAAVLERVQQKKL
DINQKVKYESRDLEYHSPITTKYKGSGMTLGDMASAALQYSDNGATNIIMERFLGGPEGMTKFMR
SIGDNEFRLDRWELELNTAIPGDKRDTSTPKAVANSLNKLALGNVLNAKVKAIYQNWLKGNTTGD
ARIRASVPADWVVGDKTGSCGAYGTANDYAVIWPKNRAPLIVSIYTTRKSKDDKHSDKTIAEASR
IAIQAID
>d1fr1a_ e.3.1.1 (A:) AMPC beta-Lactamase, class C {Citrobacter
freundii}
AAKTEQQIADIVNRTITPLMQEQAIPGMAVAIIYQGKPYYFTWGKADIANNRPVTQQTLFELGSV
SKTFNGVLGGDAIARGEIKLSDPVTQYWPELTGKQWQGISLLHLATYTAGGLPLQVPDDVTDKAA
LLRFYQNWQPQWAPGAKRLYANSSIGLFGALAVKPSGMSYEEAMSKRVLHPLKLAHTWITVPQSE
QKDYAWGYREGKPVHVSPGQLDAEAYGVKSSVIDMTRWVQANMDASQVQEKTLQQGIELAQSRYW
RIGDMYQGLGWEMLNWPVKADSIISGSDSKVALAALPAVEVNPPAPAVKASWVHKTGSTGGFGSY
VAFVPEKNLGIVMLANKSYPNPVRVEAAWRILEKLQ
>d1ga0a_ e.3.1.1 (A:) AMPC beta-Lactamase, class C {Enterobacter
cloacae, P99, cephalosporinase}
PVSEKQLAEVVANTVTPLMKAQSVPGMAVAVIYQGKPHYYTFGKADIAANKPVTPQTLFELGSIS
KTFTGVLGGDAIARGEISLDDPVTRYWPQLTGKQWQGIRMLDLATYTAGGLPLQVPDEVTDNASL
LRFYQNWQPQWKPGTTRLYANASIGLFGALAVKPSGMPYEQAMTTRVLKPLKLDHTWINVPKAEE
AHYAWGYRDGKAVRAVRVSPGMLDAQAYGVKTNVQDMANWVMANMAPENVADASLKQGIALAQSR
YWRIGSMYQGLGWEMLNWPVEANTVVEGSDSKVALAPLPVAEVNPPAPPVKASWVHKTGSTGGFG
SYVAFIPEKQIGIVMLANTSYPNPARVEAAYHILEALQ
>d1i5qa_ e.3.1.1 (A:) AMPC beta-Lactamase, class C {Escherichia coli,
cephalosporinase}
APQQINDIVHRTITPLIEQQKIPGMAVAVIYQGKPYYFTWGYADIAKKQPVTQQTLFELGSVSKT
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FTGVLGGDAIARGEIKLSDPTTKYWPELTAKQWNGITLLHLATYTAGGLPLQVPDEVKSSSDLLR
FYQNWQPAWAPGTQRLYAASSIGLFGALAVKPSGLSFEQAMQTRVFQPLKLNHTWINVPPAEEKN
YAWGYREGKAVHVSPGALDAEAYGVKSTIEDMARWVQSNLKPLDINEKTLQQGIQLAQSRYWQTG
DMYQGLGWEMLDWPVNPDSIINGSDNKIALAARPVKAITPPTPAVRASWVHKTGATGGFGSYVAF
IPEKELGIVMLANKNYPNPARVDAAWQILNALQ
>d1k55a_ e.3.1.1 (A:) Class D beta-lactamase {Pseudomonas aeruginosa, OXA-10}
SITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNDLARASKEYLPASTFKIPNAIIGLETGVIKN
EHQVFKWDGKPRAMKQWERDLTLRGAIQVSAVPVFQQIAREVGEVRMQKYLKKFSYGNQNISGGI
DKFWLEGQLRISAVNQVEFLESLYLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTES
NPGVAWWVGWVEKETEVYFFAFNMDIDNESKLPLRKSIPTKIMESEGIIG
>d1k25a4 e.3.1.1 (A:264-631) Penicillin-binding protein 2x (pbp-2x), transpeptidase domain {Streptococcus pneumoniae}
TLSSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKEGITEDFVWRDIL
YQSNYEPGSAMKVMTLASSIDNNTFPSGEYFNSSELKIADATTRDWDVNEGLTTGGMMTFLQGFA
HSSNVGMSLLEQKMGDATWLDYLKRFKFGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQ
TQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVSKEAASTTRNHMILVGTDPL
YGTMYNHYTGKPIITVPGQNVAVKSGTAQIADEKNGGYLVGSTNYIFSAVTMNPAENPDFILYVT
VQQPEHYSGIQLGEFATPILERASAMKESLNLQSPAKNLDKVT
>d1qmea4 e.3.1.1 (A:264-620) Penicillin-binding protein 2x (pbp-2x), transpeptidase domain {Streptococcus pneumoniae}
TISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDIL
YQSNYEPGSTMKVMMLAAAIDNNTFPGGEVFNSSELKIADATIRDWDVNEGLTGGRMMTFSQGFA
HSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQ
TQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKDAASLTRTNMVLVGTDPV
YGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVT
VQQPEHYSGIQLGEFANPILERASAMKDSLNL
>d1hd8a2 e.3.1.1 (A:3-262) Penicillin-binding protein 5, N-terminal domain {Escherichia coli}
LNIKTMIPGVPQIDAESYILIDYNSGKVLAEQNADVRRDPASLTKMMTSYVIGQAMKAGKFKETD
LVTIGNDAWATGNPVFKGSSLMFLKPGMQVPVSQLIRDINLQSGNDACVAMADFAAGSQDAFVGL
MNSYVNALGLKNTHFQTVHGLDADGQYSSARDMALIGQALIRDVPNEYSIYKEKEFTFNGIRQLN
RNGLLWDNSLNVDGIKTGHTDKAGYNLVASATEGQMRLISAVMGGRTFKGREAESKKLLTWGFRF
>d1ei5a3 e.3.1.1 (A:3-335) D-aminopeptidase, N-terminal domain {Ochrobactrum anthropi}
KFDTSALEAFVRHIPQNYKGPGGVVAVVKDGEVVLQHAWGFADLRTRTPMTLDTRMPICSVSKQF
TCAVLLDAVGEPELLDDALEAYLDKFEDERPAVRDLCNNQSGLRDYWALSVLCGADPEGVFLPAQ
AQSLLRRLKTTHFEPGSHYSYCNGNFRILADLIEAHTGRTLVDILSERIFAPAGMKRAELISDTA
LFDECTGYEGDTVRGFLPATNRIQWMGDAGICASLNDMIAWEQFIDATRDDESGLYRRLSGPQTF
KDGVAAPYGFGLNLHETGGKRLTGHGGALRGWRCQRWHCADERLSTIAMFNFEGGASEVAFKLMN
IALGVSSS
>d1lbea_ e.4.1.1 (A:) ADP ribosyl cyclase {Sea hare (Aplysia californica)}
IVPTRELENVFLGRCKDYEITRYLDILPRVRSDCSALWKDFFKAFSFKNPCDLDLGSYKDFFTSA
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QQQLPKNKVMFWSGVYDEAHDYANTGRKYITLEDTLPGYMLNSLVWCGQRANPGFNEKVCPDFKT
CPVQARESFWGMASSSYAHSAEGEVTYMVDGSNPKVPAYRPDSFFGKYELPNLTNKVTRVKVIVL
HRLGEKIIEKCGAGSLLDLEKLVKAKHFAFDCVENPRAVLFLLCSDNPNARECRL
>d4blca_ e.5.1.1 (A:) Catalase I {Cow (Bos taurus)}
NRDPASDQMKHWKEQRAAQKPDVLTTGGGNPVGDKLNSLTVGPRGPLLVQDVVFTDEMAHFDRER
IPERVVHAKGAGAFGYFEVTHDITRYSKAKVFEHIGKRTPIAVRFSTVAGESGSADTVRDPRGFA
VKFYTEDGNWDLVGNNTPIFFIRDALLFPSFIHSQKRNPQTHLKDPDMVWDFWSLRPESLHQVSF
LFSDRGIPDGHRHMDGYGSHTFKLVNADGEAVYCKFHYKTDQGIKNLSVEDAARLAHEDPDYGLR
DLFNAIATGNYPSWTLYIQVMTFSEAEIFPFNPFDLTKVWPHGDYPLIPVGKLVLNRNPVNYFAE
VEQLAFDPSNMPPGIEPSPDKMLQGRLFAYPDTHRHRLGPNYLQIPVNCPYRARVANYQRDGPMC
MMDNQGGAPNYYPNSFSAPEHQPSALEHRTHFSGDVQRFNSANDDNVTQVRTFYLKVLNEEQRKR
LCENIAGHLKDAQLFIQKKAVKNFSDVHPEYGSRIQALLDKYNE
>d1dgfa_ e.5.1.1 (A:) Catalase I {Human (Homo sapiens)}
RDPASDQMQHWKEQRAAQKADVLTTGAGNPVGDKLNVITVGPRGPLLVQDVVFTDEMAHFDRERI
PERVVHAKGAGAFGYFEVTHDITKYSKAKVFEHIGKKTPIAVRFSTVAGESGSADTVRDPRGFAV
KFYTEDGNWDLVGNNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLRPESLHQVSFL
FSDRGIPDGHRHMNGYGSHTFKLVNANGEAVYCKFHYKTDQGIKNLSVEDAARLSQEDPDYGIRD
LFNAIATGKYPSWTFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNRNPVNYFAEV
EQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHRLGPNYLHIPVNCPYRARVANYQRDGPMCM
QDNQGGAPNYYPNSFGAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNEEQRKRL
CENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALLDKYN
>d1a4ea_ e.5.1.1 (A:) Catalase I {Baker's yeast (Saccharomyces
cerevisiae)}
DVREDRVVTNSTGNPINEPFVTQRIGEHGPLLLQDYNLIDSLAHFNRENIPQRNPHAHGSGAFGY
FEVTDDITDICGSAMFSKIGKRTKCLTRFSTVGGDKGSADTVRDPRGFATKFYTEEGNLDWVYNN
TPVFFIRDPSKFPHFIHTQKRNPQTNLRDADMFWDFLTTPENQVAIHQVMILFSDRGTPANYRSM
HGYSGHTYKWSNKNGDWHYVQVHIKTDQGIKNLTIEEATKIAGSNPDYCQQDLFEAIQNGNYPSW
TVYIQTMTERDAKKLPFSVFDLTKVWPQGQFPLRRVGKIVLNENPLNFFAQVEQAAFAPSTTVPY
QEASADPVLQARLFSYADAHRYRLGPNFHQIPVNCPYASKFFNPAIRDGPMNVNGNFGSEPTYLA
NDKSYTYIQQDRPIQQHQEVWNGPAIPYHWATSPGDVDFVQARNLYRVLGKQPGQQKNLAYNIGI
HVEGACPQIQQRVYDMFARVDKGLSEAIKKVAE
>d1e93a_ e.5.1.1 (A:) Catalase I {Proteus mirabilis}
KKLTTAAGAPVVDNNNVITAGPRGPMLLQDVWFLEKLAHFDREVIPERRMHAKGSGAFGTFTVTH
DITKYTRAKIFSEVGKKTEMFARFSTVAGERGAADAERDIRGFALKFYTEEGNWDMVGNNTPVFY
LRDPLKFPDLNHIVKRDPRTNMRNMAYKWDFFSHLPESLHQLTIDMSDRGLPLSYRFVHGFGSHT
YSFINKDNERFWVKFHFRCQQGIKNLMDDEAEALVGKDRESSQRDLFEAIKRGDYPRWKLQIQIM
PEKEASTVPYNPFDLTKVWPHADYPLMDVGYFELNRNPDNYFSDVEQAAFSPANIVPGISFSPDK
MLQGRLFSYGDAHRYRLGVNHHQIPVNAPKCPFHNYHRDGAMRVDGNSGNGITYEPNSGGVFQEQ
PDFKEPPLSIEGAADHWNHREDEDYFSQPRALYELLSDDEHQRMFARIAGELSQASKETQQRQID
LFTKVHPEYGAGVEKAIKVLE
>d1hbza_ e.5.1.1 (A:) Catalase I {Micrococcus lysodeikticus}
TTPHATGSTRQNGAPAVSDRQSLTVGSEGPIVLHDTHLLETHQHFNRMNIPERRPHAKGSGAFGE
FEVTEDVSKYTKALVFQPGTKTETLLRFSTVAGELGSPDTWRDVRGFALRFYTEEGNYDLVGNNT
PIFFLRDPMKFTHFIRSQKRLPDSGLRDATMQWDFWTNNPESAHQVTYLMGPRGLPRTWREMNGY
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GSHTYLWVNAQGEKHWVKYHFISQQGVHNLSNDEATKIAGENADFHRQDLFESIAKGDHPKWDLY
IQAIPYEEGKTYRFNPFDLTKTISQKDYPRIKVGTLTLNRNPKNHFAQIESAAFSPSNTVPGIGL
SPDRMLLGRAFAYHDAQLYRVGAHVNQLPVNRPKNAVHNYAFEGQMWYDHTGDRSTYVPNSNGDS
WSDETGPVDDGWEADGTLTREAQALRADDDDFGQAGTLVREVFSDQERDDFVETVAGALKGVRQD
VQARAFEYWKNVDATIGQRIEDEVKRHEGDGIPGVEAGGEARI
>d1cf9a2 e.5.1.1 (A:27-597) Catalase II {Escherichia coli, HPII}
DSLAPEDGSHRPAAEPTPPGAQPTAPGSLKAPDTRNEKLNSLEDVRKGSENYALTTNQGVRIADD
QNSLRAGSRGPTLLEDFILREKITHFDHERIPERIVHARGSAAHGYFQPYKSLSDITKADFLSDP
NKITPVFVRFSTCQGGAGSADTVRDIRGFATKFYTEEGIFDLVGNNTPIFFIQDAHKFPDFVHAV
KPEPHWAIPQGQSAHDTFWDYVSLQPETLHNVMWAMSDRGIPRSYRTMEGFGIHTFRLINAEGKA
TFVRFHWKPLAGKASLVWDEAQKLTGRDPDFHRRELWEAIEAGDFPEYELGFQLIPEEDEFKFDF
DLLDPTKLIPEELVPVQRVGKMVLNRNPDNFFAENEQAAFHPGHIVPGLDFTNDPLLQGRLFSYT
DTQISRLGGPNFHEIPINRPTCPYHNFQRDGMHRMGIDTNPANYEPNSINDNWPRETPPGPKRGG
FESYQERVEGNKVRERSPSFGEYYSHPRLFWLSQTPFEQRHIVDGFSFELSKVVRPYIRERVVDQ
LAHIDLTLAQAVAKNLGIELTDDQLNITPPPDVNGLKKDPSLSLYAIPDGD
>d1buca2 e.6.1.1 (A:1-232) Butyryl-CoA dehydrogenase {Megasphaera elsdenii}
MDFNLTDIQQDFLKLAHDFGEKKLAPTVTERDHKGIYDKELIDELLSLGITGAYFEEKYGGSGDD
GGDVLSYILAVEELAKYDAGVAITLSATVSLCANPIWQFGTEAQKEKFLVPLVEGTKLGAFGLTE
PNAGTDASGQQTIATKNDDGTYTLNGSKIFITNGGAADIYIVFAMTDKSKGNHGITAFILEDGTP
GFTYGKKEDKMGIHTSQTMELVFQDVKVPAENMLGEE
>d1jqia2 e.6.1.1 (A:4-234) Butyryl-CoA dehydrogenase {Rat (Rattus norvegicus)}
VYQSVELPETHQMLRQTCRDFAEKELVPIAAQLDKEHLFPTSQVKKMGELGLLAMDVPEELSGAG
LDYLAYSIALEEISRGCASTGVIMSVNNSLYLGPILKFGSSQQKQQWITPFTNGDKIGCFALSEP
GNGSDAGAASTTAREEGDSWVLNGTKAWITNSWEASATVVFASTDRSRQNKGISAFLVPMPTPGL
TLGKKEDKLGIRASSTANLIFEDCRIPKENLLGEPG
>d3mdda2 e.6.1.1 (A:11-241) Medium chain acyl-CoA dehydrogenase {Pig (Sus scrofa)}
GFSFELTEQQKEFQATARKFAREEIIPVAAEYDRTGEYPVPLLKRAWELGLMNTHIPESFGGLGL
GIIDSCLITEELAYGCTGVQTAIEANTLGQVPLIIGGNYQQQKKYLGRMTEEPLMCAYCVTEPGA
GSDVAGIKTKAEKKGDEYIINGQKMWITNGGKANWYFLLARSDPDPKAPASKAFTGFIVEADTPG
VQIGRKEINMGQRCSDTRGIVFEDVRVPKENVLTGE
>d1egda2 e.6.1.1 (A:10-241) Medium chain acyl-CoA dehydrogenase {Human (Homo sapiens)}
LGFSFEFTEQQKEFQATARKFAREEIIPVAAEYDKTGEYPVPLIRRAWELGLMNTHIPENCGGLG
LGTFDACLISEELAYGCTGVQTAIEGNSLGQMPIIIAGNDQQKKKYLGRMTEEPLMCAYCVTEPG
AGSDVAGIKTKAEKKGDEYIINGQKMWITNGGKANWYFLLARSDPDPKAPANKAFTGFIVEADTP
GIQIGRKELNMGQRCSDTRGIVFEDVKVPKENVLIGD
>d1ivha2 e.6.1.1 (A:6-241) Isovaleryl-coa dehydrogenase {Human (Homo sapiens)}
VDDAINGLSEEQRQLRQTMAKFLQEHLAPKAQEIDRSNEFKNLREFWKQLGNLGVLGITAPVQYG
GSGLGYLEHVLVMEEISRASGAVGLSYGAHSNLCINQLVRNGNEAQKEKYLPKLISGEYIGALAM
SEPNAGSDVVSMKLKAEKKGNHYILNGNKFWITNGPDADVLIVYAKTDLAAVPASRGITAFIVEK

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GMPGFSTSKKLDKLGMRGSNTCELIFEDCKIPAANILGHEN
>d1frpa_ e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Pig (Sus scrofa)}
NIVTLTRFVMEQGRKARGTGEMTQLLNSLCTAVKAISTAVRKAGIAHLYGIAGATNVTGDQVKKL
DVLSNDLVINVLKSSFATCVLVTEEDKNAIIVEPEKRGKYVVCFDPLDGSSNIDCLVSIGTIFGI
YRKNSTDEPSEKDALQPGRNLVAAGYALYGSATMLVLAMVNGVNCFMLDPAIGEFILVDRNVKIK
KKGSIYSINEGYAKEFDPAITEYIQRKKFPPDNSAPYGARYVGSMVADVHRTLVYGGIFMYPANK
KSPKGKLRLLYECNPMAYVMEKAGGLATTGKEAVLDIVPTDIHQRAPIILGSPEDVTELLEIYQK
HA
>d1ftaa_ e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Human (Homo
sapiens)}
DVVTLTRFVMEEGRKARGTGELTQLLNSLCTAVKAISSAVRKAGIAHLYGIAGSTNVTGDQVKKL
DVLSNDLVMNMLKSSFATCVLVSEEDKHAIIVEPEKRGKYVVCFDPLDGSSNIDCLVSVGTIFGI
YRKKSTDEPSEKDALQPGRNLVAAGYALYGSATMLVLAMDCGVNCFMLDPAIGEFILVDKDVKIK
KKGKIYSLNEAYAKDFDPAVTEYIQRKKFPPDNSAPYGARYVGSMVADVHRTLVYGGIFLYPANK
KSPNGKLRLLYECNPMAYVMEKAGGMATTGKEAVLDVIPTDIHQRAPIILGSPDDVLEFLKVYEK
HS
>d1bk4a_ e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Rabbit
(Oryctolagus cuniculus)}
FDTDISTMTRFVMEEGRKAGGTGEMTQLLNSLCTAVKAISTAVRKAGIAHLYGIAGSTNVTGDQV
KKLDVLSNDLVMNMLKSSFATCVLVSEEDKNAIIVEPEKRGKYVVCFDPLDGSSNIDCLVSIGTI
FGIYRKKSTDEPSTKDALQPGRNLVAAGYALYGSATMLVLAGGSGVNSFMLDPAIGEFILVDKNV
KIKKKGNIYSLNEGYAKDFDPAVTEYIQKKKFPPDNSSPYGARYVGSMVADVHRTLVYGGIFLYP
ANKKSPDGKLRLLYECNPMAFIMEKAGGMATTGKEAILDIVPTDIHQRAPVILGSPDDVQEFLEI
YKKHAVK
>d1spia_ e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Spinach (Spinacia
oleracea)}
AATQTKARTRSKYEIETLTGWLLKQPMAGVIDAELTIVLSSISLACKQIASLVQRAGISNLTGIQ
GAVNIQGEDQKKLDVVSNEVFSSCLRSSGRTGIIASEEEDVPVAVEESYSGNYIVVFDPLDGSSN
IDAAVSTGSIFGIYSPNDECIVDSDHDDESQLSAEEQRCVVNVCQPGDNLLAAGYCMYSSSVIFV
LTIGKGVYAFTLDPMYGEFVLTSEKIQIPKAGKIYSFNEGNYKMWPDKLKKYMDDLKEPGESQKP
YSSRYIGSLVGDFHRTLLYGGIYGYPRDAKSKNGKLRLLYECAPMSFIVEQAGGKGSDGHQRILD
IQPTEIHQRVPLYIGSVEEVEKLEKYLA
>d1dcua_ e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Garden pea (Pisum
sativum)}
KRSGYEIITLTSWLLQQEQKGIIDAELTIVLSSISMACKQIASLVQRANISNLTGTQGAVNIQGE
DQKKLDVISNEVFSNCLRSSGRTGIIASEEEDVPVAVEESYSGNYIVVFDPLDGSSNLDAAVSTG
SIFGIYSPNDECLPDFGDDSDDNTLGTEEQRCIVNVCQPGSNLLAAGYCMYSSSVIFVLTIGKGV
FVFTLDPLYGEFVLTQENLQIPKSGKIYSFNEGNYKLWDENLKKYIDDLKEPGPSGKPYSARYIG
SLVGDFHRTLLYGGIYGYPRDKKSKNGKLRLLYECAPMSFIVEQAGGKGSDGHQRVLDIQPTEIH
QRVPLYIGSTEEVEKVEKYLA
>d2hhma_ e.7.1.1 (A:) Inositol monophosphatase {Human (Homo sapiens)}
WQECMDYAVTLARQAGEVVCEAIKNEMNVMLKSSPVDLVTATDQKVEKMLISSIKEKYPSHSFIG
EESVAAGEKSILTDNPTWIIDPIDGTTNFVHRFPFVAVSIGFAVNKKIEFGVVYSCVEGKMYTAR
KGKGAFCNGQKLQVSQQEDITKSLLVTELGSSRTPETVRMVLSNMEKLFCIPVHGIRSVGTAAVN
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MCLVATGGADAYYEMGIHCWDVAGAGIIVTEAGGVLMDVTGGPFDLMSRRVIAANNRILAERIAK
EIQVIPLQRDDE
>d1g0ha_ e.7.1.1 (A:) Archaeal inositol monophosphatase/fructose-1,6-bisphosphatase {Archaeon Methanococcus jannaschii, MJ0109}
MKWDEIGKNIAKEIEKEILPYFGRKDKSYVVGTSPSGDETEIFDKISEDIALKYLKSLNVNIVSE
ELGVIDNSSEWTVVIDPIDGSFNFINGIPFFAFCFGVFKNNEPYYGLTYEFLTKSFYEAYKGKGA
YLNGRKIKVKDFNPNNIVISYYPSKKIDLEKLRNKVKRVRIFGAFGLEMCYVAKGTLDAVFDVRP
KVRAVDIASSYIICKEAGALITDENGDELKFDLNATDRLNIIVANSKEMLDIILDLL
>d1inp__ e.7.1.1 (-) Inositol polyphosphate 1-phosphatase {Cow (Bos taurus), brain}
MSDILQELLRVSEKAANIARACRQQETLFQLLIEEKKEGEKNKKFAVDFKTLADVLVQEVIKENM
ENKFPGLGKKIFGEESNELTNDLGEKIIMRLGPTEEETVALLSKVLNGNKLASEALAKVVHQDVF
FSDPALDSVEINIPQDILGIWVDPIDSTYQYIKGSADITPNQGIFPSGLQCVTVLIGVYDIQTGV
PLMGVINQPFVSQDLHTRRWKGQCYWGLSYLGTNIHSLLPPVSTRSNSEAQSQGTQNPSSEGSCR
FSVVISTSEKETIKGALSHVCGERIFRAAGAGYKSLCVILGLADIYIFSEDTTFKWDSCAAHAIL
RAMGGGMVDLKECLERNPDTGLDLPQLVYHVGNEGAAGVDQWANKGGLIAYRSEKQLETFLSRLL
QHLAPVATHT
>d1ka1a_ e.7.1.1 (A:) 3';5'-adenosine bisphosphatase, PAP phosphatase {Baker's yeast (Saccharomyces cerevisiae)}
ALERELLVATQAVRKASLLTKRIQSEVISHKDSTTITKNDNSPVTTGDYAAQTIIINAIKSNFPD
DKVVGEESSSGLSDAFVSGILNEIKANDEVYNKNYKKDDFLFTNDQFPLKSLEDVRQIIDFGNYE
GGRKGRFWCLDPIDGTKGFLRGEQFAVCLALIVDGVVQLGCIGCPNLVLSSYGAQDLKGHESFGY
IFRAVRGLGAFYSPSSDAESWTKIHVRHLKDTKDMITLEGVEKGHSSHDEQTAIKNKLNISKSLH
LDSQAKYCLLALGLADVYLRLPIKLSYQEKIWDHAAGNVIVHEAGGIHTDAMEDVPLDFGNGRTL
ATKGVIASSGPRELHDLVVSTSCDVIQSR
>d1jp4a_ e.7.1.1 (A:) PIPase {Rat (Rattus norvegicus)}
HNVLMRLVASAYSIAQKAGTIVRCVIAEGDLGIVQKTSATDLQTKADRMVQMSICSSLSRKFPKL
TIIGEEDLPPGEVDQELIEDGQSEEILKQPCPSQYSAIKEEDLVVWVDPVDGTKEYTEGLLDNVT
VLIGIAYEGKAIAGIINQPYYNYQAGPDAVLGRTIWGVLGLGAFGFQLKEAPAGKHIITTTRSHS
NKLVTDCIAAMNPDNVLRVGGAGNKIIQLIEGKASAYVFASPGCKKWDTCAPEVILHAVGGKLTD
IHGNPLQYDKEVKHMNSAGVLAALRNYEYYASRVPESVKSALIP
>d1kfsa2 e.8.1.1 (A:519-928) DNA polymerase I (Klenow fragment) {Escherichia coli}
HKGPLNVFENIEMPLVPVLSRIERNGVKIDPKVLHNHSEELTLRLAELEKKAHEIAGEEFNLSST
KQLQTILFEKQGIKPLKKTPGGAPSTSEEVLEELALDYPLPKVILEYRGLAKLKSTYTDKLPLMI
NPKTGRVHTSYHQAVTATGRLSSTDPNLQNIPVRNEEGRRIRQAFIAPEDYVIVSADYSQIELRI
MAHLSRDKGLLTAFAEGKDIHRATAAEVFGLPLETVTSEQRRSAKAINFGLIYGMSAFGLARQLN
IPRKEAQKYMDLYFERYPGVLEYMERTRAQAKEQGYVETLDGRRLYLPDIKSSNGARRAAAERAA
INAPMQGTAADIIKRAMIAVDAWLQAEQPRVRMIMQVHDELVFEVHKDDVDAVAKQIHQLMENCT
RLDVPLLVEVGSGENWDQAH
>d1qtma2 e.8.1.1 (A:423-831) DNA polymerase I (Klenow fragment) {Thermus aquaticus}
EERLLWLYREVERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSR

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DQLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPDL
IHPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQRIRRAFIAEEGWLLVALDYSQIELR
VLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFGVLYGMSAHRLSQEL
AIPYEEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETLFGRRRYVPDLEARVKSVREAAERM
AFNMPVQGTAADLMKLAMVKLFPRLEEMGARMLLQVHDELVLEAPKERAEAVARLAKEVMEGVYP
LAVPLEVEVGIGEDWLSAK
>d1xwl_2 e.8.1.1 (469-876) DNA polymerase I (Klenow fragment)
{Bacillus stearothermophilus, newly identified strain as yet unnamed}
EQDRLLVELEQPLSSILAEMEFAGVKVDTKRLEQMGKELAEQLGTVEQRIYELAGQEFNINSPKQ
LGVILFEKLQLPVLKKTKTGYSTSADVLEKLAPYHEIVENILHYRQLGKLQSTYIEGLLKVVRPD
TKKVHTIFNQALTQTGRLSSTEPNLQNIPIRLEEGRKIRQAFVPSESDWLIFAADYSQIELRVLA
HIAEDDNLMEAFRRDLDIHTKTAMDIFQVSEDEVTPNMRRQAKAVNFGIVYGISDYGLAQNLNIS
RKEAAEFIERYFESFPGVKRYMENIVQEAKQKGYVTTLLHRRRYLPDITSRNFNVRSFAERMAMN
TPIQGSAADIIKKAMIDLNARLKEERLQAHLLLQVHDELILEAPKEEMERLCRLVPEVMEQAVTL
RVPLKVDYHYGSTWYDAK
>d1t7pa2 e.8.1.1 (A:211-704) T7 phage DNA polymerase {Bacteriophage
T7}
LEAVDIEHRAAWLLAKQERNGFPFDTKAIEELYVELAARRSELLRKLTETFGSWYQPKGGTEMFC
HPRTGKPLPKYPRIKTPKVGGIFKKPKNKAQREGREPCELDTREYVAGAPYTPVEHVVFNPSSRD
HIQKKLQEAGWVPTKYTDKGAPVVDDEVLEGVRVDDPEKQAAIDLIKEYLMIQKRIGQSAEGDKA
WLRYVAEDGKIHGSVNPNGAVTGRATHAFPNLAQIPGVRSPYGEQCRAAFGAEHHLDGITGKPWV
QAGIDASGLELRCLAHFMARFDNGEYAHEILNGDIHTKNQIAAELPTRDNAKTFIYGFLYGAGDE
KIGQIVGAGKERGKELKKKFLENTPAIAALRESIQQTLVESSQWVAGEQQVKWKRRWIKGLDGRK
VHVRSPHAALNTLLQSAGALICKLWIIKTEEMLVEKGLKHGWDGDFAYMAWVHDEIQVGCRTEEI
AQVVIETAQEAMRWVGDHWNFRCLLDTEGKMGPNWAICH
>d1ih7a2 e.8.1.1 (A:376-903) T4-like DNA polymerase {Bacteriophage
RB69}
QNKVIPQGRSHPVQPYPGAFVKEPIPNRYKYVMSFDLTSLYPSIIRQVNISPETIAGTFKVAPLH
DYINAVAERPSDVYSCSPNGMMYYKDRDGVVPTEITKVFNQRKEHKGYMLAAQRNGEIIKEALHN
PNLSVDEPLDVDYRFDFSDEIKEKIKKLSAKSLNEMLFRAQRTEVAGMTAQINRKLLINSLYGAL
GNVWFRYYDLRNATAITTFGQMALQWIERKVNEYLNEVCGTEGEAFVLYGDTDSIYVSADKIIDK
VGESKFRDTNHWVDFLDKFARERMEPAIDRGFREMCEYMNNKQHLMFMDREAIAGPPLGSKGIGG
FWTGKKRYALNVWDMEGTRYAEPKLKIMGLETQKSSTPKAVQKALKECIRRMLQEGEESLQEYFK
EFEKEFRQLNYISIASVSSANNIAKYDVGGFPGPKCPFHIRGILTYNRAIKGNIDAPQVVEGEKV
YVLPLREGNPFGDKCIAWPSGTEITDLIKDDVLHWMDYTVLLEKTFIKPLEGFTSAAKLDYEKKA
SLFDMFDF
>d1tgoa2 e.8.1.1 (A:348-773) T4-like DNA polymerase {Archaeon
Thermococcus gorgonarius}
STGNLVEWFLLRKAYERNELAPNKPDERELARRRESYAGGYVKEPERGLWENIVYLDFRSLYPSI
IITHNVSPDTLNREGCEEYDVAPQVGHKFCKDFPGFIPSLLGDLLEERQKVKKKMKATIDPIEKK
LLDYRQRAIKILANSFYGYYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYADTD
GFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRG
LEIVRRDWSEIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIYEQITRDLKD
YKATGPHVAVAKRLAARGIKIRPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYYIENQV
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LPAVERILRAFGYRKEDLRYQKTRQVGLGAWLKPKT
>d1qhta2 e.8.1.1 (A:348-750) T4-like DNA polymerase {Archaeon Thermococcus sp., 9on-7}
STGNLVEWFLLRKAYKRNELAPNKPDERELARRRGGYAGGYVKEPERGLWDNIVYLDFRSLYPSI
IITHNVSPDTLNREGCKEYDVAPEVGHKFCKDFPGFIPSLLGDLLEERQKIKRKMKATVDPLEKK
LLDYRQRAIKILANSFYGYYGYAKARWYCKECAESVTAWGREYIEMVIRELEEKFGFKVLYADTD
GLHATIPGADAETVKKKAKEFLKYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRG
LEIVRRDWSEIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIHEQITRDLRD
YKATGPHVAVAKRLAARGVKIRPGTVISYIVLKGSGRIGDRAIPADEFDPTKHRYDAEYYIENQV
LPAVERILKAFGY
>d1d5aa2 e.8.1.1 (A:348-756) T4-like DNA polymerase {Archaeon Desulfurococcus tok}
STGNLVEWFLLRKAYERNDVAPNKPDERELARRTESYAGGYVKEPEKGLWENIVYLDYKSLYPSI
IITHNVSPDTLNREGCREYDVAPQVGHRFCKDFPGFIPSLLGDLLEERQKVKKKMKATVDPIERK
LLDYRQRAIKILANSYYGYYAYANARWYCRECAESVTAWGRQYIETTMREIEEKFGFKVLYADTD
GFFATIPGADAETVKNKAKEFLNYINPRLPGLLELEYEGFYRRGFFVTKKKYAVIDEEDKITTRG
LEIVRRDWSEIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSRHEVPPEKLVIYEAGPHVAAA
ATVISYIVLKGPGRVGDRAIPFDEFDPAKHRYDAEYYIENQVLPAVERILRAFGYRKEDLR
>d1gcxa2 e.8.1.1 (A:348-758) T4-like DNA polymerase {Archaeon Pyrococcus kodakaraensis}
STGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYEGGYVKEPERGLWENIVYLDFRSLYPSI
IITHNVSPDTLNREGCKEYDVAPQVGHRFCKDFPGFIPSLLGDLLEERQKIKKKMKATIDPIERK
LLDYRQRAIKILANSYYGYYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYSDTD
GFFATIPGADAETVKKKAMEFLKYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRG
LEIVRRDWSEIAKETQARVLEALLKDGDVEKAVRIVKEVTEKLSKYEVPPEKLVIHEQITRDLKD
YKATGPHVAVAKRLAARGVKIRPGTVISYIVLKGSGRIGDRAIPFDEFDPTKHKYDAEYYIENQV
LPAVERILRAFGYRKEDLRYQ
>d1jx4a_ e.8.1.5 (A:) DinB homolog (DBH) {Archaeon Sulfolobus solfataricus, DNA polymerase IV}
MIVLFVDFDYFYAQVEEVLNPSLKGKPVVVCVFSGRFEDSGAVATANYEARKFGVKAGIPIVEAK
KILPNAVYLPMRKEVYQQVSSRIMNLLREYSEKIEIASIDEAYLDISDKVRDYREAYNLGLEIKN
KILEKEKITVTVGISKNKVFAKIAADMAKPNGIKVIDDEEVKRLIRELDIADVPGIGNITAEKLK
KLGINKLVDTLSIEFDKLKGMIGEAKAKYLISLARDEYNEPIRTRVRKSIGRIVTMKRNSRNLEE
IKPYLFRAIEESYYKLDKRIPKAIHVVAVTEDLDIVSRGRTFPHGISKETAYSESVKLLQKILEE
DERKIRRIGVRFSKFI
>d1im4a_ e.8.1.5 (A:) DinB homolog (DBH) {Archaeon Sulfolobus solfataricus}
HHHHHIVIFVDFDYFFAQVEEVLNPQYKGKPLVVCVYSGRTKTSGAVATANYEARKLGVKAGMPI
IKAMQIAPSAIYVPMRKPIYEAFSNRIMNLLNKHADKIEVASIDEAYLDVTNKVEGNFENGIELA
RKIKQEILEKEKITVTVGVAPNKILAKIIADKSKPNGLGVIRPTEVQDFLNELDIDEIPGIGSVL
ARRLNELGIQKLRD
>d1k1sa_ e.8.1.5 (A:) DinB homolog (DBH) {Archaeon Sulfolobus solfataricus}
MIVIFVDFDYFFAQVEEVLNPQYKGKPLVVSVYSGRTKTSGAVATANYEARKLGVKAGMPIIKAM

