

Supplementary Information for HITS-PR-HHblits: Protein Remote Homology Detection by Combining PageRank and Hyperlink-Induced Topic Search

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Online SCOP benchmark dataset S1. The SCOP benchmark dataset contains 7329 sequences from 1824 families and 1070 superfamilies, which were extracted from the Astral database. None of the sequences included has $\geq 95\%$ pairwise sequence identity to any other. See the main text for further explanation.

>d1dlwa_ a.1.1.1 (A:) Truncated hemoglobin {Ciliate (Paramecium caudatum)}
SLFEQLGGQAAVQAVTAQFYANIQADATVATFFNGIDMPNQTNKTA AFLCAALGGPNAWTGRNLKE
VHANMGVSNAQFTTVIGHLRSALTGAGVAAALVEQTVAVAETVRGDVVTV

>d1dlya_ a.1.1.1 (A:) Truncated hemoglobin {Green alga (Chlamydomonas eugametos)}
SLFAKLGGREAVEAAVDKIFYNKIVADPTVSTYFSNTDMKVQRSKQFAFLAYALGGASEWKGKDMRT
AHKDLVPHLSDVHFQAVARHLSDTLTELGVPPEDITDAMAVVASTRTEVLNMPQQ

>d1idra_ a.1.1.1 (A:) Truncated hemoglobin {Mycobacterium tuberculosis}
GLLSRLRKREPISYDKIGGHEAIEVVVEDFYVRVLADDQLSAFFSGTNMSRLKKGQVEFFAAALGGP
EPYTGAPMKQVHQGRGITMHHFSLVAGHLADALTAAGVPSETITEILGVIAPLAVDVTS

>d1scta_ a.1.1.2 (A:) Hemoglobin I {Ark clam (Scapharca inaequivalvis)}
VDAAVAKVCGSEAIKANLRRSWGVLSDIEATGLMLMSNLFTLRPDTKTYFTRLGDVQK GKANSKL
RGHAITLTYALNNFVDSLDDPSRLKCVVEKFAVNHINRKISGDAFGAIVEPMKETLKARMGNYSSDD
VAGAWAALVGVVQAAL

>d1sctb_ a.1.1.2 (B:) Hemoglobin I {Ark clam (Scapharca inaequivalvis)}
KVAELANAVVSNADQKDLLRMSWGVLSVDMEGTGLMLMANLFKTSPSAKGFARLGDVSAGKDNS
KLRGHSITLMYALQNFVDALDDVERLKCVEKFAVNHINRQISADEFG EIVGPLRQTLKARMGNYFD
EDTVAAWASLVAVVQASL

>d3sdha_ a.1.1.2 (A:) Hemoglobin I {Ark clam (Scapharca inaequivalvis)}
SVYDAAAQLTADVKKDLRDSWKVIGSDKKGNGVALMTTLFADNQETIGYFKRLGNVSQGMANDKL
RGHSITLMYALQNFIDQLDNPDDLVCVVEKFAVNHITRKISAAEFGKINGPIKKVLASKNFGDKYANA
WAKLVAVVQAAL

>d1b0b_ a.1.1.2 (-) Hemoglobin I {Clam (Lucina pectinata)}
SLSAAQKDNVKSWSAKASAAWGTAGPEFFMALFDAHDDVFAKFSGLFSGAAKGTVKNTPEMAAQA
QSFKGLVSNWVDNLDNAGALEGQCKTFAANHKARGISAGQLEAAFKVLAGFMKSYGGDEGAWTAV
AGALMGMIRPDM

>d1h97a_ a.1.1.2 (A:) Trematode hemoglobin/myoglobin {Paramphistomum epiclitum}
TLTKHEQDILLKELGPHVDTPAHIVETGLGAYHALFTAHPQYISHFSRLEGHTIENVMQSEGIKHYAR
TLTEAIVHMLKEISNDAEVKKIAAQYKGDHTSRKVTKDEFMSGEPIFTKYFQNLVKDAEGKAAVEKF
LKHVFPMAAEI

>d1vrea_ a.1.1.2 (A:) Glycera globin {Marine bloodworm (Glycera dibranchiata)}

GLSAAQRQVVASTWKDIAGSDNGAGVVGKECFKFLSAHHDMAAVFGFSGASDPGVADLGAKVLAQI
GVAVSHLGDEGKMVAEMKAVGVRHKGYGNKHIKAEIFEPLGASLLSAMEHRIGGKMNAAAKDAWA
AAYADISGALISGLQS

>d2hbg_ a.1.1.2 (-) Glycera globin {Marine bloodworm (Glycera dibranchiata)}

GLSAAQRQVIAATWKDIAGADNGAGVGGKCLIKFLSAHPQMAAVFGFSGASDPGVAALGAKVLAQIG
VAVSHLGDEGKMVAQMKAAGVVRHKGYGNKHIKAQYFEPLGASLLSAMEHRIGGKMNAAAKDAWAA
AYADISGALISGLQS

>d1a6m_ a.1.1.2 (-) Myoglobin {Sperm whale (Physeter catodon)}

VLSEGEWQLVHLVWAKVEADVAGHGQDILIRLFKSHPETLEKFDKFKHLKTEAEMKASEDLKKHGV
TVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPGDFGADAQGAMNKA
LELFRKDIAAKYKELGY

>d1mba_ a.1.1.2 (-) Myoglobin {Sea hare (Aplysia limacina)}

SLSAAEADLAGKSWAPVFANKNANGLDFLVALFEKFPDSANFFADFKGKSVADIKASPCLRDRVSSRIF
TRLNEFVNNAANAGKMSAMLSQFAKEHVGFGVGSQAQFENVRSMFPGFVASVAAPPAGADAAWTKL
FGLIIDALKAAGA

>d1mbs_ a.1.1.2 (-) Myoglobin {Common seal (Phoca vitulina)}

GLSDGEWHLVNLVWVGKVEDLAGHGQEVLRIRLFKSHPETLEKFDKFKHLKSEDDMRSEDLRKHG
NTVLTALGGILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSHKHPAEFGADAQAAMKK
ALELFRNDIAAKYKELGFHG

>d1mwca_ a.1.1.2 (A:) Myoglobin {Pig (Sus scrofa)}

GLSDGEWQLVNLVWVGKVEADVAGHGQEVLRIRLFKSHPETLEKFDKFKHLKSEDEMASEDLKKHG
NTVLTALGGILKKKGHHEAELTPLAQSHATKHKIPVKYLEFISEAIIQVLQSKHPGDFGADAQAMSK
ALELFRNDMAAKYKELGFQG

>d1dwta_ a.1.1.2 (A:) Myoglobin {Horse (Equus caballus)}

GLSDGEWQQVLNLVWVGKVEADIAGHGQEVLRIRLFTGHPETLEKFDKFKHLKTEAEMKASEDLKKHG
TVVLTALGGILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISDAIIHVLHSHKHPGDFGADAQAMTK
ALELFRNDIAAKYKELGFQ

>d2mm1_ a.1.1.2 (-) Myoglobin {Human (Homo sapiens)}

GLSDGEWQLVNLVWVGKVEADIPGHGQEVLRIRLFKSHPETLEKFDKFKHLKSEDEMASEDLKKHG
ATVLTALGGILKKKGHHEAEIKPLAQSHATKHKIPVKYLEFISEAIIQVLQSKHPGDFGADAQAMNK
ALELFRKDMASNYKELGFQG

>d1emy_ a.1.1.2 (-) Myoglobin {Asian elephant (Elephas maximus)}

GLSDGEWELVLTWVGKVEADIPGHGETVFVRLFTGHPETLEKFDKFKHLKTEGEMKASEDLKKQG
VTVLTALGGILKKKGHHEAEIQPLAQSHATKHKIPIKYLEFISDAIIHVLQSKHPAEFGADAQAMKKA
LELFRNDIAAKYKELGFQG

>d1lht_ a.1.1.2 (-) Myoglobin {Loggerhead sea turtle (Caretta caretta)}

GLSDDEWNHVLGIWAKVEPDLAAGHGQEVIRLFLQHPETQERFAKFKNLTTIDALKSSEEVKKHGTT
VLTALGRILKQKNNHEQELKPLAESHATKHKIPVKYLEFICEIIVKVIAEKHPSDFGADSQAAMKKAL
ELFRNDMASKYKEFGFQG

>d1myt_ a.1.1.2 (-) Myoglobin {Yellowfin tuna (Thunnus albacares)}

ADFDAVLKCGWGPVEADYTTMGGLVLRFLKEHPETQKLPKFKAGIAQADIAGNAAISAHGATVLKKL
GELLKAKGSHAAILKPLANSATKHKIPINNFKLISEVLVKVMHEKAGLDAGGQTALRNVMGIIIDL
EANYKELGFSG

>d1eco_ a.1.1.2 (-) Erythrocrucorin {Midge (Chironomus thummi thummi), fraction III}

LSADQISTVQASFDKVKGDPVGILYAVFKADPSIMAKFTQFAGKDLESIKGTAPFETHANRIVGFFSKII
GELPNIEADVNTFVASHKPRGVTHDQLNNFRAGFVSYMKAHTDFAGAEAAWGATLDTFFGMIFSK
M

>d2gdm_ a.1.1.2 (-) Leghemoglobin {Yellow lupin (*Lupinus luteus*)}

GALTESQAALVKSSWEEFNANIPKHTHRFFILVLEIAPAAKDLFSFLKGTSEVPQNNPELQAHAGKVF
KLVYEAAIQLEVTGVVVTDATLKNLGSVHVSKGVADAHFPVVKEAILKTIKEVVGAKWSEELNSAWT
IAYDELAIVIKKEMDDAA

>d1fsla_ a.1.1.2 (A:) Leghemoglobin {Soybean (*Glycine max*), isoform A}

VAFTEKQDALVSSFEAFKANIPQYSVVFYTSILEKAPAAKDLFSFLANGVDPTNPKLTGHAEKLFALV
RDSAGQLKASGTVVADAALGSVHAQKAVTDPQFVVVKEALLKTIKAAVGDKWSDELRAWVEVAYDE
LAAAIKKA

>d1d8ua_ a.1.1.2 (A:) Non-symbiotic plant hemoglobin {Rice (*Oryza sativa*)}

ALVEDNNAVAVSFSEEQALVLKSWAILKKDSANIALRFFLKIFEVAPSASQMFSLRNSDVPLEKNP
KLKTHAMSVFVMTCEAAAQLRKAGKVTVRDITLTKRLGATHLKYGVGDAHFEVVKFALLDTIKEEPV
ADMWSPAMKSAWSEAYDHLVAAIKQEMKPAE

>d1i3da_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Human (*Homo sapiens*)}

GHFTEEDKATITSLWGKVNVEDAGGETLGRLLVVYPWTQRFFDSFGNLSASAIMGNPKVKAHGKK
VLTSLGDAIKHLDDLKGTFAQLSELHCDKLHVDPENFKLLGNVLTVLAIHFGKEFTPEVQASWQKM
VTAVASALSSRYH

>d1irda_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Human (*Homo sapiens*)}

VLSPADKTNVKAAWGKVGGAHAGEYGAEALERMFLSFPTTKTYFPHFDLSHGSAQVKGHGKKVADAL
TNAVAHVDDMPNALSALSDLHAHKLKRVDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVS
TVLTSKYR

>d1jeba_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Human (*Homo sapiens*), zeta isoform}

SLTKTERTIIVSMWAKISTQADTIGTETLERLFLSHPQTKTYFPHFDLHPGSAQLRAHGSKVVAAVGD
AVKSIDDIGGALSSELHAYILRVDPVNFKLLSHCLLVTLAARFPADFTAEAHAAWDKFLSVVSSVLT
EKYR

>d1ibea_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Horse (*Equus caballus*)}

VLSAADKTNVKAAWSKVGGHAGEFGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGKKVGD
LTLAVGHLDDLPGALSLSNLHAHKLKRVDPVNFKLLSHCLLSTLAVHLPNDFTPAVHASLDKFLSSVS
TVLTSKYR

>d1hdsa_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Deer (*Odocoileus virginianus*)}

VLSAANKSNVKAAWGKVGGNAPAYGAQALQRMFLSFPTTKTYFPHFDLSHGSAQVKAHGQKVANA
LTKAQGHLDLPGTSLNSNLHAHKLKRVNPVNFKLLSHSLVTLASHLPTNFTPAVHANLNKFLAN
DSTVLTSKYR

>d1g08a_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Cow (*Bos taurus*)}

VLSAADKGNVKAAWGKVGGHAAEYGAELERMFLSFPTTKTYFPHFDLSHGSAQVKGHGAKVAAA
LTKAVEHLDDLPGALSELSDLHAHKLKRVDPVNFKLLSHSLVTLASHLPSDFTPAVHASLDKFLANVS
TVLTSKYR

>d1qpwa_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Pig (*Sus scrofa*)}

VLSAADKANVKAAWGKVGQAGAHGAEALERMFLGFPTTKTYFPHFNLSHGSDQVKAHGQKVAD
ALTKAUGHLDLPGALSALSDLHAHKLKRVDPVNFKLLSHCLLVTLAAHHPDDFNPSVHASLDKFLA
NVSTVLTSKYR

>d1fhja_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Maned wolf (*Chrysocyon brachyurus*)}

VLSPADKTNIKSTWDKIGGHAGDYGGAEALDRTFQSFPTTKTYFPHFDLSPGSAQVKAHGKKVADALT
TAVAHLLDLPGALSALSDDLHAYKLRVDPVNFKLLSHCLLVTLACHHPTEFTPAVHASLDKFFTAVSTV
LTSKYR

>d1hbra_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Chicken (*Gallus gallus*)}

MLTAEDKKLIQQAWEKAASHQEFGAEALTRMFTTYPQTKTYFPHFDLSPGSDQVRGHGKKVLGAL
GNAVKNVDNLSQAMAELSNLHAYNLRVDPVNFKLLSQCIQVVLAVHMGKDYTPEVHAAFDKFLSAV
SAVLAEKYR

>d1a4fa_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Bar-headed goose (*Anser indicus*)}

VLSAADKTNVKGVFSKISGHAEYGAETLERMFTAYPQTKTYFPHFDLQHGSAQIKAHGKKVVAALV
EAVNHIDDIAGALSKLSDLHAQKLRVDPVNFKFLGHCFLLVVVAIHPSALTAEVHASLDKFLCAVGTV
LTAKYR

>d1outa_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Trout (*Oncorhynchus mykiss*)}

SLTAKDKSVVKAFWGWKISGKADVVGAELGRMLTAYPQTKTYFSHWADLSPGSGPVKKHGGIIMGAI
GKAVGLMDDLVGMSALSDDLHAFKLRVDPGNFKILSHNILVTLAIHFPSDFTPEVHIAVDKFLAAVSA
ALADKYR

>d1cg5a_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Cartilaginous fish akabei (*Dasyatis akajei*)}

VLSSQNKKAIEELGNLIKANAEEAWGADALARLFELHPQTKTYFSKFSGFACNEQVKKHGRVMNA
LADATHHLDNLHLHLEDLARKHGENLLVDPHFHFLFADCIVVTLAVNLQAFTPVTHCAVDKFLLELV
AYELSSCYR

>d1t1na_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Fish (*Trematomus newnesi*)}

SLSDKDKAAVRALWSKIGKSSDAIGNDALSRMIVVYPQTKIYFSHWPDVTPGSPNIKAHGKKVMGGI
ALAVSKIDDLKTGLMELSEQHAYKLRVDPNSFKILNHCILVVISTMFPKEFTPEAHVSLDKFLSGVAL
ALAERYR

>d1spga_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Teleost fish (*Leiostomus xanthurus*)}

SLSATDKARVKALWDKIEGKSAELGAEALGRMLVSPFPQTKIYFSEWGQDLGPQTPQVRNHGAVIMA
AVGKAVKSIDNLVGGLSQLSELHAFKLRVDPANFKILAHNIIIVISMYFPGDFTPEVHLSVDKFLACLA
LALSEKYR

>d1gcva_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Houndshark (*Mustelus griseus*)}

AFTACEKQTIGKIAQVLAKSPEAYGAELARLFVTHPGSKSYFEYKDYSAGAKVQVHGGKVIKAVVK
AAEHVDDLHSHLETALHTHGKLLVDPQNFPMSECIIVTLATHLTFSPDTHCAVDKLLSAICQELS
SRYR

>d1irdb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Human (*Homo sapiens*)}

VHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPKVKAHGK
KVLGAFSDGLAHLNLDKGTFAATLSELHCDKLHVDPENFRLLGNVLCVLAHFGKEFTPPVQAAYQ
KVVAGVANALAHKYH

>d1a9we_ a.1.1.2 (E:) Hemoglobin, beta-chain {Human (*Homo sapiens*), embryonic gower II}

VHFTAEEKAAVTSLSKMNVEEAGGEALGRLLVVYPWTQRFFDSFGNLSSPSAILGNPKVKAHGKK
VLTSFGDAIKNMDNLKPAFAKLSLHCDKLHVDPENFKLLGNVMVILATHFGKEFTPEVQAAWQKL
VSAVAIALAHKY

>d1ibeb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Horse (*Equus caballus*)}

VQLSGEEKAAVLALWDKVNVEEVGGEALGRLLVVYPWTQRFFDSFGDLSNPGAVMGNPKVKAHGK
KVLHSFGEGVHHLNLDKGTFAALSELHCDKLHVDPENFRLLGNVLLVVLARHFGKDFTELQASYQ
KVVAGVANALAHKYH

>d1hdsb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Deer (*Odocoileus virginianus*)}

MLTAEKAAVTGFWGKVDVDVVGQAALGRLLVYPWTQRFFQHFGNLSSAGAVMNNPKVKAHGK
RVLDAFTQGLKHLDDLKGAFAQLSGLHCNKLHVNPQNFRLGNVLAALVARNFGGQFTPNVQALFQ
KVVAGVANALAHKYH

>d1g08b_ a.1.1.2 (B:) Hemoglobin, beta-chain {Cow (Bos taurus)}

MLTAEKAAVTAFWVGKVKVDEVGGEALGRLLVYPWTQRFFESFGDLSTADAVMNNPKVKAHGK
VLDSFSNGMKHLDDLKGTFAALSELHCDKLHVDPENFKLLGNVLLVVLARNFGKEFTPVLAADFQK
VVAGVANALAHRYH

>d1qpwb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Pig (Sus scrofa)}

VHLSAEEKEAVLGLWGKVNVEVGGEALGRLLVYPWTQRFFESFGDLNADAVMGNPKVKAHGK
KVLQSFSDGLKHLNLDLKGTFKLSLHCDQLHVDPENFRLGNVIVVVLARRLGHDFNPVQAAFQ
KVVAGVANALAHKYH

>d1fhjb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Maned wolf (Chrysocyon brachyurus)}

VHLTAEKSLVSGLWGKVNVEVGGEALGRLLVYPWTQRFFDSFGDLSTPDAVMSNAKVKAHGK
VLNSFSDDLKHLNLDLKGTFKLSLHCDKLHVDPENFKLLGNVLCVLAHHFGKEFTPVQAAYQK
VVAGVANALAHKYH

>d1jebb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Mouse (Mus musculus)}

VHLTDAEKAASGLWGKVNVEVGGEALGRLLVYPWTQRYFDSFGDLSSASAIMGNAKVKAHGK
KVITAFNDGLNHLDSLKGTFAALSELHCDKLHVDPENFRLGNMIVIVLGHHLGKDFTPAAQAAFQK
VVAGVAAALAH

>d1hbrb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Chicken (Gallus gallus)}

VHWTAEKQLITGLWGKVNVAECGAEALARLLVYPWTQRFFASFGNLSSPTAILGNPMVRAHGK
VLTSFGDAVKNLDNIKNTFSQSELHCDKLHVDPENFRLGDILIVLAAHFSKDFTEPCQAAWQKLV
RVVAHALARK

>d1a4fb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Bar-headed goose (Anser indicus)}

VHWSAEEKQLITGLWGKVNVAECGAEALARLLVYPWTQRFFSSFGNLSSPTAILGNPMVRAHGK
VLTSFGDAVKNLDNIKNTFAQLSELHCDKLHVDPENFRLGDILIVLAAHFAKEFTPDCQAAWQKL
VRVVAHALARKYH

>d1outb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Trout (Oncorhynchus mykiss)}

VEWTDKERSIISAVWGKVNIDEIGPLALARVLVYPWTQRYFGSFGNVSTPAAIMGNPKVAAHGKVV
CGALDKAVKNMGNILATYKSLSETHANKLFVDPDNFRVLADVLTIVIAAKFGASFTPEIQATWQKFM
KVVVAAMGSRYF

>d1pbb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Antarctic fish (Pagothenia bernacchii)}

VEWTDKERSIISDIFSHMDYDDIGPKALSRLVYPWTQRHFSGFGNLYNAEAIIGNANVAAHGKVL
HGLDRGVKNMDNIAATYADLSTLHSEKLVDPDNFKLLSDCITIVLAAKMGHAFTAETQGAQKFL
AVVVSALGKQYH

>d1cg5b_ a.1.1.2 (B:) Hemoglobin, beta-chain {Cartilaginous fish akabei (Dasyatis akajei)}

VKLSAQEHYIKGVWVDVHKQITAKALERVVYPWTTRLFSKLQGLFSANDIGVQGHADKVQRA
LGEAIDDLKKEINFQNLGKHQEIQVDTQNFKLLGQTFMVELALHYKKTFRPKEHAAAYKFFRLVA
EALSSNYH

>d1t1nb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Fish (Trematomus newnesi)}

VEWTDKERSIISDIFSHMDYDDIGPKALSRLVYPWTQRYFSGFGNLYNAEGIMSNANVAAHGKVV
LHGLDRGMKNMDNIADAYTDLSTLHSEKLVDPDNFKLLSDCITIVLAAKMGHAFTAETQGAQKFL
LAAVVSALGKQYH

>d1spgb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Teleost fish (Leiostomus xanthurus)}

VDWTD AERAAIKALWGKIDVGEIGPQALSRLIVYPWTQRHFKGFNISTNAAILGNAKVAEHGKTV
MGGLDRAVQNMDNIKNVYKQLSIKHSEKIHVDPDNFRLLGEIITMCVGAKFGPSAFTPEIHEAWQKF
LAVVVSALGRQYH

>d1gcvb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Houndshark (*Mustelus griseus*)}

VHWTQEERDEISKTFQGTDMKTVVTQALDRMFKVYPWTNRYFQKRTDFRSSIHAGIVVGALQDAV
KHMDDVKTFLFKDLSKKHADDLHVDPGSFHLTDCIIVELAYLRKDCFTPHIQGIWDFKFFEVVIDAIS
KQYH

>d1ch4a_ a.1.1.2 (A:) Chimeric hemoglobin beta-alpha {Synthetic, based on *Homo sapiens*
sequence}

VHLTPEEKSAVTALWGKVVNDEVGGEALGRLLVYPWTQRFESFGDLSTPDAVMGNPKVKAHGK
KVLGAFSDGLAHLNLDKGTFFATLSELHCDKLRVDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLTK
VLASVSTVLTSKYR

>d1it2a_ a.1.1.2 (A:) Hagfish hemoglobin {Inshore hagfish (*Eptatretus burgeri*)}

PIIDQGPLPTLDGDKKAINKIWPKIYKEYEQYSLNILLRFLKCFPQAQASFPKFSTKKSLEQDPEVK
HQAVVIFNKVNEIINSMDNQEEIISLKDLSQKHKTVFKVDSIWFKELSSIFVSTIDGGAEFEKLFISI
LLRSAY

>d2lhb_ a.1.1.2 (-) Lamprey globin {Sea lamprey (*Petromyzon marinus*)}

PIVDTGSVAPLSAAEKTKIRSAWAPVYSTYETSGVDILVKFFTSTPAAQEFFPKFKGLTTADELKKSD
VRWHAERIINAVDDAVASMDDEKMSMKLRNLSGKHAKSFQVDPEYFKVLA AVIADTVAAGDAGFE
KLMSMICILLRSAY

>d1ash_ a.1.1.2 (-) *Ascaris* hemoglobin, domain 1 {Pig roundworm (*Ascaris suum*)}

ANKTRELCKMSLEHAKVDTSNEARQDGDIDLYKHMFFENYPLRKYFKSREEYTAEDVQNDPFFAKQG
QKILLACHVLCATYDDRETFNAYTRELLDRHARDHVHMPPEVWTD FWKLFEEYLGKKTTLDEPTK
QAWHEIGREFAKEINK

>d1itha_ a.1.1.2 (A:) Hemoglobin {Innkeeper worm (*Urechis caupo*)}

GLTAAQIKAIQDHWFLNIKGLQAAADSIFFKYLTAYPGDLAFFHKFSSVPLYGLRSNPAYKAQTLTVI
NYLDKVV DALGGNAGALMKAKVPSHDAMGITPKHFGQLLKLVGGVFQEEFSADPTTVAAWGDAAG
VLVAAMK

>d1h1b_ a.1.1.2 (-) Hemoglobin, different isoforms {Sea cucumber (*Caudina* (*Molpadia*)
arenicola)}

GGTLAIQAQGDTLAQKKIVRKTWHQLMRNKTSFVTDVFIRIFAYDPSAQNKFPQMAGMSASQLRS
SRQMQAHAIRVSSIMSEYVEELSDILPELLATLARTHDLNKGADHYNLFAKVLMEALQAE LGSDF
NEKTRDAWAKAFSVVQAVLLVKHG

>d1h1m_ a.1.1.2 (-) Hemoglobin, different isoforms {Sea cucumber (*Caudina* (*Molpadia*)
arenicola)}

GATQSFQSVGDLTPAEKDLIRSTWDQLMTHRTGFVADV FIRIFHNDPTAQRKFPQMAGLSPAELRTS
RQMHAHAIRVSALMTTYIDEMDTEVLPELLATLTRTHDKNHVGGKNYDLFGKVLMEAIKAE LGVGF
TKQVHDAWAKTFAIVQGV LITK HAS

>d1vhba_ a.1.1.2 (A:) Bacterial dimeric hemoglobin {*Vitreoscilla stercoraria*}

LDQQTINI KATVPVLKEHGVTITTTFYKNLFAKHPEVRPLFDMGRQESLEQPKALAMTVLAAAQNI
ENLPAILPAVKKIAVKHCQAGVAAAHYPIVGQELLGAIKEVLGDAATDDILD AWGKAYGVIADVFIQVE
ADLYAQAV

>d1cxa1 a.1.1.2 (A:1-150) Flavohemoglobin, N-terminal domain {*Alcaligenes eutrophus*}

MLTQKTKDIVKATAPVLAEHGYDIKCFYQRMFEAHPELKNVFNMAHQEQGQQQALARAVYAYAE

NIEDPNSLMAVLKNIANKHASLGVKPEQYPIVGEHLLAAIKEVLGNAATDDIISAWAQAYGNLADVL
MGMESELYERSAEQPGG

>d1ew6a_ a.1.1.2 (A:) Dehaloperoxidase {Marine worm (Amphitrite ornata)}
GFKQDIATIRGDLRTYAQDIFLAFLNKYPDERRYFKNYVGKSDQELKSMKFGDHTKVFNLMMEV
ADRATDCVPLASDANTLVQMKQHSSLTGNFEKLFVALVEYMRASGQSFDSQSWDRFGKNLVSALS
SAGMK

>d1phna_ a.1.1.3 (A:) Phycocyanin {Red alga (Cyanidium caldarium)}
MKTPTTEAIAAADNQGRFLSNTLQAVNGRYQRAAASLEAARSLTNAERLINGAAQAVYSKFPYTS
QMPGPQYASSAVGKAKCARDIGYYLRMVTYCLVVGTTGPMDEYLIAGLEEINRTFDLSPSWYVEALN
YIKANHGLSGQAANEANTYIDYAINALS

>d1phnb_ a.1.1.3 (B:) Phycocyanin {Red alga (Cyanidium caldarium)}
MLDAFAKVVAQADARGEFLSNTQLDALS KMVSEGNKRLDVVN RITSNASAIVTNAARALFSEQPQLI
QPGGNAYTNRMAACL RDMEIILRYVSYAIIAGDSSILDDRCLNGLRETYQALGVP GASVAVGIEKMK
DSAIAIANDPSGITGDCSALMAEVGTYFDRAATAVQ

>d1f99a_ a.1.1.3 (A:) Phycocyanin {Red alga (Polysiphonia urceolata)}
MKTPLTEAIAAADSQGRFLSNTLQVVNGRYNRATSSLEAAKALTANADRLISGAANAVYSKFPYTT
QMPGPNYSSTAIGKAKCARDIGYYLRMVTYCLVVGTTGPMDDYLVAGLEEINRTFELSPSWYIEALKY
IKNNHGLSGDVANEANTYIDYAINALS

>d1f99b_ a.1.1.3 (B:) Phycocyanin {Red alga (Polysiphonia urceolata)}
MLDAFAKVVAQADARGEFLSNTQIDALLAIVSEGNKRLDVVNKITNNASAIVTNAARALFAEQQLIS
PGGNAYTSRRMAACL RDMEIVLRYVSYAMIAGDASVLD DRCLNGLRETYQALGTP GASVAVAIQKMK
DAALALVNDTTGTPAGDCASLVAEIATYFDRAAAA VA

>d1cpca_ a.1.1.3 (A:) Phycocyanin {Cyanobacterium (Fremyella diplosiphon)}
MKTPLTEAVAAADSQGRFLSSTEIQAFGRFRQASASLAAKALTEKASSLASGAANAVYSKFPYTT
QNGPNFASTQTGKDKCVRDIGYYLRMVTYCLVVGTTGPLDDYLIGGIAEINRTFDLSPSWYVEALKYI
KANHGLSGDPAVEANSYIDYAINALS

>d1cpcb_ a.1.1.3 (B:) Phycocyanin {Cyanobacterium (Fremyella diplosiphon)}
MLDAFAKVVSQADARGEYLSGSQIDALSALVADGNKRM DVVN RITGNSSTIVANAARSLFAEQQLIA
PGGNAYTSRRMAACL RDMEIILRYVTYAIFAGDASVLD DRCLNGLKETYLALGTPGSSVAVGVQKMK
DAALAIAGDTNGITRGDCASLMAEVASYFDKAASAVA

>d1i7ya_ a.1.1.3 (A:) Phycocyanin {Synechococcus vulcanus}
MKTPTTEAIAAADTQGRFLSNTLQAVDGRFKRAVASMEAAARALTNNAQSLIDGAAQAVYQKFPYTT
TMQGSQYASTPEGKAKCARDIGYYLRMITYCLVAGGTGPMDEYLIAGLSEINSTFDLSPSWYIEALKYI
KANHGLTGQAAVEANAYIDYAINALS

>d1i7yb_ a.1.1.3 (B:) Phycocyanin {Synechococcus vulcanus}
MLDAFAKVVAQADARGEFLTNAQFDALS NLVKEGNKRLDAVN RITSNASTIVANAARALFAEQQLI
QPGGNAYTNRMAACL RDMEIILRYVTYAILAGDSSVLD DRCLNGLRETYQALGTPGSSVAVAIQKM
KDAIAIANDPNGITPGDCSALMSEIAGYFDRAAAA VA

>d1gh0a_ a.1.1.3 (A:) Phycocyanin {Spirulina platensis}
MKTPLTEAVSVADSQGRFLSSTEIQVAFGRFRQAKAGLEAAKALTSKADSLISGAAQAVYNKFPYTTQ
MQGPNYAADQRGKDKCARDIGYYLRMVTYCLIAGGTGPMDEYLIAGIDEINRTFELSPSWYIEALKYI
KANHGLSGDAAVEANSYLDYAINALS

>d1gh0b_ a.1.1.3 (B:) Phycocyanin {Spirulina platensis}
MFDAFTKVVSQADTRGEMLSAQIDALSQMVAESNKRLDVVN RITSNASTIVSNAARSLFAEQQLI

APGGNAYTSRRMAACLRDMEIILRYVITYAVFAGDASVLEDRCLNGLRETYLALGTPGSSVAVGVGKM
KEAALAIVNDPAGITPGDCSALASEIAGYFDRAAAAVS
>d1alla_ a.1.1.3 (A:) Allophycocyanin {Spirulina platensis}
SIVTKSIVNADAEARYLSPGELDRIKSFVTSGERVRIAETMTGARERIIKQAGDQLFGKRPDVVSPGG
NAYGADMTATCLRDLDYLLRLITYGIVAGDVTPIEEIGVVGVREMYKSLGTPIEIAIEGVRAMKSVATS
LLSGADAAEAGSYFDYLIGAMS
>d1allb_ a.1.1.3 (B:) Allophycocyanin {Spirulina platensis}
MQDAITSVINSSDVQGKYLDASAIQKLKAYFATGELRVRAATTISANAANIVKEAVAKSLLYSDVTRPG
GNMYTTRRYAACIRDLDYLLRYATYAMLADGPSILDERVLNGLKETYNLSLGVPIGATVQAIQAMKEVT
AGLVGGGAGKEMGIYFDYICSGLS
>d1b33a_ a.1.1.3 (A:) Allophycocyanin {Cyanobacterium (Mastigocladus laminosus)}
SIVTKSIVNADAEARYLSPGELDRIKSFVSSGEKRLRIAQILTDNRERIVKQAGDQLFQKRPDVVSPGG
NAYGQEMTATCLRDLDYLLRLITYGIVAGDVTPIEEIGIVGVREMYKSLGTPIDAVAAGVSAMKNVASS
ILSAEDAAEAGAYFDYVAGALA
>d1b33b_ a.1.1.3 (B:) Allophycocyanin {Cyanobacterium (Mastigocladus laminosus)}
MQDAITAVINSSDVQGKYLDAALEKLSYFSTGELRVRAATTIAANAAIVKEAVAKSLLYSDITRPG
GNMYTTRRYAACIRDLDYLLRYATYAMLADGPSILDERVLNGLKETYNLSLGVPISATVQAIQAMKEVT
ASLVGPDAGKEMGVYFDYICSGLS
>d1liaa_ a.1.1.3 (A:) Phycoerythrin {Red alga (Polysiphonia urceolata)}
MKSVITTTISAADAAGRYPSTSDLQSVQGNIQRAAARLEAAEKLGSNHEAVVKEAGDACFSKYGYNK
NPGEAGENQEKINKCYRDIDHYMRLINYTLVVGGTGPLDEWGIAGAREVYRTLNLPSAAIAAFVFT
RDRLCIPRDMSAQAGVEFCTALDYLINSLS
>d1liab_ a.1.1.3 (B:) Phycoerythrin {Red alga (Polysiphonia urceolata)}
MLDAFSRVVNSDSKAAYVSGSDLQALKTFINDGNKRLDAVNYIVSNSSCIVSDAISGMICENPGLITP
GGNCYTNRMAACLRDGEIILRYVSYALLAGDASVLEDRCLNGLKETYIALGVPTNSTVRAVSIMKAA
AVCFISNTASQRKVEVIEGDCSALASEVASYCDRVAAVS
>d1b8da_ a.1.1.3 (A:) Phycoerythrin {Red alga (Griffithsia monilis)}
MKSVITTTISAADAAGRFSSDLESIQGNIQRAAARLEAAQKLSGNHEAVVKEAGDACFAKYSYLKN
AGEAGDSPEKINKCYRDIDHYMRLINYSLVGGTGPVDEWGIAGSREVYRALNLPGSAYIAAFTRD
RLCVPRDMSSQAGVEFTSALDYVINSLS
>d1b8db_ a.1.1.3 (B:) Phycoerythrin {Red alga (Griffithsia monilis)}
MLDAFSRVVVTSDAKAAYVGGSDLQSLKSFINDGNKRLDAVNYIVSNASCIVSDAVSGMICENPGLIA
PGGNCYTNRMAACLRDGEIILRYVSYALLAGDSSVLEDRCLNGLKETYIALGVPTASSRAVSIMKAT
ATAFITNTASGRKVEVAAGDCQALQAEAAASYFDKVGSSID
>d1eyxa_ a.1.1.3 (A:) Phycoerythrin {Red algae (Gracilaria chilensis)}
MKSVITTVISAADSAGRFSSDLESVQGNIQRASARLEAAEKLASNHEAVVKEAGDACFGKYGYLKN
PGEAGENQEKINKCYRDIDHYMRLVNYSLVIGGTGPLDEWGIAGAREVYRTLNLPTSAYIAAFTRD
RLCGPRDMSAQAGVEYSTALDYIINSLS
>d1eyxb_ a.1.1.3 (B:) Phycoerythrin {Red algae (Gracilaria chilensis)}
MLDAFSRVISNADAKAAYVGGSDLQALRTFISDGNKRLDAVNYIVSNSSCIVSDAISGMICENPGLITP
GGNCYTNRMAACLRDGEIILRYISYALLAGDSSVLEDRCLNGLKETYIALGVPTNSTVRAVSIMKAA
VGAFISNTASQRKGEVIEGDCSALAAEIASYCDRISAAVS
>d1qgwc_ a.1.1.3 (C:) Phycoerythrin {Cryptophyte (Rhodomonas sp.), cs24}
DAFSRVVTNADSKAAYVGGADLQALKKFISEGNKRLDSVNSIVSNASCIVSDAVSGMICENPSLISPSG

NCYTNRRMAACL RDGEIILRYVSYALLSGDASVLEDRCLNGLKETYSSLGVPANSNARAVSIMKACAV
AFVNN TASQKKLSTPQGDCSGLASEVGGYFDKVTAAIS
>d1fumb1 a.1.2.1 (B:106-243) Fumarate reductase iron-sulfur protein, C-terminal domain
{*Escherichia coli*}
MTHFIESLEAIKPYIIGNSRTADQGTNIQTPAQMAKYHQFSGCINCGLCYAACPQFGLNPEFIGPAAIT
LAHRYNEDSRDHGKKERMAQLNSQNGVWSCTFVGYCSEVCPKHVDPAAAIQQGKVESKDFLIATL
KPR
>d1qlab1 a.1.2.1 (B:107-239) Fumarate reductase iron-sulfur protein, C-terminal domain
{*Wolinella succinogenes*}
TGNWFNGMSQRVESWIHAQKEHDISKLEERIEPEVAQEVFELDRCIIEGCCIAACGTKIMREDFVGA
AGLNRVRFMIDPHDERTDEYYELIGDDDGVFGCMTLLACHDVC PKNLPLQSKIAYLRRKMVSVN
>d1h7wa1 a.1.2.2 (A:2-183) Dihydropyrimidine dehydrogenase, N-terminal domain {*Pig*
(*Sus scrofa*)}
APVLSKDVADIESILALNPRTQSHAALHSTLAKKLDKHKHWKRNPDKNCFHCEKLENNFDDIKHTTL
GERGALREAMRCLKCADAPCQKSCPTHLDIKSFITSISNKNYGA AKMIFSDNPLGLTCGMVCPTS DL
CVGGCNLYATEEGSINIGGLQQFASEVFKAMNIPQIRNPCLPSQEKMP
>d1grj_1 a.2.1.1 (2-79) GreA transcript cleavage protein, N-terminal domain {*Escherichia*
coli}
QAIPMTLRGAEKLREELDFLKS VRRPEIIAAIAEAREHGDLKENAEYHAAREQQGFCEGRIKDIEAKL
SNAQVIDVTK
>d1jj2u_ a.2.2.1 (U:) Ribosomal protein L29 (L29p) {*Archaeon Haloarcula marismortui*}
TVLHVQEIRDMPAEREAELDDLKTELLNARAVQAAGGAPENPGRIKELRKA IARIKTIQGEED
>d1fpoa1 a.2.3.1 (A:1-76) HSC20 (HSCB), N-terminal (J) domain {*Escherichia coli*}
MDYFTFLGLPARYQLDTQALSLRFQDLRQYHPDKFASGSQAEQLAAVQQSATINQAWQTLRHPLM
RAEYLLSLHG
>d1hdj_ a.2.3.1 (-) HSP40 {*Human (Homo sapiens)*}
MGKDYQTLGLARGASDEEIKRAYRRQALRYHPDKNKEPGAEEKFKEIAEAYDVLSDPRKREIFDRY
GEEGLKSGC
>d1xbl_ a.2.3.1 (-) DnaJ chaperone, N-terminal (J) domain {*Escherichia coli*}
AKQDYEILGVSKTAEEREIRKAYKRLAMKYHPDRNQGDKEAEAKFKEIKEAYEVLTD SQKRAAYDQ
YGHAAFEQ
>d1fafa_ a.2.3.1 (A:) Large T antigen, the N-terminal J domain {*Murine polyomavirus*}
MDRVLSRADKERLLELLKLPRQLWGFGRMQAYKQQSLLLHPDKGGSHALMQELNSLWGTFKTE
VYNLRMNLGGTG FQ
>d1gh6a_ a.2.3.1 (A:) Large T antigen, the N-terminal J domain {*Simian virus 40, Sv40*}
SHMREESLQ LMDLLGLERSAWGNIPLMRKAYLKKCKEFHPDKGGDEEKMKKMNTLYKKMEDGVK
YAHQPDFGGFWDATEIPT YGTDEWEQWNAFNEENLFCSEEMPSSDDEAT
>d1du2a_ a.2.4.1 (A:) Theta subunit of DNA polymerase III {*Escherichia coli*}
MLKNLAKLDQTEM DKVNVDLAAAGVAFKERYNMPVIAEAVEREQPEHLRSWFRERLIAHRLASVN
LSRLPYEPK LK
>d1fxkc_ a.2.5.1 (C:) Prefoldin alpha subunit {*Archaeon Methanobacterium*
thermoautotrophicum}
AALAEIVAQLNIYQSQVELIQQQMEAVRATISELEILEKTLSDIQGKDGSETLVPVGAGSFIKAE LKDT S
EVIMSVGAGVAIKKNFEDAMESIKSQKNELESTLQKMGENLRAITDIMMKLSPQAEELLAAVA

>d1fxka_ a.2.5.1 (A:) Prefoldin beta subunit {Archaeon Methanobacterium thermoautotrophicum}
QNVQHQLAQFQQQQQAISVQKQTVEMQINETQKALEELSRAADDAEVYKSSGNILIRVAKDELTEELQEKLETLQLREKTIERQEERVMKKLQEMQVNIQEAMK

>d1cxzb_ a.2.6.1 (B:) Effector domain of the protein kinase pkn/prk1 {Human (Homo sapiens)}
WSLLEQLGLAGADLAAPGVQQLELERERLRREIRKELKKEGAENLRRATTDLGRSLGPVELLLRGSSRRLDLLHQQLQELHAHV

>d1seta1 a.2.7.1 (A:1-110) Seryl-tRNA synthetase (SerRS) {Thermus thermophilus, strain hb27}
MVDLKRRLRQEPEVFHRAIREKGVALLDLEALLALDREVQELKKRLQEVQTERNQVAKRVPKAPPEEK EALIARGKALGEEAKRLEEALREKEARLEALLQVPLPPWPGAP

>d1eiya1 a.2.7.2 (A:6-84) Phenylalanyl-tRNA synthetase (PheRS) {Thermus thermophilus}
LAAIQNARDLEELKALKARYLGKKGLLTQEMKGLSALPLEERRKRGQELNAIKAALAALEAREKAL EEAALKEALERE

>d1a36a1 a.2.8.1 (A:641-712) Eukaryotic DNA topoisomerase I, dispensable insert domain {Human (Homo sapiens)}
EKSMNLTQKIDAKKEQLADARRDLKSAKADAKVMKDAKTKKVVESKKAQVQRLEEQLMKLEVQ ATDREENK

>d1e52a_ a.2.9.1 (A:) C-terminal, UvrC-binding domain of UvrB {Escherichia coli}
LEPDNVPMDMSPKALQQKIHELEGLMMQHAQNLEFEEAAQIRDQLHQLRELFIAS

>d1qoja_ a.2.9.1 (A:) C-terminal, UvrC-binding domain of UvrB {Escherichia coli}
SPKALQQKIHELEGLMMQHAQNLEFEEAAQIRDQLHQLRELFIAS

>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)}
DMLDLGAAKANLEKAQSELLGADEATRAEIQUIRIEANEALVKAL

>d1idsa1 a.2.11.1 (A:2-85) Fe superoxide dismutase (FeSOD) {Mycobacterium tuberculosis}
AEYTLPLDLWDYGALEPHISGQINELHHSKHHATYVKGANDAVAKLEEARAKEDHSAILLNEKNLA FNLAGHVNHTIWWKNLSP

>d1dt0a1 a.2.11.1 (A:1-83) Fe superoxide dismutase (FeSOD) {Pseudomonas ovalis}
AFELPPLPYAHDALQPHISKETLEFHHDKHHNTYVVNLNLPVPGTEFEGKTLEEIVKTSSGGIFNNA AQVWNHTFYWNCLSPN

>d3sdpa1 a.2.11.1 (A:5-83) Fe superoxide dismutase (FeSOD) {Pseudomonas ovalis}
PPLPYAHDALQPHISKETLEYHHDKHHNTYVVNLNLPVPGTPEFEGKTLEEIVKSSSGGIFNNAQV WNHTFYWNCLSP

>d1isaa1 a.2.11.1 (A:1-82) Fe superoxide dismutase (FeSOD) {Escherichia coli}
SFELPALPYAKDALAPHISAETIEYHYGKHHQTYVTNLNLIKGTAFEGKSLEEIIRSSEGGVFNNAQ VWNHTFYWNCLAP

>d1coja1 a.2.11.1 (A:2-90) Fe superoxide dismutase (FeSOD) {Aquifex pyrophilus}
VHKLEPKDHLKPQNLEGISNEQIEPHFEAHYKGYVAKYNEIQEKLADQNFADRSKANQNYSEYREL KVEETFNYMGVVLHELYFGMLTP

>d1sssa1 a.2.11.1 (A:4-92) Fe superoxide dismutase (FeSOD) {Archaeon Sulfolobus solfataricus}
 IQFKKYELPPLPYKIDALEPYISKDIIDVHYNGHHKGYVNGANSLLERLEKVVKGDLQTGQYDIQGIIR
 GLTFNINGHKLHALYWENMA

>d1b06a1 a.2.11.1 (A:3-92) Fe superoxide dismutase (FeSOD) {Archaeon Sulfolobus acidocaldarius}
 VIQLKRYEFPQLPYKVDALPYISKDIIDVHYNGHHKGYVNGANSLLDRLEKLIKGDLPQGQYDLQGI
 LRGLTFNINGHKLHAIYWNNMA

>d1ap6a1 a.2.11.1 (A:1-83) Mn superoxide dismutase (MnSOD) {Human (Homo sapiens)}
 KHSPLDLPYDYGALEPHINAQIMQLHHSKHHAFAVNNLNVTTEKYQEALAKGDVTAQIALQPALKF
 NGGGHINHSIFWTNLSP

>d1kkca1 a.2.11.1 (A:14-97) Mn superoxide dismutase (MnSOD) {Aspergillus fumigatus}
 QQYTLPLPYDALQPYISQQIMELHHKHHQTYVNGLNAALEAQKAAEATDVPKLVSVQQAIF
 FNGGGHINHSIFWKNLAP

>d1i0ha1 a.2.11.1 (A:1-90) Mn superoxide dismutase (MnSOD) {Escherichia coli}
 SYTLPSLPYAYDALEPHFDKQTMEIHHTKHHQTYVNNANALESLEPEFANLPVEELITKLDQLPADK
 KTVLRNNAAGGHANHSIFWKNLAP

>d1mnga1 a.2.11.1 (A:1-92) Mn superoxide dismutase (MnSOD) {Thermus thermophilus}
 PYPFKLPDLGYPYEALEPHIDAKTMEIHHQKHHGAYVTNLNAALEKYPYHLHGVEVEVLLRHLAALP
 QDIQTAVRNNGGGHLNHSIFWKNLAP

>d1bsma1 a.2.11.1 (A:1-86) Cambialistic superoxide dismutase {Propionibacterium shermanii}
 AVYTLPELPYDYSALPYISGEIMELHHDKHHKAYVDGANTALDKLAEARDKADFGAINKLEKDLAF
 NLAGHVNHVSFVWKNMAPKG

>d1qna1 a.2.11.1 (A:1-84) Cambialistic superoxide dismutase {Porphyromonas gingivalis}
 MTHELISLPYAVDALAPVISKETVEFHGKHLKTYVDNLNKLIGTEFENADLNTIVQKSEGGIFNNA
 GQTLNHNLYFTQFRPG

>d1dava_ a.139.1.1 (A:) Cellulosome endoglucanase SS {Clostridium thermocellum}
 MSTKLYGDVNDGKVNSTDAVALKRYVLRSGISINTDNADLNEDGRVNSTDGILKRYILKEIDTLPY
 KNG

>d1h9ea_ a.140.1.1 (A:) Thymopoietin, LAP2 {Human (Homo sapiens)}
 PEFLEDPSVLTKDKLSELVANNVTLPAGEQRKDVYVQYLYLQHLTARNRPPLPAGT

>d1h9fa_ a.140.1.1 (A:) Thymopoietin, LAP2 {Human (Homo sapiens)}
 RQEDKDDLVDTELTNEDLLDQLVKYGVNPGPIVGTTRKLYEKLLKLREQGTESRSS

>d1jeia_ a.140.1.1 (A:) Inner nuclear membrane protein emerlin {Human (Homo sapiens)}
 DNYADLSDELTTLLRRYNIPHGPPVVGSTRRLYEKKIFEYETQRRRLSPPSSS

>d1jeqa1 a.140.2.1 (A:559-609) DNA binding C-terminal domain of ku70 {Human (Homo sapiens)}
 YSEEELKTHISKGTGKFTVPMLKEACRAYGLKSGKQELLEALTKHFQD

>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}
VDAAEAVVQQKCISCHGGDLTGASAPAIKAGANYSEEEILDIIILNGQGGMPGGIAKGAEAEVAAWLA
EKK

>d1ctj_ a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553) {Monoraphidium braunii}
EADLALGKAVFDGNCAACHAGGGNNVIPDHTLQKAAIEQFLDGGFNIEAIVYQIENGKAMPWDG
RLDEDEIAGVAAYVYDQAAGNKW

>d1c53_ a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553) {Desulfovibrio vulgaris, different strains}

ADGAALYKSCVCHGADGSKQAMGVGHAVKGQKADELFKKLGADGSYGGEKKAVMTNLVKRYS
DEEMKAMADYMSKL

>d2dvh_ a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553) {Desulfovibrio desulfuricans}

ADGAALYKSCIGCHGADGSKAAMGSAKPVKGQGAEELYKKMKGYADGSYGGGERKAMMTNAVKKAS
DEELKALADYMSKL

>d1cyi_ a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553) {Chlamydomonas reinhardtii}

ADLALGAQVFNNGCAACHMGGGRNSVMPEKTLDKAALEQYLDGGFKVESIIYQVENGKAMPAWAD
RLSEEEIQAVAEYVFKQATDAAWK

>d1c6s_ a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553) {Cyanobacterium (Synechococcus elongatus)}

ADLANGAKVFSNGCAACHMGGGNVVMANKTLKKEALEQFGMYSEDAIYQVQHGNAMPAGRL
TDEQIQDVAAYVLDQAAKGWAG

>d1f1fa_ a.3.1.1 (A:) Cytochrome c6 (synonym: cytochrome c553) {Arthrospira maxima}
DVAAGASVFSANCAACHMGGGRNVIVANKTSLKSDLAKYLKGFDDDAVAAYVAVQVTNGKNAMPGFNG
RLSPLQIEDVAAYVVDQAEKGW

>d1c6ra_ a.3.1.1 (A:) Cytochrome c6 (synonym: cytochrome c553) {Green alga (Scenedesmus obliquus)}

ADLALGKQTFEANCAACHAGGNNVIPDHTLRKAAMEQFLQGGFNLEAITVQVENGKAMPASG
TLDDDEIAAVAYVYDQASGDKW

>d1gdva_ a.3.1.1 (A:) Cytochrome c6 (synonym: cytochrome c553) {Red alga (Porphyra yezoensis)}

ADLDNGEKVFSANCAACHAGGNNAIMPKTLKKDVLEANSMTIDAITYQVQNGKNAMPAGGRL
VDEDIEDAANYVLSQSEKGW

>d1c52_ a.3.1.1 (-) Cytochrome c552 {Thermus thermophilus}

QADGAKIYAQCAGCHQNGQGIPGAFPLAGHVAEILAKEGGREYLILVLLYGLQGQIEVKGMKYNGV
MSSFAQLKDEEIAAVLNHIATAWGDAAKVKGFKPFATAEEVKLRAKLTTPQVLAERKKLGLK

>d1cnoa_ a.3.1.1 (A:) Cytochrome c552 {Pseudomonas nautica}

AGDIEAGKAKAAVCAACHGQNGISQVPIYPNLAGQKEQYLVAALKAYKAGQRQGGQAPVMQGGQATA
LSDADIANLAAYYASNPAAA

>d1ql3a_ a.3.1.1 (A:) Cytochrome c552 {Paracoccus denitrificans}

ADPAAGEKVFVKCKACHKLDGNDGVPHLNGVVGRTVAGVDGFNYSDPMKAHGGDWTPEALQEFL

TNPKAVVKGTKMAFAGLPKIEDRANLIAYLEGQQ
>d1ayg_ a.3.1.1 (-) Cytochrome c552 {Hydrogenobacter thermophilus}
NEQLAKQKGCMAHDLDKAKKVGPAYADVAKKYAGRKDAVDYLAGKIKKGGSGVWGSVPMPPQNVT
DAEAKQLAQWILSIK
>d1a56_ a.3.1.1 (-) Cytochrome c552 {Nitrosomonas europaea}
DADLAKNNCIACHQVETKVVGPALKDIAAKYADKDDAATYLAGKIKGSSGVWQIPMPPNVNVS
DADAKALADWILTLK
>d1e29a_ a.3.1.1 (A:) Photosystem II associated cytochrome c549 {Synechocystis sp., pcc
6803}
VELTESTRTIPLDEAGGTTTTLTAQFTNGQKIFVDTCTQCHLQGKTKTNNVSLGLADLAGAEP
RRD
NVLALVEFLKNPKSYDGEDDYSELHPNISRPIYEMRNYTEDDIFDVAGYTLIAPKLD
ERWGGTIYF
>d1f1ca_ a.3.1.1 (A:) Photosystem II associated cytochrome c549 {Arthrospira maxima}
LTEELRTFPINAQGD TAVLSLKEIKKGQVFNAACAQCHALGVTRTNPDVNLSPEALALATPP
RDNIA
ALVDYIKNPTTYDGFVEISELHPSLKSSDIFPKMRNISEDDLNVAGYILLQPKVRGEQWG
>d1ycc_ a.3.1.1 (-) Mitochondrial cytochrome c {Baker's yeast (Saccharomyces cerevisiae)}
TEFKAGSAKKGATLFKTRCLQCHTVEKGGPHKVGPNLHGIFGRHSGQAEGYSYTDANIKKNV
LWDE
NNMSEYLTNPKKYIPGTKMAFGGLKKEKDRNDLITYLKKACE
>d1yeb_ a.3.1.1 (-) Mitochondrial cytochrome c {Baker's yeast (Saccharomyces cerevisiae)}
TEFKAGSAKKGATLFKTRCQCCHTIEEGGPNKVGPNLHGIFGRHSGQVKGYSYTDANINKN
VKWDE
DSMSEYLTNPKKYIPGTKMAFGGLKKEKDRNDLITYLKKACE
>d1ytc_ a.3.1.1 (-) Mitochondrial cytochrome c {Baker's yeast (Saccharomyces cerevisiae)}
AKESTGFKPGSAKKGATLFKTRCQCCHTIEEGGPNKVGPNLHGIFGRHSGQVKGYSYTD
AIINKNVK
WDEDSMSEYLTNPKKYIPGTKMAFAGLKKKEKDRNDLITYMTKAAK
>d1wejf_ a.3.1.1 (F:) Mitochondrial cytochrome c {Horse (Equus caballus)}
GDVEKGGKIFVQKCAQCHTVEKGGKHKTGPNLHGLFGRKTGQAPGFTYTDANKNKGITW
KEETLM
EYLENPKKYIPGTKMIFAGIKKKTEREDLIAYLKKATNE
>d1ccr_ a.3.1.1 (-) Mitochondrial cytochrome c {Rice embryos (Oryza sativa)}
ASFSEAPPGNPKAGEKIFKTKCAQCHTVDKGAGHKQGNLNGLFGRQSGTTPGYSYSTADKN
MAVI
WEENTLYDYLLNPKKYIPGTKMVFPGLKKPQERADLISYLKEATS
>d5cytr_ a.3.1.1 (R:) Mitochondrial cytochrome c {Tuna (Thunnus alalunga and Thunnus
thynnus)}
GDVAKGKKTFFVQKCAQCHTVENGGKHKVGPNLWGLFGRKTGQAEGYSYTDANKSKGIVW
NNDTL
MEYLENPKKYIPGTKMIFAGIKKKGERQDLVAYLKSATS
>d1qn2a_ a.3.1.1 (A:) Cytochrome ch {Methylobacterium extorquens}
EGDAAAGEKAFAPCKACHNFEKNGVGPTLKGVVGAKAGEGADGYAFSDALKKSGLTWDQ
ADLKQW
LADPCKKVPGTKMVFPGISDPKKVDDIIAYLTKK
>d3c2c_ a.3.1.1 (-) Cytochrome c2 {Rhodospirillum rubrum}
EGDAAAGEKVSCKLACHTFDQGGANKVGPNLFGVFENTA AHKDNAYSESYTEMKAKGLT
WTEA
NLAAYVKNPKAFVLEKSGDPKAKSKMTFKLTKDDEIENVIAYLTKL
>d1c2ra_ a.3.1.1 (A:) Cytochrome c2 {Rhodobacter capsulatus}
GDAKGEKEFNKCKTCHSIIAPDGTEIVKGAKTGNLYGVVGRTAGTYPEFKYKDSIVALG
ASGFAWT
EEDIATYVKDPGAFLEKLDKAKTGMFAKFLAKGGEDVAAYLASVVK
>d1cxc_ a.3.1.1 (-) Cytochrome c2 {Rhodobacter sphaeroides}
QEGDPEAGAKAFNQCTCHVIVDDSGTTIAGRNAKTGNLYGVVGRTAGTQADFKGYGEGM
KEAGA

KGLAWDEEHFVQYVQDPTKFLKEYTGDAAKAKGKMTFCLKKEADAHNIWAYLQQVAVRP
>d1co6a_ a.3.1.1 (A:) Cytochrome c2 {Rhodopseudomonas viridis}
QDAASGEQVFKQCLVCHSIGPGAKNKVGPVNLGLFGRHSGTIEGFAYS DANKNSGITWTEEVFREYIR
DPKAKIPGTKMIFAGVKDEQKVSDLIAYIKQFNADGSKK
>d1i8oa_ a.3.1.1 (A:) Cytochrome c2 {Rhodopseudomonas palustris}
EDAKAGEAVFKQCMTCHRADKNMVG PALAGVVGRKAGTAAGFTYSPLNHNSGEAGLVWTADNIVP
YLADPNAFLKFLTEK GKADQAVGVTKMTF KLANEQQRKDVVAYLATLK
>d1hroa_ a.3.1.1 (A:) Cytochrome c2 {Rhodopila globiformis}
SAPPGDPVEGKHLFHTICITC HTDIKGANKVGPSLYGVVGRHSGIEPGYNYSEANIKSGIVWTPDVLFK
YIEHPQKIVPGTKMGYPGQPD PQKRADIIAYLETLK
>d155c_ a.3.1.1 (-) Cytochrome c2 {Paracoccus denitrificans}
NEGDAAKGEKEFNKCKACHMIQAPDGTDIKGGKTGPNLYGVVGRKIAS EEGFKYGE GILEVAEKNP
DLTWTEANLIEYVTDPKPLVKMTDDKGAKTKMTFKMGKNQADVVAFLAQDDPDAXXXXXXXXXXX
XX
>d1cot_ a.3.1.1 (-) Cytochrome c2 {Paracoccus denitrificans}
DGDAAKGEKEFNKCKACHMIQAPDGTDIKGGKTGPNLYGVVGRKIAS EEGFKYGE GILEVAEKNPDL
TWTEADLIEYVTDPKPWLVKMTDDKGAKTKMTFKMGKNQADVVAFLAQNSPDA
>d1jdl a_ a.3.1.1 (A:) Cytochrome c2 {Rhodospirillum centenum}
GDPAKGEAVFKKCMACHRVGPDAKNLVGPAL TGVIDRQAGTAPGFNYSAINHAAGEAGLHWTPENII
AYLPDPNAFLRKFLADAGHAEQAKGSTKMVF KLPDEQERKDVVAYLKQFSP
>d1cc5_ a.3.1.1 (-) Cytochrome c5 {Azotobacter vinelandii}
GGGARS GDDVVAKYCNACHGTGLLNAPKVGDSA AWKTRADAKGGLDGLLAQSL SGLNAMPPKGT
CADCSDDELKAAIGKMSGL
>d1kx2a_ a.3.1.1 (A:) Mono-heme c-type cytochrome ScyA {Shewanella putrefaciens}
ADLQDAEAIYNKACTVCHSMGVAGAPKSHNTADWEPRLAKGVDNLVKS VKTGLNAMPPGGMCTDC
TDEDYKAAIEFMSKAK
>d1cch_ a.3.1.1 (-) Cytochrome c551 {Pseudomonas stutzeri}
QDGEALFKSKPCAACHSVDTKMVGPALKEVA AKNAGVEGAADTLALHIKNGSQGVWGPIPMPPNP
VTEEEAKILAEWVLSLK
>d1cor_ a.3.1.1 (-) Cytochrome c551 {Pseudomonas stutzeri}
EDGEALFKSKPCAACHSIDAKLVGPAFKEVA AKYAGQDGAADLLAGHIKNGSQGVWGPIPMPPNPVT
EEEAKILAEWILSQK
>d1dvva_ a.3.1.1 (A:) Cytochrome c551 {Pseudomonas aeruginosa}
EDPEVLAKNKGCMACHAIDTKMVGPAYKDVA AKYAGQAGAEAYLAQRIKNGSQGVWGPIPMPPNA
VSDDEAQT LAKWILSQK
>d451c_ a.3.1.1 (-) Cytochrome c551 {Pseudomonas aeruginosa}
EDPEVL FKNKGCVACHAIDTKMVGPAYKDVA AKFAGQAGAEELAQRIKNGSQGVWGPIPMPPNAV
SDDEAQT LAKWVLSQK
>d2mtac_ a.3.1.1 (C:) Cytochrome c551 {Paracoccus denitrificans}
APQFFNIIDGSPLNFDDAMEEGRDTEAVKH FLETGENVYNEDPEILPEAEELYAGMCSGCHGHYAEG
KIGPGLNDAYW TYPGNETDVGLFSTLYGGATGQM GPMWGS LTLDEMLRTMAWVRHLYTGDPKDA
SWLTDEQKAGFTPFQP
>d1gks_ a.3.1.1 (-) Cytochrome c551 {Ectothiorhodospira halophila}
DGESIYINGTAPTCCSCHDRGVAGAPELNAPEDWADR PSSVDELVESTLAGKGAMPAYDGRADREDL

VKAIEYMLSTL

>d05c1__ a.3.1.1 (-) Cytochrome c555 {Chlorobium thiosulfatophilum}

YDAAAGKATYDASCAMCHKTGMMGAPKVGDKAAWAPHIAKGMNVMVANSIKGYKGTGMMMPAK
GGNPKLTDAQVGNNAVAYMVGQSK

>d1dw0a_ a.3.1.1 (A:) SHP, an oxygen binding cytochrome c {Rhodobacter sphaeroides}

GDTSPAQLIAGYEEAAGAPADAERGRALFLSTQTTGGKPDTPSCTTCHGADVTRAGQTRTGKEIAPLA
PSATPDRFTDSARVEKWLGRNCNSVIGRDCTPGEKADLLAWLAAQ

>d1e8ea_ a.3.1.1 (A:) Cytochrome c'' {Methylophilus methylotrophus, strain w3a1}

DVTNAEKLVIKYTNIAHSANPMYEAPSITDGKIFFNRKFKTPSGKEAACASCHTNNPANVGNKIVTG
KEIPPLAPRVNTRKFTDIDKVEDEFKHKCNLDILGADCSPSEKANFIAYLLTETKPTK

>d1diqc_ a.3.1.1 (C:) p-Cresol methylhydroxylase, cytochrome c subunit {Pseudomonas
putida}

SQWGSKNLYDKVCGHCHKPEVGVGPVLEGRGLPEAYIKDIVRNGFRAMPAPFASVYVDDDESILTQVAE
YLSSLPA

>d1dy7b1 a.3.1.2 (B:32-135) N-terminal (heme c) domain of cytochrome cd1-nitrite
reductase {Paracoccus pantotrophus}

LAQQDVAAPGAPEGVSALSDAQYNEANKIYFERCAGCHGVLRKGATGKALTPDLTRDLGFDYLSFIT
YGSPAGMPNWTSGELSAEQVDLMANYLLLDPAAPP

>d1h9xa1 a.3.1.2 (A:42-133) N-terminal (heme c) domain of cytochrome cd1-nitrite
reductase {Paracoccus pantotrophus}

APEGVSALSDAQYNEANKIYFERCAGCHGVLRKGATGKALTPDLTRDLGFDYLSFITYGSPAGMPN
WTSGELSAEQVDLMANYLLLDPAAP

>d1hj3a1 a.3.1.2 (A:17-133) N-terminal (heme c) domain of cytochrome cd1-nitrite
reductase {Paracoccus pantotrophus}

HKTRTDNRYEPLDNLAQQDVAAPGAPEGVSALSDAQYNEANKIYFERCAGCHGVLRKGATGKALT
PDLTRDLGFDYLSFITYGSPAGMPNWTSGELSAEQVDLMANYLLLDPAAP

>d1hzua1 a.3.1.2 (A:23-117) N-terminal (heme c) domain of cytochrome cd1-nitrite
reductase {Pseudomonas aeruginosa}

VRTNGAPDMSESEFNEAKQIYFQRCAGCHGVLRKGATGKPLTPDITQQRGQYLEALITYGTPLGMP
NWGSSGELSKEQITLMAKYIQHTPPQPP

>d1nira1 a.3.1.2 (A:6-117) N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
{Pseudomonas aeruginosa}

AAEQYQGAASAVDPAHVVRTNGAPDMSESEFNEAKQIYFQRCAGCHGVLRKGATGKPLTPDITQQR
GQYLEALITYGTPLGMPNWGSSGELSKEQITLMAKYIQHTPPQPP

>d1e2rb1 a.3.1.2 (B:25-135) N-terminal (heme c) domain of cytochrome cd1-nitrite
reductase {Paracoccus denitrificans}

YEPLDNLAQQDVAAPGAPEGVTALSDAQYNEANKIYFERCAGCHGVLRKGATGKALTPDLTRDLGF
DYLSFITYASPAGMPNWTSGELSAEQVDLMANYLLLDPAAPP

>d1qksa1 a.3.1.2 (A:9-135) N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
{Paracoccus denitrificans}

DPAAALEDHKTRTDNRYEPLDNLAQQDVAAPGAPEGVTALSDAQYNEANKIYFERCAGCHGVLRK
GATGKALTPDLTRDLGFDYLSFITYASPAGMPNWTSGELSAEQVDLMANYLLLDPAAPP

>d1kb0a1 a.3.1.6 (A:579-675) Quinoprotein alcohol dehydrogenase, C-terminal domain
{Comamonas testosteroni}

TGQLLQGVKYDPAKVEAGTMLYVANCVFCHGVPGVDRGGNIPNLGYMDASYIENLPNFVFKGPAMV
RGMPDFTGKLSGDDVESLKAFIQGTADAIRP
>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)}
SDLELHPPSYPPWSHRGPLSSLDHTSIRRGFQVYKQVCSSCHSMDYVAYRHLVGVCTEDEAKALAAE
VEVQDGNEDGEMFMRPGKLSYDFPKYPNPEAARAANNALPPDLSYIVRARHGGEDYVFSLLTG
YCEPPTGVSREGLYFNPFYFPGQAIGMAPPIYNDVLEFDDGTPATMSQVAKDVCTFLRWAAE
>d1ezvd1 a.3.1.3 (D:62-260) Cytochrome bc1 domain {Baker's yeast (Saccharomyces
cerevisiae)}
MTAAEHGLHAPAYAWSHNGPFETFDHASIRRGYQVYREVCAACHSLDRVAWRTLVGVSHTNEEVRN
MAEEFEYDDEPDEQGNPKKRPGLSDYIPGPYPNEQAARAANQALPPDLSLIVKARHGGCDYIFSL
LTGYPDEPPAGVALPPGSNYPYFPGGSIAMARVLFDDMVEYEDGTPATTSQMAKDVTTFLNWCAE
>d1etpa1 a.3.1.4 (A:1-92) Cytochrome c4 {Pseudomonas stutzeri}
AGDAEAGQGKVAVCGACHGVDGNSPAPNFPKLAGQGERYLLKQLQDIKAGSTPGAPEGVGRKVLEM
TGMLDPLSDQDLEDIAAYFSSQKGSV
>d1etpa2 a.3.1.4 (A:93-190) Cytochrome c4 {Pseudomonas stutzeri}
GYADPALAKQGEKLFRRGGKLDQGMFACTGCHAPNGVGNLAGFPKLGQHAAYTAKQLTDFREGN
RTNDGDTMIMRGVAAKLSNKDIEALSSYIQLH
>d1fcd1 a.3.1.4 (C:1-80) Flavocytochrome c sulfide dehydrogenase, FCSD, cytochrome
subunit {Purple phototrophic bacterium (Chromatium vinosum)}
EPTAEMLTNNCAGCHGTHGNSVGPASPSIAQMDPMVFVEVMGFKSGEIASTIMGRIAKGYSTADFE
KMAGYFKQTYQP
>d1fcd2 a.3.1.4 (C:81-174) Flavocytochrome c sulfide dehydrogenase, FCSD, cytochrome
subunit {Purple phototrophic bacterium (Chromatium vinosum)}
AKQSFDTALADTGAKLHDKYCEKCHVEGGKPLADEEDYHILAGQWTPYLQYAMSDFREERRPMEK
KMASKLRELLKAEGDALDALFAFYASQQ
>d1eb7a1 a.3.1.5 (A:1-164) Di-haem cytochrome c peroxidase {Pseudomonas aeruginosa}
DALHDQASALFKPIEQVTELRGQPISEQRELGKCLFFDPRLSRSHVLSCNTCHNVGTGGADNVPT
SVGHGWQKGRNSPTVFNVAVFNAQFWDGRAKDLGEQAKGPIQNSVEMHSTPQLVEQTLGSIPEYV
DAFRKAFPKAGKPVSFDMALAIAYEATLV
>d1eb7a2 a.3.1.5 (A:165-323) Di-haem cytochrome c peroxidase {Pseudomonas aeruginosa}
TPDSPFDLYLKGGDKALDAQKGLKAFMDSGCSACHNGLGGQAYFPFLVKKPDASVLPDSDGK
RFAVTKTQSDYVFRAPLRNVALTAPYFHSGQVWELKDAVAIMGNAQLGKQLAPDDVENIVAFLHS
LSGKQPRVEYPLLPASTETTPRAE
>d1iqca1 a.3.1.5 (A:1-150) Di-haem cytochrome c peroxidase {Nitrosomonas europaea}
ANEPIQPIKAVTPENADMAELGKMLFFDPRLSKSGFISCSCHNLMSGGTDNITTSIGHKWQQGPIN
APTVLNSSMNLAQFWDGRAKDLKEQAAGPIANPKEMASTHEIAEKVVASMPQYRERFKKVFSGSDE
VTIDRITTAIAQFEETLV
>d1iqca2 a.3.1.5 (A:151-308) Di-haem cytochrome c peroxidase {Nitrosomonas europaea}
TPGSKFDKWLEGDKNALNQDELEGYNLFKSGCVQCHNGPAVGGSSYQKMGVFKPYETKNPAAGR
MDVTGNEADRNVFKVPTLRNIELTYPYFHDGGAATLEQAVETMGRIQLNREFNKDEVSKIVAFLKTL
TGDQPDFKLPILPPSNNDTPRSQPYE
>d1jjua1 a.3.1.7 (A:1-85) Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2

{Paracoccus denitrificans}
VTGEEVLQNAACAACHVQHEDGRWERIDAARKTPEGWDMTVTRMMRNHGVALEPEERAAIVRHLS
DTRGLSLAETEERRYILEREP
>d1jjua2 a.3.1.7 (A:86-165) Quinohemoprotein amine dehydrogenase A chain, domains 1
and 2 {Paracoccus denitrificans}
VAWDEGPDTSMTQTCGRCHSYARVALQRRTPEDWKHLVNFHLGQFPTLEYQALARDRDWWGIAQ
AEIIPFLARTYPLGEA
>d1jmx1 a.3.1.7 (A:2-85) Quinohemoprotein amine dehydrogenase A chain, domains 1 and
2 {Pseudomonas putida}
EQGPSLLQNKCMGCHIPEGNDTYSRISHQRKTPEGWLMSIARMQVMHGLQISDDDRRTLKYLADK
QGLAPSETDGVRYAMERR
>d1jmx2 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)}
KKEKSPKGGSSISPQARAFLEQVFRRKQSLNSKEKEEVAKKCGITPLQVRVWFINKRMRSK
>d1akhb_ a.4.1.1 (B:) mat alpha2 Homeodomain {Baker's yeast (Saccharomyces cerevisiae)}
TKPYRGHRFTKENVRILESWFAKNIENPYLDTKGLENLMKNTSLSRIQIKNWVSNRRRKEKTITAP
ELADLLSGEPL
>d1apl_ a.4.1.1 (C:) mat alpha2 Homeodomain {Baker's yeast (Saccharomyces cerevisiae)}
YRGHRFTKENVRILESWFAKNIENPYLDTKGLENLMKNTSLSRIQIKNWVSNRRRKEKT
>d1mnm_ a.4.1.1 (C:) mat alpha2 Homeodomain {Baker's yeast (Saccharomyces
cerevisiae)}
GLVFNVTQDMINKSTKPYRGHRFTKENVRILESWFAKNIENPYLDTKGLENLMKNTSLSRIQIKN
WVSNRRRKEKT
>d1lfb_ a.4.1.1 (-) Transcription factor LFB1 {Rat (Rattus rattus)}
RFKWGPASQQILFQAYERQKNPSKEERETLVEECNRAECIQRGVSPSQAQGLGSNLVTEVRVYNWFA
NRRKEEAFRHK
>d2lfb_ a.4.1.1 (-) Transcription factor LFB1 {Rat (Rattus rattus)}
MARIDPTKKGRRNRFKWGPASQQILFQAYERQKNPSKEERETLVEECNRAECIQRGVSPSQAQGLGS
NLVTEVRVYNWFANRRKEEAFRHKLAMDTYKLN
>d1e3oc1 a.4.1.1 (C:104-160) Oct-1 POU Homeodomain {Human (Homo sapiens)}
KRTSIETNIRVALEKSFMENQKPTSEDLTIAEQLNMEKEVIRVWFSNRRQKEKRIN
>d1hf0a1 a.4.1.1 (A:102-159) Oct-1 POU Homeodomain {Human (Homo sapiens)}
RKKRTSIETNIRVALEKSFLENQKPTSEEITMIADQLNMEKEVIRVWFSNRRQKEKRI

>d1au7a1 a.4.1.1 (A:103-160) Pit-1 POU homeodomain {Rat (Rattus norvegicus)}
KRRRTISIAAKDALERHFGEHSPSSQEIMRMAEELNLEKEVVRVWFCNRRQREKRVK

>d1ftt_ a.4.1.1 (-) Thyroid transcription factor 1 homeodomain {Rat (Rattus norvegicus)}
MRRKRRVLFSAQVYELERRFKQKYLAPEREHLASMIHLTPTQVKIWFQNHRYKMKRQAKDKA
AQQ

>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)}
METLVQARKRKRKTSIENRVRWSLETMFLKCPKPSLQQITHIANQLGLEKDVVRVWFCNRRQKGRS
S

>d1b72a_ a.4.1.1 (A:) Homeobox protein hox-b1 {Human (Homo sapiens)}
ARTFDWMKVKRNPPKTAKVSEPLGSPGLRTNFTTRQLTELEKEFHFNKYLSRARRVEIAATLEL
NETQVKIWFQNRMMKQKKRERE

>d1b72b_ a.4.1.1 (B:) pbx1 {Human (Homo sapiens)}
RKRRNFNKQATEILNEYFYSHLSNPYPSEEAKEELAKKCGITVSQVSNWFGNKRIRYKKNIGKFQEE
ANIYAA

>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)}
MKTTRVRTVLNEKQLHTLRTCYAANRPDALMKEQLVEMTGLSPRVIRVWFQNKRCCKDKRSIMM
K

>d1ig7a_ a.4.1.1 (A:) Msx-1 homeodomain {Mouse (Mus musculus)}
RKRPTPFTTAQLLALERKFRQKQYLSIAERAEFSSSLTETQVKIWFQNRRAKAKRL

>d1ahdp_ a.4.1.1 (P:) Antennapedia Homeodomain {Drosophila melanogaster}
MRKRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALSLTERQIKIWFQNRMMKWKKENKTKGE
PG

>d1san_ a.4.1.1 (-) Antennapedia Homeodomain {Drosophila melanogaster}
MTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALSLTERQIKIWFQNRMMKWKKENKTKGEPG

>d9anta_ a.4.1.1 (A:) Antennapedia Homeodomain {Drosophila melanogaster}
RQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALSLTERQIKIWFQNRMMKWKKEN

>d1b8ia_ a.4.1.1 (A:) Ultrabithorax (ubx) homeodomain {Drosophila melanogaster}
FYPWMAIAGTNGLRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALSLTERQIKIWFQNR
MMLKKEI

>d1b8ib_ a.4.1.1 (B:) Extradenticle (exd) homeodomain {Drosophila melanogaster}
RRNFSKQASEILNEYFYSHLSNPYPSEEAKEELARKCGITVSQVSNWFGNKRIRYKKN

>d1jgga_ a.4.1.1 (A:) Even-skipped homeodomain {Fruit fly (Drosophila melanogaster)}
RYRTAFTRDQLGRLEKEFYKENYVSRPRCELAAQLNLPSTIKVWFQNRMMKDKRQ

>d1ftz_ a.4.1.1 (-) Fushi Tarazu protein {Fruit fly (Drosophila melanogaster)}
MDSKRTRQTYTRYQTLELEKEFHFNRYITRRRRIDIANALSLSERQIKIWFQNRMMKSKKDRTLDSS
PEH

>d1nk3p_ a.4.1.1 (P:) VND/NK-2 protein {Fruit fly (Drosophila melanogaster)}
KKRKRRLVFTKAQTYELERRFRQRYLSAPEREHLASLIRLTPTQVKIWFQNHRYKTKRAQNE

>d1vnd_ a.4.1.1 (-) VND/NK-2 protein {Fruit fly (Drosophila melanogaster)}
ASDGLPNKKRKRRLVFTKAQTYELERRFRQRYLSAPEREHLASLIRLTPTQVKIWFQNHRYKTKRA

QNEKGYEGHP

>d1fjla_ a.4.1.1 (A:) Paired protein {Fruit fly (Drosophila melanogaster)}
KQRRSRTTFSASQLDELERAFERTQYPDIYTREELAQRNTLTEARIQVWFQNRRLRRLKQHTSVS

>d1fjlb_ a.4.1.1 (B:) Paired protein {Fruit fly (Drosophila melanogaster)}
QRRSRTTFSASQLDELERAFERTQYPDIYTREELAQRNTLTEARIQVWFQNRRLRRLK

>d1hcra_ a.4.1.2 (A:) HIN recombinase (DNA-binding domain) {Synthetic}
GRPRAINKHEQEIQSRLLLEKGHPRQQLAIIFGIGVSTLYRYFPASSIKKRMN

>d1ijwc_ a.4.1.2 (C:) HIN recombinase (DNA-binding domain) {Synthetic}
GRPRAINKHEQEIQSRLLLEKGHPRQQLAIIFGIGVSTLYRYFPASSI

>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}
MIARPTLEAHDYDREALWSKWDNASDSQRRLAEKWLPVQAADDEMLNQGISTKTAFATVAGHYQV
SASTLRDKYYQVQKFAKPDWAAALVDGRGASRRN

>d2ezh_ a.4.1.2 (-) Transposase {Bacteriophage mu}
SEFDEDAWQFLIADYLRPEKPAFRKCYERLELAAREHGWSIPS RATAFRRIQQLDEAMVVACREG

>d2ezi_ a.4.1.2 (-) Transposase {Bacteriophage mu}
MNVHKSEFDEDAWQFLIADYLRPEKPAFRKCYERLELAAREHGWSIPS RATAFRRIQQLDEAMVVA
CREGEHALM

>d1h88c1 a.4.1.3 (C:39-88) c-Myb, DNA-binding domain {Mouse (Mus musculus)}
GKTRWTREEDEKLKLVQNGTDDWKVIANYLPNRTDVQCQHRWQKVLNP

>d1h88c2 a.4.1.3 (C:89-143) c-Myb, DNA-binding domain {Mouse (Mus musculus)}
ELIKGPWTKEEDQRVIKLVQKYGPKRWSVIAKHLKGRIGKQCRERWHNHLNPEVK

>d1idz_ a.4.1.3 (-) c-Myb, DNA-binding domain {Mouse (Mus musculus)}
MEVKKTSWTEEEEDRILYQAHKRLGNRWAEIAKLLPGRTDNAIKNHWNSTMRRKV

>d1a5j_1 a.4.1.3 (1-55) b-Myb DNA binding domain {Chicken (Gallus gallus)}
GIPDLVKGPWTKEEDQKVIELVKKYGTKQWTLIAKHLKGRIGKQCRERWHNHLNP

>d1a5j_2 a.4.1.3 (56-110) b-Myb DNA binding domain {Chicken (Gallus gallus)}
EVKKSSTWTEEEEDRIIFEAHKVLGNRWAEIAKLLPGRTDNAVKNHWNSTIKRKVDV

>d1h8ac1 a.4.1.3 (C:87-143) v-Myb {Avian myeloblastosis virus}
NPELNKGPWTKEEDQRVIEHVQKYGPKRWSVIAKHLKGRIGKQCRERWHNHLNPEVK

>d1h8ac2 a.4.1.3 (C:144-191) v-Myb {Avian myeloblastosis virus}
KTSWTEEEEDRIYQAHKRLGNRWAEIAKLLPGRTDNAVKNHWNSTMRR

>d1fexa_ a.4.1.3 (A:) Rap1 {Human (Homo sapiens)}
GRIAFDADDVAILTYVKENARSPSSVTGNALWKAMEKSSLTQHSWQSLKDRYLKHLRG

>d1ba5_ a.4.1.4 (-) DNA-binding domain of human telomeric protein, htrf1 {Human (Homo
sapiens)}
RKRQAWLWEEEDKNLRSGVRKYGEGNWSKILLHYKFNNRTSVMLKDRWRMTMKKL

>d1k78a1 a.4.1.5 (A:19-81) Pax-5 {Human (Homo sapiens)}
GVNQLGGVFNVRPLPDVVRQRIVELAHQGVPRCDISRQLRVSHGCVSKILGRYYETGSIKPG

>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)}
SHSGVNVQLGGVFNVRPLPDSTRQRIVELAHSGARPCDISRILQVSNCGCVSKILGRYYATGSIRPRAI
>d6paxa2 a.4.1.5 (A:69-133) Pax-6 {Human (Homo sapiens)}
GGSKPRVATPEVVSKIAQYKQECPSIFAWWEIRDRLLESEGVTNDNIPSVSSINRVLRLNLASEKQQ
>d1pdnc_ a.4.1.5 (C:) Paired protein (prd) {Fruit fly (Drosophila melanogaster)}
QGRVNVQLGGVFINGRPLPNNIRLKIVEMAADGIRPCVISRQLRVSHGCVSKILNRYQETGSIRPGVIGG
SKPRIATPEIENRIEYKRSSPGMFSWEIREKLIREGVCDRSTAPSVSAISRLV
>d1igna1 a.4.1.6 (A:360-445) DNA-binding domain of rap1 {Baker's yeast (Saccharomyces cerevisiae)}
KASFTDEEDEFILDVVRKNPTRRTTHTLYDEISHYVPNHTGNSIRHRFRVYLSKRLEYVVEVDKFGKL
VRDDDGNLIKTKVLPPSI
>d1igna2 a.4.1.6 (A:446-594) DNA-binding domain of rap1 {Baker's yeast (Saccharomyces cerevisiae)}
KRKFSADEDYTLAIAVKKQFYRDLFQIDPDTGRSLITDEDTPTAIARRNMTMDPNHVPGSEPNFAAY
RTQSRRGPIAREFFKHFAEEHAAHTENAWRDRFRKFLAYGIDDYISYYEAEKAQNREPEPMKNLT
NRPKRPGVPTPGNYNS
>d1bw6a_ a.4.1.7 (A:) DNA-binding domain of centromere binding protein B (CENP-B) {Human (Homo sapiens)}
MGPKRRQLTFREKSRIIQEVEENPDLRKGEIARRFNIPPSTLSTILKNKRAILASE
>d1hlva1 a.4.1.7 (A:1-66) DNA-binding domain of centromere binding protein B (CENP-B) {Human (Homo sapiens)}
MGPKRRQLTFREKSRIIQEVEENPDLRKGEIARRFNIPPSTLSTILKNKRAILASERKYGVASTCR
>d1hlva2 a.4.1.7 (A:67-131) DNA-binding domain of centromere binding protein B (CENP-B) {Human (Homo sapiens)}
KTNKLSPYDKLEGLLIAWFQQIRAAGLPVKGILKEKALRIAEEELGMDFTASNGWLDLFRRRRS
>d1g2ha_ a.4.1.10 (A:) Transcriptional regulator TyrR, C-terminal domain {Haemophilus influenzae}
SAVISLDEFENKTLDEIIGFYEAQVLKLFYAEYPSTRKLAQRLGVSHTAIANKLKQYIGIK
>d1bl0a1 a.4.1.8 (A:9-62) MarA {Escherichia coli}
DAITIHSILDWIEDNLESPLSLEKVSERSGYSKWHLQRMFKKETGHSGLGQYIRS
>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}
RRLSKSAVALRLTARPILDIALQYRFDSQQTFTRAFFKQFAQTPALYRRSPEWSAFGIRPPLRLG
>d1a6i_1 a.4.1.9 (2-67) Tetracyclin repressor (Tet-repressor, TetR) {Escherichia coli}
SRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAVEILARHHDYS
>d2tct_1 a.4.1.9 (2-67) Tetracyclin repressor (Tet-repressor, TetR) {Escherichia coli}
ARLNRESVIDAALELLNETGIDGLTTRKLAQKLGIEQPTLYWHVKNKRALLDALAVEILARHHDYS
>d1jt6a1 a.4.1.9 (A:2-72) Multidrug binding protein QacR {Staphylococcus aureus}
NLKDKILGVAKELFIKNGYNATTTTGEIVKLSSESKGNLYYHFKTKENLFLEILNIEESKWQEQQWKKEQ
IKA

>d1sfe_1 a.4.2.1 (93-176) Ada DNA repair protein {Escherichia coli}
GTAFQQVWQALRTIPCGETVSYQQLANAIGKPKAVRAVASACAANKLAIVIPCHRVRGDGSLSGYR
WGVSRKAQLLRREAEN

>d1qnta1 a.4.2.1 (A:92-176) O6-alkylguanine-DNA alkyltransferase {Human (Homo sapiens)}
ESFTRQVLWKLKLVKVFGEVISYQQLAALAGNPKAARAVGGAMRGNPVPILIPCHRVCSSGAVGNY
SGGLAVKEWLLAHEGHRL

>d1mgta1 a.4.2.1 (A:89-169) O6-alkylguanine-DNA alkyltransferase {Archaeon Pyrococcus kodakaraensis}
VTPFEKKVYEWLTKNVKRGSVITYGDLAKALNTSPRAVGGAMKRNPYPIVVPCHRVAHDGIGYSS
GIEKKFLLEIEGV

>d1c20a_ a.4.3.1 (A:) DNA-binding domain from the dead ringer protein {Fruit fly (Drosophila melanogaster)}
GWSFEEQFKQVRQLYEINDDPKRKEFLDDLFSFMQKRGTPIINRLPIMAKSVLDLYELYNLVIARGGLV
DVINKKLWQEIHKGLHLPSSITSAFTLRQYMKYLYPYECEKKNLSTPAELQAAIDGNR

>d1ig6a_ a.4.3.2 (A:) MRF-2 DNA-binding domain {Human (Homo sapiens)}
RADEQAFVLVALYKYMKERKTPIERIPYLGFKQINLWTMFAQAAQKGGYETITARRQWKHIYDELGGN
PGSTSAATCTRRHYERLILPYERFIKGEEDKPLPPIKPRK

>d1bia_1 a.4.5.1 (1-63) Biotin repressor, N-terminal domain {Escherichia coli}
MKDNTVPLKLIALLANGEFHSGEQLGETLGMSSRAAINKHIQTLRDWGVDFVFTVPKGYSLPEP

>d1jhfa1 a.4.5.2 (A:2-72) LexA repressor, N-terminal DNA-binding domain {Escherichia coli}
KALTARQQEVFDLIRDHISQTMPPTRAIEAQRLGFRSPNAAEHLKALARKGVIEIVSGASRGIRLLQ
EE

>d1aoy_ a.4.5.3 (-) Arginine repressor (ArgR), N-terminal DNA-binding domain {Escherichia coli}
MRSSAKQEELVKAFKALLKEEFSSQGEIVAALQEQGFDNINQSKVSRMLTKFGAVRTRNAKMEMV
YCLPAELGVPTT

>d1b4aa1 a.4.5.3 (A:4-78) Arginine repressor (ArgR), N-terminal DNA-binding domain {Bacillus stearothermophilus}
GQRHIKIREIIMSNDIETQDELVDRLREAGFNVTQATVSRDIKEMQLVKVPMANGRYKYSPLSDQRF
NPLQKLR

>d1f9na1 a.4.5.3 (A:3-78) Arginine repressor (ArgR), N-terminal DNA-binding domain {Bacillus subtilis}
KGQRHIKIREIITSNEIETQDELVDMLKQDGYKVTQATVSRDIKELHLVKVPTNNGSYKYSPLADQRF
NPLSKLR

>d1hw5a1 a.4.5.4 (A:138-208) Catabolite gene activator protein (CAP), C-terminal domain {Escherichia coli}
DVTGRIAQTLLNLAKQPDAMTHPDGMQIKITRQEIGQIVGCSRETVGRILKMLEDQNLISAHGKTIVV
YGT

>d1ft9a1 a.4.5.4 (A:134-213) CO-sensing protein CoaA, C-terminal domain {Rhodospirillum rubrum}
DIKQRIAGFFIDHANTTGRQTQGGVIVSVDFTVVEEIANLIGSSRQTTSTALNSLIKEGYISRQGRGHYTI
PNLVRKAAA

>d1i1ga1 a.4.5.32 (A:2-61) LprA {Archaeon Pyrococcus furiosus}

IDERDKIILELEKDARTPFTEIAKKGISETAVRKRVKALEEKGIEGYTIKINPKKLG
>d1smta_a.4.5.5 (A:) SmtB repressor {Cyanobacteria (Synechococcus), pcc7942}
ELQAIAPVAQSLAEFFAVLADPNRLRLSLLARSELVGDLAQAIGVSESAVSHQLRSLRNLRLVSYR
KQGRHVYYQLQDHHIVALYQNALDHLQEC
>d1jgsa_a.4.5.28 (A:) Multiple antibiotic resistance repressor, MarR {Escherichia coli}
LFNEIPLGRLIHMVNQKKDRLLNEYLSPLDITAAQFKVLCIRCAACITPVELKKVLSVDLGALTRML
DRLVCKGWVERLPNPNDKRGVLVKLTTGGAAICEQCHQLVGDHLHQELTKNLTADEVATLEYLLKKV
LP
>d1hsja1_a.4.5.28 (A:373-487) staphylococcal accessory regulator A homolog, SarR
{Staphylococcus aureus}
MSKINDINDLVNATFQVKKFFRDTKKKFNLYEEIYILNHILRSESNEISSKEIAKCEFKPYLTKAL
QKLKDLKLLSKRSLQDERTVIVYVTDQKANIQKLISELEEYIKN
>d1fzpb_a.4.5.28 (B:) Pleiotropic regulator of virulence genes, SarA {Staphylococcus aureus}
AITKINDCFELSMVTYADKLKSLIKKEFSISFEFAVLTYSIENKEKEYLKDIIHNLNYKQPQVVKAV
KILSQEDYFDKKRNEHDERTVLILVNAQQRKKIESLLSRVNKRIT
>d1hw1a1_a.4.5.6 (A:5-78) Fatty acid responsive transcription factor FadR, N-terminal
domain {Escherichia coli}
AQSPAGFAEEYIIESIWNNRFPPGTILPAERELSELIGVTRTTLREVLQRLARDGWLTIQHGKPTKVN
NFWETS
>d1bm9a_a.4.5.7 (A:) Replication terminator protein (RTP) {Bacillus subtilis}
EEKRSSTGFLVKQRAFLKLYMITMTEQERLYGLKLEVLRFSEFKEIGFKPNHTEVYRSLHELLDDGIL
KQIKVKKEGAKLQEVVLYQFKDYEAALKYKKQLKVELDRCKKLIKALSDNF
>d1b9ma1_a.4.5.8 (A:-1-126) N-terminal domain of molybdate-dependent transcriptional
regulator ModE {Escherichia coli}
HMQAEILLTLKLQKLFADPRRISLLKHIALSGSISQGAKDAGISYKSAWDAINEMNQLSEHILVERAT
GGKGGGGAVLTRYGQRLIQLYDLAQIQKAFDVLSDDDALPLNSLLAAISRFSLQTS
>d1bjaa_a.4.5.9 (A:) Transcription factor MotA, activation domain {Bacteriophage T4}
SKVTYIHKASNDVLNEKTATILITIAKKDFITAAEVREVHPDLGNAVVNSNIGVLIKKGLVEKSGDGLIIT
GEAQDIISNAATLYAQENAPPELLK
>d1rep1_a.4.5.10 (C:15-143) RepE54 {Escherichia coli, mini-F plasmid}
SPRIVQSNLDEAAAYSLSRDQKRMLYLFVDQIRKSDGTLQEHDGICEIHVAKYAEIFGLTSAEASKDIR
QALKSFAGKEVVFYRPEEDAGDEKGYESFPWFIKPAHSPSRGLYSVHINPYLIPFFIGLQ
>d1rep2_a.4.5.10 (C:144-246) RepE54 {Escherichia coli, mini-F plasmid}
NRFTQFRLSETKEITNPYAMRLYESLCQYRKPDSGIVSLKIDWIIERYQLPQSYQRMPDFRRRFLQV
CVNEINSRTPMRLSYIEKKKGRQTTHIVFSFRDIT
>d1hqca1_a.4.5.11 (A:243-318) Holliday junction helicase RuvB {Thermus thermophilus}
LGLEKRDREILEVLILRFGGGPVGLATLATALSEDPGTLEEVHEPYLIRQGLLKRTPRGRVPTELAYRH
LGYPVV
>d1in4a1_a.4.5.11 (A:255-329) Holliday junction helicase RuvB {Thermotoga maritima}
EGLDEFDRKILKTIIEIYRGGPVGLNALAASLGVEADTLSEVYEPYLLQAGFLARTPRGRIVTEKAYKH
LKYEVP
>d1fna1_a.4.5.11 (A:277-388) CDC6, C-terminal domain {Archaeon Pyrobaculum
aerophilum}
ISEEVLIGLPLHEKLFLLAIVRSLKISHTPYITFGDAEESYKIVCEEYGERPRVHSQLWSYLNLDLREKGI

VETRQNKRGEGVRGRTTLISIGTEPLDTLEAVITKLIKEELR

>d1foka3 a.4.5.12 (A:287-386) Restriction endonuclease FokI, N-terminal (recognition) domain {Flavobacterium okeanokoites}
 VPKRVYWEMLATNLTDKKEYVRTRRALILEILIKAGSLKIEQIQDNLKKGDFDEVIETIENDIKGLINTGI
 FIEIKGRFYQLKDHLQFVIPNRGVTKQLV

>d2foka1 a.4.5.12 (A:5-143) Restriction endonuclease FokI, N-terminal (recognition) domain {Flavobacterium okeanokoites}
 IRTFGVWQNPQGFENLKRQVQVDFRNSKVHNEVKNIKIPTLVKESKIQKELVAINQHDLIYTYKEL
 VGTGTSIRSEAPCDAIHQATIADQGNKKGYIDNWSSDGLRWAHALGFIEYINKSDSFVITDVGLAYSK
 SAD

>d2foka2 a.4.5.12 (A:144-286) Restriction endonuclease FokI, N-terminal (recognition) domain {Flavobacterium okeanokoites}
 GSAIEKEILIEAISSYPPAIRILTLEDGQHLTKFDLGNLGFSGESGFTSLPEGILLDTLANAMPKDKGE
 IRNNWEGSSDKYARMIGGWLDKLGVLKQGGKEFIIPTLGKPDNKEFISHAFKITGEGLKVLRRAKGS
 TKFTR

>d2foka3 a.4.5.12 (A:287-386) Restriction endonuclease FokI, N-terminal (recognition) domain {Flavobacterium okeanokoites}
 VPKRVYWEMLATNLTDKKEYVRTRRALILEILIKAGSLKIEQIQDNLKKGDFDEVIETIENDIKGLINTGI
 FIEIKGRFYQLKDHLQFVIPNRLGKPDV

>d1f1za1 a.4.5.27 (A:169-267) TnsA endonuclease, C-terminal domain {Escherichia coli}
 NPVVKENIEWLYSVKTEEVSALLAQLSPLAHILQEKGDENIINVCKQVDIAYDLELGLTSEIRALTA
 NGFIKFNIYKSFRAKCADLCISQVVMEE

>d1fp1d1 a.4.5.29 (D:19-128) Chalcone O-methyltransferase {Alfalfa (Medicago sativa)}
 QTEDSACLSAMVLTNNLVYPAVLNAAIDLNLFEIIAKATPPGAFMSPSEIASKLPASTQHSDLPNRLDR
 MLRLLASYSVLTSTTRTIEDGGAERVYGLSMVGKYLVPDES

>d1fp2a1 a.4.5.29 (A:8-108) Isoflavone O-methyltransferase {Alfalfa (Medicago sativa)}
 RKPSEIFKAQALLYKHIFAFIDSMKSLKWAVEMNIPNIIQNHGKPISSLNLSILQVPSSKIGNVRRMLRY
 LAHNGFFEIITKEEESYALTVASELLVRGSD

>d1hsta_ a.4.5.13 (A:) Histone H5, globular domain {Chicken (Gallus gallus)}
 SHPTYSEMIAAAIRAERSRGGSSRSIQYKIKSHYKVGHNADLQIKLSIRLLAAGVLKQTKGVGASGS
 FRLAK

>d1ghc_ a.4.5.13 (-) Histone H1, globular domain {Chicken (Gallus gallus)}
 MAGPSVTEELITKAVSASKERKGLSLAALKKALAAGGYDVEKNNSRIKLGKSLVSKGLTVQTKGTGAS
 GSFRLSK

>d1e17a_ a.4.5.14 (A:) Afx (Foxo4) {Human (Homo sapiens)}
 SRRNAWGNQSYAELISQAIESAPEKRLTLAQIYEWVVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHS
 KFIKVHNEATGKSSWWMLNPEGG

>d1d5va_ a.4.5.14 (A:) Adipocyte-transcription factor FREAC-11 (s12, fkh-14) {Human (Homo sapiens)}
 MLVKPPYSYIALITMAIQNAPEKKITLNGIYQFIMDRFPFYRENKQGWQNSIRHNLSLNECFVKVPRD
 DKKPGKGSYWTLDPDSYNMFENGSL

>d2hdca_ a.4.5.14 (A:) Genesis {Rat (Rattus norvegicus)}
 VKPPYSYIALITMAILQSPQKLTLSGICEFISNRFYREKFPWQNSIRHNLSLNDCFVKIPREPGN
 PGKGNWTLDPQSEDMFDNGSFLRRRKR

>d1kq8a_ a.4.5.14 (A:) HFH-1 (HNF-3 forkhead homolog-1) {Rat (Rattus norvegicus)}
YIALITMAIRDSAGGRLTLAEINEYLMGKFPFRGYSYTGWRNSVRHNLNDCFVKVLRDPSRPWGK
DNYWMLNP

>d2bby_ a.4.5.15 (-) DNA-binding domain from rap30 {Human (Homo sapiens)}
RARADKQHVLDMLFSAFEKHQYYNLKDLVDITKQPVVYLKEILKEIGVQNVKGIHKNTWELKPEYR
HYQ

>d1i27a_ a.4.5.30 (A:) C-terminal domain of the rap74 subunit of TFIIIF {Human (Homo sapiens)}
GPLGSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTKKTGLSSEQTVNVLAQILKRLNPERKMINDK
MHFSLKE

>d1dpua_ a.4.5.16 (A:) C-terminal domain of RPA32 {Human (Homo sapiens)}
ANGLTVAQNQVLNLKACPRPEGLNFQDLKNQLKHMSVSSIKQAVDFLSNEGHIYSTVDDDDHFKSTD
AE

>d1fsha_ a.4.5.31 (A:) Segment polarity protein Dishevelled-1 {Mouse (Mus musculus)}
EAPLTVKSDMSAIVRVMQLPDSGLEIRDRMWLKITIANAVIGADVVDWLYTHVEGFKERREARKYAS
SMLKHGFLRHTV NKITFSEQCYYVFGD

>d1cf7a_ a.4.5.17 (A:) Cell cycle transcription factor e2f-dp {Human (Homo sapiens)}
SRHEKSLGLLTTKFVSLLEAKDGVLDLKLAAADTLAVRQKRRYDITNVLEGIGLIEKSKNSIQWK

>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 TFIIIE beta {Human (Homo sapiens)}
ALSGSSGYKFGVLAKIVNYMKTRHQRGDTHPLTLDEILDDETQHLDIGLKQKQWLMTEALVNNPKIE
VIDGKYAFKPKYNVR

>d1qbj_ a.4.5.19 (A:) Z-alpha domain of dsRNA-specific adenosine deaminase, ADAR1
{Human (Homo sapiens)}
SIYQDQEQRILKFLEELGEGKATTAHDLGKLGTPKKEINRVLYSLAKKGLQKEAGTPPLWKIA

>d1qgpa_ a.4.5.19 (A:) Z-alpha domain of dsRNA-specific adenosine deaminase, ADAR1
{Human (Homo sapiens)}
LSSHQFQELSIYQDQEQRILKFLEELGEGKATTAHDLGKLGTPKKEINRVLYSLAKKGLQKEAGTPPL
WKIAVSD

>d1j75a_ a.4.5.19 (A:) Dlm-1 {Mouse (Mus musculus)}
NLEQKILQVLSDDGGPVKIGQLVKKCQVPKKTNLNQLYRLKKEDRVSSPEPATWSIG

>d1dp7p_ a.4.5.20 (P:) MHC class II transcription factor RFX1 {Human (Homo sapiens)}
TVQWLLDNYETAEGVSLPRSTLYNHYLLHSQEQLKLEPVNAASFGLIRSVFMGLRTRRLGTRGNSKY
HYYGLRIKA

>d1flia_ a.4.5.21 (A:) Fli-1 {Human (Homo sapiens)}
PGSGQIQLWQFLELLSDSANASCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALR
YYYDKNIMTKVHGKRYAYKFDHFGIAQALQPHP

>d1k78b_ a.4.5.21 (B:) ETS-1 transcription factor, residues 331-440 {Mouse (Mus musculus)}
IQLWQFLELLTDKSCQSFISWTGDGWEFKLSDPDEVARRWGKRKNPKMNYEKLSRGLRYYYDK
NIIHKTAGKRYVYRFVCDLQSLGTYPEELHAMLVDK

>d2stta_ a.4.5.21 (A:) ETS-1 transcription factor, residues 331-440 {Human (Homo sapiens)}

VIPAAALAGYTGSGPIQLWQFLELLTDKSCQSFSISWTGDGWEFKLSDPDEVARRWGKRKNPKMKN
YEKLSRGLRYYYDKNIIHKTAGKRYVYRFV
>d1puee_ a.4.5.21 (E:) Transcription factor PU.1, residues 171-259 {Mouse (Mus musculus)}
KIRLYQFLDLLRSGDMKDSIWVVDKDKGTFQFSSKHKEALHRWGIQKGNRKKMTYEKMARAL
RNYGKTGEVKKVKKLTYQFSGEV
>d1awca_ a.4.5.21 (A:) GA binding protein (GABP) alpha {Mouse (Mus musculus)}
IQLWQFLELLTDKDARDICISWVGDEGEFKLNQPELVAQKWGQRKNKPTMNYEKLSRALRYYYDG
DMICKVQGRFVYKFCVCDLKTIGYSAEELNRLVIECEQKKLARM
>d1bc8c_ a.4.5.21 (C:) Serum response factor accessory protein 1a, SAP-1 {Human (Homo
sapiens)}
MDSAITLWQFLLQLLQKPQNKHMICWTSNDGQFKLLQAEEVARLWGIRKNKPNMNYDKLSRALRY
YYVKNIIKKVNGQKFVYKFVSYPEILNM
>d1hbxg_ a.4.5.21 (G:) Serum response factor accessory protein 1a, SAP-1 {Human (Homo
sapiens)}
DSAITLWQFLLQLLQKPQNKHMICWTSNDGQFKLLQAEEVARLWGIRKNKPNMNYDKLSRALRY
YVKNIIKKVNGQKFVYKFVSYPEILNMDPMTVGRIEGDCESLNFSEVSSSSKDVENGGKDKPPQPGA
KTSSRNDYIHSGLYSSFTLNSLN
>d1duxc_ a.4.5.21 (C:) Elk-1 {Human (Homo sapiens)}
VTLWQFLLQLLREQNGHIIWTSRDGGEFKLVDAEEVARLWGLRKNKTNMNYDKLSRALRYYYD
KNIIRKVSQKQKFVYKFVSYPE
>d1hks_ a.4.5.22 (-) Heat-shock transcription factor {Drosophila melanogaster}
GSGVPAFLAKLWRLVDDADTNRLICWTKDQSFVIQNAQFAKELLPLNYKHNNMASFIRQLNMY
GFHKITSIDNGGLRFDRDEIEFSHPFFKRNPFLLDQIKRK
>d1fbqa_ a.4.5.22 (A:) Heat-shock transcription factor {Milk yeast (Kluyveromyces lactis)}
PAFVNKLWSMVNDKSNEKFIHWSTSGESIVPNRERFVQEVLLKKYFKHSNFASFVRQLNMYGWHK
VQDVKSGSMLSNNDSRWEFENERH
>d2hts_ a.4.5.22 (-) Heat-shock transcription factor {Milk yeast (Kluyveromyces lactis)}
ARPAFVNKLWSMVNDKSNEKFIHWSTSGESIVPNRERFVQEVLPKYFKHSNFASFVRQLNMYGW
HKVQDVKSGSNNDSRWEFENERHA
>d1if1a_ a.4.5.23 (A:) Interferon regulatory factor 1 (IRF-1) {Mouse (Mus musculus)}
RMRPWLEMQINSNIPGLIWINKEEMIFQIPWKHAAKHGWDINKDAFLFRSWAIHTGRYKAGEKE
PDPKTWKANFRCAMNSLPDIEEVKDQSRNKGSSAVRVYRM
>d2irfg_ a.4.5.23 (G:) Interferon regulatory factor-2, IRF-2 {Mouse (Mus musculus)}
RMRMRPWLEEQINSNTIPGLKWLNKEKKIFQIPWMHAARHGWDVEKDAPLFRNWAIHTGKHQP
GIDKDPKTWKANFRCAMNSLPDIEEVKDRSIKKGNNAFRVYRMLP
>d1g3sa1 a.4.5.24 (A:4-64) Diphtheria toxin repressor (DtxR) {Corynebacterium
diphtheriae}
LVDTTEMYLRTIYELEEEGVTPLRARIAERLEQSGPTVSQTVARMERDGLVVASDRSLQM
>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}
GQVIEVPPTLIYMYVRDVPVRVAQARFLLAKIKREYGTLPFAYRWLQNDMPEGQLKLALKTLEKAGA
IYGYVPLKEI

>d1b6a_1 a.4.5.25 (375-448) Methionine aminopeptidase, insert domain {Human (Homo sapiens)}
HDDMECSHYMKNFDVGHVPIRLPRTKHLLNVINENFGTLAFCRRWLDRLGESKYLKLNLCDLG
IVDPYPPLC

>d1g4da_ a.4.5.26 (A:) mu transposase, DNA-binding domain {Bacteriophage mu}
KSIWCSPQEIMAADGMPGSVAGVHYRANVQGWTKRKKKEGVKGGKAVEYDVMSPMPTKEREQVIAH
LGLST

>d1tns_ a.4.5.26 (-) mu transposase, DNA-binding domain {Bacteriophage mu}
MELWVSPKELANLPGLPKTSAGVIYVAKKQGWQNRTRAGVKGGKAIEYNANSLPVEAKAALLLRQG
EIETSLGYFE

>d1opc_ a.4.6.1 (-) OmpR {Escherichia coli}
VIAFGKFKLNLGTREMFREDEPMPLTSGEFAVLKALVSHPREPLSRDKLMNLARGREYSAMERSIDV
QISRLRRMVEEDPAHPRIQTVWGLGYVFPD

>d1kgsa1 a.4.6.1 (A:124-225) PhoB {Thermotoga maritima}
SKSTKLVCGDLILDATKKAYRGSKEIDLTKKEYQILEYLVMNKNRVVTKEELQEHLWSFDDEVFSDV
LRSHIKNLRKKVDKGFKKKIIHTVRGIGYVARDE

>d1qqia_ a.4.6.1 (A:) PhoB {Escherichia coli}
MAVEEVIEMQGLSLDPTSHRVMAGEEPLMGPTFKLLHFFMTHPERVYSREQLLNHVWGTNVYV
EDRTVDVHIRRLRKALEPGGHDRMVQTVRGTGYRFSTRF

>d1fsea_ a.4.6.2 (A:) Germination protein GerE {Bacillus subtilis}
SKPLLTKREREVFELLVQDKTTKEIASSELFISEKTVRNHISNAMQKLGVKGRSQAVVELLRMGEELEL

>d1a04a1 a.4.6.2 (A:150-216) Nitrate/nitrite response regulator (NarL) {Escherichia coli}
ERDVNQLTPRERDILKLIQAQLPNKMIARRLDITESTVKVHVKHMLKKMKLKSVEAAVWVHQRER
F

>d1fc3a_ a.4.6.3 (A:) SpoOA {Bacillus stearothermophilus}
NKPKNLDASITSIIHEIGVPAHIKGYLYLREAIAMVYHDIELLSITKVLYPDIAKKYNTTASRVERAIR
HAIEVAWSRGNLESISLFGYTVSVSKAKPTNSEFIAMVADKLRLEHKA

>d1fox_ a.4.7.1 (-) Ribosomal protein L11, C-terminal domain {Bacillus stearothermophilus}
MTFITKTPPAVLLKKAAGIESGSGEPNRNKVATIKRDKVREIAELKMPDLNAASIEAAMRMIEGTA
RSMGIVVED

>d1qa6a_ a.4.7.1 (A:) Ribosomal protein L11, C-terminal domain {Bacillus stearothermophilus}
KTPPAVLLKKAAGIESGSGEPNRNKVATIKRDKVREIAELKMPDLNAASIEAAMRMIEGTARSMGI

>d1mmsa1 a.4.7.1 (A:71-140) Ribosomal protein L11, C-terminal domain {Thermotoga maritima}
KTPPASFLKKAAGIEKGSSEPKRKIVGKVTRKQIEEIAKTKMPDLNANSLEAAMKIIEGTAKSMGIEV
V

>d1fjgr_ a.4.8.1 (R:) Ribosomal protein S18 {Thermus thermophilus}
PSRKAKVKATLGEFDLRDYRNVEVLKRFLSETGKILPRRRTGLSGKEQRILAKTIKRARILGLLPFTE
KLVK

>d1g1xc_ a.4.8.1 (C:) Ribosomal protein S18 {Thermus thermophilus}
DLRDYRNVEVLKRFLSETGKILPRRRTGLSGKEQRILAKTIKRARILGLLPFT

>d1i94r_ a.4.8.1 (R:) Ribosomal protein S18 {Thermus thermophilus}
KPKKEAQRPSRKAKVKATLGEFDLRDYRNVEVLKRFLSETGKILPRRRTGLSGKEQRILAKTIKRA

RILGLLPFTEKLVK

>d1e3ha1 a.4.9.1 (A:263-345) Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3 {Streptomyces antibioticus}

YQDDVLEALSAAVRPELSAALTIAGKQDREAELDRVKALAAEKLLPEFEGREKEISAAYRALTKSLVR
ERVIAEKKRIDGRGV

>d1k6ya1 a.4.10.1 (A:1-46) N-terminal Zn binding domain of HIV integrase {Human immunodeficiency virus type 1}

FLDGIDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDKCKQLK

>d1wjba_ a.4.10.1 (A:) N-terminal Zn binding domain of HIV integrase {Human immunodeficiency virus type 1}

FLDGIDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDKCKQLKGEAMHGQVD

>d1e0ea_ a.4.10.1 (A:) N-terminal Zn binding domain of HIV integrase {Human immunodeficiency virus type 2}

FLEKIEPAQEEHEKYHSNVKELSHKFGIPNLVARQIVNSCAQCQK

>d1ef4a_ a.4.11.1 (A:) RNA polymerase subunit RPB10 {Archaeon Methanobacterium thermoautotrophicum}

MIPVVRCLSCGKPVSAFYFNEYQRRVADGEDPKDVLDDGLKRYCCRRMLISHVETW

>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}

NAVREGSVVEALVGLGFAAKQAEATDQVLDGELGKDGAVATSSALRAALSLGKTR

>d1f4ia_ a.5.2.1 (A:) C-terminal UBA domain of the hhr23a DNA repair protein {Human (Homo sapiens)}

QEKEAIERLKALGFEEESLVIQAYFACEKNENLAANFLLSQNFDDE

>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)}

PAPTPSSSPVPTLSPEQQEMLQAFSTQSGMNLEWSQKCLQDNNWDYTRSAQAFTHLKAKGEIPEVA
FMK

>d1aua_1 a.5.3.1 (4-96) N-terminal domain of phosphatidylinositol transfer protein sec14p {Baker's yeast (Saccharomyces cerevisiae)}