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QIAPSAIYVPMRKPIYEAFSNRIMNLLNKHADKIEVASIDEAYLDVTNKVEGNFENGIELARKIK
QEILEKEKITVTVGVAPNKILAKIIADKSKPNGLGVIRPTEVQDFLNELDIDEIPGIGSVLARRL
NELGIQKLRDILSKNYNELEKITGKAKALYLLKLAQNKYSEPVENKSKIPHGRYLTLPYNTRDVK
VILPYLKKAINEAYNKVNGIPMRITVIAIMEDLDILSKGKKFKHGISIDNAYKVAEDLLRELLVR
DKRRNVRRIGVKLDNIIIN
>d1jiha_ e.8.1.5 (A:) DNA polymerase eta {Baker's yeast (Saccharomyces cerevisiae)}
MSKFTWKELIQLGSPSKAYESSLACIAHIDMNAFFAQVEQMRCGLSKEDPVVCVQWNSIIAVSYA
ARKYGISRMDTIQEALKKCSNLIPIHTAVFKKGEDFWQYHDGCGSWVQDPAKQISVEDHKVSLEP
YRRESRKALKIFKSACDLVERASIDEVFLDLGRICFNMLMFDNEYELTGDLKLKDALSNIREAFI
GGNYDINSHLPLIPEKIKSLKFEGDVFNPEGRDLITDWDDVILALGSQVCKGIRDSIKDILGYTT
SCGLSSTKNVCKLASNYKKPDAQTIVKNDCLLDFLDCGKFEITSFWTLGGVLGKELIDVLDLPHE
NSIKHIRETWPDNAGQLKEFLDAKVKQSDYDRSTSNIDPLKTADLAEKLFKLSRGRYGLPLSSRP
VVKSMMSNKNLRGKSCNSIVDCISWLEVFCAELTSRIQDLEQEYNKIVIPRTVSISLKTKSYEVY
RKSGPVAYKGINFQSHELLKVGIKFVTDLDIKGKNKSYYPLTKLSMTITNFDII
>d1mml__ e.8.1.2 (-) MMLV reverse transcriptase {Moloney murine leukemia virus}
TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILV
PCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKD
AFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLI
LLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLK
>d1c9ra2 e.8.1.2 (A:1-429) HIV-1 reverse transcriptase {Human immunodeficiency virus type 1}
PISPIETVPVKLAPGMDGPKVKQWPLTAEAIAALVAICTAMEAEGKISKIGPENPYNTPVFAIKK
AAAAAAAALVDFRELNKRTQDFWEVQLGIPHPAGLKKKKSVTVLDVGDAYFSVPLDEDFRKYTAF
TIPSIANATPGIRYQYNVLPQGWKGSPAIFQSSMTKILEPFKKQNPDIVIYQYIDDLYVGSDLEI
GQHATKIAELRQHLLAWGLTTPDKKHAAEPPFLWMGYELHPDAWTVAPAALAAAASAAVNDIQKL
VGKLNWASQIYPGIAVRALSAAAAGTKAAAEAAAATAAAALALAAAREALAAPVHGVYYDPSKDL
IAEIQAQGQGQWTYQIYQEPFKNLKTGKYARMRGAHTNDVKQLTEAVQKITTESIVIWGKTPKFK
LPIQKETWETWWTEYWQATWIPEWEFVNTPPLVKLWYQL
>d1c9rb1 e.8.1.2 (B:) HIV-1 reverse transcriptase {Human immunodeficiency virus type 1}
PISPIETVPVKLAPGMDGPKVKQWPLTEEKIKALVEICTEMEKEGKISKIGPENPYNTPVFAIKK
KDSTKWRKLVDFRELNKRTQDFWEAALGIPHPAGLKKKKSVTVLDVGDAYFSVPLDEDFRKYTAF
TIPSINNETPGIRYQYNVLPQGWKGSPAIFQSSMTKILEPFKAQNPDIVIYQYIDDLYVGSDLEI
GQHRTKIEELRQHLLRWGLTTPDKKHQKEPPFLWMGYELHPDKWAAAAAAAAAAAAATVNDIQKL
VGKLNWAAQIYPGIAAAALSAALAGTKALTAAAPLTAAAALELAANRAAAAAAAAGVYYDPSKDL
IAEIQKQGQGQWTYQIYQEPFKNLKTGKYARMRGAHTNDVKQLTEAVQKITTESIVIWGKTPKFK
LPIQKETWETWWTEYWQATWIPEWEFVNTPPLVALWYALE
>d1har__ e.8.1.2 (-) HIV-1 reverse transcriptase {Human immunodeficiency virus type 1}
PISPIETVPVKLKPGMDGPKVAQWPLTAAKIAALVAICTEMEKEGKISKIGPENPYNTPVFAIKK
KDSTKWAKLVDFRELNKRTQDFWEVQLGIPHPAGLKKKKSVTVLDVGDAYFSVPLDEDFRKYTAF
TIPSINNETPGIRYQYNVLPQGWKGSPAIFQSSMTKILAPFKAANPDIVIYQYMDDLYVGSDLAI
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GAHRTKIEELRQHLLRWGLTT
>d1vrta2 e.8.1.2 (A:4-429) HIV-1 reverse transcriptase {Human immunodeficiency virus type 1}
PIETVPVKLKPGMDGPKVKQWPLTEEKIKALVEICTEMEKEGKISKIGPENPYNTPVFAIKKKDS
TKWRKLVDFRELNKRTQDFWEVQLGIPHPAGLKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIP
SINNETPGIRYQYNVLPQGWKGSPAIFQSSMTKILEPFRKQNPDIVIYQYMDDLYVGSDLEIGQH
RTKIEELRQHLLRWGLTTPDKKHQKEPPFLWMGYELHPDKWTVQPIVLPEKDSWTVNDIQKLVGK
LNWASQIYPGIKVRQLCKLLRGTKALTEVIPLTEEAELELAENREILKEPVHGVYYDPSKDLIAE
IQKQGQGQWTYQIYQEPFKNLKTGKYARMRGAHTNDVKQLTEAVQKITTESIVIWGKTPKFKLPI
QKETWETWWTEYWQATWIPEWEFVNTPPLVKLWYQL
>d1ceza_ e.8.1.3 (A:) T7 RNA polymerase {Bacteriophage T7}
IAKNDFSDIELAAIPFNTLADHYGERLAREQLALEHESYEMGEARFRKMFERQLKAGEVADNAAA
KPLITTLLPKMIARINDWFEEVKAKRGKRPTAFQFLQEIKPEAVAYITIKTTLACLTSADNTTVQ
AVASAIGRAIEDEARFGRIRDLEAKHFKKNVEEQLNKRVGHVYKKAFMQVVEADMLSKGLLGGEA
WSSWHKEDSIHVGVRCIEMLIESTGMVSLHRQNAGVVGQDSETIELAPEYAEAIATRAGALAGIS
PMFQPCVVPPKPWTGITGGGYWANGRRPLALVRTHSKKALMRYEDVYMPEVYKAINIAQNTAWKI
NKKVLAVANVITKWKHCPVEDIPAIEREELPMKPEDIDMNPEALTAWKRAAAAVYRKDKARKSRR
ISLEFMLEQANKFANHKAIWFPYNMDWRGRVYAVSMFNPQGNDMTKGLLTLAKGKPIGKEGYYWL
KIHGANCAGVDKVPFPERIKFIEENHENIMACAKSPLENTWWAEQDSPFCFLAFCFEYAGVQHHG
LSYNCSLPLAFDGSCSGIQHFSAMLRDEVGGRAVNLLPSETVQDIYGIVAKKVNEILQADAINGT
DNEVVTVTDENTGEISEKVKLGTKALAGQWLAYGVTRSVTKRSVMTLAYGSKEFGFRQQVLEDTI
QPAIDSGKGLMFTQPNQAAGYMAKLIWESVSVTVVAAVEAMNWLKSAAKLLAAEVKDKKTGEILR
KRCAVHWVTPDGFPVWQEYKKPIQTRLNLMFLGQFRLQPTINTNKDSEIDAHKQESGIAPNFVHS
QDGSHLRKTVVWAHEKYGIESFALIHDSFGTIPADAANLFKAVRETMVDTYESCDVLADFYDQFA
DQLHESQLDKMPALPAKGNLNLRDILESDFAFA
>d1rdr__ e.8.1.4 (-) Viral RNA-dependent RNA-polymerase {Poliovirus type 1, strain Mahoney}
VGYPIINAPSKTKLEPSAFHYVFEGVKEPAVLTKNDPRLKTDFEEAIFSKYVGNKITEVDEYMKE
AVDHYAGQLMSLDINTEQMCLEDAMYGTDGLEALDLSTSAGYPYVAMGKKKRDILNKQTRDTKEM
QKLLDTYGINLPLVTYVKDELRSKTKVEQGKSRLIEASSLNDSVAMRMAFGNLYAAFHKNPGVIT
GSAVGCDPDLFWSKIPVLMEEKLFAFDYTGYDASLSPAWFEALKMVLEKIGFGDRVDYIDYLNHS
HHLYKNKTYCVKGGMPSGCSGTSIFNSMINNLIIRTLLLKTYKGIDLDHLKMIAYGDDVIASYPH
EVDASLLAQSGKDYGLTMTPADKSATFETVTWENVTFLKRFFRADEKYPFLIHPVMPMKEIHESI
RWTKDPRNTQDHVRSLCLLAWHNGEEEYNKFLAKIRSVPIGRALLLPEYSTLYRRWLDSF
>d1c2pa_ e.8.1.4 (A:) Viral RNA-dependent RNA-polymerase {Hepatitis C virus}
HHSYTWTGALITPCAAEESKLPINALSNSLLRHHNMVYATTSRSAGLRQKKVTFDRLQVLDDHYR
DVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRNLSSKAVNHIHSVWKDLLEDT
VTPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVSTLPQVVMGSSYGFQY
SPGQRVEFLVNTWKSKKNPMGFSYDTRCFDSTVTENDIRVEESIYQCCDLAPEARQAIKSLTERL
YIGGPLTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKASAACRAAKLQDCTMLVNGDDLVVICE
SAGVQEDAASLRAFTEAMTRYSAPPGDPPQPEYDLELITSCSSNVSVAHDASGKRVYYLTRDPTT
PLARAAWETARHTPVNSWLGNIIMYAPTLWARMILMTHFFSILLAQEQLEKALDCQIYGACYSIE
PLDLPQIIERLHGLSAFSLHSYSPGEINRVASCLRKLGVPPLRVWRHRARSVRARLLSQGGRAAT
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CGKYLFNWAVKTKLKLTPIPAASQLDLSGWFVAGYSGGDIYHS
>d1khva_ e.8.1.4 (A:) Viral RNA-dependent RNA-polymerase {Rabbit
hemorrhagic disease virus}
FCGEPIDYRGITAHRLVGAEPRPPVSGTRYAKVPGVPDEYKTGYRPANLGRSDPDSDKSLMNIAV
KNLQVYQQEPKLDKVDEFIERAAADVLGYLRFLTKGERQANLNFKAAFNTLDLSTSCGPFVPGKK
IDHVKDGVMDQVLAKHLYKCWSVANSGKALHHIYACGLKDELRPLDKVKEGKKRLLWGCDVGVAV
CAAAVFHNICYKLKMVARFGPIAVGVDMTSRDVDVIINNLTSKASDFLCLDYSKWDSTMSPCVVR
LAIDILADCCEQTELTKSVVLTLKSHPMTILDAMIVQTKRGLPSGMPFTSVINSICHWLLWSAAV
YKSCAEIGLHCSNLYEDAPFYTYGDDGVYAMTPMMVSLLPAIIENLRDYGLSPTAADKTEFIDVC
PLNKISFLKRTFELTDIGWVSKLDKSSILRQLEWSKTTSRHMVIEETYDLAKEERGVQLEELQVA
AAAHGQEFFNFVCRELERQQAYTQFSVYSYDAARKILADRKR
>d1hhsa_ e.8.1.6 (A:) dsRNA phage RNA-dependent RNA-polymerase
{Bacteriophage PHI-6}
PRRAPAFPLSDIKAQMLFANNIKAQQASKRSFKEGAIETYEGLLSVDPRFLSFKNELSRYLTDHF
PANVDEYGRVYGNGVRTNFFGMRHMNGFPMIPATWPLASNLKKRADADLADGPVSERDNLLFRAA
VRLMFSDLEPVPLKIRKGSSTCIPYFSNDMGTKIEIAERALEKAEEAGNLMLQGKFDDAYQLHQM
GGAYYVVYRAQSTDAITLDPKTGKFVSKDRMVADFEYAVTGGEQGSLFAASKDASRLKEQYGIDV
PDGFFCERRRTAMGGPFALNAPIMAVAQPVRNKIYSKYAYTFHHTTRLNKEEKVKEWSLCVATDV
SDHDTFWPGWLRDLICDELLNMGYAPWWVKLFETSLKLPVYYVGAPAPEQGHTLLGDPSNPDLEVG
LSSGQGATDLMGTLLMSITYLVMQLDHTAPHLNSRIKDMPSACRFLDSYWQGHEEIRQISKSDDA
MLGWTKGRALVGGHRLFEMLKEGKVNPSPYMKISYEHGGAFLGDILLYDSRREPGSAIFVGNINS
MLNNQFSPEYGVQSGVRDRSKRKRPFPGLAWASMKDTYGACPIYSDVLEAIERCWWNAFGESYRA
YREDMLKRDTLELSRYVASMARQAGLAELTPIDLEVLADPNKLQYKWTEADVSANIHEVLMHGVS
VEKTERFLRSVMPR
>d1i50a_ e.29.1.1 (A:) RBP1 {Baker's yeast (Saccharomyces
cerevisiae)}
VGQQYSSAPLRTVKEVQFGLFSPEEVRAISVAKIRFPETMDETQTRAKIGGLNDPRLGSIDRNLK
CQTCQEGMNECPGHFGHIDLAKPVFHVGFIAKIKKVCECVCMHCGKLLLDEHNELMRQALAIKDS
KKRFAAIWTLCKTKMVCETDVPSEDDPTQLVSRGGCGNTQPTIRKDGLKLVGSWKKDRATGDADE
PELRVLSTEEILNIFKHISVKDFTSLGFNEVFSRPEWMILTCLPVPPPPVRPSISFNESQRGEDD
LTFKLADILKANISLETLEHNGAPHHAIEEAESLLQFHVATYMDNDIAGQPQALQKSGRPVKSIR
ARLKGKEGRIRGNLMGKRVDFSARTVISGDPNLELDQVGVPKSIAKTLTYPEVVTPYNIDRLTQL
VRNGPNEHPGAKYVIRDSGDRIDLRYSKRAGDIQLQYGWKVERHIMDNDPVLFNRQPSLHKMSMM
AHRVKVIPYSTFRLNLSVTSPYNADFDGDEMNLHVPQSEETRAELSQLCAVPLQIVSPQSNKPCM
GIVQDTLCGIRKLTLRDTFIELDQVLNMLYWVPDWDGVIPTPAIIKPKPLWSGKQILSVAIPNGI
HLQRFDEGTTLLSPKDNGMLIIDGQIIFGVVEKKTVGSSNGGLIHVVTREKGPQVCAKLFGNIQK
VVNFWLLHNGFSTGIGDTIADGPTMREITETIAEAKKKVLDVTKEAQANLLTAKHGMTLRESFED
NVVRFLNEARDKAGRLAEVNLKDLNNVKQMVMAGSKGSFINIAQMSACVGQQSVEGKRIAFGFVD
RTLPHFSKDDYSPESKGFVENSYLRGLTPQEFFFHAMGGREGLIDTAVKTAETGYIQRRLVKALE
DIMVHYDNTTRNSLGNVIQFIYGEDGMDAAHIEKQSLDTIGGSDAAFEKRYRVDLLNTDHTLDPS
LLESGSEILGDLKLQVLLDEEYKQLVKDRKFLREVFVDGEANWPLPVNIRRIIQNAQQTFHIDHT
KPSDLTIKDIVLGVKDLQENLLVLRGKNEIIQNAQRDAVTLFCCLLRSRLATRRVLQEYRLTKQA
FDWVLSNIEAQFLRSVVHPGEMVGVLAAQSIGEPATQMTLNTFHFAGVASKKVTSGVPRLKEILN
VAKNMKTPSLTVYLEPGHAADQEQAKLIRSAIEHTTLKSVTIASEIYYDPDPRSTVIPEDEEIIQ
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LHFSLLDEEAEQSFDQQSPWLLRLELDRAAMNDKDLTMGQVGERIKQTFKNDLFVIWSEDNDEKL
IIRCRVVRPKSLDAETEAEEDHMLKKIENTMLENITLRGVENIERVVMMKYDRKVPSPTGEYVKE
PEWVLETDGVNLSEVMTVPGIDPTRIYTNSFIDIMEVLGIEAGRAALYKEVYNVIASDGSYVNYR
HMALLVDVMTTQGGLTSVTRHGFNRSNTGALMRCSFEETVEILFEAGASAELDDCRGVSENVILG
QMAPIGTGAFDVMIDEESL
>d1i6vc_ e.29.1.1 (C:) RNA-polymerase beta {Thermus aquaticus}
KIKRFGRIREVIPLPPLTEIQVESYKKALQADVPPEKRENVGIQAAFKETFPIEEGDKGKGGLVL
DFLEYRIGDPPFSQDECREKDLTYQAPLYARLQLIHKDTGLIKEDEVFLGHLPLMTEDGSFIING
ADRVIVSQIHRSPGVYFTPDPARPGRYIASIIPLPKRGPWIDLEVEASGVVTMKVNKRKFPLVLL
LRVLGYDQETLVRELSAYGDLVQGLLDEAVLAMRPEEAMVRLFTLLRPGDPPKKDKALAYLFGLL
ADPKRYDLGEAGRYKAEEKLGVGLSGRTLVRFEDGEFKDEVFLPTLRYLFALTAGVPGHEVDDID
HLGNRRIRTVGELMADQFRVGLARLARGVRERMVMGSPDTLTPAKLVNSRPLEAALREFFSRSQL
SQFKDETNPLSSLRHKRRISALGPGGLTRERAGFDVRDVHRTHYGRICPVETPEGANIGLITSLA
AYARVDALGFIRTPYRRVKNGVVTEEVVYMTASEEDRYTIAQANTPLEGDRIATDRVVARRRGEP
VIVAPEEVEFMDVSPKQVFSLNTNLIPFLEHDDANRALMGSNMQTQAVPLIRAQAPVVMTGLEER
VVRDSLAALYAEEDGEVVKVDGTRIAVRYEDGRLVHPLRRYARSNQGTAFDQRPRVRVGQRVKKG
DLLADGPASEEGFLALGQNVLVAIMPFDGYNFEDAIVISEELLKRDFYTSIHIERYEIEARDTKL
GPERITRDIPHLSEAALRDLDEEGIVRIGAEVKPGDILVGRTSFKGEQEPSPEERLLRSIFGEKA
RDVKDTSLRVPPGEGGIVVGRLRLRRGDPGVELKPGVREVVRVFVAQKRKLQVGDKLANRHGNKG
VVAKILPVEDMPHLPDGTPVDVILNPLGVPSRMNLGQILETHLGLAGYFLGQRYISPVFDGATEP
EIKELLAEAFNLYFGKRQGEGFGVDKREKEVLARAEKLGLVSPGKSPEEQLKELFDLGKVVLYDG
RTGEPFEGPIVVGQMFIMKLYHMVEDKMHARSTGPYSLITQQPLGGKAQFGGQRFGEMEVWALEA
YGAAHTLQEMLTIKSDDIEGRNAAYQAIIKGEDVPEPSVPESFRVLVKELQALALDVQTLDEKDN
PVDVFEGL
>d1i50b_ e.29.1.2 (B:) RBP2 {Baker's yeast (Saccharomyces
cerevisiae)}
FEDESAPITAEDSWAVISAFFREKGLVSQQLDSFNQFVDYTLQDIICEDSTLILEQLAQHTTESD
NISRKYEISFGKIYVTKPMVNESDGVTHALYPQEARLRNLTYSSGLFVDVKKRTYEAIDVPGREL
KYELIAEESEDDSESGKVFIGRLPIMLRSKNCYLSEATESDLYKLKECPFDMGGYFIINGSEKVL
IAQERSAGNIVQVFKKAAPSPISHVAEIRSALEKGSRFISTLQVKLYGREGSSARTIKATLPYIK
QDIPIVIIFRALGIIPDGEILEHICYDVNDWQMLEMLKPCVEDGFVIQDRETALDFIGRRGTALG
IKKEKRIQYAKDILQKEFLPHITQLEGFESRKAFFLGYMINRLLLCALDRKDQDDRDHFGKKRLD
LAGPLLAQLFKTLFKKLTKDIFRYMQRTVEEAHDFNMKLAINAKTITSGLKYALATGNWGEQKKA
MSSRAGVSQVLNRYTYSSTLSHLRRTNTPIGRDGKLAKPRQLHNTHWGLVCPAETPEGQACGLVK
NLSLMSCISVGTDPMPIITFLSEWGMEPLEDYVPHQSPDATRVFVNGVWHGVHRNPARLMETLRT
LRRKGDINPEVSMIRDIREKELKIFTDAGRVYRPLFIVEDDESLGHKELKVRKGHIAKLMATEYQ
DIEGGFEDVEEYTWSSLLNEGLVEYIDAEEEESILIAMQPEDLEPAEANEENDLDVDPAKRIRVS
HHATTFTHCEIHPSMILGVAASIIPFPDHNQSPRNTYQSAMGKQAMGVFLTNYNVRMDTMANILY
YPQKPLGTTRAMEYLKFRELPAGQNAIVAIACYSGYNQEDSMIMNQSSIDRGLFRSLFFRSYMDQ
EKKYGMSITETFEKPQRTNTLRMKHGTYDKLDDDGLIAPGVRVSGEDVIIGKTTPISPDEEELGQ
RTAYHSKRDASTPLRSTENGIVDQVLVTTNQDGLKFVKVRVRTTKIPQIGDKFASRHGQKGTIGI
TYRREDMPFTAEGIVPDLIINPHAIPSRMTVAHLIECLLSKVAALSGNEGDASPFTDITVEGISK
LLREHGYQSRGFEVMYNGHTGKKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGR
SRDGGLRFGEMERDCMIAHGAASFLKERLMEASDAFRVHICGICGLMTVIAKLNHNQFECKGCDN
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KIDIYQIHIPYAAKLLFQELMAMNITPRLYTDRSRDF
>d1i6vd_ e.29.1.2 (D:) RNA-polymerase beta-prime {Thermus aquaticus}
KEVRKVRIALASPEKIRSWSYGEVEKPETINYRTLKPERDGLFDERIFGPIKDYECACGKYKRQR
FEAKVCERCAVEVTRSIVRRYRMAHIELATPAAHIWFVKDVPSKIATLLDLSATELEQVLYFNKY
IVLDPKAAVLDAVPVEKRQLLTDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIDARMG
AEAIQELLKELDLEKLERELLEEMKHPSRARRAKARKRLEVVRAFLDSGNRPEWMILEAVPVLPP
DLRPMVQVDGGRFATSDLNDLYRRLINRNNRLKKLLAQGAPEIIIRNEKRMLQEAVDAVIDNGRR
GSPVTNPGSERPLRSLTDILSGKQGRFRQNLLGKRVDYSGRSVIVVGPQLKLHQCGLPKRMALEL
FKPFLLKKMEEKAFAPNVKAARRMLERQRDIKDEVWDALEEVIHGKVVLLNRAPTLHRLGIQAFQ
PVLVEGQSIQLHPLVCEAFNADFDGDQMAVHVPLSSFAQAEARIQMLSAHNLLSPASGEPLAKPS
RDIILGLYYITQVRKEKKGAGMAFATPEEALAAYERGEVALNAPIVVAGRETSVGRLKFVFANPD
EALLAVAHGLLDLQDTVTTRYLGRRLETSPGRILFARIVGEAVGDEKVAQELIQMDVPQEKNSLK
DLVYQAFLRLGMEKTARLLDALKYYGFTLSTTSGITIGIDDAVIPEEKQRYLEEADRKLRQIEQA
YEMGFLTDRERYDQVIQLWTETTEKVTQAVFNNFEENYPFNPLYVMAQSGARGNPQQIRQLCGMR
GLMQKPSGETFEVPVRSSFREGLTVLEYFISSHGARKGGADTALRTADSGYLTRKLVDVAHEIVV
READCGTTNYISVPLFQMDEVTRTLRLRKRSDIESGLYGRVLAREVEALGRRLEEGRYLSLEDVH
FLIKAAEAGEVREVPVRSPLTCQTRYGVCQKCYGYDLSMARPVSIGEAVGVVAAESIGEPGTQLT
MRTFHTGGVAVGTDITQGLPRVIELFEARRPKAKAVISEIDGVVRIEEGEDRLSVFVESEGFSKE
YKLPKDARLLVKDGDYVEAGQPLTRGAIDPHQLLEAKGPEAVERYLVDEIQKVYRAQGVKLHDKH
IEIVVRQMLKYVEVTDPGDSRLLEGQVLEKWDVEALNERLIAEGKVPVAWKPLLMGVTKSALSTK
SWLSAASFQNTTHVLTEAAIAGKKDELIGLKENVILGRLIPAGTGSDFVRFTQVVDQRTLKAIE
>d1bpya2 e.9.1.1 (A:92-335) DNA polymerase beta, catalytic (31 kD)
fragment {Human (Homo sapiens)}
DTSSSINFLTRVSGIGPSAARKFVDEGIKTLEDLRKNEDKLNHHQRIGLKYFGDFEKRIPREEML
QMQDIVLNEVKKVDSEYIATVCGSFRRGAESSGDMDVLLTHPSFTSESTKQPKLLHQVVEQLQKV
HFITDTLSKGETKFMGVCQLPSKNDEKEYPHRRIDIRLIPKDQYYCGVLYFTGSDIFNKNMRAHA
LEKGFTINEYTIRPLGVTGVAGEPLPVDSEKDIFDYIQWKYREPKDRSE
>d1jn3a_ e.9.1.1 (A:) DNA polymerase beta, catalytic (31 kD) fragment
{Rat (Rattus norvegicus)}
DDTSSSINFLTRVTGIGPSAARKLVDEGIKTLEDLRKNEDKLNHHQRIGLKYFEDFEKRIPREEM
LQMQDIVLNEVKKLDPEYIATVCGSFRRGAESSGDMDVLLTHPNFTSESSKQPKLLHRVVEQLQK
VRFITDTLSKGETKFMGVCQLPSENDENEYPHRRIDIRLIPKDQYYCGVLYFTGSDIFNKNLRAH
ALEKGFTINEYTIRPLGVTGVAGEPLPVDSEQDIFDYIQWRYREPKDRSE
>d1jmsa2 e.9.1.1 (A:243-510) Terminal deoxynucleotidyl transferase
{Mouse (Mus musculus)}
DERYKSFKLFTSVFGVGLKTAEKWFRMGFRTLSKIQSDKSLRFTQMQKAGFLYYEDLVSCVNRPE
AEAVSMLVKEAVVTFLPDALVTMTGGFRRGKMTGHDVDFLITSPEATEDEEQQLLHKVTDFWKQQ
GLLLYCDILESTFEKFKQPSRKVDALDHFQKCFLILKLDHGRVHSEKSGQQEGKGWKAIRVDLVM
CPYDRRAFALLGWTGSRQFERDLRRYATHERKMMLDNHALYDRTKRVFLEAESEEEIFAHLGLDY
IEPWERNA
>d1jaja_ e.9.1.1 (A:) DNA polymerase X {African swine fever virus}
MLTLIQGKKIVNHLRSRLAFEYNGQLIKILSKNIVAVGSLRREEKMLNDVDLLIIVPEKKLLKHV
LPNIRIKGLSFSVKVCGERKCVLFIEWEKKTYQLDLFTALAEEKPYAIFHFTGPVSYLIRIRAAL
KKKNYKLNQYGLFKNQTLVPLKITTEKELIKELGFTYRIPKKRL
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>d1fa0a2 e.9.1.2 (A:3-351) Poly(A) polymerase, catalytic domain
{Baker's yeast (Saccharomyces cerevisiae)}
SQKVFGITGPVSTVGATAAENKLNDSLIQELKKEGSFETEQETANRVQVLKILQELAQRFVYEVS
KKKNMSDGMARDAGGKIFTYGSYRLGVHGPGSDIDTLVVVPKHVTREDFFTVFDSLLRERKELDE
IAPVPDAFVPIIKIKFSGISIDLICARLDQPQVPLSLTLSDKNLLRNLDEKDLRALNGTRVTDEI
LELVPKPNVFRIALRAIKLWAQRRAVYANIFGFPGGVAWAMLVARICQLYPNACSAVILNRFFII
LSEWNWPQPVILKPIEDGPLQVRVWNPKIYAQDRSHRMPVITPAYPSMCATHNITESTKKVILQE
FVRGVQITNDIFSNKKSWANLFEK
>d1f5aa2 e.9.1.2 (A:20-364) Poly(A) polymerase, catalytic domain {Cow
(Bos taurus)}
YGITSPISLAAPKETDCLLTQKLVETLKPFGVFEEEEELQRRILILGKLNNLVKEWIREISESKN
LPQSVIENVGGKIFTFGSYRLGVHTKGADIDALCVAPRHVDRSDFFTSFYDKLKLQEEVKDLRAV
EEAFVPVIKLCFDGIEIDILFARLALQTIPEDLDLRDDSLLKNLDIRCIRSLNGCRVTDEILHLV
PNIDNFRLTLRAIKLWAKRHNIYSNILGFLGGVSWAMLVARTCQLYPNAIASTLVHKFFLVFSKW
EWPNPVLLKQPEECNLNLPVWDPRVNPSDRYHLMPIITPAYPQQNSTYNVSVSTRMVMVEEFKQG
LAITDEILLSKAEWSKLFEA
>d1knya_ e.9.1.3 (A:) Kanamycin nucleotidyltransferase (KNTase)
{Staphylococcus aureus}
MNGPIIMTREERMKIVHEIKERILDKYGDDVKAIGVYGSLGRQTDGPYSDIEMMCVMSTEEAEFS
HEWTTGEWKVEVNFYSEEILLDYASQVESDWPLTHGQFFSILPIYDSGGYLEKVYQTAKSVEAQT
FHDAICALIVEELFEYAGKWRNIRVQGPTTFLPSLTVQVAMAGAMLIGLHHRICYTTSASVLTEA
VKQSDLPSGYDHLCQFVMSGQLSDSEKLLESLENFWNGIQEWTERHGYIVDVSKRIPF
>d1k8ta_ e.9.1.4 (A:) Adenylylcyclase toxin (the edema factor)
{Bacillus anthracis}
DRIDVLKGEKALKASGLVPEHADAFKKIARELNTYILFRPVNKLATNLIKSGVATKGLNVHGKSS
DWGPVAGYIPFDQDLSKKHGQQLAVEKGNLENKKSITEHEGEIGKIPLKLDHLRIEELKENGIIL
KGKKEIDNGKKYYLLESNNQVYEFRISDENNEVQYKTKEGKITVLGEKFNWRNIEVMAKNVEGVL
KPLTADYDLFALAPSLTEIKKQIPQKEWDKVVNTPNSLEKQKGVTNLLIKYGIERKPDSTKGTLS
NWQKQMLDRLNEAVKYTGYTGGDVVNHGTEQDNEEFPEKDNEIFIINPEGEFILTKNWEMTGRFI
EKNITGKDYLYYFNRSYNKIAPGNKAYIEWTDPITKAKINTIPTSAEFIKNLSSIRRSSNVGVYK
DSGDKDEFAKKESVKKIAGYLSDYYNSANHIFSQEKKRKISIFRGIQAYNEIENVLKSKQIAPEY
KNYFQYLKERITNQVQLLLTHQKSNIEFKLLYKQLNFTENETDNFEVFQKIIDE
>d1cy9a_ e.10.1.1 (A:) DNA topoisomerase I, 67K N-terminal domain
{Escherichia coli}
FVPEEFWEVDASTTTPSGEALALQVTHQNDKPFRPVNKEQTQAAVSLLEKARYSVLEREDKPTTS
KPGAPFITSTLQQAASTRLGFGVKKTMMMAQRLYEAGYITYMRTDSTNLSQDAVNMVRGYISDNF
GKKYLPESPNQYASKENSQEAHEAIRPSDVNVMAESLKDMEADAQKLYQLIWRQFVACQMTPAKY
DSTTLTVGAGDFRLKARGRILRFDGWTKVMPALRKGDEDRILPAVNKGDALTLVELTPAQHFTKP
>d1ecl__ e.10.1.1 (-) DNA topoisomerase I, 67K N-terminal domain
{Escherichia coli}
GKALVIVESPAKAKTINKYLGSDYVVKSSVGHIRDLTSGSAAKKSADSTSTKTAKKPKKPDERGA
LVNRMGVDPWHNWEAHYEVLPGKEKVVSELKQLAEKADHIYLATDLDREGEAIAWHLREVIGGDD
ARYSRVVFNEITKNAIRQAFNKPGELNIDRVNAQQARRFMDRVVGYMVSPLLWKKIARGLSAGRV
QSVAVRLVVEREREIKAFVPEEFWEVDASTTTPSGEALALQVTHQNDKPFRPVNKEQTQAAVSLL
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EKARYSVLEREDKPTTSKPGAPFITSTLQQAASTRLGFGVKKTMMMAQRLYEAGYITYMRTDSTN
LSQDAVNMVRGYISDNFGKKYLPESPNQYASKGNSQEAHEAIRPSDVNVMAESLKDMEADAQKLY
QLIWRQFVACQMTPAKYDSTTLTVGAGDFRLKARGRILRFDGWTKVMPALRKGDEDRILPAVNKG
DALTLVELTPAQHFTKPPARFSEASLVKELEKRGIGRPSTYASIISTIQDRGYVRVENRRFYAEK
MGEIVTDRLEENFRELMNYDFTAQMENSLDQVANHEAEWKAVLDHFFSDFTQQLDKAEKDPEEGG
MRPN
>d1i7da_ e.10.1.1 (A:) DNA topoisomerase III {Escherichia coli}
MRLFIAEKPSLARAIADVLPKPHRKGDGFIECGNGQVVTWCIGHLLEQAQPDAYDSRYARWNLAD
LPIVPEKWQLQPRPSVTKQLNVIKRFLHEASEIVHAGDPDREGQLLVDEVLDYLQLAPEKRQQVQ
RCLINDLNPQAVERAIDRLRSNSEFVPLCVSALARARADWLYGINMTRAYTILGRNAGYQGVLSV
GRVQTPVLGLVVRRDEEIENFVAKDFFEVKAHIVTPADERFTAIWQPSEACEPYQDEEGRLLHRP
LAEHVVNRISGQPAIVTSYNDKRESESAPLPFSLSALQIEAAKRFGLSAQNVLDICQKLYETHKL
ITFPRSDCRYLPEEHFAGRHAVMNAISVHAPDLLPQPVVDPDIRNRCWDDKKVDAHHAIIPTARS
SAINLTENEAKVYNLIARQYLMQFCPDAVFRKCVIELDIAKGKFVAKARFLAEAGWRTLLGSKER
DEENDGTPLPVVAKGDELLCEKGEVVERQTQPPRHFTDATLLSAMTGIARFVQDKDLKKILRATD
GLGTEATRAGIIELLFKRGFLTKKGRYIHSTDAGKALFHSLPEMATRPDMTAHWESVLTQISEKQ
CRYQDFMQPLVGTLYQLIDQAKRTPVRQFRGIVAP
>d1gkub3 e.10.1.1 (B:499-1054) Topoisomerase "domain" of reverse gyrase {Archaeon Archaeoglobus fulgidus}
QEFDLIKPALFIVESPTKARQISRFFGKPSVKVLDGAVVYEIPMQKYVLMVTASIGHVVDLITNR
GFHGVLVNGRFVPVYASIKRCRDCGYQFTEDRESCPKCGSENVDNSRSRIEALRKLAHDAEFVIV
GTDPDTEGEKIAWDLKNLLSGCGAVKRAEFHEVTRRAILEALESLRDVDENLVKAQVVRRIEDRW
IGFVLSQKLWERFNNRNLSAGRAQTLVLGWIIDRFQESRERRKIAIVRDFDLVLEHDEEEFDLTI
KLVEEREELRTPLPPYTTETMLSDANRILKFSVKQTMQIAQELFENGLITYHRTDSTRVSDVGQR
IAKEYLGDDFVGREWGESGAHECIRPTRPLTRDDVQRLIQEGVLVVEGLRWEHFALYDLIFRRFM
ASQCRPFKVVVKKYSIEFDGKTAEEERIVRAEGRAYELYRAVWVKNELPTGTFRVKAEVKSVPKV
LPFTQSEIIQMMKERGIGRPSTYATIVDRLFMRNYVVEKYGRMIPTKLGIDVFRFLVRRYAKFVS
EDRTRDLESRMDAIERGELDYLKALEDMYAEIKSID
>d1bjt__ e.11.1.1 (-) DNA topoisomerase II, C-terminal fragment (residues 410-1202) {Baker's yeast (Saccharomyces cerevisiae)}
RKSRITNYPKLEDANKAGTKEGYKCTLVLTEGDSALSLAVAGLAVVGRDYYGCYPLRGKMLNVRE
ASADQILKNAEIQAIKKIMGLQHRKKYEDTKSLRYGHLMIMTDQDHDGSHIKGLIINFLESSFLG
LLDIQGFLLEFITPIIKVSITKPTKNTIAFYNMPDYEKWREEESHKFTWKQKYYKGLGTSLAQEV
REYFSNLDRHLKIFHSLQGNDKDYIDLAFSKKKADDRKEWLRQYEPGTVLDPTLKEIPISDFINK
ELILFSLADNIRSIPNVLDGFKPGQRKVLYGCFKKNLKSELKVAQLAPYVSECTAYHHGEQSLAQ
TIIGLAQNFVGSNNIYLLLPNGAFGTRATGGKDAAAARYIYTELNKLTRKIFHPADDPLYKYIQE
DEKTVEPEWYLPILPMILVNGAEGIGTGWSTYIPPFNPLEIIKNIRHLMNDEELEQMHPWFRGWT
GTIEEIEPLRYRMYGRIEQIGDNVLEITELPARTWTSTIKEYLLLGLSGNDKIKPWIKDMEEQHD
DNIKFIITLSPEEMAKTRKIGFYERFKLISPISLMNMVAFDPHGKIKKYNSVNEILSEFYYVRLE
YYQKRKDHMSERLQWEVEKYSFQVKFIKMIIEKELTVTNKPRNAIIQELENLGFPRFNKEGKPYY
GSPNDEIAEQINDVKGATSDEEDEESSHEDTENVINGPEELYGTYEYLLGMRIWSLTKERYQKLL
KQKQEKETELENLLKLSAKDIWNTDLKAFEVGYQEFLQRDAEARG
>d1ab4__ e.11.1.1 (-) DNA Gyrase A {Escherichia coli}
VGRALPDVRDGLKPVHRRVLYAMNVLGNDWNKAYKKSARVVGDVIGKYHPHGDSAVYDTIVRMAQ
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PFSLRYMLVDGQGNFGSIDGDSAAAMRYTEIRLAKIAHELMADLEKETVDFVDNYDGTEKIPDVM
PTKIPNLLVNGSSGIAVGMATNIPPHNLTEVINGCLAYIDDEDISIEGLMEHIPGPDFPTAAIIN
GRRGIEEAYRTGRGKVYIRARAEVEVETIIVHEIPYQVNKARLIEKIAELVKEKRVEGISALRDE
SDKDGMRIVIEGEVVLNNLYSQTQLQVSFGINMVALHHGQPKIMNLKDIIAAFVRHRREVVTRRT
IFELRKARDRAHILEALAVALANIDPIIELIRHAPTPAEAKTALVANPWQLGNVAAMLEDAARPE
WLEPEFGVRDGLYYLTEQQAQAILDLRLQKLTGLEHEKLLDEYKELLDQIAELLRILGSADRLME
VIREELELVREQFGDKRRTEIT
>d1d3ya_ e.12.1.1 (A:) DNA topoisomerase IV, alpha subunit {Archaeon Methanococcus jannaschii}
QAKIFAQTTKMLEFAKQLLETDDFSTLREAYYVSKNWGEARFDDQQASNNVIEDLEAALGVLREH
LGFIPEEDGSSVVGPLKIIEETPEGELVVDCTKLGTGAYNIPNDVTKLNLETDADFILAIETSGM
FARLNAERFWDKHNCILVSLKGVPARATRRFIKRLHEEHDLPVLVFTDGDPYGYLNIYRTLKVGS
GKAIHLADKLSIPAARLIGVTPQDIIDYDLPTHPLKEQDIKRIKDGLKNDDFVRSFPEWQKALKQ
MLDMGVRAEQQSLAKYGLKYVVNTYLPEKIKDESTWLP
>d1dd9a_ e.13.1.1 (A:) DNA primase DnaG catalytic core {Escherichia coli}
TLYQLMDGLNTFYQQSLQQPVATSARQYLEKRGLSHEVIARFAIGFAPPGWDNVLKRFGGNPENR
QSLIDAGMLVTNDQGRSYDRFRERVMFPIRDKRGRVIGFGGRVLGNDTPKYLNSPETDIFHKGRQ
LYGLYEAQQDNAEPNRLLVVEGYMDVVALAQYGINYAVASLGTSTTADHIQLLFRATNNVICCYD
GDRAGRDAAWRALETALPYMTDGRQLRFMFLPDGEDPDTLVRKEGKEAFEARMEQAMPLSAFLFN
SLMPQVDLSTPDGRARLSTLALPLISQVPGETLRIYLRQELGNKLGILDDSQLE
>d1ee8a_ e.14.1.1 (A:) DNA repair protein MutM (Fpg) {Thermus thermophilus}
PELPEVETTRRRLRPLVLGQTLRQVVHRDPARYRNTALAEGRRILEVDRRGKFLLFALEGGVELV
AHLGMTGGFRLEPTPHTRAALVLEGRTLYFHDPRRFGRLFGVRRGDYREIPLLLRLGPEPLSEAF
AFPGFFRGLKESARPLKALLLDQRLAAGVGNIYADEALFRARLSPFRPARSLTEEEARRLYRALR
EVLAEAVELGGSTLSDQSYRQPDGLPGGFQTRHAVYGREGLPCPACGRPVERRVVAGRGTHFCPT
CQGEGP
>d1i3ja_ e.30.1.1 (A:) DNA-binding domain of intron endonuclease I-TevI {Bacteriophage T4}
KFCKCGVRIQTSAYTCSKCRNRSGENNSFFNHKHSDITKSKISEKMKGKKPSNIKKISCDGVIFD
CAADAARHFKISSGLVTYRVKSDKWNWFYIN
>d1a31a2 e.15.1.1 (A:215-430) Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment {Human (Homo sapiens)}
IKWKFLEHKGPVFAPPYEPLPENVKFYYDGKVMKLSPKAEEVATFFAKMLDHEYTTKEIFRKNFF
KDWRKEMTNEEKNIITNLSKCDFTQMSQYFKAQTEARKQMSKEEKLKIKEENEKLLKEYGFCIMD
NHKERIANFKIEPPGLFRGRGNHPKMGMLKRRIMPEDIIINCSKDAKVPSPPPGHKWKEVRHDNK
VTWLVSWTENIQGSIKYIMLN
>d1ois__ e.15.1.1 (-) Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment {Baker's yeast (Saccharomyces cerevisiae)}
DTIKWVTLKHNGVIFPPPYQPLPSHIKLYYDGKPVDLPPQAEEVAGFFAALLESDHAKNPVFQKN
FFNDFLQVLKESGGPLNGIEIKEFSRCDFTKMFDYFQLQKEQKKQLTSQEKKQIRLEREKFEEDY
KFCELDGRREQVGNFKVEPPDLFRGRGAHPKTGKLKRRVNPEDIVLNLSKDAPVPPAPEGHKWGE
IRHDNTVQWLAMWRENIFNSFKYVRLAA

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>d1g71a_ e.16.1.1 (A:) DNA primase {Archaeon Pyrococcus furiosus}
MLMREVTKEERSEFYSKEWSAKKIPKFIVDTLESREFGFDHNGEGPSDRKNQYSDIRDLEDYIRA
TSPYAVYSSVAFYENPREMEGWRGAELVFDIDAKDLPLKRCNHEPGTVCPICLEDAKELAKDTLI
ILREELGFENIHVVYSGRGYHIRILDEWALQLDSKSRERILAFISASEIENVEEFRRFLLEKRGW
FVLKHGYPRVFRLRLGYFILRVNVPHLLSIGIRRNIAKKILDHKEEIYEGFVRKAILASFPEGVG
IESMAKLFALSTRFSKAYFDGRVTVDIKRILRLPSTLHSKVGLIATYVGTKEREVMKFNPFRHAV
PKFRKKEVREAYKLWRESL
>d1jeya_ e.31.1.1 (A:) Ku70 subunit {Human (Homo sapiens)}
GRDSLIFLVDASKAMFESQSEDELTPFDMSIQCIQSVYISKIISSDRDLLAVVFYGTEKDKNSVN
FKNIYVLQELDNPGAKRILELDQFKGQQGQKRFQDMMGHGSDYSLSEVLWVCANLFSDVQFKMSH
KRIMLFTNEDNPHGNDSAKASRARTKAGDLRDTGIFLDLMHLKKPGGFDISLFYRDIISIAEDED
LRVHFEESSKLEDLLRKVRAKETRKRALSRLKLKLNKDIVISVGIYNLVQKALKPPPIKLYRETN
EPVKTKTRTFNTSTGGLLLPSDTKRSQIYGSRQIILEKEETEELKRFDDPGLMLMGFKPLVLLKK
HHYLRPSLFVYPEESLVIGSSTLFSALLIKCLEKEVAALCRYTPRRNIPPYFVALVPQEEELDDQ
KIQVTPPGFQLVFLPFADDKRKMPFTEKIMATPEQVGKMKAIVEKLRFTYRSDSFENPVLQQHFR
NLEALALDLMEPEQAVDLTLPKVEAMNKRLGSLVDEFKELVYPPDY
>d1jeyb_ e.31.1.2 (B:) Ku80 subunit {Human (Homo sapiens)}
NKAAVVLCMDVGFTMSNSIPGIESPFEQAKKVITMFVQRQVFAENKDEIALVLFGTDGTDNPLSG
GDQYQNITVHRHLMLPDFDLLEDIESKIQPGSQQADFLDALIVSMDVIQHETIGKKFEKRHIEIF
TDLSSRFSKSQLDIIIHSLKKCDISLQFFLPFSLGKEDGSGDRGDGPFRLGGHGPSFPLKGITEQ
QKEGLEIVKMVMISLEGEDGLDEIYSFSESLRKLCVFKKIERHSIHWPCRLTIGSNLSIRIAAYK
SILQERVKKTWTVVDAKTLKKEDIQKETVYCLNDDDETEVLKEDIIQGFRYGSDIVPFSKVDEEQ
MKYKSEGKCFSVLGFCKSSQVQRRFFMGNQVLKVFAARDDEAAAVALSSLIHALDDLDMVAIVRY
AYDKRANPQVGVAFPHIKHNYECLVYVQLPFMEDLRQYMFSSLKNSKKYAPTEAQLNAVDALIDS
MSLAKKDEKTDTLEDLFPTTKIPNPRFQRLFQCLLHRALHPREPLPPIQQHIWNMLNPPAEVTTK
SQIPLSKIKTLFPLIEAKKK
>d1daaa_ e.17.1.1 (A:) D-amino acid aminotransferase {Bacillus sp.,
strain YM-1}
GYTLWNDQIVKDEEVKIDKEDRGYQFGDGVYEVVKVYNGEMFTVNEHIDRLYASAEKIRITIPYT
KDKFHQLLHELVEKNELNTGHIYFQVTRGTSPRAHQFPENTVKPVIIGYTKENPRPLENLEKGVK
ATFVEDIRWLRCDIKSLNLLGAVLAKQEAHEKGCYEAILHRNNTVTEGSSSNVFGIKDGILYTHP
ANNMILKGITRDVVIACANEINMPVKEIPFTTHEALKMDELFVTSTTSEITPVIEIDGKLIRDGK
VGEWTRKLQKQFETKIP
>d1i1ka_ e.17.1.1 (A:) Branched-chain amino acid aminotransferase
{Escherichia coli}
KADYIWFNGEMVRWEDAKVHVMSHALHYGTSVFEGIRCYDSHKGPVVFRHREHMQRLHDSAKIYR
FPVSQSIDELMEACRDVIRKNNLTSAYIRPLIFVGDVGMGVNPPAGYSTDVIIAAFPWGAYLGAE
ALEQGIDAMVSSWNRAAPNTIPTAAKAGGNYLSSLLVGSEARRHGYQEGIALDVNGYISEGAGEN
LFEVKDGVLFTPPFTSSALPGITRDAIIKLAKELGIEVREQVLSRESLYLADEVFMSGTAAEITP
VRSVDGIQVGEGRCGPVTKRIQQAFFGLFTGETEDKWGWLDQVNQ
>d1ekfa_ e.17.1.1 (A:) Branched-chain amino acid aminotransferase
{Human (Homo sapiens), mitochondrial}
ASSSFKAADLQLEMTQKPHKKPGPGEPLVFGKTFTDHMLMVEWNDKGWGQPRIQPFQNLTLHPAS
SSLHYSLQLFEGMKAFKGKDQQVRLFRPWLNMDRMLRSAMRLCLPSFDKLELLECIRRLIEVDKD
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WVPDAAGTSLYVRPVLIGNEPSLGVSQPRRALLFVILCPVGAYFPGGSVTPVSLLADPAFIRAWV
GGVGNYKLGGNYGPTVLVQQEALKRGCEQVLWLYGPDHQLTEVGTMNIFVYWTHEDGVLELVTPP
LNGVILPGVVRQSLLDMAQTWGEFRVVERTITMKQLLRALEEGRVREVFGSGTACQVCPVHRILY
KDRNLHIPTMENGPELILRFQKELKEIQYGIRAHEWMFPV
>d1et0a_ e.17.1.1 (A:) Aminodeoxychorismate lyase {Escherichia coli}
MFLINGHKQESLAVSDRATQFGDGCFTTARVIDGKVSLLSAHIQRLQDACQRLMISCDFWPQLEQ
EMKTLAAEQQNGVLKVVISRGSGGRGYSTLNSGPATRILSVTAYPAHYDRLRNEGITLALSPVRL
GRNPHLAGIKHLNRLEQVLIRSHLEQTNADEALVLDSEGWVTECCAANLFWRKGNVVYTPRLDQA
GVNGIMRQFCIRLLAQSSYQLVEVQASLEESLQADEMVICNALMPVMPVCACGDVSFSSATLYEY
LAPLCE
>d2frvb_ e.18.1.1 (B:) Nickel-iron hydrogenase, large subunit {Desulfovibrio gigas}
NKIVVDPITRIEGHLRIEVEVEGGKIKNAWSMSTLFRGLEMILKGRDPRDAQHFTQRACGVCTYV
HALASVRAVDNCVGVKIPENATLMRNLTMGAQYMHDHLVHFYHLHALDWVNVANALNADPAKAAR
LANDLSPKKTTTESLKAVQAKVKALVESGQLGIFTNAYFLGGHPAYVLPAEVDLIATAHYLEALR
VQVKAARAMAIFGAKNPHTQFTVVGGCTNYDSLRPERIAEFRKLYKEVREFIEQVYITDLLAVAG
FYKNWAGIGKTSNFLTCGEFPTDEYDLNSRYTPQGVIWGNDLSKVDDFNPDLIEEHVKYSWYEGA
GAHHPYKGVTKPKWTEFHGEDRYSWMKAPRYKGEAFEVGPLASVLVAYAKKHEPTVKAVDLVLKT
LGVGPEALFSTLGRTAARGIQCLTAAQEVEVWLDKLEANVKAGKDDLYTDWQYPTESQGVGFVNA
PRGMLSHWIVQRGGKIENFQLVVPSTWNLGPRCAEGKLSAVEQALIGTPIADPKRPVEILRTVHS
YDPCIACGVH
>d1h2rl_ e.18.1.1 (L:) Nickel-iron hydrogenase, large subunit {Desulfovibrio vulgaris}
SSYSGPIVVDPVTRIEGHLRIEVEVENGKVKNAYSSSTLFRGLEIILKGRDPRDAQHFTQRTCGV
CTYTHALASTRCVDNAVGVHIPKNATYIRNLVLGAQYLHDHIVHFYHLHALDFVDVTAALKADPA
KAAKVASSISPRKTTAADLKAVQDKLKTFVETGQLGPFTNAYFLGGHPAYYLDPETNLIATAHYL
EALRLQVKAARAMAVFGAKNPHTQFTVVGGVTCYDALTPQRIAEFEALWKETKAFVDEVYIPDLL
VVAAAYKDWTQYGGTDNFITFGEFPKDEYDLNSRFFKPGVVFKRDFKNIKPFDKMQIEEHVRHSW
YEGAEARHPWKGQTQPKYTDLHGDDRYSWMKAPRYMGEPMETGPLAQVLIAYSQGHPKVKAVTDA
VLAKLGVGPEALFSTLGRTAARGIETAVIAEYVGVMLQEYKDNIAKGDNVICAPWEMPKQAEGVG
FVNAPRGGLSHWIRIEDGKIGNFQLVVPSTWTLGPRCDKNNVSPVEASLIGTPVADAKRPVEILR
TVHSFDPCIACGVH
>d1frfl_ e.18.1.1 (L:) Nickel-iron hydrogenase, large subunit {Desulfovibrio fructosovorans}
TPQSTFTGPIVVDPITRIEGHLRIMVEVENGKVKDAWSSSQLFRGLEIILKGRDPRDAQHFTQRA
CGVCTYVHALASSRCVDDAVKVSIPANARMMRNLVMASQYLHDHLVHFYHLHALDWVDVTAALKA
DPNKAAKLAASIDTARTGNSEKALKAVQDKLKAFVESGQLGIFTNAYFLGGHKAYYLPPEVNLIA
TAHYLEALHMQVKAASAMAILGGKNPHTQFTVVGGCSNYQGLTKDPLANYLALSKEVCQFVNECY
IPDLLAVAGFYKDWGGIGGTSNYLAFGEFATDDSSPEKHLATSQFPSGVITGRDLGKVDNVDLGA
IYEDVKYSWYAPGGDGKHPYDGVTDPKYTKLDDKDHYSWMKAPRYKGKAMEVGPLARTFIAYAKG
QPDFKKVVDMVLGKLSVPATALHSTLGRTAARGIETAIVCANMEKWIKEMADSGAKDNTLCAKWE
MPEESKGVGLADAPRGSLSHWIRIKGKKIDNFQLVVPSTWNLGPRGPQGDKSPVEEALIGTPIAD
PKRPVEILRTVHAFDPCIACGVH
>d1cc1l_ e.18.1.1 (L:) Nickel-iron hydrogenase, large subunit