QQEKEFLESYPQNCPPDALPGTPGNLDSAQEKALAE LRKLE DAGFIERLDDSTLLRFLRARKFDVQ
LAKEMFENCEKWRKDYGTDTILQDFH

>d1enwa_ a.5.4.1 (A:) Elongation factor TFIIS domain 2 {Baker's yeast (Saccharomyces cerevisiae)}

GSHMPRNSKNDGVDTAIYHHKLRDQVLKALYDVLAKESHPQSILHTAKAIESEMKNVNNCDTNE

AAYKARYRIIYSNVISKNNPDLKHKIANGDITPEFLATCDAKDLAPAP
>d1fjgm_ a.5.5.1 (M:) Ribosomal protein S13 {Thermus thermophilus}
ARIAGVEIPRNKRVDVALTYIYGIGKARAKEALEKTGINPATRVKDLTEAEVRLREYVENTWKLEGE
LRAEVAANIKRLMDIGCYRGLRHRRLPVRGQTRTNARTRKGPRTVAGKKKAPRK
>d1i94m_ a.5.5.1 (M:) Ribosomal protein S13 {Thermus thermophilus}
ARIAGVEIPRNKRVDVALTYIYGIGKARAKEALEKTGINPATRVKDLTEAEVRLREYVENTWKLEGE
LRAEVAANIKRLMDIGCYRGLRHRRL
>d1eija_ a.5.6.1 (A:) Hypothetical protein MTH1615 {Archaeon Methanobacterium
thermoautotrophicum}
MRQQLEMQKKQIMMQILTPEARSRLANLRLTRPDFVEQIELQLIQLAQMGVRVRSKITDEQLKELLKR
VAGKK
>d1jjcb1 a.6.1.1 (B:1-38,B:152-190) Domains B1 and B5 of PheRS-beta, PheT {Thermus
thermophilus (Thermus aquaticus)}
MRVPFSLKAYVPELESPEVLEERLAGLGFETDRIERVXEEVLDLEVTPNRPDALGLLGLARDLHA
LGYALVEPEAA
>d1jjcb2 a.6.1.1 (B:400-474) Domains B1 and B5 of PheRS-beta, PheT {Thermus
thermophilus (Thermus aquaticus)}
PPEAIPFRPEYANRLGTSYPEAEQIAILKRLGCRVEGEGPTYRVTPPSHRLDLRLEEDLVEEVARIQG
YETIPL
>d1d4ua1 a.6.1.2 (A:37-111) DNA repair factor XPA DNA- and RPA-binding domain,
C-terminal subdomain {Human (Homo sapiens)}
DKHKLITKTEAKQEYLLKDCDLEKREPPLKFIVKKNPHHSQWGMKLYLKLQIVKRSLEVWGSQEA
LEEAKEVRQ
>d1exja1 a.6.1.3 (A:3-120) Transcription activator BmrR {Bacillus subtilis}
ESYYSIGEVSKLANVSIKALRYDKIDLFKPAYVDPDTSYRYTDSQLIHLDLIKSLKYIGTPLEEMKKA
QDLEMEELFAFYTEQERQIREKLDFLSALEQTISLVKKRMKRQMEYPA
>d1jbg_ a.6.1.3 (A:) Multidrug transporter activator MtaN {Bacillus subtilis}
KYQVKQVAEISGVSIRTLHHYDNIELNPSALTDAGYRLYSADLERLQQLFFKEIGFRLDEIKEMLD
HPNFRKAALQSQKEILMKKKQRMDEMIQTIDRTLLS
>d2spca_ a.7.1.1 (A:) Spectrin {Fruit fly (Drosophila sp.)}
QNLDLQLYMRDCELAESWMSAREAFNLADDDANAGGNVEALIKKHEDFDKAINGHEQKIAALQTV
ADQLIAQNHASNLVDEKRKQVLERWRHLKEGLIEKRSRLGD
>d1aj3_ a.7.1.1 (-) Spectrin {Chicken (Gallus gallus)}
HQFFRMDDEESWIKEKLLVSSDYGRDLTGQVQNLKHKHRLEAELAAHEPAIQGVLDTGKKLSD
DNTIGKEEIQRLAQFVDHWKELKQLAAARGQ
>d1cuna1 a.7.1.1 (A:7-115) Spectrin {Chicken (Gallus gallus)}
MVHQFFRMDDEESWIKEKLLVSSDYGRDLTGQVQNLKHKHRLEAELAAHEPAIQSVLDTGKKL
SDDNTIGKEEIQRLAQFVDHWKELKQLAAARGQRLEESLEYQ
>d1cuna2 a.7.1.1 (A:116-219) Spectrin {Chicken (Gallus gallus)}
QFVANVEEEEAWINEKMTLVASEDYGDTLAAIQGLLKKHEAFETDFTVHKDRVNDVCANGEDLIKK
NNHHVENITAKMKGLKGVSDLEKAAAQRKAKLDENSA
>d1hcia1 a.7.1.1 (A:272-396) alpha-actinin {Human (Homo sapiens)}
SSAVNQENERLMEEYERLASELLEWIRRTIPWLENRTPEKTMQAMQKKLEDFRDYRRKHKPPKVQ
EKCQLEINFNTLQTKLRISNRPAFMPSEGMVSDIAGAWQRLEQAEGYEEWLLNEIRRL

>d1hcia4 a.7.1.1 (A:633-746) alpha-actinin {Human (Homo sapiens)}
HANERLRRQFAAQANAIGPWIQNKMEEIARSSIQITGALEDQMNQLKQYEHNIINYKNNIDKLEGD
HQLIQEALVFDNKHTNYTMEHIRVGVWELLLTTIARTINEVETQILTRD

>d1quua1 a.7.1.1 (A:1-124) alpha-actinin {Human (Homo sapiens)}
GSSNEIRRLERLEHLAEKFRQKASTHETWAYGKEQILLQKDYESASLTEVRALLRKHEAFESDLAAH
QDRVEQIAAIAQELNELDYHDAVNVDNRCQKICDQWDRLGTLTQKRREALERMEKLL

>d1quua2 a.7.1.1 (A:125-248) alpha-actinin {Human (Homo sapiens)}
ETIDQLHLEFAKRAAPFNWMEGAMEDLQDMFIVHSIEEIQSLITAHEQFKATLPEADGERQSIMAI
QNEVEKVIQSYNIRISSNPYSTVTMDELRTKWVKVQLVPIRQSLQEELARQHAN

>d1e2aa_ a.7.2.1 (A:) Enzyme IIa from lactose specific PTS, IIa-lac {Lactococcus lactis}
MNREEMTLGFEIVAYAGDARSKLLEALKAAENGDFAKADSLVVEAGSCIAEAHSSQTGMLAREASG
EELPYSVTMMHGQDHLMTTILLKDVIIHHLIELYKR

>d1chua1 a.7.3.1 (A:423-533) L-aspartate oxidase {Escherichia coli}
DESRVENPDERVVIQHNWHELRLFMWDYVGVIRTTKRLERLRRITMLQQEIDEYYAHFRVSNLL
ELRNLVQVAELIVRCAMMRKESRGLHFTLDYPELLTHSGPSILSP

>d1fuma1 a.7.3.1 (A:443-575) Fumarate reductase flavoprotein subunit {Escherichia coli}
DGGENWAKIRDEMGLAMEEGCGIYRTPELMQKTIDKLAELQERFKRVRITDTSSVFNTDLLYTIELG
HGLNVAECMAHSAMARKESRGAHQRLDEGCTERDDVNFLKHTLAFRDADGTTTRLEYSVKITTLP
P

>d1qlaa1 a.7.3.1 (A:458-655) Fumarate reductase flavoprotein subunit {Wolinella
succinogenes}
KGTEDVFKIKNRMKDVMDNNGIFRDGPHLEKSVKELEELYKKSKNVGIKNKRLHANPELEEAYRV
PMMLKVALCVAKGALDRTESRGAHNREDYPKRDDINWLNRTLASWPNPEQTLPTLEYEALDVNE
MEIAPRYRGYGAKGNYIENPLSVKRQEEIDKIQSELEAAGKDRHAIQEALMPYELPAKYKARNERLG
D

>d1jnra1 a.7.3.1 (A:503-643) Adenylylsulfate reductase A subunit {Archaeon Archaeoglobus
fulgidus}
TADDVNPEYILPWQGLVRLQKIMDEYAAGIATYKTNEKMLQRALELLAFLKEDLEKLAARDLHEL
MRAWELVHRVWTAEAHVHRHMLFRKETRWPGYYYRTDYPELNDEEWKCFVCSKYDAEKDEWTFE
KVPYVQVIEWSF

>d1fewa_ a.7.4.1 (A:) Smac/diablo {Human (Homo sapiens)}
SLSSEALMRRVSLVTDSTSTFLSQTTYALIEAITEYTKAVYTLTSLYRQYTSLLGKMNSEEEDEVWQV
IIGARAEMTSKHQEYKLETTWMTAVGLSEMAAEAAAYQTGADQASITARNHIQLVKLQVEEVHQLS
RKAETKLAEAQIEELKQKTQEEGEERAESEQEAYLRED

>d1g73a_ a.7.4.1 (A:) Smac/diablo {Human (Homo sapiens)}
AVPIAQKSEPHSLSSEALMRRVSLVTDSTSTDLSQTTYALIEAITEYTKAVYTLTSLYRQYTSLLGKM
NSEEEDEVWQVIIGARAEMTSKHQEYKLETTWMTAVGLSEMAAEAAAYQTGADQASITARNHIQLV
KLQVEEVHQLSRKAETKLAEAQ

>d1hx1b_ a.7.7.1 (B:) BAG-family molecular chaperon regulator-1, BAG1 {Human (Homo
sapiens)}
GNSPQEEVELKCLKHLEKSVEKIADQLEELNKELTGIQQGFLPKDLQAEALCKLDRRVKATIEQFMKI
LEEIDTLILPENFKDSRLKRKGLVKKVQAFLAECDTVEQNICQE

>d1i6za_ a.7.7.1 (A:) BAG-family molecular chaperon regulator-1, BAG1 {Mouse (Mus
musculus)}

GSPEFMLIGEKSNP EEEVELKKLKDLEVSAEKIANHLQELNKELSGIQGFLAKELQAEALCKLDRK
VKATIEQFMKILEEIDTMVLPEQFKDSRLKRKNLVKKVQVFLAECDTVEQYICQETERLQSTNLALA
E

>d1qsda_ a.7.5.1 (A:) beta-Tubulin binding post-chaperonin cofactor Rbl2p {Baker's yeast
(*Saccharomyces cerevisiae*)}

TQLDIKVKALKRLTKKEGGYYQELKDQEAHVAKLKEDKSVDPYDLKKQEEVLDDTKRLLPTLYEKIR
EFKEDLEQFLKTYQGTEDVSDARSAITSAQELLDS

>d1fjgt_ a.7.6.1 (T:) Ribosomal protein S20 {*Thermus thermophilus*}

RNLSALKRHRQSLKRRLRNKAKKSAIKTSLSKAVQLAQEGKAEALKIMRKAESLIDKAAKGSTLHK
NAAARRKSRLMRKVRQLLEAAGAPLIGGGLSA

>d1bdc_ a.8.1.1 (-) Immunoglobulin-binding protein A modules {*Staphylococcus aureus*}

TADNKFNKEQQNAFYEILHLPNLNNEQRNGFIQSLKDDPSQSANLLAEAKKLNDAPKA

>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*}

AQHDEAQQNAFYQVLNMPNLNADQRNGFIQSLKDDPSQSANVLGEAQKLNDAPKA

>d1fc2c_ a.8.1.1 (C:) Immunoglobulin-binding protein A modules {*Staphylococcus aureus*}

FNKEQQNAFYEILHLPNLNNEQRNGFIQSLKDDPSQSANLLAEA

>d2spza_ a.8.1.1 (A:) Immunoglobulin-binding protein A modules {*Staphylococcus aureus*}

VDNKFNKEQQNAFYEILHLPNLNNEQRNAFIQSLKDDPSQSANLLAEAKKLNDAPKA

>d1gab_ a.8.1.2 (-) PAB {*Peptostreptococcus magnus*}

TIDQWLLKNAKEDAIAELKKAGITSDFYFNAINKAKTVEEVNALKNEILKAHA

>d1gjta_ a.8.1.2 (A:) IgG binding protein G {*Streptococcus sp.*, group G}

MKAIFVLNAQHDEAVDANSLAEAKVLANRELDKYGVSDYYKLNINNAKTVEGVKALIDEILALP

>d1ebdc_ a.9.1.1 (C:) E3-binding domain of dihydrolipoamide acetyltransferase {*Bacillus
stearothermophilus*}

IAMPVSRKYAREKGVDIRLVQGTGKNGRVLKEDIDAFLAGG

>d1bal_ a.9.1.1 (-) E3-binding domain of dihydrolipoamide succinyltransferase {*Escherichia
coli*}

YASLEEQNNDALSPAIRLLAEHNLDAKGTGVTGGRLTREDVEKHLAKA

>d1bb_ a.9.1.1 (-) E3-binding domain of dihydrolipoamide succinyltransferase {*Escherichia
coli*}

LSPAIRLLAEHNLDAKGTGVTGGRLTREDVEKHL

>d2erl_ a.10.1.1 (-) ER-1 {*Euplotes raikovi*}

DACEQAAIQCVESACESLCTEGEDRTGCYMYIYSNCPYPV

>d1erd_ a.10.1.1 (-) ER-2 {*Euplotes raikovi*}

DPMTCEQAMASCEHTMCGYCQGPLYMTICIGITTDPECGLP

>d1erp_ a.10.1.1 (-) ER-10 {*Euplotes raikovi*}

DLCEQSALQCNEQGCHNFCSPEDKPGCLGMVWNPELCP

>d1ery_ a.10.1.1 (-) ER-11 {*Euplotes raikovi*}

DECANAAAQCSITLCNLYCGPLIEICELTMQNCEPPFS

>d1hd6a_ a.10.1.1 (A:) ER-22 {*Euplotes raikovi*}

DICDIAIAQCSLTLQCDCENTPICELAVKGSPPWS

>d1aca_ a.11.1.1 (-) Acyl-CoA binding protein {Cow (*Bos taurus*)}

SQAEFDKAAEEVKHLKTKPADEEMFLFIYSHYKQATVGDINTERPGMLDFKGGKAKWDAWNEKLGTS
KEDAMKAYIDKVEELKKKYGI

>d1hbka_ a.11.1.1 (A:) Acyl-CoA binding protein {Plasmodium falciparum}
HMAQQVFEEECVSFINGLPRITINNLNELKLDLYKYYKQSTIGNCNIKEPSAHKYIDRKKYEEAWKS
VENLNREDAQKKRYVDIVSEIFPYWQD

>d1ef1a1 a.11.2.1 (A:88-198) Moesin {Human (Homo sapiens)}
DVSEELIQDITQRLFFLQVKEGILNDDIYCPPETAVLLASYAVQSKYGDFNKEVHKSGYLAGDKLLPQR
VLEQHKLKNDQWEERIQVWHEEHRGMLREDAVLEYLKIAQDL

>d1gc7a1 a.11.2.1 (A:88-198) Radixin {Mouse (Mus musculus)}
DVSEELIQEITQRLFFLQVKEAILNDEIYCPPETAVLLASYAVQAKYGDYNKEIHKPGYLANDRLLPQR
VLEQHKLTKEQWEERIQNWHEEHRGMLREDSMMEYLKIAQDL

>d1gg3a1 a.11.2.1 (A:82-187) Erythroid membrane protein 4.1R {Human (Homo sapiens)}
PDPAQLTEDITRYYLCLQLRQDIVAGRLPCSFATLALLGSYTIQSELGDYDPELHGVDYVSDFKLAPNQ
TKELEEKVMELHKSYSRSMTPAQADLEFLENAKKLSMY

>d1h4ra1 a.11.2.1 (A:104-214) Merlin {Human (Homo sapiens)}
NAEEELVQEITQHLFFLQVKKQILDEKIYCPPEASVLLASYAVQAKYGDYDPSVHHRGFLAQEELLPKR
VINLYQMTPEMWEERITAWYAEHRGRARDEAEMEYLKIAQDL

>d1kdx_ a.12.1.1 (A:) Kix domain of CBP (creb binding protein) {Mouse (Mus musculus)}
GVRKGWHEHVTQDLRSHLVHKLVAIFPTPDPAALKDRRMENLVAYAKKVEGDMYESANSRDEYY
HLLAEKIYKIQKELEE

>d1lre_ a.13.1.1 (-) alpha-2-Macroglobulin receptor associated protein (RAP) domain 1
{Human (Homo sapiens)}
GEEFRMEKLNQLWEKAQRLHLPPVRLAELHADLKIQRDELAWKCLKLDGLDEDEGEKEARLIRNL
NVILAKYGLDGKKDAR

>d1qqva_ a.14.1.1 (A:) Thermostable subdomain from chicken villin headpiece {Chicken
(Gallus gallus)}
PTKLETFLDVLVNTAAEDLPRGVDP SRKENHLSDEDFKAVFGMTRSAFANLPLWKQQLKKEKGL
F

>d1vii_ a.14.1.1 (-) Thermostable subdomain from chicken villin headpiece {Chicken (Gallus
gallus)}
MLSDEDFKAVFGMTRSAFANLPLWKQQLKKEKGLF

>d1tbaa_ a.15.1.1 (A:) TAF(II)230 TBP-binding fragment {Fruit fly (Drosophila
melanogaster)}
EGSIGNGLDLTGILFGNIDSEGRLLQDDDGEGRGGTGFDAELRENIGSLSKLGLD SMLLEVIDLKEA

>d1ail_ a.16.1.1 (-) N-terminal, RNA-binding domain of nonstructural protein NS1
{Influenza A virus}
MDSNTVSSVFQVDCFLWHVRKQVVDQELGDAPFLDRLRRDQKSLRGRGSTLGLNIEAATHVKGQIVE
KILK

>d1a32_ a.16.1.2 (-) Ribosomal protein S15 {Bacillus stearothermophilus}
LTQERKREIIEQFKVHENDTGSPEVQIAILTEQINNLEHLRVHKKDHH SRRGLLMVGRRRLLAY
LRNKDVARYREIVEKLG L

>d1dk1a_ a.16.1.2 (A:) Ribosomal protein S15 {Thermus thermophilus}
PITKEEKQKVMQEFARFPGDTGSTEVQVALLTLRINRLSEHLKVHKKDHH SHRGLLMVGRRRLL
RYLQREDPERYRMLIEKLG I

>d1g1xb_ a.16.1.2 (B:) Ribosomal protein S15 {Thermus thermophilus}
PITKEEKQKVIQEFARFPGDTGSTEVQVALLTLRINRLSEHLKVVHKKDHSHRGLLMMVQGRRRLLR
YLQREDPERYREIVEKLGRLG

>d1d2da_ a.16.1.3 (A:) Multifunctional Glu-Pro-tRNA synthase (EPRS) second repeated
element {Chinese hamster (Cricetulus griseus)}
MVYDKIAAQGEVVRKLKAEKAPKAKVTEAVECLLSLKAHEYKEKTGKEYVPGLEHHH

>d1fyja_ a.16.1.3 (A:) Multifunctional Glu-Pro-tRNA synthase (EPRS) second repeated
element {Human (Homo sapiens)}
DSLVLNRYAVQGDVVRELKAKKAPKEDVDAAVKQLLSLKAHEYKEKTGQEQYKPGNPP

>d2hp8_ a.17.1.1 (-) p8-MTCP1 {Human (Homo sapiens)}
MPQKDPCKQKACEIQKCLQANSYMESKCAVIQELRKCCAQYPKGRSVVCSGFEKEEEENLTRKSAS
K

>d1ijxa_ a.141.1.1 (A:) Secreted Frizzled-related protein 3 (SFRP-3;fzb) {Mouse (Mus
musculus)}
AACEPVRIPCKSLPWEMTKMPNHLHHSTQANAILAMEQFEGLLGTHCSPDLLFFLCAMYAPICTID
FQHEPIKPKSV CERARQGCEPILIKYRHSWPE SLACDEL PVYDRGVCISPEAIVTAD

>d1ijya_ a.141.1.1 (A:) Frizzled 8 (FZ8) {Mouse (Mus musculus)}
ELACQEITVPLCKGIGYEYTYMPNQFNHDTQDEAGLEVHQFWPLVEIQ CSPDLKFFLC SMYTPICLE
DYKKPLPPCRSVCERAKAGCAPLMRQYGF AWPDRMRC DRLPEQGNPD TLCMDYER

>d2end_ a.18.1.1 (-) T4 endonuclease V {Bacteriophage T4 (Escherichia coli)}
TRINLTLVSELADQHLMAEYRELPRVFGAVRKHVANGKRVRDFKISPTFILGAGHVTFYDKLEFLRK
RQIELIAECLKRGFNIKDTTVQDISDIPQEFRGDYIPHEASIAISQARLDEKIAQRPTWYKYYGKAIYA

>d2lisa_ a.19.1.1 (A:) Lysin {Red abalone (Haliotis rufescens)}
HYVEPKFLNKA FEVALKVQIIAGFDRGLVKWLRVHGRTLSTVQKKALYFVNRRYMQTHWANYMLW
INKKIDALGRTPVVG DYTRLGAEIGRRIDMAYFYDFLKDKNMIPKYL PYMEEINRMRPADVPVKYM

>d3lyna_ a.19.1.1 (A:) Lysin {Green abalone (Haliotis fulgens)}
INKAYEVTMKIQIISGFDRQLTAWLRVHGRRLTNNQKKT LFFVNRRYMQTHWQNYMLVVKRRIKA
LGRPAAVGDYTRLGAEIGRRVDMVFFYNFLSGRKMIPPYSAYMAKLNALRPADVPVK

>d1gaka_ a.19.1.1 (A:) SP18 {Abalone (Haliotis fulgens)}
FDDVVVSRQE QSYVQRGMVNFLDEEMHKLVKFRFRDMRWNLGPGFVFLKKNRERMMRYCMDY
ARYSKKILQLKHL PVNKKTLTKMGRFVGYRNYGVIRELYADVFRDVQGF RGPKMTAAMRKYSSKDP
GTFPCKNE

>d1lbu_1 a.20.1.1 (1-83) Zn²⁺ DD-carboxypeptidase, N-terminal domain {Streptomyces
albus G}
DGCYTWSGTLSEGSSEAVRQLQIRVAGYPGTGAQLAIDGQFGPATKAAVQRFQSA YGLAADGIAGPA
TFNKIYQLQDD DCTP

>d1ck7a6 a.20.1.2 (A:31-107) Gelatinase A {Human (Homo sapiens)}
PSPIIKFPGDVAPKTDKELAVQYLNTFYGCPKESC NLFVLKDTLKKMQKFFGLPQTGDLDQNTIETM
RKPRCGNPDV

>d1slm_1 a.20.1.2 (16-80) Stromelysin-1 (MMP-3) {Human (Homo sapiens), fibroblast}
LVQKYLENYDDLKDVKQFVRRKDSGPVVKKIREMQKFLGLEVTGKLDSDTLEVMRKPRCGVDPV

>d1aab_ a.21.1.1 (-) HMG1, domains A and B {Rat (Rattus norvegicus)}
GKGDPKPRGKMSSYAFFVQTSREEHKKKHPDASVNFSEFSKCSERWKTMSAKEKGFEDMAKA
DKARYEREMKTYIPPKGE

>d1ckta_a.21.1.1 (A:) HMG1, domains A and B {Rat (*Rattus norvegicus*)}
KPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGFEDMAKADKARYE
REMKTY

>d1hme_a.21.1.1 (-) HMG1, domains A and B {Rat (*Rattus norvegicus*)}
FKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAACLKEK
YEKDIAAYRAK

>d1hsm_a.21.1.1 (-) HMG1, domains A and B {Hamster (*Cricetulus griseus*)}
NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAACLKEKYEKD
IAAYRAKGPDA

>d1qrva_a.21.1.1 (A:) HMG-D {*Drosophila melanogaster*}
SDKPKRPLSAYMLWLNARESIKRENPGIKVTEVAKRGGELWRAMKDKSEWEAKAAKAKDDYDRA
VKEFEANG

>d1cg7a_a.21.1.1 (A:) NHP6a {Baker's yeast (*Saccharomyces cerevisiae*)}
MVTTPREPKRTRTKKDPNAPKRALSAYMFFANENRDIVRSENPDITFGQVGKLGKWKALTP
EKQPYEAKAQADKKRYESEKELYNATLA

>d1hrza_a.21.1.1 (A:) SRY {Human (*Homo sapiens*)}
DRVKRPMNAFIVWSRDQRRKMALENPRMRNSEISKQLGYQWKMLTEAEKWPFFQEAQKLQAMH
REKYPNYKYR

>d1j46a_a.21.1.1 (A:) SRY {Human (*Homo sapiens*)}
MQDRVKRPMNAFIVWSRDQRRKMALENPRMRNSEISKQLGYQWKMLTEAEKWPFFQEAQKLQA
MHREKYPNYKYRPRRKAKMLPK

>d1i11a_a.21.1.1 (A:) Sox-5 {Mouse (*Mus musculus*)}
PHIKRPMNAFMVWAKDERRKILQAFPMHNSNISKILGSRWKAMTNLEKQPYEEQARLSKQHLE
KYPDY

>d2lefa_a.21.1.1 (A:) Lymphoid enhancer-binding factor, LEF1 {Mouse (*Mus musculus*)}
MHIKKPLNAFMLYMKEMRANVVAESTLKESAAINQILGRRWHALSREEQAKYYELARKERQLHM
LYPGWSARDNYGKKKKRKRKREK

>d1k99a_a.21.1.1 (A:) Upstream binding factor, the first HMG box {Human (*Homo sapiens*)}
MKKLLKHPDFPKKPLTPYFRFFMEKRAKYAKLHPMSNLDLTKILSKKYKELPEKKMKYIQDFQR
EKQEFERNLARFREDHPDLIQNAKK

>d1eqza_a.22.1.1 (A:) Histone H2A {Chicken (*Gallus gallus*), erythrocytes}
SGRGKQGGKARAKAKSRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAADVLEYLTAEILELAG
NAARDNKKTRIIPRHLQLAIRNDEELNKLKGVTTIAQGGVLPNIQAVLLPKKTDHKA

>d1hioa_a.22.1.1 (A:) Histone H2A {Chicken (*Gallus gallus*), erythrocytes}
KSRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAADVLEYLTAEILELAGNAARDNKKTRIIPR
HLQLAIRNDEELNKLKGVTTIAQGGVLP

>d1hq3a_a.22.1.1 (A:) Histone H2A {Chicken (*Gallus gallus*), erythrocytes}
KAKSRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAADVLEYLTAEILELAGNAARDNKKTRIIP
RHLQLAIRNDEELNKLKGVTTIAQGGVLPNIQAVLLPK

>d1aoc_a.22.1.1 (C:) Histone H2A {African clawed frog (*Xenopus laevis*)}
GKQGGKTRAKAKTRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAADVLEYLTAEILELAGNAA
RDNKKTRIIPRHLQLAVRNDEELNKLKGRVTIAQGGVLPNIQSVLLPK

>d1f66c_a.22.1.1 (C:) Histone H2A {Human (*Homo sapiens*), variant H2A.Z}
AVSRSRAGLQFPVGRIHRHLKSRRTTSHGRVGATAAVYSAAILEYLTAEVLELAGNASKDLKVKRITP

RHLQLAIRGDEELDSLKATIAGGGVIPHIHKSLLI

>d1id3c_ a.22.1.1 (C:) Histone H2A {Baker's yeast (*Saccharomyces cerevisiae*), H2A.1}
 QRSRAKAGLTFPVGRVHRLRRGNYAQRIGSGAPVYLTAVLEYLAAEILELAGNAARDNKKTRIIPRH
 LQLAIRNDELNKLGNVTIAQGGVLPNIHQNLLPKKSAKAT

>d1eqzb_ a.22.1.1 (B:) Histone H2B {Chicken (*Gallus gallus*), erythrocytes}
 VTKTQKKGDKRKRKSRKESYSIYVYKVLKQVHPDTGISSKAMGIMNSFVNDIFERIAGEASRLAHYN
 KRSTITSREIQTAVRLLLPGELAKHAVSEGTKAVTKYTSSK

>d1hiob_ a.22.1.1 (B:) Histone H2B {Chicken (*Gallus gallus*), erythrocytes}
 SYSIYVYKVLKQVHPDTGISSKAMGSMNSFVNDIFERIAGLASRLAHYNKRSTITSREIQTAVRLLLP
 ELAKHAVSEGTKAVTKHTSSK

>d1hq3b_ a.22.1.1 (B:) Histone H2B {Chicken (*Gallus gallus*), erythrocytes}
 RKESYSIYVYKVLKQVHPDTGISSKAMGIMNSFVNDIFERIAGEASRLAHYNKRSTITSREIQTAVRLL
 LPGELAKHAVSEGTKAVTKYTSS

>d1aoid_ a.22.1.1 (D:) Histone H2B {African clawed frog (*Xenopus laevis*)}
 KRRRKTRKESYAIYVYKVLKQVHPDTGISSKAMSIMNSFVNDVFERIAGEASRLAHYNKRSTITSREI
 QTAVRLLLPGELAKHAVSEGTKAVTKYTSK

>d1id3d_ a.22.1.1 (D:) Histone H2B {Baker's yeast (*Saccharomyces cerevisiae*), H2B.2}
 RKETYSSYIYKVLKQTHPDTGISQKSMNSFVNDIFERIATEASKLAAYNKKSTISAREIQTAVRLLILP
 GELAKHAVSEGTRAVTKYSSST

>d1eqzc_ a.22.1.1 (C:) Histone H3 {Chicken (*Gallus gallus*), erythrocytes}
 APATGGVKKPHRYRPGTVALREIRRYQKSTELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEAS
 EAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA

>d1eqzg_ a.22.1.1 (G:) Histone H3 {Chicken (*Gallus gallus*), erythrocytes}
 PRKQLATKAARKSAPATGGVKKPHRYRPGTVALREIRRYQKSTELLIRKLPFQRLVREIAQDFKTDLR
 FQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA

>d1hq3c_ a.22.1.1 (C:) Histone H3 {Chicken (*Gallus gallus*), erythrocytes}
 YRPGTVALREIRRYQKSTELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNL
 CAIHAKRVTIMPKDIQLARRIRGERA

>d1id3a_ a.22.1.1 (A:) Histone H3 {Baker's yeast (*Saccharomyces cerevisiae*)}
 PHRYKPGTVALREIRRFQKSTELLIRKLPFQRLVREIAQDFKTDLRFQSSAIGALQESVEAYLVSLFED
 TNLAAIHAKRVTIQKKEIKLARRLRGER

>d1eqzh_ a.22.1.1 (H:) Histone H4 {Chicken (*Gallus gallus*), erythrocytes}
 KGLGKGGAKRHRKVLDRDNIQGITKPAIRRLARRGGVKRISGLIYEETRGVLKVFLENVIRDAVITYTEH
 AKRKTVTAMDVVYALKRQGRTLYGFGG

>d1hq3d_ a.22.1.1 (D:) Histone H4 {Chicken (*Gallus gallus*), erythrocytes}
 KVLDRDNIQGITKPAIRRLARRGGVKRISGLIYEETRGVLKVFLENVIRDAVITYTEHAKRKTVTAMDVV
 YALKRQGRTLYGFGG

>d1id3b_ a.22.1.1 (B:) Histone H4 {Baker's yeast (*Saccharomyces cerevisiae*)}
 DNIQGITKPAIRRLARRGGVKRISGLIYEEVRAVLKSFLESVIRDSVITYTEHAKRKTVTSLDVVYALKR
 QGRTLYGFGG

>d1b67a_ a.22.1.2 (A:) Archaeal histone {Archaeon *Methanothermobacter thermautotrophicus*, histone A}
 GELPIAPIGRIIKNAGAERVSDDARIALAKVLEEMGEEIASEAVKLAKHAGRKTIKAEDIELARKMFK

>d1a7w_ a.22.1.2 (-) Archaeal histone {Archaeon *Methanothermobacter thermautotrophicus*, histone B}
 MELPIAPIGRIIKDAGAERVSDDARITLAKILEEMGRDIASEAIKLARHAGRKTIKAEDIELAVRRFK

>d1f1ea_a.22.1.2 (A:) Archaeal histone {Archaeon Methanopyrus kandleri}
ELPKAAIERIFRQIGIGERRLSQDAKDTIYDFVPTMAEYVANAAKSVLDASGKKTLMEEHLKALADVL
MVEGVEDYDYGELFGRATVRRILKRAGIERASSDAVDLYNKLICRATEELGEKAAEYADEDEDGRKTVQG
EDVEKAITYSMPKGGEL

>d1tafa_a.22.1.3 (A:) TAF(II)42 {Fruit fly (Drosophila melanogaster)}
PKDAQVIMSILKELNVQEYEPVVNQLEFFRYVTSILDDAKVYANHARKKTIDLDDVRLATEVTL
D

>d1tafb_a.22.1.3 (B:) TAF(II)62 {Fruit fly (Drosophila melanogaster)}
MLYGSSISAESMKVIAESIGVGLSDDAAKELAEDVSIKLRIVQDAAKFMNHAKRQKLSVRDIDMSL
KV

>d1bh9a_a.22.1.3 (A:) TAF(II)18 {Human (Homo sapiens)}
LFSKELRCMMYGFDDQNPYTESVDILEDLVIEFITEMTHKAMSI

>d1bh9b_a.22.1.3 (B:) TAF(II)28 {Human (Homo sapiens)}
FSEQLNRYEMYRRSAFPKAAIKRLIQSITGTSVSNVVIAMSGISKVVFVGEVVEEALDVCEKWGEMP
PLQPKHMRREAVRRLKSKGQIP

>d1jfa_a.22.1.3 (A:) Negative cofactor 2, NC2, alpha chain {Human (Homo sapiens)}
ARFPPARIKKIMQTDDEIGKVAAPVVIISRALELFLESLLKACQVTQSRNAKTMTTSHLKQCIE

>d1jfb_a.22.1.3 (B:) Negative cofactor 2, NC2, beta chain {Human (Homo sapiens)}
DDLTPRAAINKMIKETLPNVRVANDARELVVNCCTEFIHLISSEANEICNKSEKKTISPEHVIQALESL
GFGSYISEVKEVLQECKTVALKRRKASSRLENLGIPEEELLRQQQELFAKARQQQAELAQQEWLQ

>d1fpoa2_a.23.1.1 (A:77-171) HSC20 (HSCB), C-terminal oligomerisation domain
{Escherichia coli}
FDLASEQHTVRDTAFLMEQLELREELDEIEQAKDEARLESFIKRVKMFDRHQLMVEQLDNETW
DAAADTCRKLRLDKLRSSAEQLEEKLLDF

>d1eexg_a.23.2.1 (G:) Diol dehydratase, gamma subunit {Klebsiella oxytoca}
SARVSDYPLANKHPEWVKATATNKTLDDFTLENVLSNKVTAQDMRITPETLRLQASIAKDAGRDLA
MNFERAAELTAVPDDRILEIYNALRPYRSTKEELLAIAADDLESRYQAKICAAFVREAATLYVERKCLK
GDD

>d1mtyg_a.23.3.1 (G:) Methane monooxygenase hydrolase, gamma subunit {Methylococcus
capsulatus}
LGIHSDTRDAWVNKIAHVNTLEKAAEMLKQFRMDHTTTPFRNSYELDNDYLWIEAKLEEKVAVLK
ARAFNEVDFRHKTAFGEDAKSVLDGTVAKMNAAKDKWEAEKIHIGFRQAYKPPIMPVNYFLDGER
QLGTRLMELRNLNYYDTPLEELRKQRGVRVH

>d1mhyg_a.23.3.1 (G:) Methane monooxygenase hydrolase, gamma subunit {Methylosinus
trichosporium}
AKREPIHDNSIRTEWEAKIAKLTSDQATKFIQDFRLAYTSPFRKSYDIDVDYQYIERKIEEKLSVLKT
EKLPVADLITKATTGEDAAVEATWIAKIKAAKSKYEAEAIHIEFRQLYKPPVLPVNVFLRTDAALGT
VLMEIRNTDYYGTPLEGLRKERGVKVLHLQ

>d1om2a_a.23.4.1 (A:) Mitochondrial import receptor subunit Tom20 {Rat (Rattus
norvegicus)}
RAGLSKLPDLKDAEAVQKFFLEEIQLGEELLAQGDYEEKVDHLTNAIAVCGQPQQLLQVLQQTLP
VFQMLLTKLPTISQRIVSAQSLGEDDVE

>d1jw2a_a.23.5.1 (A:) Hemolysin expression modulating protein HHA {Escherichia coli}
MSEKPLTKTDYLMRLRRCQTIDTLERVIEKNKYELSDNELAVFYSAADHRLAELTMNKLYDKIPSSV

WKFIR

>d1nfn_ a.24.1.1 (-) Apolipoprotein E3 {Human (Homo sapiens)}

GQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELRALMDETMKELKAYKSELEEQLTPVAE
ETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRKRLLRDAD
DLQKRLAVYQA

>d2asr_ a.24.2.1 (-) Aspartate receptor, ligand-binding domain {Escherichia coli}

KSFVVSQNLREQQELTSTWDLMLQTRINLSRSAVRMMMDSSNQSNKVELLDSARKTLAQAAT
HYKFKSMAPLPEMVATSRNIDEKYKNYYTALTELIDYLDYGNTGAYFAQPTQGMQNAMGERFAQY
ALSSEKLYRDI

>d1vta_ a.24.2.1 (A:) Aspartate receptor, ligand-binding domain {Salmonella typhimurium}

GFVISNELRQQSELTSTWDLMLQTRINLSRSAARMMDASNQSSAKTDLLQNAKTTLAQAAAH
YANFKNMTPLPAMAEASANVDEKYQRYQAALAEIQFLDNGNMDAYFAQPTQGMQNALGEALGNY
ARVSENLYRQTF

>d2liga_ a.24.2.1 (A:) Aspartate receptor, ligand-binding domain {Salmonella typhimurium}

MGLLFSSLQHCQQGFVISNELRQQSELTSTWDLMLQTRINLSRSAARMMDASNQSSAKTDLL
QNAKTTLAQAAAHYANFKNMTPLPAMAEASANVDEKYQRYQAALAEIQFLDNGNMDAYFAQPTQ
GMQNALGEALGNYARVSENLYRQTFD

>d256ba_ a.24.3.1 (A:) Cytochrome b562 {Escherichia coli}

ADLEDNMETLNDNLKVIKADNAAQVKDALTKMRAAALDAQKATPPKLEDKSPDPEMKDFRHG
FDILVQGIDDALKLANEGKVKEAQAQAAEQLKTRNAYHQYR

>d2ccya_ a.24.3.2 (A:) Cytochrome c' {Rhodospirillum molischianum}

QSKPEDLLKLRQGLMQTLKSQWVPIAGFAAGKADLPADAAQRAENMAMVAKLAPIGWAKGTEALP
NGETKPEAFGSKSAEFLEGWKALATESTKLAAAAGKAGPDALKAQAATGKVCKACHEEFKQD

>d1bbha_ a.24.3.2 (A:) Cytochrome c' {Chromatium vinosum}

AGLSPEEQIETRQAGYEFMGWNMGKIKANLEGEYNAQVEAAANVIAAIANSNGMGALYGPPTDKNV
GDVKTTRVKPEFFQNMEDVGKIAREFVGAANTLAEVAATGEAEAVKTAFGDVGAAACKSCHEKYRAK

>d1e85a_ a.24.3.2 (A:) Cytochrome c' {Alcaligenes sp.}

EFAKPEDAVKYRQSALTLMAHFGRMTPVVKQAPYDAAQIKANVEVLKTLALSALPWAAFPGTEGG
DARPEIWSAASFQKQAFQDNIVKLSAAADAGDLKLRRAAFDVGASCKACHDAYRK

>d1jafa_ a.24.3.2 (A:) Cytochrome c' {Rhodocyclus gelatinosus}

QFQKPGDAIEYRQSAFTLIANHFGRVAAMAQKAPFDKVAENIALVSTLSKLPPLTAFGPGTDKGH
GTEAKPAVWSDAAGFKAAADKFAAAVDKLDAAAGKTGDFAQIKA AVGETGGACKGCHDKFKE

>d1cpq_ a.24.3.2 (-) Cytochrome c' {Rhodobacter capsulatus}

ADTKEVLEAREAYFKSLGGSMKAMTGVAKAFDAEAAKVEAAKLEKILATDVAPLFPAGTSSTDLPQG
TEAKAAIWANMDDFGAKGKAMHEAGGAVIAAANAGDGAAFGAALQKLGCTCKACHDDYREED

>d1a7va_ a.24.3.2 (A:) Cytochrome c' {Rhodopseudomonas palustris}

QTDVIAQRKAILKQMGEATKPIAAMLKGEAKFDQAVVQKSLAAIADDSKLPALFPADSKTGGDTAA
LPKIWEDKAKFDDLFAKLAAAATAAQGTIKDEASLKANIGGVLGNCKSCHDDFRACKS

>d2hmza_ a.24.4.1 (A:) Hemerythrin {Sipunculid worm (Themiste dyscrita)}

GFPIPDPCWDISFRTFYITVDDEHKTFLNGILLSSQADNADHLNELRRCTGKHFLNEQQMLQASQY
AGYAEHKKAHDDFIHKLDTWDGDVTYAKNWLNVNHIKTIDFKYRGKI

>d1hrb_ a.24.4.1 (-) Hemerythrin {Phascolopsis gouldii}

GFPIPDPCVWDPSFRTFYSIIDDEHKTFLNGIFHLAIDNADNLGELRRCTGKHFLNQEVLMEASQY
QFYDEHKKEHDFINALDNWKGDKWAKAWLVNHIKTIDFKYKGI

>d1i4ya_a.24.4.1 (A:) Hemerythrin {Phascolopsis gouldii}
GFPIPDYVWDPFRFTFYIIDEHKTFLNGIFHLAIDNADNLGELRRCTGKHFLENEQVLMQASQY
QFYDEHKKEHETFIHALDNWKGVDKWKASWLVNHIKTIDFKYKGI
>d2mhr_ a.24.4.1 (-) Myohemerythrin {Sipunculan worm (Themiste zostericola)}
GWEIPEPYVWDESRVVFYEQLEDEHKKIFKGFDCIRDNSAPNLATLVKVTNHFTHHEAMMDAAK
YSEVVPHKMKHKDFLEKIGGLSAPVDAKNVDYCKEVLVNHKGTDFKYKGL
>d1ei7a_ a.24.5.1 (A:) Tobacco mosaic virus coat protein {Tobacco mosaic virus, vulgare strain}
SYSITTPSQFVFLSSAWADPIELINLCTNALGNQFQTQQARTVVQRQFSEVWKPSQVTVRFPDSD
KVYRYNAVLDPDLTALLGAFDTRNRRIEVENQANPTTAETLDATRRVDDATVAIRSAINNLIVELIRGT
GSYNRSSFESSGLVWTS GPAT
>d1vtmp_ a.24.5.1 (P:) Tobacco mosaic virus coat protein {Tobacco mosaic virus, vulgare strain}
PYTINSPSQFVYLSSAYADPVELINLCTNALGNQFQTQQARTTVQQFADAWKPSVMTVTRFPASDF
YVYRYNSTLDPLITALLNSFDTRNRRIEVNQPAPNTTEIVNATQRVDDATVAIRASINNLANELVRGT
GMFNQAGFETASGLVWTTTPAT
>d1cgme_ a.24.5.1 (E:) Cucumber green mottle mosaic virus {Cucumber green mottle mosaic virus, strain watermelon}
AYNPITPSKLIAFSASYVPVRTLLNFLVASQGTAFQTQAGRDSFRESLSALPSSVVDINSRFPDAGFYAF
LNGPVLRPVFLSSTDRNRVIEVVDPSNPTTAESLNAVKTDDASTAARAEIDNLIESISKGFVY
DRASFEEAFSVVWSEATTSKA
>d1rmva_ a.24.5.1 (A:) Ribgrass mosaic virus {Ribgrass mosaic virus}
SYNITNSNQYQYFAAVWAEPTPMLNQCVSALSQSYQTQAGRDTVRQQFANLLSTIVAPNQRFPDTGF
RVYVNSAVIKPLYEALMKSFDTRNRRIETEEESRPSASEVANATQRVDDATVAIRSQIQLLLNELSNGH
GYMNAEFEEAILPWTTAPAT
>d3fapb_ a.24.7.1 (B:) FKBP12-rapamycin-binding domain of FKBP-rapamycin-associated protein (FRAP) {Human (Homo sapiens)}
VAILWHEMWHEGLEEARLYFGERNVKGMFVLEPLHAMMERGPQTLKETSFNQAYGRDLMEAQ
EWCRCYMKSGNVKDLTQAWDLYYHVFRRIS
>g1avo.1 a.24.8.1 (A,B:) Proteasome activator reg(alpha) {Human (Homo sapiens)}
LRVQPEAQAKVDVFREDLCTKTENLLGSYFPKKISELDAFLKEPALNEANLSNLKAPLDIXAVNCNE
KIVVLLQRLKPEIKDVIEQLNLVTTWLQLQIPRIEDGNNFGVAVQEKFELMTSLHTKLEGFHTQISK
YFSERGDVTKAAKQPHVGDYRQLVHELDEAEYRDIRLMVMEIRNAYAVLYDIILKNFEKLLKPRG
>d1dova_ a.24.9.1 (A:) alpha-catenin {Mouse (Mus musculus)}
ESQFLKEELVVAVEDVRKQGDLMKSAAGEFADDPCCSVKRGNMVRAARALLSAVTRLLILADMADV
YKLLVQLKVVEDGILKLRNAGNEQDLGIQYKALKPEVDKLNIMAARQQELKDVGNRDQMAAARGI
LQKNVPILYASQACLQHPDVAAYKANRDLIYKQLQQA VGTGISNAAQAT
>d1dowa_ a.24.9.1 (A:) alpha-catenin {Mouse (Mus musculus)}
KAHVLAASVEQATENFLEKGDKIAKESQFLKEELVVAVEDVRKQGDLMKSAAGEFADDPCCSVKRG
MVRAARALLSAVTRLLILADMADVYKLLVQLKVVEDGILKLRNAGNEQDLGIQYKALKPEVDKLN
MAAKRQQELKDVGNRDQMAAARGILQKNVPILYASQACLQHPDVAAYKANRDLIYKQLQQA VGT
SNAQA
>d1h6ga1 a.24.9.1 (A:377-507) alpha-catenin {Human (Homo sapiens)}
DLRRQLRKAVMDHVSDSFLETNVPLLVLIEAAKNGNEKEVKEYAQVFREHANKLIEVANLACISNN

EEGVKLVMSASQLEALCPQVINAALALAAKPQSKLAQENMDLFKEQWEKQVRVLTDAVDDITS
>d1h6ga2 a.24.9.1 (A:508-631) alpha-catenin {Human (Homo sapiens)}
IDDFLAVSENHILEDVNCVIALQEKDVDGLDRTAGAIRGRAARVIHVVTSEMDNYEPGVYTEKVLE
ATKLLSNTVMPRFTEQVEAAVEALSSDPAQPMDEFIDASRLVYDGIKAVLM
>d1h6gb1 a.24.9.1 (B:392-507) alpha-catenin {Human (Homo sapiens)}
DSFLETNVPLLVIEAAKNGNEKEVKEYAQVFREHANKLIEVANLACSISNNEEGVKLVMSASQLEA
LCPQVINAALALAAKPQSKLAQENMDLFKEQWEKQVRVLTDAVDDITS
>d1qkra_ a.24.9.1 (A:) Vinculin {Chicken (Gallus gallus)}
KDEEFPEQKAGEAINQPMMAARQLHDEARKWSSKGNIIAAAKRMALLMAEMSRLVRGGSGNK
RALIQCAKDIKASDEVTRLAKEVAKQCTDKRIRTNLLQVCERIPITSTQLKILSTVKATMLGRNID
EESQATEMLVHNAQNLMSVKETVREAEASIKIRTDAGFTLRWVRK
>d1k04a_ a.24.14.1 (A:) FAT domain of focal adhesion kinase {Human (Homo sapiens)}
EISPPPTANLDRSNDKVYENVVTGLVKAVIEMSSKIQPAPPEEYVPMVKEVGLALRLLATVDETIPLLP
ASTHREIEMAQKLLNSDLGELINKMKLAQQYVMTSLQQEYKKQMLTAAHALAVDAKNLLDVIDQAR
LKMLGQT
>d1k40a_ a.24.14.1 (A:) FAT domain of focal adhesion kinase {Mouse (Mus musculus)}
NDKVYENVVTGLVKAVIEMSSKIQPAPPEEYVPMVKEVGLALRLLATVDETIPLPASTHREIEMAQK
LLNSDLGELISKMKLAQQYVMTSLQQEYKKQMLTAAHALAVDAKNLLDVIDQARLKM
>d2a0b_ a.24.10.1 (-) Aerobic respiration control sensor protein, ArcB {Escherichia coli}
SKSEALLDIPMLEQYLELVGPKLITDGLAVFEKMMPGYVSVLESNLTAQDKKGIVEEGHKIKGAAGSV
GLRHLQQLGQQIQSPDLPWEDNVGEWIEEMKEEWRHDVEVLKAWVAKAT
>d1c02a_ a.24.10.2 (A:) Phosphorelay protein ypd1 {Baker's yeast (Saccharomyces cerevisiae)}
STIPSEIINWTILNEIISMDDDDSDFSKGLIHFIDQAQTTFMQMRQLDGEKNLTELNDLGHFLKGSS
AALGLQRIAWVCERIQNLGRKMQHFFPNKTELVNTLSDKSIINGINIDEDDEEIKIQVDDKDENSIYLI
LIAKALNQRLEFKLARIELSKYYNTNL
>d1i5na_ a.24.10.3 (A:) Chemotaxis protein CheA P1 domain {Salmonella typhimurium}
DISDFYQTFDEADELLADMEQHLLDLVPESPDAEQLNAIFRAAHSIKGGAGTFGFTILQETTHLME
NLLDEARRGEMQLNTDIINLFLETKDIMEQLDAYKNSEEPDAASFYICNALRQLALEAK
>d1he1a_ a.24.11.1 (A:) ExoS toxin {Pseudomonas aeruginosa}
ASSAVVFQMVQLQALPMTLKGLDKASELATLTPEGLAREHSRLASGDGALRSLSTALAGIRAGSQVE
ESRIQAGRLLERSIGGIALQQWGTGGAASQLVLDASPELRREITDQLHQVMSEVALLRQAVESEVS
>d1g4us1 a.24.11.1 (S:167-296) SptP tyrosine phosphatase {Salmonella typhimurium}
SKQPLLDIALKGLKRTLPQLEQMDGNSLRENFMASGNPLRSLMTNLQNLNKIPEAKQLNDYVT
TLTNIQVGVARFSQWGTGCGEVERWVDKASTHELTQAVKKIHVIAKELKNVTAELEKIEAGAPM
>d1hy5a_ a.24.11.1 (A:) YopE {Yersinia pestis}
TSFSDSIKQLAAETLPKYMQLNSLDAEMLQKNHDQFATGSGPLRGSITQCQGLMQFCGGELQAEAS
AILNTPVCGIPFSQWGTIGGAASAYVASGVDLTQAANEIKGLAQQMQKLLSLM
>d1f1ma_ a.24.12.1 (A:) Outer surface protein C (OspC) {Lyme disease spirochete (Borrelia burgdorferi), different strains?}
PNLTEISKKITESNAVVLAVKEVETLLTSIDELAKAIGKKIKSDVSLDNEADHNGSLMSGAYLISTLITK
KISAIKDSGELKAEIEKAKKCSEEFKAKLGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKL
FESVKNLSKAAKEMLTNSVKELTSP
>d1g5za_ a.24.12.1 (A:) Outer surface protein C (OspC) {Lyme disease spirochete (Borrelia

burgdorferi), different strains?}

PNLTEISKKITESNAVVLAVKEVETLLASIDELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAE
KLNVLKNEELKEKIDTAKQCSTFTNKLKSEHAVLGLDNLTDNAQRAILKKHANKDKGAAELEKL
FKAVENLSKAAQDTLKNVAVKELTSPIVA

>d1ggqa_ a.24.12.1 (A:) Outer surface protein C (OspC) {Lyme disease spirochete (Borrelia burgdorferi), different strains?}

GPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIGKKIHQNNGLDTENNHNGSLLAGAYAISTLI
KQKLDGLKNEGLKEKIDAAKKCSETFTNKLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELG
KLFESVEVLSKAAKEMLANSVKELTS

>d1jpn1 a.24.13.1 (A:1-88) Signal sequence recognition protein Ffh {Thermus aquaticus}
MFQQLSARLQEAIGRLRGRGRITEEDLKATLREIRRALMDADVNLVARDVFERVREEALGKQVLES
LTPAEVILATVYEALKEALGG

>d1j8mf1 a.24.13.1 (F:3-86) Signal sequence recognition protein Ffh {Archaeon Acidianus ambivalens}

LLDNLRDTRKFLTGSSSYDKAVEDFIKELQKSLISADVNVKLVFSLTNKIKERLKNKPPTYIERRE
WFIKIVYDELSNLFGG

>d1fts_1 a.24.13.1 (201-284) Signal recognition particle receptor, FtsY {Escherichia coli}
RSLKTKENLGSGFISLFRGKKIDDDLFEELEEQLLIADVGVETTRKIITNLTEGASRKQLRDAEALY
LLKEEMGEILAKVDE

>d1jr8a_ a.24.15.1 (A:) Thiol oxidase Erv2p {Baker's yeast (Saccharomyces cerevisiae)}
DDKVKKEVGRASWKYFHTLLARFPDEPTPEEREKLHTFIGLYAELYPCGECYSYHFVKLIEKYPVQTSS
RTAAAMWGCHIHNVNEYLKKDIYDCATILEDYDCGC

>d1h99a1 a.142.1.1 (A:54-168) Transcriptional antiterminator LicT {Bacillus subtilis}
GAMEKFKTLLYDIPIECMEVSEEIISYAKLQLGKLNDSIYVSLTDHINFAIQRNQGLDIKNALLWET
KRLYKDEFAIGKEALVMVKNKTGVSLPEDEAGFIALHIVNAELNEE

>d1h99a2 a.142.1.1 (A:169-275) Transcriptional antiterminator LicT {Bacillus subtilis}
MPNIINITKVMEEILSIVKYHFKIEFNEESLHYYRFVTDLKFQAQRLFNGTHMESEDDFLLDTPVKEKY
HRAYECTKKIQTYIEREYEHKLTSEDELLYLTIDIERVVK

>d1dvba1 a.25.1.1 (A:1-147) Rubrerythrin, N-terminal domain {Desulfovibrio vulgaris}
MKSLKGSRTEKNILTAFAGESQARNRYNYFGGQAKKDGQVQISDIFAETADQEREHAKRLFKFLEGG
DLEIVAAFPAGIADTHANLIASAAGEHHEYTEMYPFARIAREEGYEEIARVFASIAVAEEFHEKRFLD
FARNIKEGRV

>d1bcfa_ a.25.1.1 (A:) Bacterioferritin (cytochrome b1) {Escherichia coli}
MKGDTKVINYLKLLGNELVAINQYFLHARMFKNWGLKRLNDVEYHESIDEMKHADRYIERILFLE
GLPNLQDLGKLNIGEDVEEMLRSDLALELDGAKNLREAIGYADSVHDYVSRDMMIEILRDEEGHID
WLETELDLIQKMGLQNYLQAQIREEG

>d1jgca_ a.25.1.1 (A:) Bacterioferritin (cytochrome b1) {Rhodobacter capsulatus}
MKGDAKVIEFLNAALRSELTAISQYWVHFRLQEDWGLAKMAKKSREESIEEMGHADKIIARILFLEG
HPNLQKLDPLRIGEGPRETLECDLAGEHDALKLYREARDYCAEVGDIVSKNIFESLITDEEGHVDFLE
TQISLYDRLGPQGALLNAAPMDAA

>d1euuma_ a.25.1.1 (A:) Non-hem ferritin {Escherichia coli, ecFtnA}
LKPEMIEKLNEQMNLELYSSLLYQQMSAWCSYHTFEGAAFLRRHAQEEMTHMQRLFDYLTDTGN
LPRINTVESPFAEYSSDELQFQETYKHEQLITQKINELAHAAMTNQDYPTFNFLQWYVSEQHEEKL
FKSIIDKLSLAGKSGEGLYFIDKELSTLD

>d1krqa_ a.25.1.1 (A:) Non-hem ferritin {Campylobacter jejuni}
MLSKEVVKLLNEQINKEMYAANLYLSMSSWCYENSLDGAGAFLEFAHASEESDHAKKLITYLNETDS
HVELQEVEKQPEQNFKSLLDVFEKTYEHEQFITKSINTLVEHMLTHKDYSTFNFLQWYVSEQHEEEAL
FRGIVDKIKLIGEHNGLYLADQYIKNIALSR

>d1dpsa_ a.25.1.1 (A:) Dodecameric ferritin homolog DPS {Escherichia coli}
SKATNLLYTRNDVSDSEKKATVELLNQVIQFIDLSLITKQAHWNMRGANFIAVHEMLDGFRTALID
HLDTMAERAVQLGGVALGTTQVINSKTPKSYPLDIHNVQDHLKELADRYAIVANDVRKAIGEAKDD
DTADILTAASRDLDKFLWFIECNIE

>d1qgha_ a.25.1.1 (A:) Dodecameric ferritin homolog DPS {Listeria innocua}
VDTKEFLNHQVANLNVFTVKIHHQIHWYMRGHNFFTLHEKMDLYSEFGEQMDEVAERLLAIGGSP
FSTLKEFLENASVEEAPYTKPKTMDQLMEDLVGTLELLRDEYKQGIELTDKEGDDVTNDMLIAFKAS
IDKHIWMFKAFLGKAPLE

>d2fha_ a.25.1.1 (-) (Apo)ferritin {Human (Homo sapiens), H chain}
TSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQSHHEEREHAEKLM
KLQNRGGRIFLQDIQKPCDDWESGLNAMECALHLEKNVNSLLELHKLATDKNDPHLCDFIET
HYLNEQVKAIKELGDHVTNLRKMGAPESGLAEYLFDKHTLG

>d1aew_ a.25.1.1 (-) (Apo)ferritin {Horse (Equus caballus), L chain}
SQIRQNYSTEVEAAVNRLVNLRLASYTYLSLGFYFDRDDVALEGVCHFFRELAEEKREGAERLLKM
QNQRGGRALFQDLQKPSQDEWGTTPDAMKAAIVLEKSLNQALLDLHALGSAQADPHLCDFLESHF
LDEEVKLIKMGDHLTNIQRLVGSQAGLGEYLFERLTL

>d1h96a_ a.25.1.1 (A:) (Apo)ferritin {Mouse (Mus musculus)}
TSQIRQNYSTEVEAAVNRLVNLHLRASYTYLSLGFDFDRDDVALEGVGHFFRELAEEKREGAERLLEF
QNRGGRALFQDVQKPSQDEWGTQEAMEAALAMEKNLNQALLDLHALGSARADPHLCDFLESH
YLDKEVKLIKMGHNLNLRVAGPQPAQTGAPQGSGLGEYLFERLTLK

>d1bg7_ a.25.1.1 (-) (Apo)ferritin {Bullfrog (Rana catesbeiana)}
DSQVRQNFHRDCEAAINRMVNMELYASYTYLSMAFYFDRDDIALHNVAKFFKEQSHEEREHAEKLM
MKDQNKRGGRIVLQDVQKPERDEWGNTLEAMQAALQLEKTVNQALLDLHKGSDKVDPHLCDFLES
ETEYPEEQVKSILQGDYITNLKRLGLPQNGMGEYLFDKHTMGE

>d1mfra_ a.25.1.1 (A:) (Apo)ferritin {Bullfrog (Rana catesbeiana)}
VSQVRQNYHSDCEAAVNRLNLELYASYTYSSMYAFFDRDDVALHNVAEFFKEHSHEEREHAEKFM
KYQNKRGGRVVLQDIKKPERDEWGNTLEAMQAALQLEKTVNQALLDLHKLATDKVDPHLCDFLES
EYLEEQVKDIKRIGDFITNLKRLGLPENGMGEYLFDKHSV

>d1rcd_ a.25.1.1 (-) (Apo)ferritin {Bullfrog (Rana catesbeiana)}
SQVRQNFHQDCEAGLNRTVNLKFHSSYVYLSMASYFNRRDDVALSNFAKFFRERSEEEKEHAEKLEIY
QNQRGGRVFLQSVEKPERDDWANGLEALQTALKLQKSVNQALLDLHAVAADKSDPHMTDFLESPY
LSESVETIKKLGDHITSLLKLLWSSHPGMAEYLFNKHTLG

>d1mtyb_ a.25.1.2 (B:) Methane monooxygenase hydrolase, beta and alpha subunits
{Methylococcus capsulatus}
ERRRGLTDPMAAVILKALPEAPLDGNNKMGYFVTPRWKRLTEYEALTVYAQPNDWIAGGLDWG
DWTQKFHGGPRPSWGNETTELRTVDWFKHRDPLRRWHAPYVKDKAEWRYTDRFLQGYSDGQI
RAMNPTWRDEFINRYWGAFLENEYGLFNAHSQGAREALSDVTRVSLAFWGFDKIDIAQMIQLERGF
LAKIVPGFDESTAVPKAEWTNGEVYKSARLAVEGLWQEVFDWNEAFSVHAVYDALFGQFVRREFF
QRLAPRFGDNLTPFFINQAQTYFQIAKQGVQDLYNCLGDDPEFSDYNRTVMRNWTGKWLEPTIAA
LRDFMGLFAKLPAGTTDKKEITASLYRVVDDWIEDYASRIDFKADRDQIVKAVLAGLK

>d1mtyd_ a.25.1.2 (D:) Methane monooxygenase hydrolase, beta and alpha subunits
{Methylococcus capsulatus}

AANRAPTSVNAQEVHRWLQSFNWDFKNNRTKYATKYKMANETKEQFKLIAKEYARMEAVKDERQ
FGSLQVALTRLNAGVRVHPKWNEMTKVVSNFLEVGEYNAIAATGMLWDSAQAEEQKNGYLAQVLD
EIRHTHQCAVYVNYFAKNGQDPAGHNDARRTRTIGPLWKGMKRVFSDGFISGDAVECSLNLQLVGEA
CFTNPLIVAVTEWAAAANGDEITPTVFLSIETDELHRMANGYQTVVSIANDPASAKYLNTDLNNAFW
TQQKYFTPVLGMLFEYGSKFKVEPWVKTWDRWVYEDWGGIWIGRLGKYGVESPRSLKDAKQDAY
WAHHDLYLLAYALWPTGFFRLALPDQEEMEWFEANYPGWYDHYGKIYEWRARGCEDPSSGFIPL
MWFIEHHPIYIDRVSQVPCPSLAKGASTLRVHEYNGEMHTFSDQWGERMWLAEPERYECQNI
EQYEGRELVIAELHGLRSDGKTLIAQPHVRGDKLWTLDDIKRLNCVFKNPVKAF

>d1mhyb_ a.25.1.2 (B:) Methane monooxygenase hydrolase, beta and alpha subunits
{Methylosinus trichosporium}

KRGLTDPERAAIAAAVDPHALDTQRKYHYFIQPRWKPLSEYEQLSCYAQPNPDWIAGGLDWGDW
TQKFHGGPRPSWGNSTELRTTDWYRHRDPARRWHHPYVKDKSEEARYTQRFLAAYSSEGSIRTIDP
YWRDEILNKYFGALLYSEYGLFNAHSSVGRDCLSDTIRQTAVFAALDKVDNAQMIQMERLFIKLV
GFDASTDVPKIKWTTDPIYSGARATVQEIWQGVQDWEILWAGHAVYDATFGQFARREFFQRLATV
YGDTLTPFFTAQSQTYFQTRGAIDDLFVYCLANDSEFGAHNRTFLNAWTEHYLASSVAALKDFVGL
YAKVEKVAGATDSAGVSEALQRFVGDWKIDYADKIGFRVDVDQKVDVLAGY

>d1mhyd_ a.25.1.2 (D:) Methane monooxygenase hydrolase, beta and alpha subunits
{Methylosinus trichosporium}

NRAPVGVPEQEVHKWLQSFNWDFKENRTKYPTKYHMANETKEQFKVIAKEYARMEAAKDERQFG
TLLDGLTRLGAGNKVHPRWGETMKVISNFLEVGEYNAIAASAMLWDSATAAEQKNGYLAQVLDEIR
HTHQCAFINHYSKYHHPAGHNDARRTRAIGPLWKGMKRVFADGFISGDAVECSVNLQLVGEACF
TNPLIVAVTEWASANGDEITPTVFLSVETDELHRMANGYQTVVSIANDPASAKFLNTDLNNAFWTQ
QKYFTPVLGYLFEYGSFKFKVEPWVKTWNRWVSEDWGGIWIGRLGKYGVESPRSLRDAKRDAYWA
HHDLALAAYAMWPLGFARLALPDEEDQAWFEANYPGWADHYGKIFNEWKKLGYEDPKSGFIPYQ
WLLANGHDVYIDRVSQVFPFISLAKGTGSLRVHEFNKKHSLTDDWGERQWLIEPERYECNVEFEQ
YEGRELVIAEGHGVRSKGKTLIAQPHTRGDNLWTLLEDIKRAGCVFPDPLAKF

>d1jqca_ a.25.1.2 (A:) Ribonucleotide reductase R2 {Escherichia coli}

AYTTFSTKNDQLKEPMMFFGQPVNVARYDQKQYDIFEKLEKQLSFFWRPEEVDVSRDRIDYQALPE
HEKHIFISNLKYQTLDSIQGRSPNVALPLISIPELETWVETWAFSETIHSRSYTHIIRNIVNDPSVVF
DDIVTNEQIQKRAEGISSYDELIEMTSYWHLLEGHTVNGKTVTVSLRELKKKLYLCLMSVNALE
AIRFYVSFACSFAPAERELMEGNAKIIRLIARDEALHLTGTQHMLNLLRSGADDPMAEIAEACKQEC
YDLFVQAAQEKDWADYLFRDGS MIGLNKDILCQYVEYITNIRMQAVGLDLFPQTRSNPIPWINTW
LV

>d1r2fa_ a.25.1.2 (A:) Ribonucleotide reductase R2 {Salmonella typhimurium}

ISAINWNKIQDDKDLEVWNRLTSNFWLPEKVPLSNDIPAWQTLAAEQQLTIRVFTGLTLLDTIQNI
AGAPSLMADAITPHEEAVLSNIFMEAVHARSYSSIFSTLCQTKEVDAAYAWSEENPPLQRKAQIILA
HYVSDPELKKKIASVFLESFLFYSGFWLPMYFSSRGKLTNTADLIRLIIRDEAVHGYIYGYQIALQKL
SAIEREELKLFALDMLMELYDNEIRYTEALYAETGWVNDVKAFLCYNANKALMNLGYEALFPPEMA
DVNPAILAALSP

>d1kgna_ a.25.1.2 (A:) Ribonucleotide reductase R2 {Corynebacterium ammoniagenes}

SNEYDEYIANHTDPVKAINWNVIPDEKDLEVWDRLTGNFWLPEKIPVSNDIQSWNKMTPEQLAT
MRVFTGLTLLDTIQGTGVAISLLPDAETMHEEAVYTNIAFMESVHAKSYSNIFMTLASTPQINEAFR

WSEENENLQRKAKIIMSYYNGDDPLKKKVASTLLESFLFYSGFYLPMYLSSRAKLTNTADIIRLIIRDE
SVHGYIYIKYQYQGVKKLSEAEQEEYKAYTFDLMYDLYENEIEYTEDIYDDLGWTEDEVKRFLRYNAN
KALNNLGYEGLFPTDETKVSPAILSSLS

>d1xsm_ a.25.1.2 (-) Ribonucleotide reductase R2 {Mouse (Mus musculus)}

NPSVEDEPLLRENPRRFVVFPIEYHDIWQMYKKAESFWTAEVDSLKDIQHWEALKPDERHFISH
VLAFFAASDGIVNENLVERFSQEVQVTEARCFYGFQIAMENIHSEMYSLIDTYIKDPKEREYLFNAIE
TMPVCVKKKADWALRWIGDKEATYGERVVAAFAAVEGIFSGSFASIFWLKRRGLMPGLTFSNELISRD
EGLHCDFACLMFKHLVHKPAEQRVREIITNAVRIEQEFLTEALPVKLGIMNCTLMKQYIEFVADRLML
ELGFNKIFRVENPFDFME

>d1jk0a_ a.25.1.2 (A:) Ribonucleotide reductase R2 {Baker's yeast (Saccharomyces cerevisiae)}

LNKELETLREENRVKSDMLKEKLSKDAENHKAYLKSHQVHRHKLKEMEKEEPLLNEDKERTVLFPI
KYHEIWQAYKRAESFWTAEEDLSKDIHDWNNRMNENERFFISRVLAFFAASDGIVNENLVENFS
TEVQIPEAKSFYGFQIMIENIHSETYSLIDTYIKDPKESEFLFNAIHTIPEIGEKAEWALRWIQDADAL
FGERLVAFASIEGVVFFSGSFASIFWLKRRGMMMPGLTFSNELICRDEGLHTDFACLLFAHLKKNKPDPAIV
EKIVTEAVEIEQRYFLDALPVALLGMNADLMNQYVEFVADRLVAFGNKKYKVENPFDFMEN

>d1jk0b_ a.25.1.2 (B:) Ribonucleotide reductase R2 {Baker's yeast (Saccharomyces cerevisiae)}

FQKERHDMKEAEKDEILLMENSRRFVMFPIKYHEIWAAYKKVEASFWTAEIEELAKDTEDFQKLT
DQKTYIGNLLALSISDNLVNKYLIENFSAQLQNPEGKSFYGFQIMMENIYSEVYSMMVDAFFKDPK
NIPLFKEIANLPEVKHKAFFIERWISNDDSLYAERLVAAAKEGIFQAGNYASMFWLTDKKIMPGLAM
ANRNICRDRGAYTDFSCLLFAHLRTPKNPKIIEKIITEAVEIEKEYYSNSLPVEKFGMDLKSIIHTYIEFV
ADGLLQGFNGEKYY

>d1afra_ a.25.1.2 (A:) delta 9-stearoyl-acyl carrier protein desaturase {Castor bean (Ricinus communis)}

MPPREHVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEKCVQPDFLPDPASDGFDEQVRELR
ERAKEIPDDYFVVLVGDMITTEALPTYQTMLNTLDGVRDET GASPTSWAIWTRAWTAEENRHGDL
LNKYLYLSGRVDMRQIEKTIQYLIGSGMDPRTENSPYLGFIYTSFQERATFISHGNTARQAKEHGDIKL
AQICGTIAADEKRHETAYTKIVEKLF EIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHSAV
AQLRGVYTA KDYADILEFLVGRWKVDKLTGLSAEQKAQDYVCRLPPRIRLEERAQGRAKEAPT
PFSWIFDRQVKL

>d1rhga_ a.26.1.1 (A:) Granulocyte-colony stimulating factor (G-CSF) {Human (Homo sapiens)}

LPQSFLKCLEQVRKIQGDGAALQEKLKCATYKLCHEPELVLLGHSLGIPWAPLSSCPSQALQLAGCLS
QLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQMEELGMAPALQPTQGAMPAFASA
FQRRAGGVLVASHLQSFLEVSRYRHLA

>d1bgc_ a.26.1.1 (-) Granulocyte-colony stimulating factor (G-CSF) {Cow (Bos taurus)}

SLPQSFLKCLEQVRKIQADGAELQERLCAAHKLCHPEELMLLRHSLGIPQAPLSSCSSQSLQRLGCL
NQLHGGLFLYQGLLQALAGISPELAPTLDLQLDVTDFATNIWLQMEDLGAAPAVQPTQGAMPTFTS
AFQRRAGGVLVASHLQHRFLELAYRGLRYLA

>d1bgea_ a.26.1.1 (A:) Granulocyte-colony stimulating factor (G-CSF) {Dog (Canis familiaris)}

PLPQSFLKCLEQMRKVQADGTALQETLCATHQLCHPEPELVLLGHALGIPQPPLSSCSSQALQLMGCL
RQLHSGFLYQGLLQALAGISPELAPTLDLQLDVTDFAINIWQQMEDLGMAPAVPPTQGTMPAFTS

AFQRRAGGVLVASNLQSFLELAYRALRHFAK
>d1alu_ a.26.1.1 (-) Interleukin-6 {Human (Homo sapiens)}
LTSSERIDKQIRYILDGIALRKETCNKSNMCESSKEALAENNLNPKMAEKDGCQSGFNEETCLVK
IITGLLEFEVYLEYLQNRFESEEQARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAA
NQWLQDMTTHLILRSFKEFLQSSLRALRQM
>d1i1rb_ a.26.1.1 (B:) Interleukin-6 {Human herpesvirus 8, Kaposi's sarcoma herpes-virus}
EFEKDLLIQRLNWMLWVIDEFCRDLCYRTGICKGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKK
LADGFFEFVFLFKFLTTEFGKSVINVDVMELLTKTLGWDIQEELNKLTKTHYSPPKFDGRLLGRLQG
LKYWVRHFASFYVLSAMEKFAGQAVRVLDSIP
>d1a7m_ a.26.1.1 (-) Leukemia inhibitory factor (LIF) {Mouse (Mus musculus)}
SPLPITPVNATCAIRHPCHGNLMNQIKNQLAQLNGSANALFISYYTAQGEPFPNNLDKLCGPNVTD
PPFHANGTEKAKLVELYRMVAYLSASLTNITRDQKVLNPSAVSLHSKLNATIDVMRGLLSNVLCRLCN
KYRVGHVDVPPVPDHSDEKVFQKKKLGCCQLLGTYSKQVISVVVQAF
>d1lki_ a.26.1.1 (-) Leukemia inhibitory factor (LIF) {Mouse (Mus musculus)}
NATCAIRHPCHGNLMNQIKNQLAQLNGSANALFISYYTAQGEPFPNNVEKLCAPNMTDFPSFHGNG
TEKTKLVELYRMVAYLSASLTNITRDQKVLNPTAVSLQVKNATIDVMRGLLSNVLCRLCNKYRVGHV
DVPPVPDHSDEKAFQRKKLGCQLLGTYSKQVISVVVQAF
>d1emra_ a.26.1.1 (A:) Leukemia inhibitory factor (LIF) {Human (Homo sapiens)}
LMNQIRSQAQLNGSANALFILYYTAQGEPFPNNLEKLCGPNVTDPPFHANGTEKAKLVELYRIVVY
LGTSLGNITRDQKILNPSALSLSKLNATADILRGLLSNVLCRLCSKYHVGHVDTYGPDTSGKDVVQ
KKKLGCCQLLGGYKQVISVLAQAF
>d1a22a_ a.26.1.1 (A:) Growth hormone, somatotropin {Human (Homo sapiens)}
FPTIPLSRLFDNAMLRAHRLHQLAFDITYQEFEEAYIPKEQKYSFLQNPQTSLCFSESIPTPSNREETQ
QKSNLELLRISLLLIQSWLEPVQFLRSVFANSLVYGASDSNVYDLLKDLEERIQTLMGRLEGQIFKQTY
SKFDTDALLKNYGLLYCFRKMMDKVETFLRIVQCRSVEGSCGF
>d1axia_ a.26.1.1 (A:) Growth hormone, somatotropin {Human (Homo sapiens)}
TIPLSRLFDNAMLRAHRLHQLAFDITYQEFEEAYIPKEQKYSFLQNPQTSLCFSESIPTPSNREETQQK
SNLELLRISLLLIQSWLEPVQFLRSVFANSLVYGASDSNVYDLLKDLEERIQTLMGRLEDGSPRTGQIF
KQTYSKFDTNSHNDALLKNYGLLYCFRRDMTYVATYLRIVQCRSVEGSCGF
>d1hgu_ a.26.1.1 (-) Growth hormone, somatotropin {Human (Homo sapiens)}
PTIPLSRLFQNAMLRAHRLHQLAFDITYEYEFEEAYIPKEQKYSFLQAPQASLCFSESIPTPSNREQAQQ
KSNLQLLRISLLLIQSWLEPVGFLRSVFANSLVYGASDSNVYDLLKDLEEGIQTLMGRLEDGSPRTGQ
AFKQTYAKFDANSHNDALLKNYGLLYCFRKMMDKVETFLRIVQCRSVEGSCG
>d1huw_ a.26.1.1 (-) Growth hormone, somatotropin {Human (Homo sapiens)}
FPTIPLSRLADNAWLRADRLNQLAFDITYQEFEEAYIPKEQIHSFWWNPQTSLCFSESIPTPSNKEET
QQKSNLELLRISLLLIQSWLEPVQFLRSVFANSLVYGASDSNVYDLLKDLEEGIQTLMGRLEALLKNY
GLLYCFNKDMSKVSTYLRTVQCRSVEGSCGF
>d1f6fa_ a.26.1.1 (A:) Placental lactogen {Sheep (Ovis aries)}
AQHPPYCRNQPGKCIPLQSLFDRATTVANYNSKLAGEMVNRFDQYGGINSSESKVINCHTSSITT
PNSKAEAINTEDEKILFKLVISLLHSWDEPLHHAVTELANSKGTSPALLTKAQEIKEKAKVLVDGVEVI
QKRIHPGEKNEPYPVWSEQSSLTSQDENVRRVAFYRLFHCLHRDSSKIYTYLRILKCRILTSC
>d1cnt1_ a.26.1.1 (1:) Ciliary neurotrophic factor (CNTF) {Human (Homo sapiens)}
PHRRDLCSRSIWLARKIRSDLTALTESYVKHQGLNKNINLDSADGMPVASTDQWSELTEAERLQENL
QAYRTFHVLLARLLEDQVHFTPTGDFHQAIHTLLLQVAFAFYQIEELMILLEYKIPRNEADGMPIN

VGDGGLFEKKLWGLKVLQELSQWTVRSIHDLRFISSHQTGIP
>d1ax8_ a.26.1.1 (-) Leptin (obesity protein) {Human (Homo sapiens)}
IQKVQDDTKLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVYQQILTSMPSR
NVIQISNDLENLRDLLHVLAFSKSchLPEASGLTLDLGGVLEASGYSTEVALSRLQGSQDMLWQ
LDLSPGC
>d1evsa_ a.26.1.1 (A:) Oncostatin M {Human (Homo sapiens)}
GSCSKEYRVLLGQLQKQTDLMQDTSRLLDPYIRIQGLDVPKLRHCRERPGAFPSEETLRGLGRRGF
LQTLNATLGCVLHRLADLEQRLPKAQDLERSGLNIEDLEKLMARPNI LGLRNNIYCMAQLLDNSDT
AEPTKAGRGASQPPTPTPASDAFQRKLEGCRFLHGYHRFMHSVGRVFSKW
>d1f45b_ a.26.1.1 (B:) Heterodimeric interleukin-12 alpha chain {Human (Homo sapiens)}
QNLRAVSNMLQKARQTLFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGS
CLASRKTSFMMALCLSSIIYEDLKMVQVEFKTMNAKLLMDPKRQIFLDQNM LAVIDELMQALNFNSE
TVPQKSSLEEDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS
>d1eera_ a.26.1.2 (A:) Erythropoietin {Human (Homo sapiens)}
APPRLICDSRVLERYLLEAKEAEKITTGCAEHCSLNEKITVDPDKVNFYAWKRMEVGGQAVEVWQG
LALLSEAVLRGQALLVKSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAISNSDAASAAPLRIT
ADTFRKLFRVYSNFLRGKLLKLYTGEACRTGDR
>d2gmfa_ a.26.1.2 (A:) Granulocyte-macrophage colony-stimulating factor (GM-CSF) {Human
(Homo sapiens)}
RSPSPSTQPWEHVNAIQEARLLNLSRD TAAEMNETVEVISEMFDLQEPTCLQTRLELYKQGLRGSL
TKLKGPLTMMASHYKQHCPTPETSCATQIITFESFKENLKDFFLVIPFDCWEP
>d1hzia_ a.26.1.2 (A:) Interleukin-4 (IL-4) {Human (Homo sapiens)}
HKCDITLQAIKTLNLSLTEQKTLCTELTVTDIFAASKNTTEKETFCRAATVLRQFYSHHEKDTRCLGAT
AQQFHRHKQLIRFLKRLDRNLWGLAGLNSCPVKEANQSTLENFLERLKTIMREKYSKCSS
>d1hula_ a.26.1.2 (A:) Interleukin-5 {Human (Homo sapiens)}
IPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGGTVERLFKNLS
LIKKYIDGQKKKCGEERRRVNQFLDYLQEFLGVMNTEWI
>d1hmca_ a.26.1.2 (A:) Macrophage colony-stimulating factor (M-CSF) {Human (Homo
sapiens)}
SEYCSHMIGSGHLQSLQRLIDSQMETSCQITFEFVDQEQLKDPVCYLKKAFLVQDIMEDTMRFRDN
TPNAIAIVQLQELSLRLKSCFTKDYEEHDKACVRTFYETPLQLLEKVKNVFNETKNLLDKDWNIFSK
NCNNSFAECSSQGH
>d1etea_ a.26.1.2 (A:) Flt3 ligand {Human (Homo sapiens)}
TQDCSFQHSPISDFAVKIRELSYLLQDYPVTVASNLQDDELGGWLRLVLAQRWMERLKT VAGSK
MQGLLERVNT EIHVTKCAFQPPPSCLR FVQTNISRLQETSEQLVALKPWITRQNF SRCLELQCQP
>d1scfa_ a.26.1.2 (A:) Stem cell factor, SCF {Human (Homo sapiens)}
NVKDVTCLVANLPKDYMITLKYVPGMDVLP SHCWISEMVVQLSDSLTDL LDKFSNISEGLSNYSIIDK
LVNIVDDLVECVKENS SKDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVA SETSDCVVS
>d1scfc_ a.26.1.2 (C:) Stem cell factor, SCF {Human (Homo sapiens)}
NVKDVTCLVANLPKDYMITLKYVPGMDVLP SHCWISEMVVQLSDSLTDL LDKFSNISEGLSNYSIIDK
LVNIVDDLVECVKENS SKDLKKSFKSPEPRLFTPEEFFRIFNRSIDAF
>d3inkc_ a.26.1.2 (C:) Interleukin-2 (IL-2) {Human (Homo sapiens)}
STKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEEELKPLEEVLNL
AQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

>d1jli_ a.26.1.2 (-) Interleukin-3 (IL-3) {Human (Homo sapiens)}
ANCSIMIDEIIHHLKRPPNPLLDPNLNSEDMILMERNLRTPNLLAFVRAVKHLENASAIESILKNL
LPCLPLATAAPTRHPIHIKDGWNEFRKLTFFYLKTLNAQAQQ

>d1ga3a_ a.26.1.2 (A:) Interleukin-13 (IL-13) {Human (Homo sapiens)}
GGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEKTQRMLS
GFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLLHLKFLREGFRN

>d2ilk_ a.26.1.3 (-) Interleukin-10 (cytokine synthesis inhibitory factor, CSIF) {Human (Homo sapiens)}
TQSENSCTHFPGNLPNMLRDLRDAFSRVKTFQMKDQLDNLLLKESLLEDFKGYLGCQALSEMIQF
YLEEVMPQAENQDPDIKAHVNSLGENLKTLLRRLRCHRFLPCENKSKAVEQVKNAFNKLQEKGIY
KAMSEFDIFINYIEAYMTMKIRN

>d1vlk_ a.26.1.3 (-) Interleukin-10 (cytokine synthesis inhibitory factor, CSIF) {Epstein-Barr virus}
CDNFPQMLRDLRDAFSRVKTFQTKDEVDNLLLKESLLEDFKGYLGCQALSEMIQFYLEEVMPQAE
NQDPEAKDHVNSLGENLKTLLRRLRCHRFLPCENKSKAVEQIKNAFNKLQEKGIYKAMSEFDIFIN
YIEAYMTIK

>d1au1a_ a.26.1.3 (A:) Interferon-beta {Human (Homo sapiens)}
MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKLQFQKEDAALTIYEMLNIF
AIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSLHLKRYYGRILHYLK
AKEYSHCAWTIVRVEILRNIFYFINRLTGYLNR

>d1rmi_ a.26.1.3 (-) Interferon-beta {Mouse (Mus musculus)}
INYKQLQLQERTNIRKQCQELLEQLNGKINLTyrADFKIPMEMTEKMQKSYTAFAIQEMLNQVFLVFR
NNSSTGWNETIVVRLDELHQQTVFLKTVLEEKQEERLTWEMSSSTALHLKSYWVRVQRYLKLMK
YNSYAWMVVRAEIFRNFLIIRRLTRNFQ

>d1rh2a_ a.26.1.3 (A:) Interferon-alpha 2b {Human (Homo sapiens)}
THSLGSRRTLMMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSS
AAWDETLLDKFYTELYQLNDLEACVIQGVGTETPLMNEDSILAVRKYFQRITLYLKEKKYSPCAW
EVRRAEIMRSFSLSTNLQE

>d1b5l_ a.26.1.3 (-) Interferon-tau {Sheep (Ovis aries)}
CYLSRKLMLDARENKLLDRMNRSLPHSCLQDRKDFGLPQEMVEGDQLQKDQAFPVLYEMLQQSF
NLFYTEHSSAAWDTTLLQLCTGLQQQLDHLDTCRGQVMGEEDSELGNMDPIVTVKKYFQGIYDYL
QEKGYSDCAWEIVRVEMMRALTVSTTLQKRLTK

>d1d9ca_ a.26.1.3 (A:) Interferon-gamma {Cow (Bos taurus)}
QGQFFREIENLKEYFNASSPDVAKGGPLFSEILKNWKDESDKKIISQIVSFYFKLFENLKDQVIQRS
MDIHKQDMFQKFLNGSSEKLEDFKKLIQIPVDDLQIQRKAINELIKVMNDLS

>d1fyha1 a.26.1.3 (A:0-124) Interferon-gamma {Human (Homo sapiens)}
MQDPYVKEAENLKKYFNAGHSDVADNGTLFLGILKNWKEESDRKIMQSQIVSFYFKLFKNFKDDQS
IQKSVETIKEDMNKFFNSNKKKRDDFEKLTNYSVTDLNVQRKAIHELIVMAELGANV

>d1fyha2 a.26.1.3 (A:201-324) Interferon-gamma {Human (Homo sapiens)}
SGEFVKEAENLKKYFNAGHSDVADNGTLFLGILKNWKEESDRKIMQSQIVSFYFKLFKNFKDDQSIQ
KSVETIKEDMNKFFNSNKKKRDDFEKLTNYSVTDLNVQRKAIHELIVMAELSPAA

>d2rig_ a.26.1.3 (-) Interferon-gamma {Rabbit (Oryctolagus cuniculus)}
QDTLTRETEHLKAYLKANTSDVANGGPLFLNLRNWKEESDNKIIQSQIVSFYFKLFDNLKDHEVIK
SMESIKEDIFVKFFNSNLTKMDDFQNLTRISVDDRLVQRKAVSELSNVLNF

>d1a8h_1 a.27.1.1 (349-500) Methionyl-tRNA synthetase (MetRS) {*Thermus thermophilus*}
LADDLGNLVQRTRAMLFRFAEGRIPEPVAGEELAEGTGLAGRLRPLVRELKFHVALEEAMAYVKALN
RYINEKKPWELFKKEPEEARAVLYRVVEGLRIASILLTPAMPDKMAELRRALGGLKEEVRLEEAEERWG
LAEPRPIEEAPVLFPPK

>d1f4la1 a.27.1.1 (A:389-548) Methionyl-tRNA synthetase (MetRS) {*Escherichia coli*}
VVNLASRNAGFINKRFDGVLASELADPQLYKFTDAAEVIGEAWESREFGKAVREIMALADLANRYV
DEQAPWVVAKQEGRDADLQAICSMGINLFRVLMTYLKPVLPKLTERAEAFNLNTELTWDGIQQPLLG
HKVNPFKALYNRIDMRQVEALVEASKE

>d1ile_1 a.27.1.1 (642-821) Isoleucyl-tRNA synthetase (IleRS) {*Thermus thermophilus*}
YFLTWNVYSFFVTYANLDRPDLKNPPPPEKRPMDRWLLARMQDLIQRVTEALEAYDPTTSARAL
RDFVVEDLSQWYVRRNRFRWKNEDALDREAAATLYEALVLVATLAAPFTPFLAEVLWQNLVRSV
RLEAKESVHLADWPEADPALADEALVAQMRAVLKVVDLARAARAKSGV

>d1ffya1 a.27.1.1 (A:645-917) Isoleucyl-tRNA synthetase (IleRS) {*Staphylococcus aureus*}
YRKIRNTLRFMLGNINDFNPDTDSIPESELLEVDRYLLNRLREFTASTINNYENFDYLNIIYQEVQNF
NVELSNFYLDYGKDILYIEQRDSHIRRSMQTVLYQILVDMTKLLAPILVHTAEVWSHTPHVKEESVH
LADMPKVVEVDQALLDKWRTFMNLRDDVNRALETARNEKVIKGSLEAKVTIASNDKFNASEFLTSF
DALHQLFIVSQVKVVDKLDQATAYEHGDIVIEHADGKERCWCWNYSEDLGAVDELTHLCPRCQQVV
KSLV

>d1qu3a1 a.27.1.1 (A:645-881) Isoleucyl-tRNA synthetase (IleRS) {*Staphylococcus aureus*}
YRKIRNTLRFMLGNINDFNPDTDSIPESELLEVDRYLLNRLREFTASTINNYENFDYLNIIYQEVQNF
NVELSNFYLDYGKDILYIEQRDSHIRRSMQTVLYQILVDMTKLLAPILVHTAEVWSHTPHVKEESVH
LADMPKVVEVDQALLDKWRTFMNLRDDVNRALETARNEKVIKGSLEAKVTIASNDKFNASEFLTSF
DALHQLFIVSQVKVVDKLDQATAYEHGDIVIEHA

>d1gaxa1 a.27.1.1 (A:579-862) Valyl-tRNA synthetase (ValRS) {*Thermus thermophilus*}
ANKLYNAARFVLLSREGFQAKEDTPTLADRFRMRSRSLRGVEEITALYEALDLAQAAREVYELVWSEF
CDWYLEAAKPALKAGNAHTLRTLEEVLAVLLKLLHPMPFLTSELYQALTGKEELALEAWPEPGGR
DEEAERAFEALKQAVTAVRALKAEAGLPPAQEVRYLEGETAPVEENLEVFRFLSRADLLPERPAKA
LVKAMPRVTARMPLEGLLDVEEWRRRQEKRLKELLALAERSQRKCLASPGFREKAPKEVVEAEEARL
KENLEQAERIREALSQIG

>d1f7ua1 a.27.1.1 (A:484-607) Arginyl-tRNA synthetase (ArgRS) {*Baker's yeast*
(*Saccharomyces cerevisiae*)}
DTGPYLQYAH SRLRSVERNASGITQEKWINADFSLLKEPAKLLIRLLGQYDPVLRNAIKTHEPTTVV
TYLFLKLT HQVSSCYDVLWVAGQTEELATARLALYGAARQVLYNGMRLGLTPVERM

>d1iq0a1 a.27.1.1 (A:467-592) Arginyl-tRNA synthetase (ArgRS) {*Thermus thermophilus*}
GDTGPYVQYAHARAHSILRKAGEWGAPDLSQATPYERALALDLLDFEEAVLEAAEERTPHVLAQYLL
DLAASWNAYYNARENGQPATPVLTAPEGLRELRLSLVQSLQRTLATGLDLLGIPAPEVM

>d1acp_ a.28.1.1 (-) Acyl carrier protein {*Escherichia coli*}
STIEERVKKIIGELGKQEEVTNNASFVEDLGADSLDVELVMALEEEFDTEIPDEEA EKITTVQAAI
DYINGHQA

>d1f80d_ a.28.1.1 (D:) Acyl carrier protein {*Bacillus subtilis*}
SADTLERVTKIIVDR LGVDEADV KLEASF KEDLGADXL DVVELVMELEDEFDMEISDEDAEKIATVG
DAVNYIQ

>d1af8_ a.28.1.1 (-) Actinorhodin polyketide synthase acyl carrier protein, ACT ACP
{*Streptomyces coelicolor*, A3(2)}

MATLLTDDLRRALVECAGETDGTDLSGDFLDRFEDIGYDSLALMETAARLESRYGVSIPDDVAGRV
DTPRELLDLINGALAEAA

>d1dnya_a.28.1.2 (A:) Peptidyl carrier protein (PCP), thioester domain {Bacillus brevis}
YVAPTNAVESKLAEIWERVLGVSGIGILDNFFQIGGHSLKAMAVAAQVHREYQVELPLKVLFAQPTIK
ALAQYVAT

>d1dv5a_a.28.1.3 (A:) apo-D-alanyl carrier protein {Lactobacillus casei}
ADEAIKNGVLDILADLTGSDDVKKNLDLNLFETGLLDMSGTVQLLELQSQFGVDAPVSEFDRKEW
DTPNKIIAKVEQAQ

>d1unka_a.28.2.1 (A:) ImmeE7 protein (Im7) {Escherichia coli}
MELKNSISDYTEAEFVQLLKEIEKENVAATDDVLDVLEHFVKITEHPDGTDLIYPSDNRRDSSPEGI
VKEIKEWRAANGKPGFKQG

>d1imy__a.28.2.1 (-) ImmeE8 (Im8) {Escherichia coli}
MELKNSISDYTETEFKKIIEDIINCEGDEKKQDDNLEHFISVTEHPSGSDLIYYPEGNNDGSPPEAVI
KEWRAANGKSGFKQG

>d1emva_a.28.2.1 (A:) ImmeE9 protein (Im9) {Escherichia coli}
LKHSISDYTEAEFLQLVTTICNADTSSEEELVTLVTHFEEMTEHPSGSDLIYYPKEGDDDDSPSGIVNTV
KQWRAANGKSGFKQ

>d2eiaa1_a.28.3.1 (A:148-222) EIAV capsid protein p26 {Equine infectious anemia virus}
PKAQNIRQGAKEPYPEFVDRLLSQIKSEGHQPQEISKFLTDTLTIQNANEECRNAMRHLRPEDTLEEK
MYACRDIG

>d1qrjb1_a.28.3.1 (B:131-214) HTLV-I capsid protein {Human T-cell leukemia virus type 1}
PSWASILQGLEEYPYHAFVERLNIALDNGLPEGTPKDPILRSLAYSANKECQKLLQARGHTNSPLGD
MLRACQWTWPKDKTKVL

>d1a8o__a.28.3.1 (-) HIV capsid protein, dimerisation domain {Human immunodeficiency
virus type 1}
MDIRQGPKEPRDYVDRFYKTLRAEQASQEVKNWMTETLLVQNANPDCKTILKALGPGATLEEMM
TACQG

>d1d1da1_a.28.3.1 (A:151-230) RSV capsid protein {Rous sarcoma virus}
GPWADITQGPSEFVDFANRLIKAVEGSDLPPSARAPVIIDCFRQKSQPDIIQLIRAAPSTLTPGGEI
YVLDQRKIAP

>d1eoqa_a.28.3.1 (A:) RSV capsid protein {Rous sarcoma virus}
MDIMQGPSEFVDFANRLIKAVEGSDLPPSARAPVIIDCFRQKSQPDIIQLIRTAPSTLTPGGEIKYV
LDRQKTAP

>d1e6ia_a.29.2.1 (A:) GCN5 {Baker's yeast (Saccharomyces cerevisiae)}
RGPHDAAIQNILTELQNHAAAWPFLQPVNKEEVPDYDFIKEPMDLSTMEIKLESNKYQKMEDFIY
DARLVFNCRMYNGENTSYYKYANRLEKFFNKKVKEIPEYSHLID

>d1f68a_a.29.2.1 (A:) GCN5 {Human (Homo sapiens)}
GDQLYTTLKNLLAQIKSHPSAWPFMEPVKKSEAPDYEVIRFPIDLKTMTERLRSRYVTRKLFVAD
LQRVIANCREYNPPDSEYCRCSALEKFFYFKLKEG

>d1b91a_a.29.2.1 (A:) P300/CAF histone acetyltransferase bromodomain {Human (Homo
sapiens)}
GSHMSKEPRDPDQLYSTLKSILQVQKSHQSAWPFMEPVKRTEAPGYEVIRSPMDLKTMSERLKNR
YYVSKKLFMADLQRFVTNCKEYNAPSEYYKCANILEKFFFSKIKEAGLIDK

>d1eqfa1_a.29.2.1 (A:1359-1497) TAFII250 double bromodomain module {Human (Homo

sapiens}}
GTTVHCDYLNRPKHSIHRRTDPMVTLSSILESIINDMRDLPNTYPFHTPVNAKVVKDYKIIITRPM
DLQTLRENVRKRLYPSREEFREHLELIVKNSATYNGPKHSLTQISQSMLDLCDEKLKEKEDKLARLE
KAINP
>d1eqfa2 a.29.2.1 (A:1498-1625) TAFII250 double bromodomain module {Human (Homo sapiens}}
LLDDDDQVAFSFDLNIIVTQKMMAVPDSWPFHHPVNKKFVDPDYKVVIVNPMLEITIRKNISKHKYQ
SRESFLDDVNLILANSVKYNGPESQYTKTAQEIVNVCYQTLTEYDEHLTQLEKDICTAKEAA
>d1gm5a1 a.29.4.1 (A:7-105) RecG, N-terminal domain {Thermotoga maritima}
FTSSLFLWGEALPTLLEEFNEVEKMLKNQVNTRRIHQLLEKELDDPLENKDLEEKLQAFLDYVKEI
PNLPEARKRYRIQKSLEMIEKLRSWFLIDYLE
>d1gkza1 a.29.5.1 (A:38-185) Branched-chain alpha-ketoacid dehydrogenase kinase (BCK) {Rat (Rattus norvegicus}}
VRLTPTMMLYSGRSQDGSLLKSGRYLQQELPVRIAHRIKGFSLPFIIGCNPTILHVHELIVIRAFQKL
TDFPPIKDQADEAQYCQLVRQLLDDHKDVVTLAEGLRSRKHIEDEKLVRYFLDKTLTSLRGIRML
ATHHLALHEDKP
>d1jm6a1 a.29.5.1 (A:1003-1169) Pyruvate dehydrogenase kinase {Rat (Rattus norvegicus), isozyme 2}
ASLAGAPKYIEHFSKFSPLSMKQFLDFGSSNACEKTSFTFLRQELPVRLANIMKEINLLPDRVLSTP
SVQLVQSWYVQSLLDIMEFLDKDPEDHRTLSQFTDALVTIRNRHNDVVPTMAQGVLEYKDTYGGDP
VSNQNIQYFLDRFYLSRISIRMLINQHTLIFD
>d1buca1 a.29.3.1 (A:233-383) Butyryl-CoA dehydrogenase {Megasphaera elsdenii}
GKGFKIAMMTLDGGRIGVAAQALGIAEAALADAVEYSKQRVQFGKPLCKFQSSISFKLADMKMQIEAA
RNLVYKAACKKQEGKPFVDAIAKRVASDVAMRVTTAVQIFGGYGYSEEYPVARHMRDAKITQIY
EGTNEVQLMVTGGALLR
>d1jqia1 a.29.3.1 (A:235-387) Butyryl-CoA dehydrogenase {Rat (Rattus norvegicus}}
MGFKIAMQTLDMGRIGIASQALGIAQASLDCAVKYAENRHAFGAPLTKLQNIQFKLADMALAESAR
LLTWRAAMLKDNKKPFTKESAMAKLAASEAATAISHQAIQILGGMGYVTEMPAERYRDARITEIYE
GTSEIQRLVIAGHLLRSYR
>d3mda1 a.29.3.1 (A:242-395) Medium chain acyl-CoA dehydrogenase {Pig (Sus scrofa}}
GAGFKIAMGTDFKTRPPVAAGAVGLAQRALDEATKYALERKTFGKLLAEHQGISFLLADMAMKVEL
ARLSYQRAAWEIDSGRRNTYYASIAKAYAADIANQLATDAVQVFGGNGFNTEYPVEKLMRDAKIYQI
YEGTAIQRIIAREHIGRYK
>d1egda1 a.29.3.1 (A:242-396) Medium chain acyl-CoA dehydrogenase {Human (Homo sapiens}}
GAGFKVAMGAFDKERPVAAGAVGLAQRALDEATKYALERKTFGKLLVEHQAISFMLAEMAMKVEL
ARMSYQRAAWEVDSGRRNTYYASIAKAFAGDIANQLATDAVQILGGNGFNTEYPVEKLMRDAKIYQI
YGGTSQIQRLIVAREHIDKYKN
>d1ivha1 a.29.3.1 (A:242-392) Isovaleryl-CoA dehydrogenase {Human (Homo sapiens}}
KGVYVLMGLDLERLVLGGPLGLMQAVLDHTIPYLHVREAFGQKIGHFQLMQGMADMYTRLMA
CRQYVYNVAKACDEGHCTAKDCAGVILYSAECATQVALDGIQCFGGNGYINDFPMGRFLRDAKLYEIG
AGTSEVRRRLVIGRAFAD
>d1b6q_ a.30.1.1 (-) ROP protein {Escherichia coli}
MTKQEKALNMARFIRSQTLTLEKLNELDPDEQADICESLHDHADELYRSCLARF

>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}
 GTKQEKTALNMARFIRSQTLTLEKLNELGADEQADICESLHDHADELYRSCLARFGDDGEN

>d1nkd__a.30.1.1 (-) ROP protein {Escherichia coli}
 MTKQEKTALNMARFIRSQTLTLEKLNELADADEQADICESLHDHADELYRSCLARFG

>d1joya_a.30.2.1 (A:) EnvZ histidine kinase {Escherichia coli}
 MAAGVKQLADDRLLMAGVSHDLRTPTRIRLATEMMSEQDGYLAESINKDIEECNAIIEQFIDYLR

>d1b3qa1_a.30.2.1 (A:293-354) Histidine kinase CheA {Thermotoga maritima}
 SQTVRVIEKLDNLMGLMELVIARSRIETLKKYNIKELDESLSHLSRITLDLQNVVMKIR

>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)}
 SNAEASRVYEIIVESVNEVREDFENAGIDEQTLQDLKNIWQKKLT

>d1ytfd1_a.32.1.1 (D:5-54) Transcription factor IIA (TFIIA), N-terminal domain {Baker's
 yeast (Saccharomyces cerevisiae)}
 GYYELYRRSTIGNSLVDALDTLISDGRIEASLAMRVLETFDKVVVAETLKD

>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}
 WSTIVKLTICPTLKSMACKCEGSIATMIKKKCDK

>d1b0na1_a.34.1.1 (A:74-108) SinR repressor (dimerisation domain)-SinI anti-repressor
 complex {Bacillus subtilis}
 LDSEWEKLVDRAMTSGVSKKQFREFLDYQKWRKSQ

>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)}
 MVSQKLSQLQTEMLAALLESGLSKEALIQALG

>d1g2za_a.34.1.1 (A:) Dimerization cofactor of HNF-1 alpha {Mouse (Mus musculus)}
 MVSQKLSQLQTEMLAALLESGLSKEALIQALGE

>d1g39a_a.34.1.1 (A:) Dimerization cofactor of HNF-1 alpha {Mouse (Mus musculus)}
 MVSQKLSQLQTELLAALLESGLSKEALIQ

>d1jb6b_a.34.1.1 (B:) Dimerization cofactor of HNF-1 alpha {Mouse (Mus musculus)}
 SKLSQLQTEMLAALLESGLSKEALIQAL

>d1e3oc2_a.35.1.1 (C:1-75) Oct-1 {Human (Homo sapiens)}
 EEPDLEELEQFAKTFKQRRIKLGFTQGDVGLAMGKLYGNDFSQTTISRFEALNLSFKNMSKLPKPLLE
 KWLNDAAE

>d1au7a2 a.35.1.1 (A:5-76) Pit-1 {Rat (*Rattus norvegicus*)}
 GMRALEQFANEFKVRRIKLGYTQTNVGEALAAVHGSEFSQTTICRFENLQLSFKNACKLKAILSOWL
 EEAEQ

>d1llib_ a.35.1.2 (B:) lambda C1 repressor, DNA-binding domain {Bacteriophage lambda
 (*Escherichia coli*)}
 STKKKPLTQELEDARRLKAIYEKKKKNELGLSQESLADKLGMGQSGIGALFNGINALNAYNAALLAKI
 LKVSVEEFSPSIAREIYEMYEAVS

>d1lmb3_ a.35.1.2 (3:) lambda C1 repressor, DNA-binding domain {Bacteriophage lambda
 (*Escherichia coli*)}
 PLTQELEDARRLKAIYEKKKKNELGLSQESVADKMGMGQSGVGFALFNGINALNAYNAALLAKILKVS
 VEEFSPSIAREIYEMYEAVS

>d1r69_ a.35.1.2 (-) 434 C1 repressor, DNA-binding domain {Bacteriophage 434
 (*Escherichia coli*)}
 SISRKVKSKRIQLGLNQAELAQKVGTTQQSIEQLENGKTKRPRFLPELASALGVSVDWLLNGT

>d2cro_ a.35.1.2 (-) cro 434 {Bacteriophage 434}
 MQTLSERLKRRIALKMTQTELATKAGVKQSQIQLIEAGVTKRPRFLFEIAMALNCDPVWLQYGT

>d1adr_ a.35.1.2 (-) P22 C2 repressor, DNA-binding domain {Salmonella bacteriophage P22}
 MNTQLMGERIRARRKLRQAALGKMVGVSNAISQWERSETEPNGENLLALSALQCPDYLLK
 GDLSQTNVAY

>d1copd_ a.35.1.2 (D:) cro lambda repressor {Bacteriophage lambda (*Escherichia coli*)}
 MEQRITLKDYAMRFGQTKTAKDLGVYQSAINKAIHAGRKIFLTINADGSVYAEVVKPFPSNKKTTA

>d1d1la_ a.35.1.2 (A:) cro lambda repressor {Bacteriophage lambda (*Escherichia coli*)}
 MEQRITLKDYAMRFGQTKTAKDLGVYQSAINKAIHAGRKIFLTINADGSVYAEVVKPWPSN

>d3orca_ a.35.1.2 (A:) cro lambda repressor {Bacteriophage lambda (*Escherichia coli*)}
 EQRITLKDYAMRFGQTKTAKDLGVYQSAINKAIHAGRKIFLTINADGSVYAEVVKDGEVVKPFPSN

>d1ner_ a.35.1.2 (-) Ner {Bacteriophage mu}
 CSNEKARDWHRADVIAGLKKRKLSSALSQRQFGYAPTTLANALERHWPKEQIIANALETKEPIVW
 PSRYQAGE

>d1b0na2 a.35.1.3 (A:1-68) SinR repressor, DNA-binding domain {*Bacillus subtilis*}
 MIGQRIKQYRKEKGYSLSELAEKAGVAKSYLSSIERNLQTNPSIQFLEKVSALVDVSVHTLLDEKHET

>d1dw9a1 a.35.1.4 (A:1-86) Cyanase N-terminal domain {*Escherichia coli*}
 MIQSQINRNIRLDLADAILLSKAKKDLSEFAEADGTGLAEAFVTAALLGQQALPADAARLVGAKLDDL
 EDSILLQMIPLRGCIDD

>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*}
 MKLDEIARLAGVSRRTTASYVINGKAKQYRVSDKTVEKVMVAVVREHNYHPN

>d1uxd_ a.35.1.5 (-) Fructose repressor (FruR), N-terminal domain {*Escherichia coli*}

MKLDEIARLAGVSRTTASYVINGKAKQYRVSDKTVEKVMMAVVREHNYHPNAVAAGLRLQ
>d1dula_a.36.1.1 (A:) Signal sequence binding protein Ffh {Escherichia coli}
FDLNDFLEQKVLVRMEAIINSMTMKERAKPEIHKSRKRRIAAGSGMQVQDVNRLKQFDDMQRM
MKKM
>d1hq1a_a.36.1.1 (A:) Signal sequence binding protein Ffh {Escherichia coli}
GFDLNDFLEQLRQMKNMGGMASLMGKLPGMGQIPDNVKSQMDDKVLVRMEAIINSMTMKERAK
PEIHKSRKRRIAAGSGMQVQDVNRLKQFDDMQRMMKMK
>d2ffha2_a.36.1.1 (A:319-418) Signal sequence binding protein Ffh {Thermus aquaticus}
ELSLEDFLKQMQLKRLGPFSEILGLLPGVPGQLKVDEKAIKRLEAIVLSMTPEERKDPRLNGSRRK
RIAKSGTSTVQEVNRFKAFEEEMKALMKSLEK
>d1qb2a_a.36.1.1 (A:) SRP54M {Human (Homo sapiens)}
QFTLRDMEYEQFNIMKMGPFSQLGMIPGFGTDFMSKGNQESMARLKKLMTIMDSMNDQELDST
DGAKVFSKQPGRIQRVARGSGVSTRDVQELLQYTKFAQMVK
>d1sknp_a.37.1.1 (P:) Binding domain of Skn-1 {Caenorhabditis elegans}
GRQSKDEQLASDNELPVSAFQISEMSLSELQVVLKNESEYQRQLIRKIRRRGKNKVAARTCRQRRT
DRHDKM
>d1hloa_a.38.1.1 (A:) Max protein {Human (Homo sapiens)}
NDDIEVESDADKRAHNALERKRRDHKDSFHSLRDSVPSLQGEKASRAQILDKATEYIQYMRRKN
HTHQDIDDLKRQN
>d1an2a_a.38.1.1 (A:) Max protein {Mouse (Mus musculus)}
ADKRAHNALERKRRDHKDSFHSLRDSVPSLQGEKASRAQILDKATEYIQYMRRKNHTHQDIDD
LKRQNALLEQQVRALEKARS
>d1mdya_a.38.1.1 (A:) Myod B/HLH domain {Mouse (Mus musculus)}
MELKRKTTNADRRKAATMRERRRLSKVNEAFETLKRSTSSNPQRLPKVEILRNAIRYIEGLQALLR
D
>d1an4a_a.38.1.1 (A:) Usf B/HLH domain {Human (Homo sapiens)}
MDEKRRQAQHNEVERRRRDKINNWIWVQLSKIIPDSSMESTKSGQSKGGILSKASDYIQELRQSNHR
>d1a0aa_a.38.1.1 (A:) Pho4 B/HLH domain {Baker's yeast (Saccharomyces cerevisiae)}
MKRESHKHAEQARRNRLAVALHELASLIPAEWKQNVSAAPSKATTVEAACRYIRHLQQNGST
>d1am9a_a.38.1.1 (A:) SREBP-1a {Human (Homo sapiens)}
QSRGEKRTAHNAIEKRYRSSINDKIIELKDLVVGTEAKLNKSAVLRKAIDYIRFLQHSNQKQENLSL
RTAVHKSLSLK
>d1bod_a.39.1.1 (-) Calbindin D9K {Cow (Bos taurus)}
MKSPEELKGIFEKYDKEGDGQLSKEELKLLLQTEFPSSLKGMSTLDELFEELDKNGDGEVSFEFQVL
VKKISQ
>d1ig5a_a.39.1.1 (A:) Calbindin D9K {Cow (Bos taurus)}
KSPEELKGIFEKYAAKEGDPNQLSKEELKLLLQTEFPSSLKGPSTLDELFEELDKNGDGEVSFEFQV
LVKKISQ
>d1cb1_a.39.1.1 (-) Calbindin D9K {Pig (Sus scrofa)}
SAQKSPAELKSIFEKYAAKEGDPNQLSKEELKQLIQAEFPSSLKGPRTLDDLFQELDKNGDGEVSFEE
FQVLVKKISQ
>d1a03a_a.39.1.2 (A:) Calcyclin (S100) {Rabbit (Oryctolagus cuniculus)}
MASPLDQAIGLLIGIFHKYSGKEGDKHTLSKKELKELIQKELTIGSKLQDAEIVKLMDDLDNRNKDQEV
NFQEYITFLGALAMIYNEALKG

>d1k2ha_ a.39.1.2 (A:) Calcyclin (S100) {Rat (Rattus norvegicus), s100a1}
GSELETAMETLINVFHHAHSGKEGDKYKLSKKELKDLLQTESSFLDVQKDADAVDKIMKELDENG
GEVDFQEFVVLVAALTVACNNFFWENS

>d1qlka_ a.39.1.2 (A:) Calcyclin (S100) {Rat (Rattus norvegicus), s100b}
MSELEKAMVALIDVFHQYSGREGDKHKLKSELKELINNELSHFLEEIKEQEVVDKVMETLDEDGD
GECDFQEFMAFVSMVTTACHEFFEHE

>d1mho_ a.39.1.2 (-) Calcyclin (S100) {Cow (Bos taurus), s100b}
SELEKAVVALIDVFHQYSGREGDKHKLKSELKELINNELSHFLEEIKEQEVVDKVMETLSDGDGE
CDFQEFMAFVAMITTACHEFF

>d1a4pa_ a.39.1.2 (A:) Calcyclin (S100) {Human (Homo sapiens), P11 s100a10, calpactin}
PSQMEHAMETMMFTFHKFAGDKGYLTKEDLRVLMEKEFPGFLENQKDPLAVDKIMKDLDQCRDG
KVGFSFFSLIAGLTACNDYFVVHMKQ

>d1psra_ a.39.1.2 (A:) Calcyclin (S100) {Human (Homo sapiens), psoriasis s100a7}
SNTQAERSIIGMIDMFHKYTRRDDKIDKPSLLTMMKENFPNFLSACDKKGTNYLADVFEKKDKNED
KKIDFSEFLSLLGDIATDYHKQSHGAAPCSGGSQ

>d1qlsa_ a.39.1.2 (A:) Calcyclin (S100) {Pig (Sus scrofa), calgizzarin s100c (s100a11)}
PTETERCIESLIAIFQKHAGRDGNNTKISKTEFLIFMNTELAAFTQNQKDPGVLDLDRMMKKLDLSDG
QLDFQEFNLIGGLAIAACHDSFIKSTQK

>d1mr8a_ a.39.1.2 (A:) Calcyclin (S100) {Human (Homo sapiens), calgranulin s100a8,
MRP8}
MLTELEKALNSIIDVYHKYSLIKGNFHAVYRDDLKKLLETECPQYIRKKGADVWFKELDINTDGAVN
FQEFLLIVIKMGVAAHKKSSHEES