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{Desulfomicrobium baculatum}
VKISIDPLTRVEGHLKIEVEVKDGKVVDAKCSGGMFRGFEQILRGRDPRDSSQIVQRICGVCPTA
HCTASVMAQDDAFGVKVTTNGRITRNLIFGANYLQSHILHFYHLAALDYVKGPDVSPFVPRYANA
DLLTDRIKDGAKADATNTYGLNQYLKALEIRRICHEMVAMFGGRMPHVQGMVVGGATEIPTADKV
AEYAARFKEVQKFVIEEYLPLIYTLGSVYTDLFETGIGWKNVIAFGVFPEDDDYKTFLLKPGVYI
DGKDEEFDSKLVKEYVGHSFFDHSAPGGLHYSVGETNPNPDKPGAYSFVKAPRYKDKPCEVGPLA
RMWVQNPELSPVGQKLLKELYGIEAKKFRDLGDKAFSIMGRHVLRAEETWLTAVAVEKWLKQVQP
GAETYVKSEIPDAAEGTGFTEAPRGALLHYLKIKDKKIENYQIVSATLWNANPRDDMGQRGPIEE
ALIGVPVPDIKNPVNVGRLVRSYDPXLGCAVH
>d1e3db_ e.18.1.1 (B:) Nickel-iron hydrogenase, large subunit
{Desulfovibrio desulfuricans}
TPRSNYTGPIVVDPLTRIEGHLRIEVEVEGGVIKEARSCATLFRGIETILKGRDPRDAQHFTQRT
CGVCTYTHALASTRCLEDAINKPIPANATYIRNLVLGNQFMHDHLVHFYHLHALDFVDVTSALLA
DPAKAAKLANSISPRKATTEEFAAVQAKLKTFVASGQLGPFTNAYFLGGHEGYYMDPEANLVCTA
HYLQALRAQVEVAKGMAVFGAKNPHTQFTVAGGVTCYEALTPERIKQFRELYVKARAFIEEVYIP
DLLLVASYYKDWGKIGGTNNFMAFGEFPAPGGERDLNSRWYKPGVIYDRKVGSVQPFDPSKIEEH
VRHSWYEGKARAPFEGETNPHFTFMGDTDKYSWNKAPRYDGHAVETGPLAQMLVAYGHNHKTIKP
TIDAVLGKLNLGPEALFSTLGRTAARGIQTLVIAQQMENWLNEYENNIVKDKQIVEDYAVPTSAR
GVGFADVSRGGLSHWMTIEDGKIDNFQLVVPTTWNLGPRDDKGVPSAAEAALVGTPVADPKRPVE
ILRTIHSFDPCIACSTH
>d2frva_ e.19.1.1 (A:) Nickel-iron hydrogenase, small subunit
{Desulfovibrio gigas}
KKRPSVVYLHNAECTGCSESVLRTVDPYVDELILDVISMDYHETLMAGAGHAVEEALHEAIKGDF
VCVIEGGIPMGDGGYWGKVGGRNMYDICAEVAPKAKAVIAIGTCATYGGVQAAKPNPTGTVGVNE
ALGKLGVKAINIAGCPPNPMNFVGTVVHLLTKGMPELDKQGRPVMFFGETVHDNCPRLKHFEAGE
FATSFGSPEAKKGYCLYELGCKGPDTYNNCPKQLFNQVNWPVQAGHPCIACSEPNFWDLYSPFYS
A
>d1h2rs_ e.19.1.1 (S:) Nickel-iron hydrogenase, small subunit
{Desulfovibrio vulgaris}
LMGPRRPSVVYLHNAECTGCSESVLRAFEPYIDTLILDTLSLDYHETIMAAAGDAAEAALEQAVN
SPHGFIAVVEGGIPTAANGIYGKVANHTMLDICSRILPKAQAVIAYGTCATFGGVQAAKPNPTGA
KGVNDALKHLGVKAINIAGCPPNPYNLVGTIVYYLKNKAAPELDSLNRPTMFFGQTVHEQCPRLP
HFDAGEFAPSFESEEARKGWCLYELGCKGPVTMNNCPKIKFNQTNWPVDAGHPCIGCSEPDFWDA
MTPFYQN
>d1frfs_ e.19.1.1 (S:) Nickel-iron hydrogenase, small subunit
{Desulfovibrio fructosovorans}
KHRPSVVWLHNAECTGCTEAAIRTIKPYIDALILDTISLDYQETIMAAAGETSEAALHEALEGKD
GYYLVVEGGLPTIDGGQWGMVAGHPMIETCKKAAAKAKGIICIGTCSPYGGVQKAKPNPSQAKGV
SEALGVKTINIPGCPPNPINFVGAVVHVLTKGIPDLDENGRPKLFYGELVHDNCPRLPHFEASEF
APSFDSEEAKKGFCLYELGCKGPVTYNNCPKVLFNQVNWPVQAGHPCLGCSEPDFWDTMTPFYEQ
G
>d1cc1s_ e.19.1.1 (S:) Nickel-iron hydrogenase, small subunit
{Desulfomicrobium baculatum}
KKAPVIWVQGQGCTGCSVSLLNAVHPRIKEILLDVISLEFHPTVMASEGEMALAHMYEIAEKFNG
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NFFLLVEGAIPTAKEGRYCIVGETLDAKAHHHEVTMMELIRDLAPKSLATVAVGTCSAYGGIPAA
EGNVTGSKSVRDFFADEKIEKLLVNVPGCPPHPDWMVGTLVAAWSHVLNPTEHPLPELDDDGRPL
LFFGDNIHENCPYLDKYDNSEFAETFTKPGCKAELGCKGPSTYADCAKRRWNNGINWCVENAVCI
GCVEPDFPDGKSPFYVAE
>d1e3da_ e.19.1.1 (A:) Nickel-iron hydrogenase, small subunit {Desulfovibrio desulfuricans}
SRPSVVYLHAAECTGCSEALLRTYQPFIDTLILDTISLDYHETIMAAAGEAAEEALQAAVNGPDG
FICLVEGAIPTGMDNKYGYIAGHTMYDICKNILPKAKAVVSIGTCACYGGIQAAKPNPTAAKGIN
DCYADLGVKAINVPGCPPNPLNMVGTLVAFLKGQKIELDEVGRPVMFFGQSVHDLCERRKHFDAG
EFAPSFNSEEARKGWCLYDVGCKGPETYNNCPKVLFNETNWPVAAGHPCIGCSEPNFWDDMTPFY
QN
>d1dg4a_ e.20.1.1 (A:) DnaK {Escherichia coli}
LSLGIETMGGVMTTLIAKNTTIPTKHSQVFSTAEDNQSAVTIHVLQGERKRAADNKSLGQFNLDG
INPAPRGMPQIEVTFDIDADGILHVSAKDKNSGKEQKITIKASSGL
>d1dkza_ e.20.1.1 (A:) DnaK {Escherichia coli}
VLLLDVTPLSLGIETMGGVMTTLIAKNTTIPTKHSQVFSTAEDNQSAVSIHVLQGERKRAADNKS
LGQFNLDGINPAPRGMPQIEVTFDIDADGILHVSAKDKNSGKEQKITIKASSGLNEDEIQKMVRD
AEANAEADRKFEELVQTRNQGDHLLHSTRKQVEEAGDKLPADDKTAIESALTALETALKGEDKAA
IEAKMQELAQVSQKLMEIAQ
>d2bpr__ e.20.1.1 (-) DnaK {Escherichia coli}
SIEGRVKDVLLLDVTPLSLGIETMGGVMTTLIAKNTTIPTKHSQVFSTAEDNQSAVTIHVLQGER
KRAADNKSLGQFNLDGINPAPRGMPQIEVTFDIDADGILHVSAKDKNSGKEQKITIKASSGLNED
EIQKMVRDAEANAEADRKFEELVQTRNQGDHLLHSTRKQVEEA
>d1ckra_ e.20.1.1 (A:) DnaK {Rat (Rattus norvegicus)}
SENVQDLLLLDVTPLSLGIETAGGVMTVLIKRNTTIPTKQTQTFTTYSDNQPGVLIQVYEGERAM
TKDNNLLGKFELTGIPPAPRGVPQIEVTFDIDANGILNVSAVDKSTGKENKITITNDKGRLSKED
IERMVQEAEKYKAEDEKQRDKVSSKNSLE
>d1dqsa_ e.22.1.1 (A:) Dehydroquinate synthase, DHQS {Aspergillus nidulans}
PTKISILGRESIIADFGLWRNYVAKDLISDCSSTTYVLVTDTNIGSIYTPSFEEAFRKRAAEITP
SPRLLIYNRPPGEVSKSRQTKADIEDWMLSQNPPCGRDTVVIALGGGVIGDLTGFVASTYMRGVR
YVQVPTTLLAMVDSSIGGKTAIDTPLGKNLIGAIWQPTKIYIDLEFLETLPVREFINGMAEVIKT
AAISSEEEFTALEENAETILKAVRREVTPGEHRFEGTEEILKARILASARHKAYVVSADEREGGL
RNLLNWGHSIGHAIEAILTPQILHGECVAIGMVKEAELARHLGILKGVAVSRIVKCLAAYGLPTS
LKDARIRKLTAGKHCSVDQLMFNMALDKKNDGPKKKIVLLSAIGTPYETRASVVANEDIRVVL
>d1jq5a_ e.22.1.2 (A:) Glycerol dehydrogenase {Bacillus stearothermophilus}
AAERVFISPAKYVQGKNVITKIANYLEGIGNKTVVIADEIVWKIAGHTIVNELKKGNIAAEEVVF
SGEASRNEVERIANIARKAEAAIVIGVGGGKTLDTAKAVADELDAYIVIVPTAASTDAPTSALSV
IYSDDGVFESYRFYKKNPDLVLVDTKIIANAPPRLLASGIADALATWVEARSVIKSGGKTMAGGI
PTIAAEAIAEKCEQTLFKYGKLAYESVKAKVVTPALEAVVEANTLLSGLGFESGGLAAAHAIHNG
FTALEGEIHHLTHGEKVAFGTLVQLALEEHSQQEIERYIELYLCLDLPVTLEDIKLKDASREDIL
KVAKAATAEGETIHNAFNVTADDVADAIFAADQYAKAYKEK
>d1kq3a_ e.22.1.2 (A:) Glycerol dehydrogenase {Thermotoga maritima,
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TM0423}
HMITTTIFPGRYVQGAGAINILEEELSRFGERAFVVIDDFVDKNVLGENFFSSFTKVRVNKQIFG
GECSDEEIERLSGLVEEETDVVVGIGGGKTLDTAKAVAYKLKKPVVIVPTIASTDAPCSALSVIY
TPNGEFKRYLFLPRNPDVVLVDTEIVAKAPARFLVAGMGDALATWFEAESCKQKYAPNMTGRLGS
MTAYALARLCYETLLEYGVLAKRSVEEKSVTPALEKIVEANTLLSGLGFESGGLAAAHAIHNGLT
VLENTHKYLHGEKVAIGVLASLFLTDKPRKMIEEVYSFCEEVGLPTTLAEIGLDGVSDEDLMKVA
EKACDKNETIHNEPQPVTSKDVFFALKAADRYGRMRKNL
>d1lci__ e.23.1.1 (-) Luciferase {Firefly (Photinus pyralis)}
AKNIKKGPAPFYPLEDGTAGEQLHKAMKRYALVPGTIAFTDAHIEVNITYAEYFEMSVRLAEAMK
RYGLNTNHRIVVCSENSLQFFMPVLGALFIGVAVAPANDIYNERELLNSMNISQPTVVFVSKKGL
QKILNVQKKLPIIQKIIIMDSKTDYQGFQSMYTFVTSHLPPGFNEYDFVPESFDRDKTIALIMNS
SGSTGLPKGVALPHRTACVRFSHARDPIFGNQIIPDTAILSVVPFHHGFGMFTTLGYLICGFRVV
LMYRFEEELFLRSLQDYKIQSALLVPTLFSFFAKSTLIDKYDLSNLHEIASGGAPLSKEVGEAVA
KRFHLPGIRQGYGLTETTSAILITPEGDDKPGAVGKVVPFFEAKVVDLDTGKTLGVNQRGELCVR
GPMIMSGYVNNPEATNALIDKDGWLHSGDIAYWDEDEHFFIVDRLKSLIKYKGYQVAPAELESIL
LQHPNIFDAGVAGLPDDDAGELPAAVVVLEHGKTMTEKEIVDYVASQVTTAKKLRGGVVFVDEVP
KGLTGKLDARKIREILIKAKK
>d1amua_ e.23.1.1 (A:) Phenylalanine activating domain of gramicidin
synthetase 1 {Bacillus brevis}
GTHEEEQYLFAVNNTKAEYPRDKTIHQLFEEQVSKRPNNVAIVCENEQLTYHELNVKANQLARIF
IEKGIGKDTLVGIMMEKSIDLFIGILAVLKAGGAYVPIDIEYPKERIQYILDDSQARMLLTQKHL
VHLIHNIQFNGQVEIFEEDTIKIREGTNLHVPSKSTDLAYVIYTSGTTGNPKGTMLEHKGISNLK
VFFENSLNVTEKDRIGQFASISFDASVWEMFMALLTGASLYIILKDTINDFVKFEQYINQKEITV
ITLPPTYVVHLDPERILSIQTLITAGSATSPSLVNKWKEKVTYINAYGPTETTICATTWVATKET
IGHSVPIGAPIQNTQIYIVDENLQLKSVGEAGELCIGGEGLARGYWKRPELTSQKFVDNPFVPGE
KLYKTGDQARWLSDGNIEYLGRIDNQVKIRGHRVELEEVESILLKHMYISETAVSVHKDHQEQPY
LCAYFVSEKHIPLEQLRQFSSEELPTYMIPSYFIQLDKMPLTSNGKIDRKQLPEPDLTF
>d1ad2__ e.24.1.1 (-) Ribosomal protein L1 {Thermus thermophilus}
KRYRALLEKVDPNKIYTIDEAAHLVKELATAKFDETVEVHAKLGIDPRRSDQNVRGTVSLPHGLG
KQVRVLAIAKGEKIKEAEEAGADYVGGEEIIQKILDGWMDFDAVVATPDVMGAVGSKLGRILGPR
GLLPNPKAGTVGFNIGEIIREIKAGRIEFRNDKTGAIHAPVGKACFPPEKLADNIRAFIRALEAH
KPEGAKGTFLRSVYVTTTMGPSVRINPHS
>d1cjsa_ e.24.1.1 (A:) Ribosomal protein L1 {Archaeon Methanococcus
jannaschii}
MDREALLQAVKEARELAKPRNFTQSFEFIATLKEIDMRKPENRIKTEVVLPHGRGKEAKIAVIGT
GDLAKQAEELGLTVIRKEEIEELGKNKRKLRKIAKAHDFFIAQADLMPLIGRYMGVILGPRGKMP
KPVPANANIKPLVERLKKTVVINTRDKPYFQVLVGNEKMTDEQIVDNIEAVLNVVAKKYEKGLYH
IKDAYVKLTMGPAVKVKK
>d1dwua_ e.24.1.1 (A:) Ribosomal protein L1 {Archaeon Methanococcus
thermolithotrophicus}
MDRENILKAVKEARSLAKPRNFTQSLDLIINLKELDLSRPENRLKEQVVLPNGRGKEPKIAVIAK
GDLAAQAEEMGLTVIRQDELEELGKNKKMAKKIANEHDFFIAQADMMPLVGKTLGPVLGPRGKMP
QPVPANANLTPLVERLKKTVLINTRDKPLFHVLVGNEKMSDEELAENIEAILNTVSRKYEKGLYH
VKSAYTKLTMGPPAQIEK
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>d1dn1a_ e.25.1.1 (A:) Neuronal Sec1, NSec1 {Rat (Rattus norvegicus)}
IGLKAVVGEKIMHDVIKKVKKKGEWKVLVVDQLSMRMLSSCCKMTDIMTEGITIVEDINKRREPL
PSLEAVYLITPSEKSVHSLISDFKDPPTAKYRAAHVFFTDSCPDALFNELVKSRAAKVIKTLTEI
NIAFLPYESQVYSLDSADSFQSFYSPHKAQMKNPILERLAEQIATLCATLKEYPAVRYRGEYKDN
ALLAQLIQDKLDAYKADDPTMGEGPDKARSQLLILDRGFDPSSPVLHELTFQAMSYDLLPIENDV
YKYETSGIGEARVKEVLLDEDDDLWIALRHKHIAEVSQEVTRSLKDFSSSKRMNTGEKTTMRDLS
QMLKKMPQYQKELSKYSTHLHLAEDCMKHYQGTVDKLCRVEQDLAMGTDAEGEKIKDPMRAIVPI
LLDANVSTYDKIRIILLYIFLKNGITEENLNKLIQHAQIPPEDSEIITNMAHLGVPIVTDSTLRR
RSKPERKERISEQTYQLSRWTPIIKDIMEDTIEDKLDTKHYPYISTRSSASFSTTAVSARYGHWH
KNKAPGEYRSGPRLIIFILGGVSLNEMRCAYEVTQANGKWEVLIGSTHILTPQKLLDTLKKLNKT
DEEI
>d1epua_ e.25.1.1 (A:) Neuronal Sec1, NSec1 {Longfin inshore squid
(Loligo pealei)}
ALKTAVHEKIMNDVVLAVKKNAEWKVLIVDQLSMRMVSACCKMHEIMSEGITLVEDINRRREPLP
LLEAVYLITPTEESVKCLMADFQNPDNPQYRGAHIFFTEACPEELFKELCKSTTARFIKTLKEIN
IAFLPYESQIFSLDSPDTFQVYYNPSRAQGGIPNKERCAEQIATLCATLGEYPSVRYRSDFDENA
SFAQLVQQKLDAYRADDPTMGEGPQKDRSQLLILDRGFDPISPLLHELTFQAMAYDLLPIENDVY
KYVNTGGNEVPEKEVLLDEKDDLWVEMRHQHIAVVSQNVTKKLKQFADEKRMGTAADKAGIKDLS
QMLKKMPQYQKELSKYSTHLHLAEDCMKQYQQHVDKLCKVEQDLAMGTDADGEKIRDHMRNIVPI
LLDQKISAYDKIRIILLYIIHKGGISEENLAKLVQHAHIPAEEKWIINDMQNLGVPIIQDGGRRK
IPQPYHTHNRKERQADHTYQMSRWTPYMKDIMEAAVEDKLDTRHYPFLNGGGPRPSCQQPVSVRY
GHWHKDKGQASYKSGPRLIIFVVGGISYSEMRSAYEVTQTAKNNWEVILGSTHILTPEGLLRDLR
KISNP
>d1e2ua_ e.26.1.1 (A:) Hybrid cluster protein (prismane protein)
{Desulfovibrio vulgaris}
MFCFQCQETAKNTGCTVKGMCGKPEETANLQDLLIFVLRGIAIYGEKLKELGQPDRSNDDFVLQG
LFATITNANWDDARFEAMISEGLARRDKLRNAFLAVYKAKNGKDFSEPLPEAATWTGDSTAFAEK
AKSVGILATENEDVRSLRELLIIGLKGVAAYAEHAAVLGFRKTEIDEFMLEALASTTKDLSVDEM
VALVMKAGGMAVTTMALLDEANTTTYGNPEITQVNIGVGKNPGILISGHDLKDMAELLKQTEGTG
VDVYTHGEMLPANYYPAFKKYPHFVGNYGGSWWQQNPEFESFNGPILLTTNCLVPLKKENTYLDR
LYTTGVVGYEGAKHIADRPAGGAKDFSALIAQAKKCPPPVEIETGSIVGGFAHHQVLALADKVVE
AVKSGAIKRFVVMAGCDGRQKSRSYYTEVAENLPKDTVILTAGCAKYRYNKLNLGDIGGIPRVLD
AGQCNDSYSLAVIALKLKEVFGLDDINDLPVSYDIAWYEQKAVAVLLALLFLGVKGIRLGPTLPA
FLSPNVAKVLVENFNIKPIGTVQDDIAAMMAGK
>d1jjya_ e.26.1.2 (A:) Ni-containing carbon monoxide dehydrogenase
{Carboxydothermus hydrogenoformans}
QNLKSTDRAVQQMLDKAKREGIQTVWDRYEAMKPQCGFGETGLCCRHCLQGPCRINPFGDEPKVG
ICGATAEVIVARGLDRSIAAGAAGHSGHAKHLAHTLKKAVQGKAASYMIKDRTKLHSIAKRLGIP
TEGQKDEDIALEVAKAALADFHEKDTPVLWVTTVLPPSRVKVLSAHGLIPAGIDHEIAEIMHRTS
MGCDADAQNLLLGGLRCSLADLAGCYMGTDLADILFGTPAPVVTESNLGVLKADAVNVAVHGHNP
VLSDIIVSVSKEMENEARAAGATGINVVGICCTGNEVLMRHGIPACTHSVSQEMAMITGALDAMI
LDYQCIQPSVATIAECTGTTVITTMEMSKITGATHVNFAEEAAVENAKQILRLAIDTFKRRKGKP
VEIPNIKTKVVAGFSTEAIINALSKLNANDPLKPLIDNVVNGNIRGVCLFAGCNNVKVPQDQNFT
TIARKLLKQNVLVVATGCGAGALMRHGFMDPANVDELCGDGLKAVLTAIGEANLGGPLPPVLHM
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GSCVDNSRSVALVAALANRLGVDMDRLPVVASAAQAMHEKAVAIGTWAVTIGLPTHIGVFPPITG
SLPVTQILTSSVKDITGGYFIVELDPQVAADKLLAAINERRAGLGLPR
>d1jqka_ e.26.1.2 (A:) Ni-containing carbon monoxide dehydrogenase
{Rhodospirillum rubrum}
ETAWHRYEKQQPQCGFGSAGLCCRICLKGPCRIDPFGEGPKYGVCGADRDTIVARHLVRMIAAGT
AAHSEHGRHIALAMQHISQGELHDYSIRDEAKLYAIAKTLGVATEGRGLLAIVGDLAAITLGDFQ
NQDYDKPCAWLAASLTPRRVKRLGDLGLLPHNIDASVAQTMSRTHVGCDADPTNLILGGLRVAMA
DLDGSMLATELSDALFGTPQPVVSAANLGVMKRGAVNIAVNGHNPMLSDIICDVAADLRDEAIAA
GAAEGINIIGICCTGHEVMMRHGVPLATNYLSQELPILTGALEAMVVDVQCIMPSLPRIAECFHT
QIITTDKHNKISGATHVPFDEHKAVETAKTIIRMAIAAFGRRDPNRVAIPAFKQKSIVGFSAEAV
VAALAKVNADDPLKPLVDNVVNGNIQGIVLFVGCNTTKVQQDSAYVDLAKSLAKRNVLVLATGCA
AGAFAKAGLMTSEATTQYAGEGLKGVLSAIGTAAGLGGPLPLVMHMGSCVDNSRAVALATALANK
LGVDLSDLPLVASAPECMSEKALAIGSWAVTIGLPTHVGSVPPVIGSQIVTKLVTETAKDLVGGY
FIVDTDPKSAGDKLYAAIQERRAGL
>d1h5wa_ e.27.1.1 (A:) Upper collar protein gp10 (connector protein)
{Bacteriophage PHI29}
RQKRNRWFIHYLNYLQSLAYQLFEWENLPPTINPSFLEKSIHQFGYVGFYKDPVISYIACNGALS
GQRDVYNQATVFRAASPVYQKEFKLYNYRDMKEEDMGVVIYNNDMAFPTTPTLELFAAELAELKE
IISVNQNAQKTPVLIRANDNNQLSLKQVYNQYEGNAPVIFAHEALDSDSIEVFKTDAPYVVDKLN
AQKNAVWNEMMTFLGIKNANLEKKERMVTDEVSSNDEQIESSGTVFLKSREEACEKINELYGLNV
KVKFRYDI
>d1io1a_ e.32.1.1 (A:) F41 fragment of flagellin {Salmonella
typhimurium}
NIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELAVQSANSTNSQSDLDSIQAEITQRLN
EIDRVSGQTQFNGVKVLAQDNTLTIQVGANDGETIDIDLKQINSQTLGLDTLNVQQKYKVSDTAA
TVTGYADTTIALDNSTFKASATGLGGTDQKIDGDLKFDDTTGKYYAKVTVTGGTGKDGYYEVSVD
KTNGEVTLAGGATSPLTGGLPATATEDVKNVQVANADLTEAKAALTAAGVTGTASVVKMSYTDNN
GKTIDGGLAVKVGDDYYSATQNKDGSISINTTKYTADDGTSKTALNKLGGADGKTEVVSIGGKTY
AASKAEGHNFKAQPDLAEAAATTTENPLQKIDAALAQVDTLRSDLAAVQNRFNSAITNLGNTVNN
LTSAR
>d1htya_ e.33.1.1 (A:) Golgi alpha-mannosidase II {Fruit fly
(Drosophila melanogaster)}
CQDVVQDVPNVDVQMLELYDRMSFKDIDGGVWKQGWNIKYDPLKYNAHHKLKVFVVPHSHNDPGW
IQTFEEYYQHDTKHILSNALRHLHDNPEMKFIWAEISYFARFYHDLGENKKLQMKSIVKNGQLEF
VTGGWVMPDEANSHWRNVLLQLTEGQTWLKQFMNVTPTASWAIDPFGHSPTMPYILQKSGFKNML
IQRTHYSVKKELAQQRQLEFLWRQIWDNKGDTALFTHMMPFYSYDIPHTCGPDPKVCCQFDFKRM
GSFGLSCPWKVPPRTISDQNVAARSDLLVDQWKKKAELYRTNVLLIPLGDDFRFKQNTEWDVQRV
NYERLFEHINSQAHFNVQAQFGTLQEYFDAVHQAERAGQAEFPTLSGDFFTYADRSDNYWSGYYT
SRPYHKRMDRVLMHYVRAAEMLSAWHSWDGMARIEERLEQARRELSLFQHHDGITGTAKTHVVVD
YEQRMQEALKACQMVMQQSVYRLLTKPSIYSPDFSFSYFTLDDSRWPGSGVEDSRTTIILGEDIL
PSKHVVMHNTLPHWREQLVDFYVSSPFVSVTDLANNPVEAQVSPVWSWHHDTLTKTIHPQGSTTK
YRIIFKARVPPMGLATYVLTISDSKPEHTSYASNLLLRKNPTSLPLGQYPEDVKFGDPREISLRV
GNGPTLAFSEQGLLKSIQLTQDSPHVPVHFKFLKYGVRSHGDRSGAYLFLPNGPASPVELGQPVV
LVTKGKLESSVSVGLPSVVHQTIMRGGAPEIRNLVDIGSLDNTEIVMRLETHIDSGDIFYTDLNG
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LQFIKRRRLDKLPLQANYYPIPSGMFIEDANTRLTLLTGQPLGGSSLASGELEIMQDRRLASDDE
RGLGQGVLDNKPVLHIYRLVLEKVNNCVRPSKLHPAGYLTSAAHKASQSLLDPLDKFIFAENEWI
GAQGQFGGDHPSAREDLDVSVMRRLTKSSAKTQRVGYVLHRTNLMQCGTPEEHTQKLDVCHLLPN
VARCERTTLTFLQNLEHLDGMVAPEVCPMETAAYVSSHS
>d1knza_ e.34.1.1 (A:) NSP3 homodimer {Simian 11 rotavirus}
TQQMAVSIINSSFEAAVVAATSALENMGIEYDYQDIYSRVKNKFDFVMDDSGVKNNPIGKAITID
QALNNKFGSAIRNRNWLADTSRPAKLDEDVNKLRMMLSSKGIDQKMRVLNACFSVKRIPGKSSSI
IKCTKLMRDKLERGEVEVDDSFVDEKM
>g1jmu.1 e.35.1.1 (A:,B:) Membrane penetration protein mu1 {Reovirus}
TINVTGDGNVFKPSAETSSTAVPSLSLSPGMLNXPGGVPWIAIGDETSVTSPGALRRMTSKDIPE
TAIINTDNSSGAVPSESALVPYNDEPLVVVTEHAIANFTKAEMALEFNREFLDKLRVLSVSPKYS
DLLTYVDCYVGVSARQALNNFQKQVPVITPTRQTMYVDSIQAALKALEKWEIDLRVAQTLLPTNV
PIGEVSCPMQSVVKLLDDQLPDDSLIRRYPKEAAVALAKRNGGIQWMDVSEGTVMNEAVNAVAAS
ALAPSASAPPLEEKSKLTEQAMDLVTAAEPEIIASLVPVPAPVFAIPPKPADYNVRTLKIDEATW
LRMIPKTMGTLFQIQVTDNTGTNWHFNLRGGTRVVNLDQIAPMRFVLDLGGKSYKETSWDPNGKK
VGFIVFQSKIPFELWTAASQIGQATVVNYVQLYAEDSSFTAQSIIATTSLAYNYEPEQLNKTDPE
MNYYLLATFIDSAAITPTNMTQPDVWDALLTMSPLSAGEVTVKGAVVSEVVPAELIGSYTPESLN
ASLPNDAARCMIDRASKIAEAIKIDDDAGPDEYSPNSVPIQGQLAISQLETGYGVRIFNPKGILS
KIASRAMQAFIGDPSTIITQAAPVLSDKNNWIALAQGVKTSLRTKSLSAGVKTAVSKLSSSESIQ
NWTQGFLDKVSTHFPAP
>d2btva_ e.28.1.1 (A:) BTV inner layer core protein vp3 {Bluetongue
virus, strain 1}
VDFTVPDVQQILDDIKALAAEQVYKIVKVPSTSFRHIVTQSRDRVLRVDTYYEEMSQVGDVITED
EPEKFYSTIIKKVRFIRGKGSFILHDIPARDHRGMEVAEPEVLGVEFKNVLPVLTAEHRAMIQNA
LDGSIIENGNVATRDVDVFIGACSEPIYRIYNRLQGYIEAVQLQELRNSIGWLERLGQRKRITYS
QEVLTDFRRQDMIWVLALQLPVNPQVVWDVPRSSIANLIMNIATCLPTGEYIAPNPRISSITLTQ
RITTTGPFAILTGSTPTAQQLNDVRKIYLALMFPGQIILDLKIDPGERMDPAVRMVAGVVGHLLF
TAGGRFTNLTQNMARQLDIALNDYLLYMYNTRVQVNYGPTGEPLDFQIGRNQYDCNVFRADFATG
TGYNGWATIDVEYRDPAPYVHAQRYIRYCGIDSRELINPTTYGIGMTYHCYNEMLRMLVAAGKDS
EAAYFRSMLPFHMVRFARINQIINEDLHSVFSLPDDMFNALLPDLIAGAHQNADPVVLDVSWISL
WFAFNRSFEPTHRNEMLEIAPLIESVYASELSVMKVDMRHLSLMQRRFPDVLIQARPSHFWKAVL
NDSPEAVKAVMNLSHSHNFINIRDMMRWVLLPSLQPSLKLVLEEEAWAAANDFEDLMLTDQVYMH
RDMLPEPRLDDIERFRQEGFYYTNMLEAPPEIDRVVQYTYEIARLQANMGQFRAALRRIMDDDDW
VRFGGVLRTVRVKFFDARPPDDILQGLPFSYDTNEKGGLSYATIKYATETTIFYLIYNVEFSNTP
DSLVLINPTYTMTKVFINKRIVERVRVGQILAVLNRRFVAYKGKMRIMDITQSLKMGTKLAAPTV
>d1cola_ f.1.1.1 (A:) Colicin A {Escherichia coli}
AKDERELLEKTSELIAGMGDKIGEHLGDKYKAIAKDIADNIKNFQGKTIRSFDDAMASLNKITAN
PAMKINKADRDALVNAWKHVDAQDMANKLGNLSKAFKVADVVMKVEKVREKSIEGYETGNWGPLM
LEVESWVLSGIASSVALGIFSATLGAYALSLGVPAIAVGIAGILLAAVVGALIDDKFADALNNEI
IR
>d1a87__ f.1.1.1 (-) Colicin N {Escherichia coli}
SAKVGEITITPDNSKPGRYISSNPEYSLLAKLIDAESIKGTEVYTFHTRKGQYVKVTVPDSNIDK
MRVDYVNWKGPKYNNKLVKRFVSQFLLFRKEEKEKNEKEALLKASELVSGMGDKLGEYLGVKYKN
VAKEVANDIKNFHGRNIRSYNEAMASLNKVLANPKMKVNKSDKDAIVNAWKQVNAKDMANKIGNL
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GKAFKVADLAIKVEKIREKSIEGYNTGNWGPLLLEVESWIIGGVVAGVAISLFGAVLSFLPISGL
AVTALGVIGIMTISYLSSFIDANRVSNINNIISSVIR
>d1cii_1 f.1.1.1 (451-624) Colicin Ia {Escherichia coli}
DAINFTTEFLKSVSEKYGAKAEQLAREMAGQAKGKKIRNVEEALKTYEKYRADINKKINAKDRAA
IAAALESVKLSDISSNLNRFSRGLGYAGKFTSLADWITEFGKAVRTENWRPLFVKTETIIAGNAA
TALVALVFSILTGSALGIIGYGLLMAVTGALIDESLVEKANKFW
>d1f0la3 f.1.2.1 (A:201-380) Diphtheria toxin, middle domain {Corynebacterium diphtheriae}
CINLDWDVIRDKTKTKIESLKEHGPIKNKMSESPNKTVSEEKAKQYLEEFHQTALEHPELSELKT
VTGTNPVFAGANYAAWAVNVAQVIDSETADNLEKTTAALSILPGIGSVMGIADGAVHHNTEEIVA
QSIALSSLMVAQAIPLVGELVDIGFAAYNFVESIINLFQVVHNSYNRPAY
>d1dlc_3 f.1.3.1 (61-289) delta-Endotoxin (insectocide), N-terminal domain {Bacillus thuringiensis tenebrionis, CRYIIIA (BT13)}
TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQKIADYA
KNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNSMPSFAISGYE
VLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYTDHCVKWYNVGLDKLR
GSSYESWVNFNRYRREMTLTVLDLIALFPLYDVR
>d1ji6a3 f.1.3.1 (A:64-290) delta-Endotoxin (insectocide), N-terminal domain {Bacillus thuringiensis, CRY3bb1}
DAVGTGISVVGQILGVVGVPFAGALTSFYQSFLNTIWPSDADPWKAFMAQVEVLIDKKIEEYAKS
KALAELQGLQNNFEDYVNALNSWKKTPLSLRSKRSQDRIRELFSQAESHFRNSMPSFAVSKFEVL
FLPTYAQAANTHLLLLKDAQVFGEEWGYSSEDVAEFYHRQLKLTQQYTDHCVNWYNVGLNGLRGS
TYDAWVKFNRFRREMTLTVLDLIVLFPFYDIR
>d1ciy_3 f.1.3.1 (33-255) delta-Endotoxin (insectocide), N-terminal domain {Bacillus thuringiensis, CRYIA (A)}
YTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI
SRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYV
QAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWV
RYNQFRRELTLTVLDIVALFSNYDSRRY
>d1i5pa3 f.1.3.1 (A:1-263) delta-Endotoxin (insectocide), N-terminal domain {Bacillus thuringiensis subsp. kurstaki, CRY2AA}
MNNVLNSGRTTICDAYNVVAHDPFSFEHKSLDTIQKEWMEWKRTDHSLYVAPVVGTVSSFLLKKV
GSLIGKRILSELWGIIFPSGSTNLMQDILRETEQFLNQRLNTDTLARVNAELIGLQANIREFNQQ
VDNFLNPTQNPVPLSITSSVNTMQQLFLNRLPQFQIQGYQLLLLPLFAQAANMHLSFIRDVILNA
DEWGISAATLRTYRDYLRNYTRDYSNYCINTYQTAFRGLNTRLHDMLEFRTYMFLNVFEYVSIWS
LFK
>d1g5ma_ f.1.4.1 (A:) Bcl-2 {Human (Homo sapiens)}
HAGRTGYDNREIVMKYIHYKLSQRGYEWDAGDDVEENRTEAPEGTESEVVHLALRQAGDDFSRRY
RGDFAEMSSQLHLTPFTARGRFATVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNI
ALWMTEYLNRHLHTWIQDNGGWDAFVELYGPSMR
>d1bxla_ f.1.4.1 (A:) Apoptosis regulator Bcl-xL {Human (Homo sapiens)}
MSMAMSQSNRELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEAVKQALREAGDEFELRY
RRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRI
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AAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQERLEHHHHHH
>d1lxl__ f.1.4.1 (-) Apoptosis regulator Bcl-xL {Human (Homo sapiens)}
MSMAMSQSNRELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLAD
SPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQV
VNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTF
VELYGNNAAAESRKGQERLEHHHHHH
>d1maz__ f.1.4.1 (-) Apoptosis regulator Bcl-xL {Human (Homo sapiens)}
MSQSNRELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV
NGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNEL
FRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELY
G
>d2bida_ f.1.4.1 (A:) Proapoptotic molecule Bid {Human (Homo sapiens)}
GSMDCEVNNGSSLRDECITNLLVFGFLQSCSDNSFRRELDALGHELPVLAPQWEGYDELQTDGNR
SSHSRLGRIEADSESQEDIIRNIARHLAQVGDSMDRSIPPGLVNGLALQLRNTSRSEEDRNRDLA
TALEQLLQAYPRDMEKEKTMLVLALLLAKKVASHTPSLLRDVFHTTVNFINQNLRTYVRSLARNG
MD
>d1ddba_ f.1.4.1 (A:) Proapoptotic molecule Bid {Mouse (Mus musculus)}
MDSEVSNGSGLGAKHITDLLVFGFLQSSGCTRQELEVLGRELPVQAYWEADLEDELQTDGSQASR
SFNQGRIEPDSESQEEIIHNIARHLAQIGDEMDHNIQPTLVRQLAAQFMNGSLSEEDKRNCLAKA
LDEVKTAFPRDMENDKAMLIMTMLLAKKVASHAPSLLRDVFHTTVNFINQNLFSYVRNLVRNEMD
>d1f16a_ f.1.4.1 (A:) Proapoptotic molecule Bax {Human (Homo sapiens)}
MDGSGEQPRGGGPTSSEQIMKTGALLLQGFIQDRAGRMGGEAPELALDPVPQDASTKKLSECLKR
IGDELDSNMELQRMIAAVDTDSPREVFFRVAADMFSDGNFNWGRVVALFYFASKLVLKALCTKVP
ELIRTIMGWTLDFLRERLLGWIQDQGGWDGLLSYFGTPTWQTVTIFVAGVLTASLTIWKKMG
>d1ikpa3 f.1.5.1 (A:252-394) Exotoxin A, middle domain {Pseudomonas
aeruginosa}
EGGSLAALTAHQACHLPLETFTRHRQPRGAEQLEQCGYPVQRLVALYLAARLSWNQVDQVIRNAL
ASPGSGGDLGEAIREQPEQARLALTLAAAESERFVRQGTGNDEAGAANADVVSLTCPVAAGECAG
PADSGDALLERNY
>d1c3wa_ f.2.1.1 (A:) Bacteriorhodopsin {Halobacterium salinarum}
TGRPEWIWLALGTALMGLGTLYFLVKGMGVSDPDAKKFYAITTLVPAIAFTMYLSMLLGYGLTMV
PFGGEQNPIYWARYADWLFTTPLLLLDLALLVDADQGTILALVGADGIMIGTGLVGALTKVYSYR
FVWWAISTAAMLYILYVLFFGFSMRPEVASTFKVLRNVTVVLWSAYPVVWLIGSEGAGIVPLNIE
TLLFMVLDVSAKVGFGLILLRSRAIFG
>d1c8sa_ f.2.1.1 (A:) Bacteriorhodopsin {Halobacterium salinarum}
TGRPEWIWLALGTALMGLGTLYFLVKGMGVSDPDAKKFYAITTLVPAIAFTMYLSMLLGYGLTMV
PFGGEQNPIYWARYADWLFTTPLLLLNLALLVDADQGTILALVGADGIMIGTGLVGALTKVYSYR
FVWWAISTAAMLYILYVLFNVTVVLWSAYPVVWLIGSEGAGIVPLNIETLLFMVLDVSAKVGFGL
I
>d1e12a_ f.2.1.1 (A:) Halorhodopsin {Halobacterium salinarum}
RENALLSSSLWVNVALAGIAILVFVYMGRTIRPGRPRLIWGATLMIPLVSISSYLGLLSGLTVGM
IEMPAGHALAGEMVRSQWGRYLTWALSTPMILLALGLLADVDLGSLFTVIAADIGMCVTGLAAAM
TTSALLFRWAFYAISCAFFVVVLSALVTDWAASASSAGTAEIFDTLRVLTVVLWLGYPIVWAVGV
EGLALVQSVGATSWAYSVLDVFAKYVFAFILLRWVANNERTVAV
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>d1h68a_ f.2.1.1 (A:) Sensory rhodopsin II {Natronobacterium pharaonis}
VGLTTLFWLGAIGMLVGTLAFAWAGRDAGSGERRYYVTLVGISGIAAVAYVVMALGVGWVPVAER
TVFAPRYIDWILTTPLIVYFLGLLAGLDSREFGIVITLNTVVMLAGFAGAMVPGIERYALFGMGA
VAFLGLVYYLVGPMTESASQRSSGIKSLYVRLRNLTVILWAIYPFIWLLGPPGVALLTPTVDVAL
IVYLDLVTKVGFGFIALDAAATL
>d1hzxa_ f.2.1.1 (A:) Rhodopsin {Cow (Bos taurus)}
MNGTEGPNFYVPFSNKTGVVRSPFEAPQYYLAEPWQFSMLAAYMFLLIMLGFPINFLTLYVTVQH
KKLRTPLNYILLNLAVADLFMVFGGFTTTLYTSLHGYFVFGPTGCNLEGFFATLGGEIALWSLVV
LAIERYVVVCKPMSNFRFGENHAIMGVAFTWVMALACAAPPLVGWSRYIPEGMQCSCGIDYYTPH
EETNNESFVIYMFVVHFIIPLIVIFFCYGQLVFTVKEAAAQQQESATTQKAEKEVTRMVIIMVIA
FLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAVYNPVIYIMMNKQFRNCMVTTLCCGK
NPLGDDEASTTVSKTETSQVAPA
>d1jfpa_ f.2.1.1 (A:) Rhodopsin {Cow (Bos taurus)}
LAAYMFLLIMLGFPINFLTLYVTVQHKKLRTPLNYILLNLAVADLFMVFGGFTTTLYTSLHGYFV
FGPTGCNLEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFRFGENHAIMGVAFTWVMALACAA
PPLVGWSRYIPEGMQCSCGIDYYTPHEETNNESFVIYMFVVHFIIPLIVIFFCYGQLVFTVKEAA
AQQQESATTQKAEKEVTRMVIIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSA
VYNPVIYIMMNKQFRNCMVTTLCCGKNPLGDDEASTTVSKTETSQVAPA
>d1dxrh2 f.2.1.2 (H:1-36) Photosynthetic reaction centre, L-, M- and H-chains {Rhodopseudomonas viridis}
MYHGALAQHLDIAQLVWYAQWLVIWTVVLLYLRRED
>d1dxrl1 f.2.1.2 (L:) Photosynthetic reaction centre, L-, M- and H-chains {Rhodopseudomonas viridis}
ALLSFERKYRVRGGTLIGGDLFDFWVGPYFVGFFGVSAIFFIFLGVSLIGYAASQGPTWDPFAIS
INPPDLKYGLGAAPLLEGGFWQAITVCALGAFISWMLREVEISRKLGIGWHVPLAFCVPIFMFCV
LQVFRPLLLGSWGHAFPYGILSHLDWVNNFGYQYLNWFYNPGHMSSVSFLFVNAMALGLHGGLIL
SVANPGDGDKVKTAEHENQYFRDVVGYSIGALSIHRLGLFLASNIFLTGAFGTIASGPFWTRGWP
EWWGWWLDIPFWS
>d1dxrm1 f.2.1.2 (M:) Photosynthetic reaction centre, L-, M- and H-chains {Rhodopseudomonas viridis}
ADYQTIYTQIQARGPHITVSGEWGDNDRVGKPFYSYWLGKIGDAQIGPIYLGASGIAAFAFGSTA
ILIIILFNMAAEVHFDPLQFFRQFFWLGLYPPKAQYGMGIPPLHDGGWWLMAGLFMTLSLGSWWIR
VYSRARALGLGTHIAWNFAAAIFFVLCIGCIHPTLVGSWSEGVPFGIWPHIDWLTAFSIRYGNFY
YCPWHGFSIGFAYGCGLLFAAHGATILAVARFGGDREIEQITDRGTAVERAALFWRWTIGFNATI
ESVHRWGWFFSLMVMVSASVGILLTGTFVDNWYLWCVKHGAAPDYPAYLPATPDPASLPGAPK
>d1qovh2 f.2.1.2 (H:11-35) Photosynthetic reaction centre, L-, M- and H-chains {Rhodobacter sphaeroides}
DLASLAIYSFWIFLAGLIYYLQTEN
>d1qovl1 f.2.1.2 (L:) Photosynthetic reaction centre, L-, M- and H-chains {Rhodobacter sphaeroides}
ALLSFERKYRVPGGTLVGGNLFDFWVGPFYVGFFGVATFFFAALGIILIAWSAVLQGTWNPQLIS
VYPPALEYGLGGAPLAKGGLWQIITICATGAFVSWALREVEICRKLGIGYHIPFAFAFAILAYLT
LVLFRPVMMGAWGYAFPYGIWTHLDWVSNTGYTYGNFHYNPAHMIAISFFFTNALALALHGALVL
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SAANPEKGKEMRTPDHEDTFFRDLVGYSIGTLGIHRLGLLLSLSAVFFSALCMIITGTIWFDQWV
DWWQWWVKLPWWANIPGGING
>d1qovm1 f.2.1.2 (M:) Photosynthetic reaction centre, L-, M- and
H-chains {Rhodobacter sphaeroides}
AEYQNIFSQVQVRGPADLGMTEDVNLANRSGVGPFSTLLGWFGNAQLGPIYLGSLGVLSLFSGLM
WFFTIGIWFWYQAGWNPAVFLRDLFFFSLEPPAPEYGLSFAAPLKEGGLWLIASFFMFVAVWSWW
GRTYLRAQALGMGKHTAWAFLSAIWLWMVLGFIRPILMGSWSEAVPYGIFSHLDWTNNFSLVHGN
LFYNPFHGLSIAFLYGSALLFAMHGATILAVSRFGGERELEQIADRGTAAERAALFWRWTMGFNW
TMEGIHRWAIWMAVLVTLTGGIGILLSGTVVDNWYVWGQNHG
>d2rcrh2 f.2.1.2 (H:1-35) Photosynthetic reaction centre, L-, M- and
H-chains {Rhodobacter sphaeroides}
MVGVTAFGNFDLASLAIYSFWIFLAGLIYYLQTEN
>d1eysh2 f.2.1.2 (H:7-43) Photosynthetic reaction centre, L-, M- and
H-chains {Thermochromatium tepidum}
HYIDAAQITIWAFWLFFFGLIIYLRREDKREGYPLDS
>d1eysl1 f.2.1.2 (L:) Photosynthetic reaction centre, L-, M- and
H-chains {Thermochromatium tepidum}
AMLSFEKKYRVRGGTLIGGDLFDFWVGPFYVGFFGVVGFCFTLLGVLLIVWGATIGPTGPTSDLQ
TYNLWRISIAPPDLSYGLRMAPLTEGGLWQIITICAAGAFISWALREVEICRKLGIGFHVPFAFS
FAIGAYLVLVFVRPLLMGAWGHGFPYGILSHLDWVSNVGYQFLHFHYNPAHMLAISFFFTNCLAL
SMHGSLILSVTNPQRGEPVKTSEHENTFFRDIVGYSIGALAIHRLGLFLALSAAFWSAVCILISG
PFWTRGWPEWWNWWLELPLW
>d1eysm1 f.2.1.2 (M:) Photosynthetic reaction centre, L-, M- and
H-chains {Thermochromatium tepidum}
PEYQNIFTAVQVRAPAYPGVPLPKGNLPRIGRPIFSYWLGKIGDAQIGPIYLGLTGTLSIFFGLV
AISIIGFNMLASVHWDVFQFLKHFFWLGLEPPPPQYGLRIPPLSEGGWWLIAGLFLTLSILLWWV
RTYKRAEALGMSQHLSWAFAAAIFFYLVLGFIRPVMMGSWAKAVPFGIFPHLDWTAAFSIRYGNL
YYNPFHMLSIAFLYGSALLFAMHGATILSVSRFGGDREIDQITHRGTAAEGAALFWRWTMGFNAT
MESIHRWAWWCAVLTVITAGIGILLSGTVVDNWYLWAVKHGMAPAYPEVVTAVNPYET
>d1ocra1 f.2.1.3 (A:) Cytochrome c oxidase {Cow (Bos taurus)}
MFINRWLFSTNHKDIGTLYLLFGAWAGMVGTALSLLIRAELGQPGTLLGDDQIYNVVVTAHAFVM
IFFMVMPIMIGGFGNWLVPLMIGAPDMAFPRMNNMSFWLLPPSFLLLLASSMVEAGAGTGWTVYP
PLAGNLAHAGASVDLTIFSLHLAGVSSILGAINFITTIINMKPPAMSQYQTPLFVWSVMITAVLL
LLSLPVLAAGITMLLTDRNLNTTFFDPAGGGDPILYQHLFWFFGHPEVYILILPGFGMISHIVTY
YSGKKEPFGYMGMVWAMMSIGFLGFIVWAHHMFTVGMDVDTRAYFTSATMIIAIPTGVKVFSWLA
TLHGGNIKWSPAMMWALGFIFLFTVGGLTGIVLANSSLDIVLHDTYYVVAHFHYVLSMGAVFAIM
GGFVHWFPLFSGYTLNDTWAKIHFAIMFVGVNMTFFPQHFLGLSGMPRRYSDYPDAYTMWNTISS
MGSFISLTAVMLMVFIIWEAFASKREVLTVDLTTTNLEWLNGCPPPYHTFEEPTYVNLK
>d1ocrb2 f.2.1.3 (B:1-90) Cytochrome c oxidase {Cow (Bos taurus)}
MAYPMQLGFQDATSPIMEELLHFHDHTLMIVFLISSLVLYIISLMLTTKLTHTSTMDAQEVETIW
TILPAIILILIALPSLRILYMMDEI
>d1ocrc1 f.2.1.3 (C:) Cytochrome c oxidase {Cow (Bos taurus)}
MTHQTHAYHMVNPSPWPLTGALSALLMTSGLTMWFHFNSMTLLMIGLTTNMLTMYQWWRDVIRES
TFQGHHTPAVQKGLRYGMILFIISEVLFFTGFFWAFYHSSLAPTPELGGCWPPTGIHPLNPLEVP
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LLNTSVLLASGVSITWAHHSLMEGDRKHMLQALFITITLGVYFTLLQASEYYEAPFTISDGVYGS
TFFVATGFHGLHVIIGSTFLIVCFFRQLKFHFTSNHHFGFEAGAWYWHFVDVVWLFLYVSIYWWG
S
>d1ocrd1 f.2.1.3 (D:) Cytochrome c oxidase {Cow (Bos taurus)}
SVVKSEDYALPSYVDRRDYPLPDVAHVKNLSASQKALKEKEKASWSSLSIDEKVELYRLKFKESF
AEMNRSTNEWKTVVGAAMFFIGFTALLLIWEKHYVYGPIPHTFEEEWVAKQTKRMLDMKVAPIQG
FSAKWDYDKNEWKK
>d1ocrg1 f.2.1.3 (G:) Cytochrome c oxidase {Cow (Bos taurus)}
ASAAKGDHGGTGARTWRFLTFGLALPSVALCTLNSWLHSGHRERPAFIPYHHLRIRTKPFSWGDG
NHTFFHNPRVNPLPTGYEK
>d1ocri1 f.2.1.3 (I:) Cytochrome c oxidase {Cow (Bos taurus)}
STALAKPQMRGLLARRLRFHIVGAFMVSLGFATFYKFAVAEKRKKAYADFYRNYDSMKDFEEMRK
AGIFQSAK
>d1ocrj1 f.2.1.3 (J:) Cytochrome c oxidase {Cow (Bos taurus)}
FENRVAEKQKLFQEDNGLPVHLKGGATDNILYRVTMTLCLGGTLYSLYCLGWASFPHK
>d1ocrk1 f.2.1.3 (K:) Cytochrome c oxidase {Cow (Bos taurus)}
APDFHDKYGNAVLASGATFCVAVWVYMATQIGIEWNPSPVGRVTPKEWR
>d1ocrl1 f.2.1.3 (L:) Cytochrome c oxidase {Cow (Bos taurus)}
SHYEEGPGKNIPFSVENKWRLLAMMTLFFGSGFAAPFFIVRHQLLKK
>d1ocrm1 f.2.1.3 (M:) Cytochrome c oxidase {Cow (Bos taurus)}
ITAKPAKTPTSPKEQAIGLSVTFLSFLLPAGWVLYHLDNYKKS
>d1ar1a1 f.2.1.3 (A:) Cytochrome c oxidase {Paracoccus denitrificans}
GFFTRWFMSTNHKDIGILYLFTAGIVGLISVCFTVYMRMELQHPGVQYMCLEGARLIADASAECT
PNGHLWNVMITYHGVLMMFFVVIPALFGGFGNYFMPLHIGAPDMAFPRLNNLSYWMYVCGVALGV
ASLLAPGGNDQMGSGVGWVLYPPLSTTEAGYSMDLAIFAVHVSGASSILGAINIITTFLNMRAPG
MTLFKVPLFAWSVFITAWLILLSLPVLAGAITMLLMDRNFGTQFFDPAGGGDPVLYQHILWFFGH
PEVYIIILPGFGIISHVISTFAKKPIFGYLPMVLAMAAIGILGFVVWAHHMYTAGMSLTQQAYFM
LATMTIAVPTGIKVFSWIATMWGGSIEFKTPMLWAFGFLFLFTVGGVTGVVLSQAPLDRVYHDTY
YVVAHFHYVMSLGAVFGIFAGVYYWIGKMSGRQYPEWAGQLHFWMMFIGSNLIFFPQHFLGRQGM
PRRYIDYPVEFAYWNNISSIGAYISFASFLFFIGIVFYTLFAGKRVNVPNYWNEHADTLEWTLPS
PPPEHTFET
>d1ar1b2 f.2.1.3 (B:1-107) Cytochrome c oxidase {Paracoccus denitrificans}
QDVLGDLPVIGKPVNGGMNFQPASSPLAHDQQWLDHFVLYIITAVTIFVCLLLLICIVRFNRRAN
PVPARFTHNTPIEVIWTLVPVLILVAIGAFSLPILFRSQEMP
>d1qlec1 f.2.1.3 (C:) Cytochrome c oxidase {Paracoccus denitrificans}
AHVKNHDYQILPPSIWPFFGAIGAFVMLTGAVAWMKGITFFGLPVEGPWMFLIGLVGVLYVMFGW
WADVVNEGETGEHTPVVRIGLQYGFILFIMSEVMFFVAWFWAFIKNALYPMGPDSPIKDGVWPPE
GIVTFDPWHLPLINTLILLLSGVAVTWAHHAFVLEGDRKTTINGLIVAVILGVCFTGLQAYEYSH
AAFGLADTVYAGAFYMATGFHGAHVIIGTIFLFVCLIRLLKGQMTQKQHVGFEAAAWYWHFVDVV
WLFLFVVIYIWGR
>d1qled1 f.2.1.3 (D:) Cytochrome c oxidase {Paracoccus denitrificans}
TDHKHGEMDIRHQQATFAGFIKGATWVSILSIAVLVFLALANS
>d1ehka1 f.2.1.3 (A:) Cytochrome c oxidase {Thermus thermophilus, ba3
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type}
AYPEKKATLYFLVLGFLALIVGSLFGPFQALNYGNVDAYPLLKRLLPFVQSYYQGLTLHGVLNAI
VFTQLFAQAIMVYLPARELNMRPNMGLMWLSWWMAFIGLVVAALPLLANEATVLYTFYPPLKGHW
AFYLGASVFVLSTWVSIYIVLDLWRRWKAANPGKVTPLVTYMAVVFWLMWFLASLGLVLEAVLFL
LPWSFGLVEGVDPLVARTLFWWTGHPIVYFWLLPAYAIIYTILPKQAGGKLVSDPMARLAFLLFL
LLSTPVGFHHQFADPGIDPTWKMIHSVLTLFVAVPSLMTAFTVAASLEFAGRLRGGRGLFGWIRA
LPWDNPAFVAPVLGLLGFIPGGAGGIVNASFTLDYVVHNTAWVPGHFHLQVASLVTLTAMGSLYW
LLPNLTGKPISDAQRRLGLAVVWLWFLGMMIMAVGLHWAGLLNVPRRAYIAQVPDAYPHAAVPMV
FNVLAGIVLLVALLLFIYGLFSVLLSRERKPELAEAPLPFAEVISGPEDRRLVLAMDRIGFWFAV
AAILVVLAYGPTLVQLFGHLNPVPGWRLW
>d1ehkb2 f.2.1.3 (B:3-40) Cytochrome c oxidase {Thermus thermophilus,
ba3 type}
DEHKAHKAILAYEKGWLAFSLAMLFVFIALIAYTLATH
>d1ehkc1 f.2.1.3 (C:) Cytochrome c oxidase {Thermus thermophilus, ba3
type}
EEKPKGALAVILVLTLTILVFWLGVYAVFFARG
>d1ffta1 f.2.1.3 (A:) Ubiquinol oxidase {Escherichia coli}
VDHKRLGIMYIIVAIVMLLRGFADAIMMRSQQALASAGEAGFLPPHHYDQIFTAHGVIMIFFVAM
PFVIGLMNLVVPLQIGARDVAFPFLNNLSFWFTVVGVILVNVSLGVGEFAQTGWLAYPPLSGIEY
SPGVGVDYWIWSLQLSGIGTTLTGINFFVTILKMRAPGMTMFKMPVFTWASLCANVLIIASFPIL
TVTVALLTLDRYLGTHFFTNDMGGNMMMYINLIWAWGHPEVYILILPVFGVFSEIAATFSRKRLF
GYTSLVWATVCITVLSFIVWLHHFFTMGAGANVNAFFGITTMIIAIPTGVKIFNWLFTMYQGRIV
FHSAMLWTIGFIVTFSVGGMTGVLLAVPGADFVLHNSLFLIAHFHNVIIGGVVFGCFAGMTYWWP
KAFGFKLNETWGKRAFWFWIIGFFVAFMPLYALGFMGMTRRLSQQIDPQFHTMLMIAASGAVLIA
LGILCLVIQMYVSIRDRDQNRDLTGDPWGGRTLEWATSSPPPFYNF
>d1fftb2 f.2.1.3 (B:27-117) Ubiquinol oxidase {Escherichia coli}
SALLDPKGQIGLEQRSLILTAFGLMLIVVIPAILMAVGFAWKYRASNKDAKYSPNWSHSNKVEAV
VWTVPILIIIFLAVLTWKTTHALEPS
>d1fftc1 f.2.1.3 (C:) Ubiquinol oxidase {Escherichia coli}
HDAGGTKIFGFWIYLMSDCILFSILFATYAVLVNGTAGGPTGKDIFELPFVLVETFLLLFSSITY
GMAAIAMYKNNKSQVISWLALTWLFGAGFIGMEIYEFHHLIVNGMGPDRSGFLSAFFALVGTHGL
HVTSGLIWMAVLMVQIARRGLTSTNRTRIMCLSLFWHFLDVVWICVFTVVYLMGA
>d1c0va_ f.2.1.4 (A:) Subunit C {Escherichia coli}
MENLNMDLLYMAAAVMMGLAAIGAAIGIGILGGKFLEGAARQPDLIPLLRTQFFIVMGLVDAIPM
IAVGLGLYVMFAVA
>d1c17m_ f.2.1.4 (M:) Subunit A {Escherichia coli}
HGKSKLIAPLALTIFVWVFLMNLMDLLPIDLLPYIAEHVLGLPALRVVPSADVNVTLSMALGVFI
LILFYSIKMKGIGGFTKELTLQPFNHWAFIPVNLILEGVSLLSKPVSLGLRLFGNMYAGELIFIL
IAGLLPWWSQWILNVPWAIFHILIITLQAFIFMVLTIVYLS
>d1h6ia_ f.2.1.5 (A:) Aquaporin-1 {Human (Homo sapiens)}
LFWRAVVAEFLATTLFVFISIGSALGFKYPVGNNQTAVQDNVKVSLAFGLSIATLAQSVGHISGA
HLNPAVTLGLLLSCQISIFRALMYIIAQCVGAIVATAILSGITSSLTGNSLGRNDLADGVNSGQG
LGIEIIGTLQLVLCVLATTDRRRRDLGGSAPLAIGLSVALGHLLAIDYTGCGINPARSFGSAVIT
HNFSNHWIFWVGPFIGGALAVLIYDFILAP
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>d1fx8a_ f.2.1.5 (A:) Glycerol uptake facilitator protein GlpF {Escherichia coli}
TLKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLTAGVSGAHLNPA
VTIALWLFACFDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVDLAGTF
STYPNPHINFVQAFAVEMVITAILMGLILALTDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGF
AMNPARDFGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFGPIVGAIVGAFAYRKLIGRHL
>d1kpka_ f.2.1.13 (A:) Clc chloride channel {Escherichia coli}
QAARLRRRQLIRQLLERDKTPLAILFMAAVVGTLVGLAAVAFDKGVAWLQNQRMGALVHTADNYP
LLLTVAFLCSAVLAMFGYFLVRKYAPEAGGSGIPEIEGALEDQRPVRWWRVLPVKFFGGLGTLGG
GMVLGREGPTVQIGGNIGRMVLDIFRLKGDEARHTLLATGAAAGLAAAFNAPLAGILFIIEEMRP
QFRYTLISIKAVFIGVIMSTIMYRIFNHEVALIDVGKLSDAPLNTLWLYLILGIIFGIFGPIFNK
WVLGMQDLLHRVHGGNITKWVLMGGAIGGLCGLLGFVAPATSGGGFNLIPIATAGNFSMGMLVFI
FVARVITTLLCFSSGAPGGIFAPMLALGTVLGTAFGMVAVELFPQYHLEAGTFAIAGMGALLAAS
IRAPLTGIILVLEMTDNYQLILPMIITGLGATLLAQFTGGKPLYSAILARTLAKQEAEQL
>d1kpla_ f.2.1.13 (A:) Clc chloride channel {Salmonella typhimurium}
TPLAILFMAAVVGTLTGLVGVAFEKAVSWVQNMRIGALVQVADHAFLLWPLAFILSALLAMVGYF
LVRKFAPEAGGSGIPEIEGALEELRPVRWWRVLPVKFIGGMGTLGAGMVLGREGPTVQIGGNLGR
MVLDVFRMRSAEARHTLLATGAAAGLSAAFNAPLAGILFIIEEMRPQFRYNLISIKAVFTGVIMS
SIVFRIFNGEAPIIEVGKLSDAPVNTLWLYLILGIIFGVVGPVFNSLVLRTQDMFQRFHGGEIKK
WVLMGGAIGGLCGILGLIEPAAAGGGFNLIPIAAAGNFSVGLLLFIFITRVVTTLLCFSSGAPGG
IFAPMLALGTLLGTAFGMAAAVLFPQYHLEAGTFAIAGMGALMAASVRAPLTGIVLVLEMTDNYQ
LILPMIITCLGATLLAQFLGGKPLYSTILARTLAKQDAEQ
>d1f6ga_ f.2.1.11 (A:) Potassium chanel protein {Streptomyces lividans}
MPPMLSGLLARLVKLLLGRHGSALHWAAAGAATVLLVIVLLAGSYLAVLAERGAPGAQLITYPAA
LWWSVETATTVGYGDLYPVTLWGRCVAVVVMVAGITSFGLVTAALATWFVGREQERRGHFVRHSE
KAAEEAYTRTTRALHERFDRLERMLDDNRR
>d1jq2a_ f.2.1.11 (A:) Potassium chanel protein {Streptomyces lividans}
LWGRCVAVVVMVAGITSFGLVTAALATWFVGREQ
>d1k4cc_ f.2.1.11 (C:) Potassium chanel protein {Streptomyces lividans}
SALHWRAAGAATVLLVIVLLAGSYLAVLAERGAPGAQLITYPRALWWSVETATTVGYGDLYPVTL
WGRCVAVVVMVAGITSFGLVTAALATWFVGREQERRGH
>d1g4yb_ f.2.1.11 (B:) Small conductance potassium channel {Rat (Rattus norvegicus)}
DTQLTKRVKNAAANVLRETWLIYKNTKLVKKIDHAKVRKHQRKFLQAIHQLRSVKMEQRKLNDQA
NTLVDLAKTQLEHHHHH
>d1kkda_ f.2.1.11 (A:) Small conductance potassium channel {Rat (Rattus norvegicus)}
RKLELTKAEKHVHNFMMDTQLTKRVKNAAANVLRETWLIYKNTKLVKKIDHAKVRKHQRKFLQAI
HQLRSVKMEQRKLNDQANTLVDLAKTQ
>d1msla_ f.2.1.11 (A:) Gated mechanosensitive channel {Mycobacterium tuberculosis}
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ARGNIVDLAVAVVIGTAFTALVTKFTDSIITPLINRIGVNAQSDVGILRIGIGGGQTIDLNVLLS
AAINFFLIAFAVYFLVVLPYNTLRKKGEVEQPGDTQVVLLTEIR
>d1be3c1 f.2.1.8 (C:) Cytochrome bc1 transmembrane subunits {Cow (Bos
taurus)}
MTNIRKSHPLMKIVNNAFIDLPAPSNISSWWNFGSLLGICLILQILTGLFLAMHYTSDTTTAFSS
VTHICRDVNYGWIIRYMHANGASMFFICLYMHVGRGLYYGSYTFLETWNIGVILLLTVMATAFMG
YVLPWGQMSFWGATVITNLLSAIPYIGTNLVEWIWGGFSVDKATLTRFFAFHFILPFIIMAIAMV
HLLFLHETGSNNPTGISSDVDKIPFHPYYTIKDILGALLLILALMLLVLFAPDLLGDPDNYTPAN
PLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALAFSILILALIPLLHTSKQRSMMFRPLSQCLF
WALVADLLTLTWIGGQPVEHPYITIGQLASVLYFLLILVLMPTAGTIENKLLKW
>d1be3e2 f.2.1.8 (E:1-69) Cytochrome bc1 transmembrane subunits {Cow
(Bos taurus)}
SHTDIKVPDFSDYRRPEVLDSTKSSKESSEARKGFSYLVTATTTVGVAYAAKNVVSQFVSSMSAS
ADVL
>d1be3f1 f.2.1.8 (F:) Cytochrome bc1 transmembrane subunits {Cow (Bos
taurus)}
AVSASSRWLEGIRKWYYNAAGFNKLGLMRDDTIHENDDVKEAIRRLPENLYDDRVFRIKRALDLS
MRQQILPKEQWTKYEEDKSYLEPYLKEVIRERKEREEWAKK
>d1be3g1 f.2.1.8 (G:) Cytochrome bc1 transmembrane subunits {Cow (Bos
taurus)}
GRQFGHLTRVRHVITYSLSPFEQRAFPHYFSKGIPNVLRRTRACILRVAPPFVAFYLVYTWGTQE
FEKSKRKNPAAYENDR
>d1be3k1 f.2.1.8 (K:) Cytochrome bc1 transmembrane subunits {Cow (Bos
taurus)}
RNWVPTAQLWGAVGAVGLVSAT
>d1qcrg1 f.2.1.8 (G:) Cytochrome bc1 transmembrane subunits {Cow (Bos
taurus)}
GRQFGHLTRVRHVITYSLSPFEQRAFPHYFSKGIPNVLRRTRACILRVAPPFVAFYLVYTWGTQE
FEKSK
>d1qcrh1 f.2.1.8 (H:) Cytochrome bc1 transmembrane subunits {Cow (Bos
taurus)}
TTVREQCEQLEKCVKARERLELCDERVSSRSQTEEDCTEELLDFLHARDHCVAHKLFNSL
>d1qcrk1 f.2.1.8 (K:) Cytochrome bc1 transmembrane subunits {Cow (Bos
taurus)}
MLTRFLGPRYRQLARNWVPTAQLWGAVGAVGLVSATDSRLILDWV
>d1bccc1 f.2.1.8 (C:) Cytochrome bc1 transmembrane subunits {Chicken
(Gallus gallus)}
APNIRKSHPLLKMINNSLIDLPAPSNISAWWNFGSLLAVCLMTQILTGLLLAMHYTADTSLAFSS
VAHTCRNVQYGWLIRNLHANGASFFFICIFLHIGRGLYYGSYLYKETWNTGVILLLTLMATAFVG
YVLPWGQMSFWGATVITNLFSAIPYIGHTLVEWAWGGFSVDNPTLTRFFALHFLLPFAIAGITII
HLTFLHESGSNNPLGISSDSDKIPFHPYYSFKDILGLTLMLTPFLTLALFSPNLLGDPENFTPAN
PLVTPPHIKPEWYFLFAYAILRSIPNKLGGVLALAASVLILFLIPFLHKSKQRTMTFRPLSQTLF
WLLVANLLILTWIGSQPVEHPFIIIGQMASLSYFTILLILFPTIGTLENKMLNY
>d1bccd3 f.2.1.8 (D:196-241) Cytochrome bc1 transmembrane subunits
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{Chicken (Gallus gallus)}
PEHDHRKRMGLKMLLMMGLLVPLVYYMKRHKWSVLKSRKLAYRPPK
>d1bcce2 f.2.1.8 (E:1-69) Cytochrome bc1 transmembrane subunits
{Chicken (Gallus gallus)}
SHTDIKVPNFSDYRRPPDDYSTKSSRESDPSRKGFSYLVTAVTTLGVAYAAKNVVTQFVSSMSAS
ADVL
>d1bccf1 f.2.1.8 (F:) Cytochrome bc1 transmembrane subunits {Chicken
(Gallus gallus)}
SRWLEGIRKWYYNAAGFNKYGLMRDDTIYENDDVKEAIRRLPENLYDDRMFRIKRALDLNMRQQI
LPKEQWTKYEEDVPYLEPYLKEVIRERKEREEWDK
>d1bccg1 f.2.1.8 (G:) Cytochrome bc1 transmembrane subunits {Chicken
(Gallus gallus)}
RQFGHLTRVRHLITYSLSPFEQRPFPHYFSKGVPNVWRRLRACILRVAPPFLAFYLLYTWGTQEF
EKSKRKNPAAYVN
>d1bcch1 f.2.1.8 (H:) Cytochrome bc1 transmembrane subunits {Chicken
(Gallus gallus)}
LVDPLTTVREQCEQLEKCVKARERLELCDERVSSRSQTEEDCTEELFDFLHARDHCVAHKLFNSL
K
>d1bccj1 f.2.1.8 (J:) Cytochrome bc1 transmembrane subunits {Chicken
(Gallus gallus)}
TLTARLYSLLFRRTSTFALTIVVGALLFERAFDQGADAIYEHINEGKLWKHIKHKYENK
>d1ezvc1 f.2.1.8 (C:) Cytochrome bc1 transmembrane subunits {Baker's
yeast (Saccharomyces cerevisiae)}
MAFRKSNVYLSLVNSYIIDSPQPSSINYWWNMGSLLGLCLVIQIVTGIFMAMHYSSNIELAFSSV
EHIMRDVHNGYILRYLHANGASFFFMVMFMHMAKGLYYGSYRSPRVTLWNVGVIIFTLTIATAFL
GYCCVYGQMSHWGATVITNLFSAIPFVGNDIVSWLWGGFSVSNPTIQRFFALHYLVPFIIAAMVI
MHLMALHIHGSSNPLGITGNLDRIPMHSYFIFKDLVTVFLFMLILALFVFYSPNTLGHPDNYIPG
NPLVTPASIVPEWYLLPFYAILRSIPDKLLGVITMFAAILVLLVLPFTDRSVVRGNTFKVLSKFF
FFIFVFNFVLLGQIGACHVEVPYVLMGQIATFIYFAYFLIIVPVISTIENVLFYIGRVNK
>d1ezvd2 f.2.1.8 (D:261-306) Cytochrome bc1 transmembrane subunits
{Baker's yeast (Saccharomyces cerevisiae)}
PEHDERKRLGLKTVIILSSLYLLSIWVKKFKWAGIKTRKFVFNPPK
>d1ezve2 f.2.1.8 (E:31-86) Cytochrome bc1 transmembrane subunits
{Baker's yeast (Saccharomyces cerevisiae)}
KSTYRTPNFDDVLKENNDADKGRSYAYFMVGAMGLLSSAGAKSTVETFISSMTATA
>d1ezvf1 f.2.1.8 (F:) Cytochrome bc1 transmembrane subunits {Baker's
yeast (Saccharomyces cerevisiae)}
QSFTSIARIGDYILKSPVLSKLCVPVANQFINLAGYKKLGLKFDDLIAEENPIMQTALRRLPEDE
SYARAYRIIRAHQTELTHHLLPRNEWIKAQEDVPYLLPYILEAEAAAKEKDELDNIEVSK
>d1ezvg1 f.2.1.8 (G:) Cytochrome bc1 transmembrane subunits {Baker's
yeast (Saccharomyces cerevisiae)}
GPPSGKTYMGWWGHMGGPKQKGITSYAVSPYAQKPLQGIFHNAVFNSFRRFKSQFLYVLIPAGIY
WYWWKNGNEYNEFLYSKAGREELERVNV
>d1ezvh1 f.2.1.8 (H:) Cytochrome bc1 transmembrane subunits {Baker's
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yeast (Saccharomyces cerevisiae)}
VTDQLEDLREHFKNTEEGKALVHHYEECAERVKIQQQQPGYADLEHKEDCVEEFFHLQHYLDTAT
APRLFDKLK
>d1ezvi1 f.2.1.8 (I:) Cytochrome bc1 transmembrane subunits {Baker's
yeast (Saccharomyces cerevisiae)}
SSLYKTFFKRNAVFVGTIFAGAFVFQTVFDTAITSWYENHNKGKLWKDVKARIAA
>d1fumc_ f.2.1.9 (C:) Fumarate reductase respiratory complex
transmembrane subunits {Escherichia coli}
TTKRKPYVRPMTSTWWKKLPFYRFYMLREGTAVPAVWFSIELIFGLFALKNGPEAWAGFVDFLQN
PVIVIINLITLAAALLHTKTWFELAPKAANIIVKDEKMGPEPIIKSLWAVTVVATIVILFVALYW
>d1fumd_ f.2.1.9 (D:) Fumarate reductase respiratory complex
transmembrane subunits {Escherichia coli}
INPNPKRSDEPVFWGLFGAGGMWSAIIAPVMILLVGILLPLGLFPGDALSYERVLAFAQSFIGRV
FLFLMIVLPLWCGLHRMHHAMHDLKIHVPAGKWVFYGLAAILTVVTLIGVVTI
>d1qlac_ f.2.1.9 (C:) Fumarate reductase respiratory complex
transmembrane subunits {Wolinella succinogenes}
MTNESILESYSGVTPERKKSRMPAKLDWWQSATGLFLGLFMIGHMFFVSTILLGDNVMLWVTKKF
ELDFIFEGGKPIVVSFLAAFVFAVFIAHAFLAMRKFPINYRQYLTFKTHKDLMRHGDTTLWWIQA
MTGFAMFFLGSVHLYIMMTQPQTIGPVSSSFRMVSEWMWPLYLVLLFAVELHGSVGLYRLAVKWG
WFDGETPDKTRANLKKLKTLMSAFLIVLGLLTFGAYVKKGLEQTDPNIDYKYFDYKRTH
>d1jb0a_ f.2.1.12 (A:) Photosystem I {Synechococcus elongatus}
RVVVDNDPVPTSFEKWAKPGHFDRTLARGPQTTTWIWNLHALAHDFDTHTSDLEDISRKIFSAHF
GHLAVVFIWLSGMYFHGAKFSNYEAWLADPTGIKPSAQVVWPIVGQGILNGDVGGGFHGIQITSG
LFQLWRASGITNEFQLYCTAIGGLVMAGLMLFAGWFHYHKRAPKLEWFQNVESMLNHHLAGLLGL
GSLAWAGHQIHVSLPINKLLDAGVAAKDIPLPHEFILNPSLMAELYPKVDWGFFSGVIPFFTFNW
AAYSDFLTFNGGLNPVTGGLWLSDTAHHHLAIAVLFIIAGHMYRTNWGIGHSLKEILEAHKGPFT
GAGHKGLYEVLTTSWHAQLAINLAMMGSLSIIVAQHMYAMPPYPYLATDYPTQLSLFTHHMWIGG
FLVVGGAAHGAIFMVRDYDPAMNQNNVLDRVLRHRDAIISHLNWVCIFLGFHSFGLYVHNDTMRA
FGRPQDMFSDTGIQLQPVFAQWVQNLHTLAPGGTAPNAAATASVAFGGDVVAVGGKVAMMPIVLG
TADFMVHHIHAFTIHVTVLILLKGVLFARSSRLIPDKANLGFRFPCDGPGRGGTCQVSGWDHVFL
GLFWMYNCISVVIFHFSWKMQSDVWGTVAPDGTVSHITGGNFAQSAITINGWLRDFLWAQASQVI
GSYGSALSAYGLLFLGAHFIWAFSLMFLFSGRGYWQELIESIVWAHNKLKVAPAIQPRALSIIQG
RAVGVAHYLLGGIATTWAFFLARIISVG
>d1jb0b_ f.2.1.12 (B:) Photosystem I {Synechococcus elongatus}
ATKFPKFSQDLAQDPTTRRIWYAIAMAHDFESHDGMTEENLYQKIFASHFGHLAIIFLWVSGSLF
HVAWQGNFEQWVQDPVNTRPIAHAIWDPQFGKAAVDAFTQAGASNPVDIAYSGVYHWWYTIGMRT
NGDLYQGAIFLLILASLALFAGWLHLQPKFRPSLSWFKNAESRLNHHLAGLFGVSSLAWAGHLIH
VAIPESRGQHVGWDNFLSTMPHPAGLAPFFTGNWGVYAQNPDTASHVFGTAQGAGTAILTFLGGF
HPQTESLWLTDMAHHHLAIAVLFIVAGHMYRTQFGIGHSIKEMMDAKDFFGTKVEGPFNMPHQGI
YETYNNSLHFQLGWHLACLGVITSLVAQHMYSLPPYAFIAQDHTTMAALYTHHQYIAGFLMVGAF
AHGAIFLVRDYDPAQNKGNVLDRVLQHKEAIISHLSWVSLFLGFHTLGLYVHNDVVVAFGTPEKQ
ILIEPVFAQFIQAAHGKLLYGFDTLLSNPDSIASTAWPNYGNVWLPGWLDAINSGTNSLFLTIGP
GDFLVHHAIALGLHTTTLILVKGALDARGSKLMPDKKDFGYAFPCDGPGRGGTCDISAWDAFYLA
MFWMLNTIGWVTFYWHWKHLGVWEGNVAQFNESSTYLMGWLRDYLWLNSSQLINGYNPFGTNNLS
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VWAWMFLFGHLVWATGFMFLISWRGYWQELIETLVWAHERTPLANLVRWKDKPVALSIVQARLVG
LAHFSVGYILTYAAFLIASTAAKF
>d1jb0f_ f.2.1.12 (F:) Photosystem I {Synechococcus elongatus}
DVAGLVPCKDSPAFQKRAAAAVNTTADPASGQKRFERYSQALCGEDGLPHLVVDGRLSRAGDFLI
PSVLFLYIAGWIGWVGRAYLIAVRNSGEANEKEIIIDVPLAIKCMLTGFAWPLAALKELASGELT
AKDNEITVSPR
>d1jb0i_ f.2.1.12 (I:) Photosystem I {Synechococcus elongatus}
MMGSYAASFLPWIFIPVVCWLMPTVVMGLLFLYIEGEA
>d1jb0j_ f.2.1.12 (J:) Photosystem I {Synechococcus elongatus}
MKHFLTYLSTAPVLAAIWMTITAGILIEFNRFYPDLLFHPL
>d1jb0k_ f.2.1.12 (K:) Photosystem I {Synechococcus elongatus}
ILCNLFAIALGRYAIQSRGKGPGLPIALPALFEGFGLPELLATTSFGHLLAAGVVSGL
>d1jb0l_ f.2.1.12 (L:) Photosystem I {Synechococcus elongatus}
LVKPYNGDPFVGHLSTPISDSGLVKTFIGNLPAYRQGLSPILRGLEVGMAHGYFLIGPWVKLGPL
RDSDVANLGGLISGIALILVATACLAAYGLVSFQKGGSSSDPLKTSEGWSQFTAGFFVGAMGSAF
VAFFLLENFLVVDGIMTGLFN
>d1jb0m_ f.2.1.12 (M:) Photosystem I {Synechococcus elongatus}
MALTDTQVYVALVIALLPAVLAFRLSTELYK
>d1jb0x_ f.2.1.12 (X:) Photosystem I {Synechococcus elongatus}
PTYAFRTFWAVLLLAINFLVAAYYFAAAA
>d1eula_ f.2.1.10 (A:) Calcium ATPase {Rabbit (Oryctolagus
cuniculus)}
MEAAHSKSTEECLAYFGVSETTGLTPDQVKRHLEKYGHNELPAEEGKSLWELVIEQFEDLLVRIL
LLAACISFVLAWFEEGEETITAFVEPFVILLILIANAIVGVWQERNAENAIEALKEYEPEMGKVY
RADRKSVQRIKARDIVPGDIVEVAVGDKVPADIRILSIKSTTLRVDQSILTGESVSVIKHTEPVP
DPRAVNQDKKNMLFSGTNIAAGKALGIVATTGVSTEIGKIRDQMAATEQDKTPLQQKLDEFGEQL
SKVISLICVAVWLINIGHFNDPVHGGSWIRGAIYYFKIAVALAVAAIPEGLPAVITTCLALGTRR
MAKKNAIVRSLPSVETLGCTSVICSDKTGTLTTNQMSVCKMFIIDKVDGDFCSLNEFSITGSTYA
PEGEVLKNDKPIRSGQFDGLVELATICALCNDSSLDFNETKGVYEKVGEATETALTTLVEKMNVF
NTEVRNLSKVERANACNSVIRQLMKKEFTLEFSRDRKSMSVYCSPAKSSRAAVGNKMFVKGAPEG
VIDRCNYVRVGTTRVPMTGPVKEKILSVIKEWGTGRDTLRCLALATRDTPPKREEMVLDDSSRFM
EYETDLTFVGVVGMLDPPRKEVMGSIQLCRDAGIRVIMITGDNKGTAIAICRRIGIFGENEEVAD
RAYTGREFDDLPLAEQREACRRACCFARVEPSHKSKIVEYLQSYDEITAMTGDGVNDAPALKKAE
IGIAMGSGTAVAKTASEMVLADDNFSTIVAAVEEGRAIYNNMKQFIRYLISSNVGEVVCIFLTAA
LGLPEALIPVQLLWVNLVTDGLPATALGFNPPDLDIMDRPPRSPKEPLISGWLFFRYMAIGGYVG
AATVGAAAWWFMYAEDGPGVTYHQLTHFMQCTEDHPHFEGLDCEIFEAPEPMTMALSVLVTIEMC
NALNSLSENQSLMRMPPWVNIWLLGSICLSMSLHFLILYVDPLPMIFKLKALDLTQWLMVLKISL
PVIGLDEILKFIARNYLEG
>d1kzua_ f.3.1.1 (A:) Light-harvesting complex subunits {Purple
bacterium (Rhodopseudomonas acidophila)}
MNQGKIWTVVNPAIGIPALLGSVTVIAILVHLAILSHTTWFPAYWQGGV
>d1kzub_ f.3.1.1 (B:) Light-harvesting complex subunits {Purple
bacterium (Rhodopseudomonas acidophila)}
ATLTAEQSEELHKYVIDGTRVFLGLALVAHFLAFSATPWLH
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>d1lgha_ f.3.1.1 (A:) Light-harvesting complex subunits {Rhodospirillum molischianum}
SNPKDDYKIWLVINPSTWLPVIWIVATVVAIAVHAAVLAAPGFNWIALGAAKSAAK
>d1lghb_ f.3.1.1 (B:) Light-harvesting complex subunits {Rhodospirillum molischianum}
RSLSGLTEEEAIAVHDQFKTTFSAFIILAAVAHVLVWVWKPWF
>d1jo5a_ f.3.1.1 (A:) Light-harvesting complex subunits {Rhodobacter sphaeroides}
ADKSDLGYTGLTDEQAQELHSVYMSGLWLFSAVAIVAHLAVYIWRPWF
>d1ijda_ f.3.1.1 (A:) Light-harvesting complex subunits {Rhodopseudomonas acidophila}
MNQGKIWTVVPPAFGLPLMLGAVAITALLVHAAVLTHTTWYAAFLQ
>d1ijdb_ f.3.1.1 (B:) Light-harvesting complex subunits {Rhodopseudomonas acidophila}
AEVLTSEQAEELHKHVIDGTRVFLVIAAIAHFLAFTLTPW
>d1g90a_ f.4.1.1 (A:) Outer membrane protein A (OMPA) transmembrane domain {Escherichia coli}
APKDNTWYTGAKLGFSQYHDTGFINNNGPTHENQLGAGAFGGYQVNPYVGFEMGYDFLGRMPYKG
SVENGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVFRADTKSNVYGKNHDTGVSPVFAGGVEYA
ITPEIATRLEYQFTNNIGDAHTIGTRPDNGMLSLGVSYRFGQGEAA
>d1qjpa_ f.4.1.1 (A:) Outer membrane protein A (OMPA) transmembrane domain {Escherichia coli}
APKDNTWYTGAKLGWSQYHDTGLINNNGPTHENKLGAGAFGGYQVNPYVGFEMGYDWLGRMPYKG
SVENGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTYSNVYGKNHDTGVSPVFAGGVEYA
ITPEIATRLEYQWTNNIGDAHTIGTRPDNGMLSLGVSYRFG
>d1qj8a_ f.4.1.1 (A:) Outer membrane protein X (OMPX) {Escherichia coli}
ATSTVTGGYAQSDAQGQMNKMGGFNLKYRYEEDNSPLGVIGSFTYTEKSRTASSGDYNKNQYYGI
TAGPAYRINDWASIYGVVGVGYGKFQTTEYPTYKNDTSDYGFSYGAGLQFNPMENVALDFSYEQS
RIRSVDVGTWIAGVGYRF
>d1i78a_ f.4.4.1 (A:) Outer membrane protease OMPT {Escherichia coli}
STETLSFTPDNINADISLGTLSGKTKERVYLAEEGGRKVSQLDWKFNNAAIIKGAINWDLMPQIS
IGAAGWTTLGSRGGNMVDQDWMDSSNPGTWTDEARHPDTQLNYANEFDLNIKGWLLNEPNYRLGL
MAGYQESRYSFTARGGSYIYSSEEGFRDDIGSFPNGERAIGYKQRFKMPYIGLTGSYRYEDFELG
GTFKYSGWVESSDNDEHYDPKGRITYRSKVKDQNYYSVAVNAGYYVTPNAKVYVEGAWNRVTNKK
GNTSLYDHNNNTSDYSKNGAGIENYNFITTAGLKYTF
>g1qd6.1 f.4.2.1 (A:,C:) Outer membrane phospholipase A (OMPLA) {Escherichia coli}
AVRGSIIANMLQEXFTLYPYDTNYLIYTQTSDLNKEAIASYDWAENARKDEVKFQLSLAFPLWRG
ILGPNSVLGASYTQKSWWQLSNSEESSPFRETNYEPQLFLGFATDYRFAGWTLRDVEMGYNHDSN
GRSDPTSRSWNRLYTRLMAENGNWLVEVKPWYVVGNTDDNPDITKYMGYYQLKIGYHLGDAVLSA
KGQYNWNTGYGGAELGLSYPITKHVRLYTQVYSGYGESLIDYNFNQTRVGVGVMLNDLF
>d1hxxa_ f.4.3.1 (A:) Porin {Escherichia coli, different sequences}
AEIYNKDGNKVDLYGKAVGLHYFSKGNGENSYGGNGDMTYARLGFKGETQINSDLTGYGQWEYNF
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QGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGRNYGVVFDALGYTDMLPEFGGDTAYSDDFFV
GRVGGVATYRNSNFFGLVDGLNFAVQYLGKNERDTARRSNGDGVGGSISYEYEGFGIVGAYGAAD
RTNLQEAQPLGNGKKAEQWATGLKYDANNIYLAANYGETRNATPITNKFTNTSGFANKTQDVLLV
AQYQFDFGLRPSIAYTKSKAKDVEGIGDVDLVNYFEVGATYYFNKNMSTYVDYIINQIDSDNKLG
VGSDDTVAVGIVYQF
>d1pho__ f.4.3.1 (-) Porin {Escherichia coli, different sequences}
AEIYNKDGNKLDVYGKVKAMHYMSDNASKDGDQSYIRFGFKGETQINDQLTGYGRWEAEFAGNKA
ESDTAQQKTRLAFAGLKYKDLGSFDYGRNLGALYDVEAWTDMFPEFGGDSSAQTDNFMTKRASGL
ATYRNTDFFGVIDGLNLTLQYQGKNENRDVKKQNGDGFGTSLTYDFGGSDFAISGAYTNSDRTNE
QNLQSRGTGKRAEAWATGLKYDANNIYLATFYSETRKMTPITGGFANKTQNFEAVAQYQFDFGLR
PSLGYVLSKGKDIEGIGDEDLVNYIDVGATYYFNKNMSAFVDYKINQLDSDNKLNINNDDIVAVG
MTYQF
>d2por__ f.4.3.1 (-) Porin {Rhodobacter capsulatus}
EVKLSGDARMGVMYNGDDWNFSSRSRVLFTMSGTTDSGLEFGASFKAHESVGAETGEDGTVFLSG
AFGKIEMGDALGASEALFGDLYEVGYTDLDDRGGNDIPYLTGDERLTAEDNPVLLYTYSAGAFSV
AASMSDGKVGETSEDDAQEMAVAAAYTFGNYTVGLGYEKIDSPDTALMADMEQLELAAIAKFGAT
NVKAYYADGELDRDFARAVFDLTPVAAAATAVDHKAYGLSVDSTFGATTVGGYVQVLDIDTIDDV
TYYGLGASYDLGGGASIVGGIADNDLPNSDMVADLGVKFKF
>d3prn__ f.4.3.1 (-) Porin {Rhodopseudomonas blastica, strain
DSM2131}
MISLNGYGRFGLQYVEDRGVGLEDTIISSRLRINIVGTTETDQGVTFGAKLRMQWDDGDAFAGTA
GNAAQFWTSYNGVTVSVGNVDTAFDSVALTYDSEMGYEWSSFGDAQSSFFAYNSKYDASGALDNY
NGIAVTYSISGVNLYLSYVDPDQTVDSSLVTEEFGIAADWSNDMISLAAAYTTDAGGIVDNDIAF
VGAAYKFNDAGTVGLNWYDNGLSTAGDQVTLYGNYAFGATTVRAYVSDIDRAGADTAYGIGADYQ
FAEGVKVSGSVQSGFANETVADVGVRFDF
>d1osma_ f.4.3.1 (A:) Porin {Klebsiella pneumoniae}
AEIYNKDGNKLDLYGKIDGLHYFSDDKDVDGDQTYMRLGVKGETQINDQLTGYGQWEYNVQANNT
ESSSDQAWTRLAFAGLKFGDAGSFDYGRNYGVVYDVTSWTDVLPEFGGDTYGSDNFLQSRANGVA
TYRNSDFFGLVDGLNFALQYQGKNGSVSGEGATNNGRGALKQNGDGFGTSVTYDIFDGISAGFAY
ANSKRTDDQNQLLLGEGDHAETYTGGLKYDANNIYLATQYTQTYNATRAGSLGFANKAQNFEVAA
QYQFDFGLRPSVAYLQSKGKDLNGYGDQDILKYVDVGATYYFNKNMSTYVDYKINLLDDNSFTRS
AGISTDDVVALGLVYQF
>d1e54a_ f.4.3.1 (A:) Porin {Comamonas acidovorans}
ESSVTLFGIVDTNVAYVNKDAAGDSRYGLGTSGASTSRLGLRGTEDLGGGLKAGFWLEGEIFGDD
GNASGFNFKRRSTVSLSGNFGEVRLGRDLVPTSQKLTSYDLFSATGIGPFMGFRNWAAGQGADDN
GIRANNLISYYTPNFGGFNAGFGYAFDEKQTIGTADSVGRYIGGYVAYDNGPLSASLGLAQQKTA
VGGLATDRDEITLGASYNFGVAKLSGLLQQTKFKRDIGGDIKTNSYMLGASAPVGGVGEVKLQYA
LYDQKAIDSKAHQITLGYVHNLSKRTALYGNLAFLKNKDASTLGLQAKGVYAGGVQAGESQTGVQ
VGIRHAF
>d1af6a_ f.4.3.2 (A:) Maltoporin (also LamB protein) {Escherichia
coli}
VDFHGYARSGIGWTGSGGEQQCFQTTGAQSKYRLGNECETYAELKLGQEVWKEGDKSFYFDTNVA
YSVAQQNDWEATDPAFREANVQGKNLIEWLPGSTIWAGKRFYQRHDVHMIDFYYWDISGPGAGLE
NIDVGFGKLSLAATRSSEAGGSSSFASNNIYDYTNETANDVFDVRLAQMEINPGGTLELGVDYGR
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ANLRDNYRLVDGASKDGWLFTAEHTQSVLKGFNKFVVQYATDSMTSQGKGLSQGSGVAFDNEKFA
YNINNNGHMLRILDHGAISMGDNWDMMYVGMYQDINWDNDNGTKWWTVGIRPMYKWTPIMSTVME
IGYDNVESQRTGDKNNQYKITLAQQWQAGDSIWSRPAIRVFATYAKWDEKWGYDYTGNADNNANF
GKAVPADFNGGSFGRGDSDEWTFGAQMEIWW
>d2mpra_ f.4.3.2 (A:) Maltoporin (also LamB protein) {Salmonella typhimurium}
VDFHGYARSGIGWTGSGGEQQCFQATGAQSKYRLGNECETYAELKLGQEVWKEGDKSFYFDTNVA
YSVNQQNDWESTDPAFREANVQGKNLIEWLPGSTIWAGKRFYQRHDVHMIDFYYWDISGPGAGIE
NIDLGFGKLSLAATRSTEAGGSYTFSSQNIYDEVKDTANDVFDVRLAGLQTNPDGVLELGVDYGR
ANTTDGYKLADGASKDGWMFTAEHTQSMLKGYNKFVVQYATDAMTTQGKGQARGSDGSSSFTEKI
NYANKVINNNGNMWRILDHGAISLGDKWDLMYVGMYQNIDWDNNLGTEWWTVGVRPMYKWTPIMS
TLLEVGYDNVKSQQTGDRNNQYKITLAQQWQAGDSIWSRPAIRIFATYAKWDEKWGYIKDGDNIS
RYAAATNSGISTNSRGDSDEWTFGAQMEIWW
>d1a0tp_ f.4.3.2 (P:) Sucrose-specific porin {Enterobacterium (Salmonella typhimurium)}
SGFEFHGYARSGVIMNDSGASTKSGAYITPAGETGGAIGRLGNQADTYVEMNLEHKQTLDNGATT
RFKVMVADGQTSYNDWTASTSDLNVRQAFVELGNLPTFAGPFKGSTLWAGKRFDRDNFDIHWIDS
DVVFLAGTGGGIYDVKWNDGLRSNFSLYGRNFGDIDDSSNSVQNYILTMNHFAGPLQMMVSGLRA
KDNDERKDSNGNLAKGDAANTGVHALLGLHNDSFYGLRDGSSKTALLYGHGLGAEVKGIGSDGAL
RPGADTWRIASYGTTPLSENWSVAPAMLAQRSKDRYADGDSYQWATFNLRLIQAINQNFALAYEG
SYQYMDLKPEGYNDRQAVNGSFYKLTFAPTFKVGSIGDFFSRPEIRFYTSWMDWSKKLNNYASDD
ALGSDGFNSGGEWSFGVQMETWF
>d1by5a_ f.4.3.3 (A:) Ferric hydroxamate uptake receptor FhuA {Escherichia coli}
QESAWGPAATIAARQSATGTKTDTPIQKVPQSISVVTAEEMALHQPKSVKEALSYTPGVSVGTRG
ASNTYDHLIIRGFAAEGQSQNNYLNGLKLQGNFYNDAVIDPYMLERAEIMRGPVSVLYGKSSPGG
LLNMVSKRPTTEPLKEVQFKAGTDSLFQTGFDFSDSLDDDGVYSYRLTGLARSANAQQKGSEEQR
YAIAPAFTWRPDDKTNFTFLSYFQNEPETGYYGWLPKEGTVEPLPNGKRLPTDFNEGAKNNTYSR
NEKMVGYSFDHEFNDTFTVRQNLRFAENKTSQNSVYGYGVCSDPANAYSKQCAALAPADKGHYLA
RKYVVDDEKLQNFSVDTQLQSKFATGDIDHTLLTGVDFMRMRNDINAWFGYDDSVPLLNLYNPVN
TDFDFNAKDPANSGPYRILNKQKQTGVYVQDQAQWDKVLVTLGGRYDWADQESLNRVAGTTDKRD
DKQFTWRGGVNYLFDNGVTPYFSYSESFEPSSQVGKDGNIFAPSKGKQYEVGVKYVPEDRPIVVT
GAVYNLTKTNNLMADPEGSFFSVEGGEIRARGVEIEAKRPLSASVNVVGSYTYTDAEYTTDTTYK
GNTPAQVPKHMASLWADYTFFDGPLSGLTLGTGGRYTGSSYGDPANSFKVGSYTVVDALVRYDLA
RVGMAGSNVALHVNNLFDREYVASCFNTYGCFWGAERQVVATATFRF
>d1fepa_ f.4.3.3 (A:) Ferric enterobactin receptor FepA {Escherichia coli}
DDTIVVTAAEQNLQAPGVSTITADEIRKNPVARDVSKIIRTMPGVNLTGNSTSGQRGNNRQIDIR
GMGPENTLILIDGKPVSSRNSVRQGWRGERDTRGDTSWVPPEMIERIEVLRGPAAARYGNGAAGG
VVNIITKKGSGEWHGSWDAYFNAPEHKEEGATKRTNFSLTGPLGDEFSFRLYGNLDKTQADAWDI
NQGHQSARAGTYATTLPAGREGVINKDINGVVRWDFAPLQSLELEAGYSRQGNLYAGDTQNTNSD
SYTRSKYGDETNRLYRQNYALTWNGGWDNGVTTSNWVQYEHTRNSRIPEGLAGGTEGKFNEKATQ
DFVDIDLDDVMLHSEVNLPIDFLVNQTLTLGTEWNQQRMKDLSSNTQALTGTNTGGAIDGVSTTD
RSPYSKAEIFSLFAENNMELTDSTIVTPGLRFDHHSIVGNNWSPALNISQGLGDDFTLKMGIARA
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YKAPSLYQTNPNYILYSKGQGCYASAGGCYLQGNDDLKAETSINKEIGLEFKRDGWLAGVTWFRN
DYRNKIEAGYVAVGQNAVGTDLYQWDNVPKAVVEGLEGSLNVPVSETVMWTNNITYMLKSENKTT
GDRLSIIPEYTLNSTLSWQAREDLSMQTTFTWYGKQQPKKYNYKGQPAVGPETKEISPYSIVGLS
ATWDVTKNVSLTGGVDNLFDKRLWRAGNAQTTGDLAGANYIAGAGAYTYNEPGRTWYMSVNTHF
>d1ek9a_ f.5.1.1 (A:) Integral outer membrane protein TolC, efflux pump component {Escherichia coli}
ENLMQVYQQARLSNPELRKSAADRDAAFEKINEARSPLLPQLGLGADYTYSNGYRDANGINSNAT
SASLQLTQSIFDMSKWRALTLQEKAAGIQDVTYQTDQQTLILNTATAYFNVLNAIDVLSYTQAQK
EAIYRQLDQTTQRFNVGLVAITDVQNARAQYDTVLANELTARNNLDNAVEQLRQITGNYYPELAA
LNVENFKTDKPQPVNALLKEAEKRNLSLLQARLSQDLAREQIRQAQDGHLPTLDLTASTGISDTS
YSGSKTRGAAGTQYDDSNMGQNKVGLSFSLPIYQGGMVNSQVKQAQYNFVGASEQLESAHRSVVQ
TVRSSFNNINASISSINAYKQAVVSAQSSLDAMEAGYSVGTRTIVDVLDATTTLYNAKQELANAR
YNYLINQLNIKSALGTLNEQDLLALNNALSKPVSTNPE
>d7ahla_ f.6.1.1 (A:) Alpha-hemolysin {Staphylococcus aureus}
ADSDINIKTGTTDIGSNTTVKTGDLVTYDKENGMHKKVFYSFIDDKNHNKKLLVIRTKGTIAGQY
RVYSEEGANKSGLAWPSAFKVQLQLPDNEVAQISDYYPRNSIDTKEYMSTLTYGFNGNVTGDDTG
KIGGLIGANVSIGHTLKYVQPDFKTILESPTDKKVGWKVIFNNMVNQNWGPYDRDSWNPVYGNQL
FMKTRNGSMKAADNFLDPNKASSLLSSGFSPDFATVITMDRKASKQQTNIDVIYERVRDDYQLHW
TSTNWKGTNTKDKWTDRSSERYKIDWEKEEMTN
>d1pvl__ f.6.1.1 (-) Leucocidin K component LukF-PV {Staphylococcus aureus}
AQHITPVSEKKVDDKITLYKTTATSDSDKLKISQILTFNFIKDKSYDKDTLILKAAGNIYSGYTK
PNPKDTISSQFYWGSKYNISINSDSNDSVNVVDYAPKNQNEEFQVQQTVGYSYGGDINISNGLSG
GGNGSKSFSETINYKQESYRTSLDKRTNFKKIGWDVEAHKIMNNGWGPYGRDSYHSTYGNEMFLG
SRQSNLNAGQNFLEYHKMPVLSRGNFNPEFIGVLSRKQNAAKKSKITVTYQREMDRYTNFWNQLH
WIGNNYKDENRATHTSIYEVDWENHTVKLIDTQSKEKNPMS
>d3lkfa_ f.6.1.1 (A:) Leukocidin F (HlgB) {Staphylococcus aureus}
EGKITPVSVKKVDDKVTLYKTTATADSDKFKISQILTFNFIKDKSYDKDTLVLKATGNINSGFVK
PNPNDYDFSKLYWGAKYNVSISSQSNDSVNVVDYAPKNQNEEFQVQNTLGYTFGGDISISNGLSG
GLNGNTAFSETINYKQESYRTTLSRNTNYKNVGWGVEAHKIMNNGWGPYGRDSFHPTYGNELFLA
GRQSSAYAGQNFIAQHQMPLLSRSNFNPEFLSVLSHRQDGAKKSKITVTYQREMDLYQIRWNGFY
WAGANYKNFKTRTFKSTYEIDWENHKVKLLDTKETENNK
>d1prea2 f.8.1.1 (A:85-470) (Pro)aerolysin, pore-forming lobe {Aeromonas hydrophila}
IPTLSALDIPDGDEVDVQWRLVHDSANFIKPTSYLAHYLGYAWVGGNHSQYVGEDMDVTRDGDGW
VIRGNNDGGCDGYRCGDKTAIKVSNFAYNLDPDSFKHGDVTQSDRQLVKTVVGWAVNDSDTPQSG
YDVTLRYDTATNWSKTNTYGLSEKVTTKNKFKWPLVGETELSIEIAANQSWASQNGGSTTTSLSQ
SVRPTVPARSKIPVKIELYKADISYPYEFKADVSYDLTLSGFLRWGGNAWYTHPDNRPNWNHTFV
IGPYKDKASSIRYQWDKRYIPGEVKWWDWNWTIQQNGLSTMQNNLARVLRPVRAGITGDFSAESQ
FAGNIEIGAPVPLAADSKVRRARSVDGAGQGLRLEIPLDAQELSGLGFNNVSLSVTPAANQ
>d1pfo__ f.9.1.1 (-) Perfringolysin {Clostridium perfringens}
DITDKNQSIDSGISSLSYNRNEVLASNGDKIESFVPKEGKKAGNKFIVVERQKRSLTTSPVDISI
IDSVNDRTYPGALQLADKALVENRPTILMVKRKPININIDLPGLKGENSIKVDDPTYGKVSGAID
ELVSKWNEKYSSTHTLPARTQYSESMVYSKSQISSALNVNAKVLENSLGVDFNAVANNEKKVMIL

AYKQIFYTVSADLPKNPSDLFDDSVTFNDLKQKGVSNEAPPLMVSNVAYGRTIYVKLETTSSSKD
VQAAFKALIKNTDIKNSQQYKDIYENSSFTAVVLGGDAQEHNKVVTKDFDEIRKVIKDNATFSTK
NPAYPISYTSVFLKDNSVAAVHNKTDYIETTSTEYSKGKINLDHSGAYVAQFEVAWDEVSYDKEG
NEVLTHKTWDGNYQDKTAHYSTVIPLEANARNIRIKARECTGLAWEWWRDVISEYDVPLTNNINV
SIWGTTLYPGSSITYN
>d1svb_2 f.10.1.1 (1-302) Envelope glycoprotein, central and dimerisation domains {Tick-borne encephalitis virus}
SRCTHLENRDFVTGTQGTTRVTLVLELGGCVTITAEGKPSMDVWLDAIYQENPAKTREYCLHAKL
SDTKVAARCPTMGPATLAEEHQGGTVCKRDQSDRGWGNHCGLFGKGSIVACVKAACEAKKKATGH
VYDANKIVYTVKVEPHTGDYVAANETHSGRKTASFTISSEKTILTMGEYGDVSLLCRVASGVDLA
QTVILELDKTVEHLPTAWQVHRDWFNDLALPWKHEGAQNWNNAERLVEFGAPHAVKMDVYNLGDQ
TGVLLKALAGVPVAHIEGTKYHLKSGHVTCEVGLEKLKMKGL
>d1g5ga1 f.12.1.1 (A:33-66,A:224-454) Head and neck region of the ectodomain of NDV fusion glycoprotein {Newcastle disease virus}
DGRPLAAAGIVVTGDKAVNIYTSSQTGSIIIKLLXQITSPALTQLTIQALYNLAGGNMDYLLTKL
GVGNNQLSSLISSGLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRATYLETLSVSTTKGFASAL
VPKVVTQVGSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIYSCLSGNTSACMYSKTEGALTTPY
MTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLIDRQSCNILSLDGITLRLSGEFDATYQKNI
SIQDSQ
>d1acc__ f.11.1.1 (-) Anthrax protective antigen {Anthrax bacillus (Bacillus anthracis)}
SSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYFQSAIWSGFIKVKKSDEYT
FATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQRENPTEKGLDFKLYWTDSQNKK
EVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWIS
NIHEKKGLTKYKSSPEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSK
NEDQSTQNTDSETRTISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSL
SLAGERTWAETMGLNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQ
ILAPNNYYPSKNLAPIALNAQDDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGR
VRVDTGSNWSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGF
NEPNGNLQYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHY
DRNNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRYDML
NISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNGIKKILIFS
KKGYEIG
>g1cph.1 g.1.1.1 (B:,A:) Insulin {Cow (Bos taurus)}
FVNQHLCGSHLVEALYLVCGERGFFYTPKAXGIVEQCCASVCSLYQLENYCN
>g1pid.1 g.1.1.1 (B:,A:) Insulin {Cow (Bos taurus)}
FVNQHLCGSHLVEALYLVCGERGFFXGIVEQCCASVCSLYQLENYCN
>d1efea_ g.1.1.1 (A:) Insulin {Human (Homo sapiens)}
FVNQHLCGSHLVEALYLVCGERGFFYTPKTRRYPGDVKRGIVEQCCTSICSLYQLENYCN
>g1a7f.1 g.1.1.1 (B:,A:) Insulin {Human (Homo sapiens)}
FVNQHLCGSHLVEALELVCGERGGFYTPKXGIVEQCCTSICSLYQLENYCN
>g1g7a.1 g.1.1.1 (B:,A:) Insulin {Human (Homo sapiens)}
FVNQHLCGSHLVEALYLVCGERGFFYTPKTXGIVEQCCTSICSLYQLENYCN
>g1hui.1 g.1.1.1 (B:,A:) Insulin {Human (Homo sapiens)}