>d1e8aa_ a.39.1.2 (A:) Calcyclin (S100) {Human (Homo sapiens), calgranulin C, s100a12}
TKLEEHLGIVNIFHQYSVRKGHFDTLKSGELKQLLTKELANTIKNIKDKAVIDEIFQGLDANQDEQV
DFQEFISLVAIALKAAHYH

>d1irja_ a.39.1.2 (A:) Calcyclin (S100) {Human (Homo sapiens), s100a9 (mrp14)}
TCKMSQLERNIETIINTFHQYSVKLGHPDTLNQGEFKELVRKDLQNFLKKNKNEKVIEHIMEDLDT
NADKQLSFEEFIMLMARL

>d1sra_ a.39.1.3 (-) C-terminal (EC) domain of BM-40/SPARC/osteonectin {Human (Homo
sapiens)}
PPCLDSELTEFPLMRDWLKNVLTLYERDEDNNLLTEKQKLRVKKIHENEKRLEAGDHPVELLAR
DFEKNYNMYIFPVHWQFGQLDQHPIDGYLSHTELAPLRAPLIPMEHCTTRFFETCDLDNDKYIALD
EWAGCFGIKQKDIDKDLVI

>d1rro_ a.39.1.4 (-) Oncomodulin {Rat (Rattus norvegicus)}
SITDILSAEDIAAALQECQDPDTFEPQKFFQTSGLSKMSASQVKDIFRFIDNDQSGYLDGDELKYFLQ
KFQSDARELSETEKSLMDAADNDGDGKIGADEFQEMVHS

>d1cdp_ a.39.1.4 (-) Parvalbumin {Carp (Cyprinus carpio)}
AFAGVLNDADIAAALEACKAADSFNHKAFFAKVGLTSSKASDDVKKAFIIDDQKSGFIEEDELKFLQ
NFKADARALTDGETKTFLKAGSDGDGKIGVDEFTALVKA

>d1pvaa_ a.39.1.4 (A:) Parvalbumin {Pike (Esox lucius)}
AAKDLLKADDIKKALDAVKAEGSFNHHKFFALVGLKAMSANDVKKVFKAIDADASGFIEEELKFLV
KSFAADGRDLTDAETKAFLKAADKDGDKIGIDEFETLVHEA

>d2pvba_ a.39.1.4 (A:) Parvalbumin {Pike (Esox lucius)}
SFAGLKDADVAAALAACSAADSFKHKEFFAKVGLASKSLDDVKKAFYVIDQDKSGFIEEDELKFLQN

FSPSARALTAETKAFLADGDKDGMIGVDEFAAMIKA
>d5pal_ a.39.1.4 (-) Parvalbumin {Leopard shark (Triakis semifasciata)}
PMTKVLKADDINKAISAFKDPGTFDYKRFFHLVGLKGTDAQVKEVFEILDKDQSGFIEEEELKGVLK
GFSAHGRDLNDTETKALLAAGDSHDGKIGADEFAKMVAQA
>d1a75a_ a.39.1.4 (A:) Parvalbumin {Whiting (Merlangius merlangus)}
AGILADADCAAANKACEAADSFSYKAFFAKCGLSGKSADDIKKAFVVIDQDKSGFIEEDELKFLQVF
KAGARALTAETKAFLKAGDSGDGAIGVEEWVALVKA
>d1bu3_ a.39.1.4 (-) Parvalbumin {Silver hake (Merluccius bilinearis)}
AFSGILADADVAALKACEAADSFNKAFKAVGLTAKSADDIKKAFVVIDQDKSGFIEEDELKFLQ
VFSAGARALTAETKAFLKAGDSGDGAIGVDEWAALVKA
>d1g33a_ a.39.1.4 (A:) Parvalbumin {Rat (Rattus rattus)}
MKSADDVKKVFHILDKDKSGFIEEDELGSILKGFSSDARDLSAKETKTLMAAGDKDGDGKIGVEEFS
TLVAES
>d1rtp1_ a.39.1.4 (1:) Parvalbumin {Rat (Rattus rattus)}
SMTDLLSAEDIKKAIGAFATAADSFHKKFFQMVGLKKKSADDVKKVFHILDKDKSGFIEEDELGSILK
GFSSDARDLSAKETKTLMAAGDKDGDGKIGVEEFSTLVAES
>d1avs_ a.39.1.5 (A:) Troponin C {Chicken (Gallus gallus)}
QAEARAFLEEMIAEFKAAFDMFDADGGGDISTKELGTVMRMLGQNPTKEELDAIIEEVEDGSGTI
DFEEFLVMMVRQMK
>d1ctda_ a.39.1.5 (A:) Troponin C {Chicken (Gallus gallus)}
KSEELANAFRIFDKNADGYIDIEELGEILRATG
>d1dtla_ a.39.1.5 (A:) Troponin C {Chicken (Gallus gallus)}
YKAAVEQLTEEQKNEFKAAFDFVLGAEDGSISTKELGKVMRMLGQNPTPEELQEMIDEVDEDEGSG
TVDFDEFLVMMVRSKDDSKGSEELSDLFRMFDKNADGYIDLEELKIMLQATGETITEDDIEEL
MKDGDKNNDGRIDYDEFLEFMKGV
>d1jc2a_ a.39.1.5 (A:) Troponin C {Chicken (Gallus gallus)}
EDAKGKSEELANCFRIFDKNADGFIDIEELGEILRATGEHVIEEDIEDLMKDSKNDGRIDFDEFL
KMMEGVQ
>d1ncx_ a.39.1.5 (-) Troponin C {Chicken (Gallus gallus)}
ASMTDQQAEARAFLEEMIAEFKAAFDMFDADGGGDISTKELGTVMRMLGQNPTKEELDAIIEEVD
EDGSGTIDFEEFLVMMVRQMKEDAKGKSEELANCFRIFDKNADGFIDIEELGEILRATGEHVTEEDI
EDLMKDSKNDGRIDFDEFLKMMEGVQ
>d1smg_ a.39.1.5 (-) Troponin C {Chicken (Gallus gallus)}
ASMTDQQAEARAFLEEMIAEFKAAFDMFDADGGGDISTKALGTVMRMLGQNPTKEELDAIIEEVD
EDGSGTIDFEEFLVMMVRQMKEDA
>g1pon.1 a.39.1.5 (A:,B:) Troponin C {Chicken (Gallus gallus)}
KSEELANAFRIFDKNADGYIDIEELGEILRATGXVTEEDIEDLMKDSKNDGRIDFDEFLKMMEG
VQ
>d1tn4_ a.39.1.5 (-) Troponin C {Rabbit (Oryctolagus cuniculus)}
TDQQAEARSYLSEEMIAEFKAAFDMFDADGGGDISVKELGTVMRMLGQTPTKEELDAIIEEVEDG
SGTIDFEEFLVMMVRQMKEDAKGKSEELAEFRIFDRNADGYIDAEELAEIFRASGEHVTEEDIEESL
MKDGDKNNDGRIDFDEFLKMMEG
>d1fi5a_ a.39.1.5 (A:) Troponin C {Chicken (Gallus gallus), cardiac isoform}
MVRCKDDSKGKTEEELSDLFRMFDKNADGYIDLEELKIMLQATGETITEDDIEELMKDGDKNND

GRIDYDEFLEFMKGVE

>d1ap4_ a.39.1.5 (-) Troponin C {Human (Homo sapiens), cardiac isoform}

MDDIYKAAVEQLTEEQKNEFKAAFDIVLGAEDGCISTKELGKVMRMLGQNPTPEELQEMIDEVDE
DGSGTVDFDEFLVMMVRCMKDDS

>d1ih0a_ a.39.1.5 (A:) Troponin C {Human (Homo sapiens), cardiac isoform}

GKSEELSDLFRMFKNADGYIDLEELKIMLQATGETITEDDIEELMKDGDKNNDGRIDYDEFLEFM
KGVE

>d2scpa_ a.39.1.5 (A:) Sarcoplasmic calcium-binding protein {Sandworm (Nereis
diversicolor)}

SDLWVQKMKTYFNRIDFDKDGAITRMDFESMAERFAKESEMKAEHAKVLMDSLTGVWDNFLTAVA
GGKIDETTFINSMKEMVKNPEAKSVVEGPLPLFFRAVDTNEDNNISRDEYGIFFGMLGLDKTMAPA
SFD AIDTNN DGLLSLEEFVIAGSDFMNDGDSTNKVFWGPLY

>d2sas_ a.39.1.5 (-) Sarcoplasmic calcium-binding protein {Amphioxus (Branchiostoma
lanceolatum)}

GLNDFQKQKIKFTDFFLDMNHGDSIQDNDFEDMMTRYKEVKNKGLSDADYKSMQASLEDEWRD
LKGRADINKDDVVSWEYLAMWEKTIATCKSVADLPAWCQNRIPFLFKGMDVSGD GIVDLEEFQNY
CKNFQLQCADVPAVYNVITDGGKVTFDLNRKELYRLLTSPAADAGNTLMGQKP

>d1c7va_ a.39.1.5 (A:) Calcium vector protein {Amphioxus (Branchiostoma lanceolatum)}

EEEILRAFKVFDANGDGVDFDEFKFKIMQVGEPLTDAEVEEAMKEADEDGNGVIDIPEFMDLIKK
S

>d1j7qa_ a.39.1.5 (A:) Calcium vector protein {Amphioxus (Branchiostoma lanceolatum)}

AAPKARALGPEEKDECMKIFDIFDRNAENIAPVSDTMDMLTKLGQTYTKRETEAIMKEARGPKGDK
KNIGPEEWLTLCSKWVRQDD

>d1j7ra_ a.39.1.5 (A:) Calcium vector protein {Amphioxus (Branchiostoma lanceolatum)}

LGPEEKDECMKIFDIFDRNAENIAPVSDTMDMLTKLGQTYTKRETEAIMKEARGPKGDKKNIGPEE
WLTLCSKWVRQ

>d1ej3a_ a.39.1.5 (A:) Calcium-regulated photoprotein {Jellyfish (Aequorea aequorea),
aequorin}

LTSDFDNPRWIGRHKHMFNFDLVNHNGKISLDEM VYKASDIVINNLGATPEQAKRHKDAVEAFFGG
AGMKYGVETDWPAYIEGWKKLATDELEKYAKNEPTLIRIWGDALFDIVDKDQNGAITLDEWKAYT
KAAGIIQSSEDCEETFRVCDIDESGQLDVDEMTRQHLGFWYTMDPACEKLYGGAVP

>d1el4a_ a.39.1.5 (A:) Calcium-regulated photoprotein {Hydrozoa (Obelia longissima),
obelin}

SSKYAVKLKTFDNPRWIKRHKHMFDFLDINGNGKITLDEIVSKASDDICAKLEATPEQTKRHQVCV
EAFFRGCMEYGKEIAFPQFLDGWKQLATSELKKWARNEPTLIREWGDVDFDIFDKDGS GTITLDE
WKAYGKISGISPSQEDCEATFRHCDLNSGDLVDDEMTRQHLGFWYTLDPEADGLYGNGVP

>d1jf0a_ a.39.1.5 (A:) Calcium-regulated photoprotein {Hydrozoa (Obelia geniculata), obelin}

KYAVKLQTFDNPKWIKRHKFMFDYLDINGNGQITLDEIVSKASDDICKNLGATPAQTQRHQDCVE
AFFRGCGLYEGKETKPEFLEGWKNLANADLAKWARNEPTLIREWGDVDFDIFDKDGS GTITLDE
WKAYGRISGISPSEEDCEKTFQHCDLNSGELDVDEMTRQHLGFWYTLDPEADGLYGNGVP

>d1jfja_ a.39.1.5 (A:) EHCABP {Entamoeba (Entamoeba histolytica)}

MAEALFKEIDVNGDGAVSYYEYKAFVSKKRAIKNEQLLQLIFKSIDADNGEIDQNEFAKFYGSIQGQ
DLSDDKIGLKVLYKLMDVDGDGKLTKEEVSFFKKHGIEKVAEQVMKADANGDGYITLEEFLEFSL

>d1cmg_ a.39.1.5 (-) Calmodulin {Cow (Bos taurus)}

MKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEF
VQMMTAK

>d1fw4a_a.39.1.5 (A:) Calmodulin {Cow (Bos taurus)}

SEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEFVQMM

>d1g4yr_a.39.1.5 (R:) Calmodulin {Rat (Rattus rattus)}

ADQLTEEQIAEFKEAFSLFDKDGDTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDFPE
FLTMMARKMKDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGD
GQVNYEEFVQMMTA

>d1f70a_a.39.1.5 (A:) Calmodulin {African frog (Xenopus laevis)}

ADQLTEEQIAEFKEAFSLFDKDGDTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDFPE
FLTMMARKM

>d1extra_a.39.1.5 (A:) Calmodulin {Ciliate (Paramecium tetraurelia)}

EQLTEEQIAEFKEAFALFDKDGDTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDFPEF
LSLMARKMKEQDSEEEIEAFKVFDRDGNLISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDG
HINYEEFVRRMMVS

>d1ggwa_a.39.1.5 (A:) Cdc4p {Fission yeast (Schizosaccharomyces pombe)}

STDDSPYKQAFSLFDRHGTGRIPKTSIGDLLRACGQNPTEAELTEIESTLPAEVDMEQFLQVLNRPNG
FDMPGDPEEFVKGQVFDKDATGMIGVGELRYVLTSLGEKLSNEEMDELLKGVVPKDGMMVNYHDFV
QMILAN

>d1wdcb_a.39.1.5 (B:) Myosin Essential Chain {Bay scallop (Aequipecten irradians)}

LPQKQIQEMKEAFSMIDVDRDGFVSKEDIKAISEQLGRAPDDKELTAMLKEAPGLNFTMFLSIFSD
KLSGTDSEETIRNAFAMFDEQETKKNIEYIKDLLENMGDNFNKDEMRTFKEAPVEGGKFDYVKF
TAMIKSGE

>d1br1b_a.39.1.5 (B:) Myosin Essential Chain {Chicken (Gallus gallus)}

FSEEQTAEFKEAFQLFDRTGDGKILYSQCGDVMRALGQNPTEAELVMKVLGNPKSDEMNLKTLKFEQ
FLPMMQTIANKDQGCFFEDYVEGLRVFDKEGNGTVMGAEIRHVLVTLGEKMTREEVEQLVAGHED
SNGCINYEELVRMVLGS

>d2mysb_a.39.1.5 (B:) Myosin Essential Chain {Chicken (Gallus gallus)}

FDETEIEDFKEAFTVIDQNADGIIDKDDLRETFAMGRLNVKNEELDAMIKEASGPINFTVFLTMFG
EKLKGADPEDVIMGAFKVLDPDGKSGIKSFLLELLTGGGRFTPEEIKNMWAAFPDPVAGNVYK
NICYVITHGEDA

>d1wdcc_a.39.1.5 (C:) Myosin Regulatory Chain {Bay scallop (Aequipecten irradians)}

LSQDEIDDLKDFELDFWDRDGAVDFAKLGDVCRCLGINPRNEDVFAVGGTHKMGEKSLPFEFF
LPAYEGLMDCEQGTFFADYMEAFKTFDREGQGFISGAELRHVLTALGERLSDEDVDEIIKLTDLQEDLE
GNVKYEDFVKKVMAGPYP

>d2mysc_a.39.1.5 (C:) Myosin Regulatory Chain {Chicken (Gallus gallus)}

AAADDFKEAFLFDRTGDAKITASQVGDIALRGQNPTEAELINKILGNPSKEEMNAAITFEEFLPM
LQAAAANKDQGTFFEDFVEGLRVFDKEGNGTVMGAEIRHVLATLGEKMTREEVEELMKGQEDSNG
CINYEAFVKHIMSV

>d1auib_a.39.1.5 (B:) Calcineurin regulatory subunit (B-chain) {Human (Homo sapiens)}

SYPLEMCSHFDADEIKRLGKRFKLLDNSGSLVVEEFMSLPELQQNPLVQRVIDIFDFTDNGEVDF
KEFIEGVSQFSVKGDKQKLRFAFRIYDMKDGYSNGELFQVLKMMVGNLKDQTLQQIVDKTIIN
ADKDGDRISFEEFCVVGGLDIHKKMVVDV

>d1rec_a.39.1.5 (-) Recoverin {Cow (Bos taurus)}

LSKEILEELQLNTRKFTTEELSSWYQSFLKECPSGRITRQEFQTIYSKFFPEADPKAYAQHVFRSFDANS
DGTLDKFKEYVIALHMTSAGKTNQKLEWAFSLYDVDGNGTISKNEVLEIVTAIFKMISPEDTKHLPED
ENTPEKRAEKIWGGFFGKKDDDKLTEKEFIEGTLANKEILRLIQFEPQKVKEKLLK
>d1g8ia_ a.39.1.5 (A:) Frequenin (neuronal calcium sensor 1) {Human (Homo sapiens)}
SNSKLPKPEVVEELTRKTYFTEKEVQQWYKGFIKDCPSGQLDAAGFQKIYKQFFPFGDPTKFATFVFN
VFENKDGRIEFSEFIQALSVTSRGTLDEKLRWAFKLYDLNDGYITRNEMLDIVDAIQMVGNTVE
LPEEENTPEKRVDRIFAMMDKNADGKLTQEFQEGSKADPSIVQALSLYDGLV
>d1fpwa_ a.39.1.5 (A:) Frequenin (neuronal calcium sensor 1) {Baker's yeast
(Saccharomyces cerevisiae)}
MGAKTSKLSKDDLTCLKQSTYFDRREIQQWHKGFRLDCPSGQLAREDFVKIYKQFFPFGSPEDFANH
LFTVFDKDNNGFIHFEEFITVLTSTSRGTLEEKLSWAFELYDLNHDGYITFDEMLTIVASVYKMMGS
MVTLNEDEATPEMRVKKIFKLMKDNEDGYITLDEFREGSKVDPSIIGALNLYDGLI
>d1jbaa_ a.39.1.5 (A:) Guanylate cyclase activating protein 2, GCAP-2 {Cow (Bos taurus)}
GQQFSWEEAEENGAVGAADAAQLQEWYKKFLEECPSGTLFMHEFKRFFKVPDNEEATQYVEAMFR
AFDTNGDNTIDFLEYVAALNLVLRGTLEHKLKWTFKIYDKDRNGCIDRQELLDIVESIYKLLKACSVE
VEAEQQGKLLTPEEVVDRIFLLVDENGDGQLSLNEFVEGARRDKWVMKMLQMDLNP
>d1bjfa_ a.39.1.5 (A:) Neurocalcin {Cow (Bos taurus)}
NSKLRPEVMQDLLESTDFTEHEIQEWYKGFRLDCPSGHLSMEEFKKIYGNFFPYGDASKFAEHVFR
FDANGDGTIDFREFIIALSVTSRGKLEQKLKWAFSMYDLGNGYISKAEMLEIVQAIYKMOVSSVMKM
PEDESTPEKRTEKIFRQMDTNRDGKLSLEEFIRGAKSDPSIVRLLQC
>d1dgua_ a.39.1.5 (A:) Calcium- and integrin-binding protein, CIB {Human (Homo sapiens)}
SKELLAEYQDLTFLTKQEILLAHRRFCCELLPQEQRSVESLRAQVPFEQILSLPELKANPFKERICRVFS
TSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFDFDDGTLNREDLSRLVNCLTGEGEDTRLSAS
EMKQLIDNILEESDIDRDGTINLSEFQHVISRSPDFASSFKIVL
>d1qjta_ a.39.1.6 (A:) Eps15 {Mouse (Mus musculus)}
LSLTQLSSGNPVYEKYYRQVEAGNTGRVLALDAAFLKKSGLPDLILGKIWDLADTDGKGVLSKQEF
FVALRLVACAQNGLEVSLSSLSLAVPPPRFHD
>d1c07a_ a.39.1.6 (A:) Eps15 {Human (Homo sapiens)}
TWVVSPEAKAKYDEIFLKTDKMDGFGVSGLEVREIFLKTGLPSTLLAHIWSLCDTKDCGKLSKDQFA
LAFHLISQKLIKIDPPHVLTPEMIPPS
>d1f8ha_ a.39.1.6 (A:) Eps15 {Human (Homo sapiens)}
PWAVKPEDKAKYDAIFDSLSPVNGFSLGDKVKPVLNLSKLPVDILGRVWELSDIDHDGMLDRDEFV
AMFLVYCALEKEPVPMSLPPALVPPSKR
>d1iq3a_ a.39.1.6 (A:) Pab1 {Human (Homo sapiens)}
GSLQDNSSYPDEPWRITEEQREYYVNQFRSLQPDPSFISGSVAKNFFTKSKLSIPELSYIWELSDADC
DGALTLPEFCAAFHLIVARKNGYPLPEGLPPTLQPEFIVTD
>d1fi6a_ a.39.1.6 (A:) Reps1 {Mouse (Mus musculus)}
WKITDEQRQYYVNQFKTIQPDNLNGFIPGSAAKEFFTKSKLPILELSHIWELSDFDKDGALTLDEFCAA
FHLVVARKNYDLPEKLPESLMPK
>d1hqva_ a.39.1.8 (A:) Apoptosis-linked protein alg-2 {Mouse (Mus musculus)}
PGPGGGPGPAAGAALPDQSFLWNVFRVDKDRSGVISDNELQQALSNGTWTWTFNPVTVRSIISMFD
RENKAGVNFSEFTGVWKYITDWQNVFRTYDRDNSGMIDKNELKQALSFGYRLSDQFHDILIRKFD
RQGRGQIAFDFFIQGCIVLQRLTDIFRRYDTDQDGWIVQVSYEQYLSMVF
>d1juoa_ a.39.1.8 (A:) Sorcin {Human (Homo sapiens)}

FPGQTQDPLYGYFAAVAGQDGGQIDADELQRCLTQSGIAGGYKPFNLETCLRMVSMLEDRDMSGTMGF
NEFKELWAVLNGWRQHFISFDTRSGTVDPQELQKALTTMGFRLSPQAVNSIAKRYSTNGKITFDD
YIACCVKLRALDTSFRRRDTAQQGVVNFYDDFIQCVMSV
>d1djb1 a.39.1.7 (B:158-298) Phosphoinositide-specific phospholipase C, isozyme D1
(PLC-D!) {Rat (Rattus norvegicus)}
NKMNFKELKDFLQVDDGYARKIFRECDHSQTDSLEDEEIEIFYKMLTQRAEIDRAFEEAAGS
AETLSVERLVTFQLHQQREEEAGPALALSLIEREYEPSETAKAQRQMTKDGFLMYLLSADGNAFSLAH
RRVYQDM
>d1qasa1 a.39.1.7 (A:205-298) Phosphoinositide-specific phospholipase C, isozyme D1
(PLC-D!) {Rat (Rattus norvegicus)}
YKMLTQRAEIDRAFEEAAGSAETLSVERLVTFQLHQQREEEAGPALALSLIEREYEPSETAKAQRQMT
KDGFLMYLLSADGNAFSLAHRRVYQDM
>d1k94a_ a.39.1.7 (A:) Grancalcin {Human (Homo sapiens)}
SVYTYFSAVAGQDGEVDAEELQRCLTQSGINGTYPFSLETGRIMIAMLEDRDHTGKMGFNFKELWA
ALNAWKENFMTVDQDGGTVEHHELRLQAIGLMGYRLSPQTLTTIVKRYSKNGRIFDDYVACCVKL
RALDFFRKRDLQGGSANFIYDDFLQGTMAI
>d1kfus_ a.39.1.7 (S:) Calpain small (regulatory) subunit (domain VI) {Human (Homo
sapiens)}
THYSNIEANESEEVQRFRRLFAQLAGDDMEVSATELMNILNKVVTRHPDLKTDGFGIDTCRSMVAV
MDSDTTGKLGFEFKYLWNNIKRWQAIYKQFDTRSGTICSELPGAFEAAAGFHLNEHLYNMIIRRY
SDESGNMDFDNFISCLVRLDAMFRAFKSLDKDGTGQIQVNIQEWLQLTMY
>d1dvia_ a.39.1.7 (A:) Calpain small (regulatory) subunit (domain VI) {Rat (Rattus
norvegicus)}
EEERQFRKLVQLAGDDMEVSATELMNILNKVVTRHPDLKTDGFGIDTSRSMVAVMDSDTTGKLG
FEFKYLWNNIKKWQGIYKRFDTDRSGTIGSNELPGAFEAAAGFHLNQHIYSMIIRRYSDETGNMDFD
NFISCLVRLDAMFRAFRSLDKDGTGQIQVNIQEWLQLTMY
>d1alva_ a.39.1.7 (A:) Calpain small (regulatory) subunit (domain VI) {Pig (Sus scrofa)}
EEVRQFRRLFAQLAGDDMEVSATELMNILNKVVTRHPDLKTDGFGIDTCRSMVAVMDSDTTGKLG
FEFKYLWNNIKKWQAIYKQFDVDRSGTIGSSELPGAFEAAAGFHLNEHLYSMIIRRYSDDEGNMDFD
NFISCLVRLDAMFRAFKSLDKDGTGQIQVNIQEWLQLTMY
>d1kful1 a.39.1.7 (L:515-700) Calpain large subunit, C-terminal domain (domain IV)
{Human (Homo sapiens)}
EIEANLEEFDISEDIDDDGVRRLFAQLAGEDAEISAFELQTLRRVLAKRQDIKSDGFSIETCKIMVDM
LDSGSGKLGKLFYILWTKIQKYQKIYREIDVDRSGTMNSYEMRKALEEAGFKMPCQLHQVIVARF
ADDQLIIDFDNFVRCLVRLETFLKIFKQLDPENTGTIELDLISWLCFSVL
>d1df0a1 a.39.1.7 (A:515-700) Calpain large subunit, C-terminal domain (domain IV) {Rat
(Rattus norvegicus)}
EIEANIEEIANEEDIGDGRRLFAQLAGEDAEISAFELQTLRRVLAKREDIKSDGFSIETCKIMVDM
DEDGSGKLGKLFYILWTKIQKYQKIYREIDVDRSGTMNSYEMRKALEEAGFKLPCQLHQVIVARFA
DDELIIDFDNFVRCLVRLEILFKIFKQLDPENTGTIQLDLISWLSFSVL
>d1eg3a1 a.39.1.7 (A:85-209) Dystrophin {Human (Homo sapiens)}
HPKMTELYQSLADLNNVRFSAYRTAMKLRRLQKALCLDLLSLAACDALDQHNLKQNDQPMILQI
INCLTTIYDRLEQEHNNLVNPLCVDMCLNWLNVYDTGRTGRIRVLSFKTGIISLCKA
>d1eg3a2 a.39.1.7 (A:210-306) Dystrophin {Human (Homo sapiens)}

HLEDKYRYLQKQVASSTGFCDQRRLLGLLHDSIQIPRQLGEVASFGGSNIEPSVRSCFQFANNKPEIEA
ALFLDWMRLEPQSMVWLPVLRVAAAET
>d2cbla1 a.39.1.7 (A:178-263) Cbl {Human (Homo sapiens)}
TFRITKADAAEFWRKAFGEKTIVPWKSFQRALHEVHPISGLEAMALKSTIDLTCNDYISVFEDIFT
RLFQPWSSLLRNWNSLAV
>d1h8ba_ a.39.1.7 (A:) alpha-Actinin {Human (Homo sapiens)}
MADTDTAEQVIASFRILASDKPYILAEELRRELPPDQAQYCIKRMPPAYSGPGSVPGALDYAAFSSALYG
ESDL
>d1c3za_ a.39.2.1 (A:) Thp12-carrier protein {Yellow mealworm (Tenebrio molitor)}
ETPREKLKQHSACKAESGVSEESLNKVRNREEVDDPKLKEHAFILKRAGFIDASGEFQLDHIKTK
FKENSEHPEKVDLVAKCAVKKDTPQHSSADFFKCVHDNRS
>d1dqa_ a.39.2.1 (A:) Pheromone binding protein {Silkworm (Bombyx mori)}
SQEVMKNLSLNFQKALDECKEMTLTDAINEDFYNFWKEGYEIKNRETGCAIMCLSTKLNMLDPEG
NLHHGNAMEFAKKHGADETMAQQLIDIVHGCEKSTPANDDKCIWTLGVATCFKAEIHKLNWAPSM
DVAVGE
>d1iioa_ a.39.4.1 (A:) Hypothetical protein MTH865 {Archaeon Methanobacterium
thermoautotrophicum}
GSHMKMGVKEDIRGQIIGALAGADFPINSPEELMAALPNGPDTTCKSGDVELKASDAGQVLTADDFP
FKSAEEVADTIVNKAGL
>d1cpo_1 a.39.3.1 (0-119) Cloroperoxidase {Fungus (Caldariomyces fumago)}
EEPQSGIGYPYDNNTLPYVAPGPTDSRAPCPALNALANHGYPHDGRAISRETLQNAFLNHMGIAN
VIELALTNAFVVCYVTGSDCGSLVNLTLAEPHAFEHDSFSRKYKQGVA
>d1cpo_2 a.39.3.1 (120-298) Cloroperoxidase {Fungus (Caldariomyces fumago)}
NSNDFIDNRNFAETFTSLDVVAGKTHFDYADMNEIRLQRESLSNELDFPGWFTESKPIQNVESGF
IFALVSDFNLPNDENPLVRIDWWKYWFTNESFPYHLGWHPSPAREIEFVTSASSAVLAASVTSTP
SSLPQGAIGPQAEAVPLSFATMTPFLATNAPYYAQDPTLGPND
>d1h67a_ a.40.1.1 (A:) Calponin {Chicken (Gallus gallus)}
MPQTERQLRVWIEGATGRRIGDNFMDGLKDGVLCELINKLQPGSVQKVNDPVQNWHLKLENIGNFL
RAIKHYGVKPHDIFEANDLFENTNHTQVQSTLIALASQAKTK
>d1bkra_ a.40.1.1 (A:) beta-spectrin {Human (Homo sapiens)}
KSAKDALLLWCQMKTAGYPVNIHNFTTSWRDGMFALIHKHPDLIDFDKLLKKSNAHYNLQNA
FNLAEQHLGLTKLLDPEDISVDHPDEKSIITYVVVYYHYFSKM
>d1aoa_1 a.40.1.1 (121-251) N-terminal actin-crosslinking domain from fimbrin {Human
(Homo sapiens)}
YSEEEKYAFVNWINKALENDPCRHVIPMNPNTDDLKAVGDGIVLCKMINLSVPDTIDERAINKKK
LTPFIIQENLNALNSASAIGCHVVNIGAEDLRAGKPHLVLGLLWQIIKIGLFADIELSRNEAL
>d1aoa_2 a.40.1.1 (260-375) N-terminal actin-crosslinking domain from fimbrin {Human
(Homo sapiens)}
TLEELMKLSPEELLRWANFHLENSGWQKINNFSADIKDSKAYFHLLNQIAPKGQKEGEPRIDINMS
GFNETDDLKRAESMLQQADKLGCRQFVTPADVVSNGPKLNLAFFVANLNFN
>d1bhda_ a.40.1.1 (A:) Utrophin {Human (Homo sapiens)}
LQQTNSEKILLSWVRQTTRPYSQVNVNFTTSWTDGLAFNAVLHRHKPDLFSWVKVMSPIERL
EHAFSKAQTYLGIKLLDPEDVAVRLPDKKSIIMYLTSLFEVL
>d1qaga1 a.40.1.1 (A:31-151) Utrophin {Human (Homo sapiens)}

DVQKKTFTKWINARFSKSGKPPINDMFTDLKDGRKLLDLLEGLTGTSLPKERGSTRVHALNNVNRV
LQVLHQNNVELVNIGGTDIVDGNHKLTLGLLWSIILHWQVKDVMKDVMSDLQQTN
>d1dxxa1 a.40.1.1 (A:9-119) Dystrophin {Human (Homo sapiens)}
DSYEREDVQKKTFTKWNVAQFSKFGKQHIEFLSDLDQGRRLDLLEGLTGQKLPKEKGSTRVHAL
NNVNKALRVLQNNNVDLVNIGSTDIVDGNHKLTLGLIWNILHWQ
>d1dxxa2 a.40.1.1 (A:120-246) Dystrophin {Human (Homo sapiens)}
VKNVMKNIMAGLQQTNSEKILLSWVRQSTRNYPQVNVINFTTSWSDGLALNALIHSRPLDFDWN
SVVSQQSATQRLEHAFNIARYQLGIEKLLDPEDVDTTYDPKKSILMYITSLFQVLPQQVSIE
>d1a26_1 a.41.1.1 (662-796) Domain of poly(ADP-ribose) polymerase {Chicken (Gallus
gallus)}
KSKLAKPIQDLIKMIFDVESMKKAMVEFEIDLQKMPGLGKLSKRQIQSAYSILNEVQQAVSDGGSESQIL
DLSNRFYTLIPHDFGMKKPPLLSNLEYIQAKVQMLDNLDDIEVAYSLLRGGNEDGDKDPIDINYEK
>d1ycqa_a.42.1.1 (A:) MDM2 {African clawed frog (Xenopus laevis)}
EKLVQPTPLLSLLKSAGAQQKFTMKEVIYHLGQYIMAKQLYDEKQQHIVHCSNDPLGELFGVQFEFS
VKEPRRLYAMISRNLV SANV
>d1ycra_a.42.1.1 (A:) MDM2 {Human (Homo sapiens)}
ETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRKYDEKQQHIVYCSNDLLGDLFGVPSFS
VKEHRKIYTMIRNLVV
>d1b28a_a.43.1.1 (A:) Arc repressor {Salmonella bacteriophage P22}
MKGMSKMPQFNLRWPREVLDLVRKVAEENGMSVNSYIYQLVMESFKKEGRIGA
>d1baza_a.43.1.1 (A:) Arc repressor {Salmonella bacteriophage P22}
SKMPQVNLRWPREVLDLVRKVAEENGRSVNSEIYQRMESFKKEGRIGA
>d1bazb_a.43.1.1 (B:) Arc repressor {Salmonella bacteriophage P22}
KMPQVNLRWPREVLDLVRKVAEENGRSVNSEIYQRMESFK
>d1bdta_a.43.1.1 (A:) Arc repressor {Salmonella bacteriophage P22}
MKGMSKMPQFNLRWPREVLDLVRKVAEENGRSVNSEIYQRMESFKKEGRIG
>d1myka_a.43.1.1 (A:) Arc repressor {Salmonella bacteriophage P22}
KMLQFNLRWPREVLDLVRKVAEENGRSVNSEIYQRMESFKKEGRIG
>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}
ARDDPHFNFRMPMEVREKLFRAEANGRSMNSELLQIVQDALS KPSVPTGYRND AERLADEQSEL
V
>d2cpga_a.43.1.2 (A:) Transcriptional repressor CopG {Streptococcus agalactiae}
MKKRLTITLSESVLENLEKMAREMGLSKSAMISVALENYKKGQ
>d1irqa_a.43.1.2 (A:) Omega transcriptional repressor {Streptococcus pyogenes}
IMGDKTVRVRADLHHIIKIETAKNGGNVKEVMDQALEEYIRKYL PDKL
>d1cmba_a.43.1.2 (A:) Met repressor, MetR {Escherichia coli}
AEWSGEYISPYAEHGKQSEVKKITVSIPLKVLKILTDERTRRQVNNLRHATNSELLCEAFLHAFTGQ
PLPDDADLRKERSDEIPEAAKEIMREMGINPETWEY
>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*}

GNMGQAMSKAYATMIALEVEDKMVPVPMFNRIHTLRKPPKDEQELRQIFLDEGIDAAKFDAAYNG
>d1aqwa1 a.45.1.1 (A:77-209) Glutathione S-transferase {Human (*Homo sapiens*), class pi}
GLYKGDQQEAAALVDMVNDGVEDLRCKYISLIYTNYEAGKDDYVKALPGQLKPFETLLSQNQGGKTFI
VGDQISFADYNLLDLLLIHEVLAPGCLDAFPLLSAYVGRLSARPKLKAFLASPEYVNLPIPINGNGKQ
>d2gsra1 a.45.1.1 (A:77-207) Glutathione S-transferase {Pig (*Sus scrofa*), class pi}
YGKDQKEAALVDMVNDGVEDLRCKYATLIYTNYEAGKEKYVKELPEHLKPFETLLSQNQGGQAFVV
GSQISFADYNLLDLLRIHQVLNPSCLDAFPLLSAYVARLSARPKIKAFASPEHVNRPIPINGNGKQ
>d1glqa1 a.45.1.1 (A:79-209) Glutathione S-transferase {Mouse (*Mus musculus*), class pi}
YGKNQREAAQMDMVNDGVEDLRGKYVTLIYTNYENGKNDYVKALPGHLKPFETLLSQNQGGKAFI
VGDQISFADYNLLDLLLIHQVLAPGCLDNFPLLSAYVARLSARPKIKAFSSPEHVNRPIPINGNGKQ
>d1gtua1 a.45.1.1 (A:85-217) Glutathione S-transferase {Human (*Homo sapiens*), class mu}
LCGETEEEEKIRVDILENQTMDNHMQLGMICYNPEFEKLPKPKYLEELPEKPKLYSEFLGKRPWFAGN
KITFVDFLVYDVLDLHRIFEPKCLDAFPNLKDFISRFEGLEKISAYMKSSRFLPRPVFSKMAVWGNK
>d1hna_1 a.45.1.1 (85-217) Glutathione S-transferase {Human (*Homo sapiens*), class mu}
LCGESEKEQIREDILENQFMDSRMQLAKLCYDPDFEKLKPEYLQALPEMLKLYSQFLGKQPWFGLD
KITFVDFIAYDVLERNQVFEPSCLDAFPNLKDFISRFEGLEKISAYMKSSRFLPRPVFTKMAVFGNK
>d3gtub1 a.45.1.1 (B:85-224) Glutathione S-transferase {Human (*Homo sapiens*), class mu}
RKHNMCGETEEEEKIRVDIIENQVMDFRQTQLRLCYSSDHEKLPQYLEELPGQLKQFSMFLGKFSWF
AGEKLTFFVDFLTYDILDQNRIFDPKCLDEFPNLKAFCRFEALEKIAAYLQSDQFCKMPINNKMAQ
WGNKPVC
>d4gtua1 a.45.1.1 (A:85-217) Glutathione S-transferase {Human (*Homo sapiens*), class mu}
LCGETEEEEKIRVDILENQAMDVSNQLARVCYSPDFEKLKPEYLEELPTMMQHFSQFLGKRPWFVGD
KITFVDFLAYDVLDLHRIFEPNCLDAFPNLKDFISRFEGLEKISAYMKSSRFLPKPLYTRVAVWGNK
>d2gsta1 a.45.1.1 (A:85-217) Glutathione S-transferase {Rat (*Rattus norvegicus*), class mu}
LCGETEEERIRADIVENQVMDNRMQLIMLCYNPDFEKQKPEFLKTIPEKMKLYSEFLGKRPWFAGD
KVTYVDFLAYDILDQYHIFEPKCLDAFPNLKDFLARFEGLKKISAYMKSSRYLSTPIFSKLAQWSNK
>d1gsua1 a.45.1.1 (A:85-217) Glutathione S-transferase {Chicken (*Gallus gallus*), class mu}
MCGETEVEKQRVDVLENHMLDLRMAFARLCYSPDFEKLKPAYLEQLPGKLRQLSRFLGSRSWFVGD
KLTFVDFLAYDVLQQRMFVPDCPELQGNLSQFLQRFEALEKISAYMRSGRFMKAPIFWY TALWNN
K
>d1gsea1 a.45.1.1 (A:81-222) Glutathione S-transferase {Human (*Homo sapiens*), class alpha
(a1-1)}
LYGKDIKERALIDMYIEGIADLGEMILLPVCPPEEKDAKLALIKEKIKNRYFPFAFEKVLKSHGQDYLV
GNKLSRADIHLVELLYVEELDSSLISSFPLLKALKTRISNLPTVKKFLQPGSPRKPMPDEKSLEEARK
IFRF
>d1gula1 a.45.1.1 (A:81-220) Glutathione S-transferase {Human (*Homo sapiens*), class alpha
(a1-1)}
LFGKNLKERTLIDMYVEGTLDLLELLIMHPFLKPDDQQKEVVNMAQKAIIRYFPVFEKILRGHGQSF
LVGNQLSLADVILLQTI LALEEKIPNILSAFPFLQEYTVKLSNIPTIKRFLEPGSKKKPPPDEIYVRTVY
NIF
>d1ev4a1 a.45.1.1 (A:80-222) Glutathione S-transferase {Rat (*Rattus norvegicus*), class

alpha (a1-1)}

DLYGKDMKERALIDMYSEGILDLTEMIMQLVICPPDQKEAKTALAKDRITKNRYLPAFEKVLKSHGQD
YLVGNKLTRVDIHLLELLLYVEEFDASLLTSFPLLKAFKSRISLPLNVKKFLQPGSQRKLPM
DAKQIEE
ARKIYKF

>d1ev4c1 a.45.1.1 (C:80-208) Glutathione S-transferase {Rat (Rattus norvegicus), class alpha (a1-1)}

DLYGKDMKERALIDMYSEGILDLTEMIMQLVICPPDQKEAKTALAKDRITKNRYLPAFEKVLKSHGQD
YLVGNKLTRVDIHLLELLLYVEEFDASLLTSFPLLKAFKSRISLPLNVKKFLQPGSQRKLPM

>d1f3aa1 a.45.1.1 (A:80-221) Glutathione S-transferase {Mouse (Mus musculus), class alpha (a1-1)}

LYGKDMKERALIDMYSEGILDLTEMIGQLVLCPPDQREAKTALAKDRITKNRYLPAFEKVLKSHGQDY
LVGNRLTRVDIHLLEVLVLYVEEFDASLLTPFPLLKAFKSRISLPLNVKKFLQPGSQRKPMDAKQIQEA
RKAFKI

>d1b48a1 a.45.1.1 (A:80-222) Glutathione S-transferase {Mouse (Mus musculus), class alpha (a1-4)}

NLYGKDLKERVRIDMYADGTQDLMMIAVAPFKTPKEKEESYDLILSRAKTRYFPVFEKILKDHGEA
FLVGNQLSWADIQLLEAILMVEELSAPVLSDFPLLQAFKTRISNIPTIKKFLQPGSQRKPMDGPPYVEV
VRIVLKF

>d1ljra1 a.45.1.1 (A:80-244) Glutathione S-transferase {Human (Homo sapiens), class theta}

TPDHWYPSDLQARARVHEYLGWHADCIRGTFGIPLWVQVLGPLIGVQVPEEKVERNRTAMDQALQ
WLEDKFLGDRPFLAGQQVTLADLMALEELMQPVALGYELFEGRPRLAAWRGRVEAFLGAELCQEA
HSIILSILEQAACKTLPTPSPEAYQAMLLRIARIP

>d1pd211 a.45.1.1 (1:76-199) Glutathione S-transferase {Rat (Rattus norvegicus), class sigma}

DLAGKTELEQCQVDAVVDLDDFMSLFPWAEENQDLKERTFNDLLTRQAPHLKDLDTYLGDKIEW
FIGNYVTWADFYWDICSTLLVLPDLLGIYPRVSLRNKVQAIPASAWILKRPQTKL

>d2gsq_1 a.45.1.1 (76-202) Glutathione S-transferase {Squid (Ommastrephes sloani pacificus), class sigma}

LDGKTSLEKYRVDEITETLQDIFNDVVKIKFAPEAAKEAVQQNYEKSCKRLAPFLEGLLVSNNGGDDGF
FVGNMSTLADLHCYVALEVPLKHTPELLKDCPKIVALRKRVAECPKIAAYLKKRPVRDF

>d1eema1 a.45.1.1 (A:103-241) Glutathione S-transferase {Human (Homo sapiens), class omega}

LPDDPYEKACQKMILELFSKVPVSLVGSFIRSQNKEDYAGLKEEFRKEFTKLEEVLTNKKTTFFGGNSIS
MIDYLIWPWFERLEAMKLNEDVDHTPKLKLWMAAMKEDPTVSALLTSEKDWQGFLELYLQNSPE
ACDYGL

>d1fw1a1 a.45.1.1 (A:88-212) Glutathione S-transferase {Human (Homo sapiens), class zeta}

LLPQDPKKRASVRMISDLIAGGIQPLQNLVSLKQVGEEMQLTWAQNAITCGFNALEQILQSTAGIYCV
GDEVTMADLCLVPQVANAERFKVDLTPYPTISSINKRLLVLEAFQVSHPCRQPDPT

>d1bg5_1 a.45.1.1 (81-254) Glutathione S-transferase {Schistosoma japonicum}

MLGGCPKERAEISMLEGAVLDIRYGVSRVIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH
VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIQIDKYLKSSKYIAWPLQGWQATFFGGD
HPPKSDLVPRGSSYYQEAKSSKIMESFKNMVPPQALVNSS

>d1duga1 a.45.1.1 (A:81-220) Glutathione S-transferase {Schistosoma japonicum}

LGGCPKERAEISMLEGAVLDIRYGVSRVIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHV

THPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIQIDKYLKSSKYIAWPLQGQWQATFGGGD
HPPKSDP

>d1gne_1 a.45.1.1 (80-232) Glutathione S-transferase {Schistosoma japonicum}
MLGGCPKERAIEISMLEGAVLDIRYGVSRIAYSKDFETLKVDLFLSKLPEMLKMFEDRLCHKTYLNGDH
VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIQIDKYLKSSKYIAWPLQGQWQATFGGGD
HPPKSDLVPRGSMELDKWA

>d1fhe_1 a.45.1.1 (81-214) Glutathione S-transferase {Fasciola hepatica}
LGTTPPEERARISMIEGAAMDRLRIGFGRVCYNPKFEEVKEEYVKELPKTLKMWSDFLGRHYLTGSSV
SHVDFMLYETLDSIRYLAPHCLDEFKPKLKEFKSRIEALPKIKAYMESKRFIKWPLNGWAASFGAGDA

>d2fhea1 a.45.1.1 (A:81-216) Glutathione S-transferase {Fasciola hepatica}
IGTTSEERARVSMIEGAAVDLRQGISRISYQPKFEQLKEGYLKDLPTTMKMWSDFLGNPNYLRGTSV
SHVDFMVYEALDAIRYLEPHCLDHFPNLQQFMSRIEALPSIKAYMESNRFIKWPLNGWHAQFGGGD
APP

>d1gnwa1 a.45.1.1 (A:86-211) Glutathione S-transferase {Mouse-ear cress (Arabidopsis thaliana)}
LQTDKSNISQYAIMAIGMQVEDHQFDPVASKLAFEQIFKSIYGLTTDEAVVAEEEEAKLAKVLDVYEAR
LKEFKYLAGETFTLTLHHPAIQYLLGTPTKKLFTERPRVNEWVAEITKRPASEKVQ

>d1axda1 a.45.1.1 (A:81-210) Glutathione S-transferase {Maize (Zea mays), type I}
ELLREGNLEEAAMVDVWIEVEANQYTAALNPILFQVLISPMLGGTTDQKVVDENLEKLLKKVLEVYE
ARLTKCKYLAGDFLSLADLNHVSVTLCFLATPYASVLDAYPHVKAWWSGLMERPSVQKVAALM

>d1aw9_1 a.45.1.1 (83-217) Glutathione S-transferase {Maize (Zea mays), type III}
GTDLLPATASAAKLEVVLEVESHHFYPNASPLVFQLLVRPLLGGAPDAAVVDKHAEQALAKVLDVYE
AHLARNKYLAGDEFTLADANHASYLKTPKAGLVAARPHVKAWWEAIVARPAFQKTVAAIPLP
PPP

>d1e6ba1 a.45.1.1 (A:88-220) Glutathione S-transferase {Mouse-ear cress (Arabidopsis thaliana), class zeta}
PLLPRDLHKRAVNYQAMSIVLSGIQPHQNLAVIRYIEEKINVEEKTAWVNNAITKGFTALEKLLVNCA
GKHATGDEIYLADLFLAPQIHGAINRFQINMEPYPTLAKCYESYNELPAFQNALPEKQPDAPSST

>d1a0fa1 a.45.1.1 (A:81-201) Glutathione S-transferase {Escherichia coli}
QLLAPVNSISRYKTIEWLNYIATELHKGFTPLFRPDTPEEYKPTVRAQLEKLLQYVNEALKDEHWIC
GQRFTIADAYLFTVLRWAYAVKLNLEGLEHIAAFMQRMAERPEVQDALSAGL

>d1b8xa1 a.45.1.1 (A:81-260) Glutathione S-transferase {Escherichia coli}
LGGCPKERAIEISMLEGAVLDIRYGVSRIAYSKDFETLKVDLFLSKLPEMLKMFEDRLCHKTYLNGDHV
THPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIQIDKYLKSSKYIAWPLQGQWQATFGGGD
HPPKSDLVPRGSRRASVGSRMHYPGAFTYSPTPVTSGIGIGMSAMGS

>d1pmt_1 a.45.1.1 (81-201) Glutathione S-transferase {Proteus mirabilis}
NLIAPPKALERYHQIEWLNFLASEVHKGYSPLFSSDTPESYLPVVKNKLKSKFVYINDVLSKQKCVCG
DHFTVADAYLFTLSQWAPHVALDLTDLSHLQDYLRARIAQRPNVHSALVTEGLI

>d1f2ea1 a.45.1.1 (A:81-201) Glutathione S-transferase {Sphingomonas paucimobilis}
GLAPAEGLDRYRLLSRLSFLGSEFHKAFFVPLFAPATSDEAKAAAAESVKNHLAALDKELAGRHDHYA
GNAFSVADIYLVMLGWPAYVGDMAAYPALGAYAGKIAQRPAVGAALKAEGLA

>d1g7oa1 a.45.1.1 (A:76-215) Glutaredoxin 2 {Escherichia coli}
PLLTGKRSPAIEEWLRKVNKYANKLLLPRFAKSAFDEFSTPAARKYFVDKKEASAGNFADLLAHS DG
LIKNISDDLALDKLIVKPNVANGELSEDDIQLFPLLRNLTLVAGINWPSRVADYRDNMAKQTQINLL

SSMAI

>d1k0da1 a.45.1.1 (A:201-351) Yeast prion protein ure2p, nitrogen regulation fragment {Baker's yeast (*Saccharomyces cerevisiae*)}

LWSDDLADQSQINAWLFFQTSQGHAPMIGQALHFRYFHSQKIASAVERYTDEVRRRVYGVVEMALAER
REALVMELDTENAAAYSAGTTPMSQSRFFDYPVWLVGDKLTIADLAFVPWNNVVDRIGINIKIEFPE
VYKWKTKHMMRRPAVIKAL

>d1k0ma1 a.45.1.1 (A:92-240) Chloride intracellular channel 1 (clic1) {Human (*Homo sapiens*)}

RYPKLAALNPESNTAGLDIFAKFSAYIKNSNPALNDNLEKGLLKALKVLDNYLTSPLEGVDETS AED
EGVSQRKFLDGNELTLADCNLLPKLHIVQVCKKYRGFTIPEAFRGVHRYLSNAYAREEFAS TPCPDDE
EIELAYEQVAKAL

>d1bmta1 a.46.1.1 (A:651-740) Methionine synthase domain {*Escherichia coli*}

QAEWRSWEVNRKLEYSLVKGITFEIQDTEEARQQATRPIEVIEGPLMDGMNVVGD LFGEGKMFLP
QVVKSARVMKQAVAYLEPFIEASK

>d2tpt_1 a.46.2.1 (1-70) Thymidine phosphorylase {*Escherichia coli*}

LFLAQEIIRKKRDGHALSDEEIRFFINGIRDNTISEGQIAALAMTIFFHDMTMPERVS LTMAMRDSGT
VL

>d1brwa1 a.46.2.1 (A:1-70) Pyrimidine nucleoside phosphorylase {*Bacillus stearothermophilus*}

MRMVDLIAKKRDGKALTKEEIEWIVRGYTNQDIPDYQMSALAMAIYFRGMTEEETAAL TMAMVQS
GEMLD

>d1bf5a1 a.47.1.1 (A:136-316) STAT-1, coiled coil domain {Human (*Homo sapiens*)}

LDKQKELDSKVRNVKDKVMCIEHEIKSLEDLQDEYDFKCKTLQNRHLLKKMYLMLDNKRKEVV
HKHIELLNVTTELQNALINDELVEWKRRQQSACIGGPPNACLQQLQNWFTIVAESLQQVRQQLKKLE
ELEQKYTYEHDPIKKNKQVLWDRTFSLFQQLIQSS

>d1bg1a1 a.47.1.1 (A:136-321) STAT3b {Mouse (*Mus musculus*)}

VVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDDFDFNYKTLKSQGDMQDLN GNNQSVTRQ
KMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQIACIGGPPNIC LDRLE
NWITSLAESQLQTRQQIKKLEELQKQVSYKGDPIVQHRPMLERIVELFRNLMKSAF

>d1dn1b_ a.47.2.1 (B:) Syntaxin 1A N-terminal domain {Rat (*Rattus norvegicus*)}

DRFMDEFFEQVEEIRGFIDKIAENVEEVKRKHSAILASPNPDEKTKEELEELMSDIKKTANKVRSK
KSIEQSIEQEEGLNRSSADLRIRKTQHSTLSRKFVEVMSEYNATQSDYRERCKGRIQRQLEITGR TTT S
EELEDMLESGNPAIFASGIIMDSSISKQALSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMID
RIEYNVEHAVDYVERAV

>d1ez3a_ a.47.2.1 (A:) Syntaxin 1A N-terminal domain {Rat (*Rattus norvegicus*)}

RDRFMDEFFEQVEEIRGFIDKIAENVEEVKRKHSAILASPNPDEKTKEELEELMSDIKKTANKVRSK
LKSIEQSIEQEEGLNRSSADLRIRKTQHSTLSRKFVEVMSEYNATQSDYRERCKGRI

>d1fioa_ a.47.2.1 (A:) Sso1 {Baker's yeast (*Saccharomyces cerevisiae*)}

MHDFVGF MNKISQINRDLDKYDHTINQVDSLHKRLLTEVNEEQASHLRHSLDNFVAQATDLQFKLK
NEIKSAQRDGIHDTNKQAQAENSRQRFLKLIQDYRIVDSNYKEENKEQAKRQYMIIQPEATEDEVEA
AISDVGGQQIFSQALLNANRRGEAKTALAEVQARHQELLKLEKSMAELTQLFNDMEELVIEQQ

>d1hs7a_ a.47.2.1 (A:) Vam3p N-terminal domain {Baker's yeast (*Saccharomyces cerevisiae*)}

TNQKTKELSNLIETFAEQSRVLEKECTKIGSKRDSKELRYKIETELIPNCTSVRDKIESNILIHQNGKLS

ADFKNLKTKYQSLQSQSYNQKSLFPLK

>d2cbla2 a.48.1.1 (A:47-177) N-terminal domain of cbl (N-cbl) {Human (Homo sapiens)}
PPGTVDKKMVEKWCWKLMDKVVRLCQNPKLALKNSPPYILDLLPDTYQHLRRTILSRYEGKMETLGEN
EYFRVFMENLMKKTKQTISLFKEGKERMYEENSQPRRNLTKLSLIFSHMLAELKGIFPSGLFQGD

>d1de4c1 a.48.2.1 (C:609-756) Transferrin receptor ectodomain, C-terminal domain
{Human (Homo sapiens)}

LDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFGNAEKTDRFVMKKL
NDRVMRVEYHFLSPYVSPKESPFRRHVFWGSGSHTLPALLENLKLKQNNGAFNETLFRNQLALAT
WTIQGAANALSGDVWDI

>d1eo0a_ a.48.3.1 (A:) Transcription elongation factor TFIIS N-domain {Baker's yeast
{Saccharomyces cerevisiae}}

MDSKEVLVHVKNLEKNKSNDAAVLEILHVLDKFVPTTEKLLRETKVGVEVNKFKKSTNVEISKLVKK
MISSWKDAIN

>d1f6va_ a.49.1.1 (A:) C-terminal domain of B transposition protein {Bacteriophage mu}
GSRIAKRTAINKTKKADVKAIAADAWQINGEKELELLQQAQKPGALRILNHSLRLAAMTAHGKGERV
NEDYLRQAFRELDLVDISTLLRN

>d1i6ve_ a.143.1.1 (E:) RNA polymerase omega subunit {Thermus aquaticus}
MAEPGIDKLFMVDISKYRLTVVAKRAQQLLRHRFKNTVLEPEERPKMRTLEGLYDDPNAVTWAM
KELLTGRLFFGENLVPEDRLQKEMERLYPTEEE

>d1cfaa_ a.50.1.1 (A:) C5a anaphylotoxin {Human (Homo sapiens)}
MLQKKIEEIAAKYKHSVKKCCYDGASVNNDETCEQRAARISLGPRCIKAFTECCVVASQLRANISHK
DMC

>d1c5a_ a.50.1.1 (-) C5a anaphylotoxin {Pig (Sus scrofa domestica)}
MLQKKIEEIAAKYKYAMLKKCCYDGAYRNDETCEERAARIKIGPKCVKAFKDCCYIANQVRAEQS

>d0c3a_ a.50.1.1 (-) C3a anaphylotoxin {Human (Homo sapiens)}
SVQLTEKRMNKVKGYPKELRKCCEDGMRQNPMRFSCQRRTFISLGEACKKVFLDCCNYITELRRQ
HARASHLGLAR

>d1ocrh_ a.51.1.1 (H:) Cytochrome c oxidase subunit h {Cow (Bos taurus)}
KIKNYQTAPFDSRFPNQNRNCWQNYLDFHRCEKAMTAKGGDVSCEWYRRVYKSLCPISWVST
WDDRRAEGTFPGKI

>d1hyp_ a.52.1.1 (-) Soybean hydrophobic protein {Soybean (Glycine max)}
PSCPDLISICLNILGGSLGTVDCCALIGGLGDIEAIVCLCIQLRALGILNLRNLQLILNSCGRSYPSNAT
CPRT

>d1bwoa_ a.52.1.1 (A:) Plant non-specific lipid-transfer protein (ns-LTP) {Wheat (Triticum
aestivum), L. seeds}
IDCGHVDSLVRPCLSYVQGGPGPSGQCCDGVKNLHNQARSQSDRQSACNCLKGIARGIHNLNEDNAR
SIPPKCGVNLPTYTISLNIDCSR

>d1be2_ a.52.1.1 (-) Plant non-specific lipid-transfer protein (ns-LTP) {Barley (Hordeum
vulgare)}
LNCQVQVDSKMKPCLTYVQGGPGPSGECNGVRDLHNQAQSSGDRQTVCNCLKGIARGIHNLNNA
ASIPSKCNVNPYITISPDIDCSR

>d1fk5a_ a.52.1.1 (A:) Plant non-specific lipid-transfer protein (ns-LTP) {Maize (Zea mays)}
AISCGVASAIAPCISYARGQSGPSAGCCSGVRSLNNAARTTADRRAACNCLKNAAAGVSGLNAGNA
ASIPSKCGVSIPYITISTSTDCSRVN

>d1rzl_ a.52.1.1 (-) Plant non-specific lipid-transfer protein (ns-LTP) {Rice (*Oryza sativa*)}
ITCGQVNSAVGPCLTYARGGAGPSAACCSGVRSLKAAASTTADRRRTACNCLKNAARGIKGLNAGNAAS
IPSKCGVSVPYTISASIDCSRVS

>d1hssa_ a.52.1.2 (A:) 0.19 alpha-amylase inhibitor {Wheat (*Triticum aestivum*)}
MCYPGQAFQVPALPACRPLLRLQCNGSQVPEAVLRDCCQQLAHISEWCRCGALYSMLDSMYKEHGA
QEQQAGTGAFPRCRREVVKLTAASITAVCRLPIVVVDASGDGAYVCKDVAAYPDA

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

>d1bea_ a.52.1.2 (-) Hageman factor/amylase inhibitor {Maize (*Zea mays*)}
SCVPGWAIPHNPLPSCRWYVTSRTCGIGPRLPWPELKRRCCRELADIPAYCRCTALSILMDGAIPPGP
DAQLEGRLEDLPGPCPREVQRGFAATLVTEAECNLATISGVAECPWILG

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

>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*)}
MVDVPGFAEAWKAQFPDSEPPRMELRSVGDIEQELERAKASIRRLQEVDNQRFRMIYLQTLLAKE
K

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

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

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

>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*}
MNKTELINAVAETSGLSKKDATKAVDAVFDSITEALRKGDKVQLIGFGNFVREARAARKGRNPQTGE
EMEIPASKVPAFKPGKALKDAVK

>d1b8za_ a.55.1.1 (A:) HU protein {*Thermotoga maritima*}

MNKKELIDRVAKKAGAKKKDVKLILDITILETITEALAKGEKVQIVGFGSFEVRKAAARKGVNPQTRK
PITIPERKVPKFKPGKALKEKVK

>d1exea_a.55.1.1 (A:) Transcription factor 1, TF1 {Bacteriophage SPO1 (Bacillus subtilis)}
MNKTELIKAIAQDTGLTQVSVSKMLASFEEKIITETVAKGDKVQLTGFLNIKPVARQARKGFNPQTQEA
LEIAPSVGVSVKPGESLKKAAEGLKYEDFAK

>d1dp3a_a.55.1.2 (A:) DNA-binding domain (fragment?) of the TraM protein {Escherichia coli}
AKVQAYVSDIVYKINKIVERRRAEGAKSTDVVSFSSISTMLELGLRVYEAQMER

>d1h1ra1_a.56.1.1 (A:81-193) Aldehyde oxidoreductase, domain 2 {Desulfovibrio gigas}
QPENLHPLQKAWVLHGGAQCGFCSPGFIVSAKGLLDTNADPSREDVDRDWFQKHRNACRCTGYKPL
VDAVMDAAAVINGKKPETDLEFKMPADGRIWGSKYPRPTAVAKVTGTL

>d1dgja1_a.56.1.1 (A:81-193) Aldehyde oxidoreductase, domain 2 {Desulfovibrio desulfuricans}
APDCLHPLQHAWIQHGAAQCGFCTPGFIVSAKALLDENVAPSREDVDRDWFQKHHNICRCTGYKPLV
DAVMDAAAAILRGEKTVEEISFKMPADGRIWGSIPRPSAVAKVTGLA

>d1fo4a1_a.56.1.1 (A:93-165) Xanthine oxidase, domain 2 {Cow (Bos taurus)}
STKTRLHPVQERIAKSHGSQCGFCTPGIVMSMYTLLRNQPEPTVEEIEDAFQGNLCRCTGYRPILQGF
RTFAK

>d1jroa1_a.56.1.1 (A:85-166) Xanthine dehydrogenase chain A, domain 2 {Rhodobacter capsulatus}
DGRLLHPVQQAMIDHHGSQCGFCTPGFIVSMAAAHDRDRKDYDDL LAGNLCRCTGYAPILRAAEAAA
GEPPADWLQADAAFTL

>d1qj2a1_a.56.1.1 (A:82-161) Carbon monoxide (CO) dehydrogenase iron-sulfur protein, C-domain {Pseudomonas carboxydovorans}
APDGTLSALQEGFRMMHGLQCGYCTPGMIMRSHRLLQENPSPTEAEIRFGIGGNLCRCTGYQNIKVA
IQYAAAKINGVPPF

>d1ffva1_a.56.1.1 (A:82-157) Carbon monoxide (CO) dehydrogenase iron-sulfur protein, C-domain {Hydrogenophaga pseudoflava}
NKGVLHAVQEGFYKEHGLQCGFCTPGMLMRAYRFLQENPNPTEAEIRMGMTGNLCRCTGYQNIK
AVQYAARKLQE

>d1dj8a_a.57.1.1 (A:) Protein HNS-dependent expression A; HdeA {Escherichia coli}
NKKPVNSWTCEDFLAVDESFPQPTAVGF AEALNNKDKPEDAVLDVQGIATVTPAIVQACTQDKQANF
KDKVKG EWDKIKK

>d1g9la_a.144.1.1 (A:) poly(A) binding protein {Human (Homo sapiens)}
GPLGSAAAATPAVRTVPQYKYAAGVRNPQQHLNAQPQVTMQQPAVHVQGQEPLTASMLASAPPQE
QKQMLGERLFP LIQAMHPTLAGKITGMLLEIDNSEL LHMLESPE SLRSKVDEAVAVLQAHQAKEAAQ
KAVNSATGVPTV

>d1i2ta_a.144.1.1 (A:) hyperplastic discs protein {Human (Homo sapiens)}
HRQALGERLYPRVQAMQPAFASKITGMLLELSPAQLLLLLASEDSL RARVDEAMELIIAHG

>d1af7_1_a.58.1.1 (11-91) Chemotaxis receptor methyltransferase CheR, N-terminal domain {Salmonella typhimurium}
SVLLQMTQRLALS DAHFRRICQLIYQRAGIVLADHKRDMVYNRLVRRRLRALGLDDFGRYLSMLEAN
QNSAEWQAFINALTT

>d1e91a_a.59.1.1 (A:) Sin3B {Mouse (Mus musculus)}

ESDSVEFNNAISYVVKIKTRFLDHPEIYRSFLEILHTYQKEQLHTKGRPFGRMSEEEVFTEVANLFRG
QEDLLSEFGQFLPEAKR
>d1g1eb_a.59.1.1 (B:) Sin3A {Mouse (Mus musculus)}
SLQNNQPVEFNHAINYVVKIKNRFGQPDYKAFLEILHTYQKEQRNAKEAGGNYTPALTEQEVYQA
VARLFKNQEDLLSEFGQFLPDA
>d1bqv_a.60.1.1 (-) Ets-1 transcription factor pointed domain {Mouse (Mus musculus)}
MECADVPLLTSSKEMMSQALKATFSGFTKEQQRLGIPKDPRQWTETHVRDWVMWAVNEFSLKG
VDFQKFCMSGAALCALGKECFLELAPDFVGDILWEHLEILQKEDVK
>d1b0xa_a.60.1.2 (A:) EphA4 receptor tyrosine kinases {Mouse (Mus musculus)}
FSAVSVGDWLQAIKMDRYKDNFTAAGYTTLEAVVHMSQDDLARIGITAITHQNKILSSVQAMRTQ
MQQMHG
>d1b4fa_a.60.1.2 (A:) EphB2 receptor {Human (Homo sapiens)}
PDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVVSQMMEDILRVGVTLAGHQKKILNSIQVMR
AQMNIQS
>d1sgg_a.60.1.2 (-) EphB2 receptor {Chicken (Gallus gallus)}
YTSFNTVDEWLDAIKMSQYKESFASAGFTTFDIVSQMTVEDILRVGVTLAGHQKKILNSIQVMRAQM
>d1coka_a.60.1.2 (A:) C-terminal domain of p73 {Human (Homo sapiens)}
YHADPSLVSFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMTIWRGLQDLKQGHY
>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}
NKQERTLFKELIKTNGVGPKLALAILSGMSAQQFVNAVEREEVGALVKLPGIGKKAERLIVEMKDRF
KGLHGDLFTP
>d1bvsa2 a.60.2.1 (A:64-134) DNA helicase RuvA subunit, middle domain {Mycobacterium
leprae}
DAENRDLFLALLSVSGVGPRLAMATLAVHDAAALRQALADSDVASLTRVPGIGRRGAERIVLELADK
VGPV
>d1dgsa1 a.60.2.2 (A:401-581) NAD+-dependent DNA ligase, domain 3 {Thermus filiformis}
RWPEACPECGRHLVKEGKVHRCNPPLCPAKRFEAIRHYASRKAMDIEGLGEKLIERLLEKGLVRDVA
DLYHLRKEDLLGLERMGEKSAQNLLRQIEESKHRGLERLLYALGLPGVGEVLARNLARRFGTMDRL
EASLEELIEVEEVGELTARAIETLKDPAFRDLVRRLEAGVSMESK
>d1coo_a.60.3.1 (-) C-terminal domain of RNA polymerase alpha subunit {Escherichia coli}
FDPIILLRPVDDLELTVRSANCLKAEAIHYIGDLVQRTEVELLKTPLGKKSLEIKDVLASRGLSLGMR
LENWPPASIADE
>d1doqa_a.60.3.1 (A:) C-terminal domain of RNA polymerase alpha subunit {Thermus
thermophilus}
EQEEELDLPEELGLSTRVLHSLKEEGIESVRALLALNLKDLKNIPGIGERSLEEIKEALEKKGFTLKE
>d1b22a_a.60.4.1 (A:) DNA repair protein Rad51, N-terminal domain {Human (Homo
sapiens)}
EEESFGPQPISRLEQCCGINANDVKKLEEAGFHTVEAVAYAPKKELINIKGISEAKADKILAEAAKLVP
M
G
>d1ci4a_a.60.5.1 (A:) Barrier-to-autointegration factor, BAF {Human (Homo sapiens)}
MTTSQKHRDFVAEPMGEKPVGSLAGIGEVLGKKLEERGFDKAYVVLGQFLVLKKDEDLFREWLKDT
CGANAKQSRDCFGCLREWCDL

>d1bpya1 a.60.6.1 (A:10-91) DNA polymerase beta, N-terminal (8 kD)-domain {Human (Homo sapiens)}
TLNGGITDMLTELANFEKNVSQAIHKYNAYRKAASVIAKYPHKIKSGAEAKKLPVGVGTAKIAEKIDIEFL
ATGKLRKLEKIRQD

>d1dk2a_ a.60.6.1 (A:) DNA polymerase beta, N-terminal (8 kD)-domain {Rat (Rattus norvegicus)}
SKRKAPQETLNGGITDMLVELANFEKNVSQAIHKYNAYRKAASVIAKYPHKIKSGAEAKKLPVGVGT
IAEKIDIEFLATGKLRKLEK

>d1jmsa1 a.60.6.1 (A:148-242) Terminal deoxynucleotidyl transferase {Mouse (Mus musculus)}
KKISQYACQRRTTLNNYNQLFTDALDILAENDELRENEGSCLAFMRASSVLKSLPFPITSMKDTEGIP
CLGDKVKSHIEGIIHEDGESSEAKAVLN

>d1tfr_1 a.60.7.1 (183-305) T4 RNase H {Bacteriophage T4}
GSAEIDCMTKILKGDKKDNVASVKVRSDFWFRVEGERTPSMKTSSIVEAIANDREQAKVLLTESEYN
RYKENLVLIDFDYIPDNIA SNIVNYNSYKLP PRGKIYSYFVKAGLSKLTNSINEF

>d1bgxt1 a.60.7.1 (T:174-289) 5' to 3' exonuclease domain of DNA polymerase Taq {Thermus aquaticus}
LRPDQWADYRALTGDESDNLPGVKGIGECTARKLLEEWGSLEALLKNLDRLKPAIREKILAHMDDL
KLSWDLAKVRTDLPLEVDFAKRREPDRERLRAFLERLEFGSLLHEFGLE

>d1xo1a1 a.60.7.1 (A:186-290) T5 5'-exonuclease {Bacteriophage T5}
VDDVEQFISLKAIMGDLGDNIRGVEGIGAKRGYNIREFGNVLDIIDQLPLPGKQKYIQLNASEELLF
RNLILVDLPTYCVDAIAAVGQDVLDFKFTKDILEIAE

>d1a77_1 a.60.7.1 (209-316) Flap endonuclease-1 {Archaeon Methanococcus jannaschii}
ISLDDLIDIAIFMGTDYNPGGVKIGIGFKRAYELVRSGVAKDVLKKEVEYYDEIKRIFKEPKVTDNYLS
LKLDPKEGIIKFLVDENDFNDRVKKHVDKLYNLIANKT

>d1b43a1 a.60.7.1 (A:220-339) Fen-1 nuclease {Archaeon Pyrococcus furiosus}
LTREKLIELAILVGTDYNPGGIGIGLKKALEIVRHSKDPLAKFQKQSDVDLYAIKEFFLNPPVTDNYN
LVWRDPDEEGILKFLCDEHDFSEERVKNGLERLKKAIKSGKQSTLESWFKR

>d1d8ba_ a.60.8.1 (A:) HRDC domain from RecQ helicase {Baker's yeast (Saccharomyces cerevisiae)}
ELNNLRMTYERLRELSNLGNRMVPPVGNFMPDSILKKMAAILPMNDSAFATLGTVEDKYRRRFK
YFKATIADLSKKRSSE

>d1go3f_ a.60.8.2 (F:) RNA polymerase II subunit RBP7 (RpoF) {Archaeon Methanococcus jannaschii}
MIGKKILGERYVTVSEAAEIMYNRAQIGELSYEQGCALDYLQKFAKLDKEEAKKLV EELISLGIDEKTA
VKIADILPEDLDDLRAIYYKREL PENAE EILEIVRKYI

>d1f44a1 a.60.9.1 (A:20-129) Cre recombinase {Bacteriophage P1}
SDEVKRNLMDFRDRQAFSEHTWKMLLSVCRSWAAWCKLNNR KWFP AEPEDVRDYLLYLQARGL
AVKTIQHLGQLNMLHRRSGLPRPSDSNAVSLVMRRIRKENVDAGE

>d1a0p_1 a.60.9.1 (3-100) Recombinase XerD {Escherichia coli}
QDLARIEQFLDALWLEKNLAENTLNAYRRDL SMMVEWLHHRGLTLATAQDDLQALLAERLEGGY
KATSSARLLSAVRRLFQYLYREKFR EDDPSAHL

>d1floa1 a.60.9.1 (A:2-129) Flp recombinase {Baker's yeast (Saccharomyces cerevisiae)}
PQFDILCKTPPKVLVRQFVERFERPSGEKIALCAAELTYLCWMITHNGTAIKRATFMSYNTIISNSLSF

DIVNKSLOFKYKTQKATILEASLKKLIPAWEFTHIIPYYGQKHQSDITDIVSSLQLQFES
>d1zyna1 a.60.10.1 (A:22-144) Enzyme I of the PEP:sugar phosphotransferase system
HPr-binding (sub)domain {Escherichia coli}
DEIVIDRKKISADQVDQEVERFLSGRAKASAQLETIKTKAGETFGEEKEAIFEGHIMLLEDEELEQEII
ALIKDKHMTADAAAHEVIEGQASALEELDDEYLKERAADVDRDIGKRLLRNIGL
>d1jyga_ a.60.11.1 (A:) Hypothetical protein Yjbj {Escherichia coli}
MNKDEAGGNWKQFKGKVKEQWGWKLTDDDMTHIEGKRDQLVGKIQERYGYQKDQAEKEVVDWETR
NEYRW
>d1hiwa_ a.61.1.1 (A:) HIV-1 matrix protein (HIV-1 MA, HIVp17, p17, MA) {Human
immunodeficiency virus type 1}
VLSGGELDKWEKIRLRPGGKKQYKLBHIVWASRELERFAVNPGLLETSEGCRQILGQLQPSLQTGSE
ELRSYNTIAVLYCVHQRIDVKDTKEALDKIEEEQNKSKKKAQQAAD
>d1hiws_ a.61.1.1 (S:) HIV-1 matrix protein (HIV-1 MA, HIVp17, p17, MA) {Human
immunodeficiency virus type 1}
VLSGGELDKWEKIRLRPGGKKQYKLBHIVWASRELERFAVNPGLLETSEGCRQILGQLQPSLQTGSE
ELRSYNTIAVLYCVHQRIDVKDTKEALDKIEEEQN
>d1tam_ a.61.1.1 (-) HIV-1 matrix protein (HIV-1 MA, HIVp17, p17, MA) {Human
immunodeficiency virus type 1}
MGARASVLSGGELDRWEKIRLRPGGKKKYKLBHIVWASRELERFAVNPGLLETSEGCRQILGQLQPS
LQTGSEELRSYNTVATLYCVHQRIEIKDTKEALDKIEEEQNKSKKKAQQAAD
>d2hmx_ a.61.1.1 (-) HIV-1 matrix protein (HIV-1 MA, HIVp17, p17, MA) {Human
immunodeficiency virus type 1}
HMGARASVLSGGELDKWEKIRLRPGGKKQYKLBHIVWASRELERFAVNPGLLETSEGCRQILGQLQPS
SLQTGSEELRSYNTIAVLYCVHQRIDVKDTKEALDKIEEEQNKSKKKAQQAADTGNNSQVSQNY
>d1ed1a_ a.61.1.1 (A:) SIV matrix antigen {Simian immunodeficiency virus}
SVLSGKKADELEKIRLRPGGKKKYMLKHVVWAANELDRFGLAESLLENKEGCQKILSVLAPLVPTGS
ENLKSlyNTVcviwcihaeekvkhteeakqivqrhlvvetgtaetmp
>d1jvr_ a.61.1.2 (-) HTLV-II matrix protein {Human T-cell leukemia virus type 2}
HMQIHLGLSPTPIPKAPRGLSTHHWLNFLQAAYRLQPGPSDFDFQQLRRFLKLALKTPIWLNPIDYS
LLASLIPKGYPRVVEIINILVKNQVSPSAPAAPVPTPICPTTTPPPPPPSPEAHVPPPYVEPTTTQCF
>d1bax_ a.61.1.3 (-) Mason-pfizer monkey virus matrix protein {Simian mason-pfizer virus}
MGQELSQHERRYVEQLKQALKTRGVKVKYADLLKFFDFVKDTCPWFPQEGTIDIKRWRVRGDCFDQD
YYNTFGPEKVPVTAFSYWNLIKELIDKKE
>d1a6s_ a.61.1.4 (-) GAG polyprotein M-domain {Rous sarcoma virus}
GEAVIKVISSACKTYCGKTSKKEIGAMLSLLQEGLLMSPSDLYSPGSWDPITAALSQRAMILGKSG
ELKTWGLVLGALKAAREE
>d1heka_ a.61.1.5 (A:) EIAV matrix antigen {Equine infectious anemia virus, EIAV}
AMADIGSMGDPLTWSKALKKLEKVTVQGSQKLTGNCNWALSVDLFDHTNFVKEKDWQLRDVIP
LLEDVTQTLSGQERAFERTWWAISAVKMGLQINNVDGKASFQLLRKYE
>d1qgta_ a.62.1.1 (A:) Hepatitis B viral capsid (hbcag) {Hepatitis B virus}
MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSPEHCSPHHTALRQAILCWGELMTL
ATWVGNLEDPASRDLVVNYVNTNMGLKIRQLLWFHISCLTFGRETVLEYLVSFGVWIRTPPAYRPP
NAPILST
>d1aep_ a.63.1.1 (-) Apolipoprotein III {African locust (Locusta migratoria)}

NIAEAVQQLNHTIVNAAHELHETLGLPTPDEALNLLTEQANAFKTKIAEVTTSLKQEAKEKHQGSVAE
QLNAFARNLNNSIHDAATSLNLQDQLNSLQSALTNVGHQWQDIATKTQASAQEAWAPVQSALQEAA
EKTKEAANLQNSIQSAVQK

>d1eq1a_ a.63.1.1 (A:) Apolipoporphin-III {Manduca sexta}

DAPAGGNAFEEMEKHAKFEQKTFSEQFNSLVNSKNTQDFNKALKDGSQSVLQQLSAFSSSLQGAISD
ANGKAKEALEQARQNVKTAELRKAHPDVEKEANAFKDKLQAAVQTTVQESQKLAKEVASNMEE
TNKKLAPKIKQAYDDFVKHAEVQKKLHEAATKQ

>d1nkl_ a.64.1.1 (-) NK-lysin {Pig (Sus scrofa)}

GYFCESCRKIIQKLEDMVGPQPNEDTVTQAASQVCDKILRGLCKKIMRSFLRRISWDILTGGKPPQA
ICVDIKICKE

>d1qdma1 a.64.1.2 (A:1S-104S) (Pro)phytepsin {Barley (Hordeum vulgare)}

VVSQECKTIVSQYQQILDLLAETQPKKICSQVGLCTFDGTRGVSAGIRSVVDDPEVKSNGLRADPM
CSACEMAVVWMQNQLAQNKTDLILDYVNLNRLP

>d1e68a_ a.64.2.1 (A:) Bacteriocin AS-48 {Enterococcus faecalis}

MAKEFGIPAAVAGTVLNVVEAGGWVTTIVSILTAVGSGGLSLLAAAGRESIKAYLKKEIKKKGKRAVIA
W

>d1ain_ a.65.1.1 (-) Annexin I {Human (Homo sapiens)}

GSAVSPYPTFNPSSDVAALHKAIMVKGVDIATIDILTKRNNAQRQKAAAYLQETGKPLDETLKKAL
TGHLEEVVLLALLKTPAQFDADELRAAMKGLGTDEDTLIEILASRTNKEIRDINRVYREELKRDIAKDI
TSDTSGDFRNALLSLAKGDRSEDFGVNEDLADSDARALYEAGERRKGTDVNVFNTILTTRSYPQLRR
VFQKYTKYSKHD MNKVLDELEKGDIEKCLTAIVKCATSKPAFFAEKHLHQAMKGVGTRHKALIRIMVS
RSEIDMNDIKAFYQKMYGISLCQAILDETKGDYKILVALCGGN

>d1bo9a_ a.65.1.1 (A:) Annexin I {Human (Homo sapiens)}

TFNPSSDVAALHKAIMVKGVDIATIDILTKRNNAQRQKAAAYLQETGKPLDETLKKALTGHLEEVV
LALLK

>d1hm6a_ a.65.1.1 (A:) Annexin I {Pig (Sus scrofa)}

AMVSEFLKQAWFIDNEEQEYIKTVKSGKGGPGSAVSPYPTFNPSSDVEALHKAITVKGVDIATIEILT
KRTNAQRQKAAAYLQEKGPLDEALKKALTGHLEEVVLLALLKTPAQFDADELRAAMKGLGTDEDT
LNEILASRTNREIREINRVYKEELKRDIAKDI TSDTSGDYQKALLSLAKGDRSEDLAINDDLADTDAR
ALYEAGERRKGTDLNVFITILTTRSYPHLRRVVFQKYSKYSKHD MNKVLDELEKGDIEKCLTAIVKCAT
SKPMPFAEKHLHQAMKGVGTRHKTLIRIMVSRSEIDMNDIKACYQKLYGISLCQAILDETKGDYKILVA
LCG

>d1axn_ a.65.1.1 (-) Annexin III {Human (Homo sapiens)}

SASIVVGHRTVRDYPDFSPVDAEAIQKAIRGIGTDEKMLISILTERSNAQRQLIVKEYQAAAYGKELK
DDLKGDLSGHFEHLMVALVTPPAVFDKQLKKSMMKAGTNEALIEILTTRTSRQMKDISQAYTVY
KKSLGDDISSETSGDFRKALLTLADGRRDESLKVDEHLAKQDAQILYKAGENRWGTDEDKFTEILCL
RSFPQLKLTDFEYRNISQKDIVDSIKGELSGHFEDLLAIVNCVRNTPAFLAERLHRALKGIGTDEFTL
NRIMVSRSEIDLLDIRTEFKKHGYSLYSAIKSDTSGDYEITLLKICGGDD

>d1i4aa_ a.65.1.1 (A:) Annexin IV {Cow (Bos taurus)}

ASGFNAEDAQTLRKAMKGLGTDEDAIINVLAYRSTAQRQEIRTAYKTTIGRDLMDLLKSELGNFE
QVILGMMPTPTVLYDVQELRKAMKAGTDEGLIEILASRTPEEIRINQTYQLQYGRSLEDDIRSDTS
FMFQRVLSLSAGGRDESNYLDDALMRQDAQDLYEAGEKKWGTDEVKFLTVLCSRNRNHLHVFD
EYKRIAQKDIEQSIKSETSGSFEDALLAIVKCMRNKSAYFAERLYKSMKGLGTDDDTLIRVMVSRAEID
MLDIRANFKRLYGKSLYSFIKGDTSYDVRKVLILLICGGDD

>d1ala_ a.65.1.1 (-) Annexin V {Chicken (Gallus gallus)}

KYTRGTVTAFSPFDARADAEALRKAMKMGMTDEETILKILTSRNNNAQRQEIASAFKTLFGRDLVDDL
KSELTGKFETLMVSLMRPARIFDAHALKHAIKGAGTNEKVLTEILASRTPAEVQNIKQVVMQYEYAN
LEDKITGETSGHFQRLLVLLQANRDPDGRVEEALVEKDAQVLFQAGELKWGTDEETFITLGRSVS
HLRRVFDKYMTISGFQIEETIDRETSGDLEKLLAVVKCIRSVPAYFAETLYYSMKGAGTDDDTLIRVM
VSRSEIDLLDIRHEFRKNFAKSQMIQKDTSGDYRKALLLLCGG

>d1hvd_ a.65.1.1 (-) Annexin V {Human (Homo sapiens)}

VLRGTVTDFPGFDGRADAETLRKAMKGLGTDEESILTLLTSRNSNAQRQEISAAFKTLFGRDLLDDLKS
ELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQVYEEEEYGSLEDD
VVGDTSGYYQRMLVLLQANRDPDAGIDEAQVEQDAQALFQAGELKWGTDEEKFITIFGTRSVSHLR
KVFVKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSR
SEIDLNFIRKEFRKNFATSLYSMIKGDTSBGDYKALLLLC

>d1g5na_ a.65.1.1 (A:) Annexin V {Rat (Rattus norvegicus)}

ALRGTVTDFSGFDGRADAEVLRKAMKGLGTDEDSILNLLTARSNAQRQQIAEEFKTLFGRDLVNDM
KSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTDEKVLTEIIASRTPEELRAIKQAYEEEEYGSNLE
DDVVGDTSGYYQRMLVLLQANRDPDAIDDAQVELDAQALFQAGELKWGTDEEKFITILGTRSVSH
LRRVFDKYMTISGFQIEETIDRETSGNLENLLLAVVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVIVS
RSEIDLNFIRKEFRKNFATSLYSMIKGDTSBGDYKALLLLCGGEDD

>d1avc_1 a.65.1.1 (10-350) Annexin VI {Cow (Bos taurus)}

YRGSIRDFPDFNPSQDAETLYNAMKGFSGDKEAIINLITSRSNKQRQEICQNYKSLYGKDLIADLKYEL
TGKFERLIVGLMRPPAYADAKEIKDAISGIGTDEKCLIEILASRTNEQIHLVAAYKDAYERDLEADITG
DTSGHFRKMLVLLQGTREEDDVVSEDLVQQDVQDLYEAGELKWGTDEAQFIYILGNRSKQHLRLVF
DEYLKTTGKPIEASIRGELSGDFEKLMLAVVKIRSTAEYFAERLFAKAMKGLGTRDNTLIRIMVSRSEL
DMLDIREIFRTKYEKSLSYMIKNDTSGEYKTKLLKCGDDDAAGQFFPEAAQVAYQMWELSAVAR

>d1avc_2 a.65.1.1 (351-671) Annexin VI {Cow (Bos taurus)}

VELKGTVRPAGDFNPDADAKALRKAMKGLGTDEDTIIDITHRSNAQRQQIRQTFKSHFGRDLMADL
KSELSGDLARLILGLMPPAHDYDAKQLKKAMEGAGTDEKALIEILATRTNAEIQAINKAYKEDYHKT
LEDALSSDTSGHFKRILISLATGNREEGGERERAREDAQVAEILEIADTTSGDKSSLETRFMMILCT
RSYPDLRRVFQEFVKMTNYDVEHTIKKEMSGDVRDVFVAIVQSVKNKPLFFADKLYKSMKGAGTEE
KTLTRIMVSRSEIDLLNIRREFIEKYDKSLHQAIEGDTSGHFLKALLAICGG

>d1dm5a_ a.65.1.1 (A:) Annexin XII {Hydra vulgaris}

VVQGTVPKPHASFNREDATLRKAMKGIKGTDEKSITHILATRSNAQRQQIKTDYTTLFGKHLEDELK
SELSGNYEAAALALLRPDEFQAEQLHAAMKGLGTDKNALIDILCTQSNAQIHAIKAAFKLLYKEDLE
KEISETSGNFQRLLVSMQLGGRKEDEPVNAHAHAEDAAAIYQAGEGQIGTDESFRNAVLAATRSYPQL
HQIFHEYSKISNKITLQAIENEFSGDIKNGLLAIVKSVENRFAYFAERLHAMKGLGTSKTLIRILVSR
SEIDLANIKETFQAMYGKSLYEFIAADDCSGDYKDLLLQITGH

>d1dk5a_ a.65.1.1 (A:) Annexin 24(ca32) {Bell pepper (Capsicum annuum)}

HHHHMASLTVPAHVPSAAEDCEQLRSFAFKGWTNEKLIISILAHRTAAQRKLRQTYAETFGEDELLK
ELDRELTHDFEKLVLVWTLDPSEDAHLAKEATKRWTKSNFVVELACTRSPKELVLAREAYHARY
KKSLEEDVAYHTTGDHRKLLVPLVSSYRYGEEVDLRLAKAESKILHEKISDKAYSDDDEVIRILATRSK
AQLNATLNHYKDEHGEDILKQLEDGDEFVALLRATIKGLVYPEHYFVEVLRDAINRRGTEEDHLTRVI
ATRAEVDLKIIDEYQKRDSIPLGRAIAKDTRGDYESMLLALLGQE

>d1azsc1 a.66.1.1 (C:86-201) Transducin (alpha subunit), insertion domain {Cow (Bos taurus)}

GEKATKVQDIKNNLKEAIIETIVAAMSNLVPPVELANPENQFRVDYILSVMNVPDFDFPPEFYEHAKA
 LWEDEGVRACYERSNEYQLIDCAQYFLDKIDVIKQDDYVPSDQDLLRCR
 >d1tada1 a.66.1.1 (A:57-177) Transducin (alpha subunit), insertion domain {Cow (Bos taurus)}
 YSLEECLEFIAIIYGNTLQSI LAIVRAMTTLNIQYGDSARQDDARKLMHMADTIEEGTMPKEMSIIQ
 RLWKDSGIQACFDRASEYQLNDSAGYYLSDLERLVTGPYVPTAQDVLRSRVKT
 >d1cipa1 a.66.1.1 (A:61-181) Transducin (alpha subunit), insertion domain {Rat (Rattus norvegicus)}
 YSEEECKQYKAVVYSNTIQSIIAIRAMGRLLKIDFGDAARADDARQLFVLAGAAEEGFMTAELAGVIKR
 LWKDSGVQACFNRSREYQLNDSAAAYLNDLDRIAQPNYIPTQQDVLRTRVKT
 >d1ej5a_ a.68.1.1 (A:) Wiscott-Aldrich syndrome protein, WASP, C-terminal domain {Human (Homo sapiens)}
 SGFKHVSHVGVWPQNGFDVNNLDPDLRSLFSRAGISEAQLTDAETSKLIYDFIEDQGGLEAVRQEMR
 RQGGSGGSQSSEGLV GALMHVMQKRSRAIHSSDEGEDQAG
 >d1e79a1 a.69.1.1 (A:380-510) C-terminal domain of alpha and beta subunits of F1 ATP synthase {Cow (Bos taurus)}
 TRAMKQVAGTMKLELAQYREVAFAAQFGSDLDAATQQLLSRQVRLTELLKQGQYSPMAIEEQVAVIY
 AGVRGYLDKLEPSKITKFENAFLSHVISHQALLGKIRTDGKISEESDAKLKEIVTNFLAGFEA
 >d1e79d1 a.69.1.1 (D:358-475) C-terminal domain of alpha and beta subunits of F1 ATP synthase {Cow (Bos taurus)}
 MDPNIVGSEHYDVARGVQKILQDYKSLQDIIAILGMDELSEEDKLTVSRARKIQRFLSQPFQVAEVFTG
 HLGKLVPLKETIKGFQQLAGEYDHLPEQAFYMGPIEEAVAKADKLAE
 >d1skyb1 a.69.1.1 (B:372-502) C-terminal domain of alpha and beta subunits of F1 ATP synthase {Bacillus sp., strain ps3}
 IKAMKKVAGTLRLDLAAYRELEAFAAQFGSDLKATQANVARGARTVEVLKQDLHQPIVVEKQVLIYYA
 LTRGFLDDIPVEDVRRFEKEFYLWLDQNGQHLLHEHIRTTKDLPNEDDLNQAIEAFKKTFFVVSQ
 >d1skye1 a.69.1.1 (E:357-470) C-terminal domain of alpha and beta subunits of F1 ATP synthase {Bacillus sp., strain ps3}
 EIVGEEHYQVARKVQQTLERYKELQDIIAILGMDELSDEDKLVVHRARRIQFFLSQNFHVAEQFTGQP
 GSYVPVKETVRGFKEILEGKYDHLPEDRFRLVGRIEEEVVEKAKAMG
 >d1fx0a1 a.69.1.1 (A:373-501) C-terminal domain of alpha and beta subunits of F1 ATP synthase {Spinach (Spinacia oleracea), chloroplast}
 IKAMKKVAGKLELAQFAELEAFAQFASDLKATQNLARGQRLRELLKQPQSAPLTVEEQVMTIY
 TGTNGYLDLSLELDQVRKYLVELRTYVKTNKPEFQEIISSTKTFTEEA EALLKEAIQEQMERF
 >d1fx0b1 a.69.1.1 (B:378-485) C-terminal domain of alpha and beta subunits of F1 ATP synthase {Spinach (Spinacia oleracea), chloroplast}
 RIVGEEHYEIAQRVKETLQRYKELQDIIAILGLDELSEEDRLTVARARKIERFLSQPFVVAEVFTGSPGK
 YVGLAETIRGFQLILSGELDSLPEQAFYLVGNIDEATA
 >d1fkma1 a.69.2.1 (A:249-442) Ypt/Rab-GAP domain of gyp1p {Baker's yeast (Saccharomyces cerevisiae)}
 NSIIQRISKFDNILKDKTIINQQDLRQISWNGIPKIHRPVVWKLIGYLPVNTKRQEGFLQRKRKEYR
 DSLKHTFSDQHSRDIPWQHIEIDIPRTNPHIPLYQFKSVQNSLQRILYLWAIHPASGYVQGINDLVT
 PFFETFLTEYLPSPQIDDVEIKDPSTYMVDEQITDLEADTFWCLTKLLEQITDNYIH
 >d1fkma2 a.69.2.1 (A:443-630) Ypt/Rab-GAP domain of gyp1p {Baker's yeast

{*Saccharomyces cerevisiae*}}

GQPGILRQVKNLSQLVKRIDADLYNHVFQNEHVEFIQFAFRWMNCLLMREFQMGTVIRMWDTYLSE
TSQEVTSYSMSSNDIKPPVPTPEPRVASFVTPTKDFQSPTTALSNMTPNNAVEDSGKMRQSSLNEF
HVFVCAAFLIKWSDQLMEMDFQETITFLQNPPTKDWTTETDIEMLLSEAFIWQSLYK

>d1k5ha1 a.69.3.1 (A:301-398) 1-deoxy-D-xylulose-5-phosphate reductoisomerase,
C-terminal domain {*Escherichia coli*}

KLSALTFAAPDYDRYPCLKLAMEAFEQQAATTALNAANEITVAAFLAQQIRFTDIAALNLSVLEKM
DMREPQCVDDVLSVDANAREVARKEVMRLAS

>d1abv_ a.70.1.1 (-) N-terminal domain of the delta subunit of the F1F0-ATP synthase
{*Escherichia coli*}

SEFITVARPYAKAAFDFAVEHQSVRWQDMLFAAAEVTKNEQMAELLSGALAPETLAESFIAVCGEQ
LDENGQNLIRVMAENGRNLALPDVLEQFIHLRAVSEAT

>d1g7da_ a.71.1.1 (A:) Endoplasmic reticulum protein ERP29, C-domain {Rat (*Rattus
norvegicus*)}

PGCLPAYDALAGQFIEASSREARQAILKQGQDGLSGVKETDKKQWASQYLKIMGKILDQGEDFPASELA
RISKLIENKMSEGKKEELQRSLNILTAFRKKGAKEEL

>d1dvka_ a.72.1.1 (A:) Functional domain of the splicing factor Prp18 {Baker's yeast
{*Saccharomyces cerevisiae*}}

MRIQEAI AQDKTISVIIDPSQIGSTEGKPLLSMKCNLYIHEILSRWKASLEAYHPELFLD'TKKALFPLLL
QLRRNQLAPDLLISLATVLYHLQPKINLAVQSYMKLSIGNVAWPVIGVTSVGIHARSAHSKIQQGRN
AANIMIDERTRLWITSIKRLITFEWYTSNH

>d1ak4c_ a.73.1.1 (C:) HIV-1 capsid protein {Human immunodeficiency virus type 1}

PIVQNLQGMVHQAI SPRTLNAWVKVVEEKAFSPEVIMFSALEGATPQDLN'TMLNTVGGHQAA
MQMLKETINEEAAEWDR'LHPVHAGPIAPGQMREPRGSDIAGTTSTLQEIQGWMTHNPP'IPVGEIYK
RWIILGLNKIVRMY

>d1e6jp2 a.73.1.1 (P:11-147) HIV-1 capsid protein {Human immunodeficiency virus type 1}

VHQAI SPRTLNAWVKVVEEKAFSPEVIMFSALEGATPQDLN'TMLNTVGGHQAA MQMLKETINE
EAAEWDRVHPVHAGPIAPGQMREPRGSDIAGTTSTLQEIQGWM'TNNPP'IPVGEIYKRWIILGLNKIV
RMYSP

>d2eiaa2 a.73.1.1 (A:17-147) EIAV capsid protein p26 {Equine infectious anemia virus}

PRGYTTWVNTIQTNGLLNEASQNLFGILSVDCTSEEMNAFLDVVPGQAGQKILLDAIDKIADDWD
NRHPLPNAPLVAPPQGPIPM'TARFIRGLGVP'RRERQMEPAFDQFRQTYRQWII'EAMSEGIKVMIGK

>d1g03a_ a.73.1.1 (A:) HTLV-I capsid protein {Human T-cell leukemia virus type 1}

PVMHPHGAPPNHRPWQMKDLQAIKQEVSAAPGSPQFMQTIRLAVQQFDPTAKDLQDLLQYLCSS
LVASLHHQQLDSLISEAETRGITSYNPLAGPLRVQANNPQQQGLRREYQQLWLA'FAALPGSAKDPS
WA

>g1qrj.1 a.73.1.1 (A;B:16-130) HTLV-I capsid protein {Human T-cell leukemia virus type 1}

HHHHHSSGHIEGRHMXQMKDLQAIKQEVSAAPGSPQFMQTIRLAVQQFDPTAKDLQDLLQYLCSS
LVASLHHQQLDSLISEAETRGITGYNPLAGPLRVQANNPQQQGLRREYQQLWLA'FAALPGSAKD

>d1d1da2 a.73.1.1 (A:11-150) RSV capsid protein {Rous sarcoma virus}

WTPLEPKLITRLADTVRTKGLRSPITMAEVEALMSSPLLPHDVTNLMRVILGPAPYALWMDAWGVQ
LQTVIAAATRDPRHPANGQGRGERTNLDRLKGLADGMVGNPQGQAALLRPGELVAITASALQAFRE
VARLAEPA

>d1em9a_ a.73.1.1 (A:) RSV capsid protein {Rous sarcoma virus}

PVVIKTEGPAWTPLEPKLITRLADTVRTKGLRSPITMAEVEALMSSPLLPHDVTNLMRVILGPAPYAL
WMDAWGVQLQTVIAAATRDPRHPANGQGRGERTNLNRLKGLADGMVGNPQGQAALLRPGELVAIT
ASALQAFREVARLA

>d1jsub2 a.74.1.1 (B:310-432) Cyclin A {Human (Homo sapiens)}

TVNQFLTQYFLHQQPANCKVESLAMFLGELSLIDADPYLKYLPVIAAGAAFHLYTQVTVGQSWPESLI
RKTGYTLESCLKPCLMDLHQTYLQAPQHAQQSIREKYKNSKYHGVSLNPPETLNL

>d1vin_1 a.74.1.1 (181-308) Cyclin A {Cow (Bos taurus)}

DIHTYLREMEVKCKPKVGYMKKQPDITNSMRAILVDWLVEVGEEYKLQNETLHLAVNYIDRFLSSM
SVLRGKLQLVGTAAMLLASKFEEIYPPEVAEFVYITDDTYTKKQVLRMEHLVLKVLAFDLAA

>d1vin_2 a.74.1.1 (309-432) Cyclin A {Cow (Bos taurus)}

PTINQFLTQYFLHQQPANCKVESLAMFLGELSLIDADPYLKYLPVIAAAAFHLYTQVTVGQSWPESL
VQKTGYTLETLPCLLDLHQTYLRAPQHAQQSIREKYKNSKYHGVSLNPPETLNL

>d1jkw_1 a.74.1.1 (11-161) Cyclin H (mcs2) {Human (Homo sapiens)}

WTFSSSEQLARLRADANRKRFRCKAVANGKVLNDPVPFLEPHEEMTLCKYYEKRLLEFCVFKPAMP
RSVVGACMYFKRFLNNSVMEYHPRIIMLTCAFLACKVDEFNVSSPQFVGNLRESPLGQEKALEQIL
EYELLLIQQLNFHLIVH

>d1jkw_2 a.74.1.1 (162-287) Cyclin H (mcs2) {Human (Homo sapiens)}

NPYRPFEGFLIDLKTRYPILNPEILRKTADDFLNRIALTDAYLLYTPSQIALTAILSSASRAGITMESYL
SESLMLKENRTCLSQLDIMKSMRNLVKKYEPPEVAVLKQKLDKDRCHSAELAL

>d1bu2a1 a.74.1.1 (A:22-148) Viral cyclin {Herpes virus saimiri}

RVLNNLKRELLLPKFTSLWEIQTEVTVDNRTILLTWMHLLCESFELDKSVFPLSVSILDRLCKKKQG
TKKTLQKIGAACVLIGSKIRTVKPMTVSKLTYLSCDCFTNLELINQEKDILEALKWDTE

>d1bu2a2 a.74.1.1 (A:149-250) Viral cyclin {Herpes virus saimiri}

AVLATDFLIPLCNALKIPEDLWPQLYEAASTTICKALIQPNIALLSPLGICAGLLTTIETDNTNCRPW
TCYLEDLSSILNFSTNTVRTVKDQVSEAFSLYD

>d1f5qb1 a.74.1.1 (B:6-146) Viral cyclin {Murine herpes virus gamma 68}

FQGFLLDSSLLNEEDCRQMIYRSEREHDARMVGVNVDQHFTSQYRKVLTTWMFVCVKDLRQDNNVF
PLAVALLDLFLSTRIDRENYQSTAAVALHIAGKVRAYMPIKATQLAYLCCGATTADKLLTLEVKSLDT
LSWVADR

>d1f5qb2 a.74.1.1 (B:147-252) Viral cyclin {Murine herpes virus gamma 68}

CLSTDILICYLHIMHAPREDYLNINLCRPFKIFCALCDGRSAMKRPVLITLACMHLTMNQKYDYENR
IDGVCKSLYITKEELHQCCDLVDIAIVSFDENYFKINA

>d1g3nc1 a.74.1.1 (C:16-147) Viral cyclin {Kaposi sarcoma-associated virus}

LCEDRIFYNILEIEPRFLTSDSVFGTFQQLTSHMRKLLGTWMFVVCQYENLEPNVVALALNLLDRLL
LIKQVSKEHFQKTGSACLLVASKLRSLTPISTSSLCYAAADSFSRQELIDQEKELLEKLAWRTE

>d1g3nc2 a.74.1.1 (C:148-253) Viral cyclin {Kaposi sarcoma-associated virus}

AVLATDVTSFLLLKLVGGSQHLDFWHHEVNTLITKALVDPLTGLSPASIISAAGCALLVPANVIPQDTH
SGGVVPLASILGCDVSVLQAAVEQILTSVSDFDLRI

>d1vola1 a.74.1.2 (A:113-207) Transcription factor IIB (TFIIB), core domain {Human (Homo sapiens)}

AMMNAFKEITTMADRINLPRNKVDRTNNLFRQAYEQKSLKGRANDAIASACLYIACRQEGVPRTFK
EICAVSRISKKEIGRCFKLILKALETSD

>d1vola2 a.74.1.2 (A:208-316) Transcription factor IIB (TFIIB), core domain {Human (Homo sapiens)}

LITGDFMSRFSNLCLPKQVQMAATHIARKAVELDLVPGRSPISVAAAAIYMASQASAEKRTQKEIG
DIAGVADVTRQSYRLIYPRAPDLFPTDFKFDTPVDKLPQL
>d1aisb1 a.74.1.2 (B:1108-1205) Transcription factor IIB (TFIIB), core domain {Archaeon
Pyrococcus woesei}
NLAFALSELDRITAQLKLPRHVEEEAARLYREAVRKGLIRGRSIESVMAACVYACRLLKVPRTLDEIA
DIARVDKKEIGRSYRFIARNLNLTPKKLF
>d1aisb2 a.74.1.2 (B:1206-1300) Transcription factor IIB (TFIIB), core domain {Archaeon
Pyrococcus woesei}
VKPTDYVNKFADELGLSEKVRRAIEILDEAYKRGLTSGKSPAGLVAAALYIASLLEGEKRTQREVAEV
ARVTEVTVRNRYKELVEKLIKIVPIA
>d1guxa_ a.74.1.3 (A:) Retinoblastoma tumor suppressor domains {Human (Homo sapiens)}
NTIQQLMMILNSASDQPSLENLISYFNNCTVNPKEILKRVKDIGYIFKEKFAKAVGQCVEIGSQRYKL
GVRLYYRVMESMLKSEEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRSTSQNLDSGTDLSP
WILNVLNLKAFDFYKVIESFIKAEGNLTREMIKHLERCEHRIMESLAWLSDSPLFDLIKQSK
>d1guxb_ a.74.1.3 (B:) Retinoblastoma tumor suppressor domains {Human (Homo sapiens)}
TSLSLFYKKVYRLAYLRLNLTLCERLLSEHPELEHIIWTLFQHTLQNEYELMRDRHLDQIMMCSMYGI
CKVKNIDLKFKIIVTAYKDLPHAVQETFKRVLIKEEYDSIIVFYNSVFMQRLKTNILQYASTRPPTLSP
IPHI
>d1k8ke_ a.148.1.1 (E:) Arp2/3 complex 21 kDa subunit ARPC3 {Cow (Bos taurus)}
PAYHSSLMDPDTKLIGNMALLPIRSQFKGPAPRETKDTDIVDEAIYFKANVFFKNEYEIKNEADRTLI
YITLYISECLKKLQKCNKSKSQGEKEMYTLGITNFPPIPGEPGFPLNAIYAKPANKQEDEVMRAYLQQLR
QETGLRLCEKVFDPQNDKPSKWWTCFVKRQFMNKSLSG
>d1jfza_ a.149.1.1 (A:) RNase III endonuclease domain {Aquifex aeolicus}
GMKMLEQLEKKLGYTFKDKSLLEKALTHVSYSKKEHYETLEFLGDALVNFIVDLLVQYSPNKREGF
LSPLKAYLISEEFFNLLAQKLELHKFIRIKRGKINETIIGDVFEALWAAVYIDSGRDANFTRELFYKLFK
EDILSAIKEGR
>d1hus_ a.75.1.1 (-) Ribosomal protein S7 {Bacillus stearothermophilus}
RDVLPDIYNSKLVTRLINKIMIDGKKSQAQKILYTAFDIIRERTGKDPMEVFEQALKNVMPVLEVRA
RRVGGANYQVPVEVRPDRRVSGLRWLVQYARLRNEKTMEERLANEIMDAANNTGAAVKKKREDTH
KMAEAN
>d1rss_ a.75.1.1 (-) Ribosomal protein S7 {Thermus thermophilus}
LQPDLVYGDVLVTAFINKIMRDGKKNLAARIFYDACKIIQEKTGQEPLKVFQAVENVKPRMEVRSR
RVGGANYQVPMEVSPRRQQSLALRWLVQAANQRPERRAAVRIAHELMDAAEGKGGAVKKKEDVER
MAEANRAYAHYRW
>d1iqva_ a.75.1.1 (A:) Ribosomal protein S7 {Archaeon Pyrococcus horikoshii}
IKVMGRWSTEDVEVKDPSLKPYNLEPRLLPHTHGRHAKKHFGKANVHIVERLINKVMRSGGSHYK
VAGHFMRREHRSLSKKNVRAVEVVEAFKIEKRTGKNPIQVLVWAIENAAPREDTTSVMFGGIRYH
VAVDISPLRRLDVALRNIALGASAKCYRTKMSFAEALAEIILAANKDPKSYASKKLEIERIAESSR
>d1jr3a1 a.80.1.1 (A:243-368) gamma subunit {Escherichia coli}
TLDDDQALSLEAMVEANGERVMALINEAAARGIEWEALLVEMLGLLHRIAMVQLSPAALGNDMA
AIELRMRELARTIPPTDIQLYYQTLLIGRKELPYAPDRRMGVEMTLRALARAFHPRMPLPEP
>d1a5t_1 a.80.1.1 (208-330) delta prime subunit {Escherichia coli}
DNWQARETLCQALAYSPSGDWYSLAALNHEQAPARLHWLATLLMDALKRHHGAAQVTNVDVP
GLVAELANHLSPSRLQAILGDVCHIREQLMSVTGINRELLITDLLLLRIEHYLQPGVVLP

>d1jr3d1 a.80.1.1 (D:212-338) delta subunit {Escherichia coli}
FTPFHWVDALLMGKSKRALHILQQLRLEGSEPVILLRTLQRELLLLVNLKRQSAHTPLRALFDKHRV
WQNRRGMMGEALNRLSQTQLRQAVQLLRTTELTKQDYGQSVWAELEGLSLLLCHKPLAD

>d1iqpa1 a.80.1.1 (A:233-327) Replication factor C {Archaeon Pyrococcus furiosus}
RARPEDIREMMLLALKGNFLKAREKLEILLKQGLSGEDVLVQMHKEVFNLPIEEPKKVLLADKIGE
YNFRLVEGANIEHQLEALLAQFTLIGKK

>d1jr5a_ a.150.1.1 (A:) Anti-sigma factor Asia {Bacteriophage T4}
MNKNIDTVREIITVASILIKFSREDIVENRANFIAFLNEIGVTHEGRKLNQNSFRKIVSELTQEDKKTLI
DEFNEGFEGVYRYLEMYTNK

>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}
TPTGRTLATAVMRKHRLAERLLTDIIGLDINKVHDEASRWEHVMSDEVERRLVKVLKDVSRSPFGN
PIPLDELGV

>d1fx7a2 a.76.1.1 (A:65-144) Iron-dependent regulator {Mycobacterium tuberculosis}
TEKGRALAIAMRKHRLAERLLVDVIGLPWEEVHAEACRWEHVMSDEVERRLVKVLNNPTTSPFG
NPIPGLDELGVGPEP

>d1gpja1 a.151.1.1 (A:303-404) Glutamyl tRNA-reductase dimerization domain {Archaeon Methanopyrus kandleri}
EIPKVEKLIEEELSTVEEELEKLERRLVADVAKSLHEIKDRELERALRRLKTGDPENVLQDFAEAYT
KRLINVLTSAIMELPDEYRRAASRALRRASELNG

>d1ngr_ a.77.1.1 (-) p75 low affinity neurotrophin receptor {Rat (Rattus norvegicus)}
GNLYSSLPLTKREEVEKLLNGDTWRHLGELGYQPEHIDSFTHEACPVRALLASWGAQDSATLDALL
AALRRIQRADIVESLCSE

>d1ddf_ a.77.1.1 (-) Fas {Human (Homo sapiens)}
METVAINLSDVDLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWH
QLHGKKEAYDTLIKDLKKNLCTLAEKIQTILKDITSDSENSFRNEIQSLVLEHHHHHH

>d1a1w_ a.77.1.1 (-) FADD (Mort1) {Human (Homo sapiens)}
MDPFLVLLHSVSSLSSELTELKYLCLGRVGRKLERVQSGLDLFSMLLEQNDLEPGHTELLRELLA
SLRRHDLRRVDDFE

>d1e41a_ a.77.1.1 (A:) FADD (Mort1) {Human (Homo sapiens)}
GSHMGEEDLCAAFNVICDNVGDWRRLARQLKVSDTKIDSIEDRYPRNLTERVRESLRIWKNTKEKE
NATVAHLV GALRSCQMNLVADLVQEVQQARDLQNRSGA

>d1fada_ a.77.1.1 (A:) FADD (Mort1) {Mouse (Mus musculus)}
AAPPGEAYLQVAFDIVCDNVGRDWKRLARELVSEAKMDGIEEKYPRSLSERVRESLKVWKNAEKK
NASVAGLVKALRTCRLNLVADLVVEEAQES

>d3crd_ a.77.1.1 (-) Raidd CARD domain {Human (Homo sapiens)}
MEARDKQVLRSLRLELGAEVLEGLVLQYLYQEGILTENHIQEINAQTTGLRKTMLLLDILPSRGPKA
FDTFLDSLQEFVWVREKLLKAREEAMTDLPAG

>d1cy5a_ a.77.1.1 (A:) Apoptotic protease activating factor 1, APAF-1 {Human (Homo sapiens)}
MDAKARNCLLQHREALEKDIKTSYIMDHMISDGFLTISEEEKVRNEPTQQQRAAMLKIMILKKDND

SYVSFYNALLHEGYKDLAALLHDGIPV

>d3ygs_p_ a.77.1.1 (P:) Procaspase 9 prodomain {Human (Homo sapiens)}

SMDEADRLLRRCLRLVEELQVDQLWDVLLSRELFRRPHMIEDIQRAGSGSRRDQARQLIIDLETRG
SQALPLFISCLEDTGQDMLASFLRTNRQAG

>d1dgna_ a.77.1.1 (A:) Iceberg {Human (Homo sapiens)}

ADQLLRKKRRIFIHSVGAGTINALLDCLLEDEVISQEDMKNKVRDENDTVMDKARVLIDLVTGKGPKS
CCKFIKHLCEEDPQLASKMGLH

>d1d2za_ a.77.1.1 (A:) Pelle death domain {Drosophila melanogaster}

LDNTMAIRLLPLPVRAQLCAHLDALDVWQQLATAVKLYPDQVEQISSQKQRGRSASNEFLNIWGGQ
YNHTVQTLFALFKKLKLNAMRLIKDYVSEDLHKYI

>d1d2zb_ a.77.1.1 (B:) Tube death domain {Drosophila melanogaster}

LSSKYSRNTLRRVEDNDIYRLAKILDENSCWRKLMISIIPKGMVDVQACSGAGCLNFP AEIKKGFKYTA
QDVFAQIDEAANRLPPDQSKSQMMIDEWKTSGKLNERTVGVLLQLLVQAELFSAADFVALDFLNES
TPARPVDGPGALISLE

>d1hw1a2 a.78.1.1 (A:79-230) Fatty acid responsive transcription factor FadR, C-terminal domain {Escherichia coli}