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EVNQHLCGSELVEALELVCGERGFFYEPKXGIVEQCCTSICSLYQLENYCN
>g1qj0.1 g.1.1.1 (B:,A:) Insulin {Human (Homo sapiens)}
VNQYLCGSHLVEALYLVCGERGFFYTPKXGIVEQCCTSICSLYQLENYCN
>g1sjt.1 g.1.1.1 (B:,A:) Insulin {Human (Homo sapiens)}
FVNQHLCGSDLVEALYLVCGERGFFYTDKXGIVEQCCTSICSLYQLENYCN
>g1vks.1 g.1.1.1 (B:,A:) Insulin {Human (Homo sapiens)}
FVNQHLCGSDLVEALYLVCGERGFFYTKPTXGIVEQCCTSICSLYQLENYCN
>d1zeia_ g.1.1.1 (A:) Insulin {Pig (Sus scrofa)}
FVNQHLCGSHLVEALYLVCGERGFFYTDKAAKGIVEQCCTSICSLYQLENYCN
>g1dei.1 g.1.1.1 (B:,A:) Insulin {Pig (Sus scrofa)}
FVNQHLCGSHLVEALYLVCGERGXGIVEQCCTSICSLYQLENYCN
>g1sdb.1 g.1.1.1 (B:,A:) Insulin {Pig (Sus scrofa)}
NQHLCGSHLVEALYLVCGERGFFXGIVEQCCTSICSLYQLENYCN
>g6rlx.1 g.1.1.1 (B:,A:) Relaxin {Human (Homo sapiens)}
SWMEEVIKLCGRELVRAQIAICGMSTWXELYSALANKCCHVGCTKRSLARFC
>d1b9ga_ g.1.1.1 (A:) Insulin-like growth factor {Human (Homo sapiens)}
GPETLCGAELVDALQFVCGDRGFYFNKPGIVDECCFRSCDLRRLEMYCAPLKPAKSA
>d1igl__ g.1.1.1 (-) Insulin-like growth factor {Human (Homo sapiens)}
AYRPSETLCGGELVDTLQFVCGDRGFYFSRPASRVSRRSRGIVEECCFRSCDLALLETYCATPAKSE
>d1imxa_ g.1.1.1 (A:) Insulin-like growth factor {Human (Homo sapiens)}
ETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRAPQTGIVDECCFRSCDLRRLEMYCAPL
>d2gf1__ g.1.1.1 (-) Insulin-like growth factor {Human (Homo sapiens)}
GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRAPQTGIVDECCFRSCDLRRLEMYCAPLKPAKSA
>d3lria_ g.1.1.1 (A:) Insulin-like growth factor {Human (Homo sapiens)}
MFPAMPLSSLFVNGPRTLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRACQTGIVDECCFRSCDLRRLEMYCAPLKPAKSA
>g1bom.1 g.1.1.1 (B:,A:) Bombyxin-II {Silkworm (Bombyx mori)}
EQPQAVHTYCGRHLARTLADLCWEAGVDXGIVDECCLRPCSVDVLLSYC
>d1ehs__ g.2.1.1 (-) Heat-stable enterotoxin B {Escherichia coli}
STQSNKKDLCEHYRQIAKESCKKGFLGVRDGTAGACFGAQIMVAAKGC
>d1vib__ g.2.2.1 (-) Neurotoxin B-IV {Milky ribbon worm (Cerebratulus lacteus)}
ASATWGAAYPACENNCRKKYDLCIRCQGKWAGKRGKCAAHCIIQKNNCKGKCKKE
>d1wgta3 g.3.1.1 (A:87-129) Wheat germ agglutinin (WGA) {Wheat (Triticum vulgaris)}
IKCGSQAGGKLCPNNLCCSQWGYCGLGSEFCGEGCQNGACSTD
>d2cwga2 g.3.1.1 (A:53-86) Wheat germ agglutinin (WGA) {Wheat (Triticum vulgaris)}
ATCTNNQCCSQYGYCGFGAEYCGAGCQGGPCRAD
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>d9wgaa1 g.3.1.1 (A:1-52) Wheat germ agglutinin (WGA) {Wheat (Triticum vulgaris)}

ERCGEQGSNMECPNNLCCSQYGYCGMGGDYCGKGCQNGACWTSKRCGSQAGG

>d9wgaa2 g.3.1.1 (A:53-86) Wheat germ agglutinin (WGA) {Wheat (Triticum vulgaris)}

ATCPNNHCCSQYGHCGFGAEYCGAGCQGGPCRAD

>d9wgaa3 g.3.1.1 (A:87-129) Wheat germ agglutinin (WGA) {Wheat (Triticum vulgaris)}

IKCGSQSGGKLCPNNLCCSQWGFCGLGSEFCGGGCQSGACSTD

>d9wgaa4 g.3.1.1 (A:130-171) Wheat germ agglutinin (WGA) {Wheat (Triticum vulgaris)}

KPCGKDAGGRVCTNNYCCSKWGSCGIGPGYCGAGCQSGGCDA

>d1ehda1 g.3.1.1 (A:1-45) Isolectin VI {Stinging nettle (Urtica dioica), UDA}

ERCGSQGGGATCPGLRCCSIWGWCGDSEPYCGRTCENKCWSGERS

>d1ehda2 g.3.1.1 (A:46-89) Isolectin VI {Stinging nettle (Urtica dioica), UDA}

DHRCGAAVGNPPCGQDRCCSVHGWCGGGNDYCSGGKCQYRCSSS

>d1en2a1 g.3.1.1 (A:1-45) Isolectin VI {Stinging nettle (Urtica dioica), UDA}

ERCGSQGGGGTCPALWCCSIWGWCGDSEPYCGRTCENKCWSGERS

>d1en2a2 g.3.1.1 (A:46-86) Isolectin VI {Stinging nettle (Urtica dioica), UDA}

DHRCGAAVGNPPCGQDRCCSVHGWCGGGNDYCSGSKCQYRC

>d1hev__ g.3.1.1 (-) Hevein {Hevea brasiliensis}

EQCGRQAGGKLCPNNLCCSQWGWCGSTDEYCSPDHNCQSNCKD

>d1mmc__ g.3.1.2 (-) Antimicrobial peptide 2, AC-AMP2 {Tassel (Amaranthus caudatus)}

VGECVRGRCPSGMCCSQFGYCGKGPKYCGR

>d1f2si_ g.3.2.1 (I:) Trypsin inhibitor {Bitter gourd (Momordica charantia), linn. Cucurbitaceae, seed}

RICPRIWMECKRDSDCMAECICVMGHCG

>d1mcti_ g.3.2.1 (I:) Trypsin inhibitor {Bitter gourd (Momordica charantia), linn. Cucurbitaceae, seed}

RICPRIWMECTRDSDCMAKCICVAGHCG

>d2stai_ g.3.2.1 (I:) Trypsin inhibitor {Squash (Cucurbita maxima)}

RVCPRILMECKKDSDCLAECVCLEHGYCG

>d1ha9a_ g.3.2.1 (A:) Trypsin inhibitor {Spiny bitter cucumber (Momordica cochinchinensis), MCOTI-II}

SGSDGGVCPKILKKCRRDSDCPGACICRGNGYCG

>d2btci_ g.3.2.1 (I:) Trypsin inhibitor {Vegetable marrow (Cucurbita pepo)}

RVCPKILMECKKDSDCLAECICLEHGYCG

>d2let__ g.3.2.1 (-) Trypsin inhibitor {Jumping cucumber (Ecballium

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elaterium)}
GCPRLLMRCKQDSDCLAGCVCGPNGFCG
>d4cpai_ g.3.2.1 (I:) Carboxypeptidase A inhibitor {Potato}
ZHADPICNKPCKTHDDCSGAWFCQACWNSARTCGPYV
>d1clvi_ g.3.2.1 (I:) alpha-amylase inhibitor (AAI) {Prince's feather (Amaranthus hypochondriacus)}
CIPKWNRCGPKMDGVPCCEPYTCTSDYYGNCS
>d1kal__ g.3.3.1 (-) Kalata B1 {African plant (Oldenlandia affinis dc)}
SWPVCTRNGLPVCGETCVGGTCNTPGCTC
>d1df6a_ g.3.3.2 (A:) Cycloviolacin O1 {Plant (Viola odorata)}
SCVYIPCTVTALLGCSCSNRVCYNGIPCAE
>d1bh4__ g.3.3.3 (-) Circulin A {Chassalia parviflora}
CGESCVWIPCISAALGCSCKNKVCYRNGIP
>d1c4ea_ g.3.4.1 (A:) Gurmarin, a sweet taste-suppressing polypeptide {Gymnema sylvestre}
EQCVKKDELCIPYYLDCCEPLECKKVNWWDHKCIG
>d1dkca_ g.3.4.2 (A:) Antifungal peptide PAFP-S {Pokeweed (Phytolacca americana)}
AGCIKNGGRCNASAGPPYCCSSYCFQIAGQSYGVCKNR
>d1hyka_ g.3.5.1 (A:) Agouti-related protein {Synthetic, based on Homo sapiens sequence}
CVRLHESCLGQQVPCCDPCATCYCRFFNAFCYCRKLGTAMNPCSRT
>d1omc__ g.3.6.1 (-) Conotoxin {Sea snail (Conus geographus), G IVa}
CKSPGSSCSPTSYNCCRSCNPYTKRCY
>d1ag7__ g.3.6.1 (-) Conotoxin {Synthetic, based on Conus geographus, GS}
ACSGRGSRCPPQCCMGLRCGRGNPQKCIGAHEDV
>d1cnna_ g.3.6.1 (A:) Conotoxin {Sea snail (Conus magus), M VIIc}
CKGKGAPCRKTMYDCCSGSCGRRGKC
>d1omg__ g.3.6.1 (-) Conotoxin {Sea snail (Conus magus), M VIIa}
CKGKGAKCSRLMYDCCTGSCRSGKC
>d1mvj__ g.3.6.1 (-) Conotoxin {Conus striatus, S VIb}
CKLKGQSCRKTSYDCCSGSCGRSGKC
>d1fyga_ g.3.6.1 (A:) Conotoxin {Conus striatus, SO3}
CKAAGKPCSRIAYNCCTGSCRSGKC
>d1kcp__ g.3.6.1 (-) Conotoxin {Conus purpurascens, kappa-pVIIa}
CRIPNQKCFQHLDDCCSRKCNRFNKCV
>d1eyoa_ g.3.6.1 (A:) Conotoxin {Conus tulipa, T VIIa}
SCSGRDSRCPPVCCMGLMCSRGKCVSIYGE
>d1g1za_ g.3.6.1 (A:) Conotoxin {Conus ermineus, E VIa}
DDCIKPYGFCSLPILKNGLCCSGACVGVCADL
>d1f3ka_ g.3.6.1 (A:) Conotoxin {Conus textile, Tx VII}
CKQADEPCDVFSLDCCTGICLGVCMW
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>d1agg__ g.3.6.2 (-) omega-Agatoxin IV, IVa, IVb {Funnel web spider (Agelenopsis aperta)}
EDNCIAEDYGKCTWGGTKCCRGRPCRCSMIGTNCECTPRLIMEGLSFA
>d1oav__ g.3.6.2 (-) omega-Agatoxin IV, IVa, IVb {Funnel web spider (Agelenopsis aperta)}
KKKCIAKDYGRCKWGGTPCCRGRGCICSIMGTNCECKPRLIMEGLGLA
>d1omb__ g.3.6.2 (-) omega-Agatoxin IV, IVa, IVb {Funnel web spider (Agelenopsis aperta)}
CIAEDYGKCTWGGTKCCRGRPCRCSMIGTNCECTP
>d1eit__ g.3.6.2 (-) mu-Agatoxin-I {Funnel web spider (Agelenopsis aperta)}
ECVPENGHCRDWYDECCEGFYCSCRQPPKCICRNNN
>d1kqha_ g.3.6.2 (A:) ACTX-HI:OB4219 {Funnel-web spider (Hadronyche infensa)}
KCLAEAADCSPWSGDSCCKPYLCSCIFFYPCSCRPKGW
>d1axh__ g.3.6.2 (-) Atracotoxin-hvI (versutoxin) {Australian funnel-web spider (Hadronyche versuta)}
SPTCIPSGQPCPYNENCCSQSCTFKENENGNTVKRCD
>d1hvwa_ g.3.6.2 (A:) Atracotoxin-hvI (versutoxin) {Australian funnel-web spider (Hadronyche versuta)}
CIPSGQPCPYNENCCSQSCTGGRCD
>d1vtx__ g.3.6.2 (-) Atracotoxin-hvI (versutoxin) {Australian funnel-web spider (Hadronyche versuta)}
CAKKRNWCGKTEDCCCPMKCVYAWYNEQGSCQSTISALWKKC
>d1dl0a_ g.3.6.2 (A:) J-atracotoxin-hv1c {Australian funnel-web spider (Hadronyche versuta)}
AICTGADRPCAACCPCCPGTSCKAESNGVSYCRKDEP
>d1g9pa_ g.3.6.2 (A:) Atracotoxin-hv2a {Funnel-web spider (Hadronyche versuta)}
LLACLFGNGRCSSNRDCCELTPVCKRGSCVSSGPGLVGGILGGIL
>d1qdp__ g.3.6.2 (-) Robustoxin {Funnel-web spider (Atrax robustus)}
CAKKRNWCGKNEDCCCPMKCIYAWYNQQGSCQTTITGLFKKC
>d1qk6a_ g.3.6.2 (A:) Huwentoxin-I {Chinese bird spider (Selenocosmia huwena)}
ACKGVFDACTPGKNECCPNRVCSDKHKWCKWKL
>d1i25a_ g.3.6.2 (A:) Huwentoxin-II {Chinese bird spider (Selenocosmia huwena)}
LFECSFSCEIEKEGDKPCKKKKCKGGWKCKFNMCVKV
>d1qk7a_ g.3.6.2 (A:) Lectin SHL-I {Chinese bird spider (Selenocosmia huwena)}
GCLGDKCDYNNGCCSGYVCSRTWKWCVLAGPW
>d1d1ha_ g.3.6.2 (A:) Hanatoxin 1 {Tarantula (Grammostola spatulata)}
ECRYLFGGCKTTSDCCKHLGCKFRDKYCAWDFTFS
>d1emxa_ g.3.6.2 (A:) Heteropdatoxin 2, hptx2 {Spider (Heteropodidae
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venatoria)}
DDCGKLFSGCDTNADCCEGYVCRLWCKLDW
>d1c6wa_ g.3.6.2 (A:) Maurocalcin {Scorpio maurus}
GDCLPHLKLCKENKDCCSKKCKRRGTNIEKRCR
>d1i26a_ g.3.6.3 (A:) PTU-1 {Assassin bug (Peirates turpis)}
AEKDCIAPGAPCFGTDKPCCNPRAWCSSYANKCL
>d1jzaa_ g.3.7.1 (A:) Scorpion toxin {Centruroides sculpturatus ewing,
variant 2}
KEGYLVNKSTGCKYGCLKLGENEGCDKECKAKNQGGSYGYCYAFACWCEGLPESTPTYPLPNKSC
S
>d2sn3__ g.3.7.1 (-) Scorpion toxin {Centruroides sculpturatus ewing,
variant 3}
KEGYLVKKSDGCKYGCLKLGENEGCDTECKAKNQGGSYGYCYAFACWCEGLPESTPTYPLPNKSC
>d1b3ca_ g.3.7.1 (A:) Scorpion toxin {Centruroides sculpturatus ewing,
beta}
KDGYLVEKTGCKKTCYKLGENDFCNRECKWKHIGGSYGYCYGFGCYCEGLPDSTQTWPLPNKTC
>d1vnb__ g.3.7.1 (-) Scorpion toxin {Centruroides sculpturatus ewing,
variant 1}
KEGYLVKKSDGCKYDCFWLGKNEHCNTECKAKNQGGSYGYCYAFACWCEGLPESTPTYPLPNKSC
>d1nrb__ g.3.7.1 (-) Scorpion toxin {Centruroides sculpturatus ewing,
variant V}
KKDGYPVDSGNCKYECLKDDYCNDLCLERKADKGYCYWGKVSCYCYGLPDNSPTKTSGKCNPA
>d1aho__ g.3.7.1 (-) Scorpion toxin {Scorpion (Androctonus australis
hector), Toxin II}
VKDGYIVDDVNCTYFCGRNAYCNEECTKLKGESGYCQWASPYGNACYCYKLPDHVRTKGPGRCH
>d1cn2__ g.3.7.1 (-) Scorpion toxin {Mexican scorpion (Centruroides
noxius hoffmann), toxin II}
KEGYLVDKNTGCKYECLKLGDNDYCLRECKQQYGKGAGGYCYAFACWCTHLYEQAIVWPLPNKRC
S
>d1bcg__ g.3.7.1 (-) Scorpion toxin {Scorpion (Buthotus judaicus),
BJXTR-IT}
MKKNGYPLDRNGKTTECSGVNAIAPHYCNSECTKVYYAESGYCCWGACYCFGLEDDKPIGPMKDI
TKKYCDVQI
>d1snb__ g.3.7.1 (-) Scorpion toxin {Scorpion (Buthus martensii),
toxin m8}
GRDAYIADSENCTYFCGSNPYCNDVCTENGAKSGYCQWAGRYGNACYCIDLPASERIKEGGRCG
>d1djta_ g.3.7.1 (A:) Scorpion toxin {Chinese scorpion (Buthus
martensii), toxin m1}
VRDAYIAKPHNCVYECARNEYCNDLCTKNGAKSGYCQWVGKYGNGCWCIELPDNVPIRVPGKCH
>d1sn4a_ g.3.7.1 (A:) Scorpion toxin {Chinese scorpion (Buthus
martensii), toxin m4}
VRDAYIAKPENCVYHCAGNEGCNKLCTDNGAESGYCQWGGRYGNACWCIKLPDDVPIRVPGKCH
>d1dq7a_ g.3.7.1 (A:) Scorpion toxin {Indian red scorpion (Buthus
tamulus), neurotoxin}
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GEDGYIADGDNCTYICTFNNYCHALCTDKKGDSGACDWWVPYGVVCWCEDLPTPVPIRGSGKCR
>d1b7da_ g.3.7.1 (A:) Scorpion toxin {Scorpion (Tityus serrulatus)}
KEGYLMDHEGCKLSCFIRPSGYCGRECGIKKGSSGYCAWPACYCYGLPNWVKVWDRATNKC
>d1i6fa_ g.3.7.1 (A:) Scorpion toxin {Bark scorpion (Centruroides sculpturatus), cse-v5}
KDGYPVDSKGCKLSCVANNYCDNQCKMKKASGGHCYAMSCYCEGLPENAKVSDSATNICG
>d1lqq__ g.3.7.1 (-) alpha toxin {Leiurus quinquestriatus quinquestriatus, LQQIII}
VRDAYIAKNYNCVYECFRDSYCNDLCTKNGASSGYCQWAGKYGNACWCYALPDNVPIRVPGKCH
>d1lqi__ g.3.7.1 (-) alpha toxin {Scorpion (Leiurus quinquestriatus hebraeus)}
MVRDAYIAKNYNCVYECFRDAYCNELCTKNGASSGYCQWAGKYGNACWCYALPDNVPIRVPGKCR
>d1bmr__ g.3.7.1 (-) LQH III alpha-like toxin, LQH {Hebraei scorpion (Leiurus quinquestriatus hebraeus)}
VRDGYIAQPENCVYHCFPGSSGCDTLCKEKGGTSGHCGFKVGHGLACWCNALPDNVGIIVEGEKCHS
>d1big__ g.3.7.2 (-) Bmtx1 {Buthus martensii}
EFTDVKCTGSKQCWPVCKQMFGKPNGKCMNGKCRCYS
>d1bkt__ g.3.7.2 (-) Bmktx {Buthus martensii}
VGINVKCKHSGQCLKPCKDAGMRFGKCINGKCDCTPK
>d2bmt__ g.3.7.2 (-) Bmtx2 {Buthus martensii}
EFTNVSCSASSQCWPVCKKLFGTYRGKCMNSKCRCYS
>d1du9a_ g.3.7.2 (A:) Bmp02 neurotoxin {Chinese scorpion (Buthus martensii)}
VGCEECPMHCKGKNAKPTCDDGVCNCNV
>d1hp2a_ g.3.7.2 (A:) alpha-KTX, K+-channel blocker {Brazilian scorpion (Tityus serrulatus), Tstx-k alpha}
VFINAKCRGSPECLPKCKEAIGKAAGKCMNGKCKCYP
>d1jlza_ g.3.7.2 (A:) alpha-KTX, K+-channel blocker {Scorpion (Tityus cambridgei)}
ACGSCRKKCKGSGKCINGRCKCY
>d1mtx__ g.3.7.2 (-) Margatoxin {Scorpion (Centruroides margaritatus)}
TIINVKCTSPKQCLPPCKAQFGQSAGAKCMNGKCKCYPH
>d1sxm__ g.3.7.2 (-) Noxiustoxin {Scorpion (Centruroides noxius hoffmann)}
TIINVKCTSPKQCSKPCKELYGSSAGAKCMNGKCKCYNN
>d1txm__ g.3.7.2 (-) Maurotoxin {Scorpion (Scorpio maurus)}
VSCTGSKDCYAPCRKQTGCPNAKCINKSCKCYGC
>d1cmr__ g.3.7.2 (-) Charybdotoxin {Scorpion (Leiurus quinquestriatus hebraeus)}
CTTSKECWSVCQRLHNTSKGWCDHRGCICES
>d2crd__ g.3.7.2 (-) Charybdotoxin {Scorpion (Leiurus quinquestriatus hebraeus)}
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EFTNVSCTTSKECWSVCQRLHNTSRGKCMNKKCRCYS
>d1scy__ g.3.7.2 (-) Scyllatoxin {Scorpion (Leiurus quinquestriatus hebraeus)}
AFCNLRMCQLSCRSLGLLGKCIGDKCECVKH
>d1agt__ g.3.7.2 (-) Agitoxin {Scorpion (Leiurus quinquestriatus hebraeus)}
GVPINVSCTGSPQCIKPCKDAGMRFGKCMNRKCHCTPK
>d1chl__ g.3.7.2 (-) Chlorootoxin {Scorpion (Leiurus quinquestriatus), venom}
MCMPCFTTDHQMARKCDDCCGGKGRGKCYGPQCLCR
>d1c55a_ g.3.7.2 (A:) Butantoxin {Brazilian scorpion (Tityus serrulatus)}
WCSTCLDLACGASRECYDPCFKAFGRAHGKCMNNKCRCYT
>d1tsk__ g.3.7.2 (-) Toxin ts kappa {Scorpion (Tityus serrulatus)}
VVIGQRCYRSPDCYSACKKLVGKATGKCTNGRCDC
>d1sis__ g.3.7.2 (-) Toxin I5a {Scorpion (Buthus eupeus)}
MCMPCFTTDPNMAKKCRDCCGGNGKCFGPQCLCNR
>d1pnh__ g.3.7.2 (-) Toxin analog {Scorpion (Androctonus mauretanicus mauretanicus)}
TVCNLRRCQLSCRSLGLLGKCIGVKCECVKH
>d1acw__ g.3.7.2 (-) Toxin analog P01 {Scorpion (Androctonus mauretanicus mauretanicus)}
VSCEDCPEHCSTQKAQAKCDNDKCVCEPI
>d1sco__ g.3.7.2 (-) OSK1 TOXIN {Central asian scorpion (Orthochirus scrobiculosus)}
GVIINVKCKISRQCLEPCKKAGMRFGKCMNGKCHCTPK
>d2ktx__ g.3.7.2 (-) Kaliotoxin (KTX) {Scorpion (Androctonus mauretanicus mauretanicus)}
GVEINVKCSGSPQCLKPCKDAGMRFGKCMNRKCHCTPK
>d1lir__ g.3.7.2 (-) LQ2 toxin {Scorpion (Leiurus quinquestriatus hebraeus)}
EFTQESCTASNQCWSICKRLHNTNRGKCMNKKCRCYS
>d1c49a_ g.3.7.2 (A:) Pandinus toxin {Emperor scorpion (Pandinus imperator), PITX-Kb}
TISCTNEKQCYPHCKKETGYPNAKCMNRKCKCFGR
>d1qkya_ g.3.7.2 (A:) PI7 {Scorpion (Pandinus imperator)}
DEAIRCTGTKDCYIPCRYITGCFNSRCINKSCKCYGCT
>d1fjna_ g.3.7.3 (A:) Defensin MGD-1 {Mediterranean mussel (Mytilus galloprovincialis)}
GFGCPNNYQCHRHCKSIPGRCGGYCGGWHRLRCTCYRCG
>d1i2ua_ g.3.7.4 (A:) Heliomicin {Tobacco budworm (Heliothis virescens)}
DKLIGSCVWGAVNYTSDCNGECKRRGYKGGHCGSFANVNCWCET
>d1myn__ g.3.7.4 (-) Drosomycin {Fruit fly (Drosophila melanogaster)}
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DCLSGRYKGPCAVWDNETCRRVCKEEGRSSGHCSPSLKCWCEGC
>d1ica__ g.3.7.4 (-) Defensin A {Flesh fly (Phormia terranovae), larva}
ATCDLLSGTGINHSACAAHCLLRGNRGGYCNGKGVCVCRN
>d1gpt__ g.3.7.5 (-) gamma-Thionin {Barley (Hordeum vulgare)}
RICRRRSAGFKGPCVSNKNCAQVCMQEGWGGGNCDGPLRRCKCMRRC
>d1gps__ g.3.7.5 (-) gamma-Thionin {Wheat (Triticum turgidum)}
KICRRRSAGFKGPCMSNKNCAQVCQQEGWGGGNCDGPFRRCKCIRQC
>d1ayj__ g.3.7.5 (-) Antifungal protein 1 (RS-AFP1) {Radish (Raphanus sativus)}
EKLCERPSGTWSGVCGNNNACKNQCINLEKARHGSCNYVFPAHKCICYFPC
>d1bk8__ g.3.7.5 (-) Antimicrobial protein 1 (AH-AMP1) {Horse chestnut (Aesculus hippocastanum)}
LCNERPSQTWSGNCGNTAHCDKQCQDWEKASHGACHKRENHWKCFCYFNC
>d1jkza_ g.3.7.5 (A:) Defensin 1 (PSD1) {Pea (Pisum sativum)}
KTCEHLADTYRGVCFTNASCDDHCKNKAHLISGTCHNWKCFCTQNC
>d1brz__ g.3.7.5 (-) Brazzein {J'oublie (Pentadiplandra brazzeana)}
EDKCKKVYENYPVSKCQLANQCNYDCKLDKHARSGECFYDEKRNLQCICDYCEY
>d2cbh__ g.3.8.1 (-) Cellobiohydrolase I {Trichoderma reesei, ct-cbh I}
TQSHYGQCGGIGYSGPTVCASGTTCQVLNPYYSQCL
>d1boea_ g.3.9.1 (A:) Insulin-like growth factor-binding protein-5 (IGFBP-5) {Human (Homo sapiens)}
ALAEGQSCGVYTERCAQGLRCLPRQDEEKPLHALLHGRGVCLNEKS
>d1igra3 g.3.9.1 (A:150-299) Cys-rich domain of the type 1 insulin-like growth factor receptor {Human (Homo sapiens)}
DLCPGTMEEKPMCEKTTINNEYNYRCWTTNRCQKMCPSTCGKRACTENNECCHPECLGSCSAPDN
DTACVACRHYYYAGVCVPACPPNTYRFEGWRCVDRDFCANILSAESSDSEGFVIHDGECMQECPS
GFIRNGSQSMYCIPCEGPCP
>d1lpba1 g.3.10.1 (A:6-44) (Pro)colipase {Pig (Sus scrofa)}
GIIINLDEGELCLNSAQCKSNCCQHDTILSLSRCALKAR
>d1lpba2 g.3.10.1 (A:45-90) (Pro)colipase {Pig (Sus scrofa)}
ENSECSAFTLYGVYYKCPCERGLTCEGDKSLVGSITNTNFGICHNV
>d1pco_1 g.3.10.1 (1-44) (Pro)colipase {Pig (Sus scrofa)}
VPDPRGIIINLDEGELCLNSAQCKSNCCQHDTILSLSRCALKAR
>d1imt_1 g.3.10.1 (1-36) Intestinal toxin 1 {Black mamba (Dendroaspis polylepis polylepis)}
AVITGACERDLQCGKGTCCAVSLWIKSVRVCTPVGT
>d1imt_2 g.3.10.1 (37-80) Intestinal toxin 1 {Black mamba (Dendroaspis polylepis polylepis)}
SGEDCHPASHKIPFSGQRMHHTCPCAPNLACVQTSPKKFKCLSK
>d1edmb_ g.3.11.1 (B:) Factor IX (IXa) {Human (Homo sapiens)}
VDGDQCESNPCLNGGSCKDDINSYECWCPFGFEGKNCEL
>d1rfnb_ g.3.11.1 (B:) Factor IX (IXa) {Human (Homo sapiens)}
MTCNIKNGRCEQFCKNSADNKVVCSCTEGYRLAENQKSCEPAVPFPCGRVSVSQTSK
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>d1pfxl1 g.3.11.1 (L:47-86) Factor IX (IXa) {Pig (Sus scrofa)}
DGDQCEPNPCLNGGLCKXDINSYECWCQVGFEGKNCELDA
>d1pfxl2 g.3.11.1 (L:87-146) Factor IX (IXa) {Pig (Sus scrofa)}
TCNIKNGRCKQFCKTGADSKVLCSCTTGYRLAPDQKSCKPAVPFPCGRVSVSHSPTTLTR
>d1danl1 g.3.11.1 (L:49-86) Coagulation factor VIIa {Human (Homo sapiens)}
QCASSPCQNGGSCKDQLQSYICFCLPAFEGRNCETHKD
>d1danl2 g.3.11.1 (L:87-142) Coagulation factor VIIa {Human (Homo sapiens)}
DQLICVNENGGCEQYCSDHTGTKRSCRCHEGYSLLADGVSCTPTVEYPCGKIPILE
>d1dval1 g.3.11.1 (L:42-86) Coagulation factor VIIa {Human (Homo sapiens)}
ISYSDGDQCASSPCQNGGSCKDQLQSYICFCLPAFEGRNCETHKD
>d1f7ea_ g.3.11.1 (A:) Coagulation factor VIIa {Human (Homo sapiens)}
SDGDQCASSPCQNGGSCKDQLQSYICFCLPAFEGRNCETHKDDGSA
>d1g1sa2 g.3.11.1 (A:119-158) E-selectin, EGF-domain {Human (Homo sapiens)}
TASCQDMSCSKQGECLETIGNYTCSCYPGFYGPECEYVRD
>d1g1ta2 g.3.11.1 (A:119-157) E-selectin, EGF-domain {Human (Homo sapiens)}
TAACTNTSCSGHGECVETINNYTCKCDPGFSGLKCEQIV
>d1fjsl_ g.3.11.1 (L:) Factor X, N-terminal module {Human (Homo sapiens)}
KLCSLDNGDCDQFCHEEQNSVVCSCARGYTLADNGKACIPTGPYPCGKQTLE
>d1xkba1 g.3.11.1 (A:48-86) Factor X, N-terminal module {Human (Homo sapiens)}
DQCETSPCQNQGKCKDGLGEYTCTCLEGFEGKNCELFTR
>d1apo__ g.3.11.1 (-) Factor X, N-terminal module {Cow (Bos taurus)}
KDGDQCEGHPCLNQGHCKDGIGDYTCTCAEGFEGKNCEFSTR
>d1kigl_ g.3.11.1 (L:) Factor X, N-terminal module {Cow (Bos taurus)}
CSLDNGGCDQFCREERSEVRCSCAHGYVLGDDSKSCVSTERFPCGKFTQGR
>d1autl1 g.3.11.1 (L:49-96) Activated protein c (autoprothrombin IIa) {Human (Homo sapiens)}
QCLVLPLEHPCASLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFL
>d1autl2 g.3.11.1 (L:97-146) Activated protein c (autoprothrombin IIa) {Human (Homo sapiens)}
NCSLDNGGCTHYCLEEVGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWK
>d1eqga2 g.3.11.1 (A:33-73) Prostaglandin H2 synthase-1, EGF-like module {Sheep (Ovis aries)}
VNPCCYYPCQHQGICVRFGLDRYQCDCTRTGYSGPNCTIPE
>d1cvua2 g.3.11.1 (A:33-73) Prostaglandin H2 synthase-1, EGF-like module {Mouse (Mus musculus)}
ANPCCSNPCQNRGECMSTGFDQYKCDCTRTGFYGENCTTPE
>d1a3p__ g.3.11.1 (-) Epidermal growth factor, EGF {Mouse (Mus
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musculus)}
PGXPSSYDGYCLNGGVXMHIESLDSYTCNCVIGYSGDRCQTRDLR
>d3egf__ g.3.11.1 (-) Epidermal growth factor, EGF {Mouse (Mus musculus)}
NSYPGCPSSYDGYCLNGGVCMHIESLDSYTCNCVIGYSGDRCQTRDLRWWELR
>d1jl9a_ g.3.11.1 (A:) Epidermal growth factor, EGF {Human (Homo sapiens)}
CPLSHDGYCLHDGVCMYIEALDKYACNCVVGYIGERCQYRDL
>d3tgf__ g.3.11.1 (-) Transforming growth factor alpha {Human (Homo sapiens)}
VVSHFNDCPDSHTQFCFHGTCRFLVQEDKPACVCHSGYVGARCEHADLLA
>d1xdtr_ g.3.11.1 (R:) Heparin-binding epidermal growth factor, HBEGF {Human (Homo sapiens)}
PCLRKYKDFCIHGECKYVKELRAPSCICHPGYHGERCHGLS
>d1urk_1 g.3.11.1 (6-49) Plasminogen activator (urokinase-type) {Human (Homo sapiens)}
QVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKT
>d1hae__ g.3.11.1 (-) Heregulin-alpha, EGF-like domain {Human (Homo sapiens)}
SHLVKCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCQPGFTGARCTENVPMKVQNQEKAEELY
>d1adx__ g.3.11.1 (-) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}
QMFCNQTACPADCDPNTQASCECPEGYILDDGFICTDIDE
>d1dx5i1 g.3.11.1 (I:345-387) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}
VEPVDPCFRANCEYQCQPLDQTSYLCVCAEGFAPIPHEPHRCQ
>d1dx5i2 g.3.11.1 (I:388-422) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}
MFCNQTACPADCDPNTQASCECPEGYILDDGFICT
>d1dx5i3 g.3.11.1 (I:423-462) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}
DIDECENGGFCSGVCHNLPGTFECICGPDSALAGQIGTDC
>d1zaq__ g.3.11.1 (-) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}
EPVDPCFRANCEYQCQPLNQTSYLCVCAEGFAPIPHEPHRCQMF
>d1emo_1 g.3.11.1 (2124-2166) Fibrillin-1 fragment (residues 2124-2205) {Human (Homo sapiens)}
SAVDMDECKEPDVCKHGQCINTDGSYRCECPFGYILAGNECVD
>d1emo_2 g.3.11.1 (2167-2205) Fibrillin-1 fragment (residues 2124-2205) {Human (Homo sapiens)}
TDECSVGNPCGNGTCKNVIGGFECTCEEGFEPGPMMTCE
>d1apq__ g.3.11.1 (-) Complement protease C1R {Human (Homo sapiens)}
AVDLDECASRSKSGEEDPQPQCQHLCHNYVGGYFCSCRPGYELQEDRHSCQAE
>d1tpg_1 g.3.11.1 (51-91) Plasminogen activator (tissue-type), t-PA
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{Human (Homo sapiens)}
CSEPRCFNGGTCQQALYFSDFVCQCPEGFAGKSCEIDTRAT
>d1hz8a1 g.3.11.1 (A:1-41) Low density lipoprotein (LDL) receptor, different EGF domains {Human (Homo sapiens)}
GTNECLDNNGGCSHVCNDLKIGYECLCPDGFQLVAQRRCED
>d1hz8a2 g.3.11.1 (A:42-82) Low density lipoprotein (LDL) receptor, different EGF domains {Human (Homo sapiens)}
IDECQDPDTCSQLCVNLEGGYKCQCEEGFQLDPHTKACKAV
>d1ijqa2 g.3.11.1 (A:643-692) Low density lipoprotein (LDL) receptor, different EGF domains {Human (Homo sapiens)}
VNWCERTTLSNGGCQYLCLPAPQINPHSPKFTCACPDGMLLARDMRSCLT
>d1jv2b4 g.3.11.6 (B:532-562) Integrin beta EGF-like domains {Human (Homo sapiens)}
KGEMCSGHGQCSCGDCLCDSDWTGYYCNCTT
>d1jv2b5 g.3.11.6 (B:563-605) Integrin beta EGF-like domains {Human (Homo sapiens)}
RTDTCMSSNGLLCSGRGKCECGSCVCIQPGSYGDTCEKCPTCP
>d1gl4a2 g.3.11.5 (A:359-398) EGF-like domain of nidogen-1 {Mouse (Mus musculus)}
TCANNRHQCSVHAECRDYATGFCCRCVANYTGNGRQCVAE
>d1h4ua2 g.3.11.5 (A:367-398) EGF-like domain of nidogen-1 {Mouse (Mus musculus)}
CSVHAECRDYATGFCCRCVANYTGNGRQCVAE
>d1klo_1 g.3.11.2 (11-65) Laminin gamma1 chain {Mouse (Mus musculus)}
CPCPGGSSCAIVPKTKEVVCTHCPTGTAGKRCELCDDGYFGDPLGSNGPVRLCRP
>d1klo_2 g.3.11.2 (66-121) Laminin gamma1 chain {Mouse (Mus musculus)}
CQCNDNIDPNAVGNCNRLTGECLKCIYNTAGFYCDRCKEGFFGNPLAPNPADKCKA
>d1klo_3 g.3.11.2 (122-172) Laminin gamma1 chain {Mouse (Mus musculus)}
CACNPYGTVQQQSSCNPVTGQCQCLPHVSGRDCGTCDPGYYNLQSGQGCER
>d1nuba2 g.3.11.3 (A:53-77) Domain of BM-40/SPARC/osteonectin {Human (Homo sapiens)}
APCQNHHCKHGKVCELDENNTPMCV
>d1b9wa1 g.3.11.4 (A:1-45) Merozoite surface protein 1 (MSP-1) {Plasmodium cynomolgi}
MSSEHRCIDTNVPENAACYRYLDGTEEWRCLLYFKEDAGKCVPAP
>d1b9wa2 g.3.11.4 (A:46-89) Merozoite surface protein 1 (MSP-1) {Plasmodium cynomolgi}
NMTCKDKNGGCAPEAECKMNDKNEIVCKCTKEGSEPLFEGVFCS
>d1ceja1 g.3.11.4 (A:1-45) Merozoite surface protein 1 (MSP-1) {Plasmodium falciparum}
NISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENP
>d1ceja2 g.3.11.4 (A:46-96) Merozoite surface protein 1 (MSP-1) {Plasmodium falciparum}
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NPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSN
>d2bi6h1 g.3.12.1 (H:8-31) Bromelain inhibitor VI (cysteine protease
inhibitor) {Pineapple (Ananas comosus)}
TDTYSDCPGFCKTCKAEFGKYICL
>g2bi6.2 g.3.12.1 (L:,H:1-7,H:32-41) Bromelain inhibitor VI (cysteine
protease inhibitor) {Pineapple (Ananas comosus)}
TACSECVCPLRXEEYKCYCXDLISPNDCVK
>d1pi2__ g.3.13.1 (-) Bowman-Birk inhibitor, BBI {Soybean (Glycine
max), PI-II}
YSKPCCDLCMCTRSMPPQCSCEDRINSCHSDCKSCMCTRSQPGQCRCLDTNDFCYKPCKSR
>d1d6ri_ g.3.13.1 (I:) Bowman-Birk inhibitor, BBI {Soybean (Glycine
max)}
KPCCDQCACTKSNPPQCRCSDMRLNSCHSACKSCICALSYPAQCFCVDITDFCYEPCK
>d2bbi__ g.3.13.1 (-) Bowman-Birk inhibitor, BBI {Soybean (Glycine
max)}
DDESSKPCCDQCACTKSNPPQCRCSDMRLNSCHSACKSCICALSYPAQCFCVDITDFCYEPCKPS
EDDKEN
>d1pbia_ g.3.13.1 (A:) Bowman-Birk inhibitor, BBI {Winter pea (Pisum
sativum)}
KSACCDTCLCTKSNPPTCRCVDVGETCHSACLSCICAYSNPPKCQCFDTQKFCYKQCHNSELEEV
IKN
>d1df9c_ g.3.13.1 (C:) Bowman-Birk inhibitor, BBI {Mung bean (Vigna
radiata)}
SHDEPSESSEPCCDSCDCTKSIPPQCHCANIRLNSCHSACKSCICTRSMPGKCRCLDTDDFCYKP
CESMDKD
>d1c2aa1 g.3.13.1 (A:4-64) Bowman-Birk inhibitor, BBI {Barley
(Hordeum vulgare)}
KRPWKCCDEAVCTRSIPPICTCMDEVFECPKTCKSCGPSMGDPSRRICQDQYVGDPGPICR
>d1c2aa2 g.3.13.1 (A:65-123) Bowman-Birk inhibitor, BBI {Barley
(Hordeum vulgare)}
PWECCDKAICTRSNPPTCRCVDEVKKCAPTCKTCLPSRSRPSRRVCIDSYFGPVPPRCT
>d1tabi_ g.3.13.1 (I:) Bowman-Birk inhibitor, BBI {Adzuki bean
(Phaseolus angularis)}
SESSKPCCDQCSCTKSMPPKCRCSDIRLNSCHSACKSCACTYSIPAKCFCTDINDFCYEPCK
>d1flei_ g.3.14.1 (I:) Elafin, elastase-specific inhibitor {Human
(Homo sapiens)}
TKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ
>d2rel__ g.3.14.1 (-) Elafin, elastase-specific inhibitor {Human
(Homo sapiens)}
AQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ
>d1bx7__ g.3.15.1 (-) Hirustasin {Medicinal leech (Hirudo
medicinalis)}
GNTCGGETCSAAQVCLKGKCVCNEVHCRIRCKYGLKKDENGCEYPCSCAKA
>d1ejab_ g.3.15.1 (B:) Bdellastasin {Medicinal leech (Hirudo
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medicinalis)}

TTPCGPVTCSGAQMCEVDKCVCSDLHCKVKCEHGFKKDDNGCEYACICADAPQ

>d1skz_1 g.3.15.1 (7-58) Factor Xa inhibitor antistasin {Mexican leech (Haementeria officinalis)}

GCEEAGCPEGSACNIITDRCTCSGVRCRVHCPHGFQRSRYGCEFCKCRLEPM

>d1skz_2 g.3.15.1 (59-110) Factor Xa inhibitor antistasin {Mexican leech (Haementeria officinalis)}

KATCDISECPEGMMCSRLTNKCDCKIDINCRKTCPNGLKRDKLGCEYCECRP

>d1hic__ g.3.15.2 (-) Hirudin {Leech (Hirudo medicinalis)}

VVYTDCTESGQNLCLCEGSNVCGQGNKCILGSDGEKNQCVTGEGTPKPQSH

>d1hrti_ g.3.15.2 (I:) Hirudin {Leech (Hirudo medicinalis)}

VVYTDCTESGQNLCLCEGSNVCGQGNKCILGSDGEKNQCVTGEGTPKPQSHNDGDFEEIPEEYLQ

>d4htci_ g.3.15.2 (I:) Hirudin {Leech (Hirudo medicinalis)}

ITYTDCTESGQNLCLCEGSNVCGKGNKCILGSNGKGNQCVTGEGTPKPESHNNGDFEEIPEEYLQ

>d1dec__ g.3.15.2 (-) Decorsin {North american leech (Macrobdella decora)}

APRLPQCQGDDQEKCLCNKDECPPGQCRFPRGDADPYCE

>d1e0fi_ g.3.15.2 (I:) Haemadin {Indian leech (Haemadipsa sylvestris)}

IRFGMGKVPCPDGEVGYTCDCGEKICLYGQSCNDGQCSGDPKPSSEFEEFEIDEEEK

>d1qgma_ g.3.16.1 (A:) N-terminal domain of granulin-1 {Carp (Cyprinus carpio)}

VIHCDAATICPDGTTCSLSPYGVWYCSPFS

>d1g26a_ g.3.16.1 (A:) N-terminal domain of granulin-1 {Human (Homo sapiens)}

VVHCDMEVICPDGYTCCRLPSGAWGCCPFTQ

>d1fwoa_ g.3.16.1 (A:) Oryzain beta chain {Rice (Oryza sativa)}

DHVCDDNFSCPAGSTCSSAFGFRNLSLVWGCSPVE

>d1hy9a_ g.3.17.1 (A:) Satiety factor CART (cocaine and amphetamine regulated transcript) {Human (Homo sapiens)}

YGQVPMCDAGEQCAVRKGARIGKLCDCPRGTSCNSFLLKCL

>d1gl1i_ g.4.1.1 (I:) Protease inhibitor PMP-C {Migratory locust (Locusta migratoria)}

ISCEPGKTFKDKCNTCRCGADGKSAACTLKACPN

>d1gl0i_ g.4.1.1 (I:) Protease inhibitor PMP-D2V {Migratory locust (Locusta migratoria)}

KCTPGQVKQQDCNTCTCTPTGVWGCTLMGCQP

>d1kgma_ g.4.1.1 (A:) Protease inhibitor SGCI {Desert locust (Schistocerca gregaria)}

EVTCEPGTTFKDKCNTCRCGSDGKSAACTLKACPQ

>d1kioa_ g.4.1.1 (A:) Protease inhibitor SGCI {Desert locust (Schistocerca gregaria)}

EVTCEPGTTFKDKCNTCRCGSDGKSAACTRMACPQ

>d1kj0a_ g.4.1.1 (A:) Protease inhibitor SGTI {Desert locust

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(Schistocerca gregaria)}
EQECTPGQTKKQDCNTCNCTPTGVWACTRKGCPPH
>d1mkna_ g.5.1.1 (A:) Midkine, a heparin-binding growth factor,
N-terminal domain {Synthetic}
KKKDKVKKGGPGSECAEWAWGPCTPSSKDCGVGFREGTCGAQTQRIRCRVPCNWKKEFG
>d1mkca_ g.5.1.2 (A:) Midkine, a heparin-binding growth factor,
C-terminal domain {Synthetic}
CKYKFENWGACDGGTGTKVRQGTLKKARYNAQCQETIRVTKPC
>d2bbg__ g.6.1.1 (-) Amb V allergen {Giant ragweed (Ambrosia trifida),
pollen}
DDGLCYEGTNCGKVGKYCCSPIGKYCVCYDSKAICNKNCT
>d3ebx__ g.7.1.1 (-) Erabutoxin B (also neurotoxin B) {Sea snake
(Laticauda semifasciata)}
RICFNHQSSQPQTTKTCSPGESSCYHKQWSDFRGTIIERGCGCPTVKPGIKLSCCESEVCNN
>d1tgxa_ g.7.1.1 (A:) gamma-Cardiotoxin {Snake (Naja nigricollis)}
LKCNQLIPPFWKTCPKGKNLCYKMTMRAAPMVPVKRGCIDVCPKSSLLIKYMCCNTDKCN
>d1fas__ g.7.1.1 (-) Fasciculin {Green mamba (Dendroaspis
angusticeps)}
TMCYSHTTTSRAILTNCGENSCYRKSRRHPPKMVLGRGCGCPPGDDYLEVKCCTSPDKCNY
>d1qm7a_ g.7.1.1 (A:) Fasciculin {Green mamba (Dendroaspis
angusticeps)}
TMCYSHTTTSRAILTNCPGETNCYKKSRRHPPKMVLGRGCGCPTVAPGIKLNCCTTDKCNY
>d1ntn__ g.7.1.1 (-) Neurotoxin I {Snake (Naja naja oxiana)}
ITCYKTPIITSETCAPGQNLCYTKTWCDAWCGSRGKVIELGCAATCPTVESYQDIKCCSTDNCNP
HPKQKRP
>d1cdta_ g.7.1.1 (A:) Cardiotoxin V4II (Toxin III) {Naja mossambica
mossambica}
LKCNKLIPIAYKTCPEGKNLCYKMMLASKKMVPVKRGCINVCPKNSALVKYVCCSTDRCN
>d1kxia_ g.7.1.1 (A:) Cardiotoxin V {Taiwan cobra (Naja naja atra)}
LKCHNTQLPFIYKTCPEGKNLCFKATLKKFPLKFPVKRGCADNCPKNSALLKYVCCSTDKCN
>d2ctx__ g.7.1.1 (-) alpha-Cobratoxin {Cobra (Naja naja siamensis)}
IRCFITPDITSKDCPNGHVCYTKTWCDAFCSIRGKRVDLGCAATCPTVKTGVDIQCCSTDNCNPF
PTRKRP
>d1lsi__ g.7.1.1 (-) Long neurotoxin 1 (component LSIII) {Sea snake
(Laticauda semifasciata)}
RECYLNPHDTQTCPSGQEICYVKSWCNAWCSSRGKVLEFGCAATCPSVNTGTEIKCCSADKCNTY
P
>d1tfs__ g.7.1.1 (-) FS2 toxin {Black mamba (Dendroaspis polylepis
polylepis)}
RICYSHKASLPRATKTCVENTCYKMFIRTHREYISERGCGCPTAMWPYQTECCKGDRCNK
>d1hc9a_ g.7.1.1 (A:) Bungarotoxin {Many-banded krait (Bungarus
multicinctus), Alpha-bungarotoxin}
IVCHTTATSPISAVTCPPGENLCYRKMWCDVFCSSRGKVVELGCAATCPSKKPYEEVTCCSTDKC
NPHPKQRPG
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>d2abxa_ g.7.1.1 (A:) Bungarotoxin {Many-banded krait (Bungarus
multicinctus), Alpha-bungarotoxin}
IVCHTTATIPSSAVTCPPGENLCYRKMWCDAFCSSRGKVVELGCAATCPSKKPYEEVTCCSTDKC
NHPPKRQPG
>d1kbaa_ g.7.1.1 (A:) Bungarotoxin {Many-banded krait (Bungarus
multicinctus), kappa-bungarotoxin}
RTCLISPSSTPQTCPNGQDICFLKAQCDKFCSIRGPVIEQGCVATCPQFRSNYRSLLCCTTDNCN
H
>d1f94a_ g.7.1.1 (A:) Bucandin {Malayan krait (Bungarus candidus)}
MECYRCGVSGCHLKITCSAEETFCYKWLNKISNERWLGCAKTCTEIDTWNVYNKCCTTNLCNT
>d2cdx__ g.7.1.1 (-) Cardiotoxin CTXI {Taiwan cobra (Naja naja atra)}
LKCNKLIPIASKTCPAGKNLCYKMFMMSDLTIPVKRGCIDVCPKNSLLVKYVCCNTDRCN
>d1chvs_ g.7.1.1 (S:) Cardiotoxin II {Taiwan cobra (Naja naja atra)}
LKCNKLVPLFYKTCPAGKNLCYKMFMVSNKMVPVKRGCIDVCPKSSLLVKYVCCNTDRCN
>d1cb9a_ g.7.1.1 (A:) Cardiotoxin II {Central asian cobra (Naja naja
oxiana)}
LKCKKLVPLFSKTCPAGKNLCYKMFMVAAPHVPVKRGCIDVCPKSSLLVKYVCCNTDKCN
>d1i02a_ g.7.1.1 (A:) Cardiotoxin III {Taiwan cobra (Naja naja atra)}
LKCNKLVPLFYKTCPAGKNLCYKMFMVATPKVPVKRGCIDVCPKSSLLVKYVCCNTDRCN
>d1kbs__ g.7.1.1 (-) Cardiotoxin IV {Taiwan cobra (Naja naja atra)}
RKCNKLVPLFYKTCPAGKNLCYKMFMVSNLTVPVKRGCIDVCPKNSALVKYVCCNTDRCN
>d1cod__ g.7.1.1 (-) Cobrotoxin II (ct2) {Taiwan cobra (Naja naja
atra)}
LECHNQQSSQTPTTTGCSGGETNCYKKRWRDHRGYRTERGCGCPSVKNGIEINCCTTDRCNN
>d1g6ma_ g.7.1.1 (A:) Cobrotoxin II (ct2) {Monocled cobra (Naja
kaouthia)}
LECHNQQSSQTPTTTGCSGGENNCYKKEWRDNRGYRTERGCGCPSVKKGIGINCCTTDRCNN
>d1nea__ g.7.1.1 (-) alpha-Toxin {Snake (Naja nigricollis)}
LECHNQQSSQPPTTKTCPGETNCYKKVWRDHRGTIIERGCGCPTVKPGIKLNCCTTDKCNN
>d1ntx__ g.7.1.1 (-) alpha-Toxin {Black mamba (Dendroaspis polylepis
polylepis)}
RICYNHQSTTRATTKSCEENSCYKKYWRDHRGTIIERGCGCPKVKPGVGIHCCQSDKCNY
>d1nor__ g.7.1.1 (-) Neurotoxin II (Nt2) {Central asian cobra (Naja
naja oxiana)}
LECHNQQSSQPPTTKTCSGETNCYKKWWSDHRGTIIERGCGCPKVKPGVNLNCCRTDRCNN
>d1txb__ g.7.1.1 (-) Toxin B (long neurotoxin) {King cobra (Ophiophagus
hannah)}
TKCYVTPDATSQTCPDGQDICYTKTWCDGFCSSRGKRIDLGCAATCPKVKPGVDIKCCSTDNCNP
FPTWKRKH
>d1jgka_ g.7.1.1 (A:) Candoxin {Malayan krait (Bungarus candidus)}
MKCKICNFDTCRAGELKVCASGEKYCFKESWREARGTRIERGCAATCPKGSVYGLYVLCCTTDDC
N
>d1drs__ g.7.1.2 (-) Dendroaspin {Dendroaspis jamesoni kaimosae}
RICYNHLGTKPPTTETCQEDSCYKNIWTFDNIIRRGCGCFTPRGDMPGPYCCESDKCNL
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>d1erh__ g.7.1.3 (-) CD59 {Human (Homo sapiens)}
LQCYNCPNPTADCKTAVNCSSDFDACLITKAGLQVYNKCWKFEHCNFNDVTTRLRENELTYYCCK
KDLCN
>d1btea_ g.7.1.3 (A:) Type II activin receptor {Mouse (Mus musculus)}
ETQECLFFNANWERDRTNQTGVEPCYGDKDKRRHCFATWKNISGSIEIVKQGCWLDDINCYDRTD
CIEKKDSPEVYFCCCEGNMCNEKFSYFPEME
>d1es7b_ g.7.1.3 (B:) BMP receptor Ia ectodomain {Human (Homo sapiens)}
TLPFLKCYCSGHCPDDAINNTCITNGHCFAIIEEDDQGETTLASGCMKYEGSDFQCKDSPKAQLR
RTIECCRTNLCNQYLQPTLPP
>d1ktzb_ g.7.1.3 (B:) TGF-beta type II receptor extracellular domain {Human (Homo sapiens)}
PQLCKFCDVRFSTCDNQKSCMSNCSITSICEKPQEVCVAVWRKNDENITLETVCHDPKLPYHDFI
LEDAASPKCIMKEKKKPGETFFMCSCSSDECNDNIIFSEEY
>d1brbi_ g.8.1.1 (I:) Pancreatic trypsin inhibitor, BPTI {Cow (Bos taurus)}
AGEPPYTGPCKARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCMRTA
>d1ejmb_ g.8.1.1 (B:) Pancreatic trypsin inhibitor, BPTI {Cow (Bos taurus)}
RPDFCLEPPYTGPCRLRIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTCGGA
>d1faki_ g.8.1.1 (I:) Pancreatic trypsin inhibitor, BPTI {Cow (Bos taurus)}
APDFCLEPPYDGPCRALHLRYFYNAKAGLCQTFYYGGCLAKRNNFESAEDCMRTC
>d1g6xa_ g.8.1.1 (A:) Pancreatic trypsin inhibitor, BPTI {Cow (Bos taurus)}
RPDFCLEPPYAGACRARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTCGGA
>d3bthi_ g.8.1.1 (I:) Pancreatic trypsin inhibitor, BPTI {Cow (Bos taurus)}
DFCLEPPYTGPCHARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTCGGA
>d5pti__ g.8.1.1 (-) Pancreatic trypsin inhibitor, BPTI {Cow (Bos taurus)}
RPDFCLEPPYTGPCKARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCMRTCGGA
>d1ktha_ g.8.1.1 (A:) Collagen type VI (domain C5 from alpha 3 chain) {Human (Homo sapiens)}
ETDICKLPKDEGTCRDFILKWYYDPNTKSCARFWYGGCGGNENKFGSQKECEKVCAPV
>d1adz__ g.8.1.1 (-) Tissue factor pathway inhibitor {Human (Homo sapiens)}
DYKDDDDKLKPDFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNICE
DGPNGF
>d1irha_ g.8.1.1 (A:) Tissue factor pathway inhibitor {Human (Homo sapiens)}
EFHGPSWCLTPADRGLCRANENRFYYNSVIGKCRPFKYSGCGGNENNFTSKQECLRACKKG
>d1tfxc_ g.8.1.1 (C:) Tissue factor pathway inhibitor {Human (Homo sapiens)}
KPDFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNICEDG
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>d1aapa_ g.8.1.1 (A:) Alzheimer's amyloid B-protein precursor, APPI {Human (Homo sapiens)}

VREVCSEQAETGPCRAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCG

>d1bik_1 g.8.1.1 (25-78) Bikunin from inter-alpha-inhibitor complex {Human (Homo sapiens)}

SCQLGYSAGPCMGMTSRYFYNGTSMACETFQYGGCMGNGNNFVTEKECLQTCRT

>d1bik_2 g.8.1.1 (79-134) Bikunin from inter-alpha-inhibitor complex {Human (Homo sapiens)}

VAACNLPIVRGPCRAFIQLWAFDAVKGKCVLFPYGGCQGNGNKFYSEKECREYCGV

>d1dtx__ g.8.1.1 (-) alpha-Dendrotoxin {Green mamba (Dendroaspis angusticeps)}

EPRRKLCILHRNPGRCYDKIPAFYYNQKKKQCERFDWSGCGGNSNRFKTIEECRRTCIG

>d1bunb_ g.8.1.1 (B:) beta2-bungarotoxin, neurotoxin chain {Many-banded krait (elapid) (Bungarus multicinctus)}

RKRHPDCDKPPDTKICQTVVRAFYYKPSAKRCVQFRYGGCNGNGNHFKSDHLCRCECLEYR

>d1shp__ g.8.1.1 (-) Trypsin inhibitor {Sea anemone (Stichodactyla helianthus)}

SICSEPKKVGRCKGYFPRFYFDSETGKCTPFIYGGCGGNGNNFETLHQCRAICRA

>d1dtk__ g.8.1.1 (-) Dendrotoxin K {Black mamba (Dendroaspis polylepis polylepis)}

AAKYCKLPLRIGPCKRKIPSFYYKWKAKQCLPFDYSGCGGNANRFKTIEECRRTCVG

>d1den__ g.8.1.1 (-) Dendrotoxin I {African elapid snake (Dendroaspis polylepis polylepis)}

QPLRKLCILHRNPGRCYQKIPAFYYNQKKKQCEGFTWSGCGGNSNRFKTIEECRRTCIRK

>d1bf0__ g.8.1.1 (-) Calcicludine (cac) {Green mamba (Dendroaspis angusticeps)}

WQPPWYCKEPVRIGSCKKQFSSFYFKWTAKKCLPFLFSGCGGNANRFQTIGECRKKCLGK

>d1tocr1 g.8.1.2 (R:1A-56) Ornithodorin {Soft tick (Ornithodoros moubata)}

SLNVLCNNPHTADCNNDAQVDRYFREGTTCLMSPACTSEGYASQHECQQACFVGGED

>d1tocr2 g.8.1.2 (R:57-119) Ornithodorin {Soft tick (Ornithodoros moubata)}

HSSEMHSSCLGDPPTSCAEGTDITYYDSDSKTCKVLAASCPSGENTFESEVECQVACGAPIEG

>d1d0da_ g.8.1.2 (A:) Anticoagulant protein, factor Xa inhibitor {Soft tick (Ornithodoros moubata)}