GLNILETLARLDHESVPQLIDNLLSVRTNISTIFIRTAFRQHPDKAQEVLATANEVADHADAFEAELDY
NIFRGLAFASGNPIYGLILNGMKGLYTRIGRHYFANPEARSLALGFYHKLSALCSEGAHDQVYETVRR
YGHESGEIWHRMQKNL

>d1eyva_ a.79.1.1 (A:) Antitermination factor NusB {Mycobacterium tuberculosis}

GRHQARKRAVALLFEAEVRGISAEEVVDTRAALAEAKPDIARLHPYTA AVARGVSEHA AHIDDLITA
HLRGWTLDRLPVDRAILRVSVWELLHAADVPEPVVVDEAVQLAKELSTDDSPGFVNGVLGQVM

>d1ey1a_ a.79.1.1 (A:) Antitermination factor NusB {Escherichia coli}

MKPAARRRARECAVQALYSWQLSQNDIADVEYQFLAEQDVKDVDVLYFRELLAGVATNTAYLDGLM
KPYLSRLLLEELGQVEKAVLRALYELSKRSDVPYKVAINEAIELAKSFGAEDSHK FVNGVLDKAAPVIR
PNKK

>d1b79a_ a.81.1.1 (A:) N-terminal domain of DnaB helicase {Escherichia coli}

PPHSIEAEQSVLGGLMLDNERWDDVAERVVADDFYTRPHRHIFTEMARLQESGSPIDLITLAESLER
QGQLDSVGGFAYLAELSKNTPSAANISAYADIVRE

>d1jwea_ a.81.1.1 (A:) N-terminal domain of DnaB helicase {Escherichia coli}

MKVPPHSIEAEQSVLGGLMLDNERWDDVAERVVADDFYTRPHRHIFTEMARLQESGSPIDLITLAES
LERQGQLDSVGGFAYLAELSKNTPSAANISAYADIVRERAVVREMIS

>d1qc7a_ a.82.1.1 (A:) FliG C-terminal domain {Thermotoga maritima}

MFVFEDILKDDRISQLVLRVDTRDLALALKGASDELKEKIFKNMSKRAAALLKDELEYMGPVRLK
DVEEAQQKIINIIRRLLEEAGEIVIARGGGEELIM

>d1qc7b_ a.82.1.1 (B:) FliG C-terminal domain {Thermotoga maritima}

MFVFEDILKDDRISQLVLRVDTRDLALALKGASDELKEKIFKNMSKRAAALLKDELEYMGPVRLK
DVEEAQQKIINIIRRLLEEAGEIV

>d1crka1 a.83.1.1 (A:1-98) Creatine kinase, N-terminal domain {Chicken (Gallus gallus), mitochondria}

TVHEKRKLFPPSADYPDLRKHNNCMAECLTPAIYAKLRDCLTPNGYSLDQCIQTGVDNPGHPFIKTV
GMVAGDEESYEVFAEIFDPVIKARHNGYDPR

>d1qh4a1 a.83.1.1 (A:2-102) Creatine kinase, N-terminal domain {Chicken (Gallus gallus), brain-type}

PFSNSHNLLKMKYSVDDEYPDLSVHNNHMAKVLTLDLYKKLRDRQTSSGFTLDDVIQTGVDNPGHP
FIMTVGCVAGDEESYEVFKELFDPVIEDRHGGYKP
>d1qk1a1 a.83.1.1 (A:1-102) Creatine kinase, N-terminal domain {Human (Homo sapiens),
mitochondria}
AASERRRLYPPSAEYPLDRKHNNCMASHLTPAVYARLCDKTTPTGWTLDQCIQTGVDNPGHPFIKT
VGMVAGDEETYEVFADLFDPIQERHNGYDPRTMKH
>d2crka1 a.83.1.1 (A:8-102) Creatine kinase, N-terminal domain {Rabbit (Oryctolagus
cuniculus)}
NKYKLNKSEEEYPDLSKHNNHMAKVLTDPDYKKLRDKETPSGFTLDDVIQTGVDNPGHPFIMTVG
CVAGDEESYTVFKDLFDPIIQDRHGGFKP
>d1g0wa1 a.83.1.1 (A:2-102) Creatine kinase, N-terminal domain {Cow (Bos taurus), retinal
isoform}
PFSNSHNTLKLRFPAEDEFDLSGHNNHMAKVLTPELYAELRAKSTPSGFTVDDVIQTGVDNPGHPY
IMTVGCVAGDEESYDVFKEKELFDPIEDRHGGYKP
>d1bg0_1 a.83.1.1 (2-95) Arginine kinase {Horseshoe crab (Limulus polyphemus)}
VDQATLDKLEAGFKKLEASDCKSLLKKHLTKDVFDSIKNKKTGMGATLLDVIQSGVENLDSGVGIY
APDAESYRTFGPLFDPIIDDYHGGFKL
>d1al01_ a.84.1.1 (1:) Scaffolding protein gpD of bacteriophage procapsid {Bacteriophage
phi-X174}
EQSVRFQ TALASIKLIQASAVLDTEDDFDLTSNKVWIATDRSRARRCVEACVYGTLD FVGYP RFP A
PVEFIAAVIAYYVHPVNIQTACLIMEGA EFTENIINGVERPVKAAELFAFTLRVRAGNTDVLTD A EENV
RQKLRA
>d1l1_1 a.85.1.1 (1-109) Hemocyanin, N-terminal domain {Horseshoe crab (Limulus
polyphemus)}
TLHDKQIRVCHLFEQLSSATVIRLKNV GKLQPG AIFSCFHPDHLEEARHLYEVFWEAGDFNDFIEIAK
EARTFVNEGLFAFAAEVAVLHRDDCKGLYVP
>d1lla_1 a.85.1.1 (2-109) Hemocyanin, N-terminal domain {Horseshoe crab (Limulus
polyphemus)}
LHDKQIRICHLFEQLSSATVIGDGDKHKHSDRLKNV GKLQPG AIFSCFHPDHLEEARHLYEVFWEAG
DFNDFIEIAKEARTFVNEGLFAFAAEVAVLHRDDCKGLYVP
>d1hc_2_1 a.85.1.1 (5-135) Hemocyanin, N-terminal domain {Spiny lobster (Panulirus
interruptus)}
TGNAQKQDINHLLDKIYEPTKYPDLKDIAENFNPLGDTSIYNDHGA AVETLMKELNDHRLLEQRH
WYSLFNTRQRKEALMLFAVLNQCKEWYCFRSNAAYFRERMNEGEFVYALYVSVIHSKLG DGIVLP
>d1lla_2 a.86.1.1 (110-379) Hemocyanin {Horseshoe crab (Limulus polyphemus)}
PVQEIFPDKFIPSA AINEAFKKAHV RPEFDESPILVDVQDTGNILDPEYRLAYYREDVGINAHHWHW
HLVYPSTWNPKYFGKKDRKGELFYMHQ QMCARYDCERLSNGMHRMLPFNNFDEPLAGYAPHL
THVASGKYSPRPDGLKLRDLGDIEISEMVRMRERILDSIHLGYVISEDGSHKTLDELHGTDILGALVE
SSYESVNHEYYGNLHNWGHVTMARIHDPDGRFH EEPGVMSDTSTSLRDP IFYNWHRFIDNIFHEY
KNTLK
>d1hc_2_2 a.86.1.1 (136-398) Hemocyanin {Spiny lobster (Panulirus interruptus)}
PLYQITPHMFTNSEVIDKAYS AKMTQKPGTFNVSFTGT KKNREQRVAYFGEDIGMNIHHVTWHMDF
PFWWEDSYGYHLDRKGELFFWVHHQLTARFDFERLSNWLDPVDELHWDRIREGFAPLTSYKYGG
EFPVRPDNIHFEDVDGVAHVHDL EITESRIHEAIDHGYITDSDGHTIDIRQPKGIELLDGDI ESSKYSSN

VQYYGSLHNTAHVMLGRQGDPHGKFNLPVMEHFETATRDPSFFRLHKYMDNIFKKHTDSF
>d1js8a1 a.86.1.1 (A:2503-2791) Functional unit from octopus hemocyanin {Giant octopus
(Octopus dofleini)}

AIIRKNVNSLTPSDIKELRDAMAKVQADTSDNGYQKIASYHGIPLSCHYENGTAACCQHGMVTFPN
WHRLLTKQMEDALVAKGSHVGIPIYWDWTTTTFANLPVLVTEEKDNSFHHAHIDVANTDTTRSPRAQ
LFDDDPDKGDKSFFYRQIALALEQTDFCDFEIQFEIGHNAIHSWVGGSSPYGMSTLHYTSYDPLFYLLH
SNTDRIWSVWQALQKYRGLPYNTANCEINKLVKPLKPFNLDTNPNAVTKAHSTGATSFYHKLGYD
YDNLNFHGMTIPELEEHLKEIQH

>d1bt3a_ a.86.1.2 (A:) Catechol oxidase {Sweet potato (Ipomoea batatas)}

APIQAPEISKCVPPADLPPGAVVDNCCPPVASNIVDYKLPVTTMKVRPAAHTMDKDAIAKFAKAV
ELMKALPADDPRNFYQALVHCAYCNGGYDQVNFDPQEIQVHNSWLFPPFHRWYLYFYERILGKLI
GDPSFGLPFWNWDNPGGMVLPDFLNDSTSSLYDSNRNQSHLPPVVVDLGYNGADTDVTDQQRITD
NLALMYKQMVNAGTAELFLGKAYRAGDAPSPGAGSIETSPHIHRWVGDPRTNEDMGNFYSA
GRDIAFYCHHSNVDRMWTIWQQLAGKPRKRDYTDSDWLNATFLFYDENGQAVKVRIGDSLNDNQK
MGYKYAKTPLPWL

>d1dbha1 a.87.1.1 (A:198-404) Son of sevenless-1 (sos-1) {Human (Homo sapiens)}

EQTYDYLVKAFMAEIRQYIRELNLIKVFREPFVSNKLFSSANDVENIFSRIVDIHELKLLGHIEDTV
EMTDEGSPHPLVGSCEFEDLAEELAFDPYESYARDILRPGFHDRFLSQLSKPGAALYLSIGEGFKEAV
QYVLPRLLLAPVYHCLHYFELLKQLEEKSEDQEDKECLKQAITALLNVQSGMEKICSKSLAKRRRLSES
A

>d1by1a_ a.87.1.1 (A:) beta-pix {Human (Homo sapiens)}

MKGFDTTAINKSYNNVVLQNILETENEYSKELQTVLSTYLRLPLQTSEKLSSANISYLMGNLEEICSFQQ
MLVQSLEECTKLPEAQQRVGGCFLNLMQMKTLTYCANHPSAVNVLTEHSEELGFMETKGASSP
GILVLTGLSKPFMRDKYPTLLKELERHMEDYHTDRQDIQKSMAAFKNLSAQCQEVKRKRKELELQI
LTEAIR

>d1f5xa_ a.87.1.1 (A:) RhoGEF Vav {Mouse (Mus musculus)}

MKGDEIYEDLMRLESVPTPPKMTEYDKRCCCLREIQQTEEKYTDTLGSIQQHFMKPLQRFLKPQDM
ETIFVNIEELFSVHTHFLKELKDALAGPGATTLYQVFIKYKERFLVYGRYCSQVESASKHLDQVATARE
DVQMKLEECQRANNGRFTLRDLLMVPMPQVRLKYHLLLQELVKHTQDATEKENLRLALDAMRDL
AQC VNEVKR

>d1foea1 a.87.1.1 (A:1034-1239) GEF of TIAM1 (T-Lymphoma invasion and metastasis
inducing protein 1) {Mouse (Mus musculus)}

QLSDADKLRKVICELLETERTYVKDLNCLMERYLKPLQKETFLTQDELVDLFGNLTEMVEFQVEFLK
TLEDGVRVLPDLEKLEKVDQFKKVLFSLGGSFYADRFKLYSAFCASHTKVPKVLVAKTDTAFKAF
LDAQNPRQQHSSTLESYLIKPIQRVLKYPLLLRELFALTDASEEHYHLDVAIKTMNKVASHINEMQK
IHE

>d1boua_ a.88.1.1 (A:) LigA subunit of an aromatic-ring-opening dioxygenase LigAB
{Sphingomonas paucimobilis, formerly Pseudomonas paucimobilis}

IDVHAYLAEFDDIPGTRVFTAQRARKGYNLNQFAMSLMKAENRERFKADESAYLDEWNLTAAKAA
VLARDYNAMIDEGGNVYFLSKLFSTDGKSFQAAGSMTGMTQEYYAQMMIDGGRSPAGVRSIKGGY

>d1hbna1 a.89.1.1 (A:270-549) Alpha chain {Archaeon Methanobacterium
thermoautotrophicum}

RRARGENEPGGVPGYLAADICQSSRVNYEDPVRVSLDVVATGAMLYDQIWLGSYMSGGVGFTQYATA
AYTDNILDFTYFGKEYVEDKYGLCEAPNNMDTVLDVATEVTFYGLEQYEEYPALLEDQFGGSQRAA

VVAAAAGCSTAFATGNAQTGLSGWYLSMYLHKEQHSRLGFYGYDLQDQCGASNVFSIRGDEGLPLEL
RGPNYPNYAMNVGHQGEYAGISQAPHAARGDAFVFNPLVKIAFADDNLVFDFTNVRGEFAK GALRE
FEPAGERALITPA

>d1e6va1 a.89.1.1 (A:273-552) Alpha chain {Archaeon Methanopyrus kandleri}
RRARGENEPGGVPFGLADCVQTMRKYPDDPAKVALEVIAAGAMLYDQIWLGSYMSGGVTQYAT
AVYPDNILDDYVYVYGLEVEYVEDKYGIAEAEPSMDVVKDVATEVTLYGLEQYERYPAAMETHFGGSQRA
AVCAAAAAGCSTAFATGHAQAGLNGWYLSQILHKEGQGRGLGFYGYALQDQCGAANSLSVRSDEGLPLE
LRGPNYPNYAMNVGHLGEYAGIVQAAHAARGDAFCVHPVIKVAFADENLVFDFTNVRKEFAK GALRE
FEPAGERDLIVPA

>d1e6ya1 a.89.1.1 (A:1284-1569) Alpha chain {Archaeon Methanosarcina barkeri}
RRARGPNEPGLSFGHLSDIVQTSRVEDPAKIALEVVGAGCMLYDQIWLGSYMSGGVTQYATAAY
TDDILDNNTYYDVDYINDKYNGAATVKGDNKVKASLEVVKDIATESTLYGIETYEFPTALEDHFGG
SQRATVLAAGVACSLATGNANAGLSGWYLSMYLHKEAWGRLGFFGFDLQDQCGATNVLSYQGD
EGLPDEL RGPNYPNYAMNVGHQGGYAGIAQAHSRGRDAFTVNPLLKVCFADDLLPFNFAEPRREF
GRGAIREFVPAGERSLVIPA

>d1hbnb1 a.89.1.1 (B:189-443) Beta chain {Archaeon Methanobacterium
thermoautotrophicum}

GYALRNIMVNHVVAATLKNLQAAALSTILEQTAMFEMGDAVGAFERMHLGLAYQGMNADNLV
DLVKANGKEGTVGSVIADLVERALEDGVIVKEKELTDYKVYGTDDLAMWNAYAAAGLMAATMVNQ
GAARAAQGVSTLLYNDLIEFETGLPSVDFGKVEGTAVGFSFFSHSIYGGGGPGIFNGNHIVTRHSGK
FAIPCVAAMALDAGTQMFSPEATSGLIKEVFSQVDEFREPLKYVVEAAAAEIKNEI

>d1e6vb1 a.89.1.1 (B:190-442) Beta chain {Archaeon Methanopyrus kandleri}
GYALRNIMVNHIVAATRKNMQAVCLAATLQQTAMFEMGDALGPFERLHLLGYAYQGLNADNMVY
DIVKKHGKEGTVGTVVREVERALEDGVIEVKEELPSFKVYKANDMDLWNAYAAAGLVAAMVNVQ
GAARAAQGVSATILYNDLLEYETGLPGVDFGRAEGTAVGFSFFSHSIYGGGGPGIFHGNHIVTRHSGK
FAIPPVAAAMALDAGTQMFSPEVTSKLIGDVFGEIDEFREPMKYITEAAAAEAK

>d1e6yb1 a.89.1.1 (B:2186-2433) Beta chain {Archaeon Methanosarcina barkeri}
GFSLRNIMANHVAAISNRNAMNASALSSIYEQSGIFEMGGAVGMFERHQLLGLAYQGLNANNLLYDI
VKENGKDGTVIESVVRRAIEAGIISVDKTAPSGYNFYKANDVPKWNACAAVGTLAATLVNCGAG
RAAQNVSTLLYFNDILEKETGLPGCDYGVKVEGTAVGFSFFSHSIYGGGGPGVFNHVVTRHRSRGA
IPCVAVALDAGTQMFSIESTSGLIGDVFGAIPFREFPIKAVAGV

>d1bfg_ a.90.1.1 (-) Transcription factor STAT-4 N-domain {Mouse (Mus musculus)}
GGSQWNQVQLEIKFLEQVDQFYDDNFPMEIRHLLAQWIETQDWEVASNNETMATILLQNLLIQL
DEQLGRVSKEKNLLIHNLRIRKVLQKFGHGNPMHVAVVISNCLREERRILAAANMPI

>d1agre_ a.91.1.1 (E:) Regulator of G-protein signalling 4, RGS4 {Rat (Rattus norvegicus)}
VSQEEVKKWAESLENLINHECGLAAFKAFKSEYSEENIDFWISCEEYKKIKSPKLSPKAKKIYNEFI
SVQATKEVNLDSCTREETS RNMLEPTITCFDEAQKIFNLMEKDSYRRFLKSRFYLDLT

>d1fqia_ a.91.1.1 (A:) RGS9, RGS domain {Cow (Bos taurus)}
KLVDIPTKMRVERWAFNFSELIRDPKGRQSFQHFLRKEFSGENLGFWEACEDLKYGDQSKVKEKAE
EIYKFLAPGARRWINIDGKTMDITVKGLKHPHRYVLDAAQTHIYMLMKDSYARYLKSPIYKEMLA
KAIEP

>d1cmza_ a.91.1.1 (A:) Galpha interacting protein, GaIP {Human (Homo sapiens)}
PSPEEVQSWAQSFQKLMHSPAGRSVFRFLRTEYSEENMLFWLACEELKAEANQHVVDEKARLIYE
DYVSILSPKEVSLDSRVREGINKKMQEPSAHTFDDAQLQIYTLMHRDSYPRFLSSPTYRALL

>d1dk8a_a.91.1.1 (A:) Axin RGS-homologous domain {Human (Homo sapiens)}
GSASPTPPYLKWAESLHSLDDQDGISLFRFTFLKQEGCADLLDFWFACTGFRKLEPCDSNEEKRLKL
ARAIYRKYILDNNGIVSRQTKPATKSFIKGCIMKQLIDPAMFDQAQTEIQATMEENTYPSFLKSDIYLE
YTRTGSESPKV

>d1emua_a.91.1.1 (A:) Axin RGS-homologous domain {Human (Homo sapiens)}
PPYLKWAESLHSLDDQDGISLFRFTFLKQEGCADLLDFWFACTGFRKLEPCDSNEEKRLKLARAIYR
KYILDNNGIVSRQTKPATKSFIKGCIMKQLIDPAMFDQAQTEIQATMEENTYPSFLKSDIYLEYT

>d1iapa_a.91.1.1 (A:) p115RhoGEF {Human (Homo sapiens)}
SQFQSLEQVKRRPAHLMALLQHVALQFEPGPLLCLHADMLGSLGPKEAKKAFLDFYHSFLEKTAVL
RVPVPPNVAFELDRTRADLISEDVQRRFVQEVVQSQQVAVGRQLEDFRSKRLMGMTPEWEQELAQLE
AWVGRDRASYEARERHVAERLLMHLEEMQHTISTDEEKSAAVVNAIGLYMRHLGVRT

>d1htjf_a.91.1.1 (F:) Pdz-RhoGEF RGS-like domain {Human (Homo sapiens)}
ESDIIFQDLEKLKSRPAHLGVFLRYIFSQADPSPLLFYLCAEVYQQASPKDSRSLGKDIWNIFLEKNAP
LRVKIPEMLQAEIDSRLRNSEDARGVLCEAQEAAMPEIQEQIHDIRTKRTLGLGSLYGENDLLDLDG
DPLRERQVAEKQLAALGDILSAYAADRSAPMDFALNTYMSHAGIRL

>d1a9xa1_a.92.1.1 (A:403-555) Carbamoyl phosphate synthetase, large subunit connection
domain {Escherichia coli}
EVGATGFDPKVSLLDPEALTKIRRELKDAGADRIWYIADAFRAGLSVDGVFNLTNIDRWFLVQIEELV
RLEEKVAEVGITGLNADFLRQLKRKGFADARLAKLAGVREAEIRKLRDQYDLHPVYKRVDTCAAEFA
TDTAYMYSTYEEEECEANP

>d1b80a_a.93.1.1 (A:) Lignin peroxidase {White rot basidiomycete (Phanerochaete
chrysosporium)}
VIEKRATCSNGKTVGDASCCAWFDVLDLDDIQQLNFHGGQCGAEAHESIRLVFHDSIAISPAMEAQGKF
GGGGADGSIMIFDDIETAFHPNIGLDEIVKLQKPFVQKHGVTGDFIAFAGAVALSNCPGAPQMNFFT
GRAPATQPAPDGLVPEPFHTVDQIINRVNDAGEFDELELVWMLSAHSVAAVNDVDPTVQGLPFDST
PGIFDSQFFVETQLRGTAFFPGSGGNQGEVESPLPGEIRIQSDHTIARDSRTACEWQSFVNNQSKLVDD
FQFIFLALTQLGQDPNAMTDCSDVIPQSKPIPGNLPFSFFPAGKTIKDVEQACAETPFPTLTTLPGPET
SVQRIPPPPGA

>d1llp__a.93.1.1 (-) Lignin peroxidase {White rot basidiomycete (Phanerochaete
chrysosporium)}
ATCANGKTVGDASCCAWFDVLDLDDIQANMFHGGQCGAEAHESIRLVFHDSIAISPAMEAKGKFGGGG
ADGSIMIFDITIETAFHPNIGLDEVVAMQKPFVQKHGVTGDFIAFAGAVALSNCPGAPQMNFFTGRK
PATQPAPDGLVPEPFHTVDQIARVNDAGEFDELELVWMLSAHSVAAVNDVDPTVQGLPFDSTPGIF
DSQFFVETQFRGTLFPGSGGNQGEVESGMAGEIRIQTDHTLARDSRTACEWQSFVGNQSKLVDDFQ
FIFLALTQLGQDPNAMTDCSDVIPLSKPIPGNPGFSFFPPGKSHSDIEQACAETPFPSLVTLPGPATSV
RIPPHKA

>d1qpaa_a.93.1.1 (A:) Lignin peroxidase {White rot basidiomycete (Phanerochaete
chrysosporium)}
VACPDGVHTASNAACCAWFPVLDDIQQLNFHGGQCGAEAEALRMVVFHDSIAISPKLQSQGKFGGG
GADGSIIFFSIETTYHPNIGLDEVVAIQKPFIAKHGVTGDFIAFAGAVGVSNCPGAPQMNFLLGRPE
ATQAAPDGLVPEPFHTIDQVLARMLDAGGFDEIETVWLLSAHSIAAANDVDPTISGLPFDSTPGQFD
SQFFVETQLRGTAFFPGKTGIQGTVMSPKLGEMRLQTDHLFARDSRTACEWQSFVNNQTKLQEDFQF
IFTALSTLGHDMNAMIDCSEVIPAPKPVNFGPSFFPAGKTHADIEQACASTPFPTLITAPGPSASVARIP
PPPSPN

>d1aru_ a.93.1.1 (-) Peroxidase {*Arthromyces ramosus*}

SVTCPPGGQSTSNSQCCVWFDVLDLQTNFYQGSKCESPVVRKILRIVFHDAIGFSPALTAAGQFGGGGA
DGSIIAHSNIELAFPANGGLTDTIEALRAVGINHGVVSGFDLIQFATAVGMNSNCPGSPRLEFLTGRSNSSQ
PSPPSLIPGPGNTVTAILDRMGDAGFSPDEVVDLLAAHSLASQEGLNSAIFRSPLDSTPQVFDTQFYIE
TLLKGTTPGPGSLGFAEELSPFPGEFRMRSDALLARDSRTACRWQSMSTSSNEVMGQRYRAAMAKM
SVLGFDRNALTDCCSDVIPSAVSNNAAPVIPGGTLVDDIEVSCPSEPFPEIATASGPLPSLAPAP

>d1jdra_ a.93.1.1 (A:) Cytochrome c peroxidase, CCP {*Baker's yeast (Saccharomyces cerevisiae)*}

TTPLVHVASVEKGRSYEDFQKVYNAIALKLREDDEYDNYIGYGPVLRVRLAWHTSGTWKHDNTGGS
YGGTYRFKKEFNPNAGLQNGFKFLEPIHKEFPWISSGDLFSLGGVTAVQEMQGPKIPWRCGRVDT
PEDTTPDNGRLPDADKDADYVRTFFQRLNMNDREVALMGAHTLGKTHLKNVSGYEGPWTANNV
FDNSFYLNLLNEDWKLEKNDANNEQWDSKSGYMLPTDYSLIQDPKYLSIVKEYANDQDKFFKDF
SKAFEKLENGITFPKDAPSPFIFKTLEEQGL

>d1mn2_ a.93.1.1 (-) Manganese peroxidase {*Basidiomycetes fungus (Phanerochaete chrysosporium)*}

AVCPDGTTRVSHAACCAFIPLAQLQETIFQNECGQDAHEVIRLTFHDAIAISRSQGPKAGGGADGSML
LFPTVEPNFSANNGIDDSVNNLIPFMQKHNTISAADLVQFAGAVALSNCPCGAPRLEFLAGRPNKTIAA
VDGLIPEPQDSVTKILQRFEDAGGFTPFVSVLLASHSVARANKVDQTIDAAPFDSTPFTFDTQVFLE
VLLKGVGFPGSANNTGEVASPLPLGSGSDTGEMRLQSDFALAHDPRTACIWQGFVNEQAFMAASFR
AAMSKLAVLGHNRNSLIDCSDVVPVPKATGPAMFPASTGPDLELSCPSEFPFTLTTPQGASQSLI
AHCPCDGSMSCPGVQFNGPA

>d1apxa_ a.93.1.1 (A:) Ascorbate peroxidase {*Pea (Pisum sativum)*}

GKSYPTVSPDYQKAIEKAKRKLGRFIAEKKCAPLILRLAWHSAGTFDSKTKTGGPFGTIKHQAELAHG
ANGLDIAVRLLEPIKEQFPVSYADFYQLAGVVAVEITGGPEVFPFHGREDKPEPPPEGRLPDATKGS
DHLRDVFGKAMGLSDQDIVALS GGHTIGAAHKERSGFEGPWTSNPLIFDNSYFTELLTGEKDGLLQL
PSDKALLTDSVFRPLVEKYAADEDVFFADYAEHLKLELGFAEA

>d7atja_ a.93.1.1 (A:) Plant peroxidase {*Horseradish (Armoracia rusticana)*}

QLTPTFYDNPCPNVSNIVRDTIVNELRSDPRIAASILRLHFHDCFVNGCDASILLDNTTSFRTEKDAFG
NANSARGFPVIDRMKAAVESACPRTVSCADLLTIAAQSVTLAGGPSWRVPLGRRDSLQAFDLANA
NLPAPFFTLPLQLKDSFRNVGLNRSSDLVALSGGHTFGKNQCRFIMDRLYNFSNTGLPDPTLNTTYLQ
TLRGLCPLNGNLSALVDFDLRPTIFDNKYVNL EEQKGLIQSDQELFSSPNATDTIPLVRSFANSTQT
FFNAFVEAMDRMGNITPLTGTGQIRLNCRVVN

>d1scha_ a.93.1.1 (A:) Plant peroxidase {*Peanut (Arachis hypogaea)*}

ELSSNFYATKCPNALSTIKSAVNSAVAKEARMGASLLRLHFHDCFVQGCASVLLDDTSNFTGEKTAG
PNANSIRGFEVIDTIKSQVESLCPGVVSCADILAVAARDSVVALGGASWNVLLGRRDSTTASLSSANS
LPAPFFNLSGLISAFSNKGFTTKELVTLGSAHTIGQAQCTAFRTRIYNESNIDPTYAKSLQANCPSVGG
DTNLSPFVDVTPNKFDNAYYINLRNKKGLLHSDQQLFNGVSTDSQVTAYSNNAATFNTDFGNAMIK
MGNLSPLTGTSGQIRTNCRKTN

>d1fhfa_ a.93.1.1 (A:) Plant peroxidase {*Soybean (Glycine max)*}

QLTPTFYRETCPNLFPIVFGVIFDASFTDPRIGASLMRLHFHDCFVQGCDSVLLNNTDTIESEQDAL
PNINSIRGLDVVNDIKTAVENSCPDVSCADILAAEIASVLGGGPGWPVPLGRRDSLANTLANQ
NLPAPFFNLTQLKASFAVQGLNTLDLVTLSGGHTFGRARCSTFINRLYNFSNTGNPDPTLNTTYLEVL
RARCPQATGDNLNLDLSTPDQFDNRYSNLLQLNGLLQSDQELFSTPGADTIPIVNSFSSNQNTF
FSNFRVSMIKMGNIGVLTGDEGEIRLQCNFVNG

>d1bgp_ a.93.1.1 (-) Plant peroxidase {Barley (*Hordeum vulgare*), peroxidase 1}
AEPPVAPGLSFDYFYTQCPRAESIVREFVQEA VRKDIGLAAGLLRLHFHDCFVQGCDA SVLLDGSAT
GPGEQQAPPNLTLP SFAKAVN DIRLERECGAVVSCSDILALAARDSVVVSGGPDYRVPLGRRDS
RSFASTQDVLSDLPGSSNVQSL LALLGRLGLDATDLVTISGGHTIGLAHCSSFEDRLFPRPDPTISPTF
LSRLKRTCPAKGTD RRTVLDVRTPNVFDNKYIDLVNREGLFVSDQDLFTNAITRPIVERFAQSQQD
FFEQFGV SIGKMGQMRVRTSDQGEVRRNC SVRNPGPG

>d1qgja_ a.93.1.1 (A:) Plant peroxidase {Mouse-ear cress (*Arabidopsis thaliana*), peroxidase N}
QLSPDIYAKSCP NLVQIVRKQVAIALKAEIRMAASLIRLHFHDCFVNGCDASLLLDGADSEKLAIPNIN
SARGFEVIDTIKAAVENACPGVVSCADILTLAARDSVVLSSGGPGWRVALGRKDG LVANQNSANNLPSF
FEPLDAIIAKFVAVNLNITDVVALSGAHTFGQAKCAVFSNRLFNF TGAGNP DATLETSLLSNLQTVCP
GGNSNITAPLDRSTTDTFDNNYFKNLLEGKLLSSDQILFSSDLAVNTTKKLV EAYSRSQSLFFRDFT
CAMIRMGNISNGASGEVRTNCRVINN

>d1pa2a_ a.93.1.1 (A:) Plant peroxidase {Mouse-ear cress (*Arabidopsis thaliana*), peroxidase A2}
MQLNATFYSGTCPNASAI VRSTIQALQSDTRIGASLIRLHFHDCFVNGCDASILLDDTGSIQSEKNAG
PNVNSARGFNVVDNIKTAL ENACPGVVSCSDV LALASEASVSLAGGPSWTVLLGRRDSL TANLAGAN
SSIPSPIESLSNITFKFSAVGLNTNDLVALSGAHTFGRARCGVFNNRLFNFSGTG NPDPTLNSTLLSTL
QQLCPQNGSASTITNLDLSTPDAFDNNYFANLQSN DGLLQSDQELFSTTGSSTIAIVT SFASNQTLFFQ
AFAQSMINMGNISPLTGSNGEIRLDCKKVNGS

>g1cxp.1 a.93.1.2 (A;C:) Myeloperoxidase {Human (*Homo sapiens*)}
CPEQDKYRTITGMCNNRRSPTLGASNRA FVRWLP AEYEDGFSLPYGWT PGVKRNGFPVALARAVSN
EIVRFPTDQLTPDQERSLMFMQW GQLLDHDLDFTEPEAXVNCETSCVQQPPCFPLKIPPNDPRIKN
QADCIPFFRSCPACPGSNITIRNQINALTSFVDAS MVYGSEELARNLRNMSNQLG LLAVNQRFQDNG
RALLPFDNLHDDPCLLTNRSARIPCFLAGDTR SSEMPELTSMH TLLLREHNRLATEL KSLNPRWDG
ERLYQEARKIVGAMVQIITYRDYLPVLGPTAMRKYLP TYRSYNDSVDPRIANVFTNAFRYGH TLIQP
FMFRLDNRYQPMENPRVPLSRVFFASWRV VLEGGIDPILRGLMATPAKLN RQNQIAVDEIRERLFE
QVMRIGLDLPALNMQRSDHGLPGYN AWRRFCGLPQPETVGLTVLRNLKLARKLMEQYGT PNN
IDIWMGGVSEPLKRKGRVGPLLACIIGTQFRKLRDGR FWWENEGVFSMQQRQALAQISLPRIICDN
TGITTVSKNNIFMSNSYPRDFVNCSTLPALNLASWREA

>d1eqga1 a.93.1.2 (A:74-583) Prostaglandin H2 synthase {Sheep (*Ovis aries*)}
IWTWLRTTLRPSPSFIHFL LTHGRWLWDFVNATFIRD TLMRLVLTVRSNLIPSPPTYNIAHDYISWE
SFSNVSYTRILPSVPRDCPTPMGT KGKKQLPDAEFLSRRFLLRRKFIPDPQGTNLMFAFFAQHFTH
QFFKTS GKMGPFTKALGHGVDLGHYGDNLERQYQLR LFKDGKLYQMLNGEVYPPSV EEPVLM
HYPRGIPPQSQMAVGQEVFGLLPGLMLYATIWLREHN RVCDLLKAEHPTWGDEQLFQTARLILIGET
IKIVIEEYVQQLSGYFLQLKFDPELLFGAQFYRNRIAMEFNQLYHWHPLMPDSFRVGPQDYSYEQF
LFNTSMLVDYGV EALVDAFSRQPAGRIGGRNIDHHILHVAVDVIKESRVLRLQPFNEYRKRFRGMKP
YTSFQELTGEKEMAAELEELYGDIDALEFY PGLLEKCHPNSIFGESMIEMGAPFSLKGLLGNPICSPE
YWKASTFGGEVGFNLVKTATLKKLVCLNTKTC PYVSFHVP

>d1cvua1 a.93.1.2 (A:74-583) Prostaglandin H2 synthase {Mouse (*Mus musculus*)}
FLTRIKLLLKPTPNTVHYIL THFKGVWNIVNNIPFLRSLIMKYVLT SRSYLIDSPPTYNVHYGYKSWEA
FSNLSYYTRALPPVADDCPTPMGVKGNKELPDSKEVLEKVL RRREFIPDPQGSNMMFAFFAQHF TA
QFFKTDH KRGPFT RGLGHGVDLNHIYGETLDRQHKLRLFKDGKLYQVIGGEVYPTVKDTQVEM
IYPPHIPENLQFAVGQEVFGLVPLMMYATIWLREHQ RVCDILKQEHPEWGD EQLFQTSKLILIGETI

KIVIEDYVQHLSGYHFKLKFDPPELLFNQQFQYQNRIASEFNTLYHWHPLLPDTFNIEDQEYSFKQFLY
NNSILLEHGLTQFVESFTRQIAGRVAGGRNVPIAVQAVAKASIDQSREMKYQSLNEYRKRFLSKPYTTSF
EELTGEKEMAAELKALYSIDIDVMELYPALLVEKPRPDAIFGETMVELGAPFSLKGLMGNPICSPQYW
KPSTFGGEVGFKIINTASISLICNNVKGCPFTSFNVQ
>d1jj2o_a.94.1.1 (O:) Ribosomal protein L19 (L19e) {Archaeon Haloarcula marismortui}
TDLAQKRLAADVLDVGNRVWFNPERQGDIAITREDVRELVEGAIQAKDKKGNRGRARERQ
KKRAKGHQKAGSRKKGAGARQNSKEDWESRIRAQRTKLELRDEGTLSSSQYRDLYDKAGGGEFD
SVADLERYIDA
>d1aa7a_a.95.1.1 (A:) Influenza virus matrix protein M1 {Influenza virus}
MSLLTEVETYVLSIIPSGPLKAEIAQRLEDVFAGKNTDLEVLMEWLKTRPILSPLTKGILGFVFTLTPV
SERGLQRRRFVQNALNGNDPNNMDKAVKLYRKLKREITFHGAKEISLSYSAGALASCMGLIYNRM
GAVTTEVAFGLVCATCEQIADSQ
>d2abk__a.96.1.1 (-) Endonuclease III {Escherichia coli}
MNKAKRLEILTRLRENNPHPTTELNFSSPELLIAVLLSAQATDVSVNKATAKLYPVANTPAAMLELG
VEGVKTYIKTIGLYNSKAENIIKTCRILLEQHNGEVPEDRAALEALPGVGRKTANVVLNTAFGWPTIA
VDTHIFRVCNRTQFAPGKNVEQVEEKLLKVPAEFKVDCHHWLILHGRTYTCIARKPRCGSCIIEDLCE
YKEKVDI
>d1mun__a.96.1.2 (-) Catalytic domain of MutY {Escherichia coli}
MQASQFSAQVLDWYDKYGRKTLPWQIDKTPYKVVWLVSEVMLQQTQVATVIPYFERFMARFPTVTDL
ANAPLDEVLHLWTGLGYYARARNLHKAQQVATLHGKFPETFEVAALPGVGRSTAGAILSLSLGK
HFPILNGNVKRVLRACYAVSGWPGKKEVENKLWSLSEQVTPAVGVERFNQAMMDLGAMICTRSKP
KCSLCPLQNGCIAAANNSWALYPGKKPK
>d1keaa_a.96.1.2 (A:) Thymine-DNA glycosylase {Archaeon Methanobacterium
thermoformicum}
DATNKKRKVFVSTILTFWNTDRRDFPWRHTRDPYVILITEILLRRTTAGHVKKIYDKFFVKYKCFEDI
LKTPKSEIAKDIKEIGLSNQRAEQLKELARVVINDYGGVRPRNRKAILDLPVGVGKYTCAAVMCLAFGK
KAAMVDANFVRVINRYFGGSYENLNYNHKALWELAEITLVPGGKCRDFNLGLMDFSAIICAPRKPKC
EKCGMSKLCSSYYEK
>d1mpga1_a.96.1.3 (A:100-282) 3-Methyladenine DNA glycosylase II (gene alkA or aidA)
{Escherichia coli}
AARPGLRLPGCVDAFEQGVRAILGQLVSVAMAAKLTARVAQLYGERLDDFPEYICFPTPQRLAAADPQ
ALKALGMPLKRAEALIHLANAALEGLPMTIPGDVEQAMKTLQTFPGIGRWTANYFALRGWQAKD
VFLPDDYLIKQRFPGMTPAQIRRYAERWKPWRSYALLHIWYTEGWQPDEA
>d1ko9a1_a.96.1.3 (A:136-323) 8-oxoguanine glycosylase {Human (Homo sapiens)}
DPIECLFSFICSSNNNIARITGMVERLCQAFGPRLIQLDDVITYHGFPQLALAGPEVEAHLRKLGLGYR
ARYVSASARAILEEQGLAWLQLRESSYEEAHKALCILPGVGTKVADCICLMALDKPQAVPVDVHM
WHIAQRDYSWHPPTTSQAKGSPQTNKELGNFFRSLWGPYAGWAQAVLFSADL
>d1gln_1_a.97.1.1 (306-468) Anticodon-binding (C-terminal) domain of glutamyl-tRNA
synthetase (GluRS) {Thermus thermophilus}
DLEKLRWMNGKYIREVLSLEEVAERVKPFLREAGLSWESEAYLRRAVELMRPRFDTLKEFPEKARY
LFTEDYPVSEKAQRKLEEGPLLLKELYPRLRAQEEWTEAALEALLRGFAAEKGVKLGQVAQPLRAAL
TGSLETPGLFEILALLGKERALRRLERALA
>d1rlr_1_a.98.1.1 (10-221) R1 subunit of ribonucleotide reductase, N-terminal domain
{Escherichia coli}

RDGSTERINLDKIHRVLDWAAEGLHNVSISQVELRSHIQFYDGIKTSDIHETIIKAAADLISRDPDYQ
YLAARLAIFHLRKKAYGQFEPPALYDHVVKMVEMGKYDNHLEDYTEEEFKQMDTFIDHDRDMTF
SYAAVKQLEGKYLQNRVTGEIYESAQFLYLVAACLSNYPRETRLQYVKRFYDAVSTFKISLPTPIMS
GVRTPTRQ

>d1dnpa1 a.99.1.1 (A:201-469) FAD-binding (C-terminal) domain of DNA photolyase
{*Escherichia coli*}

PVEEKAAIAQLRQFCQNGAGEYEQRDFPAVEGTSRLSASLATGGLSPRQCLHRLLAEQPQALDGGGA
GSVWLNELIWREFYRHLITYHPSLCKHRPFIAWTDRVWQSNPAHLQAWQEGKTYPIVDAAMRQ
LNSTGWMHNRLRMITASFLVKDLLIDWREGERYFMSQLIDGDLAANNGGWQWAASGTDAAPYF
RIFNPTTQGEKFDHEGEFIRQWLPELRDVPKVVHEPWKWAQKAGVTLDYPQPIVEHKEARVQTL
AAYEAARK

>d1iqra1 a.99.1.1 (A:172-416) FAD-binding (C-terminal) domain of DNA photolyase
{*Thermus thermophilus*}

LPLPEPGEEAALAGLRAFLEAKLPRYAEERDLGEGGSRLSPYFALGVLSPLAAWEAERRGGEGA
RKWVAELLWRDFSYHLLYHFPWMAERPLDPRFQAFPWQEDEALFQAWYEGKTYVPLVDAAMREL
HATGFLSNRARMNAAQFAVKHLLLPWKRCEEAFRHLLLDGDRAVNLQGWQWAGGLGVDAAPYFR
VFNPVLQGERHDPEGRWLKRWAPEYPSYAPKDPVVDLEEARRRYLRRLARD

>d1qnf_1 a.99.1.1 (205-475) FAD-binding (C-terminal) domain of DNA photolyase {*Anacystis
nidulans*}

PVEPGETAARIARLQEFCDRAIADYDPQRNFPAEAGTSGLSPALKFGAIGIRQAWQAASAHALSRSD
ARNRIRVWQQELAWREFYQHLYHFPSLADGPYRSLWQQFPWENREALFTAWTQAQTYPIVDA
MRQLTETGWMHNRCRMIVASFLTDLIIDWRRGEQFFMQHLVDGDLAANNGGWQWSASSGMDP
KPLRIFNPASQAKKFDATATYIKRWLPELRHVHPKDLISGEITPIERRGYPAPIVNHNLKQKFKALY
NQLKAAI

>d2pgd_1 a.100.1.1 (177-473) 6-phosphogluconate dehydrogenase (6PGD) {*Sheep (Ovis
orientalis aries)*}

GAGHFVKMVHNGIEYGDMLICEAYHLMKDVGLGHEKEMAKAFEWKNKTELDSFLIEITASILKFQ
DADGKHLPLKIRDSAGQKGTGKWTASALEYGVPTLIGEAVFARCLSSLKDERIQASKKLKGPQNI
FEGDKKSFLDIRKALYASKIISYAQGFMLLRQAATEFGWTLNYGGIALMWRGGCIIRSVFLGKIKDA
DRNPGQLNLLDDFFKSAVENCQDSWRRAISTGVQAGIPMPCFTTALSFYDGYRHAMLPANLIQAQ
RDYFGAHTYELLAKPGQFIHTNWTGHGG

>d1pgja1 a.100.1.1 (A:179-478) 6-phosphogluconate dehydrogenase (6PGD) {*Trypanosoma
brucei*}

GAGSCVKMYHNSGEYAILQIWGEVFDILRAMGLNNDVAVLEDWKSKNFLKSYMLDISIAAARAK
DKDGSYLTEHVMDRIGSKGTGLWSAQEALIGVPAPSLNMAVVSQRFTMYKTERQANASNAPGITQS
PGYTLKNKSPSGPEIKQLYDSVCIAIISCYAQMFCQLREMDKVHNFGLNLPATIAATFRAGCILQGYLLK
PMTEAFEKNPNISNLMCAFQTEIRAGLQNYRDMVALITSKLEVSIPVLSASLNYVTAMFTPTLKYGQL
VSLQRDVFGRHGYERVDKDGRESFQWPELQ

>d1qnga1 a.100.1.2 (A:308-595) Acetohydroxy acid isomeroeductase, ketoacid
reductoisomerase (KARI) {*Spinach (Spinacia oleracea)*}

LEQEYKSDIFGERGILLGAVHGIVECLFRRYTESGMSEDLAYKNTVECITGVISKTISTKGMALALYNLS
EEGKKDFQAAYSASYPSMDILYECYEDVASGSEIRSVVLGRRFYEKEGLPAFPMGKIDQTRMWKV
GEKVRSVRPAGDLGPLYPFTAGVYVALMMAQIEILRKKGHSYSEIINESVIEAVDSLNPFMHARGVSF
MVDNCSTTARLGRKWAPRFDYILSQALVAVDNGAPINQDLISNFLSDPVHEAIGVCAQLRPSVDIS

VTADADFVRPELRQA

>d1f0ya1 a.100.1.3 (A:204-302) Short chain L-3-hydroxyacyl CoA dehydrogenase {Human (Homo sapiens)}

GFIVNRLLPYLMFAIRLYERGDASKEDIDTAMKLGAGYPMGPFELLDYVGLDTTKFIVDGWHEMD
AENPLHQSPSLNKLVAENKFGKKTGEGFYKYK

>d3hdha1 a.100.1.3 (A:204-302) Short chain L-3-hydroxyacyl CoA dehydrogenase {Pig (Sus scrofa)}

GFIVNRLLPYLVIEAVRLYERGDASKEDIDTAMKLGAGYPMGPFELLDYVGLDTTKFIIDGWHEMDS
QNPLFQSPAMNKLVAENKFGKKTGEGFYKYK

>d1dlja1 a.100.1.4 (A:197-294) UDP-glucose dehydrogenase (UDPGDH), middle domain {Streptococcus pyogenes}

ASEAEAVKLFANTYLALRVAYFNELDTYAESRKLNSHMIIQGISYDDRIGMHYNNPSFGYGGYSLPKD
TKQLLANYNIPQTLIEAIVSSNNVRKSYI

>d1bg6_1 a.100.1.5 (188-359) N-(1-D-carboxylethyl)-L-norvaline dehydrogenase {Arthrobacter, strain 1c}

NVLHTSLTNVNAVHPLPTLLNAARCESGTPFQYYLEGITPSVGLAEKVDAERIAIAKAFDLNVPSV
CEWYKESYGQSPATIEAVQGNPAYRGIAGPINLNTRYFFEDVSTGLVPLSELGRAVNVPTPLIDAVLD
LISSLIDTDFRKEGRTLEKLGLSGLTAAGIRSAVE

>d1evya1 a.100.1.6 (A:189-357) Glycerol-3-phosphate dehydrogenase {Trypanosome (Leishmania mexicana)}

DRSFVCWATTDTVGCEVASAVKNVLAIGSGVANGLGMGLNARAALIMRGLLEIRDLTAAALGGDGS
FGLAGLGLDLQTCSELSRNFTVGGKLGKGLPIEEIQRRTSKAVAEGVATADPLMRLAKQLKVKMPLCH
QIYEIVYKKKNPRDALADLLSCGLQDEGLPPLFK

>d1ks9a1 a.100.1.7 (A:168-291) Ketopantoate reductase PanE {Escherichia coli}

NIRAEWLRKLAVNVCVINPLTAIWNCPNGELRHHPQEIMQICEEVAAVIEREGHHTSAEDLRDYVMQ
VIDATAENISSMLQDIRALRHTEIDYINGFLLRRARAHGIAVPENTRLFEMVKKRKESE

>d1utg_ a.101.1.1 (-) Uteroglobin {Rabbit (Oryctolagus cuniculus)}

GICPRFAHVIEENLLGTPSSYETSLKEFEPDDTMKDAGMQMKKVLDSLPTTRENIMKLTKEIVKSP
LCM

>d1ccd_ a.101.1.1 (-) Clara cell 17kDa protein {Rat (Rattus norvegicus)}

SSDICPGFLQVLEALLGSESNEYAALKPFNPASDLQNAQTQLKRLVDTLPQETRINIVKLTKEILTSPL
CEQDLRV

>d1utra_ a.101.1.1 (A:) Clara cell 17kDa protein {Rat (Rattus norvegicus)}

ICPGFLQVLEALLGSESNEYAALKPFNPASDLQNAQTQLKRLVDTLPQETRINIVKLTKEILTSPLC

>d1gai_ a.102.1.1 (-) Glucoamylase {Aspergillus awamori, variant x100}

ATLDSWLSNEATVARTAILNNIGADGAWVSGADSGIVVSPSTDNPDYFYTWTRDSGLVIKTLVDLF
RNGDTDLLSTIEHYISSQAIQGVSNPSGDLSSGGLGEPKFNVDYATYGSWGRPQRDGPALRATAMI
GFGQWLLDNGYTSAAATEIVWPLVRNDLSYVAQYWNQTYDLWEEVNGSSFFTIQVHRALVEGSAF
ATAVSSCSWCDSQAPQILCYLQSFWTGSYILANFDSRSRSGKDTNTLLGSIHTFDPEAGCDDSTFQPC
SPRALANHKEVVDVFRSITLNDGLSDSEAVAVGRYPEDSYNGNPWFCLTAAAAEQLYDALYQWDK
QGSLEITDVSLDFKALYGAATGTYSSTYSYSSIVSAVKTFADGFVSIVETHAASNGSLSEQFDKSDG
DELSARDLTWSYAALLTANNRRNSVPPSWGETSASSVPGTCAATSASGTYSSTVTSWPSIVATG

>d1ayx_ a.102.1.1 (-) Glucoamylase {Baker's yeast (Saccharomyces fibuligera)}

AYPSFEAYSNYKVDRTDLETFLDKQKEVSLYLLQNIAYPEGQFNNGVPGTVIASPSTSNPDYQWT

RDSAITFLTVLSELEDNNFNNTTLAKAVEYYINTSYNLQRTSNPSPGSFDDENHKGLGEPKFNTDGSAYT
GAWGRPQNDGPALRAYAISRYLNDVNSLNEGKLVLTDSGDINFSSTEDIYKNIIPDLEYVIGYWDST
GFDLWEENQGRHFFFTSLVQQKALAYAVDIAXSFDDGDFANTLSSTASTLESYLSGSDGGFVNTDVNHI
VENPDLLQQNSRQGLDSATYIGPLLTHDIGESSSTPFVDVNEYVLQSYLLEDNKDRYSVNSAYSAG
AAIGRYPEDVYNGDGSSEGNPWFLATAYAAQVPYKLAYDAKSASNDITINKINYDFFNKYIVDLSTINS
AYQSSDSVTIKSGSDEFNTVADNLVTFGDSFLQVILDHINDDGSLNEQLNRYTGYSTGAYSLTWSSGA
LLEAIRLRNKVKALA

>d1cem_ a.102.1.2 (-) CelA cellulase {Clostridium thermocellum}

AGVPFNTKYPYGPSTSIADNQSEVTAMLKAEWEDWKSKRITSNGAGGYKRVQRDASTNYDTVSEGM
GYGLLLAVCFNEQALFDDLYRYVKSHFNGLMHWHIDANNVTSHDGGDGAATDADEDIALALIF
ADKQWGSSGAINYGQEARTLINNLNHCVEHGSYVLKPGDRWGGSSVTNPSYFAPAWYKVYAQYTG
DTRWNQVADKCYQIVEEVKKYNNGTGLVPDWCTASGTPASGQSYDYKYDATRYGWRTAVDYSWFG
DQRAKANCDMLTKFFARDGAKGIVDGYTIQGSKISNNHNASFIGPVAASMTGYDLNFAKELYRETV
AVKDSEYYGYYGNSLRLLTLLYITGNFPNPLSDL

>d1tf4a1 a.102.1.2 (A:1-460) Endo/exocellulase:cellobiose E-4, N-terminal domain
{Thermomonospora fusca}

EPAFNYAEALQKSMFFYEAQRSGKLPENNRVSWRGDSGLNDGADVGLDLTGGWYDAGDHVKFGFP
MAFTATMLAWGAIESPQYIRSGQMPYLKDNLRWVNDYFIKAHPSPNVLYVQVGDGDADHKWWG
PAEVMMPERPSFKVDPSCPGSDVAAETAAMAASSIVFADDDPAYAATLVQHAKQLYTFADTYRQVY
SDCVPAGAFYNSWSGYQDELVWGAYWLYKATGDDSYLAKAEYDYDFLSTEQQTDLRSYRWTIAWD
DKSYGTYVLLAKETGKQKYIDDANRWLDYWTVGVNGQRPVYSPGGMAVLDTWGALRYAANTAFVA
LVYAKVIDDPVRKQRYHDFAVRQINYALGDNPRNSSYVVGFGNNPPRNPHHRTAHGSWTDSIASPAE
NRHVLYGALVGGPGSPNDAYTDDRQDYVANEVATDYNAGFSSALAMLVEEYGGTPLADFPPTTEEPD
G

>d1clc_1 a.102.1.2 (135-575) CelD cellulase {Clostridium thermocellum}

AMNVYEDAFKTMALGMYLRLRCGTSSVSATYNGIHSHGPGCHTNDAYLDYINGQHTKKDSTKGWHDA
GDYNYKVVNAGITVGSMLFLAWEHFKDQLEPVALEIPEKNNSIPDFLDELKYEIDWILTMQYPDGSGR
VAHKVSTRNFGGFIMPENEHDERFFVPWSSAATADFMAMTAMAARIFRPYDPQYAEKCINAAKVSY
EFLKNNPANVFANQSGFSTGEYATVSDADDRLWAAAEMWETLGDEEYLRDFENRAAQFSKKIEAD
FDWDNVANLGMFTYLLSERPGKNPALVQSIKDSLLSTADSIVRTSQNHGYGRTLGTYYWGCGNTV
VRQTMILQVANKISPNDYVNAALDAISHVFGGRNYNRSYVTGLGINPPMNPDRRSGADGIWEPW
PGYLVGGGWPGPKDWVDIQDSYQTNEIAINWNAALIYALAGFVNYN

>d1faea_ a.102.1.2 (A:) Processive endocellulase CelF (Cel48F) {Clostridium cellulolyticum}

ASSPANKVYQDRFESMYKIKDPANGYFSEQGIPIYSIETLMVEAPDYGHVTTSEAMSYMWLEAM
HGRFSGDFTGFDKSWSVTEQYLIPTEKQPNSTMSRYDANKPATYAPEFQDPSKYPSPLDTSQPVGR
DPINSQLTSAYGTSMLYGMHWILDVDNWyGFGARADGTSKPSYINTFQRGEQESTWETIPQPCWDE
HKFGGQYGFLLDFTKDTGTPAKQFKYT NAPDADARAVQATYWADQWAKEQGKSVSTSVGKATKMG
DYLRYSFFDKYFRKIGQPSQAGTGYDAAHYLLSWYAWGGGIDSTWSWIIGSSHNHFGYQNPFAAW
VLSTDANFKPKSSNGASDWAKSLDRQLEFYQWLQSAEGAIAGGATNSWNGRYEAVPSGTSTFYGMG
YVENPVYADPGSNTWFGMQVWSMQRVAELYKTDARAKLLDKWAKWINGEIKFNADGTFQIPS
TIDWEGQPDTWNPTQGYTGANLHVKVNYGTDLGCASSLANTLTYAAKSGDETSRQNAQKLLD
AMWNNYSDSKISTVEQRGDYHRFLDQEVFVPAGWTGKMPNGDVIKSGVKFIDIRSKYKQDPEWQ
TMVAALQAGQVPTQRLHRFQAQSEFAVANGVYAILFPD

>d1fp3a_ a.102.1.3 (A:) N-acyl-D-glucosamine 2-epimerase {Pig (Sus scrofa)}

MEKERETLQAWKERVQELDRVMAFWLEHSHDREHGGFFTCLGRDGRVYDDLKYVWLQGRQVW
MYCRLYRKLRFHRPELDDAAKAGGEFLLRHARVAPPEKKCAFVLTRDGRPVKVQRSIFSECFYTMA
MNELWRVTAEARYQSEAVDMMDQIVHWVREDPSGLGRPQLPGAVASESMAMPMLLCLVEQLGE
EDEELAGRYAQLGHCARRILQHVQRDQAVLENVSEEDGEELSGCLGRHQNPGHALEAGWFLLRH
SSRSGDAKLRAHVIDTFLLLPFRSGWDADHGGLFYFQDADGLCPTQLEWAMKLWVPHSEAMIAFL
MGYSESGDPALLRLFYQVAEYTFRQFRDPEYGEWFGYLNREGKVALTIKGGPFKGC FHVPRCLAMCE
EMLSALLSRLA

>d1h54a1 a.102.1.4 (A:269-753) *Lactobacillus maltose phosphorylase*, central domain
{*Lactobacillus brevis*}

DTQESLTAAMHQLSDKVAQSSYEDLLNAHTAIWAQRWEKSDVVIKGDDESQQGIRFNLFLFSTYYG
EDARLNIGPKGFTGEKYGGATYWDTEAFAPVYLGITDPKVTRNLLMYRYKQLDGAYINAQEQLKG
ALFPMVTFDGI ECHNEWEITFEEIHRNGDIAFAIYNYTRYTGDDSYVLHEGAKVLTEISRFWADR VH
FSKRNNQYMIHGVTGADEYENNVNNDNWDNMLAQWTLKYTLEILGKVDQDTAKQLDVSDEEKT
WQDIVDRMYLPYDKDLNIFVQHDGFLDKDIEPVSSIPADQRPINQNWSDKILRSPYIKQGDV LQGI
WDFIDDYTPEQKANFDYEP LTVHESLSPAIHSVLAADLHYEDKAVELYSRTARLDLDNYNNDTT
DGLHITSMTGAWIAVVQGFAGMRVRDQGLHYAPFLPKTWTSTYFRQVFRDLIEVSVHADGPHFKL
LSGEPLTIDVAGAAAAAAAA

>d1dl2a_ a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {*Baker's yeast*
{*Saccharomyces cerevisiae*}}

GAGEMRDRIESMFLESWRDYSKHGWYDVYGP I EHTSHNMPRGNQPLGWIIVDSVDTLMLMYNSS
TLYKSEFEAEIQRSEHWINDVLD FIDAEVNVFETTIRMLGGLLSAYHLSVLEVGNKTVYLNKAIDL
GDRLALAF LSTQTGIPYSSINLHSGQAVKNHADGGASSTAEFTTLQMEFKYLAYLTGNRTY WELVER
VYEPLYKNNDLLNTYDGLVPIYTFPDTGKFGASTIRFGSRGDSFYEYLLKQYLLTHE TLYYDLYRKSME
GMKKHLLAQSKPSSLWYIGEREQGLHGQLSPKMDHLVCFMGGLLASGSTEGLSIHEARRRPF FSKSD
WDLAKGITDTCYQMYKQSSSGLAPEIVVFNDGNIKQDGWWRSSVGDFFVKPLDRHNLQRPETVESI
MFMYHLSHDHKEYREWGA EIATSF FENTCVCDCNDPKLRRFTSLSDCITLPTKKSNNMESFWLAETL
KYLYILFLDEFDLTKVFNTEAHPFPVLDEEILKSQSLTTGWSL

>d1hcua_ a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {*Trichoderma*
reesei}

KRGSPNPTRAAAVKAAFQTSWNAYHHFAFP HDDLHPVSNSFDDERNGWGSSAIDGLDTAILMGDA
DIVNTILQYVPQINF TTTAVANQGSSVFETNIRYLGGLLSAYDLLRGP FSSLATNQT LVNSLLRQAQTL
ANGLKVAFTTPSGVPDPTVFFNPTVRRSGASSNNVAEIGSLVLEWTRLSDLTG NPYAQLAQKGESYL
LNPKGSP EAWPGLIGTFVSTSNGT FQDSSGSWSGLMDSFYEYLIKMYLYDPVAF AHYKDRWVLGAD
STIGHLGSHPSTRKDLTFLSSYNGQSTSPNSGHLASFGGGNFILGGILLNEQKYIDFGIKLASSYFGTYT
QTASGIGPEGFAWVDSVTGAGGSPSSQSGFYSSAGFWVTAPYYILRPETLESLYAYRVTGDSKWQD
LAWEALSAIEDACRAGSAYSSINDVTQANGG GASDDMESFWFAEALKYAYLIFA EESDVQVQATGGN
KFVFNTEAHPFSIRS

>d1krea_ a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {*Fungus*
{*Penicillium citrinum*}}

SNQAKADAVKEAFQHAWNGYMKYAFPHDELTPVSNGHADSRNGWGASAVDALSTAVIMGKADV
NAILEHVADIDFSKTSDTVSLFETTIRYLAGMLSGYDLLQGP AKNLVDNQLDIDGLLDQSRNLADV LK
FAFDTPSGVPYNNINITSHGNDGATTNGLAVTGTLVLEWTRLSDLTGDEEYAKLSQKAESYLLKPQPS
SSEFPGLVGSSININDGQFADSRVSWNGGDSFYEYLIKMYVYDPKR FETYKDRWVLAESTIKHL
KSHPKSRPDLTFLSSYSNRNYDLSSQHLCFDGGSFLLGGTVLDRQDFIDFGLELVDGCEATYNSTLTK

IGPDSWGWDPKKVPSDQKEFYEKAGFYISSGSYVLRPEVIESFYAHRVTGKEIYRDVWVWNAFVAIN
STCRTDSGFAAVSDVNKANGGSKYDNQESFLFAEVMKYSYLAHSEDAAWQVQKGGKNTFVYNTEA
HPISVAR

>d1fo3a_ a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {Human (Homo sapiens)}

QGPVHLNRYRQKGVLDVFLHAWKGYRKFVWGHDELKPVSRSEWFGGLTLIDALDTMWILGLRKE
FEEARKWVSKKLHFEDVDVNLFESTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKIPY
SDVNIGTGVAHPPRWTSDSTVAEVTSIQLEFRELSRLTGDKKFQEAVEKVTQHIHGLSGKKDGLVPM
FINTHSGLFTHLGVFTLGARADSYEYLLKQWIQGGKQETQLLEDYVEAIEGVTRHLLRHSEPSKLT
VGELAHGRFSAKMDHLVCFPLPGTLALGVYHGLPASHMELAQELMETCYQMNRMETGLSPEIVHF
NLYPQPGRRDVEVKPADRHNLRLPETVESLFYLYRVVTGDRKYQDWGWEILQSFSRFRTRVPSGGYSSI
NNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLDAYVFNTEAHPLPIWT

>d1qaza_ a.102.3.1 (A:) Alginate lyase A1-III {Sphingomonas sp., A1}

GSHPFDAQVVKDPTASYVDVKARRTFLQSGQLDRLKAALPKEYDCTTEATPNPQQGEMVIPRRYL
SGNHGPNPDYEPVVTLYRDFEKISATLGNLYVATGKPVYATCLLNMLDKWAKADALLNYDPKSQS
WYQVEWSAATAAFALSTMMAEPNVDTAQRERVVKNLNRVARHQTSFPGGDTSCNNHNSYWRGQ
EATHIGVSKDDELFRWGLGRYVQAMGLINEDGSFVHEMTRHEQSLHYQNYAMLPLTMIAETASRQG
IDLYAYKENGRIHSARKFVFAAVKNPDLIKKYASEPQDTRAFKPGRGDLNWIEYQRARFGFADELGF
MTVPIFDPRTGGSATLLAYKP

>d1cb8a1 a.102.3.2 (A:26-335) Chondroitinase AC {Pedobacter heparinus (Flavobacterium heparinum)}

GTAELIMKRVMLDLKKPLRNMDKVAEKNLNTLQPDGSWKDVPYKDDAMTNWLPNNHLLQLETII
QAYIEKDSHYGDDKVFDQISKAFKYWYSDPKSRNWWHNEIATPQALGEMILMRYGKKPLDEAL
VHKLTERMKRGEPEKKTGANKTDIALHYFYRALLTSDEALLSFAVKELFYPVQFVHYEGLQYDYSY
LQHGPQLQISSYGAVFITGVLKLANYVRDTPYALSTEKLAIFSKYYRDSYLKAIRGSYMDFNVEGRGVS
RPDILNKKAEKKRLLVAKMIDLKHTTEEWADAIARTDSTVAAGYK

>d1egua1 a.102.3.2 (A:171-540) Hyaluronate lyase {Streptococcus pneumoniae}

KDYTDRLDDWNGIAGNQYYSKNDQMAKLNQELEGKVADSLSSISSQADRIYLWEKFSNYKTSA
NLTATYRKLEEMAKQVTNPSSRYQDETVVRTVRDSMEWMHKKHVYNSEKSIVGNWWDYEIGTPR
AINNTLSLMKEYFSDEEIKKYTDVIEKFVPDPEHFRKTTDNPFKALGGNLVDMGRVKVIAGLLRKDD
QEISSTIRSIEQVFKLVDQGEFYQDGSYDHTNVAYTGAYGNVLIDGLSLLPVIQKTKNPIDKDKMQ
TMYHWIDKSFAPLLVNGELMDMSRGRSISRANSEGHVAAVEVLRGIHRIADMSEGETKQRLQSLVKT
IVQSDSYDVFKNLKYKDISLMQSLSDAGVASVPR

>d1f1sa1 a.102.3.2 (A:249-619) Hyaluronate lyase {Streptococcus agalactiae}

EDNFTKLLDKWVDVTIGNYVYDTNDSNMQKLNQKLEDTNAKNIEAIKLSNRTFLWKDLNLNN
SAQLTATYRRELDLAKQITNPHSTIYKNEKAIRTVKESLAWLHQNFYNVNDIEGSANWWDIEIGV
PRSITGTLMLNMYFTDAEIKTYTDPIEHFVPAEYFRKTLVNPFKALGGNLVDMGRVKIIEGLLRKD
NTIIEKTSLSLKNLFTTATKAEGFYADGSYDHTNVAYTGAYGNVLIDGLTQLLPVIQKTKNPIDKDKMQ
MVYKWINQSFLPLIVKELMDMSRGRSISRANSEGHVAAVEVLRGIHRIADMSEGETKQRLQSLVKT
IITSNKFYVFNLLKSYSDIANMKNLNDSTVATKP

>d5eau_1 a.102.4.1 (21-220) 5-Epi-aristolochene synthase, N-terminal domain {Tobacco (Nicotiana tabacum)}

SPSLWGDQFLSFSIDNQVAEKYAKEIEALKEQTRNMLLATGMKLADTLNLIDTIERLGISYHFEKEID
DILDQIYNQNSCNDLCTSAQFRLLRQHGFNISPEIFSKFQDENGKFKESLASDVLGLLNLYEASHV

RTHADDILEDALAFSTIHLESAAPHLKSPLREQVTHALEQCLHKGVPRVETRFFISSIYDKEQS
>d2sqca1 a.102.4.2 (A:8-36,A:308-630) Squalene-hopene cyclase {Alicyclobacillus
acidocaldarius}

APAYARTLDRAVEYLLSCQKDEGYWWGPLXISPVWDTGLAVLALRAAGLPADHDRLVKAGEWLLD
RQITVPGDWAVKRPNLKPGGFAFQFDNVYYPDVCDTAVVVWALNTLRLPDERRRRDAMTKGFRWI
VGMQSSNGGWGAYDVDNTSDLPNHIPFSDFGEVTDPPSEDVTAHVLECFGSFGYDDAWKVIRRAVE
YLKREQKPDGWSWFRWGVNLYGTGAVVSALKAVGIDTREPYIQKALDWVEQHQNPDGGWGEDCR
SYEDPAYAGKGASTPSQTAWALMALIAGGRAESEAAARRGVQYLVETQRPDGGWDEPYTGTGFPD
FYLGYTMYRHVFPTLALGRYKQAIER

>d2sqca2 a.102.4.2 (A:37-307) Squalene-hopene cyclase {Alicyclobacillus acidocaldarius}
LSNVTMEAEYVLLCHILDRVDRDRMEKIRRYLLHEQREDGTWALYPGGPPDLDTTIEAYVALKYIGM
SRDEEPMQKALRFIQSQGGIESSRVFTRMWLALVGEYPWEKVPMPPEIMFLGKRMPLNIYEFGSW
ARATVVALSIVMSRQPVFPLPERARVPELYETDVPPRRRGAKGGGWIFDALDRALHGYQKLSVHPF
RRAAEIRALDWLLERQAGDGSWGGIQPPWFYALIALKILDMTQHPAFIKGWEGLELYGVELDYGGW
MFQAS

>d1d8db_ a.102.4.3 (B:) Protein farnesyltransferase, beta-subunit {Rat (Rattus norvegicus)}
PVWSEPLYSLRPEHARERLQDDSVETVTSIEQAKVEEKIQEVFSSYKFNHLVPRLLVQREKHFHYLK
RGLRQLTDAYECLDASRPWLCYWILHSLELLDEPIPQIVATDVCQFLELCQSPDGGFGGGPGQYPHLA
PTYAAVNALCIIGTEEAYNVINREKLLQYLYSLKQPDGSFLMHVGGVEVDVRSAYCAASVASLTNIITPDL
FEGTAEWIARCQNWEGGIGGVPMEAHGGYTFCGLAALVILKKERSLNLKSLQWVTSRQMRFEGG
FQGRCNKLVDCYSFWQAGLLPLLHRALHAQGDPALSMHWMFHQQALQEYILMCCQCPAGLLD
KPGKSRDFYHTCYCLSGLSIAQHFGSGAMLHDVVMGVPENVLQPTHVPVYNIGPDKVIQATTHFLQKP
VPGF

>d1dceb_ a.102.4.3 (B:) Rab geranylgeranyltransferase, beta subunit {Rat (Rattus
norvegicus)}

TQQKDVTIKSDAPDTLLLEKHADYIASYGSKKDDYEYCMSEYLRMSGVYWGLTVMDLMGQLHRMN
KEEILVFIKSCQHECGGVSASIGHDPHLLYTLASVQILTLYDSIHVINVDKVVAYVQSLQKEDGSFAGDI
WGEIDTRFSFCAVATLALLGKLDAINVEKAIEFVLSNMFDGGFGCRPGSESHAGQIYCTGFLAITSQ
LHQVNSDLLGWLWCERQLPSGGLNGRPEKLPDVCYSWWVLASLKIIGRLHWIDREKLRSFILACQD
EETGGFADRPGDMVDPFHFLFGIAGLSLLGEEQIKPVPSPVFCMPEEVLQRVNVQPELVS

>d1c3d_ a.102.4.4 (-) C3D, a C3 fragment and ligand for complement receptor 2 {Human
(Homo sapiens)}

MLDAERLKHILVTPSGAGEQNMIGMTPTVIAVHYLDETEQWEKFGLEKRQGALELIKKGYTQQLAF
RQPSSAAFAFVKRAPSTWLTAYVVKVFSLAVNLIADSQVLCGAVKWLILEKQKPDGVFQEDAPVIHQ
EMIGGLRNNNEKDMALTAFLISLQEAKDICEEQVNSLPGSITKAGDFLEANYMNLQRSYTVAIAGYA
LAQMGRLLKGPLLNKFLTTAKDKNRWEDPGKQLYNVEATSYALLALLQLKDFDFVPPVVRWLNEQR
YYGGGYGSTQATFMVFQALAQYQKDAP

>d1qqfa_ a.102.4.4 (A:) C3D, a C3 fragment and ligand for complement receptor 2 {Rat
(Rattus norvegicus)}

CGEQNMIGMTPTVIAVHYLDQTEQWEKFGLEKRQEALIELIKKGYTQQLAFKQPISAYAAFNNRPPST
WLTAYVSRVFSLANLIAIDSQVLCGAVKWLILEKQKPDGVFQEDGPVIHQEMIGGFRNTKEADVSLT
AFVLIALQEARDICEGQVNSLPGSINKAGEYLEASYLNLQRPYTVAIAGYALALMNKLEEPYLTKFLNT
AKDRNRWEEPQQQLYNVEATSYALLALLLKLDFDSVPPVVRWLNDERYYGGGYGSTQATFMVFQAL
AQYRADV

>d1csc_ a.103.1.1 (-) Citrate synthase {Chicken (Gallus gallus)}
ASSTNLKDVLAALIPKEQARIKTFRQQHGTTALGQITVDMSYGGMRGMKGLVYETSVLDPDEGIRFR
GFSIPECQKLLPKGGXGGEPLPEGLFWLLVTGQIPTGAQVSWLSKEWAKRAALPSHVVTMLDNFPT
NLHPMSQLSAAITALNSESNFARAYAEGILRTKYWEMVYESAMDLIAKLPVAAKIYRNLYRAGSSIG
AIDSKLDWSHNFTNMLGYTDAQFTELMRLYLTIHSDHEGGNVAHTSHLVGSALS DPYLSFAAAMN
GLAGPLHGLANQEVLGWLALQKAXXXAGADASLRDYIWNTLN SGRVVPGYGHAVLRKTDPRYTC
QREFALKHLPDPMFKLVAQLYKIVPNVLEQGAAANPWPNVDAHSGVLLQYYGMTEMNYYTVLF
GVSRALGVLAQLIWSRALGFPLERPKSMSTDGLIAL

>d1csh_ a.103.1.1 (-) Citrate synthase {Chicken (Gallus gallus)}
STNLKDVLAASLIPKEQARIKTFRQQHGNTAVGQITVDMSYGGMRGMKGLIYETSVLDPDEGIRFRGFS
IPECQKLLPKAGGGEPLPEGLFWLLVTGQIPTPEQVSWWSKEWAKRAALPSHVVTMLDNFPTNLH
PMSQLSAAITALNSESNFARAYAEGINRTKYWEFVYEDAMDLIAKLPVAAKIYRNLYRAGSSIG
AIDSKLDWSHNFTNMLGYTDPQFTELMRLYLTIHSDHEGGNVAHTSHLVGSALS DPYLSFAAAMN
GLAGPLHGLANQEVLWLSQLQKDLGADASDEKLRDYIWNTLN SGRVVPGYGHAVLRKTDPRYTC
QREFALHKLPSDPMFKLVAQLYKIVPNVLEQKAKNPWPNVDAHSGVLLQYYGMTEMNYYTVLFG
VSRALGVLAQLIWSRALGFPLERPKSMSTAGLEKLSAGG

>d2cts_ a.103.1.1 (-) Citrate synthase {Pig (Sus scrofa)}
ASSTNLKDLADLIPKEQARIKTFRQQHGNTAVGQITVDMYGGMRGMKGLVYETSVLDPDEGIRFR
GYSIPECQKMLPKAKGGEPLPEGLFWLLVTGQIPTEEQVSWLSKEWAKRAALPSHVVTMLDNFPT
NLHPMSQLSAAITALNSESNFARAYAEGIHRTKYWELIYEDCMDLIAKLPVAAKIYRNLYREGSSIG
AIDSKLDWSHNFTNMLGYTDAQFTELMRLYLTIHSDHEGGNVAHTSHLVGSALS DPYLSFAAAMN
GLAGPLHGLANQEVLVWLTQLQKEVGKDVSDKLRDYIWNTLN SGRVVPGYGHAVLRKTDPRYTC
QREFALKHLPDPMFKLVAQLYKIVPNVLEQKAKNPWPNVDAHSGVLLQYYGMTEMNYYTVLFG
VSRALGVLAQLIWSRALGFPLERPKSMSTDGLIKLVDSK

>d1aj8a_ a.103.1.1 (A:) Citrate synthase {Archaeon Pyrococcus furiosus}
LAKGLEDVYIDQTNICYIDGKEGKLYYRGYSVEELAEELSTFEEVVYLLWVGKLPSELENFKKELAK
SRGLPKEVIEIMEALPKNTHPMGALRTIISYLGNIIDSGDIPVTPPEVYRIGISVTAKIPTIVANWYRIK
NGLEYVPPKEKLSHAANFLYMLHGEEPPKEWEKAMDVALILYAEHEINASTLAVMTVGSTLSDYSSA
ILAGIGALKGPIHGGAVEEAIKQFMEIGSPEKVEEWWFKALQQKRKIMGAGHRVYKTYDPRARIFKKY
ASKLGDKCLFEIAERLERLVEEYLSKKGISINVDYWSGLVFYGMKIPIELYTTIFAMGRIAGWTAHLAE
YVSHNRRIIRPRLQYVGEIGKKYLPIELRR

>d1a59_ a.103.1.1 (-) Citrate synthase {Antarctic bacterium DS2-3R}
EPTIHKGLAGVTADVTAISKVNSDTNSLLYRGYPVQELAAKCSFEQVAYLLWNSSELPNSELKAFVNF
ERSHRKLDENVKGAIDLLSTACHPMDVARTAVSVLGHANHARAQDSSPEANLEKAMSLLATFPSVVAY
DQRRRRGEELIEPREDLDYSANFLWMTFGEEAAPEVVEAFNVSMILYAEHSFNASTFTARVITSTLA
DLHSAVTGAIGALKGPLHGGANEAVMHTFEEIGIRKDESLDEAATR SKAWMVDALAQKKKVMGFG
HRVYKNGDSRVPTMKSALDAMIHYDRPEMLGLYNGLEAAMEEAKQIKPNLDYPAGPTYNLMGFD
TEMFTPLFIAARITGWTAHIMEQVADNALIRPLSEYNGPEQRQVP

>d1dz4a_ a.104.1.1 (A:) Cytochrome P450-CAM {Pseudomonas putida}
LAPLPPHVPEHLVDFDFMYNPSNLSAGVQEAWAVLQESNVPDLVWTRCNGGHWIATRGLIREAYE
DYRHFSECPFIPREAGEAYDFIPTSM DPPEQRQFRALANQVVGMPVVDKLENRIQELACSLIESLRP
QGQCNTEDYAEPFPIRIFMLLAGLPEEDIPHLKYLTDQMTRPDGSMTFAEAKEALYDYLIPIIEQRR
QKPGTDAISIVANGQVNGRPITSDEAKRMCGLLVGGLDVTVVNFLSFSMEFLAKSPEHRQELIQRPER
IPAACEELLRRFSLVADGRILTSYEFHGVQLKKGQILLPQMLSGLDERENACPMHVDVSRQKVSHT

TFGHGSHLCLGQHLARREIIVTLKEWLTRIPDFSIAPGAQIQHKSGIVSGVQALPLVWDPATTKAV
>d1jpza_ a.104.1.1 (A:) Cytochrome P450 bm-3 {Bacillus megaterium}
TIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSQRLIKEACDESFRD
KNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMMVDIAVQLVQKWER
LNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRALDEAMNKLQRANPDDPAY
DENKRQFQEDIKVMNDLVDKIIADRKASGEQSDLLHMLNGKDPETGEPLDDENIRYQIITFLIAG
HETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVDPVPSYKQVKQLKYVGMVLNEALRLWPTAPAFS
LYAKEDTVLGGEYPLEKGDLEMLVLIPLQLHRDKTIWGDDVEEFRPERFENPSAIPQHAFKPFNGQRA
CIGQQFALHEATLVLGMMLKHFDDEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGI
>d1jfa_ a.104.1.1 (A:) Cytochrome P450-NOR, nitric reductase {Fungus (Fusarium
oxysporum)}
APSFPSRASGPEPPAEFAKL RATNPVSQVKLFDGSLAWLVTKHKDVCVATSEKLSKVRTRQGFPEL
SASGKQAAKAKPTFVMDPPEHMHQRSMVEPTFTPEAVKNLQPYIQRVDDLLEQMKQKGCANGP
VDLVKEFALPVPSYIYTLLGVPFNDLEYLTQQNAIRNGSSTAREASAANQELLDYLAILVEQRLVEP
KDDIISKLCTEQVKPGNIDKSDAVQIAFLLLVAGNATMVNMIALGVATLAQHPDQLAQLKANPSLAPQ
FVEELCRYHTASALAIKRTAKEDVMIGDKLVRANEGIIASNQSANRDEEVFENPDEFNMNRKWPPQ
DPLGFGFDHRCIAEHLAKAELTTFVSTLYQKFPDLKVAVPLGKINYTPLNRDVGIVDLPVIF
>d1jpa_ a.104.1.1 (A:) Cytochrome P450-ERYF {Saccaropolyspora erythraea}
TTVPDLESDFHVDWYRTYAE LRETAPVTPVRFLGQDAWLVTGYDEAKAALSDDLRLSSDPKKKYPG
VEVEFPAYLGFPEVDRNYFATNMGTSDPPTHTRLRKLVSQEFTVRRVEAMRPRVEQITAELLDEVGD
SGVVDIVDRFAHPLPIKVICEL LGVDEKYRGEFGRWSSEILVMDPERAEQRGQAAREVVNFILDLVER
RRTEPGDDL SALIRVQDDDDGRLSADELTSIALVLLLAGFESSVSLIGIGTYLLLTHPDQLALVRRDPS
ALPNAVEEILRYIAPPETTTTRFAAEEVEIGGVAIPQYSTVLVANGAANRDPKQFPDPHRFDVTRDRG
HLSFGQGIHFCMGRPLAKLEGEVALRALFGRFPALSLGIDADDVVWRRSLLLRGIDHLPVRLDG
>d1cpt_ a.104.1.1 (-) Cytochrome P450-TERP {Pseudomonas sp.}
MDARATIPEHIARTVILPQGYADDEVIIYPAFKWLRDEQPLAMAHIEGYDPMWIATKHADVMQIGKQ
PGLFSNAEGSEILDQNNEAFMRSISGGCPHVIDSLTSM DPPTHAYRGLTLNWFQPASIRKLEENIR
RIAQASVQRLLD FDCDFMTDCALYPLHVMTALGVPEDEPLMLKLTQDFFGVEAARRFHETI
ATFYDYFNGFTVDRRSCPKDDVMSLLANSKLDGNYIDDKYINAYYVAIATAGHDTTSSSSGGAIIGLSR
NPEQLALAKSDPALIPRLVDEAVRWTAPVKSFMRTALADTEVRGQNIKRGDRIMLSYPSANRDEEVF
SNPDEFDITRFPNRHLGFGWGAHMCLGQHLAKLEMKIFFEELLPKLKSVELSGPPRLVATNFVGGPK
NVPIRFTKA
>d1e9xa_ a.104.1.1 (A:) Cytochrome p450 14 alpha-sterol demethylase (cyp51)
{Mycobacterium tuberculosis}
MSAVALPRVSGGHDEHGHLEEFRTDPIGLMQRVRDECGDVGTFQLAGKQVVLLSGSHANEFFFRAG
DDDLDQAKAYPFMTPIFGGVFDASPERRKEMLHNAALRGEQMKGHAATIEDQVRRMIADWGEA
GEIDLLDFFAELTIYTSSACLIGKKFRDQLDGRFAKLYHELERGTDP LAYVDPYLP IESFRRRDEARNG
LVALVADIMNGRIANPPTDKSDRMLDVLI AVKAETGTPRFSADEITGMFISMMFAGHHTSSGTASW
TLIELMRHRDAYAAVIDELDELYGDGRSVSFHALRQIPQLE NVLKETLRLHPPLIILMRVAKGEFEVQG
HRIHEGLVAASPAISNRIPEDFPDPHDFVPARYEQPRQEDLLNRWTWIPFGAGRHRVCVGAFAIMQ
IKAIFSLLREYEFEMAQPPEYSYRNDHSMV VQLAQ PACVRYRRRT
>d1io7a_ a.104.1.1 (A:) CYP119 {Archaeon Sulfolobus solfataricus}
MYDWFSEMRKKDPVYYDGNIWQVFSYRYTKEVLN NFSKFSDDLTYGHERLEDLRNGKIRFDIPTRY
TMLTSDPPLHDELRSMSADIFSPQKLQTLTETFIRETTRSLLDSIDPREDDIVKKLAVPLPIIVISKILGL

PIEDKEKFKEWSDLVAFRLGKPGEIFELGKKYLELIGYVKDHLNSGTEVVSRVNSNLSDIEKLGYYIL
LLIAGNETTTNLISNSVIDFTRFNLWQRIREENLYLKAIEEALRYSPPVMRTVRKTKERVKLGDTIE
EGEYVRVWIASANRDEEVFHDGKFKFIPDRPNPNHLSFGSGIHLCLGAPLARLEARIAIEEFSKRFRHI
EILDTEKVPNEVLNGYKRLVVRLKS

>d1dt6a_a.104.1.1 (A:) Mammalian cytochrome p450 2c5 {Rabbit (*Oryctolagus cuniculus*)}
PPGPTPFPIIGNILQIDAKDISKSLTKFSECYGPVFTVYLGMPKPTVVLHGVEAVKEALVDLGEFAGRG
SVPILEKVKSLGLIAFSNAKTWKEMRRFSLMTRLNFGMGKRSIEDRIQEEARCLVEELRKTNASPCD
PTFILGCAPCNVICSVIFHNRFDYKDEEFLKLMESLHENVELLGTPWLQVYNNFPALLDYFPGIHKTL
LKNADYIKNFIMEKVKEHQKLLDVNNPRDFIDCFLIKMEQENNLEFTLESLVIAVSDLFAGTETTST
TLRYSLLLLLKHPEVAARVQEIEIRVIGRHRSPCMQDRSRMPYTDVAIHEIQRFIDLLPTNLPHAVTR
DVRFRNYFIPKGTDIITSLTSVLHDEKAFPNPKVDFDPGHFLDESGNFKSDYFMPFSAGKRMCVGEG
LARMELFLFLTSILQNFKLQSLVEPKDLITAVVNGFVSVPPSYQLCFIPIHH

>d1etob_a.105.1.1 (B:) FIS protein {*Escherichia coli*}
MFEQRVNSDVLTVSTVNSQDQVTQKPLRDSVKQALKNYFAQLNGQDVNDLYELVLAEEVEQPLDMV
MQYTLGNQTRAALMMGINRGTLRKKLKKYGMN

>d1etxa_a.105.1.1 (A:) FIS protein {*Escherichia coli*}
VLTVSTVNSQDQVTQKPLRDSVKQALKNYFAQLNGQDVNDLYELVLAEEVEQPLDMVMQYTRGNA
TRAALMMGINRGTLRKKLKKYGMN

>d1fipa_a.105.1.1 (A:) FIS protein {*Escherichia coli*}
PLRDSVKQALKNYFAQLNGQDVNDLYELVLAEEVEQALLDMVMQYTRGNQTRAALMMGINRGTLRK
KLKKYGMN

>d1ntca_a.105.1.1 (A:) DNA-binding domain of NTRC {*Salmonella typhimurium*}
MDLPGELFEASTPDSPSHLPPDSWATLLAQWADRALRSQHQNLLSEAQPELERTLLTTALRHTQGH
KQEAARLLGWGAATLTAKLKELGME

>d1g8ea_a.145.1.1 (A:) Flagellar transcriptional activator FlhD {*Escherichia coli*}
MHTSELLKHIYDINLSYLLLAQRLIVQDKASAMFRLGINEEMATTLAALTLPQMVKLAETNQLVCHF
RFDSHQITITQLTQDSRVDDLQIHTGIMLST

>d1g8eb_a.145.1.1 (B:) Flagellar transcriptional activator FlhD {*Escherichia coli*}
TSELLKHIYDINLSYLLLAQRLIVQDKASAMFRLGINEEMATTLAALTLPQMVKLAETNQLVCHFRFD
SHQTITQLTQDS

>d1jhga_a.107.1.1 (A:) Trp repressor {*Escherichia coli*}
SAAMAEQRHQEWLRFVDLLKNAYQNDLHLPLLNLMLTPDEREALGTRVRIIEELLRGEMSQRELKN
ELGAGIATITRGSNSLKAAPVELRQWLEEVLLKSD

>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*}
MTIDEIIEAIEKLTVSELAELVKKLEDKFGVTAAAPVAVAAAAPVAGAAAGAAQEEKT

>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)}

YGNMTEHDHVMHLLQNADPLKVYPPPLKGSFPENLRHLKNTMETIDWKVFESWMHHWLLFEMSRH
SLEQKPTDAPPK

>d1aora1 a.110.1.1 (A:211-605) Aldehyde ferredoxin oxidoreductase {Archaeon Pyrococcus furiosus}

IADKQKFMFLVVREKVNKLNDPVGGLPKYGTAVLVNIIENGLYPVKNFQTVGYPPYAYEQSGEAM
AAKYLVNRNKPCYACPIGCGRVNRLPTVGETEGPEYESVWALGANLGINDLASIIEANHMCDELGLDTI
STGGTLATAMELYEKGHKDEELGDAPPFRWGNTVEVLHYYIEKIAKREGFGDKLAEGSYRLAESYGH
PELSMTVKKLELPAYDPRGAEGHGLGYATNNRGGCHIKNYMISPEILGYPKMDPHDVSDDKIKMLI
LFQDLTALIDSAGLCLFTTFGLGADDYRDLLNAALGWDFTTEDYKIGERIWNAERLFLNLKAGLDP
RDDTLPKRFLPEPMPEGPNKGHTVRLKEMLPYKLRGWTEDEGKIPKEKLEELGIAEFY

>d1b25a1 a.110.1.1 (A:211-619) Formaldehyde ferredoxin oxidoreductase {Archaeon Pyrococcus furiosus}

DKEELKKLSQEAYNEILNSPGYPFWKRQGTMAAVEWCNTNYALPTRNFSDGYFEFARSIDGYTMEG
MKVQQRGCPYCNMPCGNVVLDAEGQESELDYENVALLGSNLGIGKLNESVNLRIADEMGMDTISL
GVSIAHVMEAVERGILKEGPTFGDFKGAKQLALDIAYRKGELGNLAAEGVKAMAELGTHDFAMHV
KGLEVSGYNCYIYPAMALAYGTSAIGAHHKEAWVIAWEIGTAPIEGEKAKEKVEYKISYDPIKAQKVVE
LQRLRGGLFEMLTACRLPWVEVGLSLDYYPKLLKAITGVTYTWDLYKAADRVYSLIRAYWVREFN
GKWDRKMDYPPKRWFTEGLKSGPHKGEHLDEKKYDELLSEYYRIRGWDERGIPKKEKLELDLDF
VIPELEKVTNLE

>d1d2ta_ a.111.1.1 (A:) Acid phosphatase {Escherichia blattae}

GNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAFLNDQAMYEQGRLLRNTERGKLAEDANLSSG
GVANAFSGAFGSPITEKDAPALHKLLTNMIEDAGDLATRSKDHVMRIRPFAFYGVSTCNTTEQDKL
SKNGSYPSGHTSIGWATALVLAEINPQRQNEILKRGYELGQSRVICGYHWQSDVDAARVVGSAVVATL
HTNPAFQQQLQKAKAEFAQHQK

>d1qi9a_ a.111.1.2 (A:) Haloperoxidase (bromoperoxidase) {Ascophyllum nodosum}

TCSTSDDADPTPPNERDDEAFASRVAAAKRELEGTGTVCQINNGETDLAAKFHKSLPHDDLQVD
ADAFAALEDICILNGDLSICEDVPVGNSEGDVPVGRVNPAAFAIDISGPAFSATTIPPVPTLPSPELAAQ
LAEVYWMALARDVPMQYGTDDITVTAANLAGMEGFPNLDAVSIGSDGTVDPLSQLFRATFVGVVE
TGPFIQQLVNSFTIDSITVEPKQETFAPDVNYMVDFDEWLNINQNGGPPAGPELLDDELRFVRNARD
LARVTFTDNINTEAYRGALILLGLDAFNRAVNGPFIDRQAGFVNFVNGISHYFRLIGAAELAQRSSW
YQKWQVHRFARPEALGGTLHLTIKGEINADFDLSLENAELLKRVAAINAAQNPNNVYLLPQAIQ
EGSPTHPSPSGHATQNGAFATVLKALIGLDRGGDCYPDPVYPPDDGLKLIDFRGSCLTFEGEINKLA
VNVAFGRQMLGIHYRFDGIQGLLLGETITVRTLHQELMTFAEESTFEFRLFTGEVIKLFQDGTFTIDG
FKCPGLVYTVGENCV

>d1qhba_ a.111.1.2 (A:) Haloperoxidase (bromoperoxidase) {Red algae (Corallina officinalis)}

GIPADNLQSRKASFDTRVAAAELALARGAVPSFANGEELLYRNSETGDPSFIGSFTKGLPHDDNGAII
DPDDFLAFVRAINSGDEKEIAALTLGPARDPETGLPIWRSDLANSLDLEVRGWENSSAGLTFDLEGP
DAQSVAMPPAPVLTSPELIAEMAELYLMALGRDIEFSEFDSPKNAAFIRSAIERLNGLEWFNTPAKLG
DPPAEIRRRRGEVTVGNLFRGILPGSEVGPYLSQFIIVGSKQIGSATVGNKTLVSPNAADEFDGEIAYGS
ITISQVRVIATPGRDFMTDLKVFLDVQDAADFRGFESYEPGARLIRTIRDLATWVHFDLSYEAYLNAC

LILLANGVFPDPNLPFQQEDKLDNQDVFVNFVNGSAHVLSLVTEVATRALKAVRYQKFNIHRRLRPEAT
GGLISVNKNAFLKSESVFPEVDVLEELSSILDDSSASSNEKQNIADGDVSPGKSFLLPMAFAEGSPFHP
SYGSGHAVVAGACVTILKAFFDANFQIDQVFEVDTDEDKLVKSSFPGLTVAGELNKLADNVAIGRNM
AGVHYFSDQFESLLLGEQIAIGILEEQSLTYGENFFFNLPKFDGTTIQI

>d1vns_ a.111.1.3 (-) Chloroperoxidase {*Curvularia inaequalis*}

VTPIPLPKIDEPEEYNTNYILFWNHVGLLELNRVTHTVGGPLTGPPLSARALGMLHLAIHDAYFSICPP
TDFTTFLSPDTENAAAYRLPSPNGANDARQAVAGAALKMLSSLYMKPVEQPNNPANGANISDNAYAQL
GLVLDRSVLEAPGGVDRESASFVGFEDVADVFFALLNDPRGASQEGYHPTPGRYKFDDEPTHPVLI
PVDPNPNPGPKMPFRQYHAPFYGKTTKRKFATQSEHFLADPPGLRSNADETAEYDDAVRVAIAMGGA
QALNSTKRSPWQTAQGLYWAYDGSNLIGTPPRFYNQIVRRIAVTYKKEEDLANSEVNNADFARLFAL
VDVACTDAGIFSWKEKWEFEFWRPLSGVRDDGRPDHGDPPFWLTLGAPATNTNDIPFKPPFPAYPSG
HATFGGAVFQMVERRYYNGRVGTWKDDEPDNIAIDMMISEELNGVNRDLRQPYDPTAPIEDQPGIVR
TRIVRHFDSAWELMFENAI SRIFLGVHWRFDAAAARDILIPTTTTKDVYAVDNNGATVFQNVEDIRYT
TRGTREDEEGLFPIGGVPLGIEIADEIFNNGLKPTPPEIQP

>d1sig_ a.112.1.1 (-) sigma70 subunit fragment from RNA polymerase {*Escherichia coli*}

MEGEIDIAKRIEDGINQVQCSVAEYPEAITYLLEQYNRVEAEEARLSDLITGFVDPNAEEDLAPTATHV
GSELSQEDLDDDEDEDEDEEDGDDDSADDDNSIDPELAREKFAELRAQYVVTTRDTIKAKGRSHATAQE
EILKLSEVFKQFRLVPKQFDYLVNSMRVMMDRVTRQERLIMKLCVEQCKMPKKNFITLFTGNETS
TWFNAAIAMNKPWSEKLHDVSEEVHRALQKLQIEEETGLTIEQVKDINRRMSIGEA KARRAKKE
MVEANLRLVISIAKKYTNRGLQFLDLIQEGNIGLMKAVDKFEYRRGYKFSYATWWIRQAITRSIADQ

>d1ewqa1 a.113.1.1 (A:267-541) DNA repair protein MutS, domain III {*Thermus aquaticus*}

RGQDTLFSVLDETRTAPGRRLQSWLRHPLLDGRPLEARLDRVEGFVREGALREGVRRLLYRLADL
ERLATRLELGRASPKDLGALRRSLQILPELRALLGEEVGLPDLSPKKEEALVEDPPLKVSEGLIR
EGYDPDLDALRAAHREGVAYFLELEERERERTGIPTLVKGYNAVFGYYLEVTRPYERVPKEYRPVQ
TLKDRQRYTLPEMKEKEREVYRLEALIRRRREEVFLEVRERAKRQAEALREARILAEADVYAALAE
VAVRYG

>d1e3ma1 a.113.1.1 (A:270-566) DNA repair protein MutS, domain III {*Escherichia coli*}

DAATTRNLEITQNLAGGAENTLASVLDCTVTPMGRMLKRWLHMPVRDTRVLLERQQTIGALQDF
TAGLQPVLRQVGDLERILARLALRTARPRDLARMRHAFQQLPELRAQLETVDSAPVQALREKMGEF
AELRDLLERAIIDTPVLVRDGGVIASGYNEELDEWRALADGATDYLERLEVRERERTGLDTLKVGF
NAVHGYIYQISRGQSHLAPINYMRRQTLKNAERYIPELKEYEDKVLTSKGKALALEKQLYEELFDLLL
PHLEALQQSASALAEADVLVNLAERAYTLN

>d1f5na1 a.114.1.1 (A:284-583) Interferon-induced guanylate-binding protein 1 (GBP1),
C-terminal domain {Human (*Homo sapiens*)}

GGIQVNGPRLESVLTYVNAISSGLPCMENAVLALAQIENSAAVQKAI AHYEQQMGQKVQLPTESL
QELLDLHRDSEREAIEVFIRSSFKDVDFHLFQKELAAQLEKKRDFCKQNQEASSDRCSGLLQVIFSP
EEEVKAGIYKPGGYRFLVQKLQDLKKKYEEPRKGIQAEIILQTYLKSKE SMTDAILQTDQTLTEKE
KEIEVERVKAESAQASAKMLHEMQRKNEQMMEQKERSYQEHLKQLTEKMENDRVQLLKEQERTL
ALKLQEQEQLLKEGFQKESRIMKNEIQDLQTKM

>d1bvp11 a.115.1.1 (1:1-120,1:255-349) Bluetongue virus capsid protein vp7 (BTV-10 vp7)
{Bluetongue virus}

MDTIAARALVMRACATLQEARIVLEANVMEILGIAINRYNGLTLRGVTMRPTSLAQRNEMFFMCL
DMMLSAAGINVGPIPDYQHMATIGVLATPEIPFTTEAANEIARVTGETSTWGXTLNQYPALTAEI
FNVYSFRDHTWHGLRTAILNRTTLPNMLPPIFPNDRDSILTL LLLSTLADVYTVLRPEFAIHGVNP

MPGPLTRAIARAAYV

>d1qhda1_a.115.1.2 (A:1-148,A:333-397) vp6, the major capsid protein of group A rotavirus {Bovine rotavirus}

MDVLYSLSKTLKDARDKIVEGTLYSNVSDLIQQFNQMIITMNGNEFQTGGIGNLPIRNWNFDFGLLG
TTLLNLDANYVETARNTIDYFVDFVDNVCDEMVRQSRNGIAPQSDSLIKLSGKFKRINFDSSE
YIENWNLQNRRTXSVLADASETMLANVTSVRQEYAIIPVGPVFPFGMNWTDLITNYSRSDNLQ
RVFTVASIRSMLVK

>d1tx4a_a.116.1.1 (A:) p50 RhoGAP domain {Human (Homo sapiens)}

PLPNQQFGVSLQHLQEKNPEQEPIPIVLRQVAYLQAHALTTEGIFRRSANTQVVREVQQKYNMGLP
VDFDQYNALHLPVILKTFRLPEPLTDFDLYPHVVGFLNIDESQRPATLQVLQTLPEENYQVLRFL
TAFVLQISAHSQNKMTNTNLAVVFGPNLLWAKDAAITLKAINPINTFTKFLLDHQGELF

>d1pbwa_a.116.1.1 (A:) p85 alpha subunit RhoGAP domain {Human (Homo sapiens)}

LPDLAEQFAPPDIAPPLLIKLVIAIEKKGLECYRTQSSSNLAELRQLLDCDTPSVDLEMIDVHVLA
DAFKRYLLDLPNPVIPAAYSEMISLAPEVQSSEYIQLLKKLIRSPSIPHQYWLTLYLLKHFHFKLSQT
SSKNLLNARVLSEIFSPMLFRFSAASSDNTENLIKVIEILISTEW

>d1f7ca_a.116.1.1 (A:) Graf {Chicken (Gallus gallus)}

AQLDSIGFSIIKKCIHAVETRGINEQGLYRIVGVNSRVQKLLSILMDPKTATETETEICAWEIKTITSAL
KTYLRMLPGPLMMYQFQRSFIKAAKLENQESRVSEIHSVHRLPEKNRQMLHLLMNHLAKVADNH
KQNLMTVANLGVVFGPTLLRPQEETVAAIMDIKFQNVIEILIEIENHEKIFNTVPE

>d1wer__a.116.1.2 (-) p120GAP domain {Human (Homo sapiens)}

MPEEEYSEFKELILQKELHVYALSHVCGQDRLLASILLRIFLHEKLESLLLCTLNDRISMEDEATT
LFRATTLASTLMEQYMKATATQFVHHALKDSILKIMESKQSCELSPSKLEKNEDVNTNLTHLLNILSE
LVEKIFMASEILPPTLRYYGCLQKSVQHKWPTNTTMRTRVVSGFVFLRLICPAILNPRMFNIISDPS
PIAARTLILVAKSVQNLANLVEFGAKEPYMEGVNPFIKSNKHRMIMFLDELGNVPELPTTEHSRTD
LSRDLAALHEICVAHSDELRTLSNERGAQQHVLLKLLAITELLQKQKQNYT

>d1nf1a_a.116.1.2 (A:) GAP related domain of neurofibromin {Human (Homo sapiens)}

ERLVELVTMMGDQELPIAMALANVVPCSQWDELARVLVTLFDSRHLLYQLLWNMFSKEVELADS
MQTLFRGNLASKIMTFCFKVYGATYLQKLLDPLLRIVITSSDWQHVSFEVDPTRLEPSESLEENQR
NLLQMTEKFFHAISSSSEFPQLRSVCHCLYQVVSQRFPQNSIGAVGSAMFLRFINPAIVSPYEAGILD
KKPPPIIERGLKMSKILQSIANHVLFTEEHRPFNDFVKSNFDAARRFFLDIASDCPTSDAVNHSL
SFISDGNVLALHRLWNNQEIKGYLSSNRDHKAVGRRPFDKMATLLAYLGPPE

>d1bkds_a.117.1.1 (S:) Son of sevenless-1 (sos-1) {Human (Homo sapiens)}

RLPSADVYRFAEPDSEENIIFEEGIPIKAGTVIKLIERLTYHMYADPNFVRTFLTYSRFSCKPQELLSLII
ERFEIPEPRFRKEYIQPVQLRVLNVCRHWVEHHFYDFERDAYLLQRMEEFIGTVRGKAMKKWVESI
TKIIQRKKITFQSSPPTVEWHISRPGHIETFDLLTLHPHIEIARQLTLESYDLYRAVQPSSELVGSVWTKED
KEINSPNLLKMIRHTNLTWFEKIVETENLEERVAVVSRIIEILQVFQELNNGVLEVVVSAMNSSP
VYRLDHTFEQIPSRQKILEEAHELSEDHKKYLAKLSINPPCVFFGIYLTNLIKTEEGNPEVLKRH
GKELINFSTRKVAEITGEIQYQNPYCLRVESDIKRFENLNPMGNSMEKEFTDYLFNKSLEIEPR
NPKPLPRFPKYSYPLKSPGVRPSN

>d1h6oa_a.146.1.1 (A:) TRF1 {Human (Homo sapiens)}

EDAGLVAAEAVAAGWMLDFLCLSLCRAFRDGRSEDFRTRNSAEAIHGLSSLTACQLRTIYICQFLT
RIAAGKTLDAQFENDERITPLESALMIWGSIEKEHDKLHEEIQNLIKIQAIAVCMENGNFKEAEEVFE
RIFGDPNSHMPFKSKLLMIISQKDTFHSFFQHFSYNHMEKIKSYVNYVLSEKSSFTLMAAAKVVVE

>d1h6pa_a.146.1.1 (A:) TRF2 {Human (Homo sapiens)}

AGEARLEEAVNRWVLFYFHEALRAFRGSRYGDFRQIRDIMQALLVRPLGKEHTVSRLLRVMQCLS
RIEENLDCSFDMEAEPLTESAINVLEMIKTEFTLTEAVVSSRKLVKAAVVICIKNKEFEKASKIL
KKHMSKDPPTQKLRNDLLNIIREKNLAHPVIQNFYSYETFQQKMLRFLESHLDDAEPYLLTMAKKAL
K

>d1g3jc_a.118.1.1 (C:) beta-Catenin {Human (Homo sapiens)}

HHREGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLLHQQEGAKMAVRLAGGLQKMVALLNKT
NVKFLAITTDCLQILAYGNQESKLILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSSNKPAIV
EAGGMQALGLHLTDPSQRLVQNCLWTLRNLSDAATKQEGMEGLLGLTLVQLLGSDDINVVTCAAGILS
NLTCNNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLSRHQEAEMAQNAVRLHYGL
PVVVKLLHPPSHWPLIKATVGLIRNLALCPANHAPLREQGAIPRLVQLLVRAHQDTQRRTSMGGTQ
QQFVEGVRMEEIVEGCTGALHILARDVHNRIVIRGLNTIPLFVQLLYSPIENIQRVAAGVLCCELAQDKE
AAEAIEAEGATAPLTELHLSRNEGVATYAAAVLFRMSE

>d1jdha_a.118.1.1 (A:) beta-Catenin {Human (Homo sapiens)}

AVVNLINYQDDAELATRAIPELTKLLNDEDQVVVNKAAMVHQLSKKEASRHAIMRSPQMVAIVR
TMQNTNDVETARCTAGTLHNLSHHREGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLLHQQE
GAKMAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAYGNQESKLILASGGPQALVNIMRTYTYEK
LLWTTSRVLKVLSSNKPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSDAATKQEGMEGL
LGLTLVQLLGSDDINVVTCAAGILSNLTCNNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALR
HLTSRHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLALCPANHAPLREQGAIPRL
VQLLVRAHQDTQRRTSMGGTQQFVEGVRMEEIVEGCTGALHILARDVHNRIVIRGLNTIPLFVQLL
YSPIENIQRVAAGVLCCELAQDKEAAEAIEAEGATAPLTELHLSRNEGVATYAAAVLFRMS

>d1iala_a.118.1.1 (A:) Importin alpha {Mouse (Mus musculus)}

DEQMLKRRNVSSFPDDATSPLQENRNNQGTVNWSVEDIVKGINSNLESQEQATQAARKLLSREKQ
PPIDNIIRAGLIPKFVSFLGKTDSPQIFESAWALTNIASGTSEQTKAVVDGGAIPAFISLLASPHAHISE
QAVWALGNIAGDGSFRDLVIKHGAIDPLLALLAVPDLSTLACGYLRNLTWTLNLCRNKNPAPPLD
AVEQILPTLVRLLHHNDPEVLADSCWAISSYLDGPNRIEMVVKKGVPQLVKLLGATELPIVTPALR
AIGNIVTGTDEQTKVIDAGALAVFPSLLTNPKTNIQKEATWTMSNITAGRQDQIQVVNHGLVPFLV
GVLKADFKTQKEAAWAITNYTSGGTVEQIVLVHCGIIEPLMNLSSAKDTKIIQVILDAISNIFQAAE
KLGETEKLKSIMIECGGLDKIEALQRHENESVYKASLNLEKYF

>d1ibrb_a.118.1.1 (B:) Importin beta {Human (Homo sapiens)}

ELITILEKTVSPDRLELEAAQKFLERAAVENLPTFLVELSRVLANPGNSQVARVAAGLQIKNSLTSKDP
DIKAQYQQRWLAIANARREVKNYVLQTLGTETYRPSASQCVAGIACAEIPVNQWPELIPQLVANV
TNPNSTEHMKESTLEAIGYICQDIDPEQLQDKSNEILTAIQGMRKEEPSNNVLAATNALLNSLEFT
KANFDKESERHFIMQVVCEATQCPDTRVRVAALQNLVKIMSLLYQYMETYMGPALFAITIEAMKSDI
DEVALQGIEFWSNVCDEEMDLAIEASEAAEQGRPPEHTSKFYAKGALQYLVPILTQTLTKQDENDDD
DDWNPCKAAGVCLMLLATCCEDDIPHVLPFIKEHIKPNPDWRYRDAAVMAFGCILEGPEPSQLKPL
VIQAMPTLIELMKDPSVVVRDTAAWTVGRICELLPEAAINDVYLAPLLQCLIEG

>d1qgra_a.118.1.1 (A:) Importin beta {Human (Homo sapiens)}

MELITILEKTVSPDRLELEAAQKFLERAAVENLPTFLVELSRVLANPGNSQVARVAAGLQIKNSLTSK
DPDIKAQYQQRWLAIANARREVKNYVLHRTLGTETYRPSASQCVAGIACAEIPVNQWPELIPQLVA
NVTNPNSTEHMKESTLEAIGYICQDIDPEQLQDKSNEILTAIQGMRKEEPSNNVLAATNALLNSLE
FTKANFDKESERHFIMQVVCEATQCPDTRVRVAALQNLVKIMSLLYQYMETYMGPALFAITIEAMKS
DIDEVALQGIEFWSNVCDEEMDLAIEASEAAEQGRPPEHTSKFYAKGALQYLVPILTQTLTKQDENDD
DDDWNPCKAAGVCLMLLATCCEDDIPHVLPFIKEHIKPNPDWRYRDAAVMAFGCILEGPEPSQLKPL

LVIQAMPTLIELMKDPSVVVRDTAAAWTVGRICELLPEAAINDVYLAPLLQCLIEGLSAEPRVASNVCW
AFSSLAEEAAYEAADVADDQEEPATYCLSSSFELIVQKLETTDRPDGHQNNLRSSAYESLMEIVKNSA
KDCYPAVQKTTLVIMERLQQVLQMESHISTSDRIQFNDLQSLLCATLQNVLRKVQHQDALQISDVV
MASLLRMFQSTAGSGGVQEDALMAVSTLVEVLGGEFLKYMEAFKPFLLGIGLKNYAAYQVCLAAVGLV
GDLCRALQSNIIPCDEVMQLLENLGNENVHRSVKPQILSVFGDIALAIGGEFKKYLEVVLNTLQQA
SQAQVDKSDYDMVDYLNELRESCLEAYTGIVQGLKGDQENVHPDVMLVQPRVEFILSFIDHIAGDED
HTDGVVACAAGLIGDLCTAFGKDVLLKVEARPMIHELLTEGRRSKTNKAKTLARWATKELRKLKNQ
A

>d1qbbk_a.118.1.1 (B:) Karyopherin beta2 {Human (Homo sapiens)}

YEWKPDEQGLQQILQLLKESQSPDTTIQRTVQQKLEQLNQYPDFNNYLIFVLTCLKSEDEPTRSLGL
ILKNNVKAHFQNFNGVTDVFIKSECLNIGDSSPLIRATVGILITTIASKGELQNWPDLLPKLCSLLDS
EDYNTCEGAFGALQKICEDSAEILSDVLDLDRPLNIMIPKFLQFFKHSSPKIRSHAVACVNQFIISRTQA
LMLHIDSFTENLFALAGDEEPEVRKNVCRALVMLLEVRMDRLLPHMHNIVEYMLQRTQDQDENVA
LEACEFWLTLAEQPICKDVLVRHLPKLPVLVNGMKYSIDIDIILLKGDVEEDEETIPDSEQDIRPRFHRS
RTVAQQHDEDGIEEEDDDDEIDDDDTISDWNLRKCSAAALDVLANVYRDELLPHILPLLKELLFH
HEWVVKESGILVLGAIAEGCMQGMIPYLPPELPHLIQCLSDKKALVRSITCWTLSTRYAHWVVSQPPDT
YKPLMTELLKRILDSNKRQEAACSAFATLEEEACTELVPYLAIDLTLVFAFSKYQHKNLLILYDAIG
TLADSVGHHLNKPEYIQMLMPPLIQKWNMLKDEDKDLFPLLECLSSVATALQSGFLPYCEPVYQRCV
NLVQKTLAQAMLNNAQPDQYEAPDKDFMIVALDLLSGLAEGGGNIEQLVARSNILTLMYQCMQDK
MPEVRQSSFALLGDLTKACFQHVKPCIADFMPILGTNLNPEFISVCNNATWAIGEISIQMGIEMQYPIP
MVLHQLVEIINRPNTPKTLENTAITIGRLGYVCPQEVAPMLQQFIRPWCTSLRNIRDNEEKDSAFRG
ICTMISVNPSTGVIQDFIFFCDAVASWINPKDDLDRDMFCKILHGFKNQVGDENWRRFSDQFPLPLKER
LAAFYGV

>d1ee4a_a.118.1.1 (A:) Karyopherin alpha {Baker's yeast (Saccharomyces cerevisiae)}

QELPQMTQQLNSDDMQEQLSATVKFRQILSREHRPPIDVVIQAGVVPRLVEFMRENQPEMLQLEAA
WALTNIASGTSATKVVVDADAVPLFIQLLYTGSVEVKEQAIWALGNVAGDSTDYRDYVLQCNAMEP
ILGLFNSNKPSLIRTATWTLNLCRGGKQPDPWSVVSQALPTLAKLIYSMDTETLVDACWAISYLSDG
PQEAIQAVIDVRIPKRLVELLSHESTLVQTPALRAVGNIVTGNDLQTQVVINAGVLPALRLLLSSPKENI
KKEACWTISNITAGNTEQIQAVIDANLIPPLVKLLEVAEDKTKKEACWAISNASSGGLQRPDIIRYLV
QGCIKPLCDLLEIADNRIEVTLDALENILKMGEADKEARGLNINENADFIEKAGGMEKIFNCQQNEN
DKIYEKAYKIIETYP

>d1b3ua_a.118.1.2 (A:) Constant regulatory domain of protein phosphatase 2a, pr65alpha
{Human (Homo sapiens)}