YNRLCIKPRDWIDECDSNEGGERAYFRNGKGGCDSFWICPEDHTGADYYSSYRDCFNACI

>d1dfna_ g.9.1.1 (A:) Defensin HNP-3 {Human (Homo sapiens)}

DCYCRIPACIAGERRYGTCIYQGRLWAFCC

>d1ijva_ g.9.1.1 (A:) Beta-defensin, BD {Human (Homo sapiens), HBD1}

DHYNCVSSGGQCLYSACPIFTKIQGTCYRGKAKCCK

>d1e4qa_ g.9.1.1 (A:) Beta-defensin, BD {Human (Homo sapiens), HBD2}

PVTCLKSGAICHPVFCPRRYKQIGTCGLPGTKCCKKP

>d1fd3a_ g.9.1.1 (A:) Beta-defensin, BD {Human (Homo sapiens), HBD2}

GIGDPVTCLKSGAICHPVFCPRRYKQIGTCGLPGTKCCKKP

>d1e4ta_ g.9.1.1 (A:) Beta-defensin, BD {Mouse (Mus musculus), MBD5}
NSKRACYREGGECLQRCIGLFHKIGTCNFRFKCCKFQ
>d1e4ra_ g.9.1.1 (A:) Beta-defensin, BD {Mouse (Mus musculus), MBD6}
NEPVSCIRNGGICQYRCIGLRHKIGTCGSPFKCCK
>d1bnb__ g.9.1.1 (-) Beta-defensin, BD {Cow (Bos taurus), BD12}
APLSCGRNGGVCIPIRCPVPMRQIGTCFGRPVKCCRSW
>d1ewsa_ g.9.1.1 (A:) Alpha-defensin rk-1 {Rabbit (Oryctolagus cuniculus)}
MPCSCKKYCDPWEVIDGSCGLFNSKYICCREK
>d1b8wa_ g.9.1.1 (A:) Defensin-like peptide, DLP {Duckbilled platypus (Ornithorhynchus anatinus), DLP-1}
FVQHRPRDCESINGVCRHKDTVNCREIFLADCYNDGQKCCRK
>d1d6ba_ g.9.1.1 (A:) Defensin-like peptide, DLP {Duckbilled platypus (Ornithorhynchus anatinus), DLP-2}
IMFFEMQACWSHSGVCRDKSERNCKPMAWTYCENRNQKCCEY
>d2bds__ g.9.1.1 (-) BDs-I defensin {Sea anemone (Anemonia sulcata)}
AAPCFCSGKPGRGDLWILRGTCPGGYGYTSNCYKWPNICCYPH
>d1sh1__ g.9.1.1 (-) Sea anemone neurotoxin-1 {Sea anemone (Stichodactyla helianthus)}
AACKCDDEGPDIRTAPLTGTVDLGSCNAGWEKCASYYTIIADCCRKKK
>d1atx__ g.9.1.1 (-) Sea anemone toxin IA {Sea anemone (Anemonia sulcata)}
GAACLCKSDGPNTRGNSMSGTIWVFGCPSGWNNCEGRAIIGYCCKQ
>d1ahl__ g.9.1.1 (-) Anthopleurin-A {Giant green sea anemone (Anthopleura xanthogrammica)}
GVSCLCDSDGPSVRGNTLSGTLWLYPSGCPSGWHNCKAHGPTIGWCCKQ
>d1apf__ g.9.1.1 (-) Anthopleurin-B {Giant green sea anemone (Anthopleura xanthogrammica)}
GVPCLCDSDGPRPRGNTLSGILWFYPSGCPSGWHNCKAHGPNIGWCCKK
>d1bhta1 g.10.1.1 (A:35-126) Hepatocyte growth factor {Human (Homo sapiens)}
RRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIR
>d1gmnb1 g.10.1.1 (B:42-125) Hepatocyte growth factor {Human (Homo sapiens)}
FKKSAKTTLIKIDPALKIKTKKVNTADQCADRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYI
>d1i8na_ g.10.1.2 (A:) Anti-platelet protein {Leech (Haementeria officinalis)}
ETITAGNEDCWSKRPGWKLPDNLLTKTEFTSVDECRKMCEESAVEPSCYILQINTETNECYRNNEGDVTWSSLQYDQPNVVQWHLHACS
>d1ans__ g.11.1.1 (-) Neurotoxin III (ATX III) {Sea anemone (Anemonia sulcata)}
RSCCPCYWGGCPWGQNCYPEGCSGPKV

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>d1ajj__ g.12.1.1 (-) Ligand-binding domain of low-density
lipoprotein receptor {Human (Homo sapiens)}
PCSAFEFHCLSGECIHSSWRCDGGPDCKDKSDEENCA
>d1cr8a_ g.12.1.1 (A:) Ligand-binding domain of low-density
lipoprotein receptor {Human (Homo sapiens)}
PGGCHTDEFQCRLDGLCIPLRWRCDGDTDCMDSSDEKSCEGV
>d1d2la_ g.12.1.1 (A:) Ligand-binding domain of low-density
lipoprotein receptor {Human (Homo sapiens)}
GSPPQCQPGEFACANSRCIQERWKCDGDNDCLDNSDEAPALCHQH
>d1f5ya1 g.12.1.1 (A:1-44) Ligand-binding domain of low-density
lipoprotein receptor {Human (Homo sapiens)}
GSAVGDRCERNEFQCQDGKCISYKWVCDGSAECQDGSDESQETC
>d1f5ya2 g.12.1.1 (A:45-85) Ligand-binding domain of low-density
lipoprotein receptor {Human (Homo sapiens)}
LSVTCKSGDFSCGGRVNRCIPQFWRCDGQVDCDNGSDEQGC
>d1f8za_ g.12.1.1 (A:) Ligand-binding domain of low-density
lipoprotein receptor {Human (Homo sapiens)}
ATCRPDEFQCSDGNCIHGSRQCDREYDCKDMSDEVGCVN
>d1j8ea_ g.12.1.1 (A:) Ligand-binding domain of low-density
lipoprotein receptor {Human (Homo sapiens)}
GSHSCSSTQFKCNSGRCIPEHWTCDGDNDCGDYSDETHANCTNQ
>d1ldl__ g.12.1.1 (-) Ligand-binding domain of low-density
lipoprotein receptor {Human (Homo sapiens)}
AVGDRCERNEFQCQDGKCISYKWVCDGSAECQDGSDESQETCLSVT
>d1k7ba_ g.12.1.1 (A:) soluble Tva ectodomain, sTva47 {Quail (Coturnix
coturnix)}
SCPPGQFRCSEPPGAHGECYPQDWLCDGHPDCDDGRDEWGCG
>d1ejga_ g.13.1.1 (A:) Crambin {Abyssinian cabbage (Crambe
abyssinica)}
TTCCPSIVARSNFNVCRLPGTPEALCATYTGCIIIPGATCPGDYAN
>d1bhp__ g.13.1.1 (-) beta-Purothionin {Wheat (Triticum aestivum)}
KSCCKSTLGRNCYNLCRARGAQKLCANVCRCKLTSGLSCPKDFPK
>d2plh__ g.13.1.1 (-) alpha-1-Purothionin {Wheat (Triticum aestivum)}
KSCCRSTLGRNCYNLCRARGAQKLCAGVCRCKISSGLSCPKGFPK
>d1ed0a_ g.13.1.1 (A:) Viscotoxin a3 {European mistletoe (Viscum
album)}
KSCCPNTTGRNIYNACRLTGAPRPTCAKLSGCKIISGSTCPSDYPK
>d1i5ka_ g.14.1.1 (A:) Plasminogen kringles {Human (Homo sapiens)}
ECMHGSGENYDGKISKTMSGLECQAWDSQSPHAHGYIPSKFPNKNLKKNYCRNPDRDLRPWCFTT
DPNKRWEYCDIPRC
>d1krn__ g.14.1.1 (-) Plasminogen kringles {Human (Homo sapiens)}
DCYHGDGQSYRGTSSTTTTGKKCQSWSSMTPHRHQKTPENYPNAGLTMNYCRNPDADKGPWCFTT
DPSVRWEYCNLKKC
>d1pmla_ g.14.1.1 (A:) Plasminogen kringles {Human (Homo sapiens)}
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SDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCST
>d1ceaa_ g.14.1.1 (A:) Plasminogen kringle domains {Human (Homo sapiens)}
ECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDNDPQGPWCYTTDPEKRYDYCDILEC
>d5hpga_ g.14.1.1 (A:) Plasminogen kringle domains {Human (Homo sapiens)}
DCMFGNGKGYRGKRVTTVTGTPCQDWAAQEPHRHSIFTPETNPRAGLEKNYCRNPDGDVGGPWCYTTNPRKLYDYCDVPQCAAP
>d2pf1_1 g.14.1.1 (66-156) Prothrombin kringle domain {Cow (Bos taurus)}
CAEGVGMNYRGNVSVTRSGIECQLWRSRYPHKPEINSTTHPGADLRENFCRNPDGSITGPWCYTTSPTLRREECSVPVCGQDRVTVEVIPR
>d2pf2_1 g.14.1.1 (66-146) Prothrombin kringle domain {Cow (Bos taurus)}
CAEGVGMNYRGNVSVTRSGIECQLWRSRYPHKPEINSTTHPGADLRENFCRNPDGSITGPWCYTTSPTLRREECSVPVCGQ
>d1a0ha1 g.14.1.1 (A:164-270) Meizothrombin kringle domain {Cow (Bos taurus)}
SPLLETCVPDRGREYRGRLAVTTHGSRCLAWSSEQAKALSKDQDFNPAVPLAENFCRNPDGDEEGAWCYVADQPGDFEYCDLNYCEEPVDGDLGDRLGEDPDPDAAIEG
>d2hppp_ g.14.1.1 (P:) Meizothrombin kringle domain {Cow (Bos taurus)}
CVPDRGREYRGRLAVTTSGSRCLAWSSEQAKALSKDQDFNPAVPLAENFCRNPDGDEEGAWCYVADQPGDFEYCNLNYC
>d2hpqp_ g.14.1.1 (P:) Meizothrombin kringle domain {Human (Homo sapiens)}
CVPDRGQQYQGRLAVTTHGLPCLAWASAQAKALSKHQDFNSAVQLVENFCRNPDGDEEGVWCYVAGKPGDFGYCDLNYC
>d1kdu__ g.14.1.1 (-) Urokinase-type plasminogen activator kringle domain {Human (Homo sapiens)}
TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMVHDCAD
>d3kiv__ g.14.1.1 (-) Apolipoprotein A kringle domain {Human (Homo sapiens), IV-10/M66 variant}
QCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADTGPWCFTTDPSIRWEYCNLTRC
>d1i71a_ g.14.1.1 (A:) Apolipoprotein A kringle domain {Human (Homo sapiens), IV-7 variant}
DCYHGDGQSYRGSFSTTVTGRTCQSWSSMTPHWHQRTTEYYPNGGLTRNYCRNPDAEIRPWCYTMDPSVRWEYCNLTQCPVME
>d1bhta2 g.14.1.1 (A:127-210) NK1 fragment of hepatocyte growth factor {Human (Homo sapiens)}
NCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFT

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SNPEVRYEVCDIPQCSEVE
>d1pdc__ g.14.1.2 (-) PDC-109, collagen-binding type II domain {Cow (Bos taurus)}
DYAKCVFPFIYGGKKYETCTKIGSMWMSWCSLSPNYDKDRAWKYC
>d1e88a1 g.14.1.2 (A:42-101) Fibronectin {Human (Homo sapiens)}
AVTQTYGGNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQKYSFCTDHT
>d1e88a2 g.14.1.2 (A:102-160) Fibronectin {Human (Homo sapiens)}
VLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRRDNMKWCGTTQNYDADQKFGFCPMA
>d1ck7a3 g.14.1.2 (A:217-277) Gelatinase A (MMP-2) type II modules {Human (Homo sapiens)}
EGQVVRVKYGNADGEYCKFPFLFNGKEYNSCTDTGRSDGFLWCSTTYNFEKDGKYGFCPHE
>d1ck7a4 g.14.1.2 (A:278-335) Gelatinase A (MMP-2) type II modules {Human (Homo sapiens)}
ALFTMGGNAEGQPCKFPFRFQGTSYDSCTTEGRTDGYRWCGTTEDYDRDKKYGFCPET
>d1ck7a5 g.14.1.2 (A:336-393) Gelatinase A (MMP-2) type II modules {Human (Homo sapiens)}
AMSTVGGNSEGAPCVFPFTFLGNKYESCTSAGRSDGKMWCATTANYDDDRKWGFCPDQ
>d1j7ma_ g.14.1.2 (A:) Gelatinase A (MMP-2) type II modules {Human (Homo sapiens)}
SWMSTVGGNSGGAPCVFPFTFLGNKYESCTSAGRSDGKMWCATTANYDDDRKWGFCPDQG
>d1ks0a_ g.14.1.2 (A:) Gelatinase A (MMP-2) type II modules {Human (Homo sapiens)}
RIPVKYGNADGEYCKFPFLFNGKEYNSCTDTGRSDGFLWCSTTYNFEKDGKYGFCPHEA
>d1sgpi_ g.15.1.1 (I:) Ovomucoid III domain {Turkey (Meleagris gallopavo)}
VDCSEYPKPACTAEYRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
>d3ovo__ g.15.1.1 (-) Ovomucoid III domain {Japanese quail (Coturnix coturnix japonica)}
LAAVSVDCSEYPKPACPKDYRPVCGSDNKTYSNKCNFCNAVVESNGTLTLNHFGKC
>d2ovo__ g.15.1.1 (-) Ovomucoid III domain {Silver pheasant (Lophura nycthemera)}
LAAVSVDCSEYPKPACTMEYRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
>d1hpt__ g.15.1.1 (-) Secretory trypsin inhibitor {Human (Homo sapiens)}
DSLGREAKCYNELNGCTYEYRPVCGTDGDTYPNECVLCFENRKRQTSILIQKSGPC
>d1tgsi_ g.15.1.1 (I:) Secretory trypsin inhibitor {Pig (Sus scrofa)}
TSPQREATCTSEVSGCPKIYNPVCGTDGITYSNECVLCSENKKRQTPVLIQKSGPC
>d1tbrr1 g.15.1.1 (R:1-51) Rhodniin {Bug (Rhodnius prolixus)}
EGGEPCACPHALHRVCGSDGETYSNPCTLNCAKFNGKPELVKVHDGPCEPD
>d1tbrr2 g.15.1.1 (R:52-103) Rhodniin {Bug (Rhodnius prolixus)}
EDEDVCQECDGDEYKPVCGSDDITYDNNCRLECASISSSPGVELKHEGPCRT
>d1nuba3 g.15.1.1 (A:78-135) Domain of BM-40/SPARC/osteonectin {Human (Homo sapiens)}
CQDPTSCPAPIGEFEKVCSNDNKTFDSSCHFFATKCTLEGTKKGHKLHLDYIGPCKYI
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>d2bus__ g.15.1.1 (-) Seminal plasma inhibitor IIa {Cow (Bos taurus)}
EGAQVDCAEFKDPKVYCTRESNPHCGSNGETYGNKCAFCKAVMKSGGKINLKHRGKC
>d1pce__ g.15.1.1 (-) PEC-60 peptide {Pig (Sus scrofa)}
EKQVFSRMPICEHMTESPDCSRIYDPVCGTDGVTYESECKLCLARIENKQDIQIVKDGEC
>d1an1i_ g.15.1.1 (I:) Leech derived tryptase inhibitor (LDTI-C) {Medicinal leech (Hirudo medicinalis)}
KVCACPKILKPVCGSDGRTYANSCIARCNGVSIKSEGSCP
>d1ldtl_ g.15.1.1 (L:) Leech derived tryptase inhibitor (LDTI-C) {Medicinal leech (Hirudo medicinalis)}
KKVCACPKILKPVCGSDGRTYANSCIARCNGVSIKSEGSCPTGILN
>d4sgbi_ g.15.1.2 (I:) Plant chymotrypsin inhibitor {Potato tuber (Solanum tuberosum)}
PICTNCCAGYKGCNYYSANGAFICEGQSDPKKPKACPLNCDPHIAYSKCPR
>d1ce3a_ g.15.1.2 (A:) Multidomain proteinase inhibitor {Winged tobacco (Nicotiana alata)}
MKACTLNCDPRIAYGVCPRSEEKKNDRICTNCCAGTKGCKYFSDDGTFVCEGES
>d1fyba1 g.15.1.2 (A:1-55) Multidomain proteinase inhibitor {Winged tobacco (Nicotiana alata)}
DRICTNCCAGTKGCKYFSDDGTFVCEGESDPRNPKACTLNCDPRIAYGVCPRSEE
>d1tih__ g.15.1.2 (-) Multidomain proteinase inhibitor {Winged tobacco (Nicotiana alata)}
DRICTNCCAGTKGCKYFSDDGTFVCEGESDPRNPKACPRNCDPRIAYGICPLA
>g1qh2.1 g.15.1.2 (B:,A:) Multidomain proteinase inhibitor {Winged tobacco (Nicotiana alata)}
RICTNCCAGKKGCKYFSDDGTFICEGESXKACTLNCDPRIAYGVCPR
>d2pspa1 g.16.1.1 (A:1-53) Pancreatic spasmolytic polypeptide {Pig (Sus scrofa)}
EKPAACRCSRQDPKNRVNCGFPGITSDQCFTSGCCFDSQVPGVPWCFKPLPAQ
>d2pspa2 g.16.1.1 (A:54-106) Pancreatic spasmolytic polypeptide {Pig (Sus scrofa)}
ESEECVMQVSARKNCGYPGISPEDCAARNCCFSDTIPEVPWCFFPMSVEDCHY
>d1hi7a_ g.16.1.1 (A:) PNR-2/PS2, TFF1 {Human (Homo sapiens)}
EAQTETCTVAPRERQNCGFPGVTPSQCANKGCCFDDTVRGVPWCFYPNTIDVPPEEECEF
>d1e9ta_ g.16.1.1 (A:) Intestinal trefoil factor {Human (Homo sapiens)}
EEYVGLSANQCAVPAKDRVDCGYPHVTPKECNNRGCCFDSRIPGVPWCFKPLQEAECTF
>d1pdga_ g.17.1.1 (A:) Platelet-derived growth factor BB {Human (Homo sapiens)}
EPAMIAECKTRTEVFEISRRLIDRTNANFLVWPPCVEVQRCSGCCNNRNVQCRPTQVQLRPVQVR
KIEIVRKKPIFKKATVTLEDHLACKCETVAA
>d1fltv_ g.17.1.1 (V:) Vascular endothelial growth factor, VEGF {Human (Homo sapiens)}
EVVKFMDVYQRSYCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTEESNIT
MQIMRIKPHQGQHIGEMSFLQHNKCECRPK
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>d1fzva_ g.17.1.1 (A:) Placenta growth factor-1, PLGF-1 {Human (Homo
sapiens)}
SSEVEVVPFQEVWGRSYCRALERLVDVVSEYPSEVEHMFSPSCVSLLRCTGCCGDENLHCVPVET
ANVTMQLLKIRSGDRPSYVELTFSQHVRCECRPLR
>d1ktza_ g.17.1.2 (A:) TGF-beta3 {Human (Homo sapiens)}
ENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASASPC
CVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS
>d1tgj__ g.17.1.2 (-) TGF-beta3 {Human (Homo sapiens)}
ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLY
NTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS
>d2tgi__ g.17.1.2 (-) TGF-beta2 {Human (Homo sapiens)}
ALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLY
NTINPEASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKCS
>d1klaa_ g.17.1.2 (A:) TGF-beta1 {Human (Homo sapiens)}
ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY
NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS
>d1bmp__ g.17.1.2 (-) Bone morphogenetic protein-7 (BMP-7) {Human
(Homo sapiens)}
QACKKHELYVSFRDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNATNHAIVQTLVHFINPETVP
KPCCAPTQLNAISVLYFDDSSNVILKKYRNMVVRACGCH
>d1es7a_ g.17.1.2 (A:) Bone morphogenetic protein-2 (BMP-2) {Human
(Homo sapiens)}
KSSCKRHPLYVDFSDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNSTNHAIVQTLVNSVNSKIP
KACCVPTELSAISMLYLDENEKVVLKNYQDMVVEGCGCR
>d1agqa_ g.17.1.2 (A:) Glial cell-derived neurotrophic factor, GDNF
{Rat (Rattus norvegicus)}
NRGCVLTAIHLNVTDLGLGYETKEELIFRYCSGSCEAAETMYDKILKNLSRSRRLTSDKVGQACC
RPVAFDDDLSFLDDSLVYHILRKHSAKRCGCI
>d1bnda_ g.17.1.3 (A:) Brain-derived neurotrophic
factor/neurotrophin 3 heterodimer, BDNF/NT3 {Human (Homo sapiens)}
GQLSVCDSISEWVTAADKKTAVDMSGGTVTVLEKVPVSKGQLKQYFYETKCNPMGYTKEGCRGID
KRHWNSQCRTTQSYVRALTMDSKKRIGWRFIRIDTSCVCTLTIK
>d1bndb_ g.17.1.3 (B:) Brain-derived neurotrophic
factor/neurotrophin 3 heterodimer, BDNF/NT3 {Human (Homo sapiens)}
RGEVSVCDSESLWVTDKSSAIDIRGHQVTVLGEIKTQNSPVKQYFYETRCKEARPVKNGCRGIDD
KHWNSQCKTSQTYVRALTSENNKLVGWRWIRIDTSCVCALSRK
>d1b8mb_ g.17.1.3 (B:) Neurotrophin 4 {Human (Homo sapiens)}
GELAVCDAVSGWVTDRRTAVDLRGREVEVLGEVPAAGGSPLRQYFFETRCKADNAEEGGPGAGGG
GCRGVDRRHWVSECKAKQSYVRALTADAQGRVGWRWIRIDTACVCTLLSRTGRA
>d1hcfa_ g.17.1.3 (A:) Neurotrophin 4 {Human (Homo sapiens)}
GVSETAPASRRGELAVCDAVSGWVTDRRTAVDLRGREVEVLGEVPAAGGSPLRQYFFETRCKADN
AEEGGPGAGGGGCRGVDRRHWVSECKAKQSYVRALTADAQGRVGWRWIRIDTACVCTLLSRT
>d1bet__ g.17.1.3 (-) beta-Nerve growth factor {Mouse (Mus musculus)}
GEFSVCDSVSVWVGDKTTATDIKGKEVTVLAEVNINNSVFRQYFFETKCRASNPVESGCRGIDSK
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HWNSYCTTTHTFVKALTTDEKQAAWRFIRIDTACVCVLSRKA
>d1wwwv_ g.17.1.3 (V:) beta-Nerve growth factor {Human (Homo sapiens)}
SSHPIFHRGEFSVCDSVSVWVGDKTTATDIKGKEVMVLGEVNINNSVFKQYFFETKCRDPNPVDS
GCRGIDSKHWNSYCTTTHTFVKALTMDGKQAAWRFIRIDTACVCVLSRK
>d1hcna_ g.17.1.4 (A:) Glycoprotein hormones alpha chain (Gonadotropin A, Follitropin alpha) {Human (Homo sapiens)}
QDCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYNRVT
VMGGFKVENHTACHCSTCYY
>d1hcnb_ g.17.1.4 (B:) Gonadotropin B chain {Human (Homo sapiens)}
KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES
IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD
>d1fl7b_ g.17.1.4 (B:) Follicle stimulating hormone, follitropin, beta chain {Human (Homo sapiens)}
CELTNITIAIEKEECRFCISINTAWCAGYCYTRDLVYKDPARPKIQKTCTFKELVYETVRVPGCA
HHADSLYTYPVATQCHCGKCDSDSTDCTVRGLGPSYCSFGEM
>d1jpya_ g.17.1.6 (A:) Interleukin 17F, IL-17F {Human (Homo sapiens)}
HTFFQKPESCPPVPGGSMKLDIGIINENQRVSMSRNIESRSTSPWNYTVTWDPNRYPSEVVQAQC
RNLGCINAQGKEDISMNSVPIQQETLVVRRKHQGCSVSFQLEKVLVTVGCTCVTPV
>d1aoca_ g.17.1.5 (A:) Coagulogen {Japanese horseshoe crab (Tachypleus tridentatus)}
ADTNAPICLCDEPGVLGRTQIVTTEIKDKIEKAVEAVAQESGVSGRGFSIFSHHPVFRECGKYEC
RTVRPEHSRCYNFPPFTHFKSECPVSTRDCEPVFGYTVAGEFRVIVQAPRAGFRQCVWQHKCRFG
SNSCGYNGRCTQQRSVVRLVTYNLEKDGFLCESFRTCCGCPCRSF
>d1hcc__ g.18.1.1 (-) Factor H, 15th and 16th modules {Human (Homo sapiens)}
EGLPCKSPPEISHGVVAHMSDSYQYGEEVTYKCFEGFGIDGPAIAKCLGEKWSHPPSCI
>d1hfi__ g.18.1.1 (-) Factor H, 15th and 16th modules {Human (Homo sapiens)}
EKIPCSQPPQIEHGTINSSRSSQESYAHGTKLSYTCEGGFRISEENETTCYMGKWSSPPQCE
>d1g40a1 g.18.1.1 (A:1-64) Complement control protein {Vaccinia virus}
CCTIPSRPINMKFKNSVETDANANYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGWTLFNQCIK
>d1g40a2 g.18.1.1 (A:65-126) Complement control protein {Vaccinia virus}
RRCPSPRDIDNGQLDIGGVDFGSSITYSCNSGYHLIGESKSYCELGSTGSMVWNPEAPICES
>d1g40a3 g.18.1.1 (A:127-184) Complement control protein {Vaccinia virus}
VKCQSPPSISNGRHNGYEDFYTDGSVVTYSCNSGYSLIGNSGVLCSGGEWSDPPTCQI
>d1g40a4 g.18.1.1 (A:185-243) Complement control protein {Vaccinia virus}
VKCPHPTISNGYLSSGFKRSYSYNDNVDFKCKYGYKLSGSSSSTCSPGNTWKPELPKCV
>d1ckla1 g.18.1.1 (A:1-62) CD46 (membrane cofactor protein, MCP) {Human (Homo sapiens)}
CEEPPTFEAMELIGKPKPYYEIGERVDYKCKKGYFYIPPLATHTICDRNHTWLPVSDDACYR
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>d1ckla2 g.18.1.1 (A:63-126) CD46 (membrane cofactor protein, MCP) {Human (Homo sapiens)}
ETCPYIRDPLNGQAVPANGTYEFGYQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKV
>d1c1za5 g.18.1.1 (A:244-326) beta2-glycoprotein I {Human (Homo sapiens)}
SCKLPVKKATVVYQGERVKIQEKFKNGMLHGDKVSFFCKNKEKKCSYTEDAQCIDGTIEVPKCFK
EHSSLAFWKTDASDVKPC
>d1quba1 g.18.1.1 (A:1-62) beta2-glycoprotein I {Human (Homo sapiens)}
GRTCPKPDDLPFSTVVPLKTFYEPGEEITYSCKPGYVSRGGMRKFICPLTGLWPINTLKCTP
>d1quba2 g.18.1.1 (A:63-120) beta2-glycoprotein I {Human (Homo sapiens)}
RVCPFAGILENGAVRYTTFEYPNTISFSCNTGFYLNGADSAKCTEEGKWSPELPVCAP
>d1quba3 g.18.1.1 (A:121-183) beta2-glycoprotein I {Human (Homo sapiens)}
IICPPPSIPTFATLRVYKPSAGNNSLYRDTAVFECLPQHAMFGNDTITCTTHGNWTKLPECRE
>d1quba4 g.18.1.1 (A:184-243) beta2-glycoprotein I {Human (Homo sapiens)}
VKCPFPSRPDNGFVNYPAKPTLYYKDKATFGCHDGYSLDGPEEIECTKLGNWSAMPSCKA
>d1quba5 g.18.1.1 (A:244-326) beta2-glycoprotein I {Human (Homo sapiens)}
SCKVPVKKATVVYQGERVKIQEKFKNGMLHGDKVSFFCKNKEKKCSYTEDAQCIDGTIEVPKCFK
EHTDASDVKPC
>d1ghqb1 g.18.1.1 (B:1-66) Complement receptor 2, cr2 {Human (Homo sapiens)}
AISCGSPPPILNGRISYYSTPIAVGTVIRYSCSGTFRLIGEKSLLCITKDKVDGTWDKPAPKCEY
F
>d1ghqb2 g.18.1.1 (B:67-129) Complement receptor 2, cr2 {Human (Homo sapiens)}
NKYSSCPEPIVPGGYKIRGSTPYRHGDSVTFACKTNFSMNGNKSVWCQANNMWGPTRLPTCVS
>d1elva2 g.18.1.1 (A:342-409) Complement C1S protease domain {Human (Homo sapiens)}
LDCGIPESIENGKVEDPESTLFGSVIRYTCEEPYYYMENGGGGEYHCAGNGSWVNEVLGPELPKC
VPV
>d1bgk__ g.19.1.1 (-) Sea anemone toxin k {Sea anemone (Bunodosoma granulifera), BGK}
VCRDWFKETACRHAKSLGNCRTSQKYRANCAKTCELC
>d1c2ua_ g.19.1.1 (A:) Sea anemone toxin k {Sun anemone (Stichodactyla helianthus), SHK}
RSXIDTIPKSRCTAFQCKHSAKYRLSFCRKTCGTX
>d1roo__ g.19.1.1 (-) Sea anemone toxin k {Sun anemone (Stichodactyla helianthus), SHK}
RSCIDTIPKSRCTAFQCKHSMKYRLSFCRKTCGTC
>d2ech__ g.20.1.1 (-) Echistatin {Echis carinatus}
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ECESGPCCRNCKFLKEGTICKRARGDDMDDYCNGKTCDCPRNPHKGPAT
>d1fvl__ g.20.1.1 (-) Flavoridin {Snake (Trimeresurus flavoviridis)}
GEECDCGSPSNPCCDAATCKLRPGAQCADGLCCDQCRFKKKRTICRIARGDFPDDRCTGLSNDCPRWNDL
>d1kst__ g.20.1.1 (-) Kistrin {Agkistrodon rhodostoma}
GKECDCSSPENPCCDAATCKLRPGAQCGEGLCCEQCKFSRAGKICRIPRGDMPDDRCTGQSADCPRYH
>d1mdal_ g.21.1.1 (L:) Methylamine dehydrogenase {Paracoccus denitrificans}
VDPRAKWQPQDNDIQACDYWRHCSIAGNICDCSAGSLTSCPPGTLVASGSWVGSCYNPPDPNKYITAYRDCCGYNVSGRCACLNTEGELPVYNKDANDIIWCFGGEDGMTYHCSISPVSGA
>d2bbkl_ g.21.1.1 (L:) Methylamine dehydrogenase {Paracoccus denitrificans}
TDPRAKWVPQDNDIQACDYWRHCSIDGNICDCSGGSLTNCPPGTKLATASWVASCYNPTDGQSYLIAYRDCCGYNVSGRCPCLNTEGELPVYRPEFANDIIWCFGAEDDAMTYHCTISPIVGKAS
>d1atb__ g.22.1.1 (-) Ascaris trypsin inhibitor, ATI {Pig roundworm (Ascaris Lumbricoides), variant suum}
EAEKCTKPNEQWTKCGGCEGTCAQKIVPCTRECKPPRCECIASAGFVRDAQGNCIKFEDCPK
>d1eaic_ g.22.1.1 (C:) Ascaris elastase inhibitor {Pig roundworm (Ascaris suum)}
GQESCGPNEVWTECTGCEMKCGPDENTPCPLMCRRPSCECSPGRGMRRTNDGKCIPASQCP
>d1coua_ g.22.1.1 (A:) Anticoagulant protein {Dog hookworm (Ancylostoma caninum)}
KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNKDDKCVSAEDCELDNMDFIYPGTRNP
>d1ccva_ g.22.1.1 (A:) Chymotrypsin inhibitor AMCI {Honeybee (Apis mellifera)}
EECGPNEVFNTCGSACAPTCAQPKTRICTMQCRIGCQCQEGFLRNGEGACVLPENC
>d1hx2a_ g.22.1.2 (A:) BSTI {Fire-bellied toad (Bombina bombina)}
NFVCPPGQTFQTCASSCPKTCETRNKLVLCDKKCNQRCGCISGTVLKSKDSSECVHPSKC
>d1apj__ g.23.1.1 (-) Fibrillin {Human (Homo sapiens)}
SAQDLRMSYCYAKFEGGKCSSPKSRNHSKQECCCALKGEGWGDPCELCPTEPDEAFRQICPYGSGIIVGPDDSA
>d1exta1 g.24.1.1 (A:13-71) Tumor necrosis factor (TNF) receptor {Human (Homo sapiens)}
SVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL
>d1exta2 g.24.1.1 (A:72-115) Tumor necrosis factor (TNF) receptor {Human (Homo sapiens)}
SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCF
>d1exta3 g.24.1.1 (A:116-172) Tumor necrosis factor (TNF) receptor {Human (Homo sapiens)}
NCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIEN
>d1ncfa3 g.24.1.1 (A:116-150) Tumor necrosis factor (TNF) receptor {Human (Homo sapiens)}

NCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENEC
>d1ncfb3 g.24.1.1 (B:116-155) Tumor necrosis factor (TNF) receptor {Human (Homo sapiens)}
NCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSN
>d1d0gr1 g.24.1.1 (R:21-61) Death receptor-5 (dr5) fragment {Human (Homo sapiens)}
SSPSEGLCPPGHHISEDGRDCISCKYGQDYSTHWNDLLFCL
>d1d0gr3 g.24.1.1 (R:102-128) Death receptor-5 (dr5) fragment {Human (Homo sapiens)}
KCRTGCPRGMVKVGDCTPWSDIECVHK
>d1d4va1 g.24.1.1 (A:69-114) Death receptor-5 (dr5) fragment {Human (Homo sapiens)}
PQQKRSSPSEGLCPPGHHISEDGRDCISCKYGQDYSTHWNDLLFCL
>d1d4va2 g.24.1.1 (A:115-154) Death receptor-5 (dr5) fragment {Human (Homo sapiens)}
RCTRCDSGEVELSPCTTTRNTVCQCEEGTFREEDSPEMCR
>d1d4va3 g.24.1.1 (A:155-185) Death receptor-5 (dr5) fragment {Human (Homo sapiens)}
KCRTGCPRGMVKVGDCTPWSDIECVHKESGD
>d1du3a3 g.24.1.1 (A:102-123) Death receptor-5 (dr5) fragment {Human (Homo sapiens)}
KCRTGCPRGMVKVGDCTPWSDI
>d1jmab1 g.24.1.1 (B:4-59) Cellular receptor HveA {Human (Homo sapiens)}
CKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQ
>d1jmab2 g.24.1.1 (B:60-105) Cellular receptor HveA {Human (Homo sapiens)}
MCDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYAT
>d1vgh__ g.25.1.1 (-) Heparin-binding domain from vascular endothelial growth factor {Human (Homo sapiens)}
ARQENPCGPCSERRKHLFVQDPQTCKCSCKNTDSRCKARQLELNERTCRCDKPRR
>d1afp__ g.26.1.1 (-) Antifungal protein (AGAFP) {Mold (Aspergillus giganteus)}
ATYNGKCYKKDNICKYKAQSGKTAICKCYVKKCPRDGAKCEFDSYKGKCYC
>d1e88a3 g.27.1.1 (A:1-41) Fibronectin {Human (Homo sapiens)}
YGHCVTDSGVVYSVGMQWLKTQGNKQMLCTCLGNGVSCQET
>d1fbr_1 g.27.1.1 (1-46) Fibronectin {Human (Homo sapiens)}
AEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGRITCTSR
>d1fbr_2 g.27.1.1 (47-93) Fibronectin {Human (Homo sapiens)}
NRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCERHTS
>d1qgba1 g.27.1.1 (A:17-60) Fibronectin {Human (Homo sapiens)}
SKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESKP
>d1qgba2 g.27.1.1 (A:61-109) Fibronectin {Human (Homo sapiens)}
EAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANR

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>d1tpg_2 g.27.1.1 (1-50) Tissue-type plasminogen activator, t-PA {Human (Homo sapiens)}
SYQVICRDEKTQMIYQQHQSWLRPVLRSNRVEYCWCNSGRAQCHSVPVKS
>d1icfi_ g.28.1.1 (I:) MHC class II associated p41 invariant chain fragment {Human (Homo sapiens)}
LTKCQEEVSHIPAVHPGSFRPKCDENGNYLPLQCYGSIGYCWCVFPNGTEVPNTRSRGHHNCSES
>d1e8ra_ g.29.1.1 (A:) Endo-1;4-beta-xylanase A CBDX {Pseudomonas fluorescens, subsp. cellulosa}
MGNQQCNWYGTLYPLCVTTTNGWGWEDQRSCIARSTCAAQPAPFGIVGSG
>d1e8qa_ g.55.1.1 (A:) Cellulose docking domain, dockering {Piromyces equi}
ASCWAQSQGYNCCNNPSSTKVEYTDASGQWGVQNGQWCGIDYSYGQ
>d1dtdb_ g.30.1.1 (B:) Carboxypeptidase inhibitor {Medicinal leech (Hirudo medicinalis)}
DESFLCYQPDQVCCFICRGAAPLPSEGECNPHPTAPWCREGAVEWVPYSTGQCRTTCIPYV
>d1hdla_ g.57.1.1 (A:) Serine proteinase inhibitor lekti, domain one {Human (Homo sapiens)}
KNEDQEMCHEFQAFMKNGKLFCPQDKKFFQSLDGIMFINKCATCKMILEKEAKSQ
>d1dqca_ g.31.1.1 (A:) Tachycitin {Horseshoe crab (Tachypleus tridentatus)}
YLAFRCGRYSPCLDDGPNVNLYSCCSFYNCHKCLARLENCPKGLHYNAYLKVCDWPSKAGCTSVNKECHLWKT
>d1ha8a_ g.58.1.1 (A:) Pheromone ER-23 {Euplotes raikovi}
GECEQCFSDGGDCTTCFNNGTGPCANCLAGYPAGCSNSDCTAFLSQCYGGC
>d1danl3 g.32.1.1 (L:1-48) Coagulation factor VIIa {Human (Homo sapiens)}
ANAFLEELRPGSLERECKEEQCSFEEAREIFKDAERTKLFWISYSDGD
>d2pf1_2 g.32.1.1 (36-65) Prothrombin {Cow (Bos taurus)}
SATDAFWAKYTACESARNPREKLNECLEGN
>d2pf2_2 g.32.1.1 (1-65) Prothrombin {Cow (Bos taurus)}
ANKGFLEEVRKGNLREECLEEPCSREEAFEALESLSATDAFWAKYTACESARNPREKLNECLEGN
>d1cfi__ g.32.1.1 (-) Coagulation factor IX (IXa) {Human (Homo sapiens)}
YNSGKLEEFVQGNLERECMEEKCSFEEAREVFENTERTTEFWKQYVD
>d1pfxl3 g.32.1.1 (L:1-46) Coagulation factor IX (IXa) {Pig (Sus scrofa)}
YNSGKLEEFVRGNLERECIEEKCSFEEAREVFENTEKTNEFWKQYV
>d1iodg_ g.32.1.1 (G:) Coagulation factor X {Cow (Bos taurus)}
ANSFLEEVKQGNLERECLEEACSLEEAREVFEDAEQTDEFWSKY
>d1d6ga_ g.33.1.1 (A:) Cholecystokinin A receptor, N-domain {Human (Homo sapiens)}
MDVVDSLLVNGSNITPPCELGLENETLFCLDQPRPSKEWQPAQVILL
>d1vpu__ g.34.1.1 (-) HIV-1 VPU cytoplasmic domain {Human immunodeficiency virus type 1}
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LQIDRLIDRITERAEDSGNESEGDQEELSALVERGHLAPWDVDDL
>d1isua_ g.35.1.1 (A:) HIPIP (high potential iron protein) {Rhodocyclus tenuis}
GTNAAMRKAFNYQDTAKNGKKCSGCAQFVPGASPTAAGGCKVIPGDNQIAPGGYCDAFIVKK
>d1b0ya_ g.35.1.1 (A:) HIPIP (high potential iron protein) {Allochromatium vinosum, (formerly Chromatium vinosum)}
SAPANAVAADNATAIALKYNQDATKSERVAAARPGLPPEEQQCANCQFMQADAAGATDEWKGCQLFPGKLINVNGWCASWTLKAG
>d1js2a_ g.35.1.1 (A:) HIPIP (high potential iron protein) {Allochromatium vinosum, (formerly Chromatium vinosum)}
MEFMSAPANAVAADDATAIALKYNQDATKSERVAAARPGLPPEEQHCANCQFMQADAAGATDEWKGCQLFPGKLINVNGWSASWTLKAG
>d3hipa_ g.35.1.1 (A:) HIPIP (high potential iron protein) {Chromatium purpuratum}
VPANAVTESDPAAVALKYHRDAASSERVAAARPGLPPEEQHCENCQFMNPDSAAADWKGCQLFPGKLINLSGWCASWTLRAG
>d2hipa_ g.35.1.1 (A:) HIPIP (high potential iron protein) {Ectothiorhodospira halophila}
EPRAEDGHAHDYVNEAADASGHPRYQEGQLCENCAFWGEAVQDGWGRCTHPDFDEVLVKAEGWCSVYAPAS
>d1hpi__ g.35.1.1 (-) HIPIP (high potential iron protein) {Ectothiorhodospira vacuolata}
MERLSEDDPAAQALEYRHDASSVQHPAYEEGQTCLNCLLYTDASAQDWGPCSVFPGKLVSANGWCTAWVAR
>d1eyta_ g.35.1.1 (A:) HIPIP (high potential iron protein) {Thermochromatium tepidum}
AAPANAVTADDPTAIALKYNQDATKSERVAAARPGLPPEEQHCANCQFMQANVGEGDWKGCQLFPGKLINVNGWCASWTLKAG
>d1dj7a_ g.36.1.1 (A:) Ferredoxin thioredoxin reductase (FTR), catalytic beta chain {Synechocystis sp.}
NNKTLAAMKNFAEQYAKRTDTYFCSDLSVTAVVIEGLARHKEELGSPLCPCRHYEDKEAEVKNTFWNCPCVPMRERKECHCMLFLTPDNDFAGDAQDIPMETLEEVKAS
>d1a1ga1 g.37.1.1 (A:103-131) ZIF268 {Mouse (Mus musculus)}
RPYACPVESCDRRFSDSSNLTRHIRIHTG
>d1a1ha1 g.37.1.1 (A:103-131) ZIF268 {Mouse (Mus musculus)}
RPYACPVESCDRRFSQSGSLTRHIRIHTG
>d1a1ia1 g.37.1.1 (A:103-131) ZIF268 {Mouse (Mus musculus)}
RPYACPVESCDRRFSRSADLTRHIRIHTG
>d1a1ia2 g.37.1.1 (A:132-159) ZIF268 {Mouse (Mus musculus)}
QKPFQCRICMRNFSRSDHLTTHIRTHTG
>d1a1ia3 g.37.1.1 (A:160-187) ZIF268 {Mouse (Mus musculus)}
EKPFACDICGRKFARSDERKRHTKIHLR
>d1aaya1 g.37.1.1 (A:103-131) ZIF268 {Mouse (Mus musculus)}
RPYACPVESCDRRFSRSDELTRHIRIHTG
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>d1f2ig1 g.37.1.1 (G:1093-1131) ZIF268 {Mouse (Mus musculus)}
NLLNYVVPKMRPYACPVESCDRRFSRSDELTRHIRIHTG
>d1rmd_1 g.37.1.1 (87-116) V(D)J recombination activating protein 1 (RAG1), dimerization domain {Mouse (Mus musculus)}
LMVKCPAQDCNEEVSLEKYNHHVSSHKESK
>d2drpa1 g.37.1.1 (A:103-139) Tramtrack protein (two zinc-finger peptide) {Drosophila melanogaster}
FTKEGEHTYRCKVCSRVYTHISNFCRHYVTSHKRNVK
>d2drpa2 g.37.1.1 (A:140-165) Tramtrack protein (two zinc-finger peptide) {Drosophila melanogaster}
VYPCPFCFKEFTRKDNMTAHVKIIHK
>d1paa__ g.37.1.1 (-) ADR1 {Synthetic, based on Saccharomyces cerevisiae sequence}
KAYACGLCNRAFTRRDLLIRHAQKIHSGNL
>d2adr_1 g.37.1.1 (102-130) ADR1 {Synthetic, based on Saccharomyces cerevisiae sequence}
RSFVCEVCTRAFARQEHLKRHYRSHTNEK
>d2adr_2 g.37.1.1 (131-161) ADR1 {Synthetic, based on Saccharomyces cerevisiae sequence}
PYPCGLCNRAFTRRDLLIRHAQKIHSGNLGE
>d1znf__ g.37.1.1 (-) XFIN, third domain {Xenopus laevis}
YKCGLCERSFVEKSALSRHQRVHKN
>d5znf__ g.37.1.1 (-) ZFY {Human (Homo sapiens)}
KTYQCQYCEYRSADSSNLKTHIKTKHSKEK
>d7znf__ g.37.1.1 (-) ZFY {Human (Homo sapiens)}
KTYQCQYCEKRFADSSNLKTHIKTKHSKEK
>d1ncs__ g.37.1.1 (-) SWI5 zinc-finger domains {Baker's yeast (Saccharomyces cerevisiae)}
TLPRGSIDKYVKEMPDKTFECLFPGCTKTFKRRYNIRSHIQTHLEDR
>d1zfd__ g.37.1.1 (-) SWI5 zinc-finger domains {Baker's yeast (Saccharomyces cerevisiae)}
DRPYSCDHPGCDKAFVRNHDLIRHKKSHQEKA
>d2glia1 g.37.1.1 (A:103-134) Five-finger GLI1 {Human (Homo sapiens)}
ETDCRWDGCSQEFDSQEQLVHHINSEHIHGER
>d2glia2 g.37.1.1 (A:135-167) Five-finger GLI1 {Human (Homo sapiens)}
KEFVCHWGGCSRELRPFKAQYMLVVHMRRHTGE
>d2glia3 g.37.1.1 (A:168-197) Five-finger GLI1 {Human (Homo sapiens)}
KPHKCTFEGCRKSYSRLENLKTHLRSHTGE
>d2glia4 g.37.1.1 (A:198-228) Five-finger GLI1 {Human (Homo sapiens)}
KPYMCEHEGCSKAFSNASDRAKHQNRTHSNE
>d2glia5 g.37.1.1 (A:229-257) Five-finger GLI1 {Human (Homo sapiens)}
KPYVCKLPGCTKRYTDPSSLRKHVKTVHG
>d1bbo_1 g.37.1.1 (1-28) Enhancer binding protein {Human (Homo sapiens)}
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KYICEECGIRXKKPSMLKKHIRTHTDVR
>d1bbo_2 g.37.1.1 (29-57) Enhancer binding protein {Human (Homo sapiens)}
PYHCTYCNFSFKTKGNLTKHMKSKAHSKK
>d4znf__ g.37.1.1 (-) Enhancer binding protein {Human (Homo sapiens)}
RPYHCSYCNFSFKTKGNLTKHMKSKAHSKK
>d1sp1__ g.37.1.1 (-) Transcription factor sp1 {Human (Homo sapiens)}
KKFACPECPKRFMRSDHLSKHIKTHQNKK
>d1sp2__ g.37.1.1 (-) Transcription factor sp1 {Human (Homo sapiens)}
RPFMCTWSYCGKRFTRSDELQRHKRTHTGEK
>d1bhi__ g.37.1.1 (-) Transactivation domain of cre-bp1/atf-2 {Human (Homo sapiens)}
MSDDKPFLCTAPGCGQRFTNEDHLAVHKHKHEMTLKFG
>d1ubdc1 g.37.1.1 (C:295-322) Ying-yang 1 (yy1, zinc finger domain) {Human (Homo sapiens)}
TIACPHKGCTKMFRDNSAMRKHLHTHGP
>d1ubdc2 g.37.1.1 (C:323-350) Ying-yang 1 (yy1, zinc finger domain) {Human (Homo sapiens)}
RVHVCAECGKAFVESSKLKRHQLVHTGE
>d1ubdc3 g.37.1.1 (C:351-380) Ying-yang 1 (yy1, zinc finger domain) {Human (Homo sapiens)}
KPFQCTFEGCGKRFSLDFNLRTHVRIHTGD
>d1ubdc4 g.37.1.1 (C:381-408) Ying-yang 1 (yy1, zinc finger domain) {Human (Homo sapiens)}
RPYVCPFDGCNKKFAQSTNLKSHILTHA
>d1tf3a1 g.37.1.1 (A:1-40) Transcription factor IIIA, TFIIIA {Xenopus laevis}
MKRYICSFADCGAAYNKNWKLQAHLSKHTGE
>d1tf3a2 g.37.1.1 (A:41-70) Transcription factor IIIA, TFIIIA {Xenopus laevis}
KPFPCKEEGCEKGFTSLHHLTRHSLTHTGE
>d1tf3a3 g.37.1.1 (A:71-101) Transcription factor IIIA, TFIIIA {Xenopus laevis}
KNFTCDSDGCDLRFTTKANMKKHFNRFHNIK
>d1tf6a1 g.37.1.1 (A:10-40) Transcription factor IIIA, TFIIIA {Xenopus laevis}
YKRYICSFADCGAAYNKNWKLQAHLCKHTGE
>d1tf6a4 g.37.1.1 (A:101-131) Transcription factor IIIA, TFIIIA {Xenopus laevis}
KICVYVCHFENCGKAFKKHNQLKVHQFSHTQ
>d1tf6a5 g.37.1.1 (A:132-160) Transcription factor IIIA, TFIIIA {Xenopus laevis}
QLPYECPHEGCDKRFSLPSRLKRHEKVHA
>d1tf6a6 g.37.1.1 (A:161-188) Transcription factor IIIA, TFIIIA
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{Xenopus laevis}
GYPCKKDDSCSFVGKTWTLYLKHVAECH
>d1yuja_ g.37.1.1 (A:) GAGA factor {Drosophila melanogaster}
PKAKRAKHPPGTEKPRSRSQSEQPATCPICYAVIRQSRNLRRHLELRHFAKPGV
>d1fu9a_ g.37.1.2 (A:) U-shaped transcription factor, different fingers {Fruit fly (Drosophila melanogaster)}
GSAAEVMKKYCSTCDISFNYVKTYLAHKQFYCKNKP
>d1fv5a_ g.37.1.2 (A:) U-shaped transcription factor, different fingers {Fruit fly (Drosophila melanogaster)}
GSLLKPARFMCLPCGIAFSSPSTLEAHQAYYCSHRI
>d1aw6__ g.38.1.1 (-) Gal4 {Baker's yeast (Saccharomyces cerevisiae)}
MKLLSSIEQACDICRLKKLKCSKEKPKCAKCLKNNWECRYSPK
>d1d66a1 g.38.1.1 (A:8-48) Gal4 {Baker's yeast (Saccharomyces cerevisiae)}
EQACDICRLKKLKCSKEKPKCAKCLKNNWECRYSPKTKRSP
>d1pyia1 g.38.1.1 (A:30-71) PPR1 {Baker's yeast (Saccharomyces cerevisiae)}
SRTACKRCRLKKIKCDQEFPSCKRCAKLEVPCVSLDPATGKD
>d1zmec1 g.38.1.1 (C:31-66) PUT3 {Baker's yeast (Saccharomyces cerevisiae)}
SVACLSCRKRHIKCPGGNPCQKCVTSNAICEYLEPS
>d1hwtc1 g.38.1.1 (C:59-97) Hap1 (Cyp1) {Baker's yeast (Saccharomyces cerevisiae)}
RIPLSCTICRKRKVKCDKLRPHCQQCTKTGVAHLCHYME
>d2hapc1 g.38.1.1 (C:55-97) Hap1 (Cyp1) {Baker's yeast (Saccharomyces cerevisiae)}
RKRNRIPLRCTICRKRKVKCDKLRPHCQQCTKTGVAHLCHYME
>d1cld__ g.38.1.1 (-) CD2-Lac9 {Milk yeast (Kluyveromyces lactis)}
QACDACRKKKWKCSKTVPTCTNCLKYNLDCVYS
>d2alca_ g.38.1.1 (A:) Ethanol regulon transcriptional activator ALCR DNA-binding domain {Aspergillus nidulans and Emericella nidulans}
GSMADTRRRQNHSCDPCRKGKRRCDAPENRNEANENGWVSCSNCKRWNKDCTFNWLSSQRSKNSS
>d3gata_ g.39.1.1 (A:) Erythroid transcription factor GATA-1 {Chicken (Gallus gallus)}
KRAGTVCSNCQTSTTTLWRRSPMGDPVCNACGLYYKLHQVNRPLTMRKDGIQTRNRKVSSKGKKRR
>d7gata_ g.39.1.1 (A:) Erythroid transcription factor GATA-1 {Chicken (Gallus gallus)}
MKNGEQNGPTTCTNCFTQTTPVWRRNPEGQPLCNACGLFLKLHGVVRPLSLKTDVIKKRNRNSANS
>d1gnf__ g.39.1.1 (-) Erythroid transcription factor GATA-1 {Mouse (Mus musculus)}
GSEARECVNCGATATPLWRRDRTGHYLCNACGLYHKMNGQNRPLIR
>d1dszb_ g.39.1.2 (B:) Retinoid X receptor (RXR-alpha) DNA-binding
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domain {Human (Homo sapiens)}
GSFTKHICAICGDRSSGKHYGVYSCEGCKGFFKRTVRKDLTYTCRDNKDCLIDKRQRNRCQYCRY
QKCLAMGMKREAVQEERQR
>d2nlla_ g.39.1.2 (A:) Retinoid X receptor (RXR-alpha) DNA-binding
domain {Human (Homo sapiens)}
CAICGDRSSGKHYGVYSCEGCKGFFKRTVRKDLTYTCRDNKDCLIDKRQRNRCQYCRYQKCLAMG
M
>d2nllb_ g.39.1.2 (B:) Thyroid hormone receptor (TR-beta) DNA-binding
domain {Human (Homo sapiens)}
DELCVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLHPSYSCKYEGKCVIDKVTRNQCQECRFKK
CIYVGMATDLVLDDSKRLAKRKLIEENREKRRREELEK
>d1cita_ g.39.1.2 (A:) Orphan nuclear receptor NGFI-B {Rat (Rattus
norvegicus)}
GRCAVCGDNASCQHYGVRTCEGCKGFFKRTVQKSAKYICLANKDCPVDKRRRNRCQFCRFQKCLA
VGMVKEVVRTDSLKGRRGRLPSKP
>d1hcqa_ g.39.1.2 (A:) Estrogen receptor DNA-binding domain {Human
and chicken (Homo sapiens) and (Gallus gallus)}
MKETRYCAVCNDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCPATNQCTIDKNRRKSCQACRLR
KCYEVGMMK
>d1glua_ g.39.1.2 (A:) Glucocorticoid receptor DNA-binding domain
{Rat (Rattus norvegicus)}
MKPARPCLVCSDEASGCHYGVLTCGSCKVFFKRAVEGQHNYLCAGRNDCIIDKIRRKNCPACRYR
KCLQAGMNLEARKTKK
>d1lata_ g.39.1.2 (A:) Glucocorticoid receptor DNA-binding domain
{Rat (Rattus norvegicus)}
RPCLVCSDEASGCHYGVLTCEGCKAFFKRAVEGQHNYLCKYEGKCIIDKIRRKNCPACRYRKCLQ
AGMNLE
>d2gda__ g.39.1.2 (-) Glucocorticoid receptor DNA-binding domain {Rat
(Rattus norvegicus)}
LCLVCSDEASGCHYGVLTCGSCKVFFKRAVEGQHNYLCAGRNDCIIDKIRRKNCPACRYRKCLQA
GMNLEAR
>d1dsza_ g.39.1.2 (A:) Retinoic acid receptor DNA-binding domain
{Human (Homo sapiens)}
PCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCIINKVTRNRCQYCRLQKCFEV
GMSKESVRND
>d1hra__ g.39.1.2 (-) Retinoic acid receptor DNA-binding domain {Human
(Homo sapiens)}
PPRVYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMIYTCHRDKNCVINKVTRNRCQYCRL
QKCFEVGMSKESVRN
>d1a6ya_ g.39.1.2 (A:) Orphan nuclear receptor reverb {Human (Homo
sapiens)}
LLCKVCGDVASGFHYGVHACEGCKGFFRRSIQQNIQYKRCLKNENCSIVRINRNRCQQCRFKKCL
SVGMSRDAVRFGR
>d1b8ta1 g.39.1.3 (A:1-35) Cysteine-rich (intestinal) protein, CRP,
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CRIP {Chicken (Gallus gallus)}
MPNWGGGKKCGVCQKAVYFAEEVQCEGSSFHKSCF
>d1b8ta2 g.39.1.3 (A:36-100) Cysteine-rich (intestinal) protein, CRP,
CRIP {Chicken (Gallus gallus)}
LCMVCKKNLDSTTVAVHGDEIYCKSCYGKKYGPKGKGKGMGAGTLSTDKGESLGIKYEEGQSHRP
>d1b8ta3 g.39.1.3 (A:101-143) Cysteine-rich (intestinal) protein, CRP,
CRIP {Chicken (Gallus gallus)}
TNPNASRMAQKVGGSDGCPRCGQAVYAAEKVIGAGKSWHKSCF
>d1b8ta4 g.39.1.3 (A:144-192) Cysteine-rich (intestinal) protein, CRP,
CRIP {Chicken (Gallus gallus)}
RCAKCGKSLESTTLADKDGEIYCKGCYAKNFGPKGFGFGQGAGALIHSQ
>d1ctl_1 g.39.1.3 (1-35) Cysteine-rich (intestinal) protein, CRP,
CRIP {Chicken (Gallus gallus)}
MAQKVGGSDGCPRCGQAVYAAEKVIGAGKSWHKSC
>d1a7i_1 g.39.1.3 (8-35) Cysteine-rich (intestinal) protein, CRP,
CRIP {Japanese quail (Coturnix coturnix japonica), CRP2}
NKCGACGRTVYHAEEVQCDGRSFHRCCF
>d1a7i_2 g.39.1.3 (36-67) Cysteine-rich (intestinal) protein, CRP,
CRIP {Japanese quail (Coturnix coturnix japonica), CRP2}
LCMVCRKNLDSTTVAIHDAEVYCKSCYGKKYG
>d1ibia1 g.39.1.3 (A:117-144) Cysteine-rich (intestinal) protein, CRP,
CRIP {Japanese quail (Coturnix coturnix japonica), CRP2}
AEKCSRCGDSVYAAEKVIGAGKPWHKNC
>d1ibia2 g.39.1.3 (A:145-175) Cysteine-rich (intestinal) protein, CRP,
CRIP {Japanese quail (Coturnix coturnix japonica), CRP2}
FRCAKCGKSLESTTLTEKEGEIYCKGCYAKN
>d1iml_1 g.39.1.3 (1-28) Cysteine-rich (intestinal) protein, CRP,
CRIP {Rat (Rattus rattus)}
PKCPKCDKEVYFAERVTSLGKDWHRPCL
>d1iml_2 g.39.1.3 (29-76) Cysteine-rich (intestinal) protein, CRP,
CRIP {Rat (Rattus rattus)}
KCEKCGKTLTSGGHAEHEGKPYCNHPCYSAMFGPKGFGRGGAESHTFK
>d1g47a1 g.39.1.3 (A:1-35) Pinch (particularly interesting new
Cys-His) protein {Human (Homo sapiens)}
MANALASATCERCKGGFAPAEKIVNSNGELYHEQC
>d1g47a2 g.39.1.3 (A:36-70) Pinch (particularly interesting new
Cys-His) protein {Human (Homo sapiens)}
FVCAQCFQQFPEGLFYEFEGRKYCEHDFQMLFAPC
>d1zfo__ g.39.1.4 (-) LASP-1 {Pig (Sus scrofa)}
MNPNCARCGKIVYPTEKVNCLDKFWHKACF
>d1d4ua2 g.39.1.5 (A:1-36) DNA repair factor XPA DNA- and RPA-binding
domain, N-terminal subdomain {Human (Homo sapiens)}
MEFDYVICEECGKEFMDSYLMDHFDLPTCDDCRDAD
>d1xpa_2 g.39.1.5 (98-133) DNA repair factor XPA DNA- and RPA-binding
```

domain, N-terminal subdomain {Human (Homo sapiens)}
MEFDYVICEECGKEFMDSYLMNHFDLPTCDNCRDAD
>d1jj2t_ g.39.1.6 (T:) Ribosomal protein L24e {Archaeon Haloarcula marismortui}
RECDYCGTDIEPGTGTMFVHKDGATTHFCSSKCENNADLGREARNLEWTDTAR
>d1fjgn_ g.39.1.7 (N:) Ribosomal protein S14 {Thermus thermophilus}
ARKALIEKAKRTPKFKVRAYTRCVRCGRARSVYRFFGLCRICLRELAHKGQLPGVRKASW
>d1aaf__ g.40.1.1 (-) HIV nucleocapsid {Human immunodeficiency virus type 1, different isolates}
MQRGNFRNQRKIIKCFNCGKEGHIAKNCRAPRKRGCWKCGKEGHQMKDCTERQAN
>d1eska_ g.40.1.1 (A:) HIV nucleocapsid {Human immunodeficiency virus type 1, different isolates}
NVKCFNCGKEGHTARNCRAPRKKGCWKCGKEGHQMKDCTERQ
>d1f6ua_ g.40.1.1 (A:) HIV nucleocapsid {Human immunodeficiency virus type 1, different isolates}
MQKGNFRNQRKTVKCFNCGKEGHIAKNCRAPRKKGCWKCGKEGHQMKDCTERQAN
>d1nc8__ g.40.1.1 (-) HIV nucleocapsid {Human immunodeficiency virus type 2}
AQQRKVIRCWNCGKEGHSARQCRAPRRQG
>d1cl4a_ g.40.1.1 (A:) Nucleocapsid protein from mason-pfizer monkey virus (MPMV) {Mason-pfizer monkey virus}
VPGLCPRCKRGKHWANECKSKTDNQGNPIPPH
>d1a6bb_ g.40.1.1 (B:) Zinc finger protein ncp10 {Moloney murine leukemia virus}
GERRRSQLDRDQCAYCKEKGHWAKDCPKKPRGPRGPRPQT
>d1dsqa_ g.40.1.1 (A:) Nucleic acid binding protein p14 {Mouse mammary tumor virus}
KGPVCFSCGKTGHIKRDCKEE
>d1dsva_ g.40.1.1 (A:) Nucleic acid binding protein p14 {Mouse mammary tumor virus}
PPGLCPRCKKGYHWKSECKSKFDKDGNPLPP
>d1f4la3 g.41.1.1 (A:141-175) Methionyl-tRNA synthetase (MetRS), Zn-domain {Escherichia coli}
VKGTCPKCKSPDQYGDNCEVCGATYSPTELIEPKS
>d1mea__ g.41.1.1 (-) Methionyl-tRNA synthetase (MetRS), Zn-domain {Escherichia coli}
GSDRFVKGTCPKCKSPDQYGDNCEVCGA
>d1zin_2 g.41.2.1 (126-160) Microbial and mitochondrial ADK, insert "zinc finger" domain {Bacillus stearothermophilus}
GRRICRNCGATYHLIFHPPAKPGVCDKCGGELYQR
>d1e4ya2 g.41.2.1 (A:122-156) Microbial and mitochondrial ADK, insert "zinc finger" domain {Escherichia coli}
GRRVHAPSGRVYHVKFNPPKVEGKDDVTGEELTTR
>d2ak3a2 g.41.2.1 (A:125-161) Microbial and mitochondrial ADK, insert

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"zinc finger" domain {Cow (Bos taurus), mitochondrial izozyme-3}
ARWIHPGSGRVYNIEFNPPKTMGIDDLTGEPLVQRED
>d1ak2_2 g.41.2.1 (147-176) Microbial and mitochondrial ADK, insert
"zinc finger" domain {Cow (Bos taurus), mitochondrial izozyme-2}
PQSGRSYHEEFNPPKEPMKDDITGEPLIRR
>d1aky_2 g.41.2.1 (131-168) Microbial and mitochondrial ADK, insert
"zinc finger" domain {Baker's yeast (Saccharomyces cerevisiae)}
GRLIHPASGRSYHKIFNPPKEDMKDDVTGEALVQRSDD
>d1zaka2 g.41.2.1 (A:128-158) Microbial and mitochondrial ADK, insert
"zinc finger" domain {Maize (Zea mays)}
GRRLDPVTGKIYHLKYSPPENEEIASRLTQR
>d1tfi__ g.41.3.1 (-) Transcriptional factor SII, C-terminal domain
{Human (Homo sapiens)}
KTGGTQTDLFTCGKCKKKNCTYTQVQTRSADEPMTTFVVCNECGNRWKFC
>d1pft__ g.41.3.1 (-) Transcription inititiation factor TFIIB,
N-terminal domain {Archaeon Pyrococcus furiosus}
MVNKQKVCPACESAELIYDPERGEIVCAKCGYVIEENIIDMGPEWRAFDA
>d1dl6a_ g.41.3.1 (A:) Transcription inititiation factor TFIIB,
N-terminal domain {Human (Homo sapiens)}
ASTSRLDALPRVTCPNHPDAILVEDYRAGDMICPECGLVVGDRVIDVGSEWRTFSNDK
>d1d0qa_ g.41.3.2 (A:) Zinc-binding domain of DNA primase {Bacillus
stearothermophilus}
GHRIPEETIEAIRRGVDIVDVIGEYVQLKRQGRNYFGLCPFHGEKTPSFSVSPEKQIFHCFGCGA
GGNAFTFLMDIEGIPFVEAAKRLAAKAGVDLSVYELD
>d1yua_1 g.41.3.3 (1-65) Prokariotic DNA topoisomerase I, a C-terminal
fragment {Escherichia coli}
MNGEVAPPKEDPVPLPELPCEKSDAYFVLRDGAAGVFLAANTFPKSRETRAPLVEELYRFRDRLP
>d1yua_2 g.41.3.3 (66-122) Prokariotic DNA topoisomerase I, a
C-terminal fragment {Escherichia coli}
EKLRYLADAPQQDPEGNKTMVRFSRKTKQQYVSSEKDGKATGWSAFYVDGKWVEGKK
>d1qf8a_ g.41.4.1 (A:) Casein kinase II beta subunit {Human (Homo
sapiens)}
VSWISWFCGLRGNEFFCEVDEDYIQDKFNLTGLNEQVPHYRQALDMILDLEPDEELEDNPNQSDL
IEQAAEMLYGLIHARYILTNRGIAQMLEKYQQGDFGYCPRVYCENQPMLPIGLSDIPGEAMVKLY
CPKCMDVYTPKSSRHHHTDGAYFGTGFPHMLFMVHPEYRPKRP
>d1rb9__ g.41.5.1 (-) Rubredoxin {Desulfovibrio vulgaris}
MKKYVCTVCGYEYDPAEGDPDNGVKPGTSFDDLPADWVCPVCGAPKSEFEAA
>d2rdva_ g.41.5.1 (A:) Rubredoxin {Desulfovibrio vulgaris}
MKKYVCTVCGYEYDPAEGDPDNGVKPGTAFEDVPADWVCPICGAPKSEFEPA
>d1rdg__ g.41.5.1 (-) Rubredoxin {Desulfovibrio gigas}
MDIYVCTVCGYEYDPAKGDPDSGIKPGTKFEDLPDDWACPVCGASKDAFEKQ
>d6rxn__ g.41.5.1 (-) Rubredoxin {Desulfovibrio desulfuricans, strain
27774}
MQKYVCNVCGYEYDPAEHDNVPFDQLPDDWCCPVCGVSKDQFSPA
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>d1iro__ g.41.5.1 (-) Rubredoxin {Clostridium pasteurianum}
MKKYTCTVCGYIYNPEDGDPDNGVNPGTDFKDIPDDWVCPLCGVGKDQFEEVE
>d5rxn__ g.41.5.1 (-) Rubredoxin {Clostridium pasteurianum}
MKKYTCTVCGYIYDPEDGDPDDGVNPGTDFKDIPDDWVCPLCGVGKDEFEEVEE
>d1brfa_ g.41.5.1 (A:) Rubredoxin {Archaeon Pyrococcus furiosus}
AKWVCKICGYIYDEDAGDPDNGISPGTKFEELPDDWVCPICGAPKSEFEKLED
>d1qcva_ g.41.5.1 (A:) Rubredoxin {Archaeon Pyrococcus furiosus}
AKWVLKITGYIYDEDAGDPDNGISPGTKFEELPDDWVAPITGAPKSEFEKLED
>d1dx8a_ g.41.5.1 (A:) Rubredoxin {Guillardia theta}
MEIDEGKYECEACGYIYEPEKGDKFAGIPPGTPFVDLSDSFMCPACRSPKNQFKSIKKVIAGFAE
NQKYG
>d1h7va_ g.41.5.1 (A:) Rubredoxin {Guillardia theta}
MEIDEGKYECEACGYIYEPEKGDKFAGIPPGTPFVDLSDSFMCPACRSPKNQFKSIKKVI
>d1dvba2 g.41.5.1 (A:148-191) Rubrerythrin, C-terminal domain
{Desulfovibrio vulgaris}
FLREQATKWRCRNCGYVHEGTGAPELCPACAHPKAHFELLGINW
>d1dxga_ g.41.5.2 (A:) Desulforedoxin {Desulfovibrio gigas}
ANEGDVYKCELCGQVVKVLEEGGGTLVCCGEDMVKQ
>d1dfx_2 g.41.5.2 (1-36) Desulfoferrodoxin N-terminal domain
{Desulfovibrio desulfuricans}
PKHLEVYKCTHCGNIVEVLHGGGAELVCCGEPMKHM
>d1ocrf_ g.41.5.3 (F:) Cytochrome c oxidase Subunit F {Cow (Bos
taurus)}
ASGGGVPTDEEQATGLEREVMLAARKGQDPYNILAPKATSGTKEDPNLVPSITNKRIVGCICEED
NSTVIWFWLHKGEAQRCPSCGTHYKLVPHQLAH
>d1gh9a_ g.41.6.1 (A:) Hypothetical protein MTH1184 {Archaeon
Methanobacterium thermoautotrophicum}
MYIIFRCDCGRALYSREGAKTRKCVCGRTVNVKDRRIFGRADDFEEASELVRKLQEEKYGSCHFT
NPSKRE
>d1d09b2 g.41.7.1 (B:101-153) Aspartate carbamoyltransferase,
Regulatory-chain, C-terminal domain {Escherichia coli}
ERIDNVLVCPNSNCISHAEPVSSSFAVRKRANDIALKCKYCEKEFSHNVVLAN
>d2atcb2 g.41.7.1 (B:101-152) Aspartate carbamoyltransferase,
Regulatory-chain, C-terminal domain {Escherichia coli}
ERNIDVLVCPDSNCISHAEPVSSSFAVRRADDIALKCKYCEKEFSHNVVLAN
>d1ffkw_ g.41.8.1 (W:) Ribosomal protein L37ae {Archaeon Haloarcula
marismortui}
PTGRFGPRYGLKIRVRVRDVEIKHKKKYKCPVCGFPKLKRASTSIWVCGHCGYKIAGGAYTPETV
AGKAVMKA
>d1jj2y_ g.41.8.1 (Y:) Ribosomal protein L37ae {Archaeon Haloarcula
marismortui}
RTGRFGPRYGLKIRVRVADVEIKHKKKHKCPVCGFKKLKRAGTGIWMCGHCGYKIAGGCYQPETV
AGKAVMKA
>d1jj2z_ g.41.8.2 (Z:) Ribosomal protein L37e {Archaeon Haloarcula
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marismortui}
TGAGTPSQGKKNTTTHTKCRRCGEKSYHTKKKVCSSCGFGKSAKRRDYEWQSKAGE
>d1jj22_ g.41.8.3 (2:) Ribosomal protein L44e {Archaeon Haloarcula
marismortui}
MQMPRRFNTYCPHCNEHQEHEVEKVRSGRQTGMKWIDRQRERNSGIGNDGKFSKVPGGDKPTKKT
DLKYRCGECGKAHLREGWRAGRLEFQE
>d1qyp__ g.41.9.1 (-) RBP9 subunit of RNA polymerase II {Archaeon
Thermococcus celer}
GSHMEQDLKTLPTTKITCPKCGNDTAYWWEMQTRAGDEPSTIFYKCTKCGHTWRSYE
>d1i50i1 g.41.9.1 (I:1-49) RBP9 subunit of RNA polymerase II {Baker's
yeast (Saccharomyces cerevisiae)}
MTTFRFCRDCNNMLYPREDKENNRLLFECRTCSYVEEAGSPLVYRHELI
>d1i50i2 g.41.9.1 (I:50-122) RBP9 subunit of RNA polymerase II {Baker's
yeast (Saccharomyces cerevisiae)}
TNIGETAGVVQDIGSDPTLPRSDRECPKCHSRENVFFQSQQRRKDTSMVLFFVCLSCSHIFTSDQ
KNKRTQFS
>d1i50l_ g.41.9.2 (L:) RBP12 subunit of RNA polymerase II {Baker's
yeast (Saccharomyces cerevisiae)}
ATLKYICAECSSKLSLSRTDAVRCKDCGHRILLKARTKRLVQFEAR
>d1dfea_ g.42.1.1 (A:) Ribosomal protein L36 {Thermus thermophilus}
MKVRASVKRICDKCKVIRRHGRVYVICENPKHKQRQG
>d1fre__ g.43.1.1 (-) Nuclear factor XNF7 {African clawed frog (Xenopus
laevis)}
EKCSEHDERLKLYCKDDGTLSCVICRDSLKHASHNFLPI
>d1fbva4 g.44.1.1 (A:356-434) CBL {Human (Homo sapiens)}
TPQDHIKVTQEQYELYCEMGSTFQLCKICAENDKDVKIEPCGHLMCTSCLTSWQESEGQGCPFCR
CEIKGTEPIVVDPF
>d1rmd_2 g.44.1.1 (1-86) V(D)J recombination activating protein 1
(RAG1), dimerization domain {Mouse (Mus musculus)}
NCSKIHLSTKLLAVDFPAHFVKSISCQICEHILADPVETSCKHLFCRICILRCLKVMGSYCPSCR
YPCFPTDLESPVKSFLNILNS
>d1chc__ g.44.1.1 (-) Immediate early protein, IEEHV {Equine herpes
virus type 1}
MATVAERCPICLEDPSNYSMALPCLHAFCYVCITRWIRQNPTCPLCKVPVESVVHTIESDSEFGD
QLI
>d1bor__ g.44.1.1 (-) Acute promyelocytic leukaemia proto-onkoprotein
PML {Human (Homo sapiens)}
EEEFQFLRCQQCQAEAKCPKLLPCLHTLCSGCLEASGMQCPICQAPWPLGADTPAL
>d1g25a_ g.44.1.1 (A:) TFIIH Mat1 subunit {Human (Homo sapiens)}
MDDQGCPRCKTTKYRNPSLKLMVNVCGHTLCESCVDLLFVRGAGNCPECGTPLRKSNFRVQLFED
>d1e4ua_ g.44.1.1 (A:) Not-4 N-terminal RING finger domain {Human (Homo
sapiens)}
MSRSPDAKEDPVECPLCMEPLEIDDINFFPCTCGYQICRFCWHRIRTDENGLCPACRKPYPEDPA
VYKPLSQEELQRI
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>d1jm7a_ g.44.1.1 (A:) brca1 RING domain {Human (Homo sapiens)}
MDLSALRVEEVQNVINAMQKILECPICLELIKEPVSTKCDHIFCKFCMLKLLNQKKGPSQCPLCK
NDITKRSLQESTRFSQLVEELLKIICAFQLDTGLEYAN
>d1jm7b_ g.44.1.1 (B:) bard1 RING domain {Human (Homo sapiens)}
MEPDGRGAWAHSRAALDRLEKLLRCSRCTNILREPVCLGGCEHIFCSNCVSDCIGTGCPVCYTPA
WIQDLKINRQLDSMIQLCSKLRNLLHDNELSD
>d1dcqa2 g.45.1.1 (A:247-368) Pyk2-associated protein beta ARF-GAP domain {Mouse (Mus musculus)}
LTKEIISEVQRMTGNDVCCDCGAPDPTWLSTNLGILTCIECSGIHRELGVHYSRMQSLTLDVLGT
SELLLAKNIGNAGFNEIMECCLPSEDPVKPNPGSDMIARKDYITAKYMERRYARKKH
>d1mhu__ g.46.1.1 (-) Metallothionein {Human (Homo sapiens)}
KSCCSCCPVGCAKCAQGCICKGASDKCSCCA
>d2mhu__ g.46.1.1 (-) Metallothionein {Human (Homo sapiens)}
MDPNCSCAAGDSCTCAGSCKCKECKCTSCK
>d2mrb__ g.46.1.1 (-) Metallothionein {Rabbit (Oryctolagus cuniculus)}
MDPNCSCAAAGDSCTCANSCTCKACKCTSCK
>d1mrt__ g.46.1.1 (-) Metallothionein {Rat (Rattus rattus)}
KSCCSCCPVGCAKCSQGCICKEASDKCSCCA
>d2mrt__ g.46.1.1 (-) Metallothionein {Rat (Rattus rattus)}
MDPNCSCATDGSCSCAGSCKCKQCKCTSCK
>d4mt2__ g.46.1.1 (-) Metallothionein {Rat (Rattus rattus)}
MDPNCSCATDGSCSCAGSCKCKQCKCTSCKKSCCSCCPVGCAKCSQGCICKEASDKCSCCA
>d1dfsa_ g.46.1.1 (A:) Metallothionein {Mouse (Mus musculus)}
KSCCSCCPVGCSKCAQGCVCKGAADKCTCCA
>d1dfta_ g.46.1.1 (A:) Metallothionein {Mouse (Mus musculus)}
MDPNCSCSTGGSCTCTSSCACKNCKCTSCK
>d1ji9a_ g.46.1.1 (A:) Metallothionein {Mouse (Mus musculus)}
KSCCSCCPAGCEKCAKDCVCKGEEGAKAEAEKCSCCQ
>d1dmc__ g.46.1.1 (-) Metallothionein {Crab (Callinectes sapidus), alpha and beta domains}
SPCQKCTSGCKCATKEECSKTCTKPCSCCPK
>d1dme__ g.46.1.1 (-) Metallothionein {Crab (Callinectes sapidus), alpha and beta domains}
PGPCCNDKCVCQEGGCKAGCQCTSCRCS
>d1fmya_ g.46.1.1 (A:) Metallothionein {Baker's yeast (Saccharomyces cerevisiae)}
QNEGHECQCQCGSCKNNEQCQKSCSCPTGCNSDDKCPCGN
>d1qjka_ g.46.1.1 (A:) Metallothionein {Purple sea urchin (Strongylocentrotus purpuratus)}
PDVKCVCCTEGKECACFGQDCCVTGECCKDGTCCGI
>d1qjla_ g.46.1.1 (A:) Metallothionein {Purple sea urchin (Strongylocentrotus purpuratus)}
ICTNAACKCANGCKCGSGCSCTEGNCAC
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>d1jjda_ g.46.1.1 (A:) Cyanobacterial metallothionein SmtA {Synechococcus sp., PCC 7942}
TLVKCACEPCLCNVDPSKAIDRNGLYYCSEACADGHTGGSKGCGHTGCNCHG
>d1co4a_ g.47.1.1 (A:) Zinc domain conserved in yeast copper-regulated transcription factors {Synthetic}
MVVINGVKYACDSCIKSHKAAQCEHNDRPLKILKPRGRPPTT
>d1adn__ g.48.1.1 (-) Ada DNA repair protein, N-terminal domain (N-Ada 10) {Escherichia coli}
MKKATCLTDDQRWQSVLARDPNADGEFVFAVRTTGIFCRPSCRARHALRENVSFYANASEALAAG
FRPCKRCQPDKANPRQHRLDKITHACR
>d1ptq__ g.49.1.1 (-) Protein kinase C-delta (PKCdelta) {Mouse (Mus musculus)}
HRFKVYNYMSPTFCDHCGSLLWGLVKQGLKCEDCGMNVHHKCREKVANLC
>d1faq__ g.49.1.1 (-) RAF-1 {Human (Homo sapiens)}
LTTHNFARKTFLKLAFCDICQKFLLNGFRCQTCGYKFHEHCSTKVPTMCVDW
>d1tbo__ g.49.1.1 (-) Protein kinase c-gamma {Rat (Rattus rattus)}
QTDDPRNKHKFRLHSYSSPTFCDHCGSLLYGLVHQGMKCSCCEMNVHRRCVRSVPSLCGVDHTER
R
>d1kbea_ g.49.1.1 (A:) Kinase suppressor of Ras, Ksr {Mouse (Mus musculus)}
GSVTHRFSTKSWLSQVCNVCQKSMIFGVKCKHCRLKCHNKCTKEAPACR
>d1e53a_ g.49.1.2 (A:) TFIIH p44 subunit cysteine-rich domain {Human (Homo sapiens)}
LDAFQEIPLEEYNGERFCYGCQGELKDQHVYVCAVCQNVFCVDCDVFVHDSLHCCPGCI
>d1vfya_ g.50.1.1 (A:) vps27p protein {Baker's yeast (Saccharomyces cerevisiae)}
DWIDSDACMICSKKFSLLNRKHHCRSCGGVFCQEHSSNSIPLPDLGIYEPVRVCDSCFEDYEFIV
TD
>d1joca1 g.50.1.1 (A:1348-1411) Eea1 {Human (Homo sapiens)}
KWAEDNEVQNCMACGKGFSVTVRRHHCRQCGNIFCAECSAKNALTPSSKKPVRVCDACFNDLQG
>d1dvpa2 g.50.1.1 (A:149-220) Hrs {Fruit fly (Drosophila melanogaster)}
MFTADTAPNWADGRVCHRCRVEFTFTNRKHHCRNCGQVFCGQCTAKQCPLPKYGIEKEVRVCDGC
FAALQRG
>d1zbdb_ g.50.1.1 (B:) Effector domain of rabphilin-3a {Rat (Rattus norvegicus)}
EELTDEEKEIINRVIARAEKMETMEQERIGRLVDRLETMRKNVAGDGVNRCILCGEQLGMLGSAS
VVCEDCKKNVCTKCGVETSNNRPHPVWLCKICLEQREVWKRSGAWFFKGFPKQVLPQPM
>d1f62a_ g.50.1.2 (A:) Williams-Beuren syndrome transcription factor, WSTF {Human (Homo sapiens)}
ARCKVCRKKGEDDKLILCDECNKAFHLFCLRPALYEVPDGEWQCPACQPAT
>d1fp0a1 g.50.1.2 (A:19-88) Nuclear corepressor KAP-1 (TIF-1beta) {Human (Homo sapiens)}
GTLDDSATICRVCQKPGDLVMCNQCEFCFHLDCHLPALQDVPGEEWSCSLCHVLPDLKEEDVDLQ
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ACKLN
>d1adt_2 g.51.1.1 (266-385) First Zn-domain of early E2A DNA-binding
protein, ADDBP {Human adenovirus type 5}
TGCALWLHRCAEIEGELKCLHGSIMINKEHVIEMDVTSENGQRALKEQSSKAKIVKNRWGRNVVQ
ISNTDARCCVHDAACPANQFSGKSCGMFFSEGAKAQVAFKQIKAFMQALYPNAQT
>d1adt_3 g.51.1.1 (386-529) Second Zn-domain of early E2A DNA-binding
protein, ADDBP {Human adenovirus type 5}
GHGHLLMPLRCECNSKPGHAPFLGRQLPKLTPFALSNAEDLDADLISDKSVLASVHHPALIVFQC
CNPVYRNSRAQGGGPNCDFKISAPDLLNALVMVRSLWSENFTELPRMVVPQFKWSTKHQYRNVSL
PVAHSDARQNPFDF
>d1qbha_ g.52.1.1 (A:) 2MIHB/C-IAP-1 {Human (Homo sapiens)}
GSHMQTHAARMRTFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWVEHA
KWFPRCEFLIRMKGQEFVDEIQGRYPHLLEQLLSTS
>d1f9xa_ g.52.1.1 (A:) BIR domains of XIAP {Human (Homo sapiens)}
MSDAVSSDRNFPNSTNLPRNPSMADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCG
GGLTDWKPSEDPWEQHAKWYPGCKYLLEQKGQEYINNIHLTHSLEECLVRTT
>d1g73c_ g.52.1.1 (C:) BIR domains of XIAP {Human (Homo sapiens)}
LPRNPSMADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQH
AKWYPGCKYLLEQKGQEYINNIHL
>d1g73d_ g.52.1.1 (D:) BIR domains of XIAP {Human (Homo sapiens)}
LPRNPSMADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQH
AKWYPGCKYLLEQKGQEYINNIHLTHSLEECLVRTTE
>d1i3oe_ g.52.1.1 (E:) BIR domains of XIAP {Human (Homo sapiens)}
FALDRPSETHADYLLRTGQVVDISDTIYPRNPAMYSEEARLKSFQNWPDYAHLTPRELASAGLYY
TGIGDQVQCFACGGKLKNWEPGDRAWSEHRRHFPNCFFVLGRNLNI
>d1jd5a_ g.52.1.1 (A:) BIR2 domain of DIAP1 {Fruit fly (Drosophila
melanogaster)}
GNYFPQYPEYAIETARLRTFEAWPRNLKQKPHQLAEAGFFYTGVGDRVRCFSCGGGLMDWNDNDE
PWEQHALWLSQCRFVKLMKGQLYIDTVAAKPVLAEEKEES
>d1e31a_ g.52.1.1 (A:) Anti-apoptotic protein survivin {Human (Homo
sapiens)}
TLPPAWQPFLKDHRISTFKNWPFLEGCACTPERMAEAGFIHCPTENEPDLAQCFFCFKELEGWEP
DDDPIEEHKKHSSGCAFLSVKKQFEELTLGEFLKLDRERAKNKIAKETNNKKKEFEETAKKVRRA
IEQLAA
>d1f81a_ g.53.1.1 (A:) CREB-binding transcriptional adaptor protein
CBP {Mouse (Mus musculus)}
SPQESRRLSIQRCIQSLVHACQCRNANCSLPSCQKMKRVVQHTKGCKRKTNGGCPVCKQLIALCC
YHAKHCQENKCPVPFCLNIKHK
>d1hc7a3 g.56.1.1 (A:404-477) C-terminal domain of ProRS {Thermus
thermophilus}
TRKVDTYEAFKEAVQEGFALAFHCGDKACERLIQEETTATTRCVPFEAEPEEGFCVRCGRPSAYG
KRVVFAKAY
>d1exka_ g.54.1.1 (A:) Cysteine-rich domain of the chaperone protein
DnaJ. {Escherichia coli}
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GVTKEIRIPTLEECDVCHGSGAKPGTQPQTCPTCHGSGQVQMRQGFFAVQQTCPHCQGRGTLIKD
PCNKCHGHGRVERS