AAADGDDSLYPIAVLIDELRNEDVQLRLNSIKKLSIALALGVERTRSELLPFLTDTIYDEDEVLLALA
EQLGFTTTLVGGPEYVHCLLPPELSTAVEETVVRDKAVESLRAISHEHSPSDLEAHFVPLVKRLAGG
DWFTSRTSACGLFVVCYPRVSSAVKAEQRQYFRNLCSDDTPMVRRAAASKLGEFAKVLVDNVKSEII
PMFSNLASDEQDSVRLLAVEACVNIAQLLPQEDLEALVMPTLRQAEDKSWRVRYMVAADKFTTELQK
AVGPEITKTDLVPAFQNLMDCEAEVRAAASHKVKEFCENLSADCRENVIMSQILPCIKELVSDANQ
HVKSALASVIMGLSPILGKDNTEHLLPLFLAQLKDECEVRLNIISNLDCVNEVIGIRQLSQSLLPAIV
ELAEDAKWRVRLAIEYMPPLLAGQLGVEFFDEKLNLSLMAWLVDHVYAIREAATSNLKLVKVEKFGKE
WAHATHIPKVLAMSGDPNYLHRMTTLFCINVLSEVCGQDITTKHMLPTVLRMAGDPVANVRFNVAK
SLQKIGPILDNSTLQSEVKPILEKLTQDQDQVDVKYFAQEALTVLSLA

>d1hu3a_a.118.1.2 (A:) Eukaryotic initiation factor eIF4G {Human (Homo sapiens)}

SDPENIKTQELFRKVRISILNKLTPQMFNQLMKQVSGLTVDTEERLKGVIDLVFEKAIDEPSFSVAYAN

MCRCVLTLKVPKMGNTVNFRLKLLNRCQKEFEKDKADDDVFEKKQKELEAASAPEERTRLHD
ELEEAKDKARRRSIGNIKFIGELFKLKLMLTEAMHDCVVKLLKNHDEESLECLCRLTTIGKDLDFEK
AKPRMDQYFNQMEKIVKERKTSSRIRFMLQDVIDLRLCNWVS

>d1h6ka1 a.118.1.2 (A:27-290) CBP80, 80KDa nuclear cap-binding protein {Human (Homo sapiens)}

TEDHLESICKVGEKSACSLESNLEGLAGVLEADLPNYKSKILRLLCTVARLLPEKLTITYTTLVGLLNA
RNYNFGGEFVEAMIRQLKESLKANNYNEAVYLVRFLSDLVNCHVIAAPSMVAMFENFVSVTQEEDV
PQVRRDWYVYAFSSLPWVGKELYEKKDAEMDRIFANTESYLRKRRQKTHVPMQLQVWTADKPHPQ
EEYLDCLWAQIQKLLKDRWQERHILRPYLAFDSILCEALQHNLPPFTPPPHTEDSVYPMPRVIFR

>d1h6ka2 a.118.1.2 (A:291-480) CBP80, 80KDa nuclear cap-binding protein {Human (Homo sapiens)}

MFDYTDDEPGVMPGSHSVERFVIEENLHCIKSHWKERKTCAAQLVSYPGKNKIPLNYHIVEVIFAE
LFQLPAPPHIDVMYTTLLIELCKLQPGSLPQVLAQATEMLYMRLDTMNTTCVDRFINWFSSHLSNF
QFRWSWEDWSDCLSQDPESPCKPKFVREVLEKCMRLSYHQRILDIVPPTFSALCPSN

>d1h6ka3 a.118.1.2 (A:481-790) CBP80, 80KDa nuclear cap-binding protein {Human (Homo sapiens)}

PTCIYKYGDESSNSLPGHSVALCLAVAFKSKATNDEIFSIKLDVNPQNQDDDDDEGFSFNPLKIEVFVQ
TLLHLAAKFSHSFALAKFHEVFKTLAESDEGKLVLRVMFEVWRNHPQMIAVLVDKMIRTQIVD
CAAVANWIFSELSRDFTRLFVWEILHSTIRKMNKHVLKIQKELEEAKEKLARQHDGVLEEQIERLQ
EKVESAQSEQKNLFLVIFQRFIMILTEHLVRCETDGTSVLTPWYKNCIERLQQIFLQHHQIIQYQYMTL
ENLLFTAELDPHILAVFQQFCALQA

>d1hs6a1 a.118.1.7 (A:461-610) Leukotriene A4 hydrolase C-terminal domain {Human (Homo sapiens)}

DMTLTNACIALSQRWITAKEDDLNSFNATDLKDLSSHQLNEFLAQTQLRAPLPLGHKRMQEVYNF
NAINNSEIRFRWLRLCIQSKWEDAIPALKMATEQGRMKFTRPLFKDLAAFDKSHDQAVRTYQEHK
ASMHPVTAMLVGKDLKVD

>d1b89a_ a.118.1.3 (A:) Clathrin heavy chain proximal leg segment {Cow (Bos taurus)}

RLAELEEFINGPNNNAHIQVQGDRCYDEKMYDAAKLLYNNVSNFGRLASTLVHLGEYQAAVDGARKA
NSTRTWKEVCFACVDGKEFRLAQMCGLHIVVHADELEELINYYQDRGYFEELITMLEAALGLERAH
MGMFTELAIFYSKFKPKMREHLELFWSRVNIPKVLRAAEQAHLWAEVFLYDKYEEYDIAITMM
NHPTDAWKEGQFKDIITKVANVELYRAIQFYLEFKPLLLNDLLMVLSPRLDHTRAVNYFSKVKQLP
LVKPYLRSVQNHNNKSVNESLNNLFITEEDYQALRTSIDAYDNFDNISLAQRLEKHELIEFRRIAAYLF
KG

>d1bpoa1 a.118.1.4 (A:331-487) Clathrin heavy-chain linker domain {Rat (Rattus norvegicus)}

EENIIPYITNVLQNPDLALRMAVRNNLAGAEELFARKFNALFAQGNYSAAKVAANAPKGLRTPDTI
RRFQSVPAQPGQTSPLLQYFILLDQGQLNKYESLELCRPVLQQRKQLLEKWLKEDKLECSEELGD
LVKSVDPTLALSIVYLRANVPNK

>d1c9la1 a.118.1.4 (A:331-359) Clathrin heavy-chain linker domain {Rat (Rattus norvegicus)}

EENIIPYITNVLQNPDLALRMAVRNNLAG

>d1lr_ a.118.1.5 (-) Leucine-rich repeat variant {Azotobacter vinelandii}

TPIGDCRVCFSRMSLLLTGRCTPGDACVAVESGRQIDRFFRNNPHLAVQYLADPFWERRAIVRYSVP
EALTPLIRDSDEVVRRAYAYRLPREQLSALMFDEDEDREVITVADRLPLEQLEQMAADRDRYLVRAYVV

QRIPPGRLFRFMRDEDQRVKLVAKRLPEESLGLMTQDPEPEVRRIVASRLRGDDLELLHDPDWT
VRLAAVEHASLEALRELEDPDPEVRLAIAGRL
>d1e8xa_ a.118.1.6 (A:525-725) Phosphoinositide 3-kinase (PI3K) helical domain {Pig (*Sus scrofa*)}
HPIALPKHRPTPDPEGDRVRAEMPQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPK
LFSSVKWGGQEIIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDLV
HYLLQLVQAVKFEFYPYHDSALARFLLKRGRLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCG
>d1ib2a_ a.118.1.8 (A:) Pumilio 1 {Human (*Homo sapiens*)}
GRSRLLEDFRNNRYPNLQLREIAGHIMEFSQDQHGSRFIQLKLERATPAERQLVFNEILQAAAYQLMV
DVFNGYVIQKFFEFSGLEQKLALAEIRGHVLSLALQMYGCRVIQKALEFIPSDQQNEMVRELDGHV
LKCVDQNGNHVVQKCIQVQPQSLQFIIDAFKGVFALSTHPYGCRVIQRILEHCLPDQTLPILEELH
QHTEQLVQDQYGNVVIQHVLEHGRPEDKSKIVAEIRGNVLSLQHKFASNVVEKCVTHASRTERAVLI
DEVCTMNDGPHSALYTMKDKQYANYVVQKIDVAEPGQRKIVMHKIRPHIA
>d1ho8a_ a.118.1.9 (A:) Regulatory subunit H of the V-type ATPase {Baker's yeast (*Saccharomyces cerevisiae*)}
GATKILMDSTHFNEIRSIIRSRSVAWDALARSEELSEIDASTAKALESILVKKNIGDGLSSSNAHSGFK
VNGKTLIPLIHLSTSDNEDCKKSVQNLIAELLSSDKYGD DTVKFFQEDPKQLEQLFDVSLKGFQTV
LISGFNVVSLVQNGLHNVKLVEKLLKNNLNILQNIQMDTCYVCIRLLQELAVIPEYRDVIWLHE
KKFMPTLFKILQRATDSQLATRIVATNSNHLGIQLQYHSLLLIWLTFNPFANELVQKYLSDFLDLL
KLVKITIKEKVSRLCISIILQCCSTRVKQHKKVIKQLLLGNALPTVQSLSERKYSDEELRQDISNLKEIL
ENEYQELTSFDEYVAELDSKLLCWSPPHVDNGFWSNIDEFKKDNYKIFRQLIELLQAKVRNGDVN
AKQEKIIIQVALNDITHVVPELLPESIDVLDKTTGGKADIMELLNHSDSRVKYEALKATQAIIGYTFK
>d1ycsb1 a.118.2.1 (B:327-456) 53BP2 {Human (*Homo sapiens*)}
PLALLDSSLEGEFDLVQRIIEVDDPSLPNDEGITALHNAVCAGHTEIVKFLVQFGVNVNAADSDGW
TPLHCAASCNNVQVCKFLVESGAAVFAMTYSDMQTAADKCEEMEEGYTQCSQFLYGVQEKMG
>d1awcb_ a.118.2.1 (B:) GA binding protein (GABP) beta 1 {Mouse (*Mus musculus*)}
DLGKKLLEAARAGQDDEVRI LMANGAPFTTDWLGTSPHLAAQYGHFSTTEVLLRAGVSRDARTKV
DRTPLHMAASEGHANIVEVLLKHGADVNAKDMKMTALHWATEHNHQEVEVLLIKYGADVHTQS
KFCKTAFDISIDNGNEDLAEILQ
>d1bd8_ a.118.2.1 (-) Cell cycle inhibitor p19ink4D {Human (*Homo sapiens*)}
RAGDRLSGAAARGDVQEVRRLLHRELVHPDALNRFGKTALQVMMFGSTAIALELLKQGASPNVQDT
SGTSPVHDAARTGFLDTLKVLEHGADVNVDPDGTGALPIHLAVQEGHTAVVSFLAAESDLHRRDAR
GLTPELALQRGAQDLVDILQGHM
>d1blxb_ a.118.2.1 (B:) Cell cycle inhibitor p19ink4D {Mouse (*Mus musculus*)}
VCVGDRLSGAAARGDVQEVRRLLHRELVHPDALNRFGKTALQVMMFGSPAVALLELLKQGASPNVQD
ASGTSPVHDAARTGFLDTLKVLEHGADVNALDSTGSLPIHLAIREGHSSVVSFLAPESDLHHRDASG
LTPLELARQRGAQNLMDILQGHMMIP
>d1ihba_ a.118.2.1 (A:) p18ink4C(ink6) {Human (*Homo sapiens*)}
WGNELASAAARGDLEQLTSLQNNVNVNAQNGFGR TALQVMKLG NPEIARRLLLLRGANPDLKDRT
GFAVIHDAARAGFLDTLQTLLEFQADVNIEDNEGNLPLHLAAKEGHLRVVEFLVKHTASNVGHRNH
KGDTACDLARLYGRNEVVSLMQANG
>d1a5e_ a.118.2.1 (-) Cell cycle inhibitor p16ink4A {Human (*Homo sapiens*)}
MEPAAGSSMEPSADWLATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMMG SARVAELLLL
HGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYL

RAAAGGTRGSNHARIDAAEGPSDIPD

>d1bi7b_ a.118.2.1 (B:) Cell cycle inhibitor p16ink4A {Human (Homo sapiens)}

EPSADWLATAAARGRVEEVRALLEAGANPNAPNSYGRRIQVMMMG SARVAELLLLHGAEPNCAD
PATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAA

>d1iknd_ a.118.2.1 (D:) I-kappa-B-alpha {Human (Homo sapiens)}

DGDSFLHLAIHHEEKALTEMEVIRQVKGDLAFLNFQNNLQQTPLHLAVITNQPEIAEALLGAGCDPELR
DFRGNTPLHLACEQGCLASVGVLTQSCTTPHLHSILKATNYNGHTCLHLASIHGYLGIVELLVSLGAD
VNAQEPNCNGRTALHLAVDLQNPDLVSLLLKCGADVNRVITYQGYSPYQLTWGRPSTRIQQQLGQLTLE
NLQMLPESEDEESYDTES

>d1k1aa_ a.118.2.1 (A:) bcl-3 {Human (Homo sapiens)}

EDGDTPLHIAVVQGNLPAVHRLVNLVQGGRELDIYNNLRQTPLHLAVITTLPSVVRLLVTAGASPM
ALDRHGQTA AHLACEHRSPTCLRALDLSAAPGTLDEARNYDGLTALHVAVNTECQETVQLLLERG
ADIDAVIDIKSGRSPLIHAVENNSLSMVQLLLQHGAVNAQMYSGSSALHSASGRGLLPLVRTLVRSGA
DSSLKNCHNDTPLMVARSRRVIDILRG

>d1myo_ a.118.2.1 (-) Myotrophin {Rat (Rattus norvegicus)}

MCDKEFMWALKNGDLDEVKDYVAKGEDVNRITLEGGRKPLHYAADCGQLEILEFLLLKGADINAPD
KHHITPLLSAVYEGHVSCVKLLLSKGGADKTVKGPDGLTALEATDNQAIKALLQ

>d1sw6a_ a.118.2.1 (A:) Swi6 ankyrin-repeat fragment {Baker's yeast (Saccharomyces cerevisiae)}

GPIITFTHDLTSDFLSSPLKIMKALPSPVVNDNEQMKLEAFLQRLFPFIQEMPTSLNNDSSNRNSE
GGSSNQQQHVFSFDLLQEVNDAFPNTQLNINIPVDEHGNTPLHWLTSIANLELVKHLVKHGSNRL
YGDNMGESCLVKAVKSVNNYDSGTFEALDYLYPCLILEDSMNRTILHHIITSGMTGCSAAAKYYLDI
LMGWIVKKQNRPIQSGTNEKESKPNKNGERKDSILENLDLKWIIANMLNAQDSNGDTCLNIAARL
GNISIVDALLDYGADPFIANKSGLRPVDFGAG

>d1dcqa1 a.118.2.1 (A:369-522) Pyk2-associated protein beta {Mouse (Mus musculus)}

ADTAAKLHSLCEAVKTRDIFGLLQAYADGVDLTEKIPLANGHEPDETALHLAVRSVDRTSLHIVDFLV
QNSGNLDKQTKGSTALHYCCLTDNAECLKLLLRGKASIEIANESGETPLDIAKRLKHEHCEELLTQA
LSGRFNHSHVHVEYEWRL

>d1pbv_ a.118.3.1 (-) Exchange factor ARNO {Human (Homo sapiens)}

ANEGSKTLQRNRKMAMGRKKFNMDPKKGIQFLVENELLQNTPEEIARFLYKGEGLNKTAGDYLGE
REELNLAVLHAFVDLHEFTDLNLVQALRQFLWSFRLPGEAQKIDRMMEAFQAQRYCLCNPVGFQSTD
TCYVLSFAVIMLNTSLHNPVNRDKPGLERFVAMNRRGINEGGDLPEELLRNLYDSIRNEPFKIP

>d1bc9_ a.118.3.1 (-) Cytohesin-1/b2-1 {Human (Homo sapiens)}

MKNMQRNKQVAMGRKKFNMDPKKGIQFLIENDLLKNTCEDIAQFLYKGEGLNKTAGDYLGERDEF
NIQVLHAFVELHEFTDLNLVQALRQFLWSFRLPGEAQKIDRMMEAFQAQRYCQCNGVGFQSTDTCYV
LSFAIIMLNTSLHNPVVKDKPTVERFIAMNRRGINDGGDLPEELLRNLYESIKNEPFKIPELEHHHHH
H

>d1qsaa1 a.118.5.1 (A:1-450) 70 KDa soluble lytic transglycosylase (SLT70), superhelical domain {Escherichia coli}

DSLDEQRSRYAQIKQAWDNRQMDVVEQMMPGLKDYPLYPYLEYRQITDDL MNQPAVTVTNFVRAN
PTLPPARTLQSRFVNELARREDWRGLLAFSPEKPGTTEAQCNYYYAKWNTGQSEAWQGAKEWL
TGKSQPNACDKLFSVWRASGKQDPLAYLERIRLAMKAGNTGLVTVLGQMPADYQTIASAIISLANN
PNTVLT FARTTGATDFTRQMAAVAFASVARQDAENARLMIPSLAQAQQLNEDQIQELRDIVAWRLM
GNDVTDEQAKWRDDAIMRSQSTS LIERRVRMALGTGDRRLNTWLARLPMEAKEKDEWRYWQA

DLLEERGAEAEKEILHQLMQQRGFYPMVAAQRIGEEYELKIDKAPQNVDSALTQGPENARVRELM
YWNLDNTARSEWANLVKSKSKTEQAQLARYAFNNQWWDLQSVQATIAGKLWDHLEERFP
>d1d8da_ a.118.6.1 (A:) Protein farnesyltransferase alpha-subunit {Rat (Rattus norvegicus)}
FLSLDSPTYVLYRDRAEWADIDPVPQNDGPPVQIYSEKFRDQVYDYFRAVLQRDERSERAFKLTRD
AIELNAANYTVWHFRRVLLRSLQKDLQEEMNYIIAIIIEEQPKNYQVWHHRRVLVEWLKDPQSQELEFI
ADILNQDAKNYHAWQHRQWVIQEFRLWDNELQYVDQLLKEDVRNNSVWNQRHFVISNTTGYSR
AVLEREVQYTLEMILVPHNESAWNYLKGILQDRGLSRYPNLLNQLLDLQPSHSSPYLIAFLVDIYED
MLENQCDNKEDILNKALELCEILAKEKDTIRKEYWRYIGRSLQSKHSRESIPASV
>d1jcqa_ a.118.6.1 (A:) Protein farnesyltransferase alpha-subunit {Human (Homo sapiens)}
FVSLDPSYVLYRDRAEWADIDPVPQNDGPNPQVQIYSDKFRDQVYDYFRAVLQRDERSERAFKLTR
DAIELNAANYTVWHFRRVLLKSLQKDLHEEMNYITAIIEEQPKNYQVWHHRRVLVEWLDRDPSQELE
FIADILNQDAKNYHAWQHRQWVIQEFKLDNELQYVDQLLKEDVRNNSVWNQRYFVISNTTGYN
DRAVLEREVQYTLEMILVPHNESAWNYLKGILQDRGLSKYPNLLNQLLDLQPSHSSPYLIAFLVDIY
EDMLNQCNDKEDILNKALELCEILAKEKDTIRKEYWRYIGRSLQSKH
>d1dcea1 a.118.6.1 (A:1-240,A:351-443) Rab geranylgeranyltransferase alpha-subunit,
N-terminal domain {Rat (Rattus norvegicus)}
MHGRLKVKTSEEQAEAKRLEREQKLKLYQSATQAVFQKRQAGELDESVELETSQILGANPDFATLWN
CRREVQLHLETEKSPEESAALVKAELGFLESLRVNPKSYGTWHHRCWLLSRLPEPNWARELELCA
RFLEADERNFHCWDYRRFVAAQAAVAPAEELAFDSLITRNFSNYSSWHYRSCLLPQLHPQPDSGP
QGRLPENVLLKELELVQNAFFTDPNQSAWFYHRWLLGRAEXLFRCELSVEKSTVLQSELESCKEL
QELEPENKWCLLTIILLMRALDPLLYEKETLQYFSTLKAVDPMRAAYLDDLRSKFLENSVLKMEYA
DV
>d1qjba_ a.118.7.1 (A:) zeta isoform {Human (Homo sapiens)}
MDKNELVQKAKLAEQAERYDDMAACMKSVTEQGAELSNEERNLLSVAYKNVVGARRSSWRVSSI
EQKTEGAEEKQMQMAREYREKIETELRDICNDVLSLLEKFLIPNASQAESKVFYLMKMGDYRYLAEV
AAGDDKKGIVDQSQAYQEAFAEISKKEMQPTHPIRLGLALNFSVFYIEILNSPEKACSLAKTAFDEAI
AELDTLSEESYKDSTLIMQLLRDNLTLWTSDT
>d1a17_ a.118.8.1 (-) Protein phosphatase 5 {Human (Homo sapiens)}
PPADGALKRAEELKTQANDYFKAKDYENAIKFYSQAIELNPSNAIYYGNRSLAYLRTECYGYALGDAT
RAIELDKKYIKGYRRAASNALGKFRAALRDYETVVKVKPHDKDAKMKYQECNKIVKQKAFERAI
AGDEHKRSVDSLIESMTIEDEYS
>d1elra_ a.118.8.1 (A:) Hop {Human (Homo sapiens)}
GKQALKEKELGNDAYKKKDFDTALKHYDKAKELDPTNMTYITNQAQAVYFEKGDYNKCRELCEKAIE
VGRENREDYRQIAKAYARIGNSYFKEEKYKDAIHFYNKSLAEHRTPDVLKCCQQAEEKILKEQ
>d1elwa_ a.118.8.1 (A:) Hop {Human (Homo sapiens)}
EQVNELKEKGNKALSVGNIDDALQCYSEAIKLDPHNHVLYSNRSAAYAKKGDYQKAYEDGCKTVDLK
PDWGGKYSRKAALAEFLNRFEAKRTEYEEGLKHEANNPQLKEGLQNMEAR
>d1qqa_ a.118.8.1 (A:) Vesicular transport protein sec17 {Baker's yeast (Saccharomyces
cerevisiae)}
ISDPVELLKRAEKKGVPSSGFMKLFSGSDSYKFEEAADLCVQAATYRLRKELNLAGDSFLKAADYQK
KAGNEDEAGNTYVEAYKCFKSGNSVNAVDSLENAIQIFTHRGQFRRGANFKFELGEILENDLHDYA
KAIDCYELAGEWYAQDQSVALSINKCFIKCADLKALDQYIEASDIYSKLIKSSMGNRLSQWSLKDYFL
KKGLCQLAATDAVAAARTLQEGQSEDPNFADSRESNFKSLIDAVNEGDSEQLSEHCKEFDNFMRLD
KWKITILNKIKESIQQQEDD

>d1hh8a_ a.118.8.1 (A:) Neutrophil cytosolic factor 2 (NCF-2, p67-phox) {Human (Homo sapiens)}

SLVEAISLWNEGVLAADKKDWKGALDAFSAVQDPHSRICFNIGCMYTLKNMTEAEKAFTRSINRDK
HLAVAYFQRGMLYYQTEKYDLAIKDLKEALIQLRGNQLIDYKILGLQFKLFACEVLYNIAFMYAKKEE
WKKAEELALATSMKSEPRHSKIDKAMECVWKQKLYEPVVIPVGRFRPNERQVAQL

>d1fcha_ a.118.8.1 (A:) Peroxin pex5 (peroxisomal targeting signal 1 (PTS1) receptor) {Human (Homo sapiens)}

SATYDKGYQFEEENPLRDHPQPFEGLRRLQEGDLPNVLLFEAAVQDQPKHMEAWQYLGTQAE
NEQELLAISALRRCLELKPNDQTALMALAVSFTNESLQRQACEILRDWLRYPAYAHLVTPAEEGAG
GAGLGPSCRILGSLSDSLFLEVKELFLAAVRLDPTSIDPDVQCGLGVLFNLSGEYDKAVDCFTAALSV
RPNDYLLWNKLGATLANGNQSEEAVAAYRRALELQPGYIRSRYNLGISCINLGAHREAVEHFLEALN
MQRKSRGPRGEGGAMSENIWSTLRLALSMLGQSDAYGAADARDLSTLLTMFGLPQ

>d1hxia_ a.118.8.1 (A:) Peroxin pex5 (peroxisomal targeting signal 1 (PTS1) receptor) {Trypanosoma brucei}

NNTDYPFEANNPYMYHENPMEEGLSMLKLANLAEAAAFEAVCQKEPEREAEWRSLGLTQAENEK
DGLAIIALNHARMLDPKDIHVHAALAVSHTNEHNANAALASLRAWLL

>d1ihga1 a.118.8.1 (A:197-365) Cyclophilin 40 {Cow (Bos taurus)}

GSGDShPDFPEDADVDLKDVDKILLISED LKNIGNTFFKSQNWEMAIKKYTKVLRVVEGSRAAAED
ADGAKLQPVALSCLVNLGACKLKMSDWQGAVDSCLEALEIDPSNTKALYRRAQGWQGLKEYDQALA
DLKKAQEIAPEDKAIQAELLKVKQKIKAKDKKEKAAAY

>d1iipa1 a.118.8.1 (A:197-298) Cyclophilin 40 {Cow (Bos taurus)}

GSGDShPDFPEDADVDLKDVDKILLISED LKNIGNTFFKSQNWEMAIKKYTKVLRVVEGSRAAAED
ADGAKLQPVALSCLVNLGACKLKMSDWQGAVDSCLE

>d1hz4a_ a.118.8.2 (A:) Transcription factor MalT domain III {Escherichia coli}

EIKDIREDTMHAEFNALRAQVAINDGNPDEAERLAKLALALEELPPGWFYSRIVATSVLGEVLHCKGEL
TRSLALMQQTEQMARQHDVWHYALWSLIQQSEILFAQGFLQTAWETQEKAFLINEQHLEQLPMH
EFLVRIRAQLLWAWARLDEAEASARSIEVLSSYQPQQQLQCLAMLIQCSLARGDLNARSQNLNRL
NLLGNGKYHSDWISNANKVRVIYQMTGDKAAAANWLRHTAKPEFANNHFLQGQWRNIARAQIL
LGEFEPAEIVLEELNENARSLRLMSDLNRNLLLLNQLYWQAGRKSDAQRVLLDALKLANRTGFISHF
VIEGEAMAQQLRQLIQLNLTPELEQHRAQRILREIN

>d1eyha_ a.118.9.1 (A:) Epsin 1 {Rat (Rattus norvegicus)}

HNYSEAEIKVREATSNDPWGPSSSLMSEIADLTYNVVAFFSEIMSMIWKRLNDHGKNWRHVYKAMT
LMEYLIKTSERVSQCKENMYAVQTLKDFQYVDRDGKQGVNVREKAKQLVALLRDEDRLREERA
HALKTKEKLAQTA

>d1inza_ a.118.9.1 (A:) Epsin 1 {Human (Homo sapiens)}

GSSRMSTSSLRRQMKNIHVHNYSEAEIKVREATSNDPWGPSSSLMSEIADLTYNVVAFFSEIMSMIWK
LNDHGKNWRHVYKAMTLMYLIKTSERVSQCKENMYAVQTLKDFQYVDRDGKQGVNVREKA
KQLVALLRDEDRLREER

>d1dvpa1 a.118.9.2 (A:1-145) Hrs {Fruit fly (Drosophila melanogaster)}

MFRSSFCKNLENATSHLRLEPDWPSILLICDEINQKDVTPKNAFAAIKKKMNSPNPHSSCYSLLVLES
IVKNCGAPVHEEVFTKENCCEMFSSFLESTPHENVRQKMLELVQTWAYAFRSSDKYQAIKDTMTILKA
KGHTFPPELRE

>d1elka_ a.118.9.2 (A:) Tom1 protein {Human (Homo sapiens)}

SDFLLGNPFSSPVGQRIEKATDGSLSQSEDWALNMEICDIINETEEGPKDALRAVKKRIVGNKNFHEV

MLALTVLETCVKNCGHRFHVLVASQDFVESVLVRTILPKNNPPTIVHDKVLNLIQSWADAFRSSPDLT
GVVTIYEDLRRKGLEFPM

>d1juqa_a.118.9.2 (A:) Gga3 {Human (Homo sapiens)}

ESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEGPQIAVRLLAHKIQSPQEWALQALTVEACM
KNCGRRFHNEVGKFRFLNELIKVVSPKYLGDVSEKVKTKVIELLYSWTMALPEEAKIKDAYHMLKR
QGIVQSDPPIPVDRTLI

>d1hf8a_a.118.10.1 (A:) Clathrin assembly lymphoid myeloid leukaemia protein, Calm {Rat
(Rattus norvegicus)}

GSAVSKTVCKATTHEIMGPKKKHLDYLIQCTNEMNVNIPQLADSLFERTTNSSWVVFKSLITTHHL
MVYGENERFIQYLASRNTLFNLSNFLDKSGLQGYDMSTFIRRYRYLNEKAVSYRQVAFDFTKVKRGA
DGMVMTMTEKLLKTVPPIQNQMDALLDFNVNSNELTNGVINA AFMLLFKDAIRLFAAYNEGIINLL
EKYFDMKKNQCKEGLDIYKKFLTRMTRISEFLKVAEQVGIDRGDIPDLSQAPSSLLDALEQH

>d1hx8a_a.118.10.1 (A:) AP180 (Lap) {Fruit fly (Drosophila melanogaster)}

QGLAKSVCKATTEECIGPKKKHLDYLVHCANEPNVSIPHLANLLIERSQANANWVVVYKSLITTHHLM
AYGNERFMQYLASSNSTFNLSSFLDKGTVQDGGMGVPGGRMGYDMSPFIRRYAKYLNEKSLSYRAM
AFDFCKVKRGKEEGLSRMNAEKLLKTLPLVLAQLDALLEFDCQSNDSLNGVINMSFMLLFRDLRL
FACYNDGIINLLEKYFDMNKKHARDALDLYKKFLVRMDRVGEFLKVAENVGIDKGDIPDLTKAPSSL
LDALEQHLATL

>d1kpsb_a.118.12.1 (B:) Ran-GTPase activating protein 1 (RanGAP1), C-terminal domain
{Mouse (Mus musculus)}

TDLSTFLSFPSEKLLRLGPKVSVLIVQQTDTSDPEKVVSAFLKVASVFRDDASVKTAVLDAIDALMK
KAFSCSSFNSNTFLTRLLIHMGLLKSEDKIKAIPSLHGPLMVLNHVVRQDYFPKALAPLLAFVTKPN
GALETCSFARHNLLQTYNI

>d1k8kg_a.118.13.1 (G:) Arp2/3 complex 16 kDa subunit ARPC5 {Cow (Bos taurus)}

ARFRKVDVDEYDENKFVDEDDGGDGQAGPDEGEVDSCLRQGNMTAALQAALKNPPINTKSQAVKD
RAGSIVLKVLI SFKANDIEKAVQSLDKNGVDLLMKYIYKGFESPSDNSSAVLLQWHEKALAAGGVGSI
VRVLTARKTV

>d1ocre_a.118.11.1 (E:) Cytochrome c oxidase subunit E {Cow (Bos taurus)}

SHGSHETDEEFDARWVTFYFNKPDIDAWELRKG MNTLVGYDLVPEPKIIDAALRACRRLNDFASAVRI
LEVVKDKAGPHKEIYPYVIQELRPTLNELGISTPEELGLDKV

>d1f8na1_a.119.1.1 (A:150-839) Lipoxigenase, C-terminal domain {Soybean (Glycine max),
isozyme L1}

VPSETPAPLVSYREEELKSLRGNGTGERKEYDRIYDYDVYNDLGNPDKSEKLARPVLGGSSTFPYPRR
GRTGRGPTVTDPNTEKQGEVVFYVPRDENLGHLSKDALEIGTKSLSQIVQPAFESAFDLKSTPIEFHS
FQDVHDLYEGGIKLP RDVISTIIPVIKELYRTDGQHILKFPQPHVVQVSQSAWMTDEEFAREMIAG
VNPCVIRGLEEFPPKSNLDP AIYGDQSSKITADSLDLGTYMDEALGSRRLFMLDYHDIFMPYVRQIN
QLNSAKTYATRITLFLREDGTLKPVAIELSLPHSAGDLSA AVSQVVLPAKEGVESTIWLLAKAYVIVND
SCYHQLMSHWLNTHAAMEPFVIATHRHLSVLHPYIKLLTPHYRNNMNINALARQSLINANGHIETTF
LPSKYSVEMSSAVYKNWVFTDQALPADLIKRGVAIKDPSTPHGVRLIEDYPYAADGLEIWAAIKTW
VQEYVPLYARDDDVKNDSELQHWWEAVEKGGHDLKDKPWWPKLQTLLEDLVEVCLIIIIWIASAL
HAAVNFQYPYGGIMNRPTASRRLPEKGTPEYEEMINNEKAYLRTITSKLPTLISLSVIEILSTHA
SDEVYLGQRDNPHWTS DSKALQAFQKFGNKLKEIEEKLVRNRNDPSLQGNRLGPVQLPYTLLYPSS
EEGLTFRGIPNSISI

>d1ik3a1_a.119.1.1 (A:168-857) Lipoxigenase, C-terminal domain {Soybean (Glycine max),

isozyme L3}

LPSETPAPLVKYREEELHNLRGDGTGERKEWERIYDYDVYNDLGDPAKGENHARVVLGGNDTFPYP
RRGRTGRKPTRKDPNSESRSDVYLPDEAFGHLKSSDFLTGLKSVSQNVLPQQSAFDLNFNTPRE
FDSFDEVHGLYSGGKLPDTHISKISPLVLEIFRTDGEQALKFPPPKVIQVSKSAWMTDEEFAREML
AGVNPNIIRCLKDFPPRSKLDQVYGDHTSQITKEHLEPNLEGLTVDEAIQNKRLFLLDHHDPIMPY
LRRINATSTKAYATRILFLKNDGTLRPLAIELSLPHQGDQSGAFSQVFLPADEGVESIIWLLAKAYV
VVNDSCYHQLVSHWLNTHAVVEPFIIATNRHLSVHPIYKLLHPHYRDTMNINGLARLSLVNDGGVI
EQTFWGRYSVEMSAVVYKDWVFTDQALPADLIKRGMAIEDPSCPHGIRLVIEDYPYTVDGLIWD
IKTWVHEYVFLYKSDDTLREDPELQACWKELVEVGHGDKKNEPWWPKMQTREELVEACAIHW
ASALHAAVNFGQYPYGGILNRPTLSRRFMPEKGSAYEELRKNPQKAYLKTITPKFQTLIDLSVIEIL
SRHASDEVYLGGERDNPWNTSDTRALEAFKRFGNKLAQIENKLSERNNDEKLRNRCGPVQMPYTL
LPSSKEGLTFRGIPNSISI

>d1lox_1 a.119.1.2 (113-663) 15-Lipoxygenase {Rabbit (*Oryctolagus cuniculus*)}

TGCTTVGDPQGLFQKHREQELEERRKLYQWGSWKEGLILNVAGSKLTDLPVDERFLEDKIDFEASL
AWGLAELALKNSLNILAPWKTLDNFNRFWCGRSKLARRVRDSWQEDSLFGYQFLNGANPMLLR
SVQLPARLVFPFGMEELQAQLEKELKAGTLFEADFALLDNIKANVILYCCQYLAAPLVMLKLQPDGK
LMPMVIQLHLPKIGSSPPPLFLPTDPPMVWLLAKCWWRSSDFQVHELNSHLLRGHLMAEFTVAT
MRCLPSIHPVFKLIVPHLRYTLEINVRARNGLVSDFGIFDQIMSTGGGGHVQLLQAGAFITYRSFCPP
DDLADRGLLGVESFYAQDALRLWEIISRYVQGIMGLYKTDCAVRDDLELQSWCREITEIGLQGAQK
QGFPTSLQSVAAQACHFVTMCIFTCTGQHSSIHGLQDWFTWVNPACTMRLPPPTTKDATLETVMA
TLPNLKQSSLQMSIVWQLGRDQPMVPLGQHQEYFSGPEPRAVLEKFREELAIMDKIEVRNEKLD
IPYEYLRPSIVENSVAI

>d1c1ka_a.120.1.1 (A:) gene 59 helicase assembly protein {Bacteriophage T4}

MIKLMPAGGERYIDGKSVYKLYLMIKQHMNGKYDVIKYNWCMRVSDAAYQKRRDKYFFQKLESEY
KLKELALIFISNLVANQDAWIGDISDADALVFYREYIGRLKQIKFKFEEDIRNIYYFSKKVEVSFAK
EYNPVKVQSSYIFKLLQSNISFETFILDSFLNIIDKHDEQTDNLVWNNYSIKLKAYRKILNIDSQKAKN
VFIETVKSKY

>d2tct_2 a.121.1.1 (68-208) Tetracyclin repressor (Tet-repressor, TetR) {*Escherichia coli*}

LPAAGESWQSFLRNNAMSFRRALLRYRDGAKVHLGTRPDEKQYDTVETQLRFMTENGFSRLDGLY
AISAVSHFTLGAVLEQQEHTAALTDRPAAPDENLPPLLREALQIMDSDDGEQAFHLGLESIRGFEVQ
LTALLQIV

>d1jt6a2 a.121.1.1 (A:73-187) Multidrug binding protein QacR {*Staphylococcus aureus*}

KTNREKFYLYNELSLTTEYYYYPLQNAIIEFYTEYYKTNSINEKMNKLENKYIDAYHVIFKEGNLNGEW
SINDVNAVSKIAANAVNGIVTFTHEQNINERIKLMNKFSQIFLNGLS

>d1fqva1 a.122.1.1 (A:107-145) Skp1-Skp2 dimerisation domains {Human (*Homo sapiens*)}

VSWDSLPEDELLGIFSCCLPELLKVSQVCKRWYRLASD

>d1fqvb1 a.122.1.1 (B:85-160) Skp1-Skp2 dimerisation domains {Human (*Homo sapiens*)}

IPVWDQEFLKVDQGTLELILAAANYLDIKGLLDVTCKTVANMIKGTPEEIRKTFNIKNDFTEEEEAQ
VRKENQWC

>d1fs1a1 a.122.1.1 (A:109-149) Skp1-Skp2 dimerisation domains {Human (*Homo sapiens*)}

WDSLPEDELLGIFSCCLPELLKVSQVCKRWYRLASDESLW

>d1fs1b1 a.122.1.1 (B:86-140) Skp1-Skp2 dimerisation domains {Human (*Homo sapiens*)}

PVWDQEFLKVDQGTLELILAAANYLDIKGLLDVTCKTVANMIKGTPEEIRKTFN

>d1fs2b1 a.122.1.1 (B:80-146) Skp1-Skp2 dimerisation domains {Human (*Homo sapiens*)}

KRTDDIPVWDQEFLKVDQGTLELILAANYLDIKGLLDVTCKTVANMIKGTKPEEIRKTFNIKNDFT
>d1g5ya_a.123.1.1 (A:) Retinoid-X receptor (RXR-alpha) {Human (Homo sapiens)}
PVERILEAEALAVEPKTETYVEANMGLNPSSPNPVTNICQAADKQLFTLVEWAKRIPHFSELPLDDQ
VILLRAGWNEILLASFSHRSAIVKDGILLATGLHVHRNSAHSAGVGAIFDRVLTVELVSKMRDMQMDK
TELGCLRAIVLFNPDSKGLSNPAEVEALREKVYASLEAYCKHKYPEQPGRFAKLLLRLPALRSIGLKCL
EHLFFFKLIGDTPIDTFLMEMLEAP
>d1dkfb_a.123.1.1 (B:) Retinoic acid receptor alpha (RAR-alpha) {Human (Homo sapiens)}
PEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIKTFEFAKQLPGF
TTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFAFANQLLP
LEMDDAETGLLSAICLICGDRQDLEQPDRVDMLEQPLEALKVYVRKRRPSRPHMFPKMLMKITDL
RSISAKGAERVITLKMEIPGSMPLIQEMLEN
>d1fcya_a.123.1.1 (A:) Retinoic acid receptor gamma (RAR-gamma) {Human (Homo sapiens)}
ASPQLEELITKVSKAHQETFPSLCQLGKYTTNSSADHRVQLDLGLWDFSELATKCIKIVEFAKRLP
GFTGLSIADQITLLKAACLDILMLRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFAFAGQ
LLPLEMDDTETGLLSAICLICGDRMDLEEPEKVDKLEQPLEALRLYARRRRPSQPYMFPRMLMKIT
DLRGISTKGAERAITLKMEIPGMPPLIREMLE
>d1a28a_a.123.1.1 (A:) Progesterone receptor {Human (Homo sapiens)}
QLIPPLINLLMSIEPDVIYAGHDNTKPDTSLLTSLNQLGERQLLSVVKWSKSLPGFRNLHIDDQITLI
QYSWMSLMVFGWRSYKHSVSGQMLYFAPDLILNEQRMKESFYSLCLTMWQIPQEFVKLQVSQEE
FLCMKVLNLLNTIPLEGLRSQTQFEEMRSSYIRELIKAIGLRQKGVVSSSRFYQLTKLLDNLHDLVKQ
LHLYCLNTFIQSRALSVEFPEMMSEVIAAQLPKILAGMVKPLL FHK
>d3erda_a.123.1.1 (A:) Estrogen receptor alpha {Human (Homo sapiens)}
SLALSLTADQMVSALLDAEPPILYSEYDPTPRPFSEASMMGLTNLADRELVHMINWAKRVPGFVDLT
LHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVGEMVEIFDMLLATSSRFMR
MNLQGEFVCLKSILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITDTLIHLMAGLTLQQHQHQLA
QLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEMLDAHRLH
>d1qkma_a.123.1.1 (A:) Estrogen receptor beta {Human (Homo sapiens)}
LDALSPEQLVLTLLAEPPHVLISRPSAPFTEASMMMSLTKLADKELVHMISWAKKIPGFVELSLFDQ
VRLLESCWMEVLMVGLMWRSIDHPGKLIFAPDLVDRDEGKCVGILEIFDMLLATTSRFRELKQLQ
HKEYLCVKAMILLNSSMYPLVTATQDADSSRKLHLLNAVTDALVWVIAKSGISSQQQSMRLANLL
MLLSHVRHASNKGMEHLLNMKCKNVVVPYDLLLLLEMLNAHVL
>d1qkna_a.123.1.1 (A:) Estrogen receptor beta {Rat (Rattus norvegicus)}
TLSPEQLVLTLLAEPPNVLSRPSMPFTEASMMMSLTKLADKELVHMIGWAKKIPGFVELSLLDQV
RLLESCWMEVLMVGLMWRSIDHPGKLIFAPDLVDRDEGKCVGILEIFDMLLATTSRFRELKQLQ
KEYLCVKAMILLNSSMYPLASANQEAESSRKLTHLLNAVTDALVWVIAKSGISSQQQSVRLANLLML
LSHVRHISNKGMEHLLSMKCKNVVVPYDLLLLLEMLNA
>d1i37a_a.123.1.1 (A:) Androgen receptor {Rat (Rattus norvegicus)}
IFLNVLEAIEPGVVCAGHDNNQPDSFAALLSSLNELGERQLVHVVKWAKALPGFRNLHVDDQMAVI
QYSWMGLMVFAMGWSFTNVNSRMLYFAPDLVFNEYRMHKSRMYSQCVRMRHLSQEFGWLQIT
PQEFKCMKALLLSIIPVDGLKNQKFFDELRMNYIKELDRIIACKRKNPTSCSRRFYQLTKLLDSVQPI
ARELHQFTFDLLIKSHMVSVDPEMMAEHSVQVPKILSGKVKPIYFH
>d1k7la_a.123.1.1 (A:) Peroxisome proliferator activated receptor alpha, PPAR-alpha
{Human (Homo sapiens)}

DLKSLAKRIYEAYLKNFNMNKVKARVILSGKASNNPPFVIHDMETLCMAEKTIVAKLVANGIQNKEA
EVRIFHCCQCTSVETVTELTEFAKAIPGFANLDLNDQVTLTKYGVYEAIFAMLSSVMNKDGMVAYGN
GFITREFLKSRLKPKFCDIMEPKFDFAMKFNALDSDISLVAIIICCGDRPGLLNVGHIEKMQEGIV
HVLRLHLQSNHPDDIFLFPKLLQKMADLRQLVTEHAQLVQIHKKTESDAALHPLLQEIYRDMY
>d2prga_ a.123.1.1 (A:) Peroxisome proliferator activated receptor gamma, PPAR-gamma
{Human (Homo sapiens)}
ESADLRALAKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQS
KEVAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLTKYGVHEIITMLASLMNKDGVLISE
GQGFMTREFLKSRLKPKFDFMEPKFEFAVKFNALDSDLAIFIAVIIISGDRPGLLNKPIEDIQDN
LLQALELQLKLNHPSSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIKDLY
>d2gwx_ a.123.1.1 (A:) Peroxisome proliferator-activated receptor delta, PPAR-DELTA
{Human (Homo sapiens)}
LKAFSKHIYNAYLKNFNMTKKARSILT GKASHTAPFVIHDIETLWQA EKGLVWKQLVNGLPYKEIS
VHVYFRCQCTTVETVRELTEFAKSIPSFSSFLNDQVTLTKYGVHEAIFAMLASIVNKDGLLVANGSGF
VTREFLSRLKPKFSDIIEPKFEFAVKFNALDSDLALFIAAIIICGDRPGLMNVPRVEAIQDTILRAL
EFHLQANHPDAQQLFPKLLQKMADLRQLVTEHAQMMQRIKKTETETSLHPLLQEIKDM
>d1ilga_ a.123.1.1 (A:) Pregnane x receptor, PXR {Human (Homo sapiens)}
GLTEEQRMMIRELMDAQMKTFDITFSHFKNFRLPGVLSSGCELPESLQAPSREEAAKWSQVRKDLK
SLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLPHMADMSTYMFKGIISFAKVISYFRDLPIEDQISLL
KGA AFELCQLRFNTVFNAETGTWECGRLSYCLEDTAGGFQQLLEPMLKFHYMLKQLHEEEYVL
MQAISLSPDRPGVLQHRVVDQLQEQAIFLTKSYIECNRPQPAHRFLFLKIMAMLT ELSINAQHTQR
LLRIQDIHPFATPLMQELFGI
>d1ie9a_ a.123.1.1 (A:) Vitamin D nuclear receptor {Human (Homo sapiens)}
DSL RPKLSEEQQRIIAILLDAHHKTYDPTYSDFCQFRPPVRVNDGGGSVTLELSQLSMLPHLADLVSY
SIQKVIGFAKMIPGFRDLTSEDQIVLLKSSAIEVIMLRSNESFTMDDMSWT CGNQDYKYRVSDVTKAG
HSLELIEPLIKFQVGLKKNLH EEEHVLLMAICIVSPDRPGVQDAALIEAIQDRLSNTLQTYIRCRHPP
PGSHLLYAKMIQKLADLRSLNEEHSKQYRCLSFQPECSMKLTPLVLEVFG
>d1bsxa_ a.123.1.1 (A:) Thyroid hormone receptor beta (TR-beta) {Human (Homo sapiens)}
KPEPTDEEWELIKTVTEAHVATNAQGS HWKQKRKFLPEDIGQAPIVNAPEGGKVDLEAFSHFTKIIT
PAITRVVDFAKKLPFCELPCEQIILLKGCMEIMSLRAAVRYDPESETLTLNGEMAVTRGQLKNGG
LGVVSDAIFDLGMSLSSFNLDDETEVALLQAVLLMSSDRPGLACVERIEKYQDSFLLAFEHYINYRKH
VTHFWPKLLMKVTDLRMIGACHASRFLHMKVECPTELPPLFLEVFE
>d1hg4a_ a.123.1.1 (A:) Ultraspiracle protein, usp {Drosophila melanogaster}
FSIERIIEAEQRAETQCGDRALTF LRVGPYSTVQPDYKGA VSALCQVVNKQLFQMV EYARMMPHFAQ
VPLDDQVILLKAAWIELLIANVAWCSIVSLDDGGAGGGGGGLGHDGSFERRSPGLQPQLFLNQSFYS
HRNSAIKAGVSAIFDRILSELSVKMKRLNDRRELSCLKAIIYNPDIRGIKSRAEIEMCREKVYACLDE
HCRLEHPGDDGRFAQLLLRLPALRSISLKCQDHLFLFRITSDRPLEELFLEQLEAPPPG
>d1g2na_ a.123.1.1 (A:) Ultraspiracle protein, usp {Heliothis virescens}
AAVQELSIERLLEMESLVADPSEEFQLRVGPDSNVPPKFRAPVSSLCQIGNKQIAALVVWARDIPHFS
QLEMEDQILLIKGSWNELLLFAIAWRSMEFLTEERDGDVGTGNRTTSPQLMCLMPGMTLHRNSAL
QAGVGQIFDRVLSLSLKMRTL RVDQAEYVALKAIILLNPDVKGLKNRQEVEVLREKMFLCLDEYCR
RSRSSEEGRFAALLRLPALRSISLKSFEHLFFFHLVADTSIAGYIRDALRNHA
>d1ah7_ a.124.1.1 (-) Bacterial phospholipase C {Bacillus cereus}
WSAEDKHKEGVNSHLWIVNRAIDIMSRNTTLVKQDRVAQLNEWRTLENGIYAADYENPYDNTSF

ASHFYDPDNGKTYIPFAKQAKETGAKYFKLAGESYKNKDMKQAFFYLGLSLHYLGDVNQPMHAAN
FTNLSYPQGFHISKYENFVDTIKDNKYKVTGNGYWNWKGTPPEEWIHGAAVVAKQDYSIVNDNTK
DWFVKAASVQEQYADKWRAEVTTPMTGKRLMDAQRVTAGYIQLWFDTYGDR
>d1ca1_1 a.124.1.1 (1-249) Alpha-toxin, N-terminal domain {Clostridium perfringens}
WDGKIDGTGTHAMIVTQGVSIENDLSKNEPESVRKNLEILKENMHELQLGSTYDPYDKNAYDLYQ
DHFWDPTDNNFSKDNSWYLAYSIPDTGESQIRKFSALARYEWQRGNYKQATFYLGEMHYFGDI
DTPYHPANVTAVDSAGHVKFETFAEERKEQYKINTVGCKTNEDFYADILKNKDFNAWSKEYARGFA
KTGKSIYSHASMSHSWDDWDYAAKVTLANSQKGTAGYIYRFLHDVSEGNP
>d1ak0_ a.124.1.2 (-) P1 nuclease {Penicillium citrinum}
WGALGHATVAYVAQHYSPEAASWAQGILGSSSSSYLASIASWADEYRLTSAGKWSASLHFIDAEDN
PPTNCNVDYERDCGSSGCSISAIANYTQRVSDSSLSENHAEALRFLVHFVIGDMTQPLHDEAYAVGGN
KINVTFDGYHDNLHSDWDTYMPQKLIHGHALSDAESWAKTLVQNIESGNYTAQAIGWIKGDNISEPI
TTATRNASDANALVCTVVMPHGAAALQTGDLYPTYYSVIDTIELQIAKGGYRLANWINEIH
>d1f0ja_ a.125.1.1 (A:) Catalytic domain of cyclic nucleotide phosphodiesterase 4b2b
{Human (Homo sapiens)}
SISRFGVNTENEDHLAKELEDLNKWGLNIFNVAGYSHNRPLTCIMYAIQERDLLKTFRISSDTFITY
MMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPALDAVFTDLEILAAIFAAAIAHDVDHDPGVSNQFL
INTNSELALMYNDESVLENHHLAVGFKLLQEEHCDFMNLTKKQRQTLRKMVIDMVLATDMSKHM
SLLADLKT MVETKKVTSSGVLLLDNYTDRIQVLRNMVHCADLSNPTKSLELYRQWTD RIMEEFFQ
GDKERERGMESPMCDKHTASVEKSQVGFIDYIVHPLWETWADLVQPDAQDILD TLEDNRN WYQS
MIPQAPAPPLDEQNRDCQGLMEKFQF
>d1gnia1 a.126.1.1 (A:3-196) Serum albumin {Human (Homo sapiens)}
HKSEVAHRFKDLGEENFKALVLIAFAQYLQCPFEDHVKLVNEVTEFAKTCVADESAENCDSLHTL
FGDKLCTVATLRETYGEMADCCAKQEPERNECFQHKDDNP NLPRLVRPEVDVMCTAFHDNEETF
LKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDEL RDEGKASSAKQ
>d1gnia2 a.126.1.1 (A:197-388) Serum albumin {Human (Homo sapiens)}
RLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAK
YICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADPLSLAADFVESKDVCKNYAEAKDVFLGMF
LYEYARRHPDYSVVLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLI
>d1gnia3 a.126.1.1 (A:389-584) Serum albumin {Human (Homo sapiens)}
KQNCLEFELGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSV
VLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQI
KKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKADDKETCFAEEGKKLVAASQAALG
>d1j78a1 a.126.1.1 (A:13-198) Vitamin D binding protein {Human (Homo sapiens)}
CKEFSHLGKEDFTSLSLVLYSRKFPSTFEQVSQVLKEVVSLTEACCAEGADPDCYDTRTSALSASCSCE
SNSPFPVHPGTAECCTKEGLERKLCMAALKHQPPQEFPTYVEPTNDEICEAFRDKPKEYANQFMWEY
STNYGQAPLSLLVSYTKSYLSMVGSCCTSASPTVCFLKERLQLKHL SLLTT
>d1j78a2 a.126.1.1 (A:199-386) Vitamin D binding protein {Human (Homo sapiens)}
LSNRVCSQYAAAYGEKKSRLSNLIKLAQKVPTADLEDVPLAEDITNLSKCCESASEDCMAKELPEHTV
KLCDNLSTKNSKFEDCCQEK TAMDVFCYFMPAAQLPELDPVELPTNKDVCDP GNTKVM DKYTF
ELSRRTHLPEVFLSKVLEPTLKS LGCCDVEDSTTCFNAKGPLLKELSSFIDK
>d1j78a3 a.126.1.1 (A:387-457) Vitamin D binding protein {Human (Homo sapiens)}
GQELCADYSENTFTEYKKLAERLAKLPDATPTELAKLVNKRSDFASNCCSINSPPLYCDSEIDAEL
KNI

>d1jswa_a.127.1.1 (A:) L-aspartate ammonia lyase {Escherichia coli}

MSNNIRIEEDLLGTREVPADAYYGVHTLRAIENFYISNNKISDIPEFVRGMVMVKKAAAMANKELQT
IPKSVANAIIAACDEVLNNGKCMDQFPVDVYQGGAGTSVNMNTNEVLANIGLELMGHQKGEYQYLN
PNDHVNKCQSTNDAYPTGFRIAVYSSLIKLVDAINQLREGFERKAVEFQDILKMGRTQLQDAVPMTL
GQEFRAFSILLKEEVKNIQRTAELLLEVNLGATAIGTGLNTPKEYSPLAVKKLAEVTGFPCVPAEDLIE
ATSDCGAYVMVHGALKRLAVKMSKICNDLRLSSGPRAGLNEINLPELQAGSSIMPAKVNPPVPEVV
NQVCFKVIIGNDTTVMMAAEAGQLQLNVMEPVIGQAMFESVHILTNACYNLLEKCINGITANKEVCEG
YVYNSIGIVTYLNPFIGHHNGDIVGKICAETGKSVREVVLERGLLAEELDDIFSV

>d1jswc_a.127.1.1 (C:) L-aspartate ammonia lyase {Escherichia coli}

IRIEEDLLGTREVPADAYYGVHTLRAIENFYISNNKISDIPEFVRGMVMVKKAAAMANKELQTIPKSV
ANAIIAACDEVLNNGKCMDQFPVDVYQGGAGTSVNMNTNEVLANIGLELMGHQKGEYQYLNPNH
VNKCQSTNDAYPTGFRIAVYSSLIKLVDAINQLREGFERKAVEFQDILKMGRTQLQDAVPMTLGQEFR
AFSILLKEEVKNIQRTAELLLEVNLGATAIGTGLNTPKEYSPLAVKKLAEVTGFPCVPAEDLIEATSDC
GAYVMVHGALKRLAVKMSKICNDLRLSSGPRAGLNEINLPELQAGSSIMPAKVNPPVPEVVNQVCF
KVIGNDTTVMMAAEAGQLQLNVMEPVIGQAMFESVHILTNACYNLLEKCINGITANKEVCEGYVYNS
IGIVTYLNP

>d1fura_a.127.1.1 (A:) Fumarase {Escherichia coli}

VRSEKDSMGAIDVPADKLWGAQTQRSLEHFRISTEKMPTSLIHALALTKRAAAKVNEDLGLLSEEKA
SAIRQAADEVLAGQHDEFLAIWQTGSGTQSNMNMNEVLANRASSELLGGVRGMERKVVHPNDDV
NKSQSSNDVFPTAMHVAALLALRKQLIPQLKTLTQTLNEKSRAFADIVKIGRTNLQDATPLTLGQEIS
GWWAMLEHNLKHIEYSLPHVAELALGGTAVGTGLNTHPEYARRVADELAVITCAPFVTAPNKFEEALA
TCDALVQAHGALKGLAASLMKIANDVRWLASGPCRGIGEISIPENEPGSSIMPGKVNPTQCEALMLC
CQVMGNDVAINMGGASGNFELNVFRPMVIHNFQLQSVRLLADGMESFNKHCavgIEPNRERINQLLN
ESLMLVTALNTHIGYDKAAEIAKKAHKEGLTLKAAALALGYLSEAEFDSWVRPEQM

>d1yfm_a.127.1.1 (-) Fumarase {Baker's yeast (Saccharomyces cerevisiae)}

SFRTETDAFGEIHVPADKYWGAQTQRSFQNFKIGGARERMPLPLVHAFVGLKKSAAIVNESLGGGLDP
KISKAIQQADEVASGLDDHFLVVFQGTGSGTQSNMNEVISNRAIEILGGKIGSKQVHPNHNH
QSQSSNDTFPTVMHIAASLQIQNELIPELTNLKNALEAKSKEFDHIVKIGRTHLQDATPLTLGQEFSG
YVQQVENGIQ RVAHSLKTL SFLAQQGTAVGTGLNTPGFDVKIAEQISKETGLKFQTAPNRFEALAAH
DAIVECSGALNTLACSLFKIAQDIRYLGSRPCGYHELMLENENPGSSIMPGKVNPTQNEALTQVCVQ
VMGNNAITFAGSQGFELNVFKPVMIANLLNSIRLITDAAYSFRVHCVEGIKANEPRIHELLTKSLM
LVTALNPKIGYDAASKVAKNAHKKGITLKESALELGVLTEKEFDEWVPEHML

>d1k62a_a.127.1.1 (A:) Argininosuccinate lyase/delta-crystallin {Human (Homo sapiens)}

GAVDPIMEKFNASIAADRHLWEVDVQGSKAYSRLGKAGLLTKAEMDQILHGLDKVAEEWAQGTFK
LNSNDEDIHTANERRLKEKELIGATAGKLHTGRSRNDQVVTDLRLWMRQTCSTLSGLLWELIRTMVDR
AEAERDVLFPGYTHLQRAQPIRWSHWILSHAVALTRDSERLLEVRKRINVLPLGSGAIAGNPLGVDR
ELLRAELNFGAITLNSMDATSERDFVAEFLFWRSLCMTLSRMAEDLILYCTKEFSFVQLSDAYSTGS
SLMPRKNPDSLELIRSKAGRVFGRACAGLLMTLKGLPSTYNKDLQEDKEAVFEVSDTMSAVLQVATG
VISTLQIHQENMGQALSPDMLATDLAYYLVRKGMFPRQAHEASGKAVFMAETKGVNQLSLQELQ
TISPLFSGDVICVWDYRHSVEQYALGGTARSSVDWQIRQVRALLQAQQA

>d1auwa_a.127.1.1 (A:) Argininosuccinate lyase/delta-crystallin {Domestic duck (Anas platyrhynchos), delta-crystallin}

TDPIMEKLNSSIAVDQRLSEVDIQGSMAYAKALEKAGILTKTELEKILSGLEKISEEWSKGVFVVKQSD
EDINTANERRLKEKELIGDIAGKLHTGRSRNDQVVTDLKLFMKNLSIISTHLLQLIKTLVERAAIEIDVIL

PGYTHLQKAQPIRWSQFLLSHAVALTRDSERLGEVKKRINVLPFGSGALAGNPLDIDREMLRSELEFA
SISLNSMDAISERDFVVEFLSFATLLMIHLSKMAEDLIIYSTSEFGFLTDSDAFSTGSSLMPQKKNPDSL
ELIRSKAGRVFGRLASILMVLKGLPSTYNKDLQEDKEAVFDVVDTLTAVLQVATGVISTLQISKENME
KALTPEMLATDLALYLVRKGVFPRQAHTASGKAVHLAETKGITINKLSLEDLKSISPQFSSDVSQVFN
VNSVEQYTALGGTAKSSVTTQIEQLRELMKKQK

>d1dcnb_ a.127.1.1 (B:) Argininosuccinate lyase/delta-crystallin {Domestic duck (*Anas platyrhynchos*), delta-crystallin}

DPIMAKLNSSAIYDQRLSEVDIQGSMAYAKALEKAGILTKTELAKILSGLEKISEEDIHTANERRLKELI
GDIAGKLNTGRSRNDQVVTDLKLFMKNLSIISTHLLQLIKTLVERAAIEIDVILPGYTNLQKAQPIRW
SQFLLSHAVALTRDSERLGEVKKRINVLPFGSGALAGNPLDIDREMLRSELEFASISLNSMDAISERDF
VVEFLSFATLLMIHLSKMAEDLIIYSTSEFGFLTSPDSLELIRSKGRVFGRLASILMVLKGLPSTYNK
DLQEDKEAVFDVVDTLTAVLQVATGVISTLQISKENMEKALTPEMLATDLALYLVRKGVFPRQAHTAS
GKAVHLAETKGITINNLSLEDLKSISPQFSSDVSQVFNFNNSVEQYTALGGTAKSSVTTQIEQLRELMK
KQK

>d1hy0a_ a.127.1.1 (A:) Argininosuccinate lyase/delta-crystallin {Domestic duck (*Anas platyrhynchos*), delta-crystallin}

DPIMQMLSTSISTEQRLSEVDIQASIYAKALEKAGILTKTELEKILSGLEKISEELSKGVIVVTQSDEDI
QTANERRLKELIGDIAGKLHTGRSRNEQVVTDLKLFMKNLSIISTHLLQLIKTLVERAAIEIDVILPGY
THLQKAQPIRWSQFLLSHAVALTRDSERLGEVKKRINVLPFGSGALAGNPLDIDREMLRSELEFASIS
LNSMDAISERDFVVEFLSVATLLLIHLSKMAEDLIIYSTSEFGFLTSDAFSTGSSLMPQKKNPDSLELI
RSKGRVFGRLASILMVLKGLPSTYNKDLQEDKEAVIDVVDTLTAVLQVATGVISTLQISKENMEKALT
PEMLATDLALYLVRKGMFPRQAHTASGKAVHLAETKGIANNLTLEDLKSISPLFSSDVSQVFNFNNS
VEQYTALGGTAKSSVTTQIEQLRELMKKQKE

>d1i0aa_ a.127.1.1 (A:) Argininosuccinate lyase/delta-crystallin {Turkey (*Meleagris gallopavo*), delta-crystallin}

GRFVGSVDPIEILSSSISTEQRLTEVDIQASMAYAKALEKASILTKELEKILSGLEKISEESSKGVLM
TQSDEDIQTAIERRLKELIGDIAGKLQTGRSRNEQVVTDLKLLKSSISVISTHLLQLIKTLVERAAIEID
IIMPGYTHLQKALPIRWSQFLLSHAVALTRDSERLGEVKKRITVLPFGSVLAGNPLEIDRELLRSELD
MTSITLNSIDAISERDFVVELISVATLLMIHLSKLAEDLIIFSTTEFGFVTLSDAYSTGSSLLPQKKNPDS
LELIRSKAGRVFGRLAAILMVLKGPSTFSKDLQEDKEAVLDVVDTLTAVLQVATGVISTLQINKENME
KALTPELLSTDLALYLVRKGMPIRQAQTASGKAVHLAETKGITINNLTLEDLKSISPLFASDVSQVFSV
NSVEQYTAVGGTAKSSVTAQIEQLRELLKKQK

>d1c3ca_ a.127.1.1 (A:) Adenylosuccinate lyase {*Thermotoga maritima*}

VERYSLSPMKDLWTEEAKYRRWLEVELAVTRAYEELGMIPKGVTERIRNNAKIDVELFKKIEEKTN
HDVVAFVEGIGSMIGEDSRFFHYGLTSSDVLDTANSLALVEAGKILLESLEKFCVDLWEVANRYKHTP
TIGRTHGVHAEPTSFGLKVLGWYSEMKNRVQLERAIEEVSYGKISGAVGNYPPEVEEKALSYL
GLKPEPVSTQVPRDRHAFYLSLAIVAAGIERIAVEIRHLQRTEVLEVEEPFRKQQRGSSAMPHKKN
PITCERLTGLSRMMRAYVDPSLENIALWHERDISHSSVERYVFPDATQTLYYMIVTATNVVRNMKVN
EERMKNIDLTKGLVFSQRVLLKLIKGLTRKEAYDIVQRNALKTNWSEKHFLEYLLEDEEVKKLVT
KEELEELFDISYLLKHVDHIFERFEK

>d1dofa_ a.127.1.1 (A:) Adenylosuccinate lyase {Archaeon *Pyrobaculum aerophilum*}

HVSPFDWRYGSEEIRRLFTNEAIINAYLEVERALVCALEELGVAERGCCEKVNKASVSADEVYRLERE
TGHDILSLVLLLEQKSGCRYVHYGATSNDIIDTAWALLIRRALAAVKEKARAVGDQLASMARKYKTLE
MVGRTHGQWAEPITLGFKFANYYYELIACRQLALAEFIRAKIGGAVGTMASWGELGLEVRRRVAE

RLGLPHHVITTTQVAPRESFAVLASALALMAAVFERLAVEIRELSRPEIGEVEGGGGSSAMPHKANPT
ASERIVSLARYVRALTHVAFENVALWHERDLTNSANERVWIPEALLALDEILTSALRVLKNVYIDEER
ITENLQKALPYILTEFHMNRMIKEGASRAEAYKKAKEVKALTFEYQKWPVERLIEDALSCLK
>d1f1oa_ a.127.1.1 (A:) Adenylosuccinate lyase {Bacillus subtilis}
EMSAIWTDENRFQAWLEVEILACEAWAELGVIPKEDVKVMRENASFDINRILEIEKDTRHDVVAFT
RAVSESLGEERKWVHYGLTSTDVVDTALSLLKQANDILLKDLERFVDIIEKAKEHKYTVMMGRTH
GVHAEPTTFGLKLALWHEEMKRNLERFKQAKAGIEVGKISGAVGTIANIDPFVEQYVCEKLGLKAAP
ISTQTLQRDRHADYMATLALIATSIEKFAVEIRGLQKSETREVEEFFAKGQKGSAMPHKRNPIGSEN
MTGMARVIRGYMMTAYENVPLWHERDISHSSAERIILPDATIALNYMLNRFNIVKNLTVFPENMK
RNMDRTLGLIYSQRVLLALIDTGLTREEAYDTVQPKAMEAWEKQVPPFRELVEAEKITSRLSPEKIAD
CFDYN
>d1gk2a_ a.127.1.2 (A:) Histidine ammonia-lyase (HAL) {Pseudomonas putida}
TELTLPKPGTLTQLRAIHAAPVRLQLDASAAPIDASVACVEQIIAEDRTAYGINTGFLLASTRIASH
DLENLQSRSLVLSHAAGIAPLDDDLVRLIMVLKINSLSRGFSGIRRKVIDALIALVNAEVYPHIPLKGSV
GASGDLAPLAHMSLVLLGEGKARYKGQWLSATEALAVAGLEPLTLAAKEGLALLNGTQASTAYALRG
LFYAEDLYAAAACGGLSVEAVLGSRSFPDARIHEARGQRGQIDTAACFRDLLGDSSEVSLSHKNADKV
QDPYSLRCQPQVMGACLTQLRQAAEVLGIEANAVSDNPLVFAAEGDVISGGNGHAEPVAMAADNLA
LAIAEIGLSERRISLMMDKHMSQLPPFLVENGGVNSGFMIAQVTAALASENKALSHPHSVDSLPTS
ANQEDHVSMAAAGKRLWEMAENTRGVLAIEWLGACQGLDLRKLKTSAKLEKARQALRSEVAHY
DRDRFFAPDIEKAVELLAKGSLTGLLPAGVPLPSL
>d1uby_ a.128.1.1 (-) Farnesyl diphosphate synthase {Chicken (Gallus gallus)}
SPVVVEREREFEVGFPPQIVRDLTEDGIGHPEVGDVARLKEVLQYNAPGGKCNRGLTVVAAAYRELSG
PGQKDAESLRCALAVGWCIELFQAASLVADDIMDQSLTRRGQLCWWYKKEGVGLDAINDSFLLESSVY
RVLKKYCRQRPYYVHLELFLQTAYQTELGQMLDLITAPVSKVDLSHFSEERYKAIVKYKTAFYSFYL
PVAAAMYVMVGIDSKEEHENAKAILLEMGEYFQIQDDYLDGDPALTGAVGTDIQDNKCSWLVVQCL
QRVTPEQRQLLEDNYGRKEPEKVAKVKELYEAVGMRAAFQQYEESYRRLQELIEKHSNRLPKEIFL
GLAQKIYKRQK
>d1ezfa_ a.128.1.2 (A:) Squalene synthase {Human (Homo sapiens)}
NSLKTCKYKLNQTSRFAAVIQALDGERNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLY
QPDWRFMESKEKDRQVLEDFPTISLEFRNLAEKYQTVIADICRRMGIGMAEFLDKHVTSEQEWK
YCHYVAGLVGIGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDQGGREFWPQEVWS
RYVKKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFAIPQVMAIATLAACYN
NQVFKGAVKIRKGQAVTLMMDATNMPAVKAIHYQYMEEIYHRIPSDPSSSKTRQIISTIRTQN
>d5eau_2 a.128.1.3 (221-548) 5-Epi-aristolochene synthase, C-terminal domain {Tobacco
(Nicotiana tabacum)}
KNNVLLRFAKLDFNLLQMLHKQELAQVSRWWKDLDFVTTLPYARDRVVECYFWALGVYFEPQYSQ
ARVMLVKTISMISIVDDTFDAYGTVKELEYTDAIQRWDINEIDRLPDYMKISYKAILDLYKDYEKELS
SAGRSHIVCHAIERMKEVVRNYNVESTWFIEGYTPPVSEYLSNALATTTYYLATTSYLGMKSATEQ
DFEWLSKNPKILEASVIICRVIDDTATYEVEKSRGQIATGIECCMRDYGISTKEAMAKFQNMAETAWK
DINEGLLRPTPVSTEFPLPILNLARIVEVTYIHNLDGYTHPEKVLKPHIINLLVDSIKI
>d1di1a_ a.128.1.4 (A:) Aristolochene synthase {Fungus (Penicillium roqueforti)}
TPPPTQWSYLCHPRVKEVQDEVDGYFLENWKFPSFKAVRTFLDAKFSEVTCLYFPLALDDRIHFACR
LLTVLFLIDDVLEHMSFADGEAYNNRLIPISRGDVLPDRTKPEEFILYDLWESMRAHDAELANEVLEP
TFVFMRAQTDRARLSIHELGHYLEYREKDVGKALLSALMRFSMGLRLSADELQDMKALEANCAKQ

LSVVNDIYSYDKEEEASRTGHKEGAFLLCSAVKVLAEESKLGIPATKRVLWSMTREWETVHDEIVAEEKI
ASPDGCSEAAKAYMKGLEYQMSGNEQWSKTTR

>d1ps1a_a.128.1.4 (A:) Pentalenene synthase {Streptomyces sp., UC5319}

QDVFHFIPLPGRQSPDHARAEAEQLAWPRSLGLIRSDAAAERHLRGGYADLASRFYPHATGADLDDL
GVDLMSWFFLFDLDFDGPGENPEDTKQLTDQVAAALDGPLPDTAPPIAHGFADIWRRRTCEGMTPA
WCARSARHWRNYFDGYVDEAESRFWNAPCDSSAAQYLAMRRHTIGVQPTVDLAERAGRFVPHRV
FDSAVMSAMLQIAVDVNLNLLNDIASLEKEEARGEQNNMVMILRREHGWSKRSVSHMQNEVRARL
EQYLLLESCLPKVGEIYQLDTAEREALERYRTDAVRTVIRGSYDWHRSSG

>d1jfaa_a.128.1.5 (A:) Trichodiene synthase {Fusarium sporotrichioides}

MENFPTEYFLNNTTVRLLEYIRYRDSNYTREERENLHYAYNKAHHFAQPRQQLLKVDPKRLQASL
QTIVGMVVYSWAKVSKECMADLSIHYYTYTLVLDDSKDDPYPTMVNYFDDLQAGREQAHPWWALV
NEHFPNVLRFHFGPFCSLNLRSTLDFEFGCWIEQYNFGGFPDGYDYPQFLRRMNLGHCVGASLWP
KEQFNERSLFLEITSAIAQMENWMVWVNDLMSFYKEFDDERDQISLVKNYVVSDEISLHEALEKLT
QDTLHSSKQMVAVFSDKDPQVMDTIECFMHGYVTWHLCDRRYRLSEIYEKVKEEKTEDAQKCFKFY
EQAANVGAVSPSEWAYPPVAQLANV

>d1oela1_a.129.1.1 (A:2-136,A:410-525) GroEL {Escherichia coli}

AAKDVKFGNDAGVKMLRGNVNLADAVKVTLPKGRNVVLDKSFAGPTITKDGVSVAEIELEDKFE
NMGAMVKEVASKANDAAGDGTATVLAQAIIIEGLKAVAAGMNPMDLKRIGIDKAVTVAVEELK
ALSXGVVAGGGVALIRVASKLADLRGQNEQNVGIKVALRAMEAPLRQIVLNCGEEPSVVANTVKG
GDGNYGYNAATEEYGNMIDMGILDPTKVRTSALQYAASVAGLMITTECMVTDLP

>d1ioea1_a.129.1.1 (A:2-136,A:410-526) GroEL {Paracoccus denitrificans}

AAKEVKFNSDARDRMLKGVNLLADAVKVTLPKGRNVVIDKSFAGPRITKDGVSVAKEIELSDKFEN
MGAQMVREVASRTNDEAGDGTATVLAQAIVREGLKAVAAGMNPMDLKRIGIDVATAKVVEAIKSA
ARXGIVVGGVALVQGAQVLEGLSGANSQDAGIAIIRALEAPMRQIAENAGVDGAVVAGKVRESSD
KAFGFNAQTEEYGMDFKFGVIDPAKVVRTALEDAASVAGLLITTEAMIAEKP

>d1a6da1_a.129.1.2 (A:17-145,A:404-519) Thermosome {Archaeon Thermoplasma acidophilum}

REQGKNAQRNIEAAKAIADAVRTTLGPKGMDKMLVDSIGDIIISNDGATILKEMDVEHPTAKMIVE
VSKAQDTAVGDGTTTAVVLSGELLQAETLLDQGVHPTVISNGYRLAVNEARKIIDEIAEK SXFLWGG
GAVEAELAMRLAKYANSVGGREQLAIEFAKALEIIPRTLAENAGIDPINTLIKLKADDEKGRISVGV
LDNNGVGMKAKGVVDPLRVKTHALESAVEVATMILRIDV

>d1a6db1_a.129.1.2 (B:20-144,B:404-521) Thermosome {Archaeon Thermoplasma acidophilum}

KDAMKENIEAAIAISNSVRSSLGPRGMDKMLVDSLGDIVITNDGVITLKEMDVEHPAAKMMVEVSK
TQDSFVGDGTTTAVIIAGLLQQAQGLINQNVHPTVISEGYRMASEEAKRVIDEISTKIXAYAAGGGAT
AAEIAFRLRSYAQKIGGRQQLAIEKFADAIEIPRALAENAGLDPIDILLKLRAEHAKGNKTYGINVFT
GEIEDMVKNGVIEPIRVGKQAIESATEAAIMILRIDVIA

>d1ecma_a.130.1.1 (A:) Chorismate mutase domain of P-protein {Escherichia coli}

NPLLALREKISALDEKLLALLAERRELAVEVGKAKLLSHRPVRDIDRERDLLERLITLGKAHHLDAH
YITRLFQLIIEDSVLTQQALLQQH

>d5csma_a.130.1.2 (A:) Allosteric chorismate mutase {Baker's yeast (Saccharomyces cerevisiae)}

MDFTKPETVLNLQNIRDELVRMEDSIIFKFIERSHFATCPSVYEANHPGLEIPNFKGSFLDWALSNLEI
AHSRIRRFESPDETPFFPKIQKSFLPSINYPQILAPYAPEVNYNDKIKKVYIEKIIPLSKRDGDDKNN

FGSVATRDIECLQSLRRHFHGKFAEAKFQSDIPLYTKLIKSKDVEGIMKNITNSAVEEKILERLTKKA
EYVGVDPTERRIERRISPEYLVKIYKEIVIPITKEVEVEYLLRLEE
>d1pprm1 a.131.1.1 (M:1-156) Peridinin-chlorophyll protein {Dinoflagellate (Amphidinium
carterae)}
DEIGDAAKGLGDASYAFAKEVDWNNGIFLQAPGKQLPLEALKKIDKMIVMGAAADPKLLKAAAEAH
HKAIGSISGPNVTSRADWDNVNAALGRVIASVPENMVMVDVYDSVSKITDPKVPAYMKSLVNGADA
EKAYEGFLAFKDVVKKSQVTSAAAG
>d1pprm2 a.131.1.1 (M:157-312) Peridinin-chlorophyll protein {Dinoflagellate
(Amphidinium carterae)}
PATVPSGDKIGVAAQQLSEASYPFLKEIDWLSVYMKPLPGVSAQQLKIDKMIVMGAQADGNALK
AAAEAHHKAIGSIDATGVTSAADYAAVNAALGRVIASVPKSTVMDVYNAMAGVTDTSIPLNMFASKVN
PLDANAAAKAFYTFKDVVQAAQ
>d1qq8a_ a.132.1.1 (A:) Heme oxygenase-1 (HO-1) {Human (Homo sapiens)}
PQDLSEALKEATKEVHTQAENAEFMRNFQKQVTRDGFKLVMASLYHIYVALEEEIERNKESPVFAP
VYFPEELHRKAALEQDLAFWYGPRWQEVIPYTPAMQRYVKRLHEVGRTEPELLVAHAYTRYLGDLS
GGQVLKKAQKALDLPSSGEGLAFFTFPNIASATKFKQLYRSRMNSLEMTPAVRQRVIEEAKTAFLLN
IQLFEELQELLTH
>d1dvga_ a.132.1.1 (A:) Heme oxygenase-1 (HO-1) {Rat (Rattus norvegicus)}
SQDLSEALKEATKEVHIRAENSEFMRNFQKQVSREGFKLVTASLYHIYTALEEEIERNKQNPVYAPL
YFPEELHRRAALEQDLAFWYGPHWQEAIPYTPATQHLYVKRLHEVGGTHPELLVAHAYTRYLGDLSG
GQVLKKAQKALALPSSGEGLASFTFPSIDNPTKFKQLYRARMNTLELTPEVKHRVTEEAKTAFLLNI
ELFEELQALLTE
>d1j77a_ a.132.1.2 (A:) Gram-negative bacterial heme oxygenase {Neisseria meningitidis}
ALTFAKRLKADTTAVHDSVDNLVMSVQPFVSKENYIKFLKLQSVFHKAVDHIYKDAELNKAIPLEY
MARYDAVTQDLKDLGEEPYKFDKELPYEAGNKAIGWLYCAEGSNLGAFLFKHAQKLDYNGEHGA
RHLAPHPDGRGKHWRFAVVEHLNALNLTPEAEAEAIQGAREAFAYKVVLRVETFLAADAPEGM
MPH
>d1knca_ a.152.1.1 (A:) Antioxidant defence protein AhpD {Mycobacterium tuberculosis}
SIEKLKAAALPEYAKDIKLNLSITRSSVLDQEQWLWGTLLASAAATRNQVLADIGAEATDHLASAAARH
AALGAAAIMGMNNVFYRGRGFLEGRYDDLRLPGLRMNIINPPIPKANFELWSFAVSAINGCSHCLVA
HEHTLRVTGVDREAI FEALKAAAI VSGVAQALATIEALS
>d1poa_ a.133.1.2 (-) Snake phospholipase A2 {Taiwan cobra (Naja naja atra)}
NLYQFKNMIQCTVPSRSWWDFAFYGCYCGRGGSGTPVDDLDRCCQVHDNDCYNEAEKISGCWPYFK
TYSYEQSGTLTCKGGNNACAAVCDCLAAICFAGAPYNDNDYNINLKARC
>d1pp2l_ a.133.1.2 (L:) Snake phospholipase A2 {Western diamondback rattlesnake
(Crotalus atrox)}
SLVQFETLIMKIAGRSGLLWYSAYGCYCGWGGHGLPQDATDRCCFVHDCCYKATDCNPKTVSYTYS
EENGEIICGGDDPCGTQICECDKAAAICFRDNIPSYDNKYWLFPPKDCREEPEPC
>d1bjja_ a.133.1.2 (A:) Snake phospholipase A2 {Chinese water moccasin (Agkistrodon halys
pallas), different isoforms}
NLLQFNKMIKEETGKNAIPFYAFYGCYCGWGGQKPKDGTDRCCFVHDCCYGRVNCNTKSDIYSYS
LKEGYITCGKGTNCEEQICECDRVAAEFCRRNLDTYNNGYMFYRDSKCTETSEEC
>d1jiaa_ a.133.1.2 (A:) Snake phospholipase A2 {Chinese water moccasin (Agkistrodon halys
pallas), different isoforms}

HLLQFRKMIKKMTGKEPVVSYAFYGCYCGSGGRGKPKDATDRCCFVHDCCYEKVTGCDPKWDDYTY
SWKNGTIVCGDDPCKKEVCECDKAAAICFRDNLKTYKKRYMAYPDILCSSKSEKC
>d1psj_ a.133.1.2 (-) Snake phospholipase A2 {Chinese water moccasin (*Agkistrodon halys pallas*), different isoforms}
SLIQFETLIMKVAKKS GMFWYSNYGCYCGWGGQGRPQDATDRCCFVHDCCYKVTGCDPKMDVYS
FSEENDIVCGDDPCKKEICECDRAAAICFRDNLTYNDKKYWAFGAKNCPQESEPC
>d1ppa_ a.133.1.2 (-) Snake phospholipase A2 {Eastern cottonmouth snake (*Agkistridon piscivorus*)}
SVLELGKMLQETGKNAITSYGSYGCNCGWGHGQPKDATDRCCFVHKCCYKLTDCNHKTD RYSYS
WKNKAIICEEKNPCLKEMCECDKAVAICLRENLDTYNKKYKAYFKLKCKKPDTC
>d1vapa_ a.133.1.2 (A:) Snake phospholipase A2 {Eastern cottonmouth snake (*Agkistridon piscivorus*)}
NLFQFEKLIKMTGKSGMLWYSAYGCYCGWGGQGRPQDATDRCCFVHDCCYKVTGCNPKMDIYT
YSVDNGNIVCGGTNPCKKQICECDRAAAICFRDNLKTYDSKTYWKYPKKNCKESEPC
>d1ijla_ a.133.1.2 (A:) Snake phospholipase A2 {Viper (*Deinagkistrodon acutus*)}
SLIQFETLIMKVVKKS GMFWYSAYGCYCGWGGHGRPQDATDRCCFVHDCCYKVTGCDPKMDSYT
YSEENDIVCGDDPCKREICECDRVAADC FRDNLDTYNSDTYWRYPQDCEESPEPC
>d1fe7a_ a.133.1.2 (A:) Snake phospholipase A2 {Snake (*Daboia russelli pulchella*)}
SLLEFGKMILEETGKLAIPSYSSYGCYCGWGGKTPKDATDRCCFVHDCCYGNLPDCNPKSDRYKYK
RVNGAIVCEKGTSCENRICECDKAAAICFRQNLNTYSKKYMLYPDFLCKGELKC
>d1ae7_ a.133.1.2 (-) Snake phospholipase A2 {Mainland tiger snake (*Notechis scutatus scutatus*), notexin}
NLVQFSYLIQCANHGKRPTWHYMDYGCYCGAGGSGTPVDELDRCCKIHDDCYDEAGKKGCFPKMSA
YDYCGENGPYCRNIKKKCLRFVCDV EAAFCFAKAPYNNANWNIDTKKRCQ
>d2nota_ a.133.1.2 (A:) Snake phospholipase A2 {Mainland tiger snake (*Notechis scutatus scutatus*), notechis II-5}
NLVQFSYLIQCANHGRPRTRHYMDYGCYCGWGGSGTPVDELDRCCKIHDDCYSDAEKKGCSPKMSA
YDYCGENGPYCRNIKKKCLRFVCDV EAAFCFAKAPYNNANWNIDTKKRCQ
>d1qlla_ a.133.1.2 (A:) Snake phospholipase A2 {Bothrops pirajai, Piratoxin-II (PRTX-II)}
SLFELGKMLQETGKNPAKSYGAYGCNCGVLGRGKPKDATDRCCYVHKCCYKLTGCNPKKDRYSYS
WKDKTIVCGENNPCLKELCECDKAVAICLRENLTGTYNKKYRYHLKPFCKKADK
>d1vip_ a.133.1.2 (-) Snake phospholipase A2 {Russell's viper (*Vipera russelli*)}
NLFQFAEMIVKMTGKNPLSSYSDYGCYCGWGGKGPQDATDRCCFVHDCCYEKVKSKPKLSLYSYS
FQNGGIVCGDNHCKRAVCECDRVAATCFRDNLNTYDKKYHNYPPSQCTGTEQC
>d1jlta_ a.133.1.2 (A:) Snake phospholipase A2 {Sand viper (*Vipera ammodytes meridionalis*), vipoxin}
NLFQFGDMILQKTGKEAVHSYAIYGCYCGWGGQARAQDATDRCCFAQDCCYGRVND CNPKTATYTY
SFENGDIVCGDNDLCLRAVCECDRAAAICLGENVNTYDKNYEYYSISHCTESEQC
>d1jlta_ a.133.1.2 (B:) Snake phospholipase A2 {Sand viper (*Vipera ammodytes meridionalis*), vipoxin}
NLFQFAKMINGKLGAFSVWNYISYGCYCGWGGQGT PKDATDRCCFVHDCCYGRVRCNPKLAIYSYS
FKKGNIVCGKNNGLRDICECDRVAANCFHQNKNTYNKNYKFLSSSRCRQTSEQC
>d1dpya_ a.133.1.2 (A:) Snake phospholipase A2 {Indian krait (*Bungarus caeruleus*), different isoforms}

NLIQFKNMIQCAGTRIWTAAYVAYGCYCGKGGSGTPVDELDRCCYTHDHCYNEAEKIPGCNPNIKTYSY
TCTQPNTCTDSADTCAQFLCECDRTAAICFASAPYNSNNIMLSSSTSCQ
>d1fe5a_ a.133.1.2 (A:) Snake phospholipase A2 {Indian krait (*Bungarus caeruleus*),
different isoforms}
NLIQFKNMIQCAGTRPWTAYVNYGCYCGKGGSGTPVDELDRCCYTHDNCYNEAEKIPGCNPNIKTYS
YTCTEPNLTCTDTADTCARFLCNCDRTAICFASAPYNSNNVMISSSTNCQ
>d1kvoa_ a.133.1.2 (A:) Phospholipase A2 {Human (*Homo sapiens*), synovial fluid}
NLVNFHRMIKLTGKEAALSYGFGCHCGVGGSPKDATDRCCVTHDCCYKRLEKRGCGTKFLSYK
FSNSGSRITCAKQDSCRSQLECDKAAATCFARNKTTYNKKYQYYSNKHCRGSTPRC
>d1g4ia_ a.133.1.2 (A:) Phospholipase A2 {Cow (*Bos taurus*), pancreas}
ALWQFNGMIKCKIPSSPEPLDFNNGCYCGLGGSGTPVDDLDRCCQTHDNCYKQAKKLDSCKVLVD
NPYTNNYSYSCSNNEITCSSENNACEAFICNCDRNAAICFSKVPYNKEHKNLDDKNC
>d1hn4a_ a.133.1.2 (A:) Phospholipase A2 {Pig (*Sus scrofa*), pancreas}
GISSRALWQFRSMIKCAIPGSHPLMDFNNGCYCGLGGSGTPVDELDRCCETHDNCYRDAKNLDSCK
FLVDNPTYTESYSCSNTEITCNSKNNACEAFICNCDRNAAICFSKAPYNKEHKNLDTKKYC
>d5p2pa_ a.133.1.2 (A:) Phospholipase A2 {Pig (*Sus scrofa*), pancreas}
ALFQFRSMIKCAIPGSHPLMDFNNGCYCGLGGSGTPVDELDRCCETHDNCYRDAKNLSGCYPYTE
SYSYSCSNTEITCNSKNNACEAFICNCDRNAAICFSKAPYNKEHKNLDTKKYC
>d1buna_ a.133.1.2 (A:) beta2-bungarotoxin, phospholipase A2 chain {Many-banded krait
(*Bungarus multicinctus*), elapid}
NLINFMEMIRYTIPEKWTGWEYADYGCYCGAGGSGRPIDALDRCCYVHDNCYGDAEKKHKCNPKTQS
YSYKLTKRTHIICYGAAGTCARIVCDCDRTAALCFGNSEYIEGHKNIDTARFCQ
>d1goda_ a.133.1.2 (A:) Myotoxin II {*Bothrops godmani*}
SMYQLWKMILQETGKNAVPSYGLYGCNCGVSGRGPKDATDRCCFVHKCCYKLLTDCSPKTDSYSYS
WKDKTIVCGDNNPCLQEMCECDKAVAICLRENLDTYNKNYKIYPKPLCKKADAC
>d1gmza_ a.133.1.2 (A:) Myotoxin II {Snake (*Bothrops pirajai*), piratoxin III}
DLWQFGKMILKETGKLPFPYVYTYGCYCGVGGRRGPKDATDRCCFVHDCCYKLTSCPKTDRYSYS
RKDGTIVCGENDPCRKEICECDKAAAVCFRENLDTYNKKYMSYLKSLCKKXADDC
>d1poc_ a.133.1.1 (-) Phospholipase A2 {European honeybee (*Apis mellifera*)}
IYPGTLWCGHGNKSSGPNELGRFKHTDACRTHDMCPDVMASAGESKHGLTNTASHTRLSCDCDDK
FYDCLKNSADTISSYFVGKMYFNLDTKCYKLEHPVTGCGERTEGRCLHYTVDKSKPKVYQWFDLRK
Y
>d1faza_ a.133.1.3 (A:) Prokaryotic phospholipase A2 {*Streptomyces violaceoruber*}
APADKPQVLASFTQTSASSQNAWLAANRNQSAWAAYEFDWSTDLCTQAPDNPFQFPNTACARHD
FGYRNYKAAGSFDANKSRIDSAFYEDMKRVCTGYTGEKNTACNSTAWTYQAVKIFG
>d1bxm_ a.134.1.1 (-) beta-cryptogein {*Phytophthora cryptogea*}
RGTCTATQQTAAYHTLVSILSDASFNQ CSTDSGYMILTAKALPTTAQYKLMCASTACNTMIKKIVTLN
PPNCDLTVPTSGLVLVNYSYANGFSNKCSSL
>d1g8qa_ a.135.1.1 (A:) CD81 extracellular domain {Human (*Homo sapiens*)}
FVNKDQIAKDVKQFYDQALQQAVVDDDANNAKAVVKTFFHETLDCCGSSTLTALTTSVLKNNLCPSGS
NIISNLFKEDCHQKIDDLFSGKH
>d1dvoa_ a.136.1.1 (A:) Repressor of bacterial conjugation FinO {*Escherichia coli*}
PPKWKVKKQKLAEKAAREALAKKAQARQALSILNPLTDEAVNTLKPWWPGLFDGDTPRLLA
CGIRDVLLLEDVAQRNIPLSHKKLRRAMKAITRSESYLCAMKAGACRYDTEGYVTEHISQEEVYAAER

LDKIRRQNRKAELQAVLD

>d1jjsa_ a.153.1.1 (A:) Nuclear receptor coactivator CBP/p300 ibid domain {Mouse (Mus musculus)}

ALQDLLRTLKSPSSPQQQQVLNILKSNPQLMAAFIKQRTAKYVAN

>d1kbhb_ a.153.1.1 (B:) Nuclear receptor coactivator CBP/p300 ibid domain {Mouse (Mus musculus)}

PNRSISPSALQDLLRTLKSPSSPQQQQVLNILKSNPQLMAAFIKQRTAKYVANQPGMQ

>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 marismortui}

GKSKATKKRKAKLDNQNSRVPAYVMLKTDREVQRNHKRRHWRRNDTDE

>d1jj21_ a.137.1.1 (1:) Ribosomal protein L39e {Archaeon Haloarcula marismortui}

GKSKATKKRLAKLDNQNSRVPWVWMLKTDREVQRNHKRRHWRRNDTDE

>d1g72b_ a.137.2.1 (B:) Methanol dehydrogenase, light chain {Methylophilus methylotrophus, w3a1}

YDGNCKEPCGNCWENKPGYPEKIAGSKYDPKHDPVELNKQESIKAMDARNAKRIAN

>d4aahb_ a.137.2.1 (B:) Methanol dehydrogenase, light chain {Methylophilus methylotrophus, w3a1}

YDGNCKEPCGNCWENKPGYPEKIAGSKYDPKHDPVELNKQESIKAMDARNAKRIANAKSSGNFV
FDVK

>d1h4ib_ a.137.2.1 (B:) Methanol dehydrogenase, light chain {Methylobacterium extorquens}

YDGTKCKAAGNCWEPKPGFPEKIAGSKYDPKHDPKELNKQADSIKQMEERNKKRVENFKKTGKFE
YDVAKISA

>d1gg2g_ a.137.3.1 (G:) Transducin (heterotrimeric G protein), gamma chain {Cow (Bos taurus)}

SIAQARKLVEQLKMEANIDRIKVSAAAADLMAYCEAHAKEDPLLTPVPAENPF

>d1gotg_ a.137.3.1 (G:) Transducin (heterotrimeric G protein), gamma chain {Cow (Bos taurus)}

LTEKDKLMEVDQLKKEVTLERMLVSKCCEEFRDYVEERSGEDPLVKGIPEDKNPFKE

>d1tbge_ a.137.3.1 (E:) Transducin (heterotrimeric G protein), gamma chain {Cow (Bos taurus)}

APVINIEDLTEKDKLMEVDQLKKEVTLERMLVSKCCEEFRDYVEERSGEDPLVKGIPEDKNPFKEL
K

>d1hfes_ a.137.4.1 (S:) Fe-only hydrogenase smaller subunit {Desulfovibrio desulfuricans}

VKQIKDYMLDRINGVYGADAKFPVRASQDNTQVKALYKSYLEKPLGHKSHDLLHTHWFDKSKGVKE
LTTAGKLPNPRASEFEGPYPYE

>d1ef1c_ a.137.5.1 (C:) Moesin tail domain {Human (Homo sapiens)}

AEASADLRADAMAKDRSEEERTTEAEKNERVQKHLKALTSELANARDESKKTANDMIHAENMRLG
RDKYKTLRQIRQGNTKQRIDEFESM

>d2prgc_ a.137.6.1 (C:) Nuclear receptor coactivator Src-1 {Human (Homo sapiens)}

QTSHKLVQLTTTAEQQLRHADIDTCKDVLSTGTSNSASANSSGGSCPSSHSLTERHKILHRLQLQE
GSPSDIT

>d1dp5b_ a.137.7.1 (B:) Proteinase A inhibitor IA3 {Baker's yeast (Saccharomyces

cerevisiae}}

NTDQQKVSEIFQSSKEKLQGDAAKVVSDAFMM

>d1dpjb_ a.137.7.1 (B:) Proteinase A inhibitor IA3 {Baker's yeast (Saccharomyces cerevisiae)}

TDQQKVSEIFQSSKEKLQGDAAKVVSDAFK

>d1e79i_ a.137.8.1 (I:) Epsilon subunit of mitochondrial F1F0-ATP synthase {Cow (Bos taurus)}

VAYWRQAGLSYIRYSQICAKAVRDALKTEFKANAMKTSGSTIKIVKV

>d1jjuc_ a.137.9.1 (C:) Quinohemoprotein amine dehydrogenase C chain {Paracoccus denitrificans}

MNALVGCTTSFDPGWEVDAFGAVSNLCQPMEADLYGCADPCWXPQVADTLNTYPNWSAGADDV
MQDWRKQLQSVFPETK

>d1jmxg_ a.137.9.1 (G:) Quinohemoprotein amine dehydrogenase C chain {Pseudomonas putida}

AVAGCTATTDPGWEVDAFGGVSSLCQPMEADLYGCSDPCWXPQVPDMMSTYQDWNAQASNSAE
DWRNLGTVFPKDK

>d1aqe_ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio desulfuricans, different strains}

TFEIPESVTMSPKQFEGYTPKKGDVTFNHASHMDIACQQCHHTVPDITYTIESCMTEGCHDNIKERT
EISSVERTFHTTKDKSEKSCVGCHEKRELKRQGPSDAPLACNSCHVQ

>d1i77a_ a.138.1.1 (A:) Cytochrome c3 {Desulfovibrio desulfuricans, different strains}

APAAPDKPLEFKGSQKTMFPHAVHAKVECVTCHHQVDGKESFAKCGSSGCHDDLAKGQGEKSLYY
VVHTKKELKHTNCIGCHSKVVEGKPELKKDLTACAKSKCHP

>d2cy3_ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio desulfuricans, different strains}

ADAPGDDYVISAPEGMKAKPKGDKPGALQKTVFPHTKHATVECVQCHHTLEADGGAVKKCTTSG
CHDSLEFRDKANAKDIKLVENAFHTQCIDCHKALKKDKKPTGPTACGKCHTTN

>d3cyr_ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio desulfuricans, different strains}

APAVPNKPVVEVKGSKQKTMFPHAPHEKVECVTCHHLVDGKESYAKCGSSGCHDDLAKKGEKSLYYV
VHAKGELKHTSCLACHSKVVAEKPELKKDLTGCAKSKCHP

>d2cdv_ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio vulgaris}

APKAPADGLKMDKTKQPVVFNHSTHKAVKCGDCHHPVNGKENYQKCATAGCHDNMDKKDKSAKG
YYHAMHDKGTFKSCVGCHELETAGADAANKKELTGCKGSKCHS

>d2ctha_ a.138.1.1 (A:) Cytochrome c3 {Desulfovibrio vulgaris}

APKAPADGLKMEATKQPVVFNHSTHKSVCGDCHHPVNGKEDYRKCCTAGCHDSMDKKDKSAKGY
YHVMHDKNTKFKSCVGCHEVAGADAANKKDLTGCKKSKCHE

>d1wad_ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio gigas}

VDVPADGAKIDFIAGGEKNLTVVFNHSTHKDVKCDDCHHDPGDKQYAGCTTDGCHNILDKADKSVN
SWYKVVHDAKGGAKPTCISCHKDKAGDDKELKKKLTGCKGSAHP

>d3caoa_ a.138.1.1 (A:) Cytochrome c3 {Desulfovibrio africanus}

EDMTHVPTDAFGKLERPAAVFNHDEHNEKAGIESCNACHHVWVNGVLAEDSVGTPCSDCHALE
QDGDTPGLQDAYHQQCWGCHEKQAKGPMCGECHVKN

>d1hh5a_ a.138.1.1 (A:) Cytochrome c7 (cytochrome c551.5) {Desulfuromonas acetoxidans}

ADVVTYENKKGNTVFDHKAHAEKLGCDACHEGTPAKIAIDKKSAAHKDACKTCHKSNNGPTKCGGC
HIK

>d19hca_ a.138.1.1 (A:) Nine-haem cytochrome c {Desulfovibrio desulfuricans, ATCC 27774}

AALEPTDSGAPSAIVMFPVGEKPNPKGAAMKPVVFNHLIHEKKIADCETCHHTGDPVSCSTCHTVE
GKAEGDYITLDRAMHATDIAARAKGNTPTSCVSCHQSETKERRECAGCHAITTPKDDEAWCATCHD
ITPSMTPSEMQKGIAGTLLPGDNEALAAETVLAEATVAPVSPMLAPYKVVIDALADKYEPSDFTHRR
HLTSLMESIKDDKLAQAFHDKPEILCATCHRSPLSLTPPKCGSCHTKEIDAADPGRPNLMAAYHLE
CMGCHKGMAVARPRDCTTCHKAAA

>d1duwa_ a.138.1.1 (A:) Nine-haem cytochrome c {Desulfovibrio desulfuricans, ATCC 29577}

EPTDSGAPSAIVMFPVSAKPNPKGAAMKPAVFNHLAHEKKIANCETCHHTGDPVACSTCHTTEGKA
EGNFVTLDRAMHATNIAKRAKGNTPVSCVSCHEQQTKERRECAGCHAIVTPKRDQAWCATCHNVT
SSMTPEQMQQGIGKGLPPDQNEALAAETVLNHNKPVQPLTAMQGPYKVSIDALADKYEPSNFTHRR
HMASLMERIKGDKLAEAFHNKPETLCATCHRSPLSATPPKCGSCHTKEIDPANPNRPNLKAAYHL
QCMGCHQGMNVGRPKNTDCTTCHKARP

>d1dxrc_ a.138.1.2 (C:) Photosynthetic reaction centre (cytochrome subunit)
{Rhodospseudomonas viridis}

CFEPPPATTTQTGFRGLSMGEVLHPATVKAKKERDAQYPPALAAVKAEGPPVSQVYKNVKVLGNLTE
AEFLRTMTAITEWVSPQEGCTYCHDENNLASEAKYPYVVARMLMTRAIINTNWTQHVAQTGVTC
YTCHRGTPPLPPYVRYLEPTLPLNNRETPTHVERVETRSQYVRLAKYTAYSALNYDPFTMFLANDK
RQVRVVPQTALPLVGVSRGKERRPLSDAYATFALMMSISDSLGTNCTFCHNAQTFESWGKSTPQRA
IAWWGIRMVRDLNMNYLAPLNASLPASRLGRQGEAPQADCRTCHQGVTKPLFGASRLKDYPELGPI
K

>d1eysc_ a.138.1.2 (C:) Photosynthetic reaction centre (cytochrome subunit)
{Thermochromatium tepidum}

CEGPPPGTEQIGYRGVGMENYYVKRQRALSIQANQPVESLPAADSTGPKASEVYQSVQVLKDLVGE
FTRTMVAVTTWVSPKEGCNYCHVPGNWASDDIYTKVVSRRMFELVRAANSWKAHVAETGVTCYT
CHRGNPVPKYAWVTDPGPKYPSGLKPTGQNYGSKTVAYASLPFDPLTPFLDQANEIRITGNAALAGS
NPASLKQAEWTFGLMMNISDSLGVGCTSCHNTRAFNDWTQSTPKRTTAWYAIRHVRDINQNYIWP
LNDVLPASRKGPDPLRVSCMTCHQAVNKPLYGAQMAKDYPGLYK

>d1fgja_ a.138.1.3 (A:) Hydroxylamine oxidoreductase, HAO {Nitrosomonas europaea}

DISTVPDETYDALKLDRGKATPKETYEALVKRYKDPAHGAGKGTMGDYWEPIAISIYMDPNTFYKPP
VSPKEVAERKDCVECHSDETPVWVRAWKRSTHANLDKIRNLKSDDPYKKGKLEEVENLRSMG
KLGEKETLKEVCIDCHVDVNKKDKADHTKDIRMPTADTCGTCHLREFAERESERDTMVWPNGQ
WPAGRPSHALDYTANIETTVWATMPQREVAEGCTMCHTNQNKCDNCHTRHEFSAAESRKPEACAT
CHSGVDHNNWEAYTMSKHGKLAEMNRDKWNWEVRLKDAFSKGGQNAPTCAACHMEYEGEYTH
NITRKRTRWANYPFVPGIAENITSDWSEARLDSWVLTCTQCHSERFARSYLDLMDKGTLEGLAKYQE
ANAIVHKMYEDGTLTGQKTNRPNPEPEKPGFGIFTQLFWSKGNNPASLELKVLEMGENNLAKMH
VGLAHVNPGGWTYTEGWGPMNRAYVEIQDEYTKMQELSALQARVN

>d1ft5a_ a.138.1.3 (A:) Cytochrome c554 {Nitrosomonas europaea}

ADAPFEGRKKSSCHKAQAQSWKDTAHAKAMESLKPVNKKEAKQKAKLDPKADYTDKDCVCGCH
VDGFGQKGGYTIESPKPMLTGVGCECHGPRNFRGDHRKSGQAFESKGGKTPRKDLAKKGQDFHF
EERCSACHLNYEGSPWKGAKAPYTPFTPEVDAKYTFKFDENVKEVKAMHEHYKLEGVFEGEPKFK
FHDEFQASAKPAKKGK

>d1ddca_ a.138.1.3 (A:) Dimeric di-heme split-soret cytochrome c {Desulfovibrio
desulfuricans, ATCC 27774}

RFDQVGGAFGWKPHKLDPKCAQVAYDGYWYKGFSGGFGAFYSIVGLMGEKYGAPYNQFPFAMLE

ANKGGISDWGTIYGALYGAAATFSLFWGRKEVHPMVNELFRWYEVTKLPIFNPGDAAQGVKGDLP
MSASDSVLCHISVSKWCYENKIEATSKQRSERAGRLTADAAFKAAEIINTKIDQGKDFKSTFPMQASV
SSCGECHMTKGN DANWAKGIMDCTPCHSGTAATQNK FVNH

>d1qdba_ a.138.1.3 (A:) Cytochrome c nitrite reductase {Sulfurospirillum deleyianum}
GIAGKEKSEEWAKYYP RQFDSWKKTK EYDSFTDMLAKDPALVIAWSGYAFSKDYNSPRGHYYALQD
NVNSLRTGAPVDAKTGPLPTACWTCKSPDVPRIIEEDGELEYFTGKWAKYGSQIVNVIGCANCHDD
KTAELKVRVPHLNRGLQAAGLKT FEESTHQDKRTLCAQCHVEYYFKKTEWKDAKGADKTAMVVT
LPWANGVGKDG NAGVEGMIKYYDEINFSDWTHNISKTPMLKAQH PGFEFWKSGIHGQKGVSCADC
HMPYTQEGSVKYSDHQVKENPLDSMDQSCMNCHRESESKLRGIVHQKYERKEFLNKVAFDNIGKA
HLETGKAIEAGASDEELKEVRKLRHGHQFKADMAIAAHGNYFHAP EETLRLLAAGSDDAQKARLLL
VKILAKHGVMDYIAPDFDTKDKAQKLAKVDIAALAAEKMKFKQTLEQEWKKEAKAKGRANPELYK
DVDTINDGKSSWNKK

>d1fs7a_ a.138.1.3 (A:) Cytochrome c nitrite reductase {Wolinella succinogenes}
KTAHSQGIEGKAMSEEWARYYP RQFDSWKKTK ESDNITDMLKEK PALVVAWAGY PFSKDYNAPRG
HYYALQDNINTLRTGAPVDGKTGPLPSACWTCKSPDVPRIIEQDGELEYFTGKWAKY GDEIVNTIGC
YNCHDDKSAELKSKVPYLD RGLSAAGFKTFAESTHQEK RSLVCAQCHVEYYFKKTEWKDDKGV DKT
AMVVTLPWWSK GISTEQMEAYYDEINFADWTHGISKTPMLKAQH PDWELYKTGIHGQKGVSCADCH
MPYTQEGAVKYSDHKVGNPLDNMDKSCMNCHRESEQKLDIVKQKFERKEFLQDIAFDNIGKAHL
ETGKAMELGATDAELKEIRTHIRHAQWRADMAIAGHG SFFHAPEEVLRL LASGNEEAQKARIKLVK
VLAKYGAIDYVAPDFETKEKAQKLAKVDMEAFIAEKLKFKQTLEQEWK KQAIAGRLNPESLKGVD
EKSSYYDKTKK

>d1e39a1 a.138.1.3 (A:1-102) Flavocytochrome c3 (respiratory fumarate reductase),
N-terminal domain {Shewanella frigidimarina}
ADNLAEFHVQNQECDSCHTPDGELSND SLTYENTQCVSCHGTLAEVAETTKHEHYNAHASHFPGEV
ACTSCHSAHEKSMVYCD SCHSFDNFMPYAKKWL RDE

>d1qo8a1 a.138.1.3 (A:2-102) Flavocytochrome c3 (respiratory fumarate reductase),
N-terminal domain {Shewanella frigidimarina}
TPDMGSFHADMGSCQSCHAKPIKVTDSETHENAQCKSCHGEYAELANDK LQFDPHNSHLGDINCTS
CHKGHEEPKFCNECHSFDIKPMPFSDAKKKKSWD

>d1d4ca1 a.138.1.3 (A:1-102) Flavocytochrome c3 (respiratory fumarate reductase),
N-terminal domain {Shewanella putrefaciens}
APEVLADFHGEMGGCDSCHVSDKGGVTNDNLTHENGQCVSCHGDLKELAAAAPKDKVSPHKSHLI
GEIACTSCHKGHEKSVAYCDACHSFGFDMPPFGGKWER

>d1neu_ b.1.1.1 (-) Myelin membrane adhesion molecule P0 {Rat (Rattus norvegicus)}
IVVYTDREYVGAVGSQVTLHCSFWSSEWVSDDISFTWRYQPEGGRDAISIFHYAKGQPYIDEVGT FKE
RIQWVGDP SWKDG SIVIHNL DYSDNGTFTCDVKNPPDIVGKTSQVTLYVFE

>d1eaja_ b.1.1.1 (A:) Coxsackie virus and adenovirus receptor (Car), domain 1 {Human
(Homo sapiens)}
FARLSITTP EEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPADNQKVDQV ILYSGDKIYDDYYP
DLKGRVHFTSNDL KSGDASINVTNLQLSDIGTYQCKVKKAPGVANKKIHLVVLV

>d1qfoa_ b.1.1.1 (A:) N-terminal domain of sialoadhesin {Mouse (Mus musculus)}
TWGVSSPKNVQGLSGSCLLIPCIFSYPADVPVSNGITAIWYYDYSGKRQVVIHSGDPKLVDKRFRGRA
ELMGNMDHKVCNLLLKDLKPEDSGTYNFRFEISDSNRWLDVKGTTVTVT

>d1akjd_ b.1.1.1 (D:) CD8 {Human (Homo sapiens)}

SQFRVSPDRTWNLGETVELKQCQVLLSNPTSGCSWLFQPRGAAASPTFLLYLSQNKPKAAEGLDTQR
FSGKRLGDTFVLTLSDFRRENEGYFCSALSNSIMYFSHFVVPVFLPA
>d1bqhg_b.1.1.1 (G:) CD8 {Mouse (Mus musculus)}
KPQAPELRIFPKMDAELGQKVDLVCEVLGVSQGCWLFQNSSSKLPQPTFVVYMASSHNKITWD
EKLNSSKLFAMRDTNKNKYVLTLNKFSKENEGYFCSVISNSVMYFSSVVPVLQKV
>d1cdy_1 b.1.1.1 (1-97) N-terminal domain of CD4 {Human (Homo sapiens)}
KKVVLGKKGDTVELTCTASQKKSIFHWKNSNQIKILGNQGSFLTSPKLNDRADSRSLWDQGNF
PLIKNLKIEDSDTYICEVEDQKEEVQLLV
>d1wioa2 b.1.1.1 (A:179-291) N-terminal domain of CD4 {Human (Homo sapiens)}
FQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSKSWITFDLKNKEVSVKRVTTQDP
KLQMGKKLPLHLTLPLQALPQYAGSGNLTALALEAKTGKHLHQEVNLVV
>d1cid_1 b.1.1.1 (1-105) N-terminal domain of CD4 {Rat (Rattus rattus)}
TSITAYKSEGSAEFSFPLNLGEEESLQGELRWKAEKAPSSQSWITFSLKNQKVSQKSTSNPKFQLSE
TLPLTLQIPQVSLQFAGSGNLTLLDRGILYQEVNLV
>d1hnf_1 b.1.1.1 (4-104) CD2, first domain {Human (Homo sapiens)}
TNALETWALGQDINLDIPSFQMSDDIDDIKWEKTSKDKKIAQFRKEKETFKEDTYKLFKNGTLK
IKHLKTDDQDIYKVSIDYDTKGKNVLEKIFDLKIQE
>d1hnga1 b.1.1.1 (A:2-99) CD2, first domain {Rat (Rattus norvegicus)}
DSGTVWALGHGINLNIPNFQMTDDIDEVRWERGSTLVAEFKRKMKPFLKSGAFEILANGDLKIKN
LTRDDSGTYNVTVYSTNGTRILNKALDLRILE
>d1ccza1 b.1.1.1 (A:1-93) CD2-binding domain of CD58, N-terminal domain {Human (Homo sapiens)}
FSQQIYGVVYGNVTFHVPSNVPLKEVLWKKQKDKVAELENSEFRASFSSFKNRVYLDTVSGSLTIYNTL
SSDEDEYEMESPNITDTMKFFLYVL
>d1qa9b_b.1.1.1 (B:) CD2-binding domain of CD58, N-terminal domain {Human (Homo sapiens)}
SSQQIYGVVYGNVTFHVPSNQPLKEVLWKKQKDKVAELENSEFRASFSSFKNRVYLDTKSGSLTIYNTL
SSDEDEYEMESPNITDSMKFFLYVGES
>d1dr9a1 b.1.1.1 (A:1-105) CD80, N-terminal domain {Human (Homo sapiens)}
VIHVTKEVKEVATLSCGHNVSEELAQTRIYWQKEKMMVLTMMMSGDMNIWPEYKNRTIFDITNNLS
IVILALRPSDEGTYESVVLKYEKDAFKREHLAEVTLVSK
>d1i85a_b.1.1.1 (A:) CD86 (b7-2), N-terminal domain {Human (Homo sapiens)}
MLKIQAYFNETADLPCQFANSQNSLSELVFWQDQENLVLNEVYLGKEKFDVSHSKYMGRTSFDSD
DSWTLRLHNLQIKDKGLYQCIIHHKPTGMIRIHQMNSELSVLA
>d1f97a1 b.1.1.1 (A:27-128) Junction adhesion molecule, JAM, N-terminal domain {Mouse (Mus musculus)}
KGSVYTAQSDVQVPENESIKLTCTYSGFSSPRVEWKFVQGSTTALVCYNSQITAPYADRVTFSSSGITFS
SVTRKDNGEYTCMVSEEGGQNYGEVSIHLTVL
>d1jmaa_b.1.1.1 (A:) HSV glycoprotein D {Herpes simplex virus type 1}
KYALADASLKMADPNRFRGKDLPLVDQLTDPGVRVYHIQAGLPDPFQPPSLPITVYAVLERACR
SVLLNAPSEAPQIVRGASEDVRKQPYNLTIWFRMGNCAPITVMEYTECSYNKSLGACPIRTQPR
WNYYSFSAVSEDNLGFLMHAPAFETAGTYLRLVKINDWTEITQFILEHRAKGSCKYALPLRIPPSAC
LSPQAYQQGVTVDSIGMLPRFIPENQRTVAVYSLKIAGWHGPKAPYTSTLLPPELSE
>d1igta1 b.1.1.1 (A:1-108) Immunoglobulin (variable domains of L and H chains) {Intact

IgG2a antibody Mab231 (mouse), kappa L chain}
DIVLTQSPSSLSASLGDTITITCHASQININWLSWYQQKPGNIPKLLIYKASNLHTGVPSRFSGSGSGT
GFTLTISLQPEDIATYYCQQGQSYPLTFGGGTKLEIKR
>d1igtb1 b.1.1.1 (B:1-114) Immunoglobulin (variable domains of L and H chains) {Intact
IgG2a antibody Mab231 (mouse), kappa L chain}
EVKLQESGGGLVQPGGSLKLSCATSGFTFSDYYMYWVRQTPEKRLEWVAYISNGGGSTYYPDTVKGR
FTISRDNKNTLYLQMSRLKSEDTAMYYCARHGGYYAMDYWGQGTTVTVSSA
>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}
KCAHTVSKSMSVGERVTLTCKASENVVTVSWYQQKPEQSPKLLIYGASNRYTGVPDRFTGSGSA
TDFTLTISVQAEDLADYHCGQGYSYPYTFGGGTKLEIK
>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}
VKLQESGAELARPGASVKMSCKASGYTFTTYTIHWIKRPGQGLEWIGYINPSSVYTNYNQRFKDKA
TLTRDRSSNTANIHLSSLTSDDSAVYYCVREGEVVPYWGQGTTVTVSS
>d1hzh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Intact
IgG B12 antibody (human), kappa L chain}
QVQLVQSGAEVVKPGASVKVSCQASGYRFSNFVIHWVRQAPGQRFWVWGWINPYNGNKEFSAKFQ
DRVTFADTSANTAYMELRSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIVVSS
>d1hzh1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Intact
IgG B12 antibody (human), kappa L chain}
EIVLTQSPGTLSPGERATFSCRSSHISRRVAVYQHKGPGAPRLVIHGVSNRASGISDRFSGSGSGT
DFTLTITRVEPEDFALYYCQVYGASSYTFGGGTKLERK
>d8faba1 b.1.1.1 (A:3-105) Immunoglobulin (variable domains of L and H chains) {Fab HIL
(human), lambda L chain}
ELTQPPSVSVSPGQTARITCSANALPNQYAYWYQQKPGRAPVMVIYKDTQRPSGIPQRFSSSTSGTTV
TLTISGVQAEDADYYCQAWDNSASIFGGGTKLTV
>d8fabb1 b.1.1.1 (B:1-121) Immunoglobulin (variable domains of L and H chains) {Fab HIL
(human), lambda L chain}
AVKLVQAGGGVVQGRSLRLSCIASGFTFSNYGMHWVRQAPGKGLEWVAVIWIYNGSRTYYGDSVKG
RFTISRDNKRTLYMQMNSLRTEDTAVYYCARDPDLTAFSFDYWGQGVLTVSS
>d7fabh1 b.1.1.1 (H:1-116) Immunoglobulin (variable domains of L and H chains) {Fab NEW
(human), lambda L chain}
AVQLEQSGPGLVRPSQTLSTCTVSGTSFDDYYWTWVRQPPGRGLEWIGYVYFTGTLLDPSLRGRV
TMLVNTSKNQFSLRLSSVTAADTAVYYCARNLIAGGIDVWGQGSVLTVS
>d7fabl1 b.1.1.1 (L:1-103) Immunoglobulin (variable domains of L and H chains) {Fab NEW
(human), lambda L chain}
ASVLTQPPSVSGAPGQRTISCTGSSSNIGAGHNKWKYQQLPGTAPKLLIFHNNARFSVSKSGTSATL
AITGLQAEDADYYCQSYDRSLRVFGGGTKLTVLR
>d1bafh1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab
ANO2 (mouse), kappa L chain}
DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWRQFPGNKLEWVWGYMSYSGSTRYNPSLRSR
ISITRDTSKNQFLLQLKSVTTEDTATYFCARGWPLAYWGQGTQVSVSE
>d1baf1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab ANO2

(mouse), kappa L chain}
QIVLTQSPAIMSASPGEKVTMTCSASSSVYYMYWYQQKPGSSPRLLIYDTSNLAGVPPVRFSGSGSGTS
YSLTISRMEAEDAATYYCQQWSSYPITFGVGTKLELKR
>d1a3rh1 b.1.1.1 (H:2-119) Immunoglobulin (variable domains of L and H chains) {Fab 8F5
(mouse), kappa L chain}
VQLQQSGAELVRPGASVKLSCTTSGFNIKDIYIHWVKQRPEQGLEWIGRLDPANGYTKYDPKFQGKA
TITVDTSSNTAYLHLSLTSSEDTAVYYCDGYSSYDMDYWGPGTSTVSSAKTTAP
>d1a3r11 b.1.1.1 (L:1-114) Immunoglobulin (variable domains of L and H chains) {Fab 8F5
(mouse), kappa L chain}
DIVMTQSPSSLTVTGTEKVTMTCKSSQSLNSRTQKNYLTWYQQKPGQSPKLLIYWASTRESGVPDR
FTGSGSGTDFTLISGVQAEDLAVYYCQNNYNYPLTFGAGTKLELKRADAAPT
>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}
EVQLQQSDAELVKPGASVKISCKASGYTFTDHAHWAKQKPEQGLEWIGYISPGNDDIKYNEKFKGK
ATLTADKSSSTAYMQLNSLTSSEDSAVYFCKRSYGHWGQGTTLTVSSA
>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}
DIQMTQSPASLSVSVGETVTITCRASENIYSNLAWYQQKQKSPQLLVYAATNLADGVPSRFSGSGSG
TQYSLKINSLQSEDFGSYYCQHFHWGTPYTFGGGTRLEIKRA
>d1hila1 b.1.1.1 (A:1-108) Immunoglobulin (variable domains of L and H chains) {Fab 17/9
(mouse), kappa L chain}
DIVMTQSPSSLTVTAGEKVTMSCTSSQSLFNSGKQKNYLTWYQQKPGQPPKVLIIYWASTRESGVPDR
FTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSNPLTFGGGTKLELKR
>d1hilb1 b.1.1.1 (B:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 17/9
(mouse), kappa L chain}
EVQLVESGGDLVKGPGSLKLSAASGFSFSSYGMSWVRQTPDKRLEWVATISNGGGYTYYPDSVKGR
FTISRDNANTLYLQMSLKSSEDSAMYYCARRERYDENGFAFWGQGLTVTVS
>d1dbbh1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and H chains) {Fab DB3
(mouse), kappa L chain}
QIQLVQSGPELKKPGETVKISCKASGYAFTNYGVNWWKEAPGKELKWMGWINIYTGEPTYVDDFKG
RFAFSLETSASTAYLEINLNKNETATYFCTRGDYVNWYFDVWGAGTTVTVS
>d1dbbl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab DB3
(mouse), kappa L chain}
DVVMTQIPLSLPVNLGDQASISCRSSQSLIHSNGNTYLHWYLQKPGQSPKLLMYKVSNRFYGVPPDRF
SGSGSGTDFTLKISRVEAEDLGIYFCSQSSHVPPTFGGGTKLEIK
>d1dfbh1 b.1.1.1 (H:1-126) Immunoglobulin (variable domains of L and H chains) {Fab 3D6
(human), kappa L chain}
EVQLVESGGGLVQPGRSLRLSCLASGFTFNDYAMHWVRQAPGKGLEWVSGISWDSSSIGYADSVKGR
FTISRDNANSLYLQMNLSRAEDMALYYCVKGRDYYDSGGYFTVAFDIWGQGMVTVSS
>d1dfbl1 b.1.1.1 (L:1-106) Immunoglobulin (variable domains of L and H chains) {Fab 3D6
(human), kappa L chain}
DIQMTQSPSTLSASVGDRTVITCRASQSISRWLAWYQQKPGKVPKLLIYKASSLESGVPSRFSGSGSGT
EFTLTISSLPDDFATYYCQYNSYSFGPGTKVDIKR
>d1igfh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab B1312

(mouse), kappa L chain}
EVQLVESGGDLVKPGGSLKLSAASGFTFSRCAMSWVRQTPEKRLEWVAGISSGGSYTFYPDTVKGR
FIISRNARNTLSLQMSLRSEDTAIYYCTRYSSDPFYFDYWGQTTTLTVSS
>d1igf1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab B1312
(mouse), kappa L chain}
DVLMTQTPLSLPVSLGDQASISCRSNQTILLSGDGTYLEWYLQKPGQSPKLLIYKVSNRFSGVPDRFS
GSGSGTDFTLKISRVEAEDLGVIYCFQGSHPPTFGGGTKLEIK
>d1igia1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 26-10
(mouse), kappa L chain}
DVMVTQTPLSLPVSLGDQASISCRSSQSLVHNSGNTYLNWYLQKAGQSPKLLIYKVSNRFSGVPDRFS
GSGSGTDFTLKISRVEAEDLGIYFCSQTTHVPPTFGGGTKLEIK
>d1igjb1 b.1.1.1 (B:2-114) Immunoglobulin (variable domains of L and H chains) {Fab 26-10
(mouse), kappa L chain}
VQLQQSGPELVKPGASVRMCKSSGYIFTDFYMNWVRQSHGKSLDYIGYISPYSGVTGYNQKFKGKA
TLTVDKSSSTAYMELRSLTSEDSAVYYCAGSSGNKWAMDYWGHGASVTVSSA
>d1igmh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv POT
(human) IgM, kappa L chain}
EVHLESGLLVQPGGSLRLSCLASGFTFNIFVMSWVRQAPGKGLEWVSGVFGSGGNTDYADAVKGR
RFTITRDNSKNTLYLQMNLSRAEDTAIYYCAKHRVSYVLTGFDSWGQGLTVTVSSGSASAPTL
>d1igm_l b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv POT (human)
IgM, kappa L chain}
DIQMTQSPSSLSASVGDRTITCQASQDISNYLAWYQQKPKGKAPKELRIYDASNLETGVPSRFSGSGSG
TDFTFITISLQPEDATYYCQQYQNLPLTFGPGTKVDIKRTVAAPSV
>d1dqlh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv MEZ (human)
IgM, kappa L chain}
EVQLVESGGGLVQPGGSLRLSCLASGFTFSSYAMHWVRQAPGKGLEWVAVISSDGGNKYYTDSVKGR
FTISRNDKNTLYLQMNLSRTEDTAVFYCARGNPPYSSGWGGDYWGQGMVTVSS
>d1dql_l b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv MEZ (human)
IgM, kappa L chain}
DIQMTQSPSSLSASVGDRTITCRASQDIRNDLGWYQQKPKGKAPKLIYAASSLQSGVPSRFSGSGSG
TDFTLTISLQPEDFATYYCLQQNSNWTFGGQTKVDIK
>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}
EIVLTQSPATLSLSPGERATLSCGASQSVSSNYLAWYQQKPGQAPRLLIYDASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYGSSPLTFGGGKVEI
>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}
EVQLQQWGAGLLKPSSETLSLTCVYGGFSDDYWSWIRQPPGKGLEWIGWIGINHSNSTNYNPSLKSRLV
TISVDTSKNQFSLKLSVTAADTAVYYCARPPHDTSGHYWNYWGQGLTVTVSS
>d1indh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab
Cha255 (mouse), lambda L chain}
EVTLVESGGDSVKPGGSLKLSAASGFTLSGETMSWVRQTPEKRLEWVATTLVSGGGFTFYASVKGR
FTISRDNANLNLYLQNLRSRSEDTALYFCASHRFVHWGHGTLTVSA
>d1fai1 b.1.1.1 (H:1-123) Immunoglobulin (variable domains of L and H chains) {Fab R19.9

(mouse), kappa L chain}
QVQLQQSGAELVRAGSSVKMCKASGYTFTSYGVNWWVKQRPGQGLEWIGYINPGKGYLSYNEKFKG
KTTTLTVDRSSSTAYMQLRSLTSEDAAVYFCARSFYGGSDLA VYFDSWGGTTLTVS
>d1fail1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab R19.9
(mouse), kappa L chain}
DIQMTQTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPSRFSGSGSG
TDYSLTISNLEHEDIATYFCQQGSTLPRTFGGGTKLEIKR
>d2fb4h1 b.1.1.1 (H:1-119) Immunoglobulin (variable domains of L and H chains) {Fab KOL
(human), lambda L chain}
EVQLVQSGGGVVPGRSLRLSCSSSGFIFSSYAMYWVRQAPGKGLEWVAIWDDGSDQHYADSVKGR
FTISRNDKNTLFLQMDSLRPEDTGVYFCARDGGHGFCSASCFGPDYWGQGPVTVSSA
>d2fb4l1 b.1.1.1 (L:1-109) Immunoglobulin (variable domains of L and H chains) {Fab KOL
(human), lambda L chain}
QSVLTQPPSASGTPGQRVTISCSGTSSNIGSSTVNWYQQLPGMAPKLLIYRDAMRPSGVPDRFSGSKS
GASASLAIGGLQSEDETYYCAAWDVSLNAYVFGTGTKVTVLG
>d2fbjh1 b.1.1.1 (H:1-118) Immunoglobulin (variable domains of L and H chains) {Fab J539
(mouse), kappa L chain}
EVKLESGGGLVQPGGSLKLSAASGFDFSKYWMSWVRQAPGKGLEWIGEIHPSDGTINYTPSLKDK
FIISRDNAKNSLYLQMSKVRSEDTALYYCARLHYYGYNAYWGQGLVTVSA
>d2fbjl1 b.1.1.1 (L:1-109) Immunoglobulin (variable domains of L and H chains) {Fab J539
(mouse), kappa L chain}
EIVLTQSPAITAASLGQKVTITCSASSVSSLHWYQQKSGTSPKPWIYEISKLASGVPARFSGSGSGTSYS
LTINTMEAEDAIIYCCQQWTYPLITFGAGTKLELKRAD
>d1fgvh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fab H52
(synthetic, humanised version), kappa L chain}
EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYTMHWMRQAPGKGLEWVAGINPKNGGTSYADSVKG
RFTISVDKSKNTLYLQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGLVTVSS
>d1fgvl_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fab H52
(synthetic, humanised version), kappa L chain}
DIQMTQSPSSLSASVGDRTITCRASQDINNYLNWYQQKPGKAPKLLIYYTSTLESVPSRFSGSGSG
TDYTLTISLQPEDFATYYCQQGNTLPPTFGAGTKVEIK
>d2fgwh1 b.1.1.1 (H:1-124) Immunoglobulin (variable domains of L and H chains) {Fab H52
(synthetic, humanised version), kappa L chain}
EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYTMHWMRQAPGKGLEWVAGINPKNGGTSYADSVKGR
DRFTISVDKSTSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGLVTVSS
>d1mcph1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and H chains) {Fab
MCPC603 (human), kappa L chain}
EVKLVESGGGLVQPGGSLRLSCATSGFTSDFYMEWVRQPPGKRLEWIAASRNKGNKYTTEYSASVK
GRFIVSRDTSQSILYLQMNALRAEDTAIYYCARNYYGSTWYFDVWGAGTTVTVS
>d2imn_ b.1.1.1 (-) Immunoglobulin (variable domains of L and H chains) {Fab MCPC603
(human), kappa L chain}
DIVMTQSPSSLSVSAGERVTMSCKSSQSLLYKDGKNFLAWYQQKPGQPPKLLIYGASTRESGVPDRFT
GSGSGTDFLTISVQAEDLA VYICQNDHSYPLTFGAGTKLELKR
>d1fvca_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Fab 4D5

(synthetic, humanised version), kappa L chain}
DIQMTQSPSSLSASVGDRTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGT
DFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRT
>d1fvcb_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {Fab 4D5
(synthetic, humanised version), kappa L chain}
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGR
FTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSS
>d1ggbh1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 50.1
(mouse), kappa L chain}
QVQLQESGPGILQPSQTLSTLCSFSGFSLSTYGMGVSQIRPQSGKGLEWLAHIFWDGDKRYNPSLKSR
LKISKDTSNNQVFLKITSVDTADTATYYCVQEGYIYWGQGTSVTVS
>d1ggb1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 50.1
(mouse), kappa L chain}
DIVLTQSPGSLAVSLGQRATISCRASESVDDDGNLFLHWYQQKPGQPPKLLIYRSSLISGIPDRFSGS
GSRTDFTLTINPVEADDVATYYCQSNEDPLTFGAGTKLEIK
>d1ai1h1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 59.1
(mouse), kappa L chain}
QVKLQESGPAVIKPSQSLSLTCLVSGFSITRTNYCWHWIRQAPGKGLEWMGRICYEGSIYYSPSIKSRST
ISRDTSLNKKFIQLISVTNEDTAMYYCSRENHMYETYFDVWGQGTTVTVS
>d1ai1l1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab 59.1
(mouse), kappa L chain}
DIVMTQSPASLVVSLGQRATISCRASESVDSYGKSFMHWYQQKPGQPPKVLIIYASNLESGVPARFSGS
GSRTDFTLTIDPVEADDAATYYCQNNEDPPTFGAGTKLEMRR
>d1mamh1 b.1.1.1 (H:1-119) Immunoglobulin (variable domains of L and H chains) {Fab
Yst9.1 (mouse), kappa L chain}
EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYMSWVRQPPGKALEWLGFIKADGYTTEYSASVK
GRFTISRDNQSILYLQMNTRLRAEDSATYYCTRDPYGAAYWGQGLTVTVSA
>d1mam1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab
Yst9.1 (mouse), kappa L chain}
DIQMTQTTSSLSASLGDRTVITCRASQDIYNYLNWYQQKPDGTVKLLIYYTSRLHSGVPSRFSGSGSG
TDYSLTISNLNQEEDMATYICQQGNTLPFTFGSGTKLEIKR
>d1mfa_1 b.1.1.1 (1L-111L) Immunoglobulin (variable domains of L and H chains) {Fab
SE155-4 (mouse), lambda L chain}
QIVVTQESALTTSPGETVTLTCSRSTGTVTSGNHANWVQEKPDHLFTGLIGDTNNRAPGVPARFSGS
LIGDKAALTITGAQPEDEAIYFCALWSNNHWIFGGGKTLTVLGQ
>d1mfa_2 b.1.1.1 (251H-367H) Immunoglobulin (variable domains of L and H chains) {Fab
SE155-4 (mouse), lambda L chain}
EVQVQQSGTVVARPGASVKMSCKASGYTFTNYWMHWIKRPGQGLEWIGAIYPGNSATFYNHKFR
AKTKLTAVTSTTTAYMELSSLTSEDSAVYYCTRGGHGYGYDYWGQASLTVS
>d1nbvh1 b.1.1.1 (H:1-122) Immunoglobulin (variable domains of L and H chains) {Fab
BV04-01 (mouse), kappa L chain}
EVQPVETGGGLVQPKGSLKLSAASGFNFNTNAMNWVRQAPGKGLEWVARIRSKSNYYATYYADSV
KDRFTISRDDSQNMLYLQMNLLKTEDTAMYYCVRDQTGTAWFAYWGQGLTVTVSAA
>d1teth1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and H chains) {Fab TE33

(mouse), kappa L chain}
QIQLVQSGPELKTPGETVRISCKASGYTFTTYGMSWVKQTPGKGFKWMGWINTYSGVPTYADDFKG
RFAFSLETSASTAYLQINLNKNETATYFCARRSWYFDVWGTGTTVTVS
>d1tet1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab TE33
(mouse), kappa L chain}
DVLMTQTPLSLPVSLGDQASISCKSSQSIHSSGNTYFEWYLQKPGQSPKLLIYKVSNRFSGVPDRFS
GSGSGTDFTLKISRVEAEDLGVYYCFQGSHPFTFGSGTKLEIK
>d1flrh1 b.1.1.1 (H:1-118) Immunoglobulin (variable domains of L and H chains) {Fab
4-4-20 (mouse), kappa L chain}
EVKLDDETGGLVQGRPMKLSVASGFTFSYWMNWVRQSPEKGLEWVAQIRNKPYNYETYYSDS
VKGRFTISRDDSKSSVYLQMNLRVEDMGIYYCTGSYYGMDYWGQGTSVTVSS
>d4fab1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab
4-4-20 (mouse), kappa L chain}
DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSQGNLYLRWYLQKPGQSPKVLIIYKVSNRFSGVPDRFS
GSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPWTFGGGKLEIK
>d1jfqh1 b.1.1.1 (H:302-421) Immunoglobulin (variable domains of L and H chains) {Fab
36-71 (mouse), kappa L chain}
VQLQQSGVELVRAGSSVKMSCKASGYTFTSNGINWVKQRPQGGLWIGYNNPNGYITYNEKFKGK
TTLTVDKSSNTAYMQLRSLTSEDSAVYFCARSEYGGSYKFDYWGQGTTLTVSS
>d1jfq1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab 36-71
(mouse), kappa L chain}
DIQMTQIPSSLSASLGDVRVSIASCRASQDINNFLNWWYQQKPDGTIKLLIYFTSRSQSGVPSRFSGSGSGT
DYSLTISNLEQEDIATYFCQQGNALPRTFGGGKLEIKR
>d1gigh1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and H chains) {Fab HC19
(mouse), lambda L chain}
QVQLKESGPGLVAPSQSLISITCTVSGFLISNGVHWVRQPPGKGLEWLGVIWAGGNTNYNSALMSRV
SISKDNSKSVFLKMKSLQTDAMYYCARDYDYDVFYAMDYWGQGTSVTV
>d2cgrh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains) {Fab,
anti-sweetener (mouse), kappa L chain}
RVQLLESAGELMKPGASVQISCKATGYTFSEYWIEWVKERPGHGLEWIGEILPGSGRTNYREKFKGK
ATFTADTSSNTAYMQLSSLTSEDSAVYYCTRGYSSMDYWGQGTSVTVSAA
>d2cgr1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab,
anti-sweetener (mouse), kappa L chain}
ELVMTQSPSLPVSLGDQASISCRPSQSLVHSNGNTYLHWYLQKPGQSPKLLIYRVSNRFSGVPDRFS
GSGSGTAFTLKISRVEAEDLGVYFCSQGTHVPYTFGGGKLELK
>d1figh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab 1F7
(mouse), kappa L chain}
DVQLQQSGPELEKPGASVKISCKASGFLSPGHNINWIVQRNGKSLEWIGNIDPYYGGTNNFNPKFKGK
ATLTVDKSSSTLYMHLTSLQSEDSAVYYCARRRDGNYGFTYWGQGLTVTVSA
>d1fig1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab 1F7
(mouse), kappa L chain}
ENVLTQSPAIMASAPGEKVTMACRASSSVSSTYLHWYQQKSGASPKLLIYSTSNLASGVPARFSGSGSG
TSYSLTISSVEAEDAATYYCQYSGYPLTFGAGTKLELKR
>d1frgh1 b.1.1.1 (H:218-336) Immunoglobulin (variable domains of L and H chains) {Fab

26/9 (mouse), kappa L chain}

EVLLVESGGDLVKPGGFLKLSAASGFTFSSFGMSWVRHTPDKRLEWVATISNGGGYTTYQDSVKGR
FTISRDNANTLFLFEMTSLKSEDAAGLYCARRERYDEKGFAYWGRGTLTVS

>d1frgl1 b.1.1.1 (L:1-113) Immunoglobulin (variable domains of L and H chains) {Fab 26/9
(mouse), kappa L chain}

DIVMTQSPSSLTVTAGEKVTMSCKSSQSLFNSGKRKNFLTWYHQKPGQPPELLIYWASTRESGVPDR
FSGSGSGTDFTLTITSVQAEDLAIYYCQNDYSHPLTFGAGTKLELK

>d1a2ya_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Fab D1.3
(mouse), kappa L chain}

DIVLTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQKSPQLLVYYTTTLADGVPSRFSGSGSGT
QYSLKINSLQPEDFGSYQCQHFWSPTPRTFGGGKLEIK

>d1a2yb_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {Fab D1.3
(mouse), kappa L chain}

QVQLQESGPGLVAPSQSLTCTVSGFSLTGYGVNWVRQPPGKGLEWLGMIWGDGNTDYNALKSRL
SISKDNSKSVFLKMNSLHTDDTARYYCARERDYRLDYWGQGTTLTVSS

>d1a7ql_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fab D1.3
(mouse), kappa L chain}

DIVLTQSPASLSASVGETVTITCRAGGNTHNYLAWYQQKQKSPQLLVYYTTTLAAGVPSRFSGSGSG
TQYSLKINSLQPDDFGSYQCQHFWSPTPRTFGGGKLEIK

>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}

DIVMTQSHKFMSTSVGDRVSITCKASQDVRIAWYQQKPGQSPKLLIYWASTRHTGVPDRFTGSGS
GTDFTLTISNVQSEDLADYFCQHCGSYPFTFGSGTKLEIK

>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}

QVQLQQPGSELVRPGASVKLSCKASGYTFTNYWMHWVKQRPGQGLEWIGNIYPSGSDSNYDEKFK
SKATLTVDTSSSTAYMQLSGLTSEDSAVYYCARGLAFYFDHWGQGTTLTVSS

>d1jhlh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv D11.15
(mouse), kappa L chain}

QVQLQQSGAELVRPGASVKLSCKASGYTFISYWINWVKQRPGQGLEWIGNIYPSDSTNYNQKFKDK
ATLTVDKSSSTAYMQLSSPTSEDSAVYYCTRDDNYGAMDYWGQGTTLTVTV

>d1jhll_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv D11.15
(mouse), kappa L chain}

DIELTQSPSYLVASPGETITINCRASKSISKSLAWYQEKPCKTNNLLIYSGSTLQSGIPSRFSGSGSGTDF
TLTISSLEPEDFAMVICQQHNEYPWTFGGGKLEIKR

>d1bqlh1 b.1.1.1 (H:2-116) Immunoglobulin (variable domains of L and H chains) {Fab
HyHEL-5 (mouse), kappa L chain}

VQLQQSGAELMKPGASVKISCKASGYTFSDYWIEWVKQRPGHGLEWIGEILPGSGSTNYHERFKGKA
TFTADTSSSTAYMQLNSLTSEDSGVYYCLHGNYDFDYGWQGTTLTVSS

>d1bql1 b.1.1.1 (L:1-106) Immunoglobulin (variable domains of L and H chains) {Fab
HyHEL-5 (mouse), kappa L chain}

DIVLTQSPAISASPGKVTMTCSASSSVNYMYWYQQKSGTSPKRWIYDTSKLAGVPPVRFSGSGSGT
SYSLTISSMETEDAATYYCQWGRNPTFGGGKLEIKR

>d1ic7h_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fab HyHEL-10

(mouse), kappa L chain}
DVQLQESGSLVKPSQTLTCSVTGDSITSAYWSWIRKFPGNRLEYMGYVSYSGSTYYNPSLKSRSI
TRDTSKNQYYLDLNSVTTEDTATYYCANWAGDYWGQGLTVTVSAA
>d2jelh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab JE142
(mouse), kappa L chain}
QVQLAQSGPELVPRPGSVKISCKGSGYFTTTYAMHWVKQSHAKSLEWIGLISTYSGYTNYNQKFKGK
ATMTVDKSSSTAYMELARLTSEDSAIYYCARVMGEQYFDVWGAGTTVIVSS
>d1ncbh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab
NC41 (mouse), kappa L chain}
QIQLVQSGPELKKPGETVKISCKASGYFTNYGMNWVKQAPGKGLEWMGWINTNTGEPTYGEEFK
GRFAFSLETSASTANLQINNLKNEKATFFCARGEDNFGSLSDYWGQGTTLTVSS
>d1ncbl1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab NC41
(mouse), kappa L chain}
DIVMTQSPKFMSTSVGDRVTITCKASQDVSTAVVWYQQKPGQSPKLLIYWASTRHIGVPDRFAGSGS
GTDYTLTISSVQAEDLALYYCQQHYSPPWTFGGGTKLEIKR
>d1forh1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and H chains) {Fab 17-Ia
(mouse), kappa L chain}
QGQLQQSGAELVRPGSSVKISCKASGYAFSSFWVNWVKQRPGQGLEWIGQIYPGDGDNKYNGKFKG
KATLTADKSSSTAYMQLYSLTSEDSAVYFCARSGNYPYAMDYWGQGTSVTVSSA
>d1forl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 17-Ia
(mouse), kappa L chain}
QIVLTQSPAISAFPGEKVTITCSATSSVNYMHWFQKPGTSPKLWIYSSSNLASGVPARFSGSGSGTS
YSLTISRMEAEDAATYYCQQRSSYPITFGSGTKLEIKR
>d1knoa1 b.1.1.1 (A:1-108) Immunoglobulin (variable domains of L and H chains) {Fab
CNJ206 (mouse), kappa L chain}
QIQMTQSPSSLSASLGERVSLTCRASQEISGYLSWLQKQPDGTIKRLIYAASLDVSGVPKRFSRSGSD
YSLTISSLESEDFADYYCLQYASSPYTFGGGTKLEILR
>d1knob1 b.1.1.1 (B:1-119) Immunoglobulin (variable domains of L and H chains) {Fab
CNJ206 (mouse), kappa L chain}
DVKLVESGGGLVQPGGSRKLSAASGFTFSSFGMHVVRQAPEKGLEWVAYISSGSSTIYYADTVKGRF
TISRDNPKNTLFLQMTSLRSEDTAMYCARGDYYSRGAYWGQGLTVTVSA
>d1eapb1 b.1.1.1 (B:1-124) Immunoglobulin (variable domains of L and H chains) {Fab 17E8
(mouse), kappa L chain}
EVQLQESGTELVKPGASVKISCKASGYISTDHAIHWVKQRPEQGLEWIGYISPGNGDIKYNEKFKVKA
TLTADQSSSTAYMQLNSLTSEDSAVYFCKRSYYSYVDYWGQGTTLTVSS
>d1mrdh1 b.1.1.1 (H:2-115) Immunoglobulin (variable domains of L and H chains) {Fab Jel
103 (mouse), kappa L chain}
VQLQQSGAELVKPGASVKLSCKASGYFTTSYWMQWVKQRPGQGLEWIGWIGIDPSDSTNYNQKFKGK
ATLTVDTSSSTAYMQLSSLTSEDSAVYYCANLRGYFDYWGQGTTLTVSSAK
>d1fbih1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and H chains) {Fab
F9.13.7 (mouse), kappa L chain}
QVQLQQPGAELVKPGASVKLSCKASGYFTTSYWMHWVKQGPQGLEWIGWIGIDPSDSTNYNEKFKG
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCASLYYGYGTVLDYWGQGTSVTVS
>d1fbil1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab

F9.13.7 (mouse), kappa L chain}

DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQKKPDGTVKLLIYYTSRLHSGVPSRFSGSGSG
TDYSLTIRNLEQEDIATYFCQQGYTLPYTFGGGKLEIK

>d1rmfh1 b.1.1.1 (H:1-119) Immunoglobulin (variable domains of L and H chains) {Fab R6.5 (mouse), kappa L chain}

QVQLQQSGPELVRPGVSVKISCKGSGYTFIDYAIHWVKESHAKSLEWIGVISAYSAGDTNYNQKFKGKA
TMTVDKSSNTAYLELARLTSEDSAIYYCARGGWLLLSFDYWGQGTTLTVSS

>d1rmfl1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab R6.5 (mouse), kappa L chain}

DVVMVTQSPLSLPVSLGDQASISCRSSQSLVHSNGNNYLHWYLQKSGQAPKLLIYKVSNRFSGVPDRFS
GSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPLTFGGGKLEIK

>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}

QVQLQQSGAELVRPGTSVKVSKASGYAFTNYLIQWIKRPGQGLEWIGVINPGSGGTDYNANFKGK
ATLTADKSSSIVYMQLSLTSDDSAVYFCARDFYDYDVGFDYWGQGTTLTVSS

>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}

DVVMVTQTPSLSPVSLGDQASISCSSSQSLVHSNGKTYLHWYLQKPGQSPKLLIYKVSNRFSGVPDRFS
GSGSGTYFTLKISRVEAEDLGVYFCSQSTHVPYTFGGGKLEIKR

>d1ikfh1 b.1.1.1 (H:1-126) Immunoglobulin (variable domains of L and H chains) {Fab, anti-cyclosporin A, (mouse), kappa L chain}

EVKLVESGGGLVQPGGSLKLSCATSGFTFSYYMYWVRQNSEKRLEWVAFISNGGSAFYADIVKGR
FTISRDNKNTLYLQMSRLKSEDTAMYYCTRHTLYDTLYGNYPVWFADWGWQGTTLTVSA

>d1ikfl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab, anti-cyclosporin A, (mouse), kappa L chain}

DIQMTQTTSSLSASLGDRVTISCRASQDISTYLNWYQQKPDGTVKLLIFYTSRLRSGVPSRFSGSGSGT
DYSLTISNLEQEDIATYFCQQGSRIPPTFGGGKLEIL

>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}

VQLQQSGTELMKPGRSLKISCKTTGYIFSNYWIEWVKRPGHGLEWIGKILPGGGSNTYNDKFKGKA
TFTADTSSNIAYMQLSSLTSEDSAVYYCARGEDYYAYWYVLDYWGQGTTVTVSSGGGGS

>d1lmka2 b.1.1.1 (A:201-312) Immunoglobulin (variable domains of L and H chains) {scFv dimer (L5MK16 diabody), based on: (mouse), kappa L chain}

DIELTQSPLSLPVSLGDQASISCRSSQSLVHSNGNTSLHWYLKKGQSPKLLIYKVSTRFSGVPDRFSG
SGSGTDFTLKISRVEAEDLGVYFCSQSTHVPFTFGSGTKLELK

>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}

DIELTQTPSLSPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFSGVPDRFSG
SGSGTDFTLKISRVEAEDLGVYYCFQGSHPYTFGGGKLEIKR

>d1igch1 b.1.1.1 (H:1-119) Immunoglobulin (variable domains of L and H chains) {Fab MoPC21 (mouse), kappa L chain}

DVQLVESGGGLVQPGGSRKLSAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTLHYADTVKGR
FTISRDNPKNTLFLQMTSLRSEDGMYYCARWGNYPYAMDYWGQGTSTVTVS

>d1igcl1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab

MoPC21 (mouse), kappa L chain}
NIVMTQSPKSMMSVGERVTLTCKASENVVTVVSWYQQKPEQSPKLLIYGASNRYTGVDPDRFTGSGS
ATDFTLTISSVQAEDLADYHCGQGNISYPYTFGGGKLEIKR
>d1ibgh1 b.1.1.1 (H:2-113) Immunoglobulin (variable domains of L and H chains) {Fab
40-50 (mouse), kappa L chain}
VHLVQSGPGLVAPSQSLTCTVSGFSLTTYGVHWFRQPPGKGLEWLGLIWAGGNTDYNLSALMSRLSI
NKDNSKQVFLKMNSLQADDTAMYYCARFRFASYYDYAVDYWGQGTSVTVSS
>d1ibgl1 b.1.1.1 (L:2-107) Immunoglobulin (variable domains of L and H chains) {Fab 40-50
(mouse), kappa L chain}
IVLTQSPASLAVSLGQRATISCRASKSVSTSGYSHIHWWYQQKPGQPPKLLIYLASILESGVPARFSGSGS
TDFTLNIHPVEEEDAATYYCQHSREYPLTFGAGTELELK
>d1mlbb1 b.1.1.1 (B:1-118) Immunoglobulin (variable domains of L and H chains) {Fab
D44.1 (mouse), kappa L chain}
QVQLQESGAELVMKPGASVKISCKATGYTFTSTYWIEWVKQRPGHGLEWIGELPGSGSTYYNEKFKGK
ATFTADTSSNTAYMQLSSLTSEDSAVYYCARGDGNVGYWGQGTTLTVSSAS
>d1a14h_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fab NC10
(mouse), kappa L chain}
QVQLQQSGAELVKPGASVRMSCKASGYTFTNYNMYWVKQSPGQGLEWIGIFYPGNGDTSYNQKFK
DKATLTADKSSNTAYMQLSSLTSEDSAVYYCARGSGSYRYDGGFDYWGQGTTVTV
>d1a14l_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fab NC10
(mouse), kappa L chain}
DIELTQTSSLSASLGDRVTISCRASQDISNYLNWYQQNPDGTVKLLIYYTSLNHSEVPSRFSGSGSGT
DYSLTISNLEQEDIATYFCQQDFTLPFTFGGGTAA
>d1nmb1_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fab NC10
(mouse), kappa L chain}
DIQMTQTSSLSASLGDRVTISCRASQDISNYLNWYQQNPDGTVKLLIYYTSLNHSEVPSRFSGSGSG
TDYSLTISNLEQEDIATYFCQQDFTLPFTFGGGTKLEIRRA
>d1bm3h1 b.1.1.1 (H:1-125) Immunoglobulin (variable domains of L and H chains)
{Anti-integrin Fab OPG2 (mouse), kappa L chain}
EVQLVQSGGGLVNPGRSLKLSAASGFTFSSYGMSSWVRQTPEKRLEWVAASGGGTYIHYPDSVKGR
FTISRDNKNNLYLQMSLRSEDALYCTRHPFYRYDGGNYAMDHWGQGTSVTVSA
>d1nsh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab N10
(mouse), kappa L chain}
DVQLQESGPGLVKPSQSLTCTVTGYSITSDYAWNWRQFPGNKLEWVMGYITYSGTTSYNPSLKSRI
SISRDTSKNQFFMQLNSVTTEDTGTIFYCTRNGDWDWGQGTTLTVSSA
>d1nsh1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab N10
(mouse), kappa L chain}
DIVLTQSPSSLAVSLGQRATISCRASQSVSTSSFRYMHWWYQQKPGQPPRLLIKYASNLESGVPARFSGS
GSGTDFTLNIHPVEEEDTATYYCQHSWEIPYTFGGGKLEIK
>d1iaih1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and H chains) {Fab
730.1.4 (mouse), kappa L chain}
QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWWKQAPGKGLKWMWINTYTGPEPTYADDFK
GRFAFSLETSASTAYLQINNKNEDTATYFCARDGYYENYYAMDYWGQGTSVTVSS
>d1iail1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab

730.1.4 (mouse), kappa L chain}

DIVMTQSHKFMSTSVGDRVSITCKASQDVSTAVAWYQQKPGQSPKLLIYSASYQYTGVPDRFTGSGSR
TDFFTTINSVQAEDLAVYYCHQHYSTPFTFGSGTKLEIKR

>d1iaii1 b.1.1.1 (I:1-121) Immunoglobulin (variable domains of L and H chains) {Fab 409.5.3
(mouse), kappa L chain}

EVKLVQESGGGLVQPGGSMKLSVCVASGFTFNWMSWVRQSPKGLWVAEIRLNSDNFATHYAESV
KGFIIISRDDSKSRLYLQMNLSRAEDTGIYYCVRPLFYAVDYWGQTSVTVSS

>d1iaim1 b.1.1.1 (M:1-109) Immunoglobulin (variable domains of L and H chains) {Fab
409.5.3 (mouse), kappa L chain}

DIQLTQSPAFMAASPGEKVTITCSVSSSISSNLHWYQQKSETSPKPWIYGTSNLASGVPVRFSGSGSG
TSYSLTSSMEAEADAATYYCQWNSYPYTFGGGTKLEIKR

>d1plgh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains) {Polysialic
acid-binding Fab (mouse), kappa L chain}

QIQLQQSGPELVKPGASVKISCKASGYTFTDYYIHVVKQRPGEGLWIGWIYPGSGNTKYNEKFKGK
ATLTVDTSSSTAYMQLSSLTSESAVYFCARGGKFAMDYWGQTSVTVSS

>d1plgl1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Polysialic
acid-binding Fab (mouse), kappa L chain}

DVVMVTQTPSLPVLGDAQISCRSSQSLVHNSGNTYLYWYLQKPGQSPKPLIYRVSNRFSGVPDRFS
GSGSGTDFTLKISRVEAEDLGVYFCFQGTHTVYTFGGGTRLEIK

>d1aj7h1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab 48G7
(mouse/human), kappa L chain}

QVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHVVKQRPEQGLEWIGRIDPANGNTKYDPKFQK
KATITADTSSNTAYLQSSLTSEDTAVYYCASYGGIYWGQTTTLTVSSA

>d1gafh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab 48G7
(mouse/human), kappa L chain}

QVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHVVKQRPKQGLEWIGRIDPANVDTKYDPKFQD
KATITADTSSKTTYLQSSLTSEDTAVYYCASYGGIYWGQTTTLTVSS

>d1gaf1 b.1.1.1 (L:1-109) Immunoglobulin (variable domains of L and H chains) {Fab 48G7
(mouse/human), kappa L chain}

DIQMTQSPSSLSASLGERVSLTCRASQEIINGYLGLWVQKPDGTIKRLIYAASLHSGVPKRFSGSRSGS
DYSLTSSLESEDFADYYCLQYASYPRTFGGGTKVEIKRT

>d1vgeh1 b.1.1.1 (H:1-122) Immunoglobulin (variable domains of L and H chains) {Fab
TR1.9 (mouse/human), kappa L chain}

QVKLLEQSGAEVKKPGASVKVSKASGYSFTSYGLHWVRQAPGQRLEWMGWISAGTGNTKYSQKF
RGRVTFTRDTSATTAYMGLSSLRPEDTAVYYCARDPYGGGKSEFDYWGQGLTVTVSS

>d1vge1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab TR1.9
(mouse/human), kappa L chain}

ELVMTQSPSSLSASVGDVNIACRASQGISSALAWYQQKPGKAPRLIYDASNLESGVPSRFSGSGSGT
DFTLTSSLPEDFAIYYCQFNSYPLTFGGGTKVEIK

>d1yuhb1 b.1.1.1 (B:1-118) Immunoglobulin (variable domains of L and H chains) {Fab
anti-nitrophenol (mouse), lambda L chain}

QVQFQQSGAELVKPGASVKLSCKASGYTFTSYLMHWIKRPRGRGLEWIGRIDPNNVTKFNEKFKS
KATLTVDKPSSSTAYMELSSLTSESAVYYCARYAYCRPMDYWGQTTVTVSS

>d1ucbh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab

CBR96 (mouse/human), kappa L chain}
EVNLVESGGGLVQPGGSLKVCVTSFGFTFSDYYMYWVRQTPEKRLEWVAYISQGGDITDYPDTVKGR
FTISRDNANSYLYLQMSRLKSEDTAMYYCARGLDDGAWFAYWGQGLVTVSV
>d1ucbl1 b.1.1.1 (L:4-108) Immunoglobulin (variable domains of L and H chains) {Fab
CBR96 (mouse/human), kappa L chain}
MTQIPVSLPVSLGDQASISCRSSQIIVHNNNGNTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGS
GTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGSGTKLEIKR
>d1dvfc_ b.1.1.1 (C:) Immunoglobulin (variable domains of L and H chains) {Fv E5.2 (mouse),
kappa L chain}
DIQLTQSPSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPSRFSGSGSGT
DYSLTISNLEQEDIATYFCQQGNTLPWTFGGGKLEIK
>d1dvfd_ b.1.1.1 (D:) Immunoglobulin (variable domains of L and H chains) {Fv E5.2
(mouse), kappa L chain}
QVQLQQSGTELKSGASVKLSCTASGFNIKDTHMNWVKQRPEQGLEWIGRIDPANGNIQYDPKFRG
KATITADTSSNTAYLQSLTSEDVAVYYCATKVIYYQGRGAMDYWGQGTTLTVS
>d1ghfh1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab
GH1002 (mouse), kappa L chain}
VQLQQSGPELKKPGETVKISCKLWYFTFDYGMNWVKQAPGKGLKWMGWIQTNTEPTYGAEFKG
RFAFSLETSFTAYKQINNLKNEDEMATYFCARVEAGFDYWAQGTTLTVSS
>d1ghf1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab
GH1002 (mouse), kappa L chain}
DIQMTQTTSSLSASLGDRVTISCRSQDISNSLNWYQQKPDGTVKLLIYYTSRLHSGVPSRFSGSGTG
TDYSLTISNLEQEDFATYFCQQGNTLPYTFGGGKLEIK
>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}
QVKLQQSGPGLVQPSQSLTCTVSGFSLTCYGVHWVRQSPGKGLEWLGVIWSSGGTDYNAAFISRLS
ITKDNSKSVVFFKMNSLQPNDRAIYYCARRGGDFWQGTTVTVS
>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), kappa L chain}
DVVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDSGVPDRFT
GSGSGTDFTLKISRVEAEDLGVYYCWQGTTFPRTFGGGKLEIK
>d1kelh1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab 28B4
(mouse), kappa L chain}
EVKLVESGGGLGQPGGSLRLSCATSGFTFTDYFYNWARQPPGKALEWLGFIKAKAGYTTTEYSASVK
GRFTISRDNQGILYLQMNTLRAEDSATYYCARWGSYAMDYWGQGTSSV
>d1kell1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 28B4
(mouse), kappa L chain}
DVLMTQTPLSLPVSLGDQASISCRFSQSIVHSNGNTYLEWYLQKSGQSPKLLIYKVSNRFSGVPDRFS
GSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGGKLEIK
>d1osph1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and H chains) {Fab
184.1 (mouse), kappa L chain}
EVQLQESGPSLVKPSQTLTCSVTGEPITSGFWDWIRKFPGNKLEFMGYIRYGGGTYYNPSLKSPISI
TRDTSKNHYYLQNSVVTEDTATYYCARSRDYGGSSGFAFWGEGTLTVSA
>d1ospl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 184.1

(mouse), kappa L chain}
DIQMSQSSSSFSVSLGDRVTITCKASEDIYSRLAWYQQKPGNAPRLLISGATSLETWVPSRFSGSDSGK
DYTLSITSLQTEDVATYFCQYWSPPPTFGGGTKLEIK
>d1fj1a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab LA-2
(mouse), kappa L chain}
DIQMTQSPSSLSATLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGNPSRFSGSGSG
RDYSFSISNLEAEDIAIYYCLQYDNLQRTFGGGTKVEIK
>d1fj1b1 b.1.1.1 (B:1-114) Immunoglobulin (variable domains of L and H chains) {Fab LA-2
(mouse), kappa L chain}
QIQLVQSGPELKKPGETVKISCKASGYTFTDYSMYWVKQAPGKGLKRMGWINTETGEPTYADDFKG
RFALSLDTSASTAYLHISNLKNETATYFCARGLDSWGQTSVTVSSA
>d1cloh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab A5B7
(mouse), kappa L chain}
EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYIMNWVRQPPGKALEWLGFIGNKANGYTTEYSASV
KGRFTISRDKSQSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQTTLVSS
>d1clo1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab A5B7
(mouse), kappa L chain}
QTVLSQSPAILSASPGEKVTMTCRASSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTS
YSLTISRVEAEDAATYYCQHWSSKPPTFGGGTKLEIK
>d1ad0a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab
A5B7 (engineered human construct), kappa L chain}
QTVLTQSPSSLSVSVGDRVTITCRASSVTYIHWYQQKPGGLAPKSLIYATSNLASGVPSRFSGSGSGTDY
TFTISSLQPEDATYYCQHWSSKPPTFGGGTKVEVCR
>d1ad0b1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Fab
A5B7 (engineered human construct), kappa L chain}
EVQLLESGGGLVQPGGSLRLSCATSGFTFTDYIMNWVRQAPGKGLEWLGFIGNKANGYTTEYSASVK
GRFTISRDKSKSTLYLQMNTLQAEDSAIYYCTRDRGLRFYFDYWGQTLTVSS
>d1mimh1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab
CHI621 (mouse), kappa L chain}
QLQQSGTVLARGASVKMSCKASGYFTRYWMHWIKRPGQGLEWIGAIYPGNSDTSYNQKFEKG
AKLTAVTSASTAYMELSSLTHEDSAIVYCSRDIYGYFDYWGQTTLVSS
>d1miml1 b.1.1.1 (L:1-105) Immunoglobulin (variable domains of L and H chains) {Fab
CHI621 (mouse), kappa L chain}
QIVSTQSPAIMSASPGEKVTMTCSASSRSYMQWYQQKPGTSPKRWIYDTSKSLASGVPARFSGSGSGT
SYSLTISMEAEEDAATYYCHQRSSYTFGGGTKLEIKR
>d1afvh1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and H chains) {Fab 25.3
(mouse), kappa L chain}
QVQLQQPGSVLVRPGASVKLSCKASGYTFTSSWIHWAKRPGQGLEWIGEIHPNSGNTNYNEKFKG
KATLTVDTSSSTAYVDLSSLTSEDSAVYYCARWRYGSPYYFDYWGQTTLVSS
>d1afvl1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 25.3
(mouse), kappa L chain}
DIVLTQSPASLAVSLGQRATISCRASESVDNYGISFMNWFQQKPGQPPKLLIYAASNLSGVPARFSGS
SGGTDFSLNIHPMEEEDTAMYFCQQSKEVPLTFGAGTKVELKR
>d2mpah1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and H chains)

{Bactericidal Fab MN12H2, (mouse), kappa L chain}
EVNLQQSGTVLARPGASVRMCKASGYSFTSYWLHWIKQRPGQGLEWIGGIYPGNRDTRYTQRFKD
KAKLTAVTSANTAYMELSSLTNEDSAVYYCSIIYFDYADFIMDYWGQGTTVTVSS
>d2mpal1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains)
{Bactericidal Fab MN12H2, (mouse), kappa L chain}
DIVMTQTPLSLPVSLGDKASISCRSSQALVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPDRFS
GSGSGTDFTLKISRVEAEDLGVFFCSQSTHVPRTFGGGTKLEIK
>d1qkzh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab
MN14C11.6 (mouse), kappa L chain}
DVKLVESGGGLVVKPGRSLKLSAASGFTFSDYYMFWVRQTPEQRLEWVATISDGGAYTYYPDSVKGR
FTISRDNANKNNLYLQMNSLKSEDTGMYCARDPLEYYGMDYWGQGTSAVSS
>d1qkzl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab
MN14C11.6 (mouse), kappa L chain}
NIVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYTVSNRFSGVPDRFS
GSGSGTDFTLKISRVEAEDLGVIYFCSQSTHFPTFGGGTKLEIK
>d1pskh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab
against a ganglioside (mouse), kappa L chain}
EVQLQQSGPELVKPGASVKISCKTSGYFTFKYTMHWVKQSHGKSLEWIGDINPNNGGTNYNQKFKG
TATLTVHKSSTTAYMELRSLTSEDSAVYYCTSKSFDYWGQGTTLTVSS
>d1pskl1 b.1.1.1 (L:1-106) Immunoglobulin (variable domains of L and H chains) {Fab
against a ganglioside (mouse), kappa L chain}
QIVLTQSPAISASPGKVTITCSASSSVSNHWFQQKPGTTPKLIWYSTSTLASGVPGRFSGSGGTSY
SLTISRMAEDAATYYCQQRSGYPFTFGSGTKLEIK
>d1yejh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab D2.3
(mouse), kappa L chain}
EMQLQQSGAELLRPGTSVKLSCKTSGYIFTSYWIHWVKQRSGQGLEWIARIYPGTGSTYYNEKFKGK
ATLTADKSSSTAYMQLSTLKSSEDSAVYFCTRWFIPVREDYVMDYWGQGLTVTVSS
>d1yejl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab D2.3
(mouse), kappa L chain}
DIVMTQSPLTSLVTIGQPASISCKSSQSLLYSNGKTYLNWLLQRPQSPKRLIHLVSKLDSGVPDRITGS
GSGTDFTLKISRVEAADLGVIYCVQGTTHFPYTFGGGKLEIL
>d1yedb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Fab D2.4
(mouse), kappa L chain}
AVKLQQSGPELVKPGTSVKLSCKTSGYIFTSYWIHWLQSSGQGLEWIARIYPGTGGTYNEKFKGKA
TLTADKSSSTAYMQLSSLKSEDSAVYFCTRWFVTVRENYAMDYWGQGLTVTVSS
>d1yeeh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab D2.5
(mouse), kappa L chain}
EVKLQESGAELVLRPGASVKLSCKTSGYIFTSYWIHWVKQRAAAGLEWIARIYPGTGSSYYNVKFKGK
ATLTADKSSSTAYMQLSSLKSDSAVYFCVWRWFIPVREDYVLDYWGQGLTVTVSS
>d1cfvh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv 4155
(mouse), kappa L chain}
QVQLQESGGGLVNLGGSMTLSCVASGFTFNTYYMSWVRQTPEKTLVLAAINSDEGIYYPDTLTKGR
VTISRDNAKKTLYLQMSLNFEDTALYICARLNYAVYGM DYWGQGTTVTVSS
>d1cfvl_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv 4155 (mouse),

kappa L chain}

DIELTQSPPLSPVSLGDQVSISSCRSSQSLVSNRRNYLHWYLOKPGQSPKLVYKVSNRFSGVPDRFSG
SGSGTDFTLKISRVAEEDLGLYFCSQSSHVPLTFGSGTKLEIKR

>d1hyxh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab 6D9
(mouse), kappa L chain}

EVKLLESGGGLVKPGGSLKLSAASGFTFSNYAMSWVRQTPEKRLEWVVISISSGGSIYYLDSVKGRFT
VSRDNARNILYLQMTSLRSEDAMFYFCARVSHYDGRDWFYFDVWGAGTSVTVSS

>d1hyxl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 6D9
(mouse), kappa L chain}

ELVMTQTPLSLPVSLGDQASISCRSSQTIVHSNGDTYLDWFLQKPGQSPKLLIYKVSNRFSGVPDRFS
GSGSGTDFTLKISRVEAEDLGVYYCFQGSHPPTFGGGTKLEIK

>d2hrph1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab
F11.2.32 (mouse), kappa L chain}

DVQLVESGGGLVQPGGSRKLSAASGFTFMRFGMHWVRQAPEKGLEWVAYISSGSSTIYYADTVKGR
FTISRDNPKNTLFLQMTSLRSEDALYYCARSGGIERYDGTYYVMDYWGQTSVTVSS

>d2hrpl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab
F11.2.32 (mouse), kappa L chain}

DTVLTQSPASLAVSLGQRATISCRASESVDYGKSFMNWFQKPGQPPKLLIYAASNQGGSGVPARFSG
SGSGTDFSLHIHPMEEDDSAMYFCQKSKEVPWTFGGGKLEIK

>d2ap2a_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {scFv C219,
(mouse sequence-based), kappa L chain}

FVRDIVMTQSPSSLTVTAGEKVTMSCKSSQSLNLSGNQKNYLTWYQQKPGQPPKLLIYWASTRESGV
PDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEP

>d2ap2b_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {scFv C219,
(mouse sequence-based), kappa L chain}

EVQLQQSGAELVRPGASVKLSCTASGFNIKDDFMHWVKRPEQGLEWIGRIDPANDNTKYAPKFQD
KATIIADTSSNTAYLQLSSTSEDVAVYYCARREVSYYSPLDVWGAGTTVTVPSG

>d1nfde1 b.1.1.1 (E:2-107) Immunoglobulin (variable domains of L and H chains) {Fab H57
(hamster), lambda L chain}

YELIQSSASVTVGETVKITCSGDQLPKNFAYWFQKSDKNILLIYMDNKRPSGIPERFSGSTSGTTA
TLTISGAQPEDEAAYYCLSSYGDNDLVFGSGTQLTVLR

>d1nfd1 b.1.1.1 (F:1-114) Immunoglobulin (variable domains of L and H chains) {Fab H57
(hamster), lambda L chain}

EVYLVESGGDLVQPGSSLVKLSAASGFTFSDFWVWVRQAPGKGLEWVGRIKNIPNNYATEYADSVR
GRFTISRDDSRNSIYLQMNRLRVDATAIYYCTRAGRFDHFDYWGQGMVTVSSA

>d2h1ph1 b.1.1.1 (H:301-420) Immunoglobulin (variable domains of L and H chains) {Fab
2H1 (mouse), kappa L chain}

DVKLVESGGGLVKLGGSLKLSAASGFTFSSYFLSWVRQTPEKRLELVATINSNGDKTYHPDTMKGRF
TISRDNKNTLYLQMSLKSEDALYYCARRDSSASLYFDYWGQGTTLTVSS

>d2h1pl1 b.1.1.1 (L:1-113) Immunoglobulin (variable domains of L and H chains) {Fab 2H1
(mouse), kappa L chain}

DVVMTQTPLSLPVSLGDPASISCRSSQSLVHSNGNTYLHWYLOKPGQSPKLLIYKVSNRFSGVPDKFS
GSGSGTDFTLKISRVEAEDQGVYFCSQSTHVPWTFGGGKLEIKR

>d1aqkh1 b.1.1.1 (H:1-123) Immunoglobulin (variable domains of L and H chains) {Fab

B7-15A2 (human), lambda L chain}
EVQLVESGGGVVQPGRSLRLSCAASGFTFNYYAIHWVRQAPGKGLEWVAFISYDGSKNYYADSVKGR
FTISRDNKNTLFLQMNSLRPEDTAIYYCARVLFQQQLVLYAPFDIWGQGTMVTVSS
>d1aqkl1 b.1.1.1 (L:1-111) Immunoglobulin (variable domains of L and H chains) {Fab
B7-15A2 (human), lambda L chain}
ENVLTQPPSVSGAPGQRVTISCTGSNSNIGAGFTVHWYQHLPGTAPKLLIFANTNRPSGVPDRFSGSK
SGTSASLAITGLQAEDEADYYCQSYDSSLSARFGGGTRLTVLG
>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)}
ELVLTQSPSSMYASLGERVTITCKASQDINSYLNWFQQKPGKSPKTLIYRTNRLVDGVPSRFRSGSGSQ
DYSLTISSLEYEDMGIYYCLQYDEFPTYFGSGTKLEIK
>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)}
QVQLQSGAELMKPGASVKISCKATGYTFSSYWIEWVKRPGHGLEWIGEILPGSGSTNYNEKFKGK
ATFTADTSSNTAYMQLSSLTSEDSAVYYCARGHSYFYDGDYWGQGTSVTVSS
>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)}
DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPSRFRSGSGSG
QDYSLTISSLEYEDMGIYYCLQYDEFPTYFGSGTKLEIK
>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}
EVKQLQESGGDLVQPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVASINNGGRTYYPDTVKG
RFTISRDNKNTLYLQMSLSEDTAMYYCVRHEYYYAMDYWGQGTTVTVSS
>d1ar1d_ b.1.1.1 (D:) Immunoglobulin (variable domains of L and H chains) {Fv against
Paracoccus denitrificans cytochrome c oxidase (mouse), kappa L chain}
DIELTQTPVLSASVGETVTITCRASENIYSYLAWYQQKQKSPQFLVYNAKTLGEGVPSRFRSGSGSGT
QFSLKINLLPEDFGSYQCQHHYGTPLTFGGGKLEIK
>d1ae6h1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab
CTM01 (mouse), kappa L chain}
QIQLQSQGPELVKPGASVKISCKASGYTFTDYYINWMKQKPGQGLEWIGWIDPGSGNTKYNEKFKG
KATLTVDTSSTAYMQLSSLTSEDTAVYFCAREKTTYYYAMDYWGQGTSVTVSAA
>d1ae6l1 b.1.1.1 (L:1-106A) Immunoglobulin (variable domains of L and H chains) {Fab
CTM01 (mouse), kappa L chain}
DIVMTQAAPSPVTPGESLSISCRSSKSLHNSGDTFLYWFLQRPQSPQLLIYRMSNLASGVPDRFS
GSGSGTAFTLRVSRVEAEDVGVYYCMQHLEYPFTFGAGTKLELK
>d1ad9a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab
CTM01 (human construct), kappa L chain}
DIQMTQSPSTLSASVGDRTITCRSSKSLHNSGDTFLYWFLQKPGKAPKLLMYRMSNLASGVPSRF
SGSGSGTEFTLTISLQPDDEFATYYCMQHLEYPFTFGQGTKVEVCR
>d1ad9b1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Fab
CTM01 (human construct), kappa L chain}
EIQLVQSGAEVKKPGSSVKVCKASGYTFTDYYINWMRQAPGQGLEWIGWIDPGSGNTKYNEKFKG
RATLTVDTSNTAYMELSSLRSEDTAFYFCAREKTTYYYAMDYWGQGLTVTVSS
>d1fgh1 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}
EIQLQQSGAELVRPGALVKLSCKASGFNIKDYMHVWVKQRPEQGLEWIGLIDPENGNTIYDPKFQGK
ASITADTSSNTAYLQLSSLTSED TAVYYCARDNSYFDYWGQTTTLTVSS
>d1fgn1 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}
DIKMTQSPSSMYASLGERVTITCKASQDIRKYLNWYQQKPKWSPKTLIYYATSLADGVPSRFSGSGSG
QDYSLTISSESDDTATYYCLQHGESPYTFGGGTKLEINR
>d1jpth1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains)
{Anti-human tissue humanised factor Fab D3H44}
EVQLVESGGGLVQPGGSLRLSCAASGFNIKEYMHVWRQAPGKGLEWVGLIDPEQGNTIYDPKFQD
RATISADNSKNTAYLQMNSLRAEDTAVYYCARDTAAAFDYWGQGLTVTVSS
>d1jptl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains)
{Anti-human tissue humanised factor Fab D3H44}
DIQMTQSPSSLSASVGDRTITCRASRDIKSYLNWYQQKPGKAPKVLIIYATSLAEGVPSRFSGSGSGT
DYTLTISLQPEDFATYYCLQHGESPWTFGGGTKVEIK
>d1jrhh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab A6
(mouse), kappa L chain}
AVKLQESGPGILKPSQTLTCSFSGFSLTTYGMGVGWIRQSSGKLEWLAHIWDDDKYYNPSLKS
RLTISKDTSRNQVFLKITSVATADTATYYCARRAPFYGNHAMDYWGQTTTVTVSS
>d1jrhl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab A6
(mouse), kappa L chain}
SVEMTQSPSSFSVSLGDRVTITCKASEDIYNRLAWYQQKPGNAPRLISGATSLETEVPSRFSGSGSGK
DYTLTISLQTEDVATYYCQYQYWTWTFGGGTKLEIK
>d1gpoh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab M41
(artificial design)}
EVKLQESGSLVKPSQTLTCSVTGDSITSDFWSWIRQFPGNRLEYMGFVQYSGETAYNPSLKSRSI
TRDTSKNQYYLDLNSVTTEDTAVYYCANWHGDYWGQTTTVTVSS
>d1gpol1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab M41
(artificial design)}
DIELTQSPATLSVTPGNSVSI SCRASQSLVNEDGNTYLFWYQQKSHESPRLIKYASQSISGIPSRFSGSG
SGTDFTLINSVETEDLAVYFCQITDWPFTFGGGGTKLEIK
>d1kb5h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab
Desire-1 (mouse), kappa L chain}
EVQLQQSGPELEKPGASVKISCKASGYSFTGYNMNWVKQSNKGSLEWIGNIDPYYGGISYNQKFKGR
ATLTVDKSSSTAYMQLKSLTSEDSAVYYCARSRTDLYYFDYWGQTTTLTVSS
>d1kb5l1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab
Desire-1 (mouse), kappa L chain}
DIQMTQSPASLSASVGETVTITCRASKNIYSYLAWYQQKQKSPQLLVYNAKTLGEGVPSRFSGSGSG
TQFSLKINSLQPEDFGSYQCQHHYGTPTFGGGGTKLEIKR
>d1a4jb1 b.1.1.1 (B:1-119) Immunoglobulin (variable domains of L and H chains) {Diels
alder catalytic Fab (mouse), kappa L chain}
QVQLLES GPPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTYTGEPYADDFK
GRFAFSLETSASTAYLQINNLKNEDTATYFCVQAERLRRTFDYWGAGTTTVTVSS
>d1a4ka1 b.1.1.1 (A:1-112) Immunoglobulin (variable domains of L and H chains) {Diels

alder catalytic Fab (mouse), kappa L chain}
ELVMTQTPLSLPVSLGDQASISCRSSQSLHNSGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPDRFS
GSGSGTDFTLKISRVEAEDLGVYFCSQVTHVPPTFGGGTKLEIKRTVAA
>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}
QIQLVQSGPELKKPGETVKISCKASGYMFTNYGMNWVKQAPGKALKLMGWINPYTGESTFADDFKG
RFAFFLETSATTAYLQINLNKNEDMATYFCARGTTIVRAMDYWGQGTSLTVSSAKTTPP
>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}
ELVMTQTPLSLPVSLGDQASISCRSSQSLVHNSGNTYLHWYLQKPGQSPKFLIYKVSNRFSGVPDRFG
GSGSGTDFILKISRVEAEDLGVYFCFQSTHFFPTFGGGTKLEIKSADAA
>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}
EVQLEESGPELVRPGTSVKISCKASGYTFTNYWLGWVKQRPGHGFEWIGDIYPGGVYTTNNEKFRG
KAILTADTSSSTAYMQLSSLTSEDSAVYFCARAGGYTGGDYWGQGTSLTVSS
>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}
DIVLTQAAFSNPVTLGASASISCRSSKSLNLSNGIHMWYWLQKPGQSPQLLIYQMSKSLASGAPDRFSG
SGSGTDFTLRISRVEAEDVGVYCAQNLELPYTFGGGTKLEIK
>d1ay1h1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab TP7
(mouse), kappa L chain}
EVQLQESGPGLVKPYQSLSLCTVTGYSITSDYAWNWIRQFPGNKLEWMGYITYSGTTDYNPSLKSRI
SITRDTSKNQFFLQLNSVTTEDTATYYCARYYYGYWYFDVWVGQGTTLTVSS
>d1ay1l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab TP7
(mouse), kappa L chain}
DIQMTQSPAISASPGKEKVTMTCSASSSVSYMYWYQQKPGSSPRLIYDSTNLSGVPVRFSGSGSGT
SYSLTISRMEAEDAATYYCQWSTYPLTFGAGTKLELK
>d1dsfh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Anticancer Fv
B1 (mouse)}
QLVESGGGLVLPKPGGSLKLSAASGFIFSDNYMYWVRQTPEKCLEWVATISDGGTYIDYSDSVKGRFTI
SRDNAKNNLYLQMSSLRSEDGMYCYGRSPYYDYAPFTYWGQGTSLTVSA
>d1dsfl_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Anticancer Fv B1
(mouse)}
DVVMTQTPLSLPVSLGDQASISCRSSQNLVHSDGKTYLHWFLQKPGQSPTLLIYKVSNRFSGVPDRFS
GSGSGTDFILKISRVEAEDLGVYFCSQSTHVPLTFGCGTKLELK
>d1a6ta1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab
Mab1-IA (mouse), kappa L chain}
QSVLSQSPAILSASPGKVMITCSPSSSVSYMQWYQQKPGSSPKPWIYSTSNLASGVPGRFSGGGSGTS
FSLTISGVEAEDAATYYCQYSSHPLTFGGGTKLELK
>d1a6tb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Fab
Mab1-IA (mouse), kappa L chain}
EVQLQQSGPDLVLPKPGASVKISCKASGYSFSTYYMHWVKQSHGKSLEWIGRVDPDNGGTSFNQKFKG
KAILTVDKSSSTAYMELGSLTSEDSAVYYCARRDDYFDVWVGQGTSLTVSS
>d1a6wh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv B1-8

(mouse), lambda L chain}
QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKYNEKFK
SKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDYYGSSYFDYWGGQTTVTVSS
>d1a6wl_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv B1-8
(mouse), lambda L chain}
AVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPARFSGSLI
GNKAALTITGAQTEDEAIYFCALWYSNHWFVGGGTKLTVLE
>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}
QVQLLES GA EVK KPGSSVKVSKASGDTFIRYSFTWVRQAPGQGLEWMGRIITILDVAHYAPHLQGR
VTITADKSTSTVYLELRNLRSDDTAVYFCAGVYEGEAGEGEYRNNGLKHWGQGLTVTVTSA
>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}
ELELTQSPATLSVSPGERATLSCRASESVSSDLAWYQQKPGQAPRLLIYGASTRATGVPARFSGSGGA
EFTLTISLQSEDFAVYYCQQYNNWPPRYTFGQGRLEIK
>d12e8h1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab 2E8
(mouse), kappa L chain}
EVQLQQSGAEVVRSGASVKLSCTASGFNIKDYIHWVKQRPEKGLEWIGWIDPEIGDTEYVPKFQGK
ATMTADTSSNTAYLQLSSLTSEDTAVYYCNAGHDYDRGRFPYWGQGLTVTVSAA
>d12e8l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 2E8
(mouse), kappa L chain}
DIVMTQSQKFMSTSVGDRVSITCKASQNVGTAVAWYQQKPGQSPKLMISASNRYTGVPDRFTGSGS
GTDFTLTISNMQSEDLADYFCQQYSSYPLTFGAGTKLELK
>d1adqh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {IgM
rheumatoid factor Fab (human), lambda L chain}
EVQLVESGGGLVQPGRSLRLSCVTSQFTFDDYAMHWVRQSPGKGLEWVSGISWNTGTIIYADSVKGR
FIISRDNAKNSLYLQMNSLRVEDTALYYCAKTRSYVVAEYFHYWGQGLVTVSS
>d1adql1 b.1.1.1 (L:2-107) Immunoglobulin (variable domains of L and H chains) {IgM
rheumatoid factor Fab (human), lambda L chain}
YVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLLVYDDSDRPPGIPERFSGSNGNT
ATLTISRVEAGDEADYYCQVWDSSTHDAVFGGGTKLTVLG
>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}
DIQMTQTTSSLSASLGDRVTISCSASQDISSYLNWYQQKPEGTVKLLIYTTSSLHSGVPSAFSGSGSGT
DYSLTISNLEPEDFATYYCQQYSKFPWTFGGGTKLEIK
>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}
QITLKESGPGIVQPSQPFRLTCTFSGFSLSTSGIGVTWIRQPSGKGLEWLATIWWDDDNRYNPSLKS
LTVSKDTSNNQAFNMMTVETADTAIYYCAQSAITSVTDSAMDHWGQTSVTVSS
>d1bvka_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Humanized
anti-lysozyme Fv HuLys11 (mouse), kappa L chain}
DIQMTQSPSSLSASVGDRTITCRASGNIHNYLAWYQQKPGKAPKLLIYTTTTLADGVPSRFSGSGSG
TDYFTFISLQPEDIATYYCQHFWSWTPRTFGGQTKVEIKR
>d1bvkb_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {Humanized

anti-lysozyme Fv HuLys11 (mouse), kappa L chain}
QVQLQESGPGLVKPSQTLSTCTVSGFSLTGYGVNWRQPPGRGLEWIGMIWGDGNTDYNALKSR
VTMLKDTSKNQFSLRSLSSVTAADTAVYYCARERDYRLDYWGQGSGLTVSS
>d1a0qh1 b.1.1.1 (H:2-114) Immunoglobulin (variable domains of L and H chains) {Fab
29G11 (mouse), kappa L chain}
VQLQESDAELVKPGASVKISCKASGYTFTDTHVIHWVKQKPEQGLEWIGYISPGNGDIKYNEKFKGKA
TLTADKSSSTAYMQLNSLTSEDSAVYLCRKYGRSNVDYWGQGTTLTVSSA
>d1a0ql1 b.1.1.1 (L:2-108) Immunoglobulin (variable domains of L and H chains) {Fab
29G11 (mouse), kappa L chain}
IELTQSPSSLSASLGGKVTITCKASQDIKYYIGWYQHKPGKQPRLLIHYTSTLLPGIPSRFRGSGSGRDY
SFSISNLEPEDIATYYCLQYYNLRFTFGGGTKLEIKR
>d1fnsh1 b.1.1.1 (H:215-336) Immunoglobulin (variable domains of L and H chains) {Fab
NMC-4 (mouse), kappa L chain}
QVQLKESGPGLVAPSQSLSTCTVSGFSLTDYGVWVWRQPPGKGLEWLGMIWGDGSTDYNSALKSRL
SITKDNSKSVFLKMNSLQTDITARYYCVDRPADYGNVDYALDYWGQGTSTVTVSS
>d1fnsl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab
NMC-4 (mouse), kappa L chain}
DIQMTQSPSSLSASLGRVTISCSASQDINKYLNWYQQKPDGAVKLLIFYSSTLHSGVPSRFRSGSGSGT
DYSLTISNLEPEDIATYYCQYKLPWTFGGGKLEVK
>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}
QVQLQPGAELVRPGASVKLSCKASGYTLTTYWMNWFKQRPDQGLEWIGRIDPYDSETHYNQKFK
DKAILTVDRSSSTAYMQLSSTSEDSAVYYCTRFLQITTHYGMIDYWGQGTSTVTVSS
>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}
QVQLQQSGAELMKPGPSVKISCKATGYSFSTYFIEWIRQRPGHGLEWIGEILPGSDNTNFNEKFKDR
ATFTADTPSNTAYMQLSSTSEDSAVYYCARPTGRLWFSYWGQGTTLTVSA
>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}
QIILTQSPAIMSASPGKVTMTCSASSDISYMHWYQQKSDTSPKIWIYDTSKLGASVGPARGSGSGSGT
YSLTISTMEAEDAATYYCHQRSSYPTFGGGTKLEIK
>d35c8h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Catalytic
Fab 5C8 (mouse), kappa L chain}
EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHVWVKQKPEQGLEWIAQIDPANGNTKYDPKFKG
KATITADTSSNTAYLHLSSTSEDSAVYYCAADPPYYGHGDYWGQGTTLTVSS
>d35c8l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic
Fab 5C8 (mouse), kappa L chain}
DIVLTQSPAIMSASLGERVTMTCTASSVSSSNLHWYQQKPGSSPKLWIYSTSNLASGVPARGSGSGSG
TSYSLTISMEEDAATYYCHQYHRSPYTFGGGKLEIK
>d1a5fh1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and H chains)
{Anti-E-selectin Fab (mouse), kappa L chain}
EVALQQSGAELVKPGASVKLSAASGFTIKDAYMHVWVKQKPEQGLEWIGRIDSGSSNTNYDPTFKGK
ATITADSSNTAYLQMSSTSEDTAVYYCARVGLSYWYAMDYWGQGTSTVTVSS
>d1axth1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Catalytic

Fab 33F12 (mouse), kappa L chain}
EVKLEESGGGLVQPGGSMKLSVVSGLTFSRFWMSWVRQSPEKGLEWVAEIRLKS DNYATHYAESVK
GKFTISRDDSKSRLYLQMNSLRTE DTGIYYCKIYFYSFSYWGGTLVTVSA
>d1axtl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic
Fab 33F12 (mouse), kappa L chain}
ELVMTQTPLSLPVSLGDQASISCRSSQSLVHSYGNTFLNWYLQKSGQSPKLLIYKVS NRFSGVPDRFS
GSGSGTDFTLKISRVEAEDLG VYFCSQGTHVPYTFGGG TKLEIK
>d1b2wh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains)
{Humanized and chimeric anti-gamma-interferon Fab}
EVQLVQSGGGV VQPGRSLKLSCLASGYIFTSSWINWVKQRPGRGLEWIGRIDPSDGEVHYNQDFKDR
FTISRDKSKNTLYLQMNSLRPEDTAVYYCARGFLPWFADWGQGT LVTVSS
>d1b2wl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains)
{Humanized and chimeric anti-gamma-interferon Fab}
DIQMTQSPSTLSASVGDRTITCKASENVD TYVSWYQQKPGKAPKLLIYGASNRYTGVP SRFSGSGSG
TDFTLTISSLQPDDFATYYCGQSYNYPFTFGQGTKVEVK
>d1b4jh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains)
{Humanized and chimeric anti-gamma-interferon Fab}
EVQLQQPGADLVMPGAPVKLSCLASGYIFTSSWINWVKQRPGRGLEWIGRIDPSDGEVHYNQDFKD
KATLTVDKSSSTAYIQLNSLTSEDSAVYYCARGFLPWFADWGQGT LVTVSA
>d1b4jl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains)
{Humanized and chimeric anti-gamma-interferon Fab}
NIVMTQSPKSMYVSIGERVTL SCKASENVD TYVSWYQQKPEQSPKLLIYGASNRYTGVPDRFTGSGSA
TDFTLTISSVQAEDLADYHCGQSYNYPFTFGSGTKLEIK
>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}
DIKMTQSPSFLSASVGDRTLNCKASQ NIDKYL N WYQQKLGESPKLLIYNTN NLQTGIPSRFSGSGSG
TDFTLTISSLQPEDVATYFCLQHISRPRTFGTG TKLELK
>d1bfo1 b.1.1.1 (B:1-121) Immunoglobulin (variable domains of L and H chains)
{CAMPATH-1G igg2b monoclonal fab (rat), kappa L chain}
EVKLLES GGGLVQPGGSMRLSCAGSGFTFTDFYMNWIRQPAGKAPEWLG FIRDKAKGYTTEYNPSV
KGRFTISRDN TQNMLYLQMN TLRAEDTATYYCAREGHTAAPFDYWGQGMVTVSS
>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}
QVQLQESGPG LVRPSQTLSLTCTVSGFTFTDFYMNWVRQPPGRGLEWIGFIRDKAKGYTTEYNPSVK
GRVTMLVDTSKNQFSLRLSSVTAADTAVYYCAREGHTAAPFDYWGQGS LVTVSS
>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}
DIQMTQSPSSLSASVGDRTITCKASQ NIDKYL N WYQQKPGKAPKLLIYNTN NLQTGVPSRFSGSGSG
TDFTF TISSLQPEDIATYYCLQHISRPRTFGQGTKVEIK
>d1bj1h1 b.1.1.1 (H:1-123) Immunoglobulin (variable domains of L and H chains) {VEGF
neutralizing Fab-12 (mouse), kappa L chain}
EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWVRQAPGKGLEWV GWINTYTG EPTYAADFKR
RFTFSLDTSKSTAYLQMN SLRAEDTAVYYCAKYPHY YGSSHWYFDVWGQGT LVTVSS
>d1bj1j1 b.1.1.1 (J:1-107) Immunoglobulin (variable domains of L and H chains) {VEGF

neutralizing Fab-12 (mouse), kappa L chain}
DIQMTQSPSSLSASVGDRTITCSASQDISNYLNWYQQKPGKAPKVLIIYFTSSLHSGVPSRFSGSGSGT
DFTLTISLQPEDFATYYCQQYSTVPTWTFGGGTKLEIK
>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}
DVLMTQTPVLSVSLGDQASISCRSSQSIVHSTGNTYLEWYLQKPGQSPKLLIYKISNRFSGVPDRFSG
SGSGTDFTLKISRVEAEDLGVIYCFQASHAPRTFSGGKLEIK
>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}
EVILVESGGGLVPGGSLKLSAASGFTFSSYTMWVVRQTPEKRLEWVATISSGGGNTYYPDSVKGRF
TISRDNKNNLYLQMSLRSEDALYCYARYRYEAWFASWGQGLVTVSA
>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}
DIKMTQSPSSMYTSLGERVTITCKASQDINSFLTWFLQKPGKSPKTLIYRANRLMIGVPSRFSGSGSG
QTYSLTISSEYEDMGIYYCLQYDDFPLTFGAGTKLDLK
>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}
QDQLQQSGAELVRPGASVKLSCKALGYIFTDYIEHWVKQTPVHGLEWIGGIHPGSSGTAYNQKFKGK
ATLTADKSSTTAFMELSSLTSEDSAVYYCTRKYDYGQGLVTVSA
>d1f58h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains)
{Anti-gp120 (HIV-1) Fab 58.2, (mouse), kappa L chain}
DVQLQQSGPDLVKPSQSLTCTVTGYSITSGYSWHWIRQFPGNKLEWGMGYIHYSAGTNYNPSLKS
ISITRDTSKNQFFLQLNSVTTEDTATYYCAREEAMPYGNQAYYYAMDCWGQGTTVTVSS
>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}
DIVLTQSPASLAVSLGQRATISCKASQGVDFDGFASFMNWYQQKPGQPPKLLIFAASTLESGIPARFSGR
GSGTDFTLNIHPVEEEDAATYYCQQSHEDPLTFGAGTKLEIK
>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}
EVQLQQSGAELVQPGASVKLSCTASGFNIKDTYIMHWVKQRPEKGLEWIGRIDPASGNTKYDPKFQD
KATITADTSSNTAYLQLSSLTSEDVAVYYCAGYDYGDFDYWGQGT
>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}
DIQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQKSPQLLVYNAKTLADGVPSRFSGSGSG
TQYSLKINSLQPEDFGSYCQHFVSTPWTWTFGGGTKLEIK
>d1sbsh1 b.1.1.1 (H:1-123) Immunoglobulin (variable domains of L and H chains) {Anti-HCG
Fab 3A2, (mouse), kappa L chain}
EVNLEESGGGLVQPGGSMKLSCLVASGFTFSNYWMNWVRSPEKGLEWVADIRLKSNNYATLYAESV
KGRFTISRDDSKSSVYLQMNNLRAEDTGIYYCTRGAAYRYDYAMDYWGQGTSTVTVSS
>d1sbsl1 b.1.1.1 (L:1-113) Immunoglobulin (variable domains of L and H chains) {Anti-HCG
Fab 3A2, (mouse), kappa L chain}
DIVMSQSPSSLAVSVGEKVTMTCKSSQSLYSSNQMNLYLAWYQQKPGQSPKLLIYWASTRESGVPDR
FTGSGSGTDFLTISSEVAEDLAVYYCQYHSPFTFGSGTKLEIK
>d1sm3h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains)

{Tumor-specific Fab SM3, (mouse), lambda L chain}
QVQLQESGGGLVQPGGSMKLSCLVASGFTFSNYWMNWVRRQSPEKGLEWVAEIRLKSNNYATHYAESV
KGRFTISRDDSKSSVYLQMNRLRAEDTGIYYCTGVGQFAYWGQGT'TVTVSS
>d2pcpa1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 6B5,
(mouse), kappa L chain}
DVLMTQTPLSLPVS LGDQASISCRSSQTIVHSNGNTYLEWYLQKPGQSPKLLIYKVTNRFSGVPDRFS
GSGSGTDFTLKISRVEAEDLG VYYCFQGT HAPYTFGGG TKLEIK
>d2pcpb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Fab 6B5,
(mouse), kappa L chain}
EVQLQQSGPELVKPGASVKMSCKASGYTFTDYIHWNKQSHGKSLEWIGYIYPNNGGNGYNHKFKG
KATLTVDKSSSTAYMDVRTLTSEDSAVYYCGRSTWDDFDYWGQGT'TLTVSS
>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}
ELVMTQTPKFMSTTVGDRVSITCKASQNVGTPVAWYQQKPGQSPKLLIYSASNRYTGVPDRFTGSGS
GTDFTLTISNMQSEDLADYFCQYSSYPLTFGGG TKVEIK
>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}
QVQLLES GAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGMIDPNSSG GTKYNEKFKS
KATLTVDKPSNTAYMQLSSLTSEDSAVYYCTRRDMDYWGAGT'TVTVSS
>d1cf8h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Catalytic
Fab 19A4 (mouse), kappa L chain}
DVQLQESGPGLVKPSQSLTCTVTGYSITSGYAWN WIRQFPGNKLEW MGYIRYSGDTRYNPSLKSRI
SITRDTSKNQFFLQLNSVTTEDTATYYCAIGYGNSDYWGQGT'LVTVSA
>d1cf8l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic
Fab 19A4 (mouse), kappa L chain}
DIVLTQSPTIMSVSPGEKVTLTCSASSVSSNYVYWYQQKPGSSPKVWIYSTSNLASGVPARFSGSGSG
TSYSLTISMEAEADAASYFCLQWSSFPYTFGGG TKLELK
>d1c12a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab
directed against the musk odorant traseolide, (mouse), kappa L chain}
DIELTQSPSSMSVSLGDTVSITCHASQGISSNIGWLQQKPGKSFKGLIYHGTNLEDGVP SRFSGSGSGA
DYSLTISSESEDFADYYCVQYVQFPFTFGSGTKLEIK
>d1c12b1 b.1.1.1 (B:301-413) Immunoglobulin (variable domains of L and H chains) {Fab
directed against the musk odorant traseolide, (mouse), kappa L chain}
QVQLQESGPGLVKPSQSLTCTVTGYSITSDYAWN WIRQFPGNKLEW MGYISYSGSTSYSPSLKSRIS
LTRDTSKNQFFLQLNSVTTEDTATYYCVTSLTWLLRRKRSYWGQGT'TVTVSS
>d1dlfh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Anti-dansyl Fv,
(mouse), kappa L chain}
EVKLEESGGGLVQPGGSMKLSCLASGFTFSDAWMDWVRRQSPEKGLEWVAEIRNKANNHATYYAES
VKGRFTISRDDSKRRVYLQMNRLRAEDTGIYYCTGIYYHYPPWFAYWGQGT'LVTVS
>d1dlf_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Anti-dansyl Fv,
(mouse), kappa L chain}
DVVMTQTPLSLPVS LGNQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVS NRFSGVPDRFS
GSGSGTDFTLKISRVEAEDLG VYFCSQSTHVPFTFGSGTKLEIKR
>d43c9a_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Sterolytic and

amidolytic Fv 43c9, (mouse), kappa L chain}
DVVMTQTPSSLAMSVGQKVTMSCKSSQSLNINQKNYLAWYQQKPGQSPKLLVFASTRESGVPD
RFIGSGSGTDFTLTISSVQAEDQADYFCQQHYRAPRTFGGGTKLEIK
>d43c9b_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {Sterolytic and
amidolytic Fv 43c9, (mouse), kappa L chain}
GQVQLVESGPGLVAPSQSLTCTVSGISLSRYNVHWVRQSPGKGLEWLGMIWGGGSIEYNPALKSRL
SISKDNSKSKIFLKMNSLQTDSDAMYYCVSYGYGGDRFSYWGQGLTVTS
>d1bz7a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab R24,
(mouse), kappa L chain}
DIQMTQITSSLSVSLGDRVIISCRASQDIGNFLNWXQQKPDGSLKLLIYYTSRLQSGVPSRFSGWGSGT
DYSLTISNLEEEEDIATFFCQQGKTLPTYTFGGGTKLEIK
>d1bz7b1 b.1.1.1 (B:1-122) Immunoglobulin (variable domains of L and H chains) {Fab R24,
(mouse), kappa L chain}
DVQLVESGGGLVQPGGSRKLSAASGFTFSNFGMHVWRQAPEKGLEWVAYISSGGSSINYADTVKGR
FTISRDNPKNTLFLQMTSLRSEDTAIYYCTRGGTGTRSLYYFDYWGQGLTVSS
>d1ct8a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic
Fab 7C8, (mouse), kappa L chain}
ELVMTQTPATLSVTPGDSVLSLSCRASQSVSNKLHWYQQKSHESPRLLIKFASQSIPGIPSRFSGSGSGS
DFTLSINSVETEDFGIYFCHQTHGRPLTFGAGTKLELK
>d1ct8b1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Catalytic
Fab 7C8, (mouse), kappa L chain}
QVKLLESGAVLVKPGASVKLSCKTSGFTFSSSYINWLKQKPGQSLEWIAWIYAGSGGTVYNQHFTDK
ARLTVDTSSSTAYMQFSSLTTEDSAIYYCARYRYDEGFAYWGQGLTVTVSA
>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}
DIQMTQSPPSLSASLGDKVTITCQASQDINKYIAWYQQKPGKAPRQLIRYTSILVLGTPSRFSGSGSGR
DFSFSISNVASEDIASYYCLQYGNLYTFGAGTKLEIK
>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}
EVKLESGPGLVQPSQTLTCTVSGFPLTTNGVSWVRQPPGKLEWIAAIISSGGSPYYNSALKSRLSI
NRDTSKSKVFLKMNSLQTEDTAIYFCTREDGWNYFDYWGPGTMVTVSS
>d1f3rb2 b.1.1.1 (B:139-257) Immunoglobulin (variable domains of L and H chains) {scFv
MAB198, (rat), kappa L chain}
DIKLTQSPSLLSASVGDRTLSCKGQSNINNYLAWYQQKLGAPKLLIYNTNSLQTGIPSRFSGSGSGT
DYTLTISSLQPEDVATYFCYQYNNGYTFGAGTKLELKAAEQKLISEEDLN
>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}
DIVLTQSPATLSVTPGDSVLSLSCRASQSSINNLHWYQQKSHESPRLLIKYASQSIGIPSRFSGSGSGTDF
TLSINSVETEDFGMYFCQQSNWPYTFGGGTKLEIK
>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}
EVQLQESGPPSLVKPSQTLTCTSVTGDSVTSYWSWIRKFPNGKLEYMGYISYSGSTYYHPSLKRISI

TRDTSKNQYYLQLNSVTTEDTATYYCASWGGDVWGAGTTVTVSS
>d1ejoh1 b.1.1.1 (H:2501-2619) Immunoglobulin (variable domains of L and H chains)
{Anti-FMDV Fab 4C4, (mouse), kappa L chain}
QMLVESGGDLVKPGGSLKLSAASGFTFSSYTMWVRQTPEKRLEWVATISSGGAYTYYPDSVKGRF
TISDDNAESTLYLQMSSLRSED TAMYYCVRRAFSDVGFASWGHRTLTVSA
>d1ejol1 b.1.1.1 (L:2001-2111) Immunoglobulin (variable domains of L and H chains)
{Anti-FMDV Fab 4C4, (mouse), kappa L chain}
DIVLTQSPASLAVSLGQRATISCRASESVDSYGN SFMHWYQQKPGQPPKLLIYRASNLESGIPARFSGS
GSRTDFTLTINPVEADDVATYYCQSQSNEDPLTFGAGTKLELK
>d1cr9h1 b.1.1.1 (H:1-110) Immunoglobulin (variable domains of L and H chains)
{Anti-prion Fab 3F4, (mouse), kappa L chain}
KVKLQQSGAELVRSGASVKLSCTASGFNIKDYIQWVKQRPEQGLEWIGWIDPENGSEYAPRFQ GK
ATMTADTLN TAYLQLSSLTSED TAVYYCNADLHDYWGQGTTLTVSS
>d1cr9l1 b.1.1.1 (L:1-106A) Immunoglobulin (variable domains of L and H chains)
{Anti-prion Fab 3F4, (mouse), kappa L chain}
DVVMTQTPLSLSVTIGQPASISCKSSQLLSDGKTYLIWVVFQRPQGSPKRLIFLVSKRDSGVPDRFTG
SGSGTDFTLKISRVEADVGVYYCWQGFHPHTVGGGTKLEIA
>d1qfwh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains)
{Anti-[gonadotropin alpha subunit] Fv, kappa L chain}
QLQQSGAELVKPGASVKLSCKASDYTF TSYWMHWVKQRPGQGLEWIGEINPTNGRTYYNEKFKSK
ATLVAASASTAAMQASLTSEDSAVYYCARRYGN SFDYWGQGTTLTVSS
>d1qfwl_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains)
{Anti-[gonadotropin alpha subunit] Fv, kappa L chain}
DIELTQSPDSLAVSLGQRATISCRASESVDSYGN SFM QWYQQKPGQPPKLLIYRASNLESGIPARFSGT
GSRTDFTLTINPVEADDVATYYCQQSDEYPYMYTFGGGTKLEIKR
>d1qfwi_ b.1.1.1 (I:) Immunoglobulin (variable domains of L and H chains)
{Anti-[gonadotropin beta subunit] Fv, kappa L chain}
QVQLQESGGH LVKPGGSLKLSAASGF AFSDFMSWIRQTPEKRLEWVASITNVGTYTYYPGSVKGR
FSISRDNARNTLN LQMSSLRSED T ALYFCARQG TAAQPYWYFDVWGAGTTVTVS
>d1qfwm_ b.1.1.1 (M:) Immunoglobulin (variable domains of L and H chains)
{Anti-[gonadotropin beta subunit] Fv, kappa L chain}
DIELTQSPKSM SMSVGERVTL SCKASET VDSFVSWYQQKPEQSPKLLIFGASNRFSGVPDRFTGSGSA
TDFTLTISSVQAEDFADYHCGQTYNHPYTFGGGTKLEIKR
>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}
DIVLTQSPASLAVSLGQRATISCRASKSVSTSGYGYMHW NQQKPGQPPRLIYLVSNLESGV PARFSGS
GSGTDFTLNIHPVEEEDAATYYCQHIREPLTFGGGTKLEIK
>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}
DVQLQESGPGLVKPSQSLSLTCTVTGYSISSDYAWN WIRQFPGNKLEW MGYISYSGSTSYNPSLKSRIS
ITRDTSKNQFFLQLSSVTTEDTATYYCARGYYGSSHSPVWGAGTTVTVSS
>d1dqdh1 b.1.1.1 (H:1-122) Immunoglobulin (variable domains of L and H chains) {Fab
HGR-2 F6, (mouse), kappa L chain}
EVQLQESGPSLVKPSQTLTLTCSVTGDSITSGYWNWIRKFPGNKLEYMGYISYSGSTYYNPSLKSRLSI

TRDTSRNQYYLQLKSVTPEDTATYYCASPPGYGSGPYAMDYWGQTSVTVSS
>d1dqd1 b.1.1.1 (L:1-106) Immunoglobulin (variable domains of L and H chains) {Fab HGR-2 F6, (mouse), kappa L chain}
DIVLSQSPAIMSASPGEKVTITCSASSSVSYMHWFQKPGTSPKLCIYTTSNLASGVPARFSGSGSGTS
YSLTISRMEAEDAATYYCQQRSTYPPTFGSGTKLEIK
>d1deea1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab of human IgM RF 2A2}
DIQMTQSPSSLSASVGDRTITCRTSQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGT
DFTLTISLQPEDFATYYCQSYSAPRTFGQGTKVEIK
>d1deeb1 b.1.1.1 (B:501-621) Immunoglobulin (variable domains of L and H chains) {Fab of human IgM RF 2A2}
QVQLVESGGGVVQPGKSLRLSCAASGFTFSGYGMHWVRQAPGKGLEWVALISYDESNKYADSVKGR
FTISRDNKNTLYLQMNSLRAEDTAVYYCAKVKFYDPTAPNDYWGQGLVTVSS
>d1qnzh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Anti-HIV Fv 0.5B, (mouse), kappa L chain}
QVQLQQSGAELVKPGASVKMSCKASGYTFTTYPIEWMKQNHGKSLEWIGNFHPYSDDTNYNEKFK
GKAKLTVEKSSSTVYLEFSRLTSDDSAVYYCAIHYGSAYAMDYWGQTSVTVSS
>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}
EVQLEESGGGLVTPGGSLRLSCAASGYVFSTYDMSWVRQTPEKRLEWVAFISSGGGRTSYPDTVKGR
FTISRDDAKNTLYLQMSLQSEDAMYYCTRHFYAVLDYWGRGTTLVSS
>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}
QAVVTQESALTTSPGETVTLTCSRSTGTVTTSNYANWVQEKPDHLFTGLIGATNNRAAGVPRFSGS
LIGKAALTITGAQTEDEAIYFCALWYSGHWVFGGGTKLTVLG
>d1f11b1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains)
{Anti-Pres2 Fab F124, (mouse), kappa L chain}
EVQLQQSGPELVKPGASVKMSCKASGYTFTDYMKWVKQSHGKSLEWIGDINPNNGGTGYNQKFK
GKATLTVDKSSSTAYMQLNSLTSEDSAVYYCANDYGSTYGFAYWGQGLVTVSA
>d1f3dh1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and H chains) {Catalytic
Fab 4B2, (mouse), kappa L chain}
EIQLQQSGPELVKPGASVKVSKASGYSFIDYNIHWVKQSHGKSLEWIGYIVPYSGGTTFNQKFKGKA
TLTVDKSSSTAFMHLNSLTFEDSAVYYCANDYDGVYWGQGTTLTVSS
>d1f3dj1 b.1.1.1 (J:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic
Fab 4B2, (mouse), kappa L chain}
DVLMTQTPLSLPVS LGDQVSISCRSSQSIFHSDGKTYLEWHLQKPGQSPKLLIYKVKRFSGVPDRFS
GSGSGTDFTLKISRVEAEDLGVYYCFQGSHPYTFGGGTKLEIK
>d1fh5h1 b.1.1.1 (H:4-120) Immunoglobulin (variable domains of L and H chains) {Fab
MAK33, (human), kappa L chain}
SGGGLVKPAGSLKLSAASGFTFSSYYMYWVRQTPDKRLEWVATISDGGSYTYYPDSVKGRFTISR
NAKNNLYLQMSLKSEDTAMYYCARDAMDYWGQGLVTVSA
>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}
NIVLTQSPKMSVSVGERVTLSCASENVDYVFWFQKPKDQSPKLLLYGPSNRYTGVPDRFTGSGST

TDFTLTISSVQAEDLADYHCGQSYSPYTFGGGKLEIK

>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}

QVQLQQPGTELVRPGASVILSCKASGYTFTSYWINWVKQRPGQGLEWVGNIFPSDSYTNYNQKFKD
KATLTVDKSSSTAYMQVNSPTSEDSAVYYCTRGARDTWFAFWGQGLTVTVSV

>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)}

QVQLLEPGTELVKPGASVKLSCRASGYSTSYWMHWVKQRPGQGLEWIGLIDPSNGRTNFNDKFKS
RATLTVDTSSTAYMQLSSLTSEDSAVYYCVRIAYWGQGLTVTVSS

>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)}

EIQLTQSPSSLSASLGERVSLTCRTSQEISGYLSWLQKQPDGTIKRLIYDATKLDGAPKRFSGSRSGSD
YSLTISSLESEDFADYYCLQYASFPRTFGGGKLEIK

>d1etza1 b.1.1.1 (A:1-110) Immunoglobulin (variable domains of L and H chains) {Anti-sweetener Fab NC10.14, (mouse), lambda L chain}

FAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYAIWVQEKPDHLFSGLIGGTNNRVPGVPARFSGSLI
GDKAALVTGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG

>d1etzb1 b.1.1.1 (B:1-126) Immunoglobulin (variable domains of L and H chains) {Anti-sweetener Fab NC10.14, (mouse), lambda L chain}

QVTLKESGPGILQPSQTLTCSFSGFSLSTSGMGVGVWIRQPSGEGLEWLADIWWNDKKYYNPSLKS
RLTVSKDTSSNQVFLKITSVDTSATYHCARRTFSYYYGSSFYFDNWGQGTTLTVSS

>d1emth1 b.1.1.1 (H:1-116) Immunoglobulin (variable domains of L and H chains) {Anti-C60 fullerene Fab, (mouse), kappa L chain}

QVHLQESGPELVRPGASVKISCKTSGYVFSSWMNWVKQRPGQGLKWIGRIYPGNGNTNYNEKFKG
KATLTADKSSNTAYMQLSSLTSVDSAVYFCATSSAYWGQGLLTVSA

>d1emtl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Anti-C60 fullerene Fab, (mouse), kappa L chain}

DIQMTQTSSLSASLGDRTVTFSCSASQDISNYLNWYQKQPDGTIKLLIYYTSSLRSGVPSRFSGSGSGT
DYSLTINNLEPEDIATYFCQQYSRLPFTFGSGTKLEIK

>d1fl3a1 b.1.1.1 (A:2-116) Immunoglobulin (variable domains of L and H chains) {Blue fluorescent Fab 19G2, (mouse), kappa L chain}

AALLESGGGLVKPGGSLKLSCTASGITFSRYIMSWVRQIPEKRLEWVASISSGGITYYPDSVAGRFTISR
DNVRNILYLQMSSLRSEDTALYYCARGQGRPYWGQGTSVTVSA

>d1fl3b1 b.1.1.1 (B:2-113) Immunoglobulin (variable domains of L and H chains) {Blue fluorescent Fab 19G2, (mouse), kappa L chain}

AALTQSPVSNPVTLGTSASISCRSTKSLHNSGITYLYWYLQKPGQSPQLLIYQMSNLAGVPNRFSSS
GSGTDFTLRINTVEAEDVGVYYCAQNLELPPTFGAGTKLELKR

>d1dzba1 b.1.1.1 (A:1-117) Immunoglobulin (variable domains of L and H chains) {Anti-lysozyme scFv 1F9, (mouse), kappa L chain}

QVKLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKYDPKFQG
KATITADTSSNTAYLQLSSLTSEDVAVYYCARWDWYFDVWGQGTTVTVSSG

>d1dzba2 b.1.1.1 (A:201-307) Immunoglobulin (variable domains of L and H chains) {Anti-lysozyme scFv 1F9, (mouse), kappa L chain}

DIELTQSPSSMYTSLGERVTITCKASQDINSYLRWFQKQKPGKSPKTLIYYATSLADGVPSRFSGSGSQ

DYSLTISSLESDDTTTYCLQHGESPYTFGGGTKLEIK
>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}
QVKLQQSGAELVRSVSVKLSCTASGFNIKDSYMHVLRQGPQGLEWIGWIDPENGDTTEYAPKFQG
KATFTTDTSSNTAYLQLSSLTSEDVAVYYCNEGTPTPGYFFDYWGQGTTVTVSSG
>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}
ENVLTQSPAIMASAPGKVTITCSASSSVSYMHWFQKPKGTSPKLWIYSTSNLASGVPARFSGSGSGTS
YSLTISRMEAEDAATYYCQQRSSYPLTFGAGTKLELK
>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}
EVQLQQSGAELARPGASVKMSCKASGYTFTSYTMHWVKQRPGQGLEWIGYINPSSGYSNYNQKFKD
KATLTADKSSSTAYMQLSSLTSEDSAVYYCSRPPVRLGYNFDYWGQGSTLTVSS
>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}
EIVLTQSPAITAASLGQKVTITCSASSSVSYMHWYQQKSGTSPKPKWIYEISKLASGVPARFSGSGSGTSY
SLTISSMEAEDAATYYCQQWNYPFTFGSGTKLEIK
>d1dl7h_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv M3C65,
(human), lambda L chain}
QVQLKESGPGLVAPSQSLTCTVSGFSLTGYGVNWRVQPPGKGLEWLGMIWGDGSTDYNSALKSRL
NISKDKSKSQVFLRMYSLQTDDETARYYCARDYGPYWGQGTTLTVSS
>d1dl7l_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv M3C65,
(human), lambda L chain}
QAVVTQESALTTSPGETVTLTCSRSTGAVTTSNYANWVQEKPDHLFTGLIGGTRKHTPGAPARFSGSL
IGDKAALTITGAQTEDEAIYFCALWYSNHVWFVGGGTKLTVL
>d1egjh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab
against cytokine receptor common beta chain domain 4, (mouse), kappa L chain}
EVQLQQSGPELVKPGTSVKMSCKASGYTFTDYMKVWKHSHGKSLEWIGDINPSNGGTLYNQKFKG
KATLTVDKSSSTASMQLSRLTSEDSAVYYCSRGDGIHGGFAYWGQGTTVTVSS
>d1egjl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab
against cytokine receptor common beta chain domain 4, (mouse), kappa L chain}
NIVLTQSPASLAVSLGQRATISCRANESVSYGDSFMHWYQQKPGQPPKLLIYLASNLASGVPARFSGS
GSRTDFTLTIDPVETDDAATYYCQQNNEPWTFGGGTKLEIK
>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
GKAKLTAVTSASTAYMEVSSLTNEEDSAVYYCTRRSYKYYALDYWGQGTSTVTVSS
>d1fe8h1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab RU5,
(mouse), kappa L chain}
DVKLVQSGPGLVAPSQSLTCTVSGFSLTTYGVSWVRQPPGKGLEWLGVIWGDGNTTYHSALISRLSI
SKDNSRSQVFLKLNLSLHTDDTATYYCAGNYYGMDYWGQGTSTVTVSS
>d1fe8l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab RU5,
(mouse), kappa L chain}
DIAMTQTSSLSASLGQKVTISCRASQDIGNYLNWYQQKPDGTVRLLIYYTSRLHSGVPSRFSGSGS

TDYSLTISNLESEDIATYFCQNGGTPWTFGGGTKLEVK

>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}

EVKLQESGAGLVQPSQSLTCSVTGYSITSGYYWNWIRLFPGNKLEWVGYISNVGDNNYNPSLKDR
LSITRDTSKNQFFLKLNSVTTEDTATYYCARSEYYSVTGYAMDYWGQTTVTVSSAWRHP

>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}

DIELTQTPVSLAASLGDRVTISCRASQDINNFLNWFYQKPDGTIKLLIYYTSSLHAGVPSRFSGSGSGT
DYSLTISNLEPEDIATYFCQHHLKFPWTFGAGTKLEIK

>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}

QLQQSGAELVRSGASVKLSCATSDFNIDYIHWVRQRPEQGLEWIGWLDPENGDTEAPKFQGKA
TMTADTSSNTAYLQLSSLTSEASAVYYCNAISTTRDYALDYWGQTSVTVSS

>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}

DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSRNQMNYLSWYQQKPGQSPKLLIYWASTRESGVPDR
FTGSGSGTDFTLTISVKAEDLAVYYCQYYHYRTFGGGTRLEIR

>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}

GVQLQESGPGLVKPSQSLTCTVTGYSITSDYAWNWIRQFPGNKLEWIMGYITYSGSTGYNPSLKSR
SITRDTSKNQFFLQLNSVTTEDTATYYCASYYDDYTWFTYWGQGLTVTSA

>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}

DVQMTQTPLTSLVTIGQPASISCESSQSLLYSNGKTYLNWLLQRPQSPKRLIYLVSKLDSGVPDRFTG
SGSGTDFTLRISRVEAEDLGVYYCVQGTHTFPRTFGGGTKLEIK

>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
TKATLTVDKSSNTAYMQLSSLTSEDSAVYYCARSPDYWGQGTTLTVSS

>d1e4wl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Anti-TGFalpha Fab TAB2, (mouse), kappa L chain}

DIQMTQTPSSLSASLGDRVTISCRASQDISHYLNWFYQKPDGTVKLLIYYTSTLHSGVPSRFSGSGSGT
DYSLTISNLEEDIAFYFCQGGALPFTFGSGTKLAIK

>d1h8na1 b.1.1.1 (A:3-109) Immunoglobulin (variable domains of L and H chains) {Anti-ampicillin scFv, (mouse), kappa L chain}

KDIVLTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQKPGQSPKLLIYWASTRHTGVPDRFTGSG
SGTDFTLTISNVQSEDLADYFCQYSSYPLTFGAGTKLEL

>d1h8na2 b.1.1.1 (A:132-243) Immunoglobulin (variable domains of L and H chains) {Anti-ampicillin scFv, (mouse), kappa L chain}

QVQLQESGGELVRPGASVKLSCKASGYTFTSYWINWVKQRPGQGLEWIGNIYPSDSTNYNQKFKD
KATLTVDKSSSTAYMQLSSLTSEDSAVYFCARWGYWGQGLTVTSA

>d1i7za1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab GNC92H2, (mouse/human chimera), kappa L chain}

DLVLTQSPASLAVSLGQRATISCRASKSVSTSGYNYMHWYQKPGQPPKLLIYLASNLASGVPARFSGS

GSGETDFTLNIHPVEEEDAATYYCLYSREFPPWTFGGGTKLEIK

>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
GRFAFSLATSASTAYLQIINLNKNETATYFCETYDSPLGDYWGQGTTVTVSS

>d1iqda1 b.1.1.1 (A:2-108) Immunoglobulin (variable domains of L and H chains) {Fab B02C11 against the C2 domain of factor VIII, (human), kappa L chain}

IALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQKQKPGQAPRLLIYGASTRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQKYGTSAITFGQGTTRLEIK

>d1iqdb1 b.1.1.1 (B:1-114) Immunoglobulin (variable domains of L and H chains) {Fab B02C11 against the C2 domain of factor VIII, (human), kappa L chain}

QVQLVQSGAEVKKPGASVKVSKVSGYTLTELPVHWVRQAPGKGLEWVGSFDPESGESIYAREFQGS
VTMTADTSTNIAYMELSSLRSDDTAVYYCAVPDPAFDIWDGQGMVTVSS

>d1fn4a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 198 against acetylcholine receptor, (rat)}

DIKLTQSPSLLSASVGDVTLSCCKGSQINNYLAWYQKLGAEAPKLLIYNTNSLQTGIPSRFSGSGSGT
DYTLTISSLQPEDVATYFCYQYNNGYTFGAGTKLELKR

>d1fn4b1 b.1.1.1 (B:1-106) Immunoglobulin (variable domains of L and H chains) {Fab 198 against acetylcholine receptor, (rat)}

QVQLLESGLVLRPSETLSLTCTVSGFSLTSFVSVWVRHPSGKGPPEWMGRMWDYDGYTAYNSALKSRL
SISRDTSKNQVFLKMNSLQTDGTYCYTRDLYGGYPLGFYDFDFWGP

>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}

QIQLVQSGPELKKPGETVTRISCKASDYSFMTSGMQWVQMPGKGLKWIGWLNTQSGVPEYAEDFKG
RFAFSLETSATTAYLQIINLNKNETATYFCATWGGNSAYWGQGTTLTVSS

>d1jp5a1 b.1.1.1 (A:1-112) Immunoglobulin (variable domains of L and H chains) {scFv 1695, (mouse), kappa L chain}

DILMTQTPLYLPVSLGDQASISCRSSQTIVHNNGNTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFS
GSGSGTDFTLKISRVEAEDLGIYYCFQGSHPPTFGGKLEIK

>d1jp5a2 b.1.1.1 (A:128-247) Immunoglobulin (variable domains of L and H chains) {scFv 1695, (mouse), kappa L chain}

EVQLQQSGPELKKPGETVKISCKATNYAFTDYSMHVVKQAPGGDLKYVGVWINTETDEPTFADDFKG
RFAFSLDTSTSTAFQLINLNKNETATYFCVDRDRHDYGEIFTYWGQGTTVTVSS

>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}

QVQLVESGGGLVQPGGSLRLSCATSGFTFTDYMSWVRQPPGKALEWLGFIKANKANGYTTTEYSASVK
GRFTISRDNQSILYLQMNLTLEAEDSATYYCARDGSYAMDYWGQGTSTVTVSS

>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}

QVQLQQPGAELVKPGASVKLSCKASGYTFTSDWIHWVKQRPGHGLEWIGEIIPSYGRANYNEKIQKK
ATLTADKSSSTAFMQLSSLTSEDSAVYYCARERGDYFAVWGAGTTVTVSS

>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}

DILLTQSPAILSVPGERVDFSCRASQSIGTDIHWYQRTNGSPRLLIKYASESISGIPSRFSGSGSGTDF

TLINSVSEDIANYCQQSNRWPFTFGSGTKLEIK

>d1jguh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 1D4, (mouse), kappa L chain}

EVKLVESRGGLVKPGGSLQLSCAASGFTFSGYAMSWFRLTPEKRLEWVASIYNGFRIHYLDSVKGRFT
ISSDYARNILYLQMSTLRSEDTAMYYCSRGDAYSRYFDVWGAGTTVTVSA

>d1jgul1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 1D4, (mouse), kappa L chain}

EVVMTQSPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPDRFS
GSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK

>d1i8ma1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Anti ssDNA Fab, (mouse), kappa L chain}

ELQMTQSPASLSASVGETVTITCRASENIYSYLAWYQQKQKSPQLLVYNAKTLAEGVPSRFSGSGSG
TQFSLKINSLQPEDFGSYQCQHHYGTPLTFGAGTKLELK

>d1i8mb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Anti ssDNA Fab, (mouse), kappa L chain}

QVKLLESPELVKPGASVKMSCKASGYTFTSYVMHWVKQKPGQGLEWIGYINPYNDGTYNEKFKG
KATLTSDKSSSTAYMELSSLTSEDSAVYYCVRGGYRPPYAMDYWGQGTSVTVSS

>d1jv5b_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {Anti-blood group A Fv, (human), kappa L chain}

QVQLQQPGAELVKPGTSVKLSCKASGYNFTSYWINWVKLRPGQGLEWIGDIYPGSGITNYNEKFKSK
ATLTVDTSSSTAYMQLSSLASEDSALYYCAGQYGNLWFAYWGQGLVTVS

>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}

QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMQWVKQRPGQGLEWIGEIDPSDYSYTNYNQKFK
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}

DIVLTQSPASLAVSLGQRATISCKASQSDYDGDYSYMNWYQQKPGQPPKLLIYAASNLESIGIPARFSGS
GSGTDFTLNIHPVEEEDAATYYCQSNEDPRTFGGGTKLEIK

>d1jnha1 b.1.1.1 (A:1-108) Immunoglobulin (variable domains of L and H chains) {Anti-estradiol Fab 10G6D6, (mouse), lambda L chain}

QAVVTQESALTTSPGETVTLTCRSSGAIITSHYANWIQEKPDHLFTGLISGTNNRAPGVPARFSGSLI
GDKAALTITGAQTEDEAIYICALWFSNQFIFGSGTKVTV

>d1jnbb1 b.1.1.1 (B:1-117) Immunoglobulin (variable domains of L and H chains) {Anti-estradiol Fab 10G6D6, (mouse), lambda L chain}

EVQLQQSGAELARPGASVKLSVRTSGYSFTTYWMQWVRQRPGQGLEWIAAIYPGDDDARYTQKFK
GKATLTADRSSSIVYLQLNSLTSEDSAVYSCSRGRSLYTTMDYWGQGTSVTV

>d1jnlh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Anti-estradiol Fab 17E12E5, (mouse), kappa L chain}

EVQLQQSGAELVKPGASVRLSCSASGFNIKDTYMFVWVKRPEQGLDWIGRINPANGISKYDPRFQGK
ATLTADTSSNTAYLQLDNLTS EDTAVYYCAIEKDLPWGQGLVTVSV

>d1jnl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Anti-estradiol Fab 17E12E5, (mouse), kappa L chain}

QIVMTQTPASLSASVGETVTITCRASGNIYNYLAWYQQKQKSPQLLVYNAKTLVDGVPLRFSGSGSG

TQYSLKINSLQPEDFGNYCHHFWNTPYTFGGGKLEIK
>d1vhp_ b.1.1.1 (-) Immunoglobulin (variable domains of L and H chains) {VH-P8 domain (human), camelized monomer}
EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKEREIVSAVSGSGGSTYYADSVKGRF
TISRDNKNTLYLQMNSLRAEDTAVYYCARLKKYAFDYWGQGLVTVSS
>d1jtpa_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Camel (Camelus dromedarius), anti-lysozyme antibody}
DVQLQASGGGSVQAGGSLRLSCAASGYTIGPYCMGWFRQAPGKEREGVAAINMGGGITYYADSVKGR
FTISQDNAKNTVYLLMNSLEPEDTAIYYCAADSTIYASYECGHGLSTGGYGYDSWGQGTQVTVSSRR
>d1bzqk_ b.1.1.1 (K:) Immunoglobulin (variable domains of L and H chains) {Camel (Camelus dromedarius), anti-RNase A antibody}
QVQLVESGGGLVQAGGSLRLSCAASGYAYTYIYMGWFRQAPGKEREGVAAMDSGGGGTLYADSVKGR
FTISRDKGKNTVYLMNSLKPEDTATYYCAAGGYELRDRTYQWGWQGTQVTVSSRGR
>d1f2xk_ b.1.1.1 (K:) Immunoglobulin (variable domains of L and H chains) {Camel (Camelus dromedarius), antibody cab-ca05}
QVQLVESGGGSVQAGGSLRLSCAASGYTVSTYCMGWFRQAPGKEREGVATILGGSTYYGDSVKGRFTI
SQDNAKNTVYLMNSLKPEDTAIYYCAGSTVASTGWCSRLRPYDYHYRGQGTQVTVSS
>d1hcv_ b.1.1.1 (-) Immunoglobulin (variable domains of L and H chains) {Llama (Lama glama), anti-gonadotropin alpha subunit VH domain}
VQLQESGGGLVQAGGSLRLSCAASGRTGTYDMGWFRQAPGKERESVAAINWDSARTYYASSVRGRF
TISRDNAAKTVYLMNSLKPEDTAVYTCGAGEGGTWDSWGQGTQVTVSS
>d1qd0a_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Llama (Lama glama), anti-RR6 VH domain}
QVQLQESGGGLVQAGGSLRLSCAASGRAASGHGHYGMGWFRQVPGKEREFVAAIRWSGKETWYKD
SVKGRFTISRDNAAKTTVYLMNSLKGEDTAVYYCAARPVRVADISLPVGFQDYWGQGTQVTVSS
>d1i3ua_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Llama (Lama glama), the dye RR1-binding Vhh domain}
VQLQESGGGLVQAGDSLKLSCEASGDSIGTYVIGWFRQAPGKERIYLATIGRNLVGPSPDFYTRYADSVK
GRFAVSRDNAKNTVNLQMNSLKPEDTAVYYCAAKTWTWGGNDPNNWNYWGQGTQVTV
>d1ivla_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {VL domain (kappa) of antibody M29B, dimer synthetic}
DIELTQSPATLSVTPGNSVSIKSCRASQSIGNRLFYQKSHESPRLLIKYASQSIGIPSRFSGSGSGTDF
TLSINSVETEDLAVYFCQVSEWPFQTFGGGKLEIK
>d1bwwa_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL (kappa) dimer REI (human)}
TPDIQMTQSPSSLSASVGDRTITCQASQDIKYLNWYQQKPGKAPKLLIYEASNLQAGVPSRFSGSGS
GTDYTFITISLQPEDATYYCQYQSLPYTFGGGKLEIK
>d2rhe_ b.1.1.1 (-) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL (lambda) dimer RHE (human)}
ESVLTQPPSASGTPGQRVTISCTGSATDIGSNSVIWYQQVPGKAPKLLIYNDLLPSGVSDRFSASKSG
TSASLAISGLESEDEADYYCAAWNDSLDEPGFGGKLTVLGQPK
>d1bjma1 b.1.1.1 (A:1-111) Immunoglobulin (variable domains of L and H chains) {Bence-Jones lambda L chain dimer LOC (human)}
ESVLTQPPSASGTPGQRVTISCSGSSNIGENSVTWYQHLSGTAPKLLIYEDNSRASGVSDRFSASKSG

TSASLAISGLQPEDETDYYCAAWDDSLDVAVFGTGTKVTVLG
>d1wtla_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL (kappa) dimer WAT (human)}
DIQMTQSPSSLSASVGDRTITCRASQDITNYVNWVFQQRPGQAPKVLIIYGASILETGVPSPRFSGSGSGT
DFTFTISLQPEDIATYYCQYDTLPLTFGGGTKVDIKR
>d1b0wa_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL (kappa) dimer BRE (human)}
DIQMTQSPSSLSASVGDRTITCQASQDISDYLIWYQQKLGKAPNLLIYDASTLETGVPSPRFSGSGSGT
EYFTFTISLQPEDIATYYCQYDDLPTFGGQTKVEIKR
>d1eeqa_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL (kappa) domain LEN (human)}
DIVLTQSPDSLAVSLGERATINCKSSQSVLDSSNSKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRF
SGSGSGTDFLTISLQAEDVAVYYCQYYSHYPYFSGGQTKLEIK
>d1lila1 b.1.1.1 (A:2-107) Immunoglobulin (variable domains of L and H chains) {Bence-Jones lambda L chain dimer CLE (human)}
YEVTQPPSLVSPGQTARITCSGEKLGDAYVCWYQQRPGQSPVVVIYQDNRRPSGIPERFSGSSSGNTA
TLTISGTQTLDEADYYCQVWDSNASVVFVGGGKTLTVLG
>d1cd0a_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL (lambda) dimer JTO (human)}
NFMLNQPHSVSESPGKTVTISCTRSSGNIDSNYVQWYQQRPGSAPITVIYEDNQRPSGVPDRFAGSID
RSSNSASLTISGLKTEDEADYYCQSYDARNVVFVGGGTRTLTVLG
>d2cd0a_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL (lambda) dimer WIL (human)}
NFLLTQPHSVSESPGKTVTISCTRSSGSIANNVHWYQQRPGSSPTTVIFEDDHRPSGVPDRFSGSVD
TSSNSASLTISGLKTEDEADYYCQSYDHNNQVVFVGGGKTLTVLG
>d1b6da1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Bence-Jones kappa L chain DEL (human)}
DIQMTQSPSSLSASVGDRTITCQASQDISSYLNWYQQKPGKAPKLLIHAASSLETGVPSPRFSGSGSGT
DFSFTISLQPEDLATYYCQYDSLPLTFGGGKTKVEIK
>d1ek3a_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Kappa-4 VL REC (human)}
DIVMTQSPDSLAVSPGERATINCKSSQNLLDSSFDTNTLAWYQQKPGQPPKLLIYWASSRESGVPDR
FSGSGSGTDFLTISLQAEDVAVYYCQYYSTPPTFGGQTKVEIKR
>d1mcoh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains) {Intact antibody (lambda) MCG (human)}
PLVLQESGPGLVKPEALSLTCTVSGDSINTILYYWSWIRQPPGKGLEWIGYIYSGSTYGNPSLKSRVT
ISVNTSKNQFYKLSVTAADTAVYYCARVPLVVPWPWGQGLTVTVSS
>d1dcla1 b.1.1.1 (A:1-111) Immunoglobulin (variable domains of L and H chains) {Lambda L chain dimer MCG (human)}
PSALTQPPSASGSLGQSVTISCTGTSSNVGGYNYVSWYQQHAGKAPKVIIEVVKRPSGVPDRFSGSK
SGNTASLTVSGLQAEDVAVYYCQSSYEGSDNFVFGTGTKVTVLG
>d1mcww1 b.1.1.1 (W:1-111) Immunoglobulin (variable domains of L and H chains) {Heterologous L chain dimer MCG-WEIR hybrid (human)}
ESALTQPASVSGSPGQSITVSCAGHTSDVADSNSISWFQQHPDKAPKLLIYAVTFRPSGIPLRFSGSKSG

NTASLTISGLLPDDEADYFCMSYLSASVFGSGTKVTVLR
>d1ac6a_b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}
DSVTQTEGQVALSEEDFLTIHCNYSASGYPALFWYVQYPGEGPQFLFRASRDKEKGSRRGFTEATYNKE
ATSFHLQKASVQESDSAVYYCALSGGNNKLTFGAGTKLTIKP
>d1b88a_b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}
MQQVRQSPQSLTVWEGETAILENCSYENSADFYFPWYQQFPGEGPALLISILSVSNKKEDGRFTIFFNKR
REKKLSLHIADSQPGDSATYFCAASASFGDNSKLIWGLGTSLVVNP
>d1d9ka_b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}
QVRQSPQSLTVWEGETTILNCSYEDSTFDYFPWYRQFPGKSPALLIAISLVSNNKKEDGRFTIFFNKR
KKLSLHITDSQPGDSATYFCAATGSFNKLTFGAGTRLAVSPY
>d1fo0a_b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}
KVTQTQTSISVMEKTTVTMDCVYETQDSSYFLFWYKQTASGEIVFLIRQDSYKKENATVGHYSLNFQ
KPKSSIGLIITATQIEDSAVYFCAMRGDYGGSGNKLIFGTGTLTSVKP
>d1h5ba_b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}
GDQVEQSPSALSHEGTDALRCNFTTTMRSVQWFRQNSRGLISLFLYASGTEKENGRLKSAFDSER
ARYSTLHIRDAQLEDSTYFCAAEASSGSWQLIFGSGTQLTVMPVT
>d1i9ea_b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}
QSVTQPDARVTVSEGASLQLRCKYSYSATPYLFWYVQYPRQLQLLLKYYSGBPVPVQGVNGFEAEFS
KSNSSFHLRKASVHWSDSAVYFCAVSGFASALTFGSGTKVIVLPYIQN
>d1kb5a_b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}
QQVRQSPQSLTVWEGETAILENCSYEDSTFNYPWYQQFPGEGPALLISIRSVSDKKEDGRFTIFFNKR
EKKLSLHITDSQPGDSATYFCAARYQGGRALIFGTGTTVSVSPGSAD
>d1nfda1_b.1.1.1 (A:1-117) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}
DSVTQTEGLVTVTEGLPVKLNCTYQTTYLTIAFFWYVQYLNEAPQVLLKSSTDNKRTEHQGFHATLH
KSSSSFHLQKSSAQLSDSALYYCALSEGNYKYVFGAGTRLKVIAH
>d1bd2d1_b.1.1.1 (D:1-117) T-cell antigen receptor {Human (Homo sapiens), alpha-chain}
QQVKQNSPQLSVQEGRISILNCDYTNMFDYFLWYKYPAEPTFLISSIKDNADGRFTVFLNKSA
KHLHLHIVPSQPGDSAVYFCAAMEGAQKLVFGQGTRLTINPN
>d1fytd1_b.1.1.1 (D:1-117) T-cell antigen receptor {Human (Homo sapiens), alpha-chain}
QSVTQLGSHVSVSEGALVLLRCNYSSVPPYLFWYVQYPNQGLQLLLKYTSAATLVKINGFEAEFKK
SETSFHLTKPSAHMSDAAEYFCAVSESPFGNEKLTFGTGTRLTIPN
>d1qrnd1_b.1.1.1 (D:1-117) T-cell antigen receptor {Human (Homo sapiens), alpha-chain}
KEVEQNSGPLSVPEGAIASLNCTYSDRGSQFFWYRQYSGKSPELIMSIYSNGDKEDGRFTAQLNKAS
QYVSLLRDSQPSDSATYLCVTTDSWGKLQFGAGTQVVVTPD
>d1bec_1_b.1.1.1 (3-117) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}
AVTQSPRNKVAVTGGKVTLSQCQTNNHNNMYWYRQDTGHGLRLIHYSYGAGSTEKGDIPDGYKASR
PSQEQFSLILELATPSQTSVYFCASGGGRGSYAEQFFGPGTRTLVLE
>d1fo0b_b.1.1.1 (B:) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}
VTLLEQNPRWRLVPRGQAVNLRILKNSQYPWMSWYQQDLQKQLQWLFTLRSPGDKEVKSPLGAD
YLATRVTDELRLQVANMSQGRTLYCTCSADRVGNTLYFGEGRSLIV
>d1kb5b_b.1.1.1 (B:) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}
VTLLEQNPRWRLVPRGQAVNLRILKNSQYPWMSWYQQDLQKQLQWLFTLRSPGDKEVKSPLGAD
YLATRVTDELRLQVANMSQGRTLYCTCSAAPDWGASAETLYFGSGTRTLVL
>d1nfdb1_b.1.1.1 (B:1-117) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}

DSGVVQSPRHIIKEKGRSVLTCIPISGHSNVVWYQQLGKELKFLIQHYEKVERDKGFLPSRFSVQQF
DDYHSEMNSALELEDSAMYFCASSLRWGDEQYFGPGTRLTVLE
>d1tcrb1 b.1.1.1 (B:1-117) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}
EAAVTQSPRNKVAVTGGKVTLSNQTNNHNNMYWYRQDTGHGLRLIHYSYGAGSTEKGDIPDGKY
ASRPSQENFSLILELATPSQTSVYFCASGGGGTLYFGAGTRLSVLE
>d1bd2e1 b.1.1.1 (E:3-118) T-cell antigen receptor {Human (Homo sapiens), beta-chain}
GVTQTPKFQVLKTGQSMTLQCAQDMNHEYSWYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVS
RSTTEDFPLRLLSAAPSQTSVYFCASSYPGGGFYEQYFGPGTRLTVTE
>d1fyte1 b.1.1.1 (E:3-118) T-cell antigen receptor {Human (Homo sapiens), beta-chain}
KVTQSSRYLVKRTGKVFLECVQDMDHENMFWYRQDPGLGLRLIYFSYDVKMKEKGDIPGYSVSR
EKKERFSLILESASTNQTSMYLCASSSTGLPYGYTFGSGTRLTVVE
>d1hxma1 b.1.1.1 (A:1-120) T-cell antigen receptor {Human (Homo sapiens), gamma-chain}
AIELVPEHQTVPSIGVPATLRCSMKGEAIGNYYINWYRKTQGNMTFIYREKDIYGPFGKDNFQGDI
DIAKNLAVLKILAPSERDEGSYYCACDTLGMGGEYTDKLIKIFGKGRVTVPEPR
>d1hxmb1 b.1.1.1 (B:1-123) T-cell antigen receptor {Human (Homo sapiens), delta-chain}
AGHLEQPQISSTKTLKARLECVVSGITISATSVYWYRERPEVIQFLVSISYDGTVRKESGIPSGKFE
VDRIPETSTSTLIHNVKQDIATYYCALWEAQQLGKKIKVFGPGTKLIITD
>d1tvda_ b.1.1.1 (A:) T-cell antigen receptor {Human (Homo sapiens), delta-chain}
DKVTQSSPDQTVASGSEVLLCTYDVTVSNPDLFWYRIRPDYSFQFVFGDDSRSEGADFTQGRFSV
KHILTQKAFHLVISPVRTEDSATYYCAFTLPPPTDKLIFGKGRVTVPEP
>d1ah1_ b.1.1.1 (-) Immunoreceptor CTLA-4 (CD152), N-terminal fragment {Human (Homo sapiens)}
AMHVAQPAVVLASSRGIA SFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELTFLDDSICT
TGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPPPYLIGINGTQIYVIDPEPCPDSDQEPK
>d1i8lc_ b.1.1.1 (C:) Immunoreceptor CTLA-4 (CD152), N-terminal fragment {Human (Homo sapiens)}
MHVAQPAVVLASSRGIA SFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELTFLDDSICT
GTSSGNQVNLTIQGLRAMDTGLYICKVELMYPPPYLIGINGTQIYVIDPE
>d1dqta_ b.1.1.1 (A:) Immunoreceptor CTLA-4 (CD152), N-terminal fragment {Mouse (Mus musculus)}
IQVTQPSVVLASSHGVA SFVCEYSPSHNTDEVTVLRQNTDQMTVEVCATTFTEKNTVGFLDYPFCS
GTFNESRVNLTIQGLRAVD TGLYLCKVELMYPPPYFVGMGNGTQIYVIDP
>d3frua1 b.1.1.2 (A:179-269) Fc (IgG) receptor, alpha-3 domain and beta subunit {Rattus norvegicus}
KEPPSMRLKARPGNSGSSVLTCAAFSFPPELKFRLRNLASGSGNCSTGPNGDGSFHAWSLLEVK
RGDEHHYQCQVEHEGLAQPLTVDL
>d3frub1 b.1.1.2 (B:) Fc (IgG) receptor, alpha-3 domain and beta subunit {Rat (Rattus norvegicus)}
IQKTPQIQVYSRHPPEKPNFLNCYVSQFHPPQIEIELLKNKIPNIEMSDLSFSKDWSFYILAHT
EFTPTETDVYACRVKHVTLKEPKVTWDRDM
>d1bmg_ b.1.1.2 (-) Class I MHC, beta2-microglobulin and alpha-3 domain {Cow (Bos taurus)}
IQRPPKIQVYSRHPPEKPNYLNCYVYGFHPPQIEIDLLKNGEKIKSEQSDLSFSKDWSFYLLSHAE
FTPNSKDQYSCRVKHVTLEQPRIVKWDRDL

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

TDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTELVETRPAGDGTFFQKWA
VVVPSGQEQRYTCHVQHEGLPKPLTLRWE

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

MIQRTPKIQVYSRHPAENGKSNFLNCYVSGFHPDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLY
TEFTPTEKDEYACRVNHVTLSPKIVKWDRDM

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

ADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTELVETRPAGDRTFQKWA
VVVPSGEEQRYTCHVQHEGLPKPLTLRWE

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

AEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTELVETRPAGDGTFFQKWA
AVVPSGEEQRYTCHVQHEGLPEPLTLRW

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

LEPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQQDGEGHTQDTELVETRPAGDGTFFQKWA
VVVPSGEEQRYTCHVQHEGLPEPVTLRW

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

QQVPPLVKVTHHVTSSVTLRCRALNYYPQNTMKWLKDKQPMDAKEFEPKDVLPNGDGTYYQGW
TLAVPPGEEQRYTCQVEHPGLDQPLIVW

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

TDSPKAHVTHHSRPEDKVTLCWALGFYPADITLTWQLNGEELIQDMELVETRPAGDGTFFQKWA
VVVPLGKEQYVYCHVYHQGLPEPLTLRW

>d1fzkb1 b.1.1.2 (B:) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), H-2KB}

IQKTPQIQVYSRHPPEKPNILNCYVTQFHPPHIEIQMLKNGKIPKVMESDMSFSKDWSFYLAH
TEFTPTEKDEYACRVKHDSMAEPTVYVDRDM

>d1jpfa1 b.1.1.2 (A:182-276) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), H-2DB}

TDSPKAHVTHHPRSKGEVTLRCWALGFYPADITLTWQLNGEELTQDMELVETRPAGDGTFFQKWA
VVVPLGKEQNYTCRVYHEGLPEPLTLRWE

>d1mhca1 b.1.1.2 (A:182-276) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), H-2M3}

ADPPKAHVTHHPRPKGDVTLRCWALGFYPADITLTWQKDEEDLTQDMELVETRPAGDGTFFQKWA
VVVPSGEEQRYTCYVHHEGLTEPLALKWRS

>d1qo3a1 b.1.1.2 (A:182-275) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), H-2DD}

TDPPKAHVTHHRRPEGDVTLRCWALGFYPADITLTWQLNGEELTQEMELVETRPAGDGTFFQKWA
VVVPLGKEQKYTCHVEHEGLPEPLTLRW

>d1k8da1 b.1.1.2 (A:182-274) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), IB QA-2}
TDPPKAHVTHHPRSYPGAVTLRCWALGFYPADITLTWQLNGEELTQDMELVETRPAGDGTFFQKWAS
VVVPLGKEQNYTCHVNHEGLPEPLTLRW

>d1ed3a1 b.1.1.2 (A:182-275) Class I MHC, beta2-microglobulin and alpha-3 domain {Rat (Rattus norvegicus), RT1-AA}
SDPPEAHVTLHPRPEGDVTLRCWALGFYPADITLTWQLNGEDLTQDMELVETRPAGDGTFFQKWAS
VVVPLGKEQNYTCRVEHEGLPKPLSQRWE

>d1zaga1 b.1.1.2 (A:184-277) Zinc-alpha-2-glycoprotein, ZAG {Human (Homo sapiens)}
QDPPSVVVVTSHQAPGEKKKLCLAYDFYPGKIDVHWTRAGEVQEPELRGDVHLHNGNGTYQSWVVV
AVPPQDTAPYSCHVQHSSLAQPLVVPWEA

>d1hyrc1 b.1.1.2 (C:181-274) MHC I homolog {Human (Homo sapiens), Mic-a}
TVPPMVNVTRSEASEGNITVTCRASGFYPWNITLSWRQDGVSLSHDTQQWGDVLPDNGTYQTTW
ATRQCQEEQRFTCYMEHSGNHSTHPVPS

>d1c16a1 b.1.1.2 (A:181-276) MHC I homolog {Mouse (Mus musculus), t22}
RSDPPKAHVTRHPRPEGDVTLRCWALGFYPADITLTWQLNGEELTQDMELVETRPAGDGTFFQKWA
AVVVPLGKEQSYTCHVYHEGLPEPLILRWGG

>d1exua1 b.1.1.2 (A:177-267) MHC-related Fc receptor {Human (Homo sapiens)}
KEPPSMRLKARPSSPGFSVLTCSAFSFPPELQLRFLRNLAAAGTGQDFGPNSDGSFHASSSLTVKS
GDEHHYCCIVQHAGLAQPLRVEL

>d1igtb3 b.1.1.2 (B:236-361) Immunoglobulin (constant domains of L and H chains) {Intact IgG2a antibody Mab231 (mouse), kappa L chain}
PCPPCKCPAPNLLGGPSVFIFPPKIKDVLMLISLPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQ
THREDYNSTLRVVSALPIQHQDWMMSGKEFKCKVNNKDLPAPIERTISKPKG

>d1igtb4 b.1.1.2 (B:363-474) Immunoglobulin (constant domains of L and H chains) {Intact IgG2a antibody Mab231 (mouse), kappa L chain}
SVRAPQVYVLPPEEEMTKKQVTLTCMVTDMPEDIYVEWTNNGKTELNYKNTEPVLDSGYSYFM
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}
GCKPCICTVPEVSSVFIFPPKPKDTHLITVTPKVTCVVVDISKDDPEVQFSWFVDNVEVHTAQTQPRE
EQFNSTFRVVSALPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKG

>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}
KPRAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQSDGQAPENYKNTQPIMDTDGSYFVY
SKLNVQKSNWEAGNTFTCSVLHEGLHNHHTTEKSLSH

>d1hzh3 b.1.1.2 (H:236-359) Immunoglobulin (constant domains of L and H chains) {Intact IgG B12 antibody (human), kappa L chain}
THTCPPEPPELLGGPSVFLFPPKPKDTHLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA

>d8faba2 b.1.1.2 (A:106-208) Immunoglobulin (constant domains of L and H chains) {Fab HIL (human), lambda L chain}
LGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPIKAGVETTTTPSKQSNKYA
ASSYLSLTPEQWKSRSYSCQVTHEGSTVEKTVAP

>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}
GSASAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGGKYAATS
QVLLPSKDV MAGTDEHVVCKVQHPNGNKEKNVPLPV

>d2fb4l2 b.1.1.2 (L:110-214) Immunoglobulin (constant domains of L and H chains) {Fab
KOL (human), lambda L chain}
QPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAA
SSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS

>d2ig2h2 b.1.1.2 (H:120-231) Immunoglobulin (constant domains of L and H chains) {Fab
KOL (human), lambda L chain}
STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPQVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT
VPSSSLGTQTYICNVNHKPSNTKVDKRVKPKCDKTHTCPPCP

>d2fbjh2 b.1.1.2 (H:119-220) Immunoglobulin (constant domains of L and H chains) {Fab
J539 (mouse), kappa L chain}
ESARNPTIYPLTLPPALSSDPVIIGCLIHDFPSGTMNVTWKGSGKDITTVNFPPALASGGRYTMSNQL
TLPAVECEPEGESVKCSVQHDSNPVQELDVNCSG

>d1mfb12 b.1.1.2 (L:112-212) Immunoglobulin (constant domains of L and H chains) {Fab
SE155-4 (mouse), lambda L chain}
PKSSPSVTLFPPSSEELTNKATLVCTITDFYPGVVTVDWKVDGTPVTQGMETTQPSKQSNNKYMA
SSYLTLTARAWERHSSYSCQVTHEGHTVEKSLRA

>d1teth2 b.1.1.2 (H:113-213) Immunoglobulin (constant domains of L and H chains) {Fab
TE33 (mouse), kappa L chain}
SAKTTPPSVYPLAPGSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSS
PRPSETVTCNVAHPASSTKVDKKIIVPR

>d2jelh2 b.1.1.2 (H:114-226) Immunoglobulin (constant domains of L and H chains) {Fab
JE142 (mouse), kappa L chain}
AATTPPSVYPLAPGGQNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLAADLYTLSSSV
TVPSSPRPSETVTCNVAHPASSTKVDKKIAPG

>d2jell2 b.1.1.2 (L:109-212) Immunoglobulin (constant domains of L and H chains) {Fab
JE142 (mouse), kappa L chain}
ADAAPTIVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIGD GARQNGVLNSWTDQDSKDSTYS
MSSTLTLTKDEYERHNSYTCEATHKTS DSPIVKSFNRN

>d1eapb2 b.1.1.2 (B:125-221) Immunoglobulin (constant domains of L and H chains) {Fab
17E8 (mouse), kappa L chain}
AKTTPPSVYPLAPGCGD TTGSSVTLGCLVKGYFPESVTVTWNSGGLSSSVHTFPALLQSGLYTMSSSV
TVPGGGWPSATVTCVAHPASSTTVDKKL

>d1yuhb2 b.1.1.2 (B:119-218) Immunoglobulin (constant domains of L and H chains) {Fab
anti-nitrophenol (mouse/human), lambda L chain}
AATTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGALSSGVHTFPAVLQSDLYTLSSSV
TVPASTWPSTVTCNVAHPASSTAVDKKIIVPR

>d1clzh2 b.1.1.2 (H:115-231) Immunoglobulin (constant domains of L and H chains) {Fab
MBR96 (mouse), kappa L chain}
TTTAPSVYPLVPGSDTSGSSVTLGCLVKGYFPEPVTKWNYGALSSGVRTVSSVLQSGFYSLSSLVTV
PSSTWPSQTVICNVAHPASKTELIKRIEPR

>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}
SASTTAPSVYPLAPVSGDQTNSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSV
TVTSSPWPSETITCNVAHPASSTKVDKKEPRGC

>d1kelh2 b.1.1.2 (H:116-218) Immunoglobulin (constant domains of L and H chains) {Fab 28B4 (mouse), kappa L chain}
TVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTL
SSSVTVPSSRPSETVTCNVAHPASSTKVDKIVP

>d1osph2 b.1.1.2 (H:121-218) Immunoglobulin (constant domains of L and H chains) {Fab 184.1 (mouse), kappa L chain}
AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSGLYTMSSSV
TVPSSTWPSQTVTCSVAHPASSTTVDKKLE

>d1nfd2 b.1.1.2 (E:108-215) Immunoglobulin (constant domains of L and H chains) {Fab H57 (hamster), lambda L chain}
GPKSSPKVTVFPPSPEELRTNKATLVCLVNDYFPGSATVTWKANGATINDGVKTTKPSKQGQNYMT
SSYLSLTADQWKSHNRVSCQVTHEGETVEKSLSPAECLE

>d1nfd2 b.1.1.2 (F:115-228) Immunoglobulin (constant domains of L and H chains) {Fab H57 (hamster), lambda L chain}
TTTAPSVYPLAPACDSTTSTTDVTLGCLVKGYFPEPVTVSWNSGALTSVHTFPSVLHSGLYSLSSSV
TVPSSTWPKQPITCNVAHPASSTKVDKKEPR

>d1aqkl2 b.1.1.2 (L:112-216) Immunoglobulin (constant domains of L and H chains) {Fab B7-15A2 (human), lambda L chain}
QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVNAGVETTKPSKQSNKYAAS
SYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPAECSE

>d1a4kh2 b.1.1.2 (H:120-211) Immunoglobulin (constant domains of L and H chains) {Diels alder catalytic Fab (mouse), kappa L chain}
SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSL
GTQTYICNVNHKPSNTKVDKKV

>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}
SVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSP
RPSETVTCNVAHPASSTKVDKIVPR

>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}
RADAAPTVSIFPPSSEQLTSGGASVVCFLNDFYPKDINVAWAIDGSAAANGVLNSWTDQDSKDYSTYS
MSSTLTLTADYEYAANSYTCAATHKTSTSPIVKSFNANEC

>d1a5fh2 b.1.1.2 (H:121-217) Immunoglobulin (constant domains of L and H chains) {Anti-E-selectin Fab (mouse), kappa L chain}
AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSV
SVPTSTETVTCNVAHPASSTKVDKIVPR

>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}
RANAAPTVSIFPPSTEQLATGGASVCLMKNFYPRDISVKWKIDGTERNGVLNSVTDQDSADSTYSM
SSTLSLTADYQSHNLYTCQVVHKTSSSPVVAKNFNRNEC

>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}

AKTTAPSVYPLVPVCGGTTGSSVTLGCLVKGYFPEPVTWTWNSGSLSSGVHTFPALLQSGLYTLSSSVT
VTSNTWPSQTITCNVAHPASSTKVDKKEIPRV

>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}

LTVSSAETTPPSVYPLAPGTAALKSSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTL
TSSVTVPSSTWPSQTVTCNVAHPASSTKVDKIVPRNCGGDC

>d1sm3h2 b.1.1.2 (H:114-213) Immunoglobulin (constant domains of L and H chains)
{Tumor-specific Fab SM3, (mouse), lambda L chain}

AKTTPPTVYPLAPGSNAASQSMVTLGCLVKGYFPEPVTVTWNSGSLASGVHTFPAVLQSDLYTLSSSV
TVPSSTWPSETVTCNVAHPASSTKVDKIVPR

>d1c12b2 b.1.1.2 (B:414-513) Immunoglobulin (constant domains of L and H chains) {Fab
directed against the musk odorant traseolide, (mouse), kappa L chain}

ASTKGPSVYPLAPGSKAAASMTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVT
VPSSRPSETVTCNVAHPASSTKVDKIVPE

>d1r24b2 b.1.1.2 (B:123-217) Immunoglobulin (constant domains of L and H chains) {Fab
R24, (mouse), kappa L chain}

ATTTAPSVYPLVPGSDTSGSSVTLGCLVKGYFPGPVTVKWNYGALSSGVRTVSSVLQSGFYLSLSSVT
VPSSTWPSQTVICNVAHPASKTDLIK

>d1c5da2 b.1.1.2 (A:107-213) Immunoglobulin (constant domains of L and H chains) {Fab
against the main immunogenic region of the human muscle acetylcholine receptor, (rat),
kappa L chain}

RADAAPTVISIFPPSTEQLATGGASVVCLMNNFYPRDISVKWKIDGTERRDGLDSVTDQDSKDYSTYS
MSSTLSLTKADYESHNLTYTCEVVHKTSSSPVVKSFNRNEC

>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}

AQTTAPSVYPLAPGCGDTSSTVTLGCLVKGYFPEPVTVTWNSGALSSDVHTFPAVLQSGLYTLTSSV
TSSTWPSQTVTCNVAHPASSTKVDKKLERR

>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}

AKTTPPPVYPLVPGSLAQTNMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSV
TVPSSTWPSETVTCNVAHPASSTKVDKIEP

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

GSASAPTLFPLVSCENSNPSTVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGGKYAATSQ
VLLPSKDVAQGTNEHVCKVQHPNGNKEKDVPL

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

AKTTPPSVYPLAPGSAAQTNMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSV
TVPSSTWPSETVTCNVAHPASSTKVDKIVPRDC

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

AKTTPPSVYPLAVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSE
TVTCNVAHPASSTKVDKKIVPR
>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)}
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV
TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC
>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)}
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS
LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
>d1fe8h2 b.1.1.2 (H:116-216) Immunoglobulin (constant domains of L and H chains) {Fab
RU5, (mouse), kappa L chain}
AETTAPSVYKLEPVSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTW
PSQSITCNVAHPASSTKVDKKIEPRG
>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}
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV
TVPSSSLGTATYTCNVDPHKPSNTKVDKRV
>d1fn4b2 b.1.1.2 (B:107-208) Immunoglobulin (constant domains of L and H chains) {Fab
198 against acetylcholine receptor, (rat)}
TMVTVSSVFPLAPGSAQTNSMVTGCLVKGYFPEPVTVTWNSGALSSGVHTFPAVLQSGLYTLTSSV
TVPSSTWSSQAVTCNVAHPASSTKVDKKIVPRDC
>d1jguh2 b.1.1.2 (H:114-212) Immunoglobulin (constant domains of L and H chains)
{Catalytic Fab 1D4, (mouse), kappa L chain}
AKTTAPSVYPLAPVCGDGTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVT
VTSSTWPSQSITCNVAHPASSTKVDKKIEP
>d1jgul2 b.1.1.2 (L:108-214) Immunoglobulin (constant domains of L and H chains)
{Catalytic Fab 1D4, (mouse), kappa L chain}
RADAAPTIVSIFPPSSEQLTSGGASVVCFLNNFYPKDIVKWKIDGSRQNGVLNSWTDQDSKDSTYS
MSSTLTTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
>d1mcoh2 b.1.1.2 (H:118-219) Immunoglobulin (constant domains of L and H chains)
{Intact antibody (lambda) MCG (human)}
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFQPPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV
TVPSSSLGTQTYICNVNHKPSNTKVDKRVAPEL
>d1adqa1 b.1.1.2 (A:238-341) Immunoglobulin (constant domains of L and H chains) {Fc
(human) IgG1 class}
PSVFLFPPKPKDITLMISRTPEVTCVVVDVSDVQEDPQVQFNWYVDGQVHNAKTKPREQQFNSTYRVV
SVLTVLHQNWLDGKEYKCKVSNKGLPSSIEKTISKAKG
>d1dn2a1 b.1.1.2 (A:237-341) Immunoglobulin (constant domains of L and H chains) {Fc
(human) IgG1 class}
GPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHENPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
>d1dn2a2 b.1.1.2 (A:342-443) Immunoglobulin (constant domains of L and H chains) {Fc
(human) IgG1 class}

QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS
KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSL
>d1fc2d1 b.1.1.2 (D:238-341) Immunoglobulin (constant domains of L and H chains) {Fc
(human) IgG1 class}
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPQVKFNWYVDGVQVHNAKTKPREQQYNSTYRVV
SVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKAKG
>d1fp5a1 b.1.1.2 (A:336-438) Immunoglobulin (constant domains of L and H chains) {Fc
(human) IgE}
VSAYLSRPSFDLFIKRSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL
PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSG
>d1fp5a2 b.1.1.2 (A:439-543) Immunoglobulin (constant domains of L and H chains) {Fc
(human) IgE}
PRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFF
VFSRLEVTRAWEQKDEFICRAVHEAASPSQTVQRAVSV
>d1i1ca1 b.1.1.2 (A:239-341) Immunoglobulin (constant domains of L and H chains) {Fc (rat)
IgG}
SVFIFPPKTKDVLGGGLTPKVTCTVVVDISQNDPEVRFVSWFIDVVEVHTAQTHAPEKQSNSTLRSVSEL
PIVERDWLNGKTFKCKVNSGAFPAPIEKSISKPEG
>d1i1ca2 b.1.1.2 (A:342-443) Immunoglobulin (constant domains of L and H chains) {Fc (rat)
IgG}
TPRGPQVYTMAPPKEEMTQSQVSITCMVKGFYPPDIYTEWKMNQPPQENYKNTPTMDTDGYSYFL
YSKLNVKKETWQQGNTFTCSVLHEGLENEHTEKLSLH
>d1pfc_ b.1.1.2 (-) Immunoglobulin (constant domains of L and H chains) {Fc (guinea pig)}
RTISKAKGPPRIPEVYLLPPPRNELSKKKVSLTCMITGFYPADINVEWDSSEPSDYKNTPPVFDTDGS
FFLYSRLKVDTDANNNGESFTCSVMHEALPNHVIQKSISRSPG
>d1cqka_ b.1.1.2 (A:) Immunoglobulin (constant domains of L and H chains) {Fc MAK33
(mouse)}
PAAPQVYTIPPPQMAKDLVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYS
KLNQKSNWEAGNTFTCSVLHEGLHNHHTKLSLH
>d1g84a_ b.1.1.2 (A:) Immunoglobulin (constant domains of L and H chains) {C epsilon2
domain from IgE (human)}
SRDFTPTVKILQSSSDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGELAS
TQSELTLSQKHWLSDRITYTCQVTYQGHTFEDSTKSA
>d1tca2 b.1.1.2 (A:118-213) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}
IQNPEPAVYALKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDATVLDKAMDSKSNGAIAWSNQ
TSFTCQDIFKETNATYPSSDVPC
>d1bd2d2 b.1.1.2 (D:118-203) T-cell antigen receptor {Human (Homo sapiens), alpha-chain}
IQNPDPAVYQLRDSKSSDKSVCLFTDFDSQTNVSQKSDVYITDKTVLDMRSMDFKSNSAVAWSNK
SDFACANAFNNSIIPEDTF
>d1bec_2 b.1.1.2 (118-246) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}
DLRQVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVWNGKEVHSGVSTDPQAYKESN
YSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVQTQNISAEAWGRAD
>d1bd2e2 b.1.1.2 (E:119-247) T-cell antigen receptor {Human (Homo sapiens), beta-chain}
DLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFYPDHVELSWVWNGKEVHSGVSTDPQPLKEQP

ALNDSRYALSSRLRVSATFWQDPRNHFRQCQVQFYGLSENDEWTQDRAKPVTQIVSAEAWGRAD
>d1hxma2 b.1.1.2 (A:121-206) T-cell antigen receptor {Human (Homo sapiens),
gamma-chain}
SQPHTKPSVFMKNGTNAVCLVKEFYPKDIRINLVSSKKITEFDPAIVISPSGKYNAVKLGKYEDSNSV
TCSVQHDKTVHSTDFE
>d1hymb2 b.1.1.2 (B:124-230) T-cell antigen receptor {Human (Homo sapiens), delta-chain}
KQLDADVSPKPTIFLPSIAETKLQKAGTYLCLLEKFFPDVIKIHWEKKSNTILGSQEGNTMKTNDTY
MKFSLWTVPEKSLDKEHRCIVRHENKNGVDQEIIFFPI
>d1cd1a1 b.1.1.2 (A:186-279) CD1, beta2-microglobulin and alpha-3 domain {Mouse (Mus
musculus)}
QEKPVAWLSSVPSAHGHRQLVCHVSGFYKPKVWVMWMRGDQEQGTHRGDFLPNADETWYLQ
ATLDVEAGEEAGLACRVKHSSLGGQDIILYW
>d1hdma1 b.1.1.2 (A:94-196) Class II MHC, C-terminal domains of alpha and beta chains
{Human (Homo sapiens), HLA-DM}
SRGFPIAEVFTLPLEFGKPNLVCVSNLFPMLTVNWHDSVPVEGFGPTFVSAVDGLSFQAFSYL
NFTPEPSDIFSCIVTHEPDRYTAIAYWVPRNALPS
>d1hdmb1 b.1.1.2 (B:88-185) Class II MHC, C-terminal domains of alpha and beta chains
{Human (Homo sapiens), HLA-DM}
TRPPSVQVAKTTPFNTREPVMLACYVWGFYPAEVTITWRKNGKLMHSSAHKTAQPNGDWTYQTL
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}
RRVEPKVTVYPSKTQPLQHNNLLVCSVSGFYPGSIEVRWFRNGQEEKAGVVSTGLIQNGDWTFQTLV
MLETVPRSGEVYTCQVEHPSVTSPLTVEWRA
>d1fv1a1 b.1.1.2 (A:82-181) Class II MHC, C-terminal domains of alpha and beta chains
{Human (Homo sapiens), HLA-DR2}
ITNVPPEVTVLNPNVRELREPVLICFIDKFTPPVVNVTWLRNGKPVTTGVSETVFLPREDHLFRKF
HYLPFLPSTEDVYDCRVEHWGLDEPLLKHWEFD
>d1fv1b1 b.1.1.2 (B:93-190) Class II MHC, C-terminal domains of alpha and beta chains
{Human (Homo sapiens), HLA-DR2}
RRVEPKVTVYPARTQLQHNNLLVCSVNGFYPGSIEVRWFRNSQEEKAGVVSTGLIQNGDWTFQTL
VMLETVPRSGEVYTCQVEHPSVTSPLTVEWRA
>d1d5zb1 b.1.1.2 (B:93-190) Class II MHC, C-terminal domains of alpha and beta chains
{Human (Homo sapiens), HLA-DR4}
RRVYPEVTVYPAKTQPLQHNNLLVCSVNGFYPGSIEVRWFRNGQEEKTGVVSTGLIQNGDWTFQTL
VMLETVPRSGEVYTCQVEHPSLTSPLTVEWRA
>d1jk8a1 b.1.1.2 (A:85-181) Class II MHC, C-terminal domains of alpha and beta chains
{Human (Homo sapiens), HLA-DQ8}
EVPEVTVFSKSPVTLGQPNTLCLVDNIFPPVVNITWLSNGHSVTEGVSETSFLSKSDHSFFKISYLTF
PSDDEIYDCKVEHWGLDEPLLKHWEPE
>d1jk8b1 b.1.1.2 (B:95-192) Class II MHC, C-terminal domains of alpha and beta chains
{Human (Homo sapiens), HLA-DQ8}
VEPTVTISPSRTEALNHHNLLVCSVTDYFPAQIKVRWFRNDQEETTGVVSTPLIRNGDWTFQILVML
EMTPQRGDVYTCHVEHPSLQNPIIVEWRAQS

>d1iaka1 b.1.1.2 (A:82-181) Class II MHC, C-terminal domains of alpha and beta chains
{Mouse (Mus musculus), I-AK}

ATNEAPQATVFPKSPVLLGQPNTLICFVDNIFPPVINITWLRNSKSVTDGVYETSFFVNRDYSFHKLS
YLTFIPSDDDIYDCKVEHWGLEEPVLKHWEPE

>d1iakb1 b.1.1.2 (B:93-190) Class II MHC, C-terminal domains of alpha and beta chains
{Mouse (Mus musculus), I-AK}

RLEQPSVVISLSRTEALNHHNTLVCSVTDYFPAKIKVRWFRNGQEETVGVSSSTQLIRNGDWTFQVLV
MLEMTPRRGEVYTCHVEHPSLTSPITVEWRA

>d1fnga1 b.1.1.2 (A:82-182) Class II MHC, C-terminal domains of alpha and beta chains
{Mouse (Mus musculus), I-EK}

DANVAPEVTVLSRSPVNLGEPNILICFIDKFSPPVVNVTWLRNGRPVTEGVSETVFLPRDDHLFRKF
HYLTFPSTDDFYDCEVDHWGLEEPLRKHWEFEE

>d1fngb1 b.1.1.2 (B:93-188) Class II MHC, C-terminal domains of alpha and beta chains
{Mouse (Mus musculus), I-EK}

RRVEPTVTVYPTKTQPLEHHNLLVCSVSDFYPGNIEVRWFRNGKEEKTGIVSTGLVRNGDWTFQTL
VMLETVPQSGEVYTCQVEHPSLTDPTVEW

>d2iada1 b.1.1.2 (A:83-186) Class II MHC, C-terminal domains of alpha and beta chains
{Mouse (Mus musculus), I-AD}

TNEAPQATVFPKSPVLLGQPNTLICFVDNIFPPVINITWLRNSKSVTDGVYETSFLVNRDHSFHKLSY
LTFIPSDDDIYDCKVEHWGLEEPVLKHWEPEISSADLVPR

>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)}

TNEAPQATVFPKSPVLLGQPNTLICFVDNIFPPVINITWLRNSKSVTDGVYETSFLVNRDHSFHKLSY
LTFIPSDDDIYDCKVEHWGLEEPVLKHWSS

>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)}

RLEQPNVAISLSRTEALNHHNTLVCSVTDYFPAKIKVRWFRNGQEETVGVSSSTQLIRNGDWTFQVLV
MLEMTPHQGEVYTCHVEHPSLKSPITVEWS

>d1k8ia1 b.1.1.2 (A:93-191) Class II MHC, C-terminal domains of alpha and beta chains
{Mouse (Mus musculus), H2-DM}

VSRGLPVAEFTLKPFEFGKPNLVCFISNLFPPPTLTVNWQLHSAPVEGASPTSISAVDGLTFQAFSYL
NFTPEPFDLYSCTVTHEIDRYTAIAYWVPQ

>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)}

FPKDPEIHLSGPLEAGKPITVKCSVADVYPFDRLEIDLLKGDHLMKSQEFLEADRKSLETKSLEVTF
TPVIEDIGKVLVCRAKLHIDEMDSVPTVRQAVKELQVYISP

>d1iam_1 b.1.1.3 (83-185) Second domain of intercellular cell adhesion molecule-1 (ICAM-1)
{Human (Homo sapiens)}

YWTPPERVELAPLPSWQPVGKQLTLRCQVEGGAPRAQLTVVLLRGEKELKREPAVGEPAEVTTTVLVR
RDHHGAQFSCRTELDLRPQGLELFENTSAPYQLQTF

>d1ic1a1 b.1.1.3 (A:83-190) Second domain of intercellular cell adhesion molecule-1 (ICAM-1) {Human (Homo sapiens)}
YWTPERVELAPLPSWQPVGKNLTLRCQVEGGAPRANLTVVLLRGEKELKREPAVGEPAEVTTTVLV
RRDHHGANFSCRTELDLRPQGLELFENTSAPYQLQTFVLPAT

>d1zxq_1 b.1.1.3 (87-192) Second domain of intercellular cell adhesion molecule-2 (ICAM-2) {Human (Homo sapiens)}
PPRQVILTLQPTLVAVGKSFTIECRVPTVEPLDSLTLFLFRGNETLHYETFGKAAPAPQEATATFNSTA
DREDGHRNFSCLAVLDLMSRGGNIFHKHSAPKMLEIY

>d1cdy_2 b.1.1.3 (98-178) CD4 {Human (Homo sapiens)}
FGLTANS DTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTL SVSQLELQDSGTWTCTVLQNQ
KKVEFKIDIVVLA

>d1wioa4 b.1.1.3 (A:292-363) CD4 {Human (Homo sapiens)}
MRATQLQKNLTCEVWGPTSPKMLSLKLENKEAKVSKREKAVVWLNPEAGMWQCLLSDSGQVLL
ESNIKVLP

>d1cid_2 b.1.1.3 (106-177) CD4 {Rat (Rattus rattus)}
VMKVTQPDSNTLTCEVMGPTSPKMRLILKQENQEARVSRQEKVIQVQAPEAGVWQCLLSEGEVVK
MDSKIQV

>d1hnf_2 b.1.1.3 (105-182) CD2, second domain {Human (Homo sapiens)}
RVSKPKISWTCINTTLTCEVMNGTDPELNLYQDGKHLKLSQRVITHKWTTSLSAKFKCTAGNKVSKE
SSVEPVSCPEK

>d1ccza2 b.1.1.3 (A:94-171) CD2-binding domain of CD58, second domain {Human (Homo sapiens)}
EMVSKPMIYWEC SNATLTCEVLEGT DVELKLYQGKEHLRSLRQKTMSYQWTNLRAPFKCKAVNRVS
QESEMEVVNCP E

>d1dr9a2 b.1.1.3 (A:106-200) CD80, second domain {Human (Homo sapiens)}
ADFPTPSISDFEIPTS NIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD FNMT
TNHSFMCLIKYGH LRVNQT FNWNTA

>d1vcaa2 b.1.1.4 (A:1-90) N-terminal domain of vascular cell adhesion molecule-1 (VCAM-1) {Human (Homo sapiens)}
FKIETTPESRYLAQIGDSVSLTCSTTGCESPFFSWRTQIDSPLNGKVTNEGTTSTLTMNPV SFGNEHSY
LCTATCESRKLEKGIQVEIYS

>d1iam_2 b.1.1.4 (1-82) N-terminal domain of intracellular adhesion molecule-1, ICAM-1 {Human (Homo sapiens)}
QTSVSPSKVILPRGGSVLVTCSTSCDQPKLLGIETPLPKKELLPLGNNRKYVYELSNVQEDSQPMCYSN
CPDGQSTAKTFLTV

>d1zxq_2 b.1.1.4 (1-86) N-terminal domain of intracellular adhesion molecule-2, ICAM-2 {Human (Homo sapiens)}
KVFEVHVRPKKLAVEPKGSLEVNCSTTCNQPEVGGLETSLNKILLDEQAQWKHYLVS NISHD TVLQC
HFTCSGKQESMNSNVSVYQ

>d1epfa1 b.1.1.4 (A:1-97) Neural cell adhesion molecule (NCAM) {Rat (Rattus norvegicus)}
LQVDIVPSQGEISVGESKFFLCQVAGDAKDKDISWFSPNGEKLSPNQQRISVVW NDDDSSTLTIYAN
IDDAGIYKCVVTAEDGTQSEATVNVKIFQ

>d1epfa2 b.1.1.4 (A:98-189) Neural cell adhesion molecule (NCAM) {Rat (Rattus norvegicus)}

KLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIHWKHKGRDVILKKDVRFIVLSNNYLQIRGIKKTDE
GTYRCEGRILARGEINFKDIQVIV
>d1ie5a_b.1.1.4 (A:) Neural cell adhesion molecule (NCAM) {Chicken (Gallus gallus)}
GKDIQVIVNPPSVRARQSTMNATANLSQSVTLACDADGFPEPTMTWTKDGEPIEQEDNEEKYSFN
YDGSELIKKVKDSDEAEYICIAENKAGEQDATIHLKVFAK
>d1gsma1_b.1.1.4 (A:1-90) Mucosal addressin cell adhesion molecule-1 (MADCAM-1)
{Human (Homo sapiens)}
VKPLQVEPEPVAVALGASRQLTCRLACADRGASVQWRGLDTSLGAVQSDTGRSVLTVRNASLSAA
GTRVCVCGSCGGRTFQHTVQLLVY
>d1gsma2_b.1.1.4 (A:91-206) Mucosal addressin cell adhesion molecule-1 (MADCAM-1)
{Human (Homo sapiens)}
AFPNQLTVSPAALVPGDPEVACTAHKVTVPDPNALSFSLLVGGQELEGAQALGPEVQEEEEEPQGDE
DVLFRVTERWRLPPLGTPVPPALYQATMRLPGLLELSHRQAIPVLIETR
>d1fhga_b.1.1.4 (A:) Telokin {Turkey (Meleagris gallopavo)}
AEEKPHVKPYFTKTILDMEVVEGSAARFDCKVEGYPDPEVMWFKDDNPVKESRHFQIDYDEEGNC
SLTISEVCGDDDAKYTCKAVNSLGEATCTAELLVETM
>d1g1ca_b.1.1.4 (A:) Titin {Human (Homo sapiens), different modules}
SMEAPKIFERIQSQTVGQSDAHFRVRVVGKPDPECEWYKNGVKIERSDRIYWYWPEDNVCELVIR
DVTGEDSASIMVKAINIAGETSSHAFLLVQAK
>d1nct_b.1.1.4 (-) Titin {Human (Homo sapiens), different modules}
SKTTLAARILTKPRSMTVYEGESARFSCD TDGEPVPTVTWLRKGQVLSTSARHQVTTTKYKSTFEISS
VQASDEGNYSVVENSEGKQEAFTLTIQK
>d1koa_1_b.1.1.4 (6265-6361) Twitchin {Nematode (Caenorhabditis elegans)}
QPRFIVKPYGTEVGEQSANFYCRVIASSPPVVTWHKDDRELKQSVKYMKRYNGNDYGLTINRVKGD
DKGEYTVRAKNSYGTKEEIVFLNVTRHSEP
>d1wiu_b.1.1.4 (-) Twitchin {Nematode (Caenorhabditis elegans)}
LKPKILTASRKIKIKAGFTHNLEVDFIGAPDPTATWTVGDSGAALAPPELLVDKSSSTTSIFFPSAKRAD
SGNYKLVKKNELGEDEAIFEVIVQ
>d1tiu_b.1.1.4 (-) Twitchin {Human (Homo sapiens), Ig repeat 27}
LIEVEKPLYGVEVFGETAHFEIELSEPDVHGQWKLKGQPLTASPDCIIEDGKKHILHNCQLGMTG
EVSFQAANAKSAANLKVKEL
>d1iray1_b.1.1.4 (Y:1-101) Type-1 interleukin-1 receptor {Human (Homo sapiens)}
DKCKEREEKIILVSSANEIDVRPCPLNPNEHKGITWYKDDSKTPVSTEQASRIHQHKEKLWFVPAK
VEDSGHYCVVRNSSYCLRIKISAKFVENEPNLC
>d1iray2_b.1.1.4 (Y:102-204) Type-1 interleukin-1 receptor {Human (Homo sapiens)}
YNAQAIFKQKLPVAGDGGGLVCPYMEFFKNENNELPKLQWYKDCCKPLLDNIHFSGVKDRILVMNVA
EKHRGNYTCHASYTYLGKQYPITRVIEFITLEENKPT
>d1iray3_b.1.1.4 (Y:205-311) Type-1 interleukin-1 receptor {Human (Homo sapiens)}
RPVIVSPANETMEVDLGSQIQLICNVTGQLSDIAYWKWNGSVIDEDDPVLGEDYYSVENPANKRRST
LITVLNISEIESRFYKHPFTCFANKTHGIDAAYIQLIYPV
>d1cvsc1_b.1.1.4 (C:149-250) Fibroblast growth factor receptor, FGFR {Human (Homo
sapiens), FGFR1}
MPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPQPTLRWLKNGKEFKPDHRIGGYKVRYATW
SIIMDSVVPKDGNYTCIVENEYGSINHTYQLDVVER

>d1cvsc2 b.1.1.4 (C:251-359) Fibroblast growth factor receptor, FGFR {Human (Homo sapiens), FGFR1}
SPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVN
TTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVL

>d1ev2e1 b.1.1.4 (E:150-250) Fibroblast growth factor receptor, FGFR {Human (Homo sapiens), FGFR2}
NKRAPYWTNTEKMEKRLHAVPAANTVKFRCPAGGNPMPMTMRWLKNGKEFKQEHRIGGYKVRNQ
HWSLIMESVVP SDKGNYTCVVENEYGSINH TYHLDVVE

>d1ev2e2 b.1.1.4 (E:251-360) Fibroblast growth factor receptor, FGFR {Human (Homo sapiens), FGFR2}
RSPHRPILQAGLPANASTVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYGPDGLPYLKVLKAAGV
NTTDKEIEVLYIRNVTFEDAGEYTCLAGNSIGISFHSAWLTVL

>d1biha1 b.1.1.4 (A:5-98) Hemolin {Moth (Hyalophora cecropia)}
KYPVLKDQPAEVLFRENNPTVLECIIEGNDQGVKYSWKKDGKSYNWQEHNAALRKDEGSLVFLRPQ
ASDEGHYQCFAETPAGVASSRVISFRKT

>d1biha2 b.1.1.4 (A:99-209) Hemolin {Moth (Hyalophora cecropia)}
YLIASPAKTHEKTPIEGRPFQLDCVLPNAYPKPLITWKKRLSGADPNADVDFDRRITAGPDGNLYFT
IVTKEDVSDIYKYVCTAKNAAVDEEVVLEVEYEIKGVTKDNSGY

>d1biha3 b.1.1.4 (A:210-306) Hemolin {Moth (Hyalophora cecropia)}
KGEPVPQYVSKDMMAKAGDVTMIYCMYGSNPMGYPNYFKNGKDVNGNPEDRITRHNRTSGKRLLF
KTTLPEDEGVYTCEVDNGVGKPKHSLKLTVV

>d1biha4 b.1.1.4 (A:307-395) Hemolin {Moth (Hyalophora cecropia)}
SAPKYEQKPEKIVIVKQGQDVTIPCKVTGLPAPNVVWVSHNAKPLSGGRATVTD SGLVIKGVKNGDKG
YYGCRATNEHGDKYFETLVQVN

>d1cs6a1 b.1.1.4 (A:7-103) Axonin-1 {Ckicken (Gallus gallus)}
RSYGPVFEEQPAHTLFPESAEKVTLCRARANPPATYRWKMNGTELKMGPD SRYRLVAGDLVISN
PVKAKDAGSYQCVATNARGTVVSREASLRF

>d1cs6a2 b.1.1.4 (A:104-208) Axonin-1 {Ckicken (Gallus gallus)}
GFLQEFSAEERDPVKITEGWGVMFTCSPPPHYPALS YRWLLNEFPNFIPADGRRFVSQTTGNLYIAK
TEASDLGNYS CFATSHIDFITKSVFSKFSQLSLAAEDA

>d1cs6a3 b.1.1.4 (A:209-299) Axonin-1 {Ckicken (Gallus gallus)}
RQYAPSIKAKFPADTYALTGMVTLECFAGNPVPQIKWRKLDGSQTSKWLSSEPLLHIQNVDFEDE
GTYECEAENIKGRD TYQGRIIIHA

>d1cs6a4 b.1.1.4 (A:300-388) Axonin-1 {Ckicken (Gallus gallus)}
QPDWLDVITDTEADIGSDLRWSCVASGKPRPAVRWLRDGQPLASQNRIEVSGGELRFSKLVLEDSG
MYQCVAENKHGTVYASAELTVQA

>d1gl4b_ b.1.1.4 (B:) Perlecan Ig3 domain {Mouse (Mus musculus)}
PIMVTVEEQRSQSVRPGADVTFICTAKSKSPAYTLVWTRLHNGKLP SRAMDFNGILTIRNVQPSDAG
TYVCTGSNMFAMDQGTATLHVQ

>d1f97a2 b.1.1.4 (A:129-238) Junction adhesion molecule, JAM, C-terminal domain {Mouse (Mus musculus)}
VPPSKPTISVPSSVTIGNRAVLTCSEHDGSPPEYSWFKD GISMLTADAKKTRAFMNSSFTIDPKSGDL
IFDPVTA FDSGEYYCQAQNGYGTAMRSEAAHMDAVELNVGG

>d1flt_x_ b.1.1.4 (X:) Second domain of the Flt-1 receptor {Human (Homo sapiens)}

GRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEI
GLLTCEATVNGHLYKTNYLTHRQT

>d1he7a_b.1.1.4 (A:) NGF binding domain of trkA receptor {Human (Homo sapiens)}
SHMPASVQLHTAVEMHHWCIPFSVDGQPAPSLRWLFNGSVLNETSFIFTEFLEPAANETVRHGCLRL
NQPTHVNNNGNYTLAANPFGQASASIMAAFMDNPFENPE

>d1wwwx_b.1.1.4 (X:) NGF binding domain of trkA receptor {Human (Homo sapiens)}
VSFPASVQLHTAVEMHHWCIPFSVDGQPAPSLRWLFNGSVLNETSFIFTEFLEPAANETVRHGCLRL
NQPTHVNNNGNYTLAANPFGQASASIMAAFMDNP

>d1wwbx_b.1.1.4 (X:) Ligand binding domain of trkB receptor {Human (Homo sapiens)}
VHFAPTITFLESPTSDHHWCIPFTVKGNPKPALQWFYNGAILNESKYICTKIHVTNHTEYHGCLQLD
NPTHMNNGDYTLIAKNEYGKDEKQISAHFMGWPGID

>d1wwca_b.1.1.4 (A:) NT3 binding domain of trkC receptor {Human (Homo sapiens)}
TVYYPPRVVSLEPELRLEHCIEFVVRGNPPPTLHWHLHNGQPLRESKIIHVEYYQEGEISEGCLLFNK
PTHYNNNGNYTLIAKNPLGTANQTINGHFLKEFPVDE

>d1fcga1_b.1.1.4 (A:4-88) Fc gamma receptor ectodomain (CD32) {Human (Homo sapiens),
IIa}
APPKAVLKLEPPWINVLQEDSVTLTCQGARSPESDSIQWFHNGNLIPHTHTQPSYRFKANNNDSGEYT
CQTGQTSLSDPVHLTVLF

>d1fcga2_b.1.1.4 (A:89-174) Fc gamma receptor ectodomain (CD32) {Human (Homo
sapiens), IIa}
EWLVLQTPHLEFQEGETIMLRCHSWKDKPLVKVTFQNGKSKFSLDPTFSIPQANHSHSGDYHC
TGNIGYTLFSSKPVTITVQV

>d2fcba1_b.1.1.4 (A:6-90) Fc gamma receptor ectodomain (CD32) {Human (Homo sapiens),
IIb}
APPKAVLKLEPQWINVLQEDSVTLTCRGTHSPESDSIQWFHNGNLIPHTHTQPSYRFKANNNDSGEY
TCQTGQTSLSDPVHLTVLS

>d2fcba2_b.1.1.4 (A:91-178) Fc gamma receptor ectodomain (CD32) {Human (Homo
sapiens), IIb}
EWLVLQTPHLEFQEGETIVLRCHSWKDKPLVKVTFQNGKSKKFSRSDPNFSIPQANHSHSGDYHC
TGNIGYTLYSSKPVTITVQAPA

>d1fnla1_b.1.1.4 (A:3-86) Fc gamma receptor ectodomain (CD32) {Human (Homo sapiens),
III}
EDLPKAVVFLEPQWYSVLEKDSVTLKCGAYSPEDNSTQWFHNESLISSQASSYFIDAATVNDSGEY
RCQTNLSTLSDPVQLEV

>d1fnla2_b.1.1.4 (A:87-175) Fc gamma receptor ectodomain (CD32) {Human (Homo sapiens),
III}
HIGWLLLQAPRWVFKEDPIHLRCHSWKNTALHKVTYLQNGKDRKYFHHNSDFHIPKATLKDSGS
YFCRGLVGSKNVSSETVNITITQA

>d1f2qa1_b.1.1.4 (A:4-85) IgE high affinity receptor alpha subunit {Human (Homo sapiens)}
KPKVSLNPPWNRIFKGENVTLCNGNFFEVSSSTKWFHNGSLSEETNSSLNIVNAKFEDSGEYKQC
HQQVNESEPVYLEVFS

>d1f2qa2_b.1.1.4 (A:86-174) IgE high affinity receptor alpha subunit {Human (Homo
sapiens)}
DWLLLQASAEVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYY

CTGKVVQLDYESEPLNITVIKAPR
>d1efxd1 b.1.1.4 (D:4-103) Killer cell inhibitory receptor {Human (Homo sapiens), kir2dl3}
VHRKPSLLAHPGRLVKSEETVILQCWSDVRFEFLLHREGKFKDTHLHIGEHHDGVSKANFSIGPM
MQDLAGTYRCYGSVTHSPYQLSAPSDPLDIVITG
>d1efxd2 b.1.1.4 (D:104-200) Killer cell inhibitory receptor {Human (Homo sapiens),
kir2dl3}
LYEKPSLSAQPGPTVLAGESVTLSCSSRSSYDMYHLSREGEAHECRFSAGPKVNGTFQADFPLGPATH
GGTYRCFGSFRDSPYEWSSSDPLLVSVI
>d1nkr_1 b.1.1.4 (6-101) Killer cell inhibitory receptor {Human (Homo sapiens), p58-cl42
kir}
RKPSLLAHPGPLVKSEETVILQCWSDVMFEHFLHREGMFNDTLRLIGEHHDGVSKANFSISRMTQ
DLAGTYRCYGSVTHSPYQVSAPSDPLDIVI
>d1nkr_2 b.1.1.4 (102-200) Killer cell inhibitory receptor {Human (Homo sapiens), p58-cl42
kir}
IGLYEKPSLSAQPGPTVLAGENVTLSCSSRSSYDMYHLSREGEAHERRLPAGPKVNGTFQADFPLGPA
THGGTYRCFGSFDSPYEWSSSDPLLVSVT
>d1g0xa1 b.1.1.4 (A:2-97) Ligand binding domain of lir-1 (ilt2) {Human (Homo sapiens)}
HLPKPTLWAEPGSVITQGSVTLRCQGGQETQEYRLYREKKTAPWITRIPQELVKKGQFPISITWEH
AGRYRCYYGSDTAGRSESSDPLELVVTG
>d1g0xa2 b.1.1.4 (A:98-198) Ligand binding domain of lir-1 (ilt2) {Human (Homo sapiens)}
AYIKPTLSAQPSVVNSGGNVTLQCDSQVAFDGFILCKEGEDEHPQCLNSQPHARGSSRAIFSVGPVS
PSRRWWYRCYAYDSNSPYEWSLPSDLLELLVLG
>d1f42a1 b.1.1.4 (A:1-87) The p40 domain of interleukin-12 (IL-12 beta chain), N-terminal
domain {Human (Homo sapiens)}
IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQY
TCHKGGEVLSHSLLLHKKED
>d1bjba1 b.1.1.4 (A:101-186) CD3 gamma chain ectodomain fragment {Mouse (Mus
musculus)}
KKDGSQTNKAKNLVQVDGSRGDGSVLLTCGLTDKTIKWLKDGSIISPLNATKNTWNLGNNAKDPRG
TYQCQGAKETSNPLQVYYRM
>d1bjba2 b.1.1.4 (A:1-100) CD3 epsilon chain ectodomain fragment {Mouse (Mus musculus)}
DDAENIEYKVSISGTSVELTCPLSDENLKWENKQELPQKHDKHLVLQDFSEVEDSGYVVCYTPAS
NKNTYLYLKARVGSADDAKKDAKKDDAKKDDA
>d1k3ia1 b.1.1.5 (A:538-639) Galactose oxidase, C-terminal domain {Fungi (Fusarium spp)}
GNLATRPKITRTSTQSVKVGGRITISTDSSISKASLIRYGTATHTVNTDQRRIPPLTLNNGGNSYSFQVP
SDSGVALPGYWMLFVMNSAGVPSVASTIRVTQ
>d1qba_1 b.1.1.5 (781-885) Bacterial chitinase, c-terminal domain {Serratia marcescens}
GETHFVDTQALEKDWLRFANILGQRELAKLDKGGVAYRPLVPGARVAGGKLEANIALPGLGIEYSTD
GGKQWQRYDAKAKPAVSGEVQVRSVSPDGKRYRAEKV
>d1svb_1 b.1.1.5 (303-395) Envelope glycoprotein, domain III (C-terminal) {Tick-borne
encephalitis virus}
TYTMCDKTKFTWKRAPTDSGHDTVMMEVTFSGTKPCRIPVRAVAHGSPDVNVAMLITPNPTIENN
GGGFIEMQLPPGDNIIYVGELSHQWFQK
>d1cgt_1 b.1.1.5 (495-579) Cyclodextrin glycosyltransferase, domain E {Bacillus circulans,

different strains}
ETTPPTIGHVGPVPMGKPGNVVTIDGRGFGSTKGTVYFGTTAVTGAAITSWEDTQIKVTIPSVAAGNYAV
KVAASGVNSNAYNNFTI
>d1kcla1 b.1.1.5 (A:496-581) Cyclodextrin glycosyltransferase, domain E {Bacillus circulans,
different strains}
TATPTIGHVGPMMAKPGVTITIDGRGFGSSKGTVYFGTTAVSGADITSWEDTQIKVKIPAVAGGNYNI
KVANAAGTASNVDNFEV
>d1cyg_1 b.1.1.5 (492-574) Cyclodextrin glycosyltransferase, domain E {Bacillus
stearothermophilus}
ESTPIIGHVGPMMGQVGHQVTIDGEGFGTNTGTVKFGTTAANVVSWSNNQIVVAVPNVSPGKYNITV
QSSSGQTSAAAYDNFEV
>d1qhoa1 b.1.1.5 (A:496-576) Cyclodextrin glycosyltransferase, domain E {Bacillus
stearothermophilus, maltogenic alpha-amylase}
ASAPQIGSVAPNMGIPGNVVTIDGKGFSTTQGTVTFFGGVTATVKSWSNRIEVYVPNMAAGLTDVKV
TAGGVSSNLYSYNI
>d1pama1 b.1.1.5 (A:497-582) Cyclodextrin glycosyltransferase, domain E {Bacillus sp.,
strain 1011}
TTPIIGNVGPMMAKPGVTITIDGRGFGSGKGTVYFGTTAVTGADIVAWEDTQIQVKIPAVPGGIYDIRV
ANAAGAASNIYDNFEVL
>d1ciu_1 b.1.1.5 (496-578) Cyclodextrin glycosyltransferase, domain E
{Thermoanaerobacterium thermosulfurigenes, EM1}
SNSPLIGHVGPMTKAGQTITIDGRGFGTTSQVFLFGSTAGTIVSWDDTEVKVKVPSVTPGKYNISLK
TSSGATSNTYNNINI
>d1smaa1 b.1.1.5 (A:1-123) Maltogenic amylase, N-terminal domain {Thermus sp.}
MRKEAIHHRSTDNFAYAYDSETLHLRLQTKKNDVDHVELLFGDPYEWHDGAWQFQTMPMRKTGS
DGLFDYWLAEVKPPYRRLRYGFVLRAGGEKLVYTEKGFYHEAPSDDTAYYFCFPFLHRV
>d1bvza1 b.1.1.5 (A:1-120) Maltogenic amylase, N-terminal domain {Thermoactinomyces
vulgaris, TVAI}
MLLEAIFHEAKGSYAYPISETQLRVRLRAKKGDVVRCEVLYADRYASPEEELAHALAGKAGSDERFDY
FEALLECSTKRKVKYVFLLTGPQGEAVYFGETGFSAERSKAGVFQYAYIHRSE
>d1eh9a1 b.1.1.5 (A:1-90) Glycosyltrehalose trehalohydrolase, N-terminal domain
{Archaeon Sulfolobus solfataricus, km1}
TFAYKIDGNEVIFTLWAPYQKSVKLVLEKGLYEMERDEKGYFTITLNNVKVRDRYKYVLDDASEIPD
PASRYQPEGVHGSPSQIIQESKE
>d1bf2_1 b.1.1.5 (1-162) Isoamylase, N-terminal domain {Pseudomonas amyloclavata}
AINSMSLGASYDAQANITFRVYSSQATRIVLYLYSAGYGVQESATYTLSPAGSGVWAVTVPVSSIKAA
GITGAVYYGYRAWGPNWPYASNWGWKGSQAGFVSDVDANGDRFNPNKLLLDPYAQEVSQDPLNPSN
QNGNVFASGASYRTTDSGIYAPKGVVLV
>d1lla_3 b.1.1.5 (380-628) Hemocyanin, C-terminal domain {Horseshoe crab (Limulus
polyphemus)}
PYDHDVLFNFPDIQVQDVTLHARVDNVVHTFMREQUELELKHGINPGNARSIKARYYHLDHEPFSYAV
NVQNNSASDKHATVRIFLAPKYDELGNEIKADELRRRTAIELDKFKTDLHPGKNTVVRHSLDSSVTLS
HQPTFEDLLHGVGLNEHKSEYCSGWPSHLLVPKGNIKGMEYHLFVMLTDWDDKDKVDGSESVACV
DAVSYCGARDHKYPDKKPMGPFDRPIHTEHISDFLTNNMFIKDIKIFHE

>d1hc2_3 b.1.1.5 (399-653) Hemocyanin, C-terminal domain {Spiny lobster (Panulirus interruptus)}

PPYTHDNLEFGSMVVNGVAIDGELITFFDEFQYSLINAVDSGENIEDVEINARVHRLNHNEFTYKITM
SNNNDGERLATFRIFLCPIEDNNGITLTLDEARWFCIELDKFFQKVPSGPETIERSKDSSTVTPDMP
SFQSLKEQADNAVNGGHDLDL SAYERSCGIPDRMLLPKSKPEGMEFNLYVAVTDGDKDTEGHNGGH
DYGGTHAQCGVHGEAYPDNRPLGYPLERRIPDERVIDGVSNIKHVVKIVHHL

>d1js8a2 b.1.1.5 (A:2792-2892) C-terminal domain of octopus hemocyanin {Giant octopus (Octopus dofleini)}

EDRVFAGFLLRTIGQSADVNFVCTKDGECTFGGTFCILGGEHEMFWAFDRLFKYDITTSKHLRLD
AHDDFDIKVTIKIDGHVLSNKYLSPPTVFLAPA

>d1clc_2 b.1.1.5 (35-134) CelD cellulase, N-terminal domain {Clostridium thermocellum}

IETKVSAAKITENYQFDSRIRLNSIGFIPNHSKKATIAANCSTFYVVKEDGTIVYTGTATSMFDNDTKE
TVYIADFSSVNEEGTYLAVPGVGKSVNFKI

>d1f1sa2 b.1.1.5 (A:171-248) Hyaluronate lyase precatalytic domain {Streptococcus agalactiae}

SEHPQPVTQTIEKSVNTALNKNYVFNKADYQYTLTNPSLGKIVGGILYPNATGSTTVKISDKSGKIIKE
VPLSVTAST

>d1edqa1 b.1.1.5 (A:24-132) Chitinase A, N-terminal domain {Serratia marcescens}

AAPGKPTIAWGNTKFAIVEVDQAATAYNNLVKVKNAADVSVSWNLWNGDTGTTAKVLLNGKEAWS
GPSTGSSGTANFKVKNKGGRYQMVALCNADGCTASDATEIVVAD

>d1f13a1 b.1.1.5 (A:5-190) Transglutaminase N-terminal domain {Human (Homo sapiens)}

RTAFGGRRVPPNNSNAEEDDLPTVELQGVVPRGVNLQEFNLVTSVHLFKERWDTNKVDHHTDKY
ENNKLIVRRGQSFYVQIDFSRPYDPRRDLFRVEYVIGRYPQENKGTYPVPIVSELQSGKWGAKIVMR
EDRSVRLSIQSSPKCIVGKFRMYAVWTPYGLRTRSRNPETDTYILFNPWCED

>d1g0da1 b.1.1.5 (A:6-140) Transglutaminase N-terminal domain {Red sea bream (Chrysophrys major)}

GLIVDVNGRSHENNLAHRTREIDRERLIVRRGQPFSTLQCSDSLPPKHHLELVHLGKRDEVVIKQV
KEHGARDKWWFNQGAQDEILLTLHSPANAVIGHYRLAVLVMSPDGHIVERADKISFHMLFNPWC
RD

>d1eut_1 b.1.1.5 (403-505) Sialidase, "linker" domain {Micromonospora viridifaciens}

GICAPFTIPDVALEPGQVTVPVAVTNQSGIAVPKPSLQLDASPDWQVQGSVEPLMPGRQAKGQVTIT
VPAGTTPGRYRVGATLRTSAGNASTTFTVTVGLLD

>d1ksr_ b.1.1.5 (-) F-actin cross-linking gelation factor (ABP-120), one repeat (ROD 4) {Slime mold (Dictyostelium discoideum), different domains}

ADPEKSYAEGPGLDGGECFQPSKFKIHAVDPDGVHRTDGGDGFVVITIEGPAPVDPVMVDNGDGTID
VEFEPKEAGDYVINLTLDGDVNGFVKPTVTVKPA

>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}

KPAPSAEHSYAEGGLVKVFDNAPAEFTIFAVDTKGVARTDGGDPFEVAINGPDGLVVDKAVTDNND
GTYGVVYDAPVEGNYNVNVTLRGNPIKNMPIDVKCIE

>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}

GANGEDSSFGSFTFTVAAKNKKGEVKTYGGDKFEVSITGPAEEITLDAIDNQDGTYYTAAAYSLVGNRFR
STGVKLNKGHIEGSPFKQVLGNPGKKNPEVKSFTTTRTAN

>d1ds6b_b.1.1.5 (B:) Rho GDP-dissociation inhibitor 1, RhoGDI {Human (Homo sapiens)}
GNYKPPPQKSLKELQEMDKDDESLIKYKKTLLGDGPVVTPKAPNVVVTRTLVLCESAPGPITMDLT
GDLEALKKETIVLKEGSEYRVKIHFKVNRDIVSGLKYVQHTYRTGVKVDKATFMVGSYGPREEEYFL
TPVEEAPKGMLARGTYHNKSFDDDDKQDHLSWEWNLSIKKEWG

>d1foa_b.1.1.5 (A:) Rho GDP-dissociation inhibitor 1, RhoGDI {Human (Homo sapiens)}
MVPNVVVVTGLTLVCCSAPGPLELDLTGDLESFKKQSFVLKEGVEYRIKISFRVNREIVSGMKYIQHTYR
AGVAIDATDYMVGSYGPRAEEYFLTPVEEAPKGMLARGSYSIKSRFTDDDKTDHLSWEWNFTIKK
DWK

>d1hh4e_b.1.1.5 (E:) Rho GDP-dissociation inhibitor 1, RhoGDI {Human (Homo sapiens)}
HSVNYKPPAQKSIQEIQLDKDDESLRKYKEALLGRVAVSADPNVNVVVVTGLTLVCCSAPGPLELDL
TGDLESFKKQSFVLKEGVEYRIKISFRVNREIVSGMKYIQHTYRKGVKIDKTDYMVGSYGPRAEEYEF
LTPVEEAPKGMLARGSYSIKSRFTDDDKTDHLSWEWNLTIKKDW

>d1rhoa_b.1.1.5 (A:) Rho GDP-dissociation inhibitor 1, RhoGDI {Human (Homo sapiens)}
VAVSADPNVNVVVVTGLTLVCCSAPGPLELDLTGDLESFKKQSFVLKEGVEYRIKISFRVNREIVSGMK
YIEHTYRKGVKIDKTDYMVGSYGPRAEEYFLTPVEEAPKGMLARGSYSIKSRFTDDDKTDHLSWE
WNLTIKKDWK

>d1ajw_b.1.1.5 (-) Rho GDP-dissociation inhibitor 1, RhoGDI {Cow (Bos taurus)}
AVSADPNVNVVVTRTLVLCSTAPGPLELDLTGDLESFKKQSFVLKEGVEYRIKISFRVNREIVSGMKY
IQHTYRKGVKIDKTDYMVGSYGPRAEEYFLTPMEEAPKGMLARGSYNIKSRTDDDRTDHLSWE
WNLTIKKEWKD

>d1doab_b.1.1.5 (B:) Rho GDP-dissociation inhibitor 1, RhoGDI {Cow (Bos taurus)}
EPTAEQLAQIAAENEDEHSVNYKPPAQKSIQEIQLDKDDESLRKYKEALLGRVAVSADPNVNVV
VTRTLVLCSTAPGPLELDLTGDLESFKKQSFVLKEGVEYRIKISFRVNREIVSGMKYIQHTYRKGVKID
KTDYMVGSYGPRAEEYFLTPMEEAPKGMLARGSYNIKSRTDDDRTDHLSWEWNLTIKKEWKD

>d1ayra2_b.1.1.5 (A:183-368) Arrestin {Cow (Bos taurus), visual arrestin}
DMGQPRAEASWQFFMSDKPLRLAVLSKEIYYHGEPVTVAVTNSTTEKTVKKIKVLVEQVTNVVL
YSSDYIYKTVAAEEAQEKVPPNSSLTKTTLVPLLANNRERRGIALDGKIKHEDTNLASSTIIEGIDKT
VMGILVSYQIKVKLTVSGLLGELTSSEVATEVPPFRLMHPQPDPDTAKA

>d1cf1a1_b.1.1.5 (A:10-182) Arrestin {Cow (Bos taurus), visual arrestin}
HVIFKKISRDKSVTIYLGKRDYIDHVERVEPVDGVLVDPELVKGRVYVSLTCAFRYQEDIDVMGLS
FRRDLYFSQVQVFPVVGASGATTRLQESLIKKLGANTYPFLFTFPDYLPDQVQVGVKSCGVD
FEIKAFATHSTDVEEDKIPKSSVRLIRKQVHAPR

>d1cf1a2_b.1.1.5 (A:183-393) Arrestin {Cow (Bos taurus), visual arrestin}
DMGQPRAEASWQFFMSDKPLRLAVLSKEIYYHGEPVTVAVTNSTTEKTVKKIKVLVEQVTNVVL
YSSDYIYKTVAAEEAQEKVPPNSSLTKTTLVPLLANNRERRGIALDGKIKHEDTNLASSTIIEGIDKT
VMGILVSYQIKVKLTVSGLLGELTSSEVATEVPPFRLMHPQPDPDTAKESFQDENFVFEEFARQNLKD
AGEYKE

>d1g4ma1_b.1.1.5 (A:5-175) Arrestin {Cow (Bos taurus), beta-arrestin 1}
GTRVFKKASPNGLTVYLGKRDYIDHVERVEPVDGVLVDPEYKERRVYVTLTCAFRYQREDLDVL
GLTFRKDLFVANVQSFPPAPEDKKPLTRLQERLIKLGEGHAYPFTFEIPPNLPCSVTLQPGPEDTGKA
CGVDYEVKAFCAENLEEKIHKRNSVRLVIRKQVYAP

>d1g4ma2_b.1.1.5 (A:176-393) Arrestin {Cow (Bos taurus), beta-arrestin 1}
ERPGPQPTAETTRQFLMSDKPLHLEASLDKEIYYHGEPISVNVHVTNNTNKTVKKIKISVRQYADICL
FNTAQYKCPVAMEEADDTVAPSSTFCKVYTLTPFLANNREKRLALDGKIKHEDTNLASSTLLREGA

NREILGIIVSYKVKVVLVSRGGLLGDASSDVAVELPFTLMHPKPKEEPPHREVPEHETPVDTNLIE
LDTNDDDIVFEDFAR
>d1a02n1 b.1.1.5 (N:577-678) Transcription factor NFATC, C-terminal domain {Human
(Homo sapiens)}
LPMVERQDTSCLVYGGQQMILTGQNFTSESKVVFTEKTTDGQQIWEMEATVDKDKSQPNMLFVEI
PEYRNKHIRTVPKVNIFYVINGKRKRKRSQPQHFTYHPV
>d1imhc1 b.1.1.5 (C:368-468) Transcription factor TONEBP, C-terminal domain {Human
(Homo sapiens)}
VPEILKKSLSHSCSVKGEVFLIGKNFLKGTQVIFQENVSDENSWKSEAEIDMELFHQNHLIVKVPY
HDQHTLPVSVGIYVVTNAGRSHDVQPFTYTPD
>d1bfs_ b.1.1.5 (-) p50 subunit of NF-kappa B transcription factor, C-terminal domain
{Mouse (Mus musculus)}
ASNLKIVRMDRTAGCVTGGEEIYLLCDKVQKDDIQIRFYEEEEENGGVWEGFGDFSPDTHVHRQFAIVF
KTPKYKDVNITKPASVFLVQLRRKSDLETSEPKPFLYYPE
>d1a3qa1 b.1.1.5 (A:227-327) p52 subunit of NF-kappa B (NFkB), C-terminal domain
{Human (Homo sapiens)}
NLKISRMDKTAGSVRGGDEVYLLCDKVQKDDIEVRFYEDDENGWQAFGDFSPDTHVHKQYVIVFRTF
PYHKMKIERPVTVFLQLKRKRGGDVSDSKQFTYYP
>d1bfta_ b.1.1.5 (A:) p65 subunit of NF-kappa B (NFkB), C-terminal domain {Mouse (Mus
musculus)}
TAEIKICRVNRNSGSLGGDEIFLLCDKVQKEDIEVYFTGPGWEARGSFQADVHRQVAIVFRTPPYA
DPSLQAPVRVSMQLRRPSDRELSEPMFQYLPD
>d1ikna1 b.1.1.5 (A:192-303) p65 subunit of NF-kappa B (NFkB), C-terminal domain
{Mouse (Mus musculus)}
AELKICRVNRNSGSLGGDEIFLLCDKVQKEDIEVYFTGPGWEARGSFQADVHRQVAIVFRTPPYAD
PSLQAPVRVSMQLRRPSDRELSEPMFQYLPDTPDRHRIEEKRK
>d1nfia1 b.1.1.5 (A:190-314) p65 subunit of NF-kappa B (NFkB), C-terminal domain
{Human (Homo sapiens)}
NTAELKICRVNRNSGSLGGDEIFLLCDKVQKEDIEVYFTGPGWEARGSFQADVHRQVAIVFRTPPY
ADPSLQAPVRVSMQLRRPSDRELSEPMFQYLPDTPDRHRIEEKRKRTYETFKSIMK
>d1ahm_ b.1.1.5 (-) Major mite allergen {House-dust mite (Dermatophagoides farinae), Der
f 2}
DQVDVKDCANNEIKKVMVDGCHGSDPCIHRGKPFLEALFDANQNTKTAKIEIKASLDGLEIDVPGI
DTNACHFVKCPLVKGQYDIKYTWNVPKIAPKSENVVTVKLGDNGLACAIATHGKIRD
>d1a9v_ b.1.1.5 (-) Major mite allergen {House-dust mite (Dermatophagoides
pteronyssinus), Der p 2}
SQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNTKTAKIEIKASIDGLEVDVPGID
PNACHYMKCPLVKGQYDIKYTWNVPKIAPKSENVVTVKVMGDDGLACAIATHAKIRD
>d1soxa1 b.1.1.5 (A:344-466) Sulfite oxidase, C-terminal domain {Chicken (Gallus gallus)}
ELPVQSAVTQPRGAAVPPGELTVKGYAWSGGREVVVDVSLDGGRTWKVARLMGDKAPPRAW
AWALWELTVPEAGTELEIVCKAVDSSYVQPDVAPIWNLRGVLSTAWHRVRSVQD
>d1cvra1 b.1.1.5 (A:351-432) Gingipain R (RgpB), C-terminal domain {Porphyromonas
gingivalis}
PTEMQVTAPANISASAQTFEVACDYNGAIATLSDDGDMVGTAVKDGKAIKLNESIADETNLTLTVVG

YNKVTVIKDVKVE

>d1h6ta1 b.1.1.6 (A:241-321) Internalin B {*Listeria monocytogenes*}

ECLNKPINHQSNNLVVPNTVKNTDGLVTPPEIISDDGDYKPNVVKWHLPEFTNEVSFIFYQPVTIGKAK
ARFHGRVTQPLKE

>d1h6ua1 b.1.1.6 (A:263-343) Internalin H {*Listeria monocytogenes*}

TITNQPVFYNNLVVPNVVKGPSGAPIAPATISDNGTYASPNLTWNLTFSINNVSYTFNQSVTFKNTT
VPFSGTVTQPLTE

>d1ehxa_ b.1.1.6 (A:) Cellulosomal scaffoldin protein CipC, module x2.1 {*Clostridium
cellulolyticum*}

MQDPTINPTSISAKAGSFADTKITLTPNGNTFNGISELQSSQYTKGTNEVTLLASYLNTLPENTTKTLT
FDFGVGTKNPKLTITVLPKDIPGLE

>d1im3d_ b.1.1.6 (D:) Cytomegalovirus protein US2 {*Human cytomegalovirus*}

PWFQIEDNRCYIDNGKLFARGSVGNMSRFVDFPKADYGGVGENLYVHADDVEFVPGESLKWNVNRN
LDVMPIFETLALRLVLQGDVIWLRCVPEL

>d1jjua3 b.1.1.6 (A:274-351) Quinohemoprotein amine dehydrogenase A chain, domains 4
and 5 {*Paracoccus denitrificans*}

AAPQVLAVAPARLKIGEETQLRVAGTGLGSDLTLPPEGVAGSVESAGNGVTVLKLTATGTPGPVSLELGG
QKVDLVAYD

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

RPDRISIVPDLTIARIGGNGGPIPKVPAQFEAMGWLNGPDGQPGTGDDIALGAFPASWATDNFDEEA
EKMQDAKYAGSIDDTGLFTPAEAGPNPERPMQTNNAGNLKVIATVDAEGEPLSAEAHLYATVQRFV
DAPIR

>d1jmx3 b.1.1.6 (A:282-363) Quinohemoprotein amine dehydrogenase A chain, domains 4
and 5 {*Pseudomonas putida*}

GKARLLAVQPAFIKAGGESEITLVGSLGAGKPDLAGVEVTEVLEQTPTLVRLKARAAADAKPGQREV
AVGTLKGVNLAVYD

>d1jmx4 b.1.1.6 (A:364-494) Quinohemoprotein amine dehydrogenase A chain, domains 4
and 5 {*Pseudomonas putida*}

KVEEVKVVPAFSIARIGENGASVPKVQGRFEAEAWGKDANGQPLRIGYLPASWKVEPFNERAVEDE
DVKFAGKMQADGVFVPGGAGPNPERKMMTNAGNLKVIATLADGGQTGEGHMIVTVQRWNNPPL
P

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

SGTTNTVAAYNLTWKSTNFKTILEWEPKPVNQVYTVQISTKSGDWKSKCFYTTDTECDLTDEIVKDV
KQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLET

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

NLGQPTIQSFEQVGTKVNVTVEDERTLVRRNNTFLSLRDVFGKDLIYTLYYWKSSSQEKGEFRSGKK
TAKTNTNEFLIDVDKGENYCFVSVQAVIPSRTVNRKSTDSPVECMG

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

TVAAYNLTWKSTNFKTILEWEPKPVNQVYTVQISTKSGDWKSKCFYTTDTECDLTDEIVKDVKQTYL
ARVFSYPAXEPLYENSPEFTPYLET

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

TGRAYNLTWKSTNFKTILEWEPKSIDHVYTVQISTRLENWWSKFLTAETECDLTDEVVKDVGQTY
MARVLSYPARNGNTTGFPEEPPFRNSPEFTPYLDTNL

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

GQPTIQSFEQVGTGLNVTVQDARTLVRRNGTFLSLRAVFGKDLNYTLYYWRASSTGKKTATTNTNEF
LIDVDKGENYCFSVQAVIPSRKRKQRSPELTECT

>d1fna_ b.1.2.1 (-) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

RDLEVVAATPTSLISWDAPAVTVRYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVDYITIVYA
VTGRGDPASSKPISINYRTEI

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

PLSPPTNLHLEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVVHADQSSCTFDNLSP
GLEYNVSVYTVKDDKESVPISDIIPA

>d1fnf_2 b.1.2.1 (1236-1326) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

VPPPTDLRFTNIGPDTMRVTWAPPSIDLTNFLVRYSPVKNEEDVAELSPSDNAVVLNLLPGTEY
VVSVSSVYEQHESTPLRGRQKTG

>d1fnf_3 b.1.2.1 (1327-1415) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

LDSPTGIDFSDITANSFTVHVIAPRATITGYRIRHHPEHFSGRPREDRVPHSRNSITLNLTPGTEYV
SIVALNGREESPLLIQQST

>d1fnha1 b.1.2.1 (A:3-92) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

PAPTDLKFTQVTPSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSSSVVSGLMVATKYE
VSVYALKDTLTSRPAQGVVTTLE

>d1fnha2 b.1.2.1 (A:93-182) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

NVSPRRARVTDATETTITISWRKTETITGFQVDAVPANGQTPIQRTIKPDVRSYTTITGLQPGTDYKI
YLYTLNDNARSSPVVIDASTA

>d1fnha3 b.1.2.1 (A:183-271) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

IDAPSNLRFATTPNSLLVSWQPPRARITGYIIRHAEHSGRPREVPRPRPGVTEATITGLEPGTEYTIY
VIALKNNQKSEPLIGRKKKT

>d1j8ka_ b.1.2.1 (A:) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

NIDRPKGLAFTDQVDSIKIAWESPQGQVSRYRVYSSPEDGIHELFPAPDGEEDTAELQGLRPGSEY
TVSVVALHDDMESQPLIGTQSTAIPA

>d2fnba_ b.1.2.1 (A:) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

MRGSEVPQLTDLDFVDITDSSIGLRWTPLNSSTIIGYRITVVAAGEGIPFEDFVDSVGYTITVGLLEPGI
DYDISVITLINGGESAPTTLTQQT

>d2mfn_1 b.1.2.1 (1-92) Fibronectin, different Fn3 modules {Mouse (Mus musculus)}

GLDSPTGFDSSDITANSFTVHVVAPRAPITGYIIRHAEHSGRPRQRDRVPPSRNSITLNLNPGTEY
VVSIIAVNGREESPLLIQQATVS

>d2mfn_2 b.1.2.1 (93-184) Fibronectin, different Fn3 modules {Mouse (Mus musculus)}

DIPRDLEVIASPTSLISWEPPAVSVRYRITYGETGGNSPVQEFTVPGSKSTATINNIKPGADYTITLY
AVTGRGDPASSKPVSYNYKT

>d1qr4a1 b.1.2.1 (A:1-87) Tenascin {Chicken (Gallus gallus)}

DNPKDLEVSDPTETTLRWRPVAKFDRYRLTYVSPSGKKNEMEIPVDSTSFILRGLDAGTEYTISL
VAEKGRHKSPTTIKGSTV

>d1qr4a2 b.1.2.1 (A:88-175) Tenascin {Chicken (Gallus gallus)}
VGSPKGISFSDITENSATVSWTPPRSRSVDSYRVSYVPITGGTPNVVTVDGSKTRTKLVKLVPGVDYNV
NIISVKGFESEEPISGILKT

>d1ten_ b.1.2.1 (-) Tenascin {Human (Homo sapiens)}
RLDAPSQIEVKDVTDTTALITWFKPLAEIDGIELTYGIKDVPGDRTTIDLTEENQYSIGNLKPDT EYE
VSLISRRGDMSSNPAKETFTT

>d1cfb_1 b.1.2.1 (610-709) Neuroglian, two amino proximal Fn3 repeats {Drosophila
melanogaster}
IVQDVPNAPKLTGITCQADKAEIHWEQQGDNRSPI LH YTIQFNTSFTPASWDAAYEKVPNTDSSFVV
QMSPWANYTFRVIAFNKIGASPPSAHSDSCTTQ

>d1cfb_2 b.1.2.1 (710-814) Neuroglian, two amino proximal Fn3 repeats {Drosophila
melanogaster}
PDVPFKNPDNVVVGQGT EPNLVISWTPMPEIEHNAPNFHYVSWKRDIPAAA WENNNIFDWRQN
NIVIADQPTFVKYLIKVVAINDRGESNVAAEEVVGYSGEDR

>d1qg3a1 b.1.2.1 (A:1126-1217) Integlin beta-4 subunit {Human (Homo sapiens)}
DLGAPQNPNAKAAGSRKIHFNLPPSGKPMGYRVKYWIQGDSESEAHLLDSKVPSVELTNLYPYCD
YEMKVCAYGAQGEGPYSSLVSCRTHQ

>d1qg3a2 b.1.2.1 (A:1218-1320) Integlin beta-4 subunit {Human (Homo sapiens)}
EVPSEPGRLAFNVVSSVTQLSWAEP AETNGEITAYEVCYGLVNDNRP IGP MKKVLVDNPKNRMLL
IENLRESQPYRYTVKARNGAGWGP EREAIINLATQP

>d1axib1 b.1.2.1 (B:32-130) Growth hormone receptor {Human (Homo sapiens)}
EPKFTKCRSPERETF SCHWTDEVHHGTKNEGPIQLFYTRRNTQEWTQE WKECPDYVSAGENSCYF
NSSFTSIAIPYCIKLT SNGGTVDEKCF SVDEIVQ

>d1axib2 b.1.2.1 (B:131-236) Growth hormone receptor {Human (Homo sapiens)}
PDPPIALNWTL LNVS LTGIHADIQVRWEAPRNADIQKGWMVLEYELQYKEVNETKWKMMDPILTT
SVPVYSLKVDKEYEVRVRSKQRNSGNYGEFSEVLYVTLPQM

>d1eerb1 b.1.2.1 (B:8-116) Erythropoietin (EPO) receptor {Human (Homo sapiens)}
DPKFESKAALLAARGPEELLCF TERLEDLVCFWEEAASAGVGP GQYSFSYQLEDEPWKLCRLHQAPT
ARGAVRFWCSLPTADTSSFVPLELRVTAASGAPRYHRVIHIN

>d1eerb2 b.1.2.1 (B:117-220) Erythropoietin (EPO) receptor {Human (Homo sapiens)}
EVLVLLDAPVGLVARLADESGHVLRWLPPPETPMTSHIRYEVDVSAGQGAGSVQRVEILEGRTECVL
SNLRGRTRYTF AVRARMAEPSFGGF WSEWSEPVSLLT

>d1bp3b1 b.1.2.1 (B:202-300) Prolactin receptor {Human (Homo sapiens)}
LPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNYS LTYHREGETLMHECPDYITGGPNSCHFGKQ
YTSMWRTYIMMVNATNQMGSSFSDELYVDVTYI

>d1bp3b2 b.1.2.1 (B:301-404) Prolactin receptor {Human (Homo sapiens)}
VQPDPPLELAVEVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAAEWEIH FAGQQTEF
KILSLHPGQKYL VQRCKPDHGYWSAWSPATFIQIPS

>d1f6fb1 b.1.2.1 (B:5-100) Prolactin receptor {Rat (Rattus norvegicus)}
GKPEIHKCRSPDKETFTCWWNPGTDGGLPTNYS LYSKEGEKTTYECPDYKTS GPNSCFFSKQYTSI
WKIYIITVNATNQMGSSSDPLYVDVTYI

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

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

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

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

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

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

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

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

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

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

>d1fyhb2 b.1.2.1 (B:110-223) Interferon-gamma receptor alpha chain {Human (Homo sapiens)}
IGPPKLDIRKEEQIMIDIFHPSVFNVDGEQVDYDPETTCYIRVYNVYVRMNGSEIQYKILTQKEDD
CDEIQCQLAIPVSSLNSQYCVSAEGLVHVWGVTTTEKSKEVCITIFN

>d1bqua1 b.1.2.1 (A:5-99) Cytokine receptor gp130 cytokine-binding domains {Human (Homo sapiens)}
GLPPEKPKNLSCIVNEGKKMRCEWDGGRETHLETNFTLKSEWATHKFKADCKAKRDTPTSCTVDYS
TVYFVNIEVWVEAENALGKVTSDHINFDPV

>d1bqua2 b.1.2.1 (A:100-214) Cytokine receptor gp130 cytokine-binding domains {Human (Homo sapiens)}

YKVKPNPPHNLSVINSEELSSILKLTWTNPSIKSVIILKYNIQYRTKDASTWSQIPPEDTASTRSSFTVQ
DLKPFTEYVFRIRCMKEDGKGYWSDWSEEASGITYEDRPSKEPSF
>d1i1ra1 b.1.2.1 (A:2-101) Cytokine receptor gp130 cytokine-binding domains {Human
(Homo sapiens)}
LLDPCGYISPESPVVQLHSNFTAVCVLKEKCMDYFHVNANYIVWKTNHFTIPKEQYTIINRTASSVTF
TDIASLNIQLTCNLTFGQLEQNVYGITIISG
>d1j7vr1 b.1.2.1 (R:2-100) Interleukin-10 receptor 1, IL-10R1 {Human (Homo sapiens)}
GTELPSPPSVWFEEFFHHILHWTPIPQQSESTCYEVALLRYGIESWNSISQCSQTLSDYDLTAVTLDL
HSNGYRARVRAVDGSRHSQWTVTNTRFSVD
>d1j7vr2 b.1.2.1 (R:101-206) Interleukin-10 receptor 1, IL-10R1 {Human (Homo sapiens)}
EVTLTGVSVNLEIHNGFILGKIQLPRPKMAPAQDTYESIFSHFREYEIAIRKVPQGQFTFTHKKVKHEQF
SLLTSGEVGEFCVQVKPSVASRSNKGMSKEECISLT
>d1bpv__ b.1.2.1 (-) Type I titin module {Human (Homo sapiens)}
SPIDPPGKPVPLNITRHTVTLKWAKPEYTGFKITSYIVEKRDLPNRGLKANFNSILENEFTVSGLT
EDAAYEFRVIAKNAAGAISPPSEPSDAITCRDDVEA
>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)}
GIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLS
AERVRGDNKEYEYSVEQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDII
>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)}
KPDPPKNLQLKPLKNSRQVEVSWEYPTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVI
CRKNASISVRAQDRYSSSWSEWASVPCS
>d1b4ra_ b.1.3.1 (A:) Polycystein-1, PKD-1 {Human (Homo sapiens)}
ATLVGPHGPLASGQLAAFHIAAPLPTATRWDGFGSAEVDAAAGPAASHRYVLPGRYHVTAVLALGA
GSALLGTDVQVEA
>d1jz8a1 b.1.4.1 (A:220-333) beta-Galactosidase, domains 2 and 4 {Escherichia coli}
TQISDFHVATRFDNDFSRAVLEAEVQMCCELRDYLRVTVSLWQGETQVASGTAPFGGEIIDERGGYA
DRVTLRLNVENPKLWSAEIPNLYRAVVELHTADGTLIEAEACDVGFR
>d1jz8a2 b.1.4.1 (A:626-730) beta-Galactosidase, domains 2 and 4 {Escherichia coli}
FFQFRLSGQTIEVTSEYLFHRSDNELLHWMVALDGKPLASGEVPLDVAPQGKQLIELPELPQESAG
QLWLTVRVVQPNATAWSEAGHISAWQQWRLAENLSVTL
>d1bhga1 b.1.4.1 (A:226-328) beta-Glucuronidase {Human (Homo sapiens)}
TYIDDITVTTVEQDGLVNYQISVKGSNLFKLEVRLDAENKVVANGTGTQGQLKVPVSLWVWPYL
MHERPAYLSLEVQLTAQTSGLPVSDFYTLPGVIRT
>d1f13a2 b.1.5.1 (A:516-627) Transglutaminase, two C-terminal domains {Human (Homo
sapiens)}
SNVDMDFEVENAVLGKDFKLSITFRNNSHNRYTITAYLSANITFYTGVPKAEFKKETFDTVLEPLSFK
KEAVLIQAGEYMGQLLEQASLHFFVTARINETRDVLAKQKSTVL
>d1f13a3 b.1.5.1 (A:628-728) Transglutaminase, two C-terminal domains {Human (Homo
sapiens)}
TIPEIIIKVRGTQVVGSDMTVTVEFTNPLKETLRNVVHLDGPGVTRPMKKMFREIRPNSTVQWEE
VCRPWVSGHRKLIASMSDSL RHVYGELDVQIQR
>d1g0da2 b.1.5.1 (A:472-583) Transglutaminase, two C-terminal domains {Red sea bream

(Chrysophrys major)}
 RLQLSIKHAQPVFGTDFDVFIVEVKNEGGRDAHAQLTMLAMAVTYNSLRRGECQRKTISVTVPAHKA
 HKEVMRLHYDDYVRCVSEHHLIRVKALLDAPGENGPIMTVANIPLS
 >d1g0da3 b.1.5.1 (A:584-684) Transglutaminase, two C-terminal domains {Red sea bream
 (Chrysophrys major)}
 TPELLVQVPGKAVVWEPLTAYVSFTNPLPVPLKGGVFTLEGAGLLSATQIHVNGAVAPSGKVSVKLSF
 SPMRTGVRKLLVDFDSDRLKDVKGVTTVVVHKK
 >d1ncia_ b.1.6.1 (A:) N-cadherin (neural) {Mouse (Mus musculus)}
 GSDWVIPPINLPENSRRGPFQELVRIRSGRDKNLSLRYSVTGPADQPPTGIFIINPISGQLSVTKPLDR
 ELIARFHLRAHAVDINGNQVENPIDIVINVID
 >d1ncia2 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)}
 VIPPISCPENEKGEFKNLVQIKSNRDKETKVFYSITGQADKPPVGVFIERETGWLKVTQPLDREAI
 AKYILYSHAVSSNGEAVEDPMEIVITVTDQ
 >d1edha2 b.1.6.1 (A:102-213) E-cadherin (epithelial) {Mouse (Mus musculus)}
 NDNRPEFTQEVFEGSVAEGAVPGTSVMKVSATDADDDVNTYNAAIAYTIVSQDPELPHKNMFTVNR
 DTGVISVLTSGLDRESYPTYTLVVQAADLQGEGLSTTAKAVITVKD
 >d2mcm_ b.1.7.1 (-) Macromycin {Streptomyces macromomyceticus}
 APGVTVPATGLSNGQTVTVSATGLTPGTVYHVQCAVVEPGVIGCDATTSTDVTADAAGKITAQLKV
 HSSFQAVVGADGTPWGTVNCKVVSCSAGLSDSGEGAAQAITFA
 >d1noa_ b.1.7.1 (-) Neocarzinostatin {Streptomyces carzinostaticus}
 AAPTATVTPSSGLSDGTVVKVAGAGLQAGTAYDVGQCAWVDTGVLACNPADFSSTADANGSASTSL
 TVRRSFEGLFDGTRWGTVDCTTAACQVGLSDAAGNGPEGVAISFN
 >d1acx_ b.1.7.1 (-) Actinoxanthin {Actinomyces globisporus, number 1131}
 APAFSVSPASGSDGQSVSVSVAAGETYYIAQCAPVGGQDACNPATATSFTTDSASGAASFVTRKSY
 AGQTPSGTPVGSVDCATDACNLGAGNSGLNLGHVALTFG
 >d1hzka_ b.1.7.1 (A:) Antitumor antibiotic C-1027 apoprotein {Streptomyces globisporus}
 APAFSVSPASGLSDGQSVSVSVAAGETYYIAQCAPVGGQDACNPATATSFTTDSASGAASFVVRK
 SYTGSTPEGTPVGSVDCATAACNLGAGNSGLDLGHVALTFG
 >d1akp_ b.1.7.1 (-) Kedarcidin (apo form) {Actinomycete, strain L585-6}
 ASAAVSVSPATGLADGATVTVSASGFATSTSATALQCAILADGRGACNVAEFHDFSLSGGEGTTSVVVR
 RSFTGYVMPDGPEVGAVDCDTAPGGCEIVVGGNTGEYGNAAISFG
 >d1cbja_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Cow (Bos taurus)}
 ATKAVCVLKGDPVQGTIHFQAKGDTVVVVTGSITGLTEGDHGFHVHQFGDNTQGCTSAGPHFNPLSK
 KHGGPKDEERHVGLGNVTADKNGVAIVDIVDPLISLSGEYSIIGRTMNVVHEKPDDLGRGGNEESTK
 TGNAGSRLACGVIGIAK
 >d1azva_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Human (Homo sapiens)}
 ATKAVCVLKGDPVQGIINFEQKESNGPVKVGSIKRLTEGLHGFHVHEFGDNTAGCTSAGPHFNPL
 SRKHGGPKDEERHVGLGNVTADKDGADVSIEDSVISLSGDHCHIGRTLNVVHEKADDLKGKGGNEES
 TKTGNAGSRLACGVIGIAQ
 >d1xsoa_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {African clawed frog (Xenopus
 laevis)}

VKAVCVLAGSGDVKGVVHFEQQDEGAVSVEGKIEGLTDGLHGFHIVFGDNTNGCMSAGSHFNPEN
KNHGAPGDTDRHVGDLDGNVTAEGGVAQFKITDSLISLKGPNSSIIGRTAVVHEKADDLKGKGNDESLK
TGNAGGRLACGVIGYSP

>d1srda_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Spinach (Spinacia oleracea)}
ATKKAVAVLKGTSNVEGVVTLTQEDDGPTTVNVRISGLAPGKHGFHLHEFGDTTNGCMSTGPHFNP
DKKTHGAPEDVHRHAGDLGNIVANTDGVAEATIVDNQIPLTGPNSVVGRALVVHELEDDLKGGGHE
LSPTTGNAGGRLACGVVGLTPV

>d1jcv_ b.1.8.1 (-) Cu,Zn superoxide dismutase, SOD {Baker's yeast (Saccharomyces cerevisiae)}
VQAVAVLKGDAGVSGVVKFEQASESEPTTVSYEIAGNPNAERGFHIIHEFGDATNGCVSAGPHFNPFK
KTHGAPTDEVHRHVGDMGNVKTDENGVAKGSFKDSLKILIGPSTSVVGRSVVIHAGQDDLKGGDTEESL
KTGNAGPRPACGVIGLTN

>d1yaia_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Photobacterium leiognathi}
QDLTVKMTDLQTGKPVGTIELSQNKYGVVFTPELADLTPGMHGFHIIHQNGSCASSEKDGKVVLLGA
AGGHYDPEHTNKHGFPWTDDNHKGDLPALFVSANGLATNPVLAPRLTLKELKGHAIMIHAGGDNH
SDMPKALGGGGARVACGVIQ

>d1eso_ b.1.8.1 (-) Cu,Zn superoxide dismutase, SOD {Escherichia coli}
ASEKVEMNLVTSQGVGQSISVTTITETDKGLEFSPDLKALPPGEHGFHIIHAKGSCQPATKDGKASAAE
SAGGHLDPQNTGKHEGPEGAGHLGDLPALVVNNDGKATDAVIAPRLKSLDEIKDKALMVHVGGDN
MSDQPKPLGGGGERYACGVIK

>d1eqwa_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Salmonella typhimurium}
NTLTVKMNDALSSGTGENIGEITVSETPYGLLFTPHLNLTPGIHGFHVHTNPSCMPGMKDGKEVPA
LMAGGHLDPKTKHGLGPNYNDKHLGDLPLVNVNADGTATYPLLAPRLKSLSELKSHSLMIHKGGD
NYSKPAPLGGGGARFACGVIE

>d2apsa_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Actinobacillus pleuropneumoniae}
EKLVVQVQQLDPVKGNKDVGTVEITESAYGLVFTPHLHGLAQGLHGFHIIHQNPSCPEKEDGKLVAG
LGAGGHWDPKETKQHGYPWSDNAHLGDLPALFVEHDGSATNPVLAPRLKKLDEVKGHSLMIHEGG
DNHSDHPAPLGGGGPRMACGVIK

>d1ej8a_ b.1.8.1 (A:) Copper chaperone for superoxide dismutase, C-terminal domain
{Baker's yeast (Saccharomyces cerevisiae)}
SSAVAILETFQKYTIDQKKDTAVRGLARIVQVGENKTLFDITVNGVPEAGNYHASIHEKGDVSKGVES
TGKVVWHKFDEPIECFNESDLGKNLYSGKTFLSAPLPTWQLIGRSFVISKSLNHPENEPSSVKDYSFLG
VIAR

>d1jk9b1 b.1.8.1 (B:74-245) Copper chaperone for superoxide dismutase, C-terminal
domain {Baker's yeast (Saccharomyces cerevisiae)}
GKPNSSAVAILETFQKYTIDQKKDTAVRGLARIVQVGENKTLFDITVNGVPEAGNYHASIHEKGDVSK
GVESTGKVVWHKFDEPIECFNESDLGKNLYSGKTFLSAPLPTWQLIGRSFVISKSLNHPENEPSSVKDY
SFLGVIARSAGVWENNKQVCACTGKTVWEERKDALA

>d1do5a_ b.1.8.1 (A:) Copper chaperone for superoxide dismutase, C-terminal domain
{Human (Homo sapiens)}
QNLGAAVAILGGPGTVQGVVRFQLTPERCLIEGTIDGLEPGLHGLHVHGYGDLTNNCNSCGNHFNPN
DGASHGGPQSDRHRGDLGNVRADADGRAIFRMEDEQLKVWDVIGRSLIIDEGEDDLGRGGHPLSK
ITGNSGERLACGIIARSAGLF

>d1d7ca_ b.1.9.1 (A:) Cytochrome domain of cellobiose dehydrogenase {Fungus

(Phanerochaete chrysosporium)}
ESASQFTDPTTGFQFTGITDPVHDVTYGFFVFPPLATSGAQSTEFIGEVAPIASKWIGIALGGAMNND
LLLVAWANGNIVSSSTRWATGYVQPTAYTGTATLTLPETTINSTHWKWWVFRQCQCTEWNNGGID
VTSQGVLAFAFSNVAVDDPSDPQSTFSEHTDFGFFGIDYSTAHSANYQNYLNGDSG
>d1i8aa_b.1.9.2 (A:) Xylanase 10A {Thermotoga maritima}
MVATAKYGTPVIDGEIDEIWNTTEEIETKAVAMGSLDKNATAKVRVLWDENYLVLAIVKDPVLNKD
NSNPWEQDSVEIFIDENNHKTGYEDDDAQFRVNYMNEQTFGTGGSPARFKTAVKLIIEGGYIVEAAI
KWKTIKPTPNTVIGFNIQVNDANEKGQRVGIISWSDPTNNSWRDPSKFGNLRLIK
>d1qtsa1_b.1.10.1 (A:692-824) Alpa-adaptin AP2, N-terminal subdomain {Mouse (Mus
musculus)}
GSPGIRLGSSEDNFARFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFLNFTPTLICA
DDLQTNLNLQTKPVDPTVDGGAQVQVNVNIECISDFTEAPVLNIQFRYGGTFQNVSVKLPITLNK
>d1e42a1_b.1.10.1 (A:705-824) Beta2-adaptin AP2, N-terminal subdomain {Human (Homo
sapiens)}
GGYVAPKAVWLPVAVKAKGLEISGTFTHRQGHYMEMNFTNKALQHMTDFAIQFNKNSFGVIPSTPL
AIHTPLMPNQSIDVSLPLNTLGPVMKMEPLNQLQAVKNNIDVFYFSCLIPLNV
>d1jv2a1_b.1.15.1 (A:439-598) Thigh, calf-1 and calf-2 domains of integrin alpha {Human
(Homo sapiens)}
PVITVNAGLEVYPSILNQDNKTCSLPGTALKVSCFNVRFLKADGKGVLPKLNQVVELLLDKLKQKG
AIRRALFLYSRSPSHSKNMTISRGLMQCEELIAYLRDESEFRDKLTPITIFMEYRLDYRTAADTTGLQ
PILNQFTPANISRQAHILLDCGE
>d1jv2a2_b.1.15.1 (A:599-737) Thigh, calf-1 and calf-2 domains of integrin alpha {Human
(Homo sapiens)}
DNVCKPKLEVSVDSDQKKIYIGDDNPLTLIVKAQNQGEYAEELIVSIPLQADFIGVVRNNEALARLS
CAFKTENQTRQVVCDLGNPMKAGTQLLAGLRFVSHQQSEMDTSVKFDLQIQSSNLFDKVSPVVSHK
VDLA
>d1jv2a3_b.1.15.1 (A:738-956) Thigh, calf-1 and calf-2 domains of integrin alpha {Human
(Homo sapiens)}
VLAAVEIRGVSSPDHVFLPIPNWEHKENPETEEDVGPVVQHIYELRNNGPSSFSKAMLHLQWPYKY
NNNTLLYLHYDIDGPMNCTSDMEINPLRIKISSLQTTEKNDTVAGQGERDHLITKRDLALSEGDIHT
LGCGVAQCLKIVCQVGRDLRGKSAILYVKSLLWTETFMNKENQNHSLKSSASFNVIEFPYKNLPIE
DITNSTLVTTNVTWGIQ
>d1jv2b1_b.1.15.1 (B:55-106,B:355-434) Hybrid domain of integrin beta {Human (Homo
sapiens)}
EFPVSEARVLEDRPLSDKSGDSSQVTQVSPQRIALRLRPDDSKNFSIQVRQXVELEVRDLPEELSLSF
NATCLNNEVIPGLKSCMGLKIGDTVFSIEAKVRGCPQEKEKSFTIKPVGFKDSLIVQVTFDCD
>d1qpxa1_b.1.11.1 (A:1-124) Pilus chaperone PapD, N-domain {Escherichia coli}
AVSLDRTRAVFDGSEKSMTLDISNDNKQLPYLAQAWIENENQEKIITGPVIATPPVQRQLDPGAKSMV
RLSTTPDISKLPQDRESLFYFNLREIPRSEKANVVQIALCTKIKLFYRPAAIKTRP
>d1quna1_b.1.11.1 (A:1-121) Periplasmic chaperone FimC {Escherichia coli}
GVALGATRVYIPAGQKQVQLAVTNNDENSTYLIQSWVENADGVKDGRFIVTPPLFAMKGGKENTLRI
LDATNNQLPQDRESLFWMNVKAIPSMDSKLTENTLQLAISRKLYYRPAKLA
>d1mspa_b.1.11.2 (A:) Major sperm protein, alpha isoform (recombinant), ph 4.6 {Pig
roundworm (Ascaris suum)}

SVPPGDINTQPSQKIVFNAPYDDKHTYHIKITNAGGRRIGWAIKTTNMRRLSVDPPCGVLDPKKVL
MAVSCDTFNAATEDLNNDRITIEWTNTPDGAAKQFRREWFQGDGMVRRKNLPIEYNL
>d4kbp1 b.1.12.1 (A:9-120) Purple acid phosphatase, N-terminal domain {Kidney bean
(Phaseolus vulgaris)}
RDMPLDSDVFRVPPGYNAPQQVHITQGDLVGRAMIISWVTMDEPGSSAVRYWSEKNGRKRIAGK
MSTYRFFNYSSGFIHHTTIRKLYNTKYYYEVGLRNTTRRFSFITPP
>d1dqia_ b.1.13.1 (A:) Superoxide reductase (SOR) {Archaeon Pyrococcus furiosus}
MISSETIRSGDWKGEKHVPVIEYEREGELVKVKVQVGKEIPHPNTEHHIRYIELYFLPEGENFVYQVG
RVEFTAHGESVNGPNTSDVYTEPIAYFVLKTKKKGKLYALSVCNIHGLWENEVTL
>d1dfx_1 b.1.13.1 (37-125) Desulfoferrodoxin C-terminal domain {Desulfovibrio
desulfuricans}
VEGSTDGAMEKHVPVIEKVDGGYLIKVGSVPHMEEKHWIEWIELLADGRSYTKFLKPGDAPEAFF
AIDASKVTAREYCNLHGHWKAEN
>d1f00i1 b.1.14.1 (I:658-752) Intimin {Escherichia coli}
ASITEIKADKTTAVANGQDAITYTVKVMKGDKPVSNQEVTFTTTLGKLSNSTEKTDNNGYAKVTLTS
TTPGKSLVSARVSDVAVDVKAPEVEFFT
>d1f00i2 b.1.14.1 (I:753-841) Intimin {Escherichia coli}
TLTIDDGNIEIVGTGVKGLPTVWLQYGQVNLKASGGNGKYTWRSANPAIASVDASSGQVTLKEKGT
TTISVISSDNQTATYTIATPNS
>d1cwva1 b.1.14.1 (A:503-596) Invasin {Yersinia pseudotuberculosis}
LTLTAAVIGDGAPANGKTAITVEFTVADFEGKPLAGQEVVITTNNGALPNKITEKTDANGVARIALTN
TTDGVTVVTAEEVQQRQSVDFHFVKG
>d1cwva2 b.1.14.1 (A:597-692) Invasin {Yersinia pseudotuberculosis}
TIAADKSTLAAVPTSHADGLMASTITLELKDITYGDPQAGANVAFDTTLGNMGVITDHNDGTYSAPLT
STTLGVATVTVKVDGAAFSVPSVTVNFT
>d1cwva3 b.1.14.1 (A:693-795) Invasin {Yersinia pseudotuberculosis}
ADPIPDAGRSSFTVSTPDILADGTMSSTLSFVVDKNGHFISGMQGLSFTQNGVPPVSPITEQPDSYT
ATVVGNSVGDVTITPQVDTLILSTLQKKISLFPV
>d1cwva4 b.1.14.1 (A:796-886) Invasin {Yersinia pseudotuberculosis}
PTLTGILVNGQNFATDKGFPKTIFKNATFQLQMDNDVANNTQYEWSSFTPNVSVNDQGVVITYQT
YSEVAVTAKSKKFPYSVSYRFYP
>d1f0la1 b.2.1.1 (A:381-535) Diphtheria toxin, C-terminal domain {Corynebacterium
diphtheriae}
SPGHKTQPFLHDGYAVSWNTVEDSIIRTGFQGESGHDIKITAENTPLPIAGVLLPTIPGKLDVNKSKT
HISVNGRKIRMRCRAIDGDVTFCRPKSPVYVGNVHANLHVAFHRSSEKIHSNEISSDSIGVLGYQK
TVDHTKVNSKLSLFFEIKS
>d1exh_ b.2.2.1 (-) Exo-1,4-beta-D-glycanase (cellulase, xylanase), cellulose-binding domain,
CBD {Cellulomonas fimi}
ASSGPAGCQVLWGVNQWNTGFTANVTVKNTSSAPVDGWTLTFSFSPGQVQTQAWSSTVTQSGSAV
TVRNAPWNGSIPAGGTAQFGFNGSHTGTNAAPTAFSLNGTPCTVG
>d1e5ba_ b.2.2.1 (A:) Endo-1,4-beta xylanase D, xylan binding domain, XBD {Cellulomonas
fimi}
TGCSVTATRAEEWSDGFNVTYSVSGSSAWTVNLALNGSQTIQASWNANVTGSGSTRVTPNGSGNT
FGVTVMKNGSSTTPAATCAGS

>d1hejc_ b.2.2.1 (C:) Endo-1,4-beta xylanase D, xylan binding domain, XBD {Cellulomonas fimi}

TGSCSVSAVRGEEWADRFNVTYSVSGSSSWVVTLGLNGGQSVQSSWNAALTGSSGTVTARPNGSGNS
FGVTFYKNGSSATPGATCATG

>d1nbca_ b.2.2.2 (A:) Cellosomal scaffolding protein A, scaffoldin {Clostridium thermocellum}
NLKVEFYNSNPSTTTNSINPQFKVTNTGSSAIDLKTLRYYYTVDGQKDQTFWCDHAAIIGSNGSY
NGITSNVKGTFFVKMSSSTNNADTYLEISFTGGTLEPGAHVQIQGRFAKNDWSNYTQSNDFYFKSASQ
FVEWDQVTAYLNGVLVWGKEP

>d1g43a_ b.2.2.2 (A:) Cellosomal scaffolding protein A, scaffoldin {Clostridium cellulolyticum}

AGTGVVSVQFNNGSSPASSNSIYARFKVTNTSGSPINLADLKLRYYYTQDADKPLTFWCDHAGYMSG
SNYIDATSKVTGSFKAVSPAVTNADHYLEVALNSDAGSLPAGGSIEIQTRFARNDWSNFDQSNDFWSY
TAAGSYMDWQKISAFVGGTLAYGSTP

>d1tf4a2_ b.2.2.2 (A:461-605) Endo/exocellulase:cellobiose E-4, C-terminal domain
{Thermomonospora fusca}

PEIFVEAQINTPGTTTFTEIKAMIRNQSGWPARMLDKGTFRYWFTLDEGVDPADITVSSAYNQCATPE
DVHHVSGDLYVEIDCTGEKIFPGGQSEHREVVQFRIAGGPGWDPSNDWSFQIGNELAPAPYIVLY
DDGVPVWGTAP

>d1anu_ b.2.2.2 (-) Cohesin domain {Clostridium thermocellum, cellulosome, various
modules}

VVVEIGKVTGSVGTVEIPVYFRGVPSKGIANCDFVFRYDPNVLEIIGIDPGDIIVDPNPTKSFDTAIYP
DRKIIVFLFAEDSGTGAYAITKDGVF AKIRATVKSSAPGYITFDEVGGFADNDLVEQKVSFIDGGVNV

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

AVRIKVDTVNAKPGDTRIPVRFSGIPSKGIANCDFVYSYDPNVLEIIEIEPGELIVDPNPTKSFDTAVY
PDRKMIVFLFAEDSGTGAYAITEDGVFATIVAKVKSGAPNGLSVIKFVEVGGFANNDLVEQKTQFFDG
GVNVG

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

ASLKVTVTGANGKPGDVTVPVTFADVAKMKNVGT CNFYLGYDASLLEVVSVDAGPIVKNAAVNFSS
SASNGTISFLFDNTITDELITADGVFANIKFKLKSVTAKTTTPVTFKDGGAFDGTMSKIASVTKTNG
SVTIDPG

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

DQQLVDQLSQLKLNKMLDNRAGENGVDCAALGADWASCNRVLF TLSNDGQAIDGKDWVIYFHSP
RQTLRVDNDQFKIAHLTGDLKLEPTAKFSGFPAGKAVEIPVVAEYWQLFRNDFLPRWYATSGDAKP
KMLANTDTENLDQFVAPFTGDQWKRTKDDKNILMTPASRFV

>d1amx_ b.2.3.1 (-) Collagen-binding domain of adhesin {Staphylococcus aureus}

TSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVSKDITIKDQIQGGQQLDLSTLNINVTGTHSNYYS
GQSAITDFEKAFFPGSKITVDNTKNTIDVTIPQGYGSYNSFSINYKTKITNEQQKEFVNNSQAWYQEHG
KEEVNGKSFNHTVHN

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

FACKTANGTAIPIGGGSANVYVNLAPVVNVGQNLVVDLSTQIFCHNDYPETITDYVTLQRGSAYGGVL
SNFSGTVKYSYSSYPFTTSETPRVVYNSRTDKPWPVALYLPVSSAGGVAIKAGSLIAVLILRQTNNY
NSDDFQFVWNIYANNDVVVPT

>d1qunb2_b.2.3.2 (B:159-279) Mannose-specific adhesin FimH {Escherichia coli}
GGCDVSARDVTVTLDPDYPGSVPIPLTVYCAKSQNLGYLSGTTADAGNSIFTNTASFSPAQGVGVQLTR
NGTIIPANNTVSLGAVGTSASVSLGLTANYARTGGQVTAGNVQSIIGVTFVYQ

>d1pdkb_b.2.3.2 (B:) PapK pilus subunit {Escherichia coli}
LLDRPCHVSGDSL NKHVFKTRASRDFWYPPGRSPTE SFVIRLENCHATAV GKIVTLTFKGT EEAAL
PGHLKVTGVNAGRLGIALLDTDGSSLLKPGTSHNKGQGEKVTGNSLELPFGAYVVATPEALRTKSVV
PGDYEATATFELTYR

>d1j8ra_b.2.3.3 (A:) PapG adhesin receptor-binding domain {Escherichia coli}
WNNIVFYS LGDVNSYQGGNVVITQRPFITSWRPGIATVTWNQCNGPEFADGFWAYYREYIAWVVF
PKKVM TQNGYPLFIEVHNKGSWSEENTGDNDSYFFLKGYKWDERAFDAGNLCQKPGEITRLTEKF
DDIIFKVALPADLPLGDYSVKIPY TSGMQRHFASYLGARFKIPYNVAKTLPRENEMLFLFKNIGG

>d1edya_b.2.4.1 (A:) alpha-1-macroglobulin {Rat (Rattus norvegicus)}
EAPFTLKVNTLPLNFDKAEHHRKFQIHINVS YIGERPNSNMVIVDVKMVSGFIPVKPSVKKLQDQSN
IQRTEVNTNHVLIYIEKLTNQTMGFSFAVEQDIPVKNLKPAPVKVYDYYETDEFAIEEYSAPFSSDS

>d1bv8a_b.2.4.1 (A:) alpha-2-macroglobulin {Human (Homo sapiens)}
EEFPFALGVQTLPQTCD EPKAHTSFQISLSVSYTGSRASNAIVDVKMVSGFIPLKPTVKMLERSNH
VSRTEVSSNHVLIYLDKVSNTLSLFFTVLQDVPVRDLKPAIVKVYDYYETDEFAIAEYNAPCSKDLG
NA

>d1ayoa_b.2.4.1 (A:) alpha-2-macroglobulin {Cow (Bos taurus)}
EFPFALEVQTLPQTCDGPKAHTSFQISLSVSYIGSRPASNAIVDVKMVSGFIPLKPTVKMLERSNV
RTEVSNHVL IYLDKVTNETLTLTFTVLQDIPVRDLKPAIVKVYDYYETDEFAVAEYSAPCS

>d1ycsa_b.2.5.1 (A:) p53 tumor suppressor, DNA-binding domain {Human (Homo sapiens)}
VPSQKTYQGSYGFRLGFLHSGTAKSVTCTYSPALNKMFCQLAKTCPVQLWVDSTPPPGRTRVRA
MAIYKQSQHMTEVRRCPHHERCSDSDGLAPPQH LIRVEGNL RVEYLDDRNTFRHSVVVPYEPPEVGS
DCTTIHYNMCMNSSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPRDRRTEEE

>d1hu8a_b.2.5.1 (A:) p53 tumor suppressor, DNA-binding domain {Mouse (Mus musculus)}
TYQGNYG FHLGFLQSGTAKSVMCTYSPPLNKLFCQLAKTCPVQLWVSATPPAGSRVRAMAIYKKSQ
HMTEVRRCPHHERCSDGDGLAPPQH LIRVEGNLAPEYLED RQTFRHSVVVPYEPPEAGSEYTTIHY
K YMCNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVRVCACPRDRRTEEE

>d1a02n2_b.2.5.1 (N:399-576) Transcription factor NFATC, DNA-binding domain {Human (Homo sapiens)}
WPLSSQSGSYELRIEVQPKPHHRAHYETEGSRGAVKAPTGGHPVVQLHGYMENKPLGLQIFIGT
ADE RILKPHAFYQVHRITGKTVTTTSYEKIVGNTKVLEIPLPKNNMRATIDCAGILKLRNADIELR
KGET DIGRKNTRVRLVFRVHIPESGRIVSLQTASNPIECSQSAHE

>d1a66a_b.2.5.1 (A:) Transcription factor NFATC, DNA-binding domain {Human (Homo sapiens)}
MKDWQLPSHSGPYELRIEVQPKSHH RARYETEGSRGAVKASAGGHPIVQLHGYLENEPLMLQLFI
GTT ADDRLLRPHAFYQVHRITGKTVSTTSHEAILSNTKVLEIPLLPENSMRAVIDCAGILKLRN
SDIELRKG ETDIGRKNTRVRLVFRVHVPQPSGRTL SLQVASNPIECSQRS

>d1imhc2_b.2.5.1 (C:188-367) Transcription factor TONEBP, DNA-binding domain {Human (Homo sapiens)}
KKSPMLCGQYPVKSEGKELKIVVQPETQHRARYLTEGSRG SVKDRTQQGFPTVKLEGHNEPVVLQV
F VGNDSGRVKPHGFYQACRVTGRNTTPCKEVDIEGTTVIEVGLDPSNNMTLAVDCV GILKLRNAD
VEA RIGIAGSKKKSTRARLVFRVNIMRKDGSTLTLQTPSSPILCTQPAG

>d1nfka2 b.2.5.1 (A:39-250) p50 subunit of NF-kappa B (NFkB), N-terminal domain {Mouse (Mus musculus)}

GPYLQILEQPKQRGFRFRYVCEGPSHGGLPGASSEKNKKSYPQVKICNYVGPAAKVVIVQLVTNGKNIHL
HAHSLVGKHCEDGVCTVTAGPKDMVVGAFANLILHVTKKKVFETLEARMTEACIRGYNPGLLVHSD
LAYLQAEGGGDRQLTDREKEIIRQAAVQQTKEMDLSVVRLMFTAFLPDSTGSFTRRLEPVVSDAIYDS
KAPNASNLKI

>d1a3qa2 b.2.5.1 (A:37-226) p52 subunit of NF-kappa B (NFkB), N-terminal domain {Human (Homo sapiens)}

GPYLVIVEQPKQRGFRFRYVCEGPSHGGLPGASSEKGRKTYPTVKICNYEGPAKIEVDLVTHSDPPRA
HAHSLVGKQCSELGICAVSVGPKDMTAQFNLLGVLHVTKKNMMGTMIQKLQRQLRSRPQGLTEAE
QRELEQEAKELKKVMDLSIVRLRFSFAFLRSLPLKPVISQPIHDSKSPGAS

>d1ikna2 b.2.5.1 (A:19-191) p65 subunit of NF-kappa B (NFkB), N-terminal domain {Mouse (Mus musculus)}

PYVEIIEQPKQRGMFRFRYKCEGRSAGSIPGERSTDTTKTHPTIKINGYTGPGTVRISLVTKDPPHRPH
HELVGKDCRDGYEADLCPDRSIHSFQNLGIQCVKCRDLEQAISQRIQTNNNPFHVPIEEQRGDYDL
NAVRLCFQVTVRDPAGRPLLLTPVLSHPHIFDNRAPNT

>d1nfia2 b.2.5.1 (A:20-189) p65 subunit of NF-kappa B (NFkB), N-terminal domain {Human (Homo sapiens)}

YVEIIEQPKQRGMFRFRYKCEGRSAGSIPGERSTDTTKTHPTIKINGYTGPGTVRISLVTKDPPHRPH
HELVGKDCRDGFYEAELCPDRCIHSFQNLGIQCVKCRDLEQAISQRIQTNNNPFQVPIEEQRGDYDL
NAVRLCFQVTVRDPGRPLRLPPVLPHPHIFDNRAP

>d1bvoa_ b.2.5.1 (A:) Dorsal homologue Gambif1 {African malaria mosquito (Anopheles gambiae)}

PYVEITEQPHPKALFRYCEGRSAGSIPGVNTTAEQKTFPSIQVHGYRGRAVVVVSCVTKEGPEHKP
HPHNLVGKEGCKKGVCTVEINSTTMSYTFNNLGIQCVKCKDVEEALRLRQEIRVDPFRTGFGHAKEP
GSIDLNAVRLCFQVFLEGQQRGRFTEPLTPVSDIYDCK

>d1xbra_ b.2.5.1 (A:) T domain from Brachyury transcription factor {African clawed frog (Xenopus laevis)}

ELKVSLEERDLWTRFKELTNEMIVTKNGRRMFPVLKVSMGLDPNAMYTLLDFVAADNHRWKY
VNGEWPVPGGKPEPQAPSCVYIHPDSPNFGAHWMKDPVSFSKVKLTNKMNGGGQIMLNSLHKYEPR
IHIVRVGGTQRMITSHSFQVIAVTAYQNEEITALKIKHNPFAKAFDAKERN

>d1bf5a2 b.2.5.1 (A:317-568) STAT-1, DNA-binding domain {Human (Homo sapiens)}

FVVERQPCMPHQPRLVLTGTVQFTVKLRLLVKLQELNYNLKVKVLFDKDVNERNTVKGFRKFN
LGTHTKVMNMEESTNGSLAAEFRHLQLKEQKNAGTRTNEGPLIVTEELHLSLFSFETQLCQPGLVIDLE
TTSLPVVVISNVSQPLSGWASILWYNMLVAEPRNLSFFLTPPCARWAQLSEVLSWQFSSVTKRGLNV
DQLNMLGEKLLGPNASPDGLIPWTRFCKENINDKNFPFWLWIESILELIKHH

>d1bg1a2 b.2.5.1 (A:322-575) STAT3b {Mouse (Mus musculus)}

VVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPENYQLKIKVCIDKDSGDVAALRGRKFNILG
TNTKVMNMEESNNGSLSAEFKHLTLREQRGNGGRANCDASLIVTEELHLITFETEVYHQGLKIDLE
THSLPVVVISNICQMPNAWASILWYNMLTNNPKNVNFFTTPPIGTWDQVAEVLVSWQFSSVTKRGLS
IEQLTTLAEKLLGPGVNYSGCQITWAKFCKENMAGKGFVWVLDNIIDLKVKY

>d1e50q_ b.2.5.1 (Q:) Acute myeloid leukemia 1 protein (AML1), RUNT domain {Human (Homo sapiens)}

LVRTDSPNFLCSVLPHTHWRCNKTLPIAFKVVVALGDVPDGLTVTMAGNDENYSAELRNATAAMKNQ

VARFNDLRFVGRSGRGKSFTLTITVFTNPPQVATYHRAIKITVD
>d1h9da_ b.2.5.1 (A:) Acute myeloid leukemia 1 protein (AML1), RUNT domain {Human (Homo sapiens)}
VLADHPGELVRTDSPNFLCSVLPHTHWRCNKTLPIAFKVVVALGDVDPDGLVTVMAGNDENYSaelRN
ATAAMKNQVARFNDLRFVGRSGRGKSFTLTITVFTNPPQVATYHRAIKITVDGPREPRR
>d1hcz_1 b.2.6.1 (1-167,231-250) Cytochrome f, large domain {Turnip (Brassica rapa)}
YPIFAQQNYENPREATGRIVCANCHLASKPVDIEVPQAVLPDPTVFEAVVKIPYDMQLKQVLANGKKG
ALNVGAVLILPEGFELAPPDRISPEMKEKIGNLSFQNYRPNKKNILVIGPVPVPGQKYSEITFPILAPDPAT
NKDVHFLKYPIYVGGNRGRGQIYPDGSKSNXPVGGFGQDAEIVLQDPLR
>d1e2wa1 b.2.6.1 (A:1-168,A:233-251) Cytochrome f, large domain {Chlamydomonas reinhardtii}
YPVFAQQNYANPREANRIVCANCHLAQKAVEIEVPQAVLPDPTVFEAVIELPYDKQVKQVLANGKKG
DLNVGMVLILPEGFELAPPDRVPAEIKEKVGNYLYQPYSPKKNILVIGPVPVPGKQYSEMVPVILSPDP
AKNKNVSYLYPIYFGNRGRGQVYPDGKSNFXNVGGFGQAETEIVLQNPAPAR
>d1ci3m1 b.2.6.1 (M:1-169,M:232-249) Cytochrome f, large domain {Phormidium laminosum}
YPFWAQQNYANPREATGRIVCANCHLAAKPAEIEVPQAVLPDSVFKAVVKIPYDHSVQVQADGSKG
PLNVGAVLMLPEGFTIAPEDRIPEEMKEEVGPSYLFQPYADDKQNVLVGPLPGDEYEEIVFPVLSNP
PATNKSVAFGKYSIHLGANRGRGQIYPTGEKSNXNVGGFGQKDTEIVLQSPN
>d1i31a_ b.2.7.1 (A:) Second domain of Mu2 adaptin subunit (ap50) of ap2 adaptor {Rattus norvegicus}
IGWRREGIKYRRNELFLDVLESVNLLMSPQGQVLSAHVSGRVVMKSYLSGMPECKFGMNDKIVIEK
QGKGTADETSKSGKQSIADDCTFHQCVRLSKFDSERSISFIPPDGEFELMRYRTTKDIILPFRVIPLVR
EVGRTKLEVKVVIKSNFKPSLLAQKIEVRIPTPLNTSGVQVICMKGKAKYKASENAIVWKIKRMAGM
KESQISAEIELLPTNDKKKWARPPISMNFVFPFAPSGLKVRYLKVFEPLNYSDDHVIKWVRYIGRSG
IYETRC
>d1cgt_2 b.3.1.1 (580-684) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus circulans, different strains}
LTGDQVTVRFVNNASTTLGQNLVLTGNVAELGNWSTGTAIGPAFNQVIHQYPTWYYDVSVPAGKQ
LEFKFFKKNSTITWESGSNHTFTTPASGTATVTVNWQ
>d1kcl2 b.3.1.1 (A:582-686) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus circulans, different strains}
LSGDQVSVRFVNNATTALGQNVYLTGSVSELGNWDPKAIGPMYNQVVYQYPNWYYDVSVPAGKT
IEFKFLKQGSTVTWEGGSNHTFTAPSSGTATINVNWQP
>d1cyg_2 b.3.1.1 (575-680) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus stearothermophilus}
LTNDQVSVRFVNNATTNLGQNIYIVGNVYELGNWDTSKAIGPMFNQVVYSYPTWYIDVSVPEGKTI
EFKFIKKDSQGNVTWESGSNHVYTTPTNTTGKIIVDWQN
>d1qhoa2 b.3.1.1 (A:577-686) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus stearothermophilus, maltogenic alpha-amylase}
LSGTQTSVVFVKSAPPTNLGDKIYLTGNIPELGNWSTDTSGAVNNAQGPLLAPNYPDFVYVFSVPA
GKTIQFKFFIKRADGTIQWENGSNHVATTPTGATGNITVTWQN
>d1pama2 b.3.1.1 (A:583-686) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus sp., strain 1011}

TGDQVTVRFVINNATTALGQNVFLTGNVSELGNWDPNNAIGPMYNQVVYQYPTWYYDVSVPAGQTI
EFKFLKKQGSTVTWEGGANRTFTTPTSGTATVNVNWQP
>d1ciu_2 b.3.1.1 (579-683) Cyclodextrin glycosyltransferase, C-terminal domain
{Thermoanaerobacterium thermosulfurigenes, EM1}
LTGNQICVRFVNNASTVYGENVYLTGNVAELGNWDTSKAIGPMFNQVVYQYPTWYYDVSVPAGTT
IQFKFIKNGNTITWEGGSNHTYTPSSSTGTVIVNWQQ
>d1acz_ b.3.1.1 (-) Glucoamilase, granular starch-binding domain {Aspergillus niger}
CTTPTAVAVTFDLTATTTYGENIYLVGSISQLGDWETSDGIALSADKYTSSDPLWYVTVTLPAGESFEY
KFIRIESDDSVESDPNREYTPQACGTSTATVTDTR
>d1cqya_ b.3.1.1 (A:) beta-amylase {Bacillus cereus}
TPVMQTIIVKNVPTTIGDVTYITGNRAELGSWDTKQYPIQLYDSDSHSNDWRGNVVLPAERNIEFKAF
IKSKDGTVKSWQTIQQSWNPVPLKTTSTSSW
>d1h8la1 b.3.2.1 (A:305-383) Carboxypeptidase D, a regulatory domain {Crested duck
(Lophonetta specularioides)}
GIWGFVLDATDGRGILNATISVADINHPVTTYKGDYWRLLVQGTYKVTASARGYDPVTKTVEVDSK
GGVQVNFNLSRT
>d1vcbc_ b.3.3.1 (C:) VHL {Human (Homo sapiens)}
LRSVNSREPSQVIFCNRSPRVLPVWLNFDGEPQPYPTLPPGTGRRHSYRGHLWLFRDAGTHDGLL
VNQTELFVPSLNVGQPIFANITLPVYTLKERCLQVVRSLVKPENYRRLDIVRSLYEDLEDHPNVQKD
LERLTQE
>d1f86a_ b.3.4.1 (A:) Transthyretin (synonym: prealbumin) {Human (Homo sapiens)}
CPLMVKVLDAVRGSPAINVAVHVFRKAADDTWEPFASGKTSESGELHGLTTEEEFVEGIYKVEIDTKS
YWKALGISPFHEHAEVVFTANDSGPRRYTIAALLSPYSYSTMAVVTN
>d1ttba_ b.3.4.1 (A:) Transthyretin (synonym: prealbumin) {Human (Homo sapiens)}
GPTGTGESKCPMLMVKVLDAVRGSPAINVAVHVFRKAADDTWEPFASGKTSESGELHGLTTEEEFVEG
IYKVEIDTKSYWKALGISPFHEHAEVVFTANDSGPRRYTIATLLSPYSYSTTAVVTNPKE
>d1gkea_ b.3.4.1 (A:) Transthyretin (synonym: prealbumin) {Rat (Rattus norvegicus)}
SKCPLMVKVLDAVRGSPAVDVAVKVFKKTADGSWEPFASGKTAESGELHGLTTDEKFTEGVYRVELD
TKSYWKALGISPFHEYADEVVFTANDSGHRHYTIAALLSPYSYSTTAVVSNPQN
>d1tfpa_ b.3.4.1 (A:) Transthyretin (synonym: prealbumin) {Chicken (Gallus gallus)}
CPLMVKVLDAVRGSPAANVAVKVFKAADGTWQDFATGKTTEFGIEHELTTTEEQFVEGVYRVEFDT
SSYWKGLGLSPFHEYADVFTANDSGHRHYTIAALLSPFSYSTTAVVS
>d1d2oa1 b.3.5.1 (A:535-624) B repeat unit of collagen binding surface protein (cna)
{Staphylococcus aureus}
ETTSSIGEKVWDDKDNQDGKRPEKVSNNLLANGEKVKTLDVDTSETNWKYEFKDLPKYDEGKKIEY
TVTEDHVKDYYTTDINGTTITNKYTP
>d1d2oa2 b.3.5.1 (A:625-721) B repeat unit of collagen binding surface protein (cna)
{Staphylococcus aureus}
GETSATVTKNWDDNNNQDGKRPTEIKVELYQDGKATGKTAILNESNNWHTWTGLDEKAKGQQV
KYTVEELTKVKGYTTHVDNNDMGNLITTNKYTP
>d1dmha_ b.3.6.1 (A:) Catechol 1,2-dioxygenase {Acinetobacter calcoaceticus}
VKIFNTQDVQDFLRVASGLEQEGGNPRVKQIHRVLSPLYKAIEDLNITSDEYWAGVAYLNQLGANQE
AGLLSPGLGFDHYLDMRMDAEDAALGIENATPRITIEGPLYVAGAPESVGYARMDGSDPNGHTLILH
GTIFDADGKPLPNAKVEIWHANTKGFYSHFDPTGEQQAFNMRRSITDENGQYRVRTILPAGYGCPP

EGPTQQLLNQLGRHGHRPAHIHYFVSADGHRKLTTQINVAGDPYTYDDFAYATREGLVDDAVEHTDP
EAIKANDVEGPFAEMVFDLKLTRLVDGVDNQQVDRPRLAV

>d3pcca_ b.3.6.1 (A:) Protocatechuate-3,4-dioxygenase, alpha chain {Pseudomonas
aeruginosa}

PIELLPETPSQTAGPYVHIGLALAAAGNPTRDQEIWNRLAKPDAPGEHILLGQVYDGNHGLVDRDSF
LEVWQADANGEYQDAYNLENANFSFGRTATTFDAGEWTLHTVKPGVVNNAAGVPMAPHINISLFA
RGINIHLHTRLYFDDEAQAANAKCPVLNLIQQRRETLIAKRCEVDGKTAYRFDIRIQEGEGETVFFDF

>d1eo9a_ b.3.6.1 (A:) Protocatechuate-3,4-dioxygenase, alpha chain {Acinetobacter
calcoaceticus, adp1}

ELKETPSQTGGPYVHIGLLPKQANIEVFEHNLDNNLVQDNTQGQRIRLEGQVFDGLSLPLRDVLEIOW
QADTNGVYPSQADTQGGKQVDPNFLGWGRTGADFGTGFWSFNTIKPGAVPGRKGSTQAPHISLIIFAR
GINIGLHTRVYFDDEAEANAKDPVLNSIEWATRRQTLVAKREERDGEVVYRFDIRIQENETVFFDI

>d3pccm_ b.3.6.1 (M:) Protocatechuate-3,4-dioxygenase, beta chain {Pseudomonas
aeruginosa}

PAQDNSRFVIRDRNWHPKALTPDYKTSIARSPRQALVSIPQSISSETTGPNFSLGFGAHDHDLNLFN
NGGLPIGERIIVAGRVVDQYGKPPVNTLVEMWQANAGGRYRHKNDRYLAPLDPNFGGVRCLTDS
GYYSFRTIKPGYPWRNGPNDWRPAHIHFISGSPSIATKLITQLYFEGDPLIPMCPIVKSANPEAVQQ
LIAKLDMMNANPMDCLAYRFDIVLRGQRKTHFE

>d1eo9b_ b.3.6.1 (B:) Protocatechuate-3,4-dioxygenase, beta chain {Acinetobacter
calcoaceticus, adp1}

IIWGAYAQRNTEHPPAYAPGYKTSVLRSPKNALISIAETLSEVTAPHFSADKFGPKDNDLILNYAKDG
LPIGERVIVHGYVRDQFGRPVKNALVEVWQANASGRYRHPNDQYIGAMPNFGGCGRMLTDDNGY
YVFRTIKPGYPWRNRINEWRPAHIHFSLIADGWAQRLISQFYFEGDTLIDSCPILKTIPSEQRRALI
ALEDKSNFIEADSRCYRFDITLRGRRATYFENDLT

>d1c3ga1 b.4.1.1 (A:180-259) Heat shock protein 40 Sis1 {Baker's yeast (Saccharomyces
cerevisiae)}

ETVQVNLVPSLEDLFGVKKKSFKIGRKGPHGASEKTQIDIQLKPGWKAGTKITYKNQGDYNPQTGRR
KTLQFVIQEKSH

>d1c3ga2 b.4.1.1 (A:260-349) Heat shock protein 40 Sis1 {Baker's yeast (Saccharomyces
cerevisiae)}

NFKRDGDDLIYTLPLSFKESLLGFSKTIQTIDGRTLPLSRVQPVQPSQTSTYPGQGMPTPKNPSQRGN
LIVKYKVDYPISLNDKRAID

>d1hd8a1 b.105.1.1 (A:263-356) Penicillin-binding protein 5, C-terminal domain
{Escherichia coli}

FETVNPLKVGKEFASEPVWFGSDRASLGVDKDVYLTIPRGRMKDLKASYVLNSELHAPLQKNQV
VGTINFQLDGKTIEQRPLVVLQEIPEGN

>d1hoe_ b.5.1.1 (-) alpha-Amylase inhibitor tendamistat {Streptomyces tendae}

DTTVSEPAVSCVTLYQSWRYSQADNGCAETVTVKVVYEDDTEGLCYAVAPGQITTVGDGYIGSHGHA
RYLARCL

>d1aac_ b.6.1.1 (-) Amicyanin {Paracoccus denitrificans}

DKATIPSESPFAAAEVADGAIVVDAKMKYETPELVHVKVGDVTVTWINREAMPNHFVAGVLGEAA
LKGPMMKKEQAYSFTFTEAGTYDYHCTPHPFMRGKVVVE

>d1id2a_ b.6.1.1 (A:) Amicyanin {Paracoccus versutus (Thiobacillus versutus)}

QDKITVTSEKPVAAADVPADAVVVGIEKMKYLTPEVTIKAGETVYVWVNGEVMPHNVAFKKGIVGED

AFRGEMMTKDQAYAITFNEAGSYDYFCTPHPFMRGKVIVE

>d1plc_ b.6.1.1 (-) Plastocyanin {Poplar (*Populus nigra*), variant italica}

IDVLLGADDGSLAFVFPSEFSISPGEKIVFKNNAGFPHNIVFDEDSIPSGVDASKISMSEEDLLNAKGET
FEVALSNKGEYSFYCSPHQGAGMVGKVTVN

>d9pcy_ b.6.1.1 (-) Plastocyanin {French bean (*Phaseolus vulgaris*)}

LEVLLGSGDGLVFPSEFSVPSGKIVFKNNAGFPHNVVFEDEDEIPAGVDAVKISMPEEELLNAPGE
TYVVTLDTKGTYSFYCSPHQGAGMVGKVTVN

>d1pla_ b.6.1.1 (-) Plastocyanin {Parsley (*Petroselinum crispum*)}

AEVKLGSDDGGLVFPSSFTVAAGEKITFKNNAGFPHNIVFDEDEVPAVNAEKISQPEYLNAGAGETY
EVTLTEKGTYKFYCEPHAGAGMKGEVTVN

>d1ag6_ b.6.1.1 (-) Plastocyanin {Spinach (*Spinacia oleracea*)}

VEVLLGGDDGSLAFLPGDFSVASGEEIVFKNNAGFPHNVVFEDEDEIPSGVDAKISMSEEDLLNAPGE
TYKVTLTEKGTYKFYCSPHQGAGMVGKVTVN

>d1bypa_ b.6.1.1 (A:) Plastocyanin {White campion (*Silene pratensis*)}

AEVLLGSSDGLAFVPSDLSIASGEKITFKNNAGFPHNDLFDKKEVPAGVDVTKISMPEEDLLNAPGE
EYSVTLTEKGTYKFYCAPHAGAGMVGKVTVN

>d1iuz_ b.6.1.1 (-) Plastocyanin {Sea lettuce (*Ulva pertusa*)}

AQIVKLGDDGSLAFVPSKISVAAGEAIEFVNNAGFPHNIVFEDEDAVPAGVDADAISYDDYLNSKGET
VVRKLSTPGVYGVYCEPHAGAGMKMTITVQ

>d2plt_ b.6.1.1 (-) Plastocyanin {Green alga (*Chlamydomonas reinhardtii*)}

DATVKLGADSGALEFVPKTLTIKSGETVNFVNNAGFPHNIVFEDEDAIPSGVNADAISRDDYLNAPGET
YSVKLTAAGEYGYCEPHQAGMVGKIIVQ

>d7pcy_ b.6.1.1 (-) Plastocyanin {Green alga (*Enteromorpha prolifera*)}

AAIVKLGDDGSLAFVPPNITVGAGESIEFINNAGFPHNIVFEDEDAVPAGVDADAISAEDYLNSKGQT
VVRKLTPGTYGVCYCDPHSGAGMKMTITVQ

>d1kdj_ b.6.1.1 (-) Plastocyanin {Fern (*Adiantum capillus-veneris*)}

AKVEVGDEVGNFKFPDSITVSAGEAVEFTLVGETGHNIVFDIPAGAPGTVASELKAASMDENDLLSE
DEPSFKAKVSTPGTYTFYCTPHKSANMKGTLTVK

>d1nin_ b.6.1.1 (-) Plastocyanin {*Anabaena variabilis*}

ETYTVKLGSDKGLLVFEPKLTIKPGDVEFLNKNVPPHNVVFDAAALNPAKSADLAKSLSHKQLLMS
PGQSTSTTFPADAPAGEYTFYCEPHRGAGMVGKITVAG

>d1bawa_ b.6.1.1 (A:) Plastocyanin {Cyanobacterium (*Phormidium laminosum*)}

ETFTVKMGADSGLLQFEPANVTVHPGDTVKWVNNKLPPHNILFDDKQVPGASKELADKLSHSQLM
FSPGESYEITFSSDFPAGTYTYCAPHRGAGMVGKITVEG

>d1pcs_ b.6.1.1 (-) Plastocyanin {Cyanobacterium (*Synechocystis* sp.), pcc 6803}

ANATVKMGSDSGALVFEPSTVTIKAGEEVKWVNNKLSPHNIVFDADGVPADTAAKLSHKGLLFAAG
ESFTSTFTEPGTYTYCEPHRGAGMVGKVVVE

>d1bxva_ b.6.1.1 (A:) Plastocyanin {Cyanobacterium (*Synechocystis* sp.), pcc 7942}

QTVAIKMGADNGMLAFEPSTIEIQAGDTVQWVNNKLAPHNVVVEGQPELSHKDLAFSPGETFEATF
SEPGTYTYCEPHRGAGMVGKIVVQ

>d2b3ia_ b.6.1.1 (A:) Plastocyanin {Photosynthetic prokaryote (*Prochlorothrix hollandica*)}

ASVQIKMGTDKYAPLYEPKALSISAGDTVEFVMNKVGNVPHNIVFDKVPAGESAPALSNTKLAIAPGSFY
SVTLGTPGTYSFYCTPHRGAGMVGTTITVE

>d1paz_ b.6.1.1 (-) Pseudoazurin {*Alcaligenes faecalis*, strain s-6}

ENIEVHMLNKGAEAMVFEPAYIKANPGDVTFTFIPVDKGHNVESIKDMIPEGAEKFKSKINENYVLT
VTQPGAYLVKCTPHYAMGMIALIAVGDSPANLDQIVSAKKPKIVQERLEK VIA
>d1pmy_ b.6.1.1 (-) Pseudoazurin {Methylobacterium extorquens, strain am1}
DEVAVKMLNSGPGMMVFDPALVRLKPGDSIKFLPTDKGHNVETIKGMAPDGADYVKTTVGQEA
VKFDKEGVYGFKCAPHYMMGMVALVVVGDKRDNLEAAKSVQHNLTKQKRLDPLFAIQ
>d1bqk_ b.6.1.1 (-) Pseudoazurin {Achromobacter cycloclastes}
ADFEVHMLNKGKDGAMVFEPASLKVAPGDVTFTFIPTDKGHNVETIKGMIPDGAEAFKSKINENYKV
TFTAPGVYGVKCTPHYGMGMVGVVQVGDAPANLEAVKGAKNPKAQERLDAALAALGN
>d1adwa_ b.6.1.1 (A:) Pseudoazurin {Thiosphaera pantotropha}
ATHEVHMLNKGESGAMVFEPAFVRAEPGDVINFPVPTDKSHNVEAIKEILPEGVESFKSKINESYTLTV
TEPLYGVKCTPHFGMGMVGLVQVGDAPENLDAAKTAKMPKKARERMDAELAQVN
>d2cbp_ b.6.1.1 (-) Plantacyanin {Cucumber (Cucumis sativus)}
AVYVVGGSGGWTFNTESWPKGKRFRAFDILLFNYNPSMHNVVVVNQGGFSTCNTPAGAKVYTSGR
DQIKLPKGQSYFICNFPGHQCQSGMKIAVNAL
>d1f56a_ b.6.1.1 (A:) Plantacyanin {Spinach (Spinacia oleracea)}
AVYNIGWSFNNGARGKSFRAFDVLFVKYIKGQHNVAVNGRGYASCSAPRGARTYSSGQDRIKLTR
GQNYFICSPGHCGGGMKIAINAK
>d1azca_ b.6.1.1 (A:) Azurin {Alcaligenes denitrificans}
AQCEATIESNDAMQYNLKEMVVDKSKCKQFTVHLKHVKGMAKVAMGHNVVLTKEADKQGVATDG
MNAGLAQDYVKAGDTRVIAHTKVIGGGESDSVTFDVSCLTPGEAYAYFCSFPGHWAMMKGTLKLSN
>d1dyza_ b.6.1.1 (A:) Azurin {Alcaligenes xylosoxidans, NCIMB (11015), different isoforms}
AQCEATVESNDAMQYNVKEIVVDKSKCKQFTMHLKHVKGMAKVAMGHNLVLTQDADKQAVATDGM
GAGLAQDYVKAGDTRVIAHTKVIGGGESDSVTFDVSIAAGENYAYFCSFPGHWAMMKGTLKLG
>d1rkra_ b.6.1.1 (A:) Azurin {Alcaligenes xylosoxidans, NCIMB (11015), different isoforms}
AECSVDIAGNDGMQFDKKEITVSKCKQFTVNLKHPGKLAKNVMGHNVVLTQADMVQAVNDGM
AAGLDNNYVKKDDARVIAHTKVIGGGESDSVTFDVSCLAAGEDYAYFCSFPGHFALMKGVLLKLV
>d1cc3a_ b.6.1.1 (A:) Azurin {Pseudomonas aeruginosa}
AECSVDIQNDQMVFNTNAITVDKSKCKQFTVNLVSHPGNLPKNVMGHNVVLTSTAADMVQVVDGM
ASGLDKDYLPDDSRVIAHTKLVIGSGEKDSVTFDVSCLKEGEQYMFCELCGINHALMKGTLTLK
>d1jzga_ b.6.1.1 (A:) Azurin {Pseudomonas aeruginosa}
AECSVDIQNDQMVFNTNAITVDKSKCKQFTVNLVSHPGNLPKNVMGHNVVLTSTAADMVQVVDGM
ASGLDKDYLPDDSRVIAHTKLVIGSGEKDSVTFDVSCLKEGEQYMFCTFPGHSALMKGTLTLK
>d1joi_ b.6.1.1 (-) Azurin {Pseudomonas fluorescens}
AECKVTVDSTDQMSFNTKAIEIDKSKCTFTVELTHSGSLPKNVMGHNVVLTSSAADMPGIASDGM
GIDKNYLKEGDTRVIAHTKIIGAGEKDSVTFDVSCLAAGTDYAFFCSFPGHISM MKGTVTVK
>d1nwpa_ b.6.1.1 (A:) Azurin {Pseudomonas putida}
AECKVTVDSTDQMSFNTKDIAIDKSKCTFTVELTHSGSLPKNVMGHNLVISKEADMVQPIATDGLSAG
IDKQYLKDGARVIAHTKVIGAGEKDSVTFDVSCLAAGEKYGFFCSFPGHISM MKGTVTVK
>d1cuoa_ b.6.1.1 (A:) Azurin {Methylobacterium sp. j}
ASCETTTSVGD TMTYSTRSISVPASCAEFTVNFHKGHMPKTMGMGHNVVLTAKSADVGDVAKEGAH
AGADNNFVTPGDKRVIAFTPIIGGGEKTSVKFKVSALS KDEAYTYFCSYPGHFSMMRGTLLKLEE
>d1qhqa_ b.6.1.1 (A:) Auracyanin {Chloroflexus aurantiacus}
ANAPGGSNVVNETPAQTVEVRAAPDALAFAQTSLSLPANTVVRLDFVNQNNLGVQHNWVLVNNGD
DVAAA VNTAAQNNADALFVPPDPNLAALAWTAMLNAGESGSVTFRTAPPGTYLYICTFPGHYLAGM

KGTLTVTP

>d1e30a_b.6.1.1 (A:) Rusticyanin {Thiobacillus ferrooxidans}

LDTTWKEATLPQVKAMLEKDTGKVSQDVTYSGKTVHVVAADVLPGFPPSFEVHDKKNPTLEIPA
GATVDVTFINTNKGFGHSFDITKKGPPYAVMPVIDPIVAGTGFSPVPKDGKFGYTNFTWHPTAGTYY
YVCQIPGHAATGQFGKIVVK

>d1jer_b.6.1.1 (-) Stellacyanin {Cucumber (Cucumis sativus)}

MQSTVHIVGDNTGWSVPSSPNFYQWAAGKTFRVGDSLQFNFPANAHNVHEMETKQSFACNFVN
SDNDVERTSPVIERLDELGMHYFVCTVGTGTHCSNGQKLSINVVAAN

>d1ibya_b.6.1.4 (A:) Red copper protein nitrosocyanin {Nitrosomonas europaea}

EHNFNVINAYDTTIPELNVEGVTVKNIRAFNVLNPEPETLVVKKGDAVKVVVENKSPISEGFSIDAFG
VQEVKAGETKTISFTADKAGAFIWCQLHPKNIHLPGLTNVVE

>d1qnia1_b.6.1.4 (A:451-581) Nitrous oxide reductase, C-terminal domain {Pseudomonas
nautica}

KIYERNDPYFASCRAQAEKDGVTLESDNKVIRGDKVVRVYMTSVAPQYGMTDFKVKEGDEVTVYIT
NLDMVEDVTHGFCMVNHGVSMEISPQQTASVTFITAGKPGVYWYYCNWFCHALHMEMVGRMLVE
AA

>d1fwa1_b.6.1.4 (A:452-581) Nitrous oxide reductase, C-terminal domain {Paracoccus
denitrificans}

SVWDRNDPMWAETRAQAEADGVDIDNWTEEVIRGDKVVRVYMTSVAPQYGMTDFKVKEGDEVTVI
VTNLDEIDDLTHGFTMGNYGVAMEIGPQMTSSVTFVAANPGVYWYYCQWFCHALHMEMRGRMLV
EPK

>d1cyx_b.6.1.2 (-) Quinol oxidase (CyoA) {Escherichia coli}

KPITIEVVSMDWKWFFIYPEQGIATVNEIAFPANTPVYFKVTSNSVMHSHFFIPRLGSQIYAMAGMQT
RLHLIANEPGTYDGCIEICGPGHSGMKFKAIATPDRAAFDQWVAKAKQSPNTMSDMAAFEKLAAP
SEYNQVEYFSNVKPDFADVINKFM

>d1ftb1_b.6.1.2 (B:118-283) Quinol oxidase (CyoA) {Escherichia coli}

KPLAHDEKPITIEVVSMDWKWFFIYPEQGIATVNEIAFPANTPVYFKVTSNSVMNSFFIPRLGSQIYA
MAGMQTRLHLIANEPGTYDGISASYSYSGPGFSGMKFKAIATPDRAAFDQWVAKAKQSPNTMSDMAA
FEKLAAPSEYNQVEYFSNVKPDFADVINKFMA

>d1ocrb1_b.6.1.2 (B:91-227) Cytochrome c oxidase {Cow (Bos taurus)}

NNPSLTVKTMGHQWYWSYEYTDYEDLSFDSYMIPTSELKPGELRLLEVDNRVLPMEMTIRMLVSS
EDVLHSAVPSLGLKTDIAPGRLNQTTLMSRPGLYYGQCSEICGSNHSFMPIVLELVPLKYFEKWSA
SML

>d1ar1b1_b.6.1.2 (B:108-252) Cytochrome c oxidase {Paracoccus denitrificans}

NDPDLVIKAIGHQWYWSYEYPNDGVAFDALMLEKEALADAGYSEDEYLLATDNPVVVPVGGKVLVQ
VTATDVIHAWTIPAFVAVKQDAVPGRIAQLWFSVDQEGVYFGQCSELCGINHAYMPIVVKAVSQEKYEA
WLAGAKEEFAA

>d2cuaa_b.6.1.2 (A:) Cytochrome c oxidase {Thermus thermophilus, ba3 type}

AGKLERVDPTTVRQEGPWADPAQAVVQTGPNQYTVYVLAFAFGYQPNPIEVPQGAEIFKITSPDVI
HGFHVEGTNINVEVLPGEVSTVRYTFKRPGEYRIICNQYCGLGHQNMFGTIVVKE

>d2cuab_b.6.1.2 (B:) Cytochrome c oxidase {Thermus thermophilus, ba3 type}

AYTLATHTAGVIPAGKLERVDPTTVRQEGPWADPAQAVVQTGPNQYTVYVLAFAFGYQPNPIEVPQG
AEIVFKITSPDVIHGFHVEGTNINVEVLPGEVSTVRYTFKRPGEYRIICNQYCGLGHQNMFGTIVVKE

>d1nif_1_b.6.1.3 (8-166) Nitrite reductase, NIR {Achromobacter cycloclastes}

DISTLPRVKVDLVKPPFVHAHDQVAKTGPRVVEFTMTIEEKKLVIDREGTEIHAMTFNGSVPGPLMV
VHENDYVELRLINPDTNTLLHNIDFHAATGALGGGALTQVNPGEETTLRFKATKPGVFVYHCAPEG
MVPWHVTSGMNGAIMVLPDGLKDEK

>d1nif_2 b.6.1.3 (167-340) Nitrite reductase, NIR {*Achromobacter cycloclastes*}
GQPLTYDKIYYVGEQDFYVPKDEAGNYKKYETPGEAYEDAVKAMRTLTPTHIVFNGAVGALTGDHAL
TAAVGERVLVVHSQANRDTRPHLIGGHGDYVWATGKFRNPPDLQETWLIPGGTAGAAFYTFRQPG
VYAYVNHNLIEAFELGAAGHFVKVTGEWNDDLMTSVVKPASM

>d1j9qa1 b.6.1.3 (A:4-166) Nitrite reductase, NIR {*Alcaligenes faecalis*, strain s-6}
ATAAEIAALPRQKVELVDPPFVHAHSQVAEGGPKVVEFTMVIEEKKIVIDDAGTEVHAMAFNGTVPG
PLMVVHQQDDYLELTINPETNTLMHNINFHAATGALGGGGLTEINPGEKTLRFKATKPGVFVYHCA
PPGMVPHVSVGMNGAIMVLPREGLHDGK

>d1j9qa2 b.6.1.3 (A:167-339) Nitrite reductase, NIR {*Alcaligenes faecalis*, strain s-6}
GKALTYDKIYYVGEQDFYVPRDENGKYKKYEPGDAYEDTVKVMRTLTPTHVVFNGAVGALTGDKA
MTAAVGEKVLIVHSQANRDTRPHLIGGHGDYVWATGKFNTPPDQETWFIPGGAAGAAFYTFQQ
PGIYAYVNHNLIEAFELGAAAHFKVTGEWNDDLMTSVLAPSG

>d1gs7a1 b.6.1.3 (A:1-159) Nitrite reductase, NIR {*Alcaligenes xylosoxidans*}
QDADKLPHTKVTLVAPPQVHPHEQATKSGPKVVEFTMTIEEKKMVIDDKGTTLQAMTFNGSMPGP
TLVVHEGDYVQLTLVNPATNAMPHNVDHFGATGALGGAKLTNVNPGEQATLRFKADRSGTFVYHCA
PEGMVPWHVSVGMSGTLMVLPDGLKDP

>d1gs7a2 b.6.1.3 (A:160-336) Nitrite reductase, NIR {*Alcaligenes xylosoxidans*}
QGKPLHYDRAYTIGFDLYIPKGPDKYKDYATLAESYGDTVQVMRTLTPSHIVFNGKVGALTGANAL
TAKVGETVLLIHSQANRDTRPHLIGGFWDVWETGKFANPPQRDLETWFIRGGSAGAAALYTFKQPG
VYAYLNHNLIIEAFELGAAGHIKVEGKWNDLMLKQIKAPAPIPR

>d1nds1 b.6.1.3 (A:11-166) Nitrite reductase, NIR {*Alcaligenes xylosoxidans*}
GLPRVAVDLVAPPLVHPHSQVAAGAPKVQFRMSIEEKKMVADDDGTTAQAMTFNGSVPGPTLVVH
EGDYIELTLVNPATNSMPHNVDHFAATGALGGAGLTQVVPGEAVLRFKADRSGTFVYHCAPAGMV
PWHVSVGMNGALMVLPRDGLRDAA

>d1nds2 b.6.1.3 (A:167-340) Nitrite reductase, NIR {*Alcaligenes xylosoxidans*}
GAALAYDRVYTIGESDLYVPKAADGNYSYDYPALASAYADTVAVMRTLTPSHAVFNGAVGALTGANALT
AAVGESVLIHSQANRDSRPHLIGGHGDVWVWTTGKFANPPQLNMFIPGGSAAAALYTFKQPGT
YAYLSHNLIEAMELGAAAQASVEGQWDDDLMTSVAAPGPA

>d1kbva1 b.6.1.3 (A:13-163) Nitrite reductase, NIR {*Neisseria gonorrhoeae*, AniA}
ELPVIDAVTTHAPEVPPAIDRDYPKVRVKMETVEKTMKMDDGVEYRYWTFDGDVPMIRVREG
DTVEVEFSNPSSTVPHNVDFHAATGQGGGAAATFTAPGRTSTFSFKALQPLIYIYHCAVAPVGMHI
ANGMYGLLVEPKGLPKV

>d1kbva2 b.6.1.3 (A:164-314) Nitrite reductase, NIR {*Neisseria gonorrhoeae*, AniA}
DKEFYIVQGFYTKGKKAQGLQPFDMKAVAEQPEYVFNHVGALTGDNALKAKAGETVRMYV
GNGGPNLVSSFHVICEIFDKVYVEGGKLINENVQSTIVPAGGSAIVEFKVDIPGNYTLVDHSIFRAFNK
GALGQLKVEGAENPEIM

>d1kv7a1 b.6.1.3 (A:31-170) multi-copper oxidase CueO {*Escherichia coli*}
RPTLPIPDLLTTDARNRIQLTIGAGQSTFGGKTATTWGYNGNLLGPAVKLQRGKAVTVDIYNQLTEET
TLHWHGLEVPGEVDGGPQGIIPPGKRSVTLNVDQPAATCWFHPHQHGKTGRQVAMGLAGLVVIE
DDEILKL

>d1kv7a2 b.6.1.3 (A:171-335) multi-copper oxidase CueO {*Escherichia coli*}

MLPKQWGIDDVPVIVQDKKFSADGQIDYQLDVMTAAVGFWDGDTLLTNGAIYPQHAAPRGWLRRL
LNGCNARSLNFATSDNRPLYVIASDGGLLPEPVKSELVLMGERFEVLVEVNDNKPFDLVTLVPSQ
MGMAIAPFDKPHPVMRIQPIAISASGALPDTLS

>d1kv7a3 b.6.1.3 (A:336-516) multi-copper oxidase CueO {Escherichia coli}
SLPALPSLEGLTVRKLQLSMDPMLDMMGMQMLMEKYGDQAMAGMDHSQMMGHMGMHGNMNHM
NHGGKFDHANKINGQAFDMNKPMFAAAKQYERWVISGVGDMMLHPFHIGTQFRILSENGK
PPAAHRAGWKDTVKEGVSEVLVKNHDAPKEHAYMAHCHLLEHEDTGMMLGFTV

>d1aoza1 b.6.1.3 (A:1-129) Ascorbate oxidase {Zucchini (Cucurbita pepo medullosa)}
SQIRHYKWEVEYMFAPNCNENIVMGINGQFPGPTIRANAGDSVVVELTNKLHTEGVVHWHGILQ
RGTPWADGTASISQCAINPGETFFYNFTVDNPGTFFYHGHLMQRSAGLYGSLIVDPPQGKKE

>d1aoza2 b.6.1.3 (A:130-338) Ascorbate oxidase {Zucchini (Cucurbita pepo medullosa)}
PFHYDGEINLLSDWWHQSIHKQEVGLSSKPIRWIGEPQTILLNGRGQFDCSIAAKYDSNLEPCKLKG
SESCAPYIFHVSPKTYRIRIASTTALAALNFAIGNHQLLVVEADGNYVQPFYTSDDIYSGESYSVLIT
TDQNPSENYWVSVGTRARHPNTPPGLTLLNLPNSVSKLPTSPPPQTPAWDDFDRSKNFYRITAA
MGSPK

>d1aoza3 b.6.1.3 (A:339-552) Ascorbate oxidase {Zucchini (Cucurbita pepo medullosa)}
PPVKFNRRIFLLNTQNVIYVYKWAINDVSLALPPTPYLGAMKYNLLHAFDQNPPEVFPEDYDIDT
PPTNEKTRIGNGVYQFKIGEVVDVILQANMMKENLSETHPWHLHGDFWVLGYGDGKFSAEES
SLNLKNPPLRNTVVIFPYGWTAIRFVADNPGVWAFHCHIEPHLMGMGVVFAEGVEKVGRIPTKAL
ACGGTAKSLINPKNP

>d1hfua1 b.6.1.3 (A:1-131) Laccase {Inky cap fungus (Coprinus cinereus)}
AIVNSVDTMTLTNANVSPDGFTRAGILVNGVHGPLIRGGKDNFELNVVNDLDNPTMLRPTSIHWH
GLFQRGTNWADGADGVNQCPISPGHAFLYKFTPAGHAGTFWYHSHFGTQYCDGLRGPVVIYDDND

>d1hfua2 b.6.1.3 (A:132-303) Laccase {Inky cap fungus (Coprinus cinereus)}
PHAALYDEDDENTIITLADWYHIPAPSIQGAAQPDATLINGKGRYVGGPAAELSIVNVEQGKRYMR
LISLSCDPNWQFSIDGHELTIEVDGELTEPHTVDRLQIFGTGRYSFVLDANQPVDNYWIRAQPNKGR
NGLAGTFANGVNSAILRYAGANADPTTSANPNPAQL

>d1hfua3 b.6.1.3 (A:304-503) Laccase {Inky cap fungus (Coprinus cinereus)}
NEADLHALIDPAAPGIPTGAADVNLRFQLGFSGRFTINGTAYESPSVPTLLQIMSGAQSANDLLPA
GSVYELPRNQVVELVVPAGVLGGPHFHLHGAFSVVRSAGSSTYNFVNPVKRDVVSLGVTGDEVTI
RFVTDNPGPWFHCHIEFHLMNGLAIVFAEDMANTVDANNPPVEWAQLCEIYDDLPEATSITV

>d1kcw_1 b.6.1.3 (1-192) Ceruloplasmin {Human (Homo sapiens)}
KEKHYYIGIETTWDYASDHGEKKLISVDTEHSNIYLQNGPDRIGRLYKKALYLQYTDDEFRTTIEKPV
WLGFLGPIIKAETGDKVYVHLKNLASRPYTFHSHGITYYKEHEGAIYPDNTTDFQRADDKVYPGEQY
TYMLLATEEQSPGEGDGNVTRIVYHSHIDAPKDIASGLIGPLIICKKDSLDEKEK

>d1kcw_2 b.6.1.3 (193-338) Ceruloplasmin {Human (Homo sapiens)}
HIDREFVVMFVVDENFSWYLEDNIKTYCSEPEKVDKDNEDFQESNRMYSVNGYTFGSLPGLSMCA
EDRVKWFYLFMGNEVDVHAFFHGQALTNKNYRIDTINLFPATLFDAYMVAQNPGEWMLSCQNLN
HLKAGLQAFFQVQEC

>d1kcw_3 b.6.1.3 (347-553) Ceruloplasmin {Human (Homo sapiens)}
IRGKHVRHYIAAEIHWNYAPSGIDIFTKENLTAPGSDSAVFFEQGTTRIGGSYKLVYREYTDASFT
NRKERGPEEHLGILGPVIWAEVGDITRVTFHNKGAYPLSIEPIGVRFNKNNEGTYYSNPNPQRSRV
PPSASHVAPTETFTYEWTVPKVEGPTNADPVCLAKMYSAVDPTKDIFTGLIGPMKICKKGLHANG
RQK

>d1kcw_4 b.6.1.3 (554-705) Ceruloplasmin {Human (Homo sapiens)}
DVDKEFYLFPTVFDENESLLEDNIRMFTTAPDQVDKEDEDFQESNKMHSMNGFMYGNQPGLTMC
KGDSVVWYLFWSAGNEADVHGIYFSGNTYLWRGERRDANLFPQTSLLTHMWPDTTEGTFNVECLTT
DHYTGGMKQKYTVNQCRQSED

>d1kcw_5 b.6.1.3 (706-884) Ceruloplasmin {Human (Homo sapiens)}
STFYLGERTYYIAAVEVEWDYSPQREWEKELHHLQEQNVSNAFLDKGEFYIGSKYKKVVYRQYTDS
TFRVPVERKAEHEHLGILGPQLHADVGDVKIIFKNMATRPYSIHAGVQTESSTVTPPLPGETLTYV
WKIPERSGAGTEDSACIPWAYYSTVDQVKDLYSGLIGPLIVCRRP

>d1kcw_6 b.6.1.3 (892-1040) Ceruloplasmin {Human (Homo sapiens)}
RRKLEFALLFLVFDENESWYLDNIIKTYSDHPEKVNKDDEEFIESNKMHAINGRMFGNLQGLTMHV
GDEVNWYLMGMGNEIDLHTVHFHGHFSFYKHRGVYSSDVDFDIFPGTYQTLEMFPRTPGIWLHCH
VTDHIHAGMETTYTVLQN

>d1qasa2 b.7.1.1 (A:626-756) PI-specific phospholipase C isozyme D1 (PLC-D1), C-terminal domain {Rat (Rattus norvegicus)}
WRPERLRVRIISGQQLPKVNKNKNSIVDPKVIVEIHGVGRDTGSRQTAVITNNGFNPRWDMEFEFEV
TVPDLALVRFMVEDYDSSSKNDFIGQSTIPWNSLKQGYRHVHLLSKNGDQHPSATLQVFKISIQD

>d1rlw_ b.7.1.1 (-) Domain from cytosolic phospholipase A2 {Human (Homo sapiens)}
SSHKFTVVVLRATKVTKGAFGDMLDTPDPYVELFISTTPDSRKRTRHFNNDINPVWNETFEFILD
NQENVLEITLMDANYVMDETLGTATFTVSSMKVGEKKEVPPFIFNQVTEMVLEMSLEVASS

>d1d5ra1 b.7.1.1 (A:188-351) Pten tumor suppressor (Phosphoinositide phosphatase), C-terminal domain {Human (Homo sapiens)}
YRPVALLFHKMMFETIPMFSGGTCNPQFVVCQLKVKIYSSNSGPTRREDKFMFYFEPQPLPVCGLDIK
VEFFHKQNKMLKKDKMFHFWVNTFFIPGPEEVDNDKEYLVLTLTKNLDLKDANKDKANRYFSPNFK
VKLYFTKTV

>d1e8xa2 b.7.1.1 (A:357-522) Phosphoinositide 3-kinase (PI3K) {Pig (Sus scrofa)}
CDRKRFRVKIRGIDIPVLPRTADLTVFVEANIYQGVLCQRRRTSPKPFTEEVLWNVWLEFSIKIKDLP
KGALLNLQIYCGKAPALSGKTSAEEMPSPEKGAQLLYVNNLLIDHRFLLRHGEYVLMWQVLSGKG
EDQGSFNADKLTSATNPDKENSMSISILLDN

>d1e8ya2 b.7.1.1 (A:357-522) Phosphoinositide 3-kinase (PI3K) {Human (Homo sapiens)}
CDRKRFRVKIRGIDIPVLPRTADLTVFVEANIYQGVLCQRRRTSPKPFTEEVLWNVWLEFSIKIKDLP
KGALLNLQIYCGKAPALSSKASAESPSESKGKVRLLYVNNLLIDHRFLLRRGEYVLMWQVLSGKGE
DQGSFNADKLTSATNPDKENSMSISILLDN

>d1bda_ b.7.1.1 (A:) Domain from protein kinase C delta {Rat (Rattus norvegicus)}
MAPFLRISFNSYELGSLQAEDDASQPFCAVKMKEALTTDRGKTLVQKKPTMYPEWKSTFDAHIYEG
RVIQIVLMRAAEDPMSEVTGVSVLAERCKKNGKAEFWLDLQPQAKVLMCVQYFLE

>d1gmia_ b.7.1.1 (A:) Domain from protein kinase C epsilon {Rat (Rattus rattus)}
MVFVNGLLKIKICEAVSLKPTAWSLRDAVGRPQTFLLDPIYALNVDDSRIGQTATKQKTNSPAWHD
EFVTDVCNKRKIELAVFHDAPIGYDDFVANCTIQFEELLQNGSRHFEDWIDLEPEGKVYVIIDLSGSS
G

>d1bna_ b.7.1.2 (A:) Synaptogamin I {Rat (Rattus norvegicus)}
EKLGLQYSLDYDFQNNQLLVGIIQAAELPALDMGGTSDPYVKVFLLPDKKKKFKETKVHRKTLNPVF
NEQFTFKVPYSELGGKTLVMAVYDFDRFSKHDIIGEFKVPMTVDFGHVTEEWRDLQSAEK

>d1dqva1 b.7.1.2 (A:295-424) Synaptogamin I {Rat (Rattus norvegicus)}
GAPCGRISFALRYLYGSDQLVVRILQALDLPKDSNGFSDPYVKIYLLPDRKKKFQTKVHRKTLNPIFN

ETFQFSVPLAELAQRKLHFSVYDFDRFSRHDLIGQVVLDNLELAEQPPDRPLWRDILEGG
>d1dqva2 b.7.1.2 (A:425-569) Synaptogamin I {Rat (Rattus norvegicus)}
SEKADLGELNFSCLYPTAGLLTVTIKASNLKAMDLTGFSDPYVKASLISEGRRLKRRKTSIKKNTLN
PTYNEALVFDVAPESVENVGLSIAVVDYDCIGHNEVIGVCRVGPEAADPHGREHWAEMLANPRKPV
EHWHQLVEEK
>d1k5wa_ b.7.1.2 (A:) Synaptogamin I {Rat (Rattus norvegicus)}
KLGDICFSLRYVPTAGKLTVVILEAKNLKMDVGGSDPYVKIHLMQNGKRLKKKKTTIKNTLNPY
YNESFSFEVPFEQIQKVQVVVTVLDYDKIGKND AIGKVFVGYNSTGAELRHWSMLANPRRPIAQW
HTLQVEEEVDAMLAV
>d1rsy_ b.7.1.2 (-) Synaptogamin I {Rat (Rattus norvegicus)}
GGGILDSMVEKEEPKEEKLKGLQYSLDYDFQNNQLLVGIIQAAELPALDMGGTSDPYVKVFLLPDK
KKKFETKVRKTLNPFVNEQFTFKVPYSELGGKTLVMAVYDFDRFSKHDIIGEFKVP MNTVDFGHV
TEEWRDLQSA
>d1dsya_ b.7.1.2 (A:) C2 domain from protein kinase c (alpha) {Rat (Rattus norvegicus)}
TEKRGRIYLKAEVTDEKLHVTVRDAKNLIPMDPNGLSDPYVKLKLIPDPKNESKQKTKTIRSTLNPQ
WNESFTFKLKPSPDKDRRLSVEIWDWDRTRNDFMGSLSFGVSELMKMPASGWYKLLNQEEGEYY
NVPIPE
>d1a25a_ b.7.1.2 (A:) C2 domain from protein kinase c (beta) {Rat (Rattus norvegicus)}
ERRGRIYIQAHDREVLIVVVRDAKNLVPMDPNGLSDPYVKLKLIPDPKSESKQKTKTIKCSLNPEWN
ETFRFQLKESDKDRRLSVEIWDWDLTSRNDFMGSLSFGISELQKAGVDGWFKLLSQEEGEYFNV
>d3rpb_a_ b.7.1.2 (A:) C2b-domain of rabphilin {Rat (Rattus norvegicus)}
RGKILVSLMYSTQQGLIVGIIRCVHLAAMDANGYSDPFVKLWLPDMGKKAKHKTQIKKTLNPEF
NEEFFYDIKHSDLAKKSLDISVWDYDIGKSNDYIGGCQLGISAKGERLKHWECLKNKDKKIERWHQ
LQENH
>d1qpxa2 b.7.2.1 (A:125-215) PapD {Escherichia coli}
NEVWQDQLILNKVSGGYRIENPTPYVTVIGLGGSEKQAEEGEFETVMLSPRSEQTVKSANYNTPYL
SYINDYGGRPVLSFICNGSRCSVK
>d1quna2 b.7.2.1 (A:122-205) FimC {Escherichia coli}
LPPDQAAEKLRFRRSANSLTLINPTPYLTVTELNAGTRVLENALVPPMGESAVKLPDAGSNITYRTI
NDYGALTPKMTGVME
>d1who_ b.7.3.1 (-) Pollen allergen PHL P 2 {Timothy grass (Phleum pratense)}
VPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELREHGSEWVAMTKGEGGVWTFDSEEPLQGPFN
FRFLTEKGMKNVFDVPEKYTIGATYAP
>d1dcea2 b.7.4.1 (A:241-350) Rab geranylgeranyltransferase alpha-subunit, insert domain
{Rat (Rattus norvegicus)}
PHDVLCCVHVSREEACLSVCFSRPLTVGSRMGTLLL MVDEAPLSVEWRTPDGRNRPSHWLCLDPA
ASLNDQLPQHTFRVIWTGSDSQKECVLLKDRPECWCRDSATDEQ
>d1czya1 b.8.1.1 (A:350-501) TNF receptor associated factor 2 (TRAF2) {Human (Homo
sapiens)}
YDGVFIWKISDFPRKRQEAVAGRIPAIFSPAFYTSRYGYKMCLRIYLNQDGTGRGTHLSLFFVVMKGP
NDALLRWPFNQKVTLMLLDQNNREHVIDAFRPDVTSSSFQRPVNDMNIASGCPLFCPVSKMEAKN
SYVRDDAIFIKAIVDLTGL
>d1flka1 b.8.1.1 (A:350-504) TNF receptor associated factor 3 (TRAF3) {Human (Homo
sapiens)}

YNGVLIWKIRDYKRRKQEAVMGKTLISLQPFYTGYPFYKMCARVYLNQDGMGKTHLSLFFVIMR
GEYDALLPWPFKQKVTMLMDQGSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFAQTVLEN
GTYIKDDTIFIKVIVDTSDLDPD

>d1k2fa_b.8.1.2 (A:) SIAH, seven in absentia homolog {Mouse (Mus musculus)}
SVLFPCKYASSGCEITLPHTEKAEHEELCEFRPYSCPCGASCKWQGS�DAVMPHLMHQHKSITTLQ
GEDIVFLATDINLPGAVDWVMMQSCFGFHFMLVLEKQEKYDGHQQFFAIVQLIGTRKQAENFAYRLE
LNGHRRRLTWEATPRSIHEGIATAIMNSDCLVFDTSIAQLFAENGLGINVTISM

>d2bn2a_b.9.1.1 (A:) Neurophysin II {Cow (Bos taurus)}
AMSDLELRQCLPCGPGGKGRFCGFSICCGDELGCFVGTAEALRCQEENYLPSPCQSGQKPCGSGGRCA
AAGICCNDESCVTEPEC

>d1kvp_b.10.1.1 (-) Bacteriophage capsid proteins {Bacteriophage phi-X174}
SNIQTGAERMPHDLSHLGLAGQIGRLITISTTPVIAGDSFEMDAVGALRSLRRLGLAIDSTVDIFTF
YVPHRHVYGEQWIKFMKDGVNATPLPTVNTTGYIDHAAFLGTINPDTNKIPKHLFQGYLNIYNNYF
KAPWMPDRTEANPNELNQDDARYGFRCCHLKNIWTAPLPPETELSRQMTTSTGMAPVTTKFRDV
PNLSGTPLIFRDNKGRITIKTGQLGIGPVDAGFLVAQNTAQAANGERAIPSNLWADLSNATSIDIMGLQ
AAYANLHTDQERDYFMQRYRDVISSFGGKTSYDADNRPLLVMRSNLWASGYDVGDTQDQTSLGQFSG
RVQQTYKHSVPRFFVPEHGTMTLALVRFPPATKEIQYLNAKGALTYTDIAGDPVLYGNLPPREISM
KDVFRSGDSSKKFKIAEGQWYRYAPSYVSPAYHLLLEGFPFIQEPSPGDLQERVLIRHHHDYDQCFQSVQ
LLQWNSQVKFNVTVYRNLPTRDSIMTS

>d2bpa1_b.10.1.1 (1:) Bacteriophage capsid proteins {Bacteriophage phi-X174}
SNIQTGAERMPHDLSHLGLAGQIGRLITISTTPVIAGDSFEMDAVGALRSLRRLGLAIDSTVDIFTF
YVPHRHVYGEQWIKFMKDGVNATPLPTVNTTGYIDHAAFLGTINPDTNKIPKHLFQGYLNIYNNYF
KAPWMPDRTEANPNELNQDDARYGFRCCHLKNIWTAPLPPETELSRQMTTSTTSIDIMGLQAYAY
NLHTDQERDYFMQRYRDVISSFGGKTSYDADNRPLLVMRSNLWASGYDVGDTQDQTSLGQFSGRVQQ
TYKHSVPRFFVPEHGTMTLALVRFPPATKEIQYLNAKGALTYTDIAGDPVLYGNLPPREISMKDV
RSGDSSKKFKIAEGQWYRYAPSYVSPAYHLLLEGFPFIQEPSPGDLQERVLIRHHHDYDQCFQSVQ
NSQVKFNVTVYRNLPTRDSIMTS

>d2bpa2_b.10.1.1 (2:) Bacteriophage capsid proteins {Bacteriophage phi-X174}
MFQTFISRHNSNFFSDKLVLTSVTPASSAPVLQTPKATSSSTLYFDSLTVNAGNGGFLHCIQMDTSVNA
ANQVVSVDGADIAFDADPKFFACLVRFESSVPTLPTAYDVYPLNGRHDGGYYTVKDCVTIDVLPRT
GNNVYVGFVWSNFTATKCRGLVSLNQVIKEIICLQPLK

>d1gff1_b.10.1.1 (1:) Bacteriophage capsid proteins {Bacteriophage G4}
VPHDLSHLVFEAGKIGRLKTISWTPVVAGDSFECMDVGAIRLSPLRRLGLAVDSRVDIFSFIYIPHRHIYG
QQWINFMKDGVNASPLPPVTCSSGWDASAAYLGTIPSSSTLKVPKFLHQGYLNIYNNYFKPPWSDDLTY
ANPSNMPSEDKWGVVANLKSNIWTAPLPPDTRTSENMTTGTSTIDIMGLQAYAYAKLHTEQERDYF
MTRYRDIMKEFGGHTSYDGDNRPLLLMRSEFWASGYDVGDTQSSLGQFSGRVQQTFNHKVPRFY
VPEHGVIMTLAVTRFPPTHEMEMHYLVGKENLTYTDIACDPALMANLPPREVSLKEFFHSSPDSAKF
KIAEGQWYRTQPDRVAFYPYALDGFYFYSALPSTDLKDRVLVNTNNYDEIFQSMQLAHWNMQTKF
NINVYRHMPTRDSIMTS

>d1gff2_b.10.1.1 (2:) Bacteriophage capsid proteins {Bacteriophage G4}
MFQKFISKHNAPINSTQLAATKTPAVAAPVLSVPLSRSTILINATTTAVTTTHSGLCHVVRIDETNPTN
HHALSIAGSLSNVPADMIAFAIRFEVADGVVPTAVPALYDVYPIETFNNGKAISFKDAVTIDSHPRVTG
NDVYAGIMLWSNAWTASTISGVLSVNQVNREATVLQPLK

>d1stma_b.10.1.2 (A:) SPMV coat protein {Satellite panicum mosaic virus}

AAATSLVYDTCYVTLTERATTSFQRQSFPTLKGMDRAFQVVAFTIQGVSAAPLMYNARLYNPGDTD
SVHATGVQLMGTVPRTVRLTPRVGQNNWFFGNTEEAETILAIIDGLVSTKGANAPSNTVIVTGCFLRA
PSELQSS

>d1a34a_b.10.1.2 (A:) STMV coat protein {Satellite tobacco mosaic virus}

TGDNSNVVTMIRAGSYPKVNPTPTWVRAIPFEVSVQSGIAFKVPVGSLSANFRDTSFTSVTVMSVR
AWTQLTPPVNEYSFVRLKPLFKTGDSTEEFEGRASININTRASVGYRIPTNLRQNTVAADNVCEVRSN
CRQVALVISCCFN

>d2stv_b.10.1.2 (-) STNV coat protein {Satellite tobacco necrosis virus}

TMRAVKRMINTHLEHKRFALINSGNTNATAGTVQNLNNGIIGDDINQRSGDQVRIVSHKLHVRGTA
ITVSQTFRFIWRDNMNRGTTPTVLEVLNTANFMSQYNPITLQQRFTILKDVTLNCSLTGESIKDRI
INLPGQLVNYNGATAVAASNGPGAIFMLQIGDSLVLGLWDSSYEAVYTDA

>d1smva_b.10.1.2 (A:) SMV coat protein {Sesbania mosaic virus}

GAITVLHCELTAIEIGVTDIVVSELVMPYTVGTWLRGVADNWSKYSWLSVRYTYIPSCPSSTAGSIH
MGFQYDMADTVPVSVNKLNLRGYVSGQVWGSAGLCFINNSRCSDTSTAISTTLDVSELGKKWYPY
KTSADYATAVGVVDVNIATDLVPARLVIALLDGSSSTAVAAGRIYDITYTIQMIEPTASALNL

>d1smvc_b.10.1.2 (C:) SMV coat protein {Sesbania mosaic virus}

QAGISMAPSAQGAMVRIRNPAVSSSRGAIIVLHCELTAIEIGVTDIVVSELVMPYTVGTWLRGVADN
WSKYSWLSVRYTYIPSCPSSTAGSIHMGFQYDMADTVPVSVNKLNLRGYVSGQVWGSAGLCFINN
SRCSDTSTAISTTLDVSELGKKWYPYKTSADYATAVGVVDVNIATDLVPARLVIALLDGSSSTAVAAGRIY
DITYTIQMIEPTASALNL

>d1f2na_b.10.1.2 (A:) RYMV capsid protein {Rice yellow mottle virus}

LSSNTWPLHSVEFLADFKRSSTSADATTYDCVPFNLPRVWLSLARCYSMWKPTRWDVVYLPEVSATV
AGSIEMCFLYDYADTIPRYTGKMSRTAGFVTSSVWYGAEGCHLLSGGSARNAVVASMDCSRVGWKR
TSSIPSSVDPNVNTILPARLAVRSSIKPTVSDTPGKLYVIASMVLRDPVDPTLNT

>d1f2nc_b.10.1.2 (C:) RYMV capsid protein {Rice yellow mottle virus}

AEPQLQRAPVAQASRISGTVPGPLSSNTWPLHSVEFLADFKRSSTSADATTYDCVPFNLPRVWLSL
ARCYSMWKPTRWDVVYLPEVSATVAGSIEMCFLYDYADTIPRYTGKMSRTAGFVTSSVWYGAEGCHLLS
GGSARNAVVASMDCSRVGWKRVTSSIPSSVDPNVNTILPARLAVRSSIKPTVSDTPGKLYVIASMV
LRDPVDPTLNT

>d1bmv1_b.10.1.2 (1:) BPMV coat protein {Bean pod mottle virus}

SISQQTWVNQMATVRTPLNFDSSKQSFQFVVDLLGGGISVDKTGDWITLVQNSPISNLLRVAWKK
GCLMVKVVMSGNAAVKRSDWASLVQVFLTNSNSTEHFDACRWTKSEPHSWELIFPIEVCGPNNNGFE
MWSSEWANQTSWHLSDVDPKQSTTFDVLGIGSQNFEIAGNTLMPAFSVPQ

>d1bmv2_b.10.1.2 (2:) BPMV coat protein {Bean pod mottle virus}

METNLFKLSLDDVETPKGSMLDLKISQSKIALPKNTVGGTILRSDLLANFLTEGNFRASVDLQRTHRI
KGMIKMVATVGIPENTGIALACAMNSSIRGRASSDIYTICSQDCELWNPACTKAMTMSFNPNPCSDA
WSLEFLKRTGFHCDIICVTGWTATPMQDVQVTIDWFISSQECVPRTYCVLNPQNPVFLNRWGMKLT
FPQGTSRSVKRMPLSIGGAGAKSAILMNMPNAVLSMWRYFVGDVFEVSKMTSPYIKCTVSFFIAF
GNLADDTINFEAFPHKLVQFGEIQEKVVLKFSQEEFLTAWSTQVRPATTLLADGCPYLYAMVHDSSVS
TIPGDFVIGVKLTHIENMCAYGLNPGISGSRLLGITIPQ

>d1a6ca1_b.10.1.2 (A:1-176) TRSV capsid protein {Tobacco ringspot virus}

AVTVVPDPTCCGTLSEFKVPKDAKKGKHLGTFDIRQAIMDYGGLHSQEWCAKGIVNPTFTVRMHAPR
NAFAGLSIACTFDYKRIDLPALGNECPPSEMFELPTKVFMLKDADVHEWQFNYGELTGHLGNWA
NVATQPTLYFFVASTNQVTMAADWQCIVTMHVDMGPVIDRFELN

>d1a6ca2_b.10.1.2 (A:177-348) TRSV capsid protein {Tobacco ringspot virus}
PTMTWPIQLGDTFAIDRYEAKEIKLDGSTSMLSISYNFGGPVKHSHKHAISYSRAVMSRNLGWSGTI
SGSVKSVSSLFCTASFVIFPWECEAPPTLRQVLWGPQHIMHGDGQFEIAIKTRLHSAATTEEGFGRGLG
ILPLSGPIAPDAHVGSYEFIVHINTWRPDSQVHPPM

>d1a6ca3_b.10.1.2 (A:349-513) TRSV capsid protein {Tobacco ringspot virus}
FSSSELYNWFTLTNLKPDANTGVVNFDPGYIHDFASKDATVTLASNPLSWLVAATGWHYGEVDLCI
SWSRSKQAQAQEGSVSITTNRYRDWGAYWQGQARIYDLRRTEAEIPIFLGSYAGATPSGALGKQNYVRI
SIVNAKDIVALRVCLRPKSIKFWGRSATLF

>d4sbva_b.10.1.2 (A:) SBMV coat protein {Southern bean mosaic virus, cow pea strain}
SSMDVTILSHCELSTELAVTVTIVVTSELVMPFTVGTWLRGVAQNWSKYAWVAIRYTYLPSCPTTTSG
AIHMGFQYDMADTLPVSVNQLSNLKGVTGPVWEGQSGLCFVNNTKCPDTSRAITIALDITNEVSEK
RYPFKTATDYATAVGVNANIGNILVPARLVTAMEGGSSKTAVNTGRLYASYTIRLIEPIAAALNL

>d4sbvc_b.10.1.2 (C:) SBMV coat protein {Southern bean mosaic virus, cow pea strain}
QAGVSMAPIAQGTMVKLRPPMLRSSMDVTILSHCELSTELAVTVTIVVTSELVMPFTVGTWLRGVAQ
NWSKYAWVAIRYTYLPSCPTTTSGAIHMGFQYDMADTLPVSVNQLSNLKGVTGPVWEGQSGLCFV
NNTKCPDTSRAITIALDITNEVSEKRYPFKTATDYATAVGVNANIGNILVPARLVTAMEGGSSKTAVNT
GRLYASYTIRLIEPIAAALNL

>d2tbva_b.10.1.2 (A:) TBSV coat protein {Tomato bushy stunt virus}
GGVTVTSHREYLTQVNNSSGFVVNGGIVGNSLQLNPSNGTLFSWLPALASNFDQYSFNSVVLVDYVPL
CGTTEVGRVALYFDKDSQDPEPADRVELANFGVLKETAPWAEAMLRIPTDKVKRYCND SATVDQKLI
DLGQLGIATYGGAGADAVGELFLARSVTLYFPQPTNTLLSSKRLDLTGLADATGPGYLVLRTPVTLT
HTFRATGTFNLSGGLRCLTSLTLGATGAVVINDIL AIDNVGTASDYFLNCTVSSLPATVTFTVSGVAAGI
LLVGRARANVVNLL

>d2tbvc_b.10.1.2 (C:) TBSV coat protein {Tomato bushy stunt virus}
IITHVGGVGGSIMAPVAVSRQLVGSKPFTGRTSGGVTVTSHREYLTQVNNSSGFVVNGGIVGNSLQL
NPSNGTLFSWLPALASNFDQYSFNSVVLVDYVPLCGTTEVGRVALYFDKDSQDPEPADRVELANFGVL
KETAPWAEAMLRIPTDKVKRYCND SATVDQKLI DLGQLGIATYGGAGADAVGELFLARSVTLYFPQP
TNTLLSSKRLDLTGLADATGPGYLVLRTPVTLTHTFRATGTFNLSGGLRCLTSLTLGATGAVVINDIL
AIDNVGTASDYFLNCTVSSLPATVTFTVSGVAAGILLVGRARANVVNLL

>d1cwpa_b.10.1.2 (A:) Cowpea chlorotic mottle virus {Host: cowpea (*Vigna unguiculata*),
(L.)}

KAIKAWTGYSVSKWTASCAAAEAKVTSAITISLPNELSSERNKQLKVGRVLLWLGLLPSVSGTVKSCV
TETQTAAASFQVALAVADNSKDVVAAMYPEAFKGITLEQLAADLIYLYSSAALTEGDVIVHLEVEH
VRPTFDDSFPTVY

>d1c8na_b.10.1.2 (A:) TNV coat protein {Tobacco necrosis virus}
NSTVVSNSELILNLTPIALAYTVQSLPLIATQPAWLGTIADNYSKWRWVSLRIIYSPKCPTTTSGTVAM
CLSYDRNDVAPGSRVQLSQT YKAINFPPYAGYDGAAILNTDVTPTS AIYVDVDVTRFDKAWYSTIGTA
AFAALTAFDQNQFCPCTVHIGSDGGPAVAVPPGDIFFKYVIELIEPINPTMN

>d1c8nc_b.10.1.2 (C:) TNV coat protein {Tobacco necrosis virus}
GVSRRAGGFVTAPVIGAMVTRPTVPRFGMRGNSTVVSNSELILNLTPIALAYTVQSLPLIATQPAWLGTI
ADNYSKWRWVSLRIIYSPKCPTTTSGTVAMCLSYDRNDVAPGSRVQLSQT YKAINFPPYAGYDGAAIL
NTDVTPTS AIYVDVDVTRFDKAWYSTIGTAAFAALTAFDQNQFCPCTVHIGSDGGPAVAVPPGDIFFK
YVIELIEPINPTMN

>d1auya_b.10.1.2 (A:) TYMV coat protein {Turnip yellow mosaic virus}

SPLTIKQPFQSEVLFAGTKDAEASLTIANIDSVSTLTTFYRHASLESWVTHPTLQAPTFPTTVGVCW
VPAQSPVTPAQITKTYGGQIFCIGGAIQTLSP LIVKCPLEMMQPRVKDSIQYLDSPKLLISITAQPTAPPA
STCIITVSGTLSMHSPLITDTST

>d1auyb_b.10.1.2 (B:) TYMV coat protein {Turnip yellow mosaic virus}

MEIDKELAPQDRTVTVATVLPVAVPGSPPLTIKQPFQSEVLFAGTKDAEASLTIANIDSVSTLTTFYRHA
SLESWVTHPTLQAPTFPTTVGVCWVPAQSPVTPAQITKTYGGQIFCIGGAIQTLSP LIVKCPLEMM
QPRVKDSIQYLDSPKLLISITAQPTAPPASTCIITVSGTLSMHSPLITDTST

>d1e57a_b.10.1.2 (A:) PHMV coat protein {Physalis mottle virus}

SPAIVLPFQFEATTFGTAETAQVSLQTADPITKLTAPYRHAQIVECKAILTPTDLAVSNPLTVYLAWV
PANSAPPTQILRVYGGQSFVLGGAISSAAKTIEVPLNLDVSNRMLKDSVTTYDTPKLLAYSRAPTNPS
KIPTASIQISGRIRLSKPMLIAN

>d1e57b_b.10.1.2 (B:) PHMV coat protein {Physalis mottle virus}

VVKVKQASIPAGSILSQPNTEQSPAIVLPFQFEATTFGTAETAQVSLQTADPITKLTAPYRHAQIVEC
KAILTPTDLAVSNPLTVYLAWVPAVSPATPTQILRVYGGQSFVLGGAISSAAKTIEVPLNLDVSNRMLK
DSVTTYDTPKLLAYSRAPTNPSKIPTASIQISGRIRLSKPMLIAN

>d1ddla_b.10.1.2 (A:) DYMV coat protein {Desmodium yellow mottle tymovirus}

MEQDKILAHQASLNTKPSLLPPPVGNNPPVISYFPQITLASLGTEAADSVSIIASNSVLATYTYALYRHA
QLKHLKATHPTYMAPKYPTSVALVWVPANSTATSTQVLDTYGGLHFCIGGSVNSVKPIDVEANLTNL
NPIIKASTTFTDTPKLLYYSKAQATAPTSPTCYLTIQGGQIELSSPLLQASS

>d1f15a_b.10.1.2 (A:) CMV coat protein {Cucumber mosaic virus, strain fny}

ERCRPGYTFTSITLKPPKIDRGSYYGKRLLLPDSVTEYDKKLVSRQLQIRVNPLPKFDSTVWVTVRKP
ASSDLSVAAISAMFADGASPVLVYQYAASGVQANNKLLYDLSAMRADIGDMRKYAVLVYSKDDALET
DELVLHVDIEHQRIPTSGVLPV

>d1f15b_b.10.1.2 (B:) CMV coat protein {Cucumber mosaic virus, strain fny}

DANFRVLSQQLSRLNKTAAAGRPTINHPTFVGSERCPRGYTFTSITLKPPKIDRGSYYGKRLLLPDSV
TEYDKKLVSRQLQIRVNPLPKFDSTVWVTVRKPASSDLSVAAISAMFADGASPVLVYQYAASGVQAN
NKLLYDLSAMRADIGDMRKYAVLVYSKDDALETDELVLHVDIEHQRIPTSGVLPV

>d2bbva_b.10.1.3 (A:) Nodavirus capsid protein {Black beetle virus}

LTRLSQPGLAFLKCAFAPDFNTDPGKGPDRFEGKVVTRKDVLNQSFNFTANRDTFILIAPTPGVAY
WVADVPAGTFPISTTTFNANVFPGFNSMFGNAAASRSQVSSFRYASMNVIYPTSNLMQFAGSITV
WKCPVKLSNVQFPVATTPATSALVHTLVGLDGLAVGPDNFSSEFIKGVFSQSVCNEPDFEFSIDILEGI
QTLPPANVTVATSGQPFNLAAGAEAVSGIVGWGNMDTIVIRVSAPTGAVNSAILKTWACLEYRPNPN
AMLYQFGHDSPPCDEVALQEYRTVARSLPVAVIAAQN

>d2bbvc_b.10.1.3 (C:) Nodavirus capsid protein {Black beetle virus}

TQTAPVPQQNVKQPRRRNRARRNRQGRAMNMGALTRLSQPGLAFLKCAFAPDFNTDPGKGI
PDRFEGKVVTRKDVLNQSFNFTANRDTFILIAPTPGVAYWVADVPAGTFPISTTTFNANVFPGFNSM
FNAAASRSQVSSFRYASMNVIYPTSNLMQFAGSITVWKCPVKLSNVQFPVATTPATSALVHTLVGL
DGLAVGPDNFSSEFIKGVFSQSVCNEPDFEFSIDILEGIQTLPPANVTVATSGQPFNLAAGAEAVSGIV
GWGNMDTIVIRVSAPTGAVNSAILKTWACLEYRPNPNAMLYQFGHDSPPCDEVALQEYRTVARSLP
VAVIAAQN

>d1nova_b.10.1.3 (A:) Nodavirus capsid protein {Nodamura virus}

NMLKMSAPGLDFLKCAFASPDFSTDPGKGPDKFQGLVLPKHKHCLTQSITFTPGKQTMLLVAPIPIA
CLKAEANVGASFSVPLASVEFPQFDQLFGTSATDAAANVTAFRYASMAAGVYPTSNLMQFAGSIQV
YKIPLKQVLNSYSQTVATVPPTNLAQNTIAIDGLEALDALPNNNYSGSFIEGCYSQSVCNEPEFEFHPI

MEGYASVPPANVTNAQASMFTNLTFSGARYTGLGDMDAIAILVTTPTGAVNTAVLKVWACVEYRPN
PNSTLYEFARESPANDEYALAAAYRKIARDIPIAVACKDN

>d1novc_b.10.1.3 (C:) Nodavirus capsid protein {Nodamura virus}

RRRAAPRQQRQQRNQRASNQRPRRRARRTRRRQQRMAATNNMLKMSAPGLDFLKCAFASPDFSTD
PGKGIPDKFQGLVLPKKHCLTQSITFTPGKQTMLLVAPIPGIACLKAEANVGASFSGVPLASVEFPFGFD
QLFGTSATDTAANVTAFRYASMAAGVYPTS NLMQFAGSIQVYKIPLKQVLNSYSQTVATVPPTNLAQ
NTIAIDGLEALDALPNNNYSGSFIEGCYSQSVCNEPEFEFHPIMEGYASVPPANVTNAQASMFTNLTF
SGARYTGLGDMDAIAILVTTPTGAVNTAVLKVWACVEYRPNPNSTLYEFARESPANDEYALAAAYRKIA
RDIPIAVACKDN

>g1f8v.1 b.10.1.3 (A:,D:) Nodavirus capsid protein {Pariacoto virus}

NRRNKARKVVSSTALVPMAPASQRTGPAPRKPRKRNQALVRNPRLTDAGLAFKCAFAAPDFSVD
PGKGIPDNFHGRTLAIKDCNTTSVFTPNNTDTYIVVAPVPGFAYFRAEVAVGAQPTTFVGVPPYPTAT
NFGAGSQNGLPAVNNYSKFRYASMACGLYPTS NMMQFSGSVQVWRVDLNLSEAVNPAVTAITPAPG
VFANFVDKRINGLRGIRPLAPRDNYSGNFIDGAYTFAFDKSTDFEWCDFVRSLEFSESNVLGAATAM
KLLAPGGGTDTTLTGLGNVNTLVYKISTPTGAVNTAILRTWNCIELQPYTDSALFQFSGVSPPFDPLA
LECYHNLKMRFPVAVSSRENXSKFWEGVLRVLNQISGTLVIPGPVGTISAGVHQLTGMYM

>g1f8v.2 b.10.1.3 (B:,E:) Nodavirus capsid protein {Pariacoto virus}

NPRLTDAGLAFKCAFAAPDFSVDPGKGIPDNFHGRTLAIKDCNTTSVFTPNNTDTYIVVAPVPGFAY
FRAEVAVGAQPTTFVGVPPYPTATNFGAGSQNGLPAVNNYSKFRYASMACGLYPTS NMMQFSGSVQV
WRVDLNLSEAVNPAVTAITPAPGVFANFVDKRINGLRGIRPLAPRDNYSGNFIDGAYTFAFDKSTDFE
WCDFVRSLEFSESNVLGAATAMKLLAPGGGTDTTLTGLGNVNTLVYKISTPTGAVNTAILRTWNCIE
LQPYTDSALFQFSGVSPPFDPLALECYHNLKMRFPVAVSSRENXSKFWEGVLRVLNQISGTLVIP

>d1dncv_b.10.1.3 (-) Galleria mellonella densovirus capsid protein {Wax moth (Galleria mellonella), densovirus}

VYIIPRPFNSFGKKLSTYTKSHKFMIFGLANNVIGPTGTGTTAVNRLTTCLAEIPWQKLPLYMNQSE
FDLLPPGSRVVECNVIVFRNTNRIAFETSSTVTQKATLNQISNVQTAIGLNKLGWGINRAFTAFQSDQ
PMIPTATTAPKYEPVTGDTGYRGMIAIDYDGADSTNDTAFGNAGNYPHHQVSSFTFLQNYCYMYQQT
NQGTGGWPCLAEHLQQFDSKTVNNQCLIDVTYKPKMGLIKSPLNYKIIGQPTVKGTSVGDNLVNM
RGAVVTNPPEATQNVAESTHNLTRNFPADLFNIYSDIEKSQVLHKGPGWGHENPQIQPSVHIGIQA
VPA LTTGALLINSSPLNSWTDSMGYIDVMSCTVMEAQPTHFPFSTEANTNPGNTIYRINLTPNSLTS
AFN GLYNGATLGN

>d1b35a_b.10.1.3 (A:) Cricket paralysis virus (CRPV) {Host: australian black field cricket (Teleogryllus commodus)}

VMGEDQQIPRNEAQHGVPISIDTHRISNNWSPQAMCIGEKVVSIRQLIKRFGIFGDANTLQADGSSF
VVAPFTVTSPTKTLTSTRNYTQFDYYYYLYAFWRGSMRIKMAETQDGTGTPRKKTNFTWFVRFM
NSLQDSFNLSLSTSSAVTTTVLPSGTINMGPSTQVIDPTVEGLIEVEVPYNNISHITPAVTIDDGT
PSM EDYLKGHSPCLLTFSPRDSISATNHIITASFMRALGDDFSFMYLLGVPPLVNVARA

>d1b35b_b.10.1.3 (B:) Cricket paralysis virus (CRPV) {Host: australian black field cricket (Teleogryllus commodus)}

ENSHIENEDKRLTSEQKEIVHFVSEGVTPSTTALPDIVNLSTNYLDKNTREDRIHSIKDFLSRPIIIATN
LWSVSDPVEKQLYTANFPEVLISNAMYQDKLKGFGVLRATLVVKVQVNSQPFPQQGRLMLQYIPYAQY
MPNRVTLINETLQGRSGCPRTDLELSVGTEVEMRIPYVSPHLYNLTITGQGSFGSIYVVVYQLHDQV
SGTGSIEYTVWAHLEDVDVQYPTGANIFTGNEAYIKGTSRYDAAQKAHAA

>d1b35c_b.10.1.3 (C:) Cricket paralysis virus (CRPV) {Host: australian black field cricket

{Teleogryllus commodus}

SKPTVQKGIGECKLRGQGRMANFDGMDMSHKMALSSTNEIETNEGLAGTSLDVMDSLRSVLSIPNY
WDRFTWKTSDVINTVLWDNYVSPFKVKPYSATITDRFRCTHMGKVANAFTYWRGSMVYTFKFKVK
TQYHSGRLRISFIPYYNTTISTGTPDVSRTQKIVVDLRTSTAVSFVTPYIGSRPWLYCIRPESSWLSKD
NTDGALMYNCVSGIVRVEVLNQLVAAQNVFSEIDVICEVNGGPDLEFAGPTCPRYVPYAGDFTLADT
RKIEAERTQEYSNNED

>d1sida_b.10.1.4 (A:) Murine polyomavirus coat protein vp1 {Murine polyoma virus, strain small-plaque 16}

KACPRPAPVPKLLIKGGMEVLDLVTGPDSVTEIEAFLNPRMGQPPTPELTEGGQYYGWSRGINLATS
DTEDSPGNNTLPTWSMAKLQLPMLNEDLTCDTLQMWEAVSVKTEVVGSGSLLDVHGFNKPTDTV
NTKGISTPVEGSQYHVFVAVGGEPDLQGLVTDARTKYKEEGVVTIKTITKKDMVNKDQVLNPISKAK
LDKDGMYPVEIWHPPAKNENTRYFGNYTGGTTTTPPVLQFTNTLTTVLLDENGVGPLCKGEGLYLS
CVDIMGWRVTRNYDVHHWRGLPRYFKITLRKRWVKNPYPMASLISSLFNNMLPQVQGPMEGEN
TQVEEVRYDGTPEVPGDPMTRYVDRFGKTKTVFPG

>d1vpsa_b.10.1.4 (A:) Murine polyomavirus coat protein vp1 {Murine polyoma virus, strain small-plaque 16}

GGMEVLDLVTGPDSVTEIEAFLNPRMGQPPTPELTEGGQYYGWSRGINLATS DTEDSPGNNTLPT
WSMAKLQLPMLNEDLTCDTLQMWEAVSVKTEVVGSGSLLDVHGFNKPTDTVNTKGISTPVEGSQY
HVFVAVGGEPDLQGLVTDARTKYKEEGVVTIKTITKKDMVNKDQVLNPISKAKLDKDGMYPVEIWH
PDKNENTRYFGNYTGGTTTTPPVLQFTNTLTTVLLDENGVGPLCKGEGLYLSCVDIMGWRVTRNY
DVHHWRGLPRYFKITLRKRWVK

>d1fmd1_b.10.1.4 (1:) Foot-and-mouth disease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

TTTTGESADPVTTTVENYGGGETQVQRRHHTDVAFLVDRFVKVTVSDNQHTLDVMQAHKDNIVGAL
LRAATYYFSDLEIAVHTHTGKLTWVWPNGAPVSALNNTTNPAYHKGPVTRLALPYTAPHRVLATAYTG
TTTTYASARGDLAHLTTTHAAHLPTSFNFGAVKAETITELLVRMKRAELYCPRPILPIQPTGDRHKQP
LVAPAKQ

>d1fmd2_b.10.1.4 (2:) Foot-and-mouth disease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

DKKTEETLLEDRLTTRNGHTTSTTQSSVGVTFGYATAEDSTSGPNTSALETRVHQAERFFKMALF
DWVPSQNFQGHMHKVVLPHEPKGVYGLVKSAYMRNGWDVEVTAVGNQFNGGCLLVALVPEMGDI
SDREKYQLTLYPHQFINPRTNMTAHITVPYVGVNRYDQYKQHRPWTLVVMVAVPLTNTAGAQQIK
VYANIAPTNVHVAGELPSKE

>d1fmd3_b.10.1.4 (3:) Foot-and-mouth disease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

GIFPVACSDGYGNMVTTPDKTADPAYGKVYNPPRTALPGRFTNYLDVAEACPTFLMFENVYPVSTRT
DGQRLAKFDVSLAAKHMSNTYLAGLAQYYTQYTGTINLHFMFTGPTDAKARYMVAVVPPGMDAP
DNPEEAHCHIAEWDGTGLNSKFTFSIPYISAADYTYTASHEAETTCVQGWVCVYQITHGKADADALV
VSASAGKDFELRLPVDARQQ

>d1qqp1_b.10.1.4 (1:) Foot-and-mouth disease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

TTSAGESADPVTTTVENYGGGETQIQRRQHTDVSFIMDRFVKVTPQNQINILDLMQVPSHTLVGALLR
ASTYYFSDLEIAVKHEGDLTWVWPNGAPEKALDNTTNPAYHKAPLTRLALPYTAPHRVLATVYNGEC
RYSRNAVPNLRGDLQVLAQKVARTLPTSFNYGAIKATRVTELLYRMKRAETYCPRLLAIHPTEARH

KQKIVAPVK

>d1qqp2_b.10.1.4 (2:) Foot-and-mouth disease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

DKKTEETLLEDRILTRNGHTTSTTQSSVGVTYGYATAEDFVSGPNTSGLETRVVQAERFFKTHLFD
WVTSDFSFRCHLLELPTDHKGVYGLTDSYAYMRNGWDVEVTAVGNQFNGGCLLVAMVPELCSIQK
RELYQLTLFPHQFINPRTNMTAHITVPFVGVNRYDQYKVHHPWTLVVMVAVPLTVNTEGAPQIKVYA
NIAPTNVHVAGEFPSKE

>d1qqp3_b.10.1.4 (3:) Foot-and-mouth disease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

GIFPVACSDGYGLVTTDPKTADPVYGVFNPPRNQLPGRFTNLLDVAEACPTFLRFEGGVVYVTTK
TDSDRVLAQFDMSLAAKHMSNTFLAGLAQYYTQYSGTINLHFMFTGPTDAKARYMVAYAPPGMEP
PKTPEAAAHCIAEWDGTGLNSKFTFSIPYLSAADYTYTASDVAETTNNVQGWVCLFQITHGKADGDAL
VVLASAGKDFELRLPVDARAE

>d1c8da_b.10.1.4 (A:) Parvovirus (panleukopenia virus) capsid {Host: dog (Canis familiaris)}

GVGISTGTFNNTQTEFKFLENGWVYITANSSRLVHLNMPESNYRRVVVNNMDKTAVNGNMALDDI
HAEIVTPWVSLVDANAWGVWFNPGDWQLIVNTMSELHLVSFEQEIFNVVVKTVSESATQPPTKVYN
NDLTASLMVALDSNNTMPFPAAMRSETLGFYPWKPTIPTPWRYFFQWDRTLIPSHTGTSPTPTNI
YHGTDPPDDVQFYTIENSVPVHLLRTGDEFATGTFDFCKPCRLTHTWQTNRALGLPPFLNSLPQSEG
DTNFGDIGVQQDKRRGVTTQMGNTNYITEATIMRPAEVGYSAPYYSFEASTQGPFKTPIAAGRGAQT
DENQAADGNPRYAFGRQHGGQTTTTGETPERFTYIAHQDTGRYPEGDWQININFLPVTNDNVLL
PTDPIGGKTGINYTNIFNTYGPLTALNNVPPVYPNGQIWDKEFDTDLKPRLHVNAPFVCQNNCPGQL
FVKVAPNLNTQYDPDASANMSRIVTYSDFWWKGKLVFKAKLRASHTWNPIQQMSINVDNQFNYP
SNIGGMKIVYEKSQLAPRKLY

>d1k3va_b.10.1.4 (A:) Parvovirus (panleukopenia virus) capsid {Host: pig (Sus scrofa)}

GVGVSTGTFNNTQTEFQYLGEGLVRITAHASRLIHLNMPHEHYKRIHVLSSESGVAGQMVQDDAHT
QMVTWPVSLIDANAWGVWFNPADWQLISNNMTEINLVSFQEIEFNVVVKTVTESATSPPTKIYNNDLT
ASLMVALDTNNTLPYTPAAPRSETLGFYPWLPKPTKPTQYRYLSCIRNLNPPTYTGQSQQITDSIQTGL
HSDIMFYTIENAVPIHLLRTGDEFSTGIYHFDTKPLKLTHTSWQTNRSGLPPLKLTTEPTTEGDQHPGT
LPAANTRKGYHQTINNSYTEATAIRPAQVGYNTPYMNFYNSGGPFLTPIVPTADTQYNDDEPNQAI
RFTMDYQHGHLLTSSQELERYTFNPQSKCGRAPKQQFNQQAPLNLENTNNGTLLPSDPIGGKSNMH
FMNTLNNTYGPLTALNNTAPVFPNGQIWDKELDTDLKPRLHVTAPFVCKNNPPGQLFVKIAPNLTD
FNADSPQQPRIITYSNFWWKGTLTFTAKMRSSNMWNPQQHTTTAENIGNYIPTNIGGIRMFPEYSQ
LIPRKLY

>d1mvma_b.10.1.4 (A:) MVM coat protein {Murine minute virus, strain i}

GVGVSTGSYDNQTHYRFLGDGWVEITALATRLVHLNMPKSENYCRIRVHNTTDTSVKGNMAKDDA
HEQIWTWPVSLVDANAWGVWLQPSDWQYICNTMSQLNLVSLDQEIEFNVVVKTVTEQDSGGQAIKIY
NNDLTACMMVAVDSNNILPYTPAANSMETLGFYPWKPTIASPYRYFFCVDRDLSVTYENQEGTIEH
NVMGTPKGMNSQFFTIENTQQITLLRTGDEFATGTYFDNPNVVKLTHTWQTNRQLGQPLLSTFPE
ADTDAGTLTAQGSRHGATQMEVNVWSEAIRTPAQVGFQPHNDFEASRAGPFAAPKVPADVQGG
MDREANGSVRYSYGKHGENWAAHGPAPERWTWDETDFGSGRDRDGFISAPLVPPPLNGILT
ANPIGTKNDIHFNSVFNYSYGLTTFSSHPSVYPQGGQIWDKELDLEHKPRLHITAPFVCKNNAPGQML
VRLGPNLTDQYDPNGATLSRIVTYGTFWKGKLTMRAKLRANTTWNPVYQVSVEDNGNSYMSVTK
WLPATGNMQSVPLITRPVARNY

>d1hxs1_b.10.1.4 (1:) Poliovirus {Poliovirus type 1, strain Mahoney}
GSSSTDNTVRETVGAATSRDALPNTEASGPTHSEIPALTAVETGATNPLVPSDTVQTRHVVQHRSRS
ESSIESFFARGACVTIMTVDNPASTTNKDKLFAVWKITYKDTVQLRRKLEFFTYSRFDMELTFVVT
NFTETNNGHALNQVYQIMYVPPGAPVPEKWDDYTWQTSSNPSIFYTYGTAPARISVPYVVISNAYSH
FYDGFSGVPLKQSAALGDSLYGAASLNDFGILAVRVVNDHNPTKVTSKIRVYLKPKHIRVWCPRPP
RAVAYYGGVDYKDGTLTPLSTKDLTTY

>d1hxs2_b.10.1.4 (2:) Poliovirus {Poliovirus type 1, strain Mahoney}
ACGYSDRVLQTLGNSTITTQEAANSVVAYGRWPEYLRDSEANPVDQPTPEPDVAACRFYTLDTVSW
TKESRGWWKLPDALRDMGLFGQNMYYHYLGRSGYTVHVQCNASKFHQGALGVFAVPEMCLAG
DSNTTTMHTSYQNANPGEKGGTFTGTFTPDNNQTSARRFCPVDYLLGNGTLLGNAFVFPHQIINL
RTNNCATLVLPYVNSLSIDSMVKHNNWGIAILPLAPLNFASSEPEIPITLTIAPMCCEFNGLRNITLP
RLQ

>d1hxs3_b.10.1.4 (3:) Poliovirus {Poliovirus type 1, strain Mahoney}
GLPVMNTPGSNQYLTDNFQSPCALPEFDVTPPIDIPGEVKNMELAEIDTMIPFDLSATKKNTE
MYRVRLSDKPHTDDPILCLSLSPASDPRLSHTMLGEILNYTHWAGSLKFTFLFCGSMMATGKLLVS
YAPPGADPPKRRKEAMLGTHVIWDIGLQSSCTMVVPWISNTTYRQTIDDSFTEGGYISVIFYQTRIVV
PLSTPREMDILGFVSACNDFSVRLLRDTHIEQKA

>d1pov0_b.10.1.4 (0:) Poliovirus {Poliovirus type 1, strain Mahoney}
GAQVSSQKVGAHENSNRAYGGSTINYTTINYRDSASNAASKQDFSQDPSKFTEPIKDVLIKTAPMLN
SPNIEACGYSDRVLQTLGNSTITTQEAANSVVAYGRWPEYLRDSEANPVDQPTPEPDVAACRFYTL
TVSWTKESRGWWKLPDALRDMGLFGQNMYYHYLGRSGYTVHVQCNASKFHQGALGVFAVPEM
CLAGDSNTTTMHTSYQNANPGEKGGTFTGTFTPDNNQTSARRFCPVDYLLGNGTLLGNAFVFPHQ
IINLRTNNCATLVLPYVNSLSIDSMVKHNNWGIAILPLAPLNFASSEPEIPITLTIAPMCCEFNGLRNI
TLPRQL

>d1pov1_b.10.1.4 (1:) Poliovirus {Poliovirus type 1, strain Mahoney}
QHRSRSESSIESFFARGACVTIMTVDNPASTTNKDKLFAVWKITYKDTVQLRRKLEFFTYSRFDMELT
FVV TANFTETNNGHALNQVYQIMYVPPGAPVPEKWDDYTWQTSSNPSIFYTYGTAPARISVPYVVIS
NAYSHFYDGFSGVPLKQSAALGDSLYGAASLNDFGILAVRVVNDHNPTKVTSKIRVYLKPKHIRVW
CPRPPRAVAYYGGVDYKDGTLTPLSTKDLTTY

>d1eah1_b.10.1.4 (1:) Poliovirus {Poliovirus type 2, strain Lansing}
ANNLPDTQSSGPAHSETPALAVETGATNPLVPSDTVQTRHVIQKRTRSESTVESFFARGACVAIIEV
DNDAPTKRASKLFSVWKITYKDTVQLRRKLEFFTYSRFDMEFFVVTSNYTDANNGHALNQVYQI
MYIPPGAPIGKWNNDYTWQTSSNPSVFYTYGAPPARISVPYVGIANAYSHFYDGFAGVPLAGQASTE
GDSLYGAASLNDFGSLAVRVVNDHNPTKLTISKIRVYMKPKHVRVWCPRPPRAVPPYGGVDYKDG
LAPLPGKGLTTY

>d1eah2_b.10.1.4 (2:) Poliovirus {Poliovirus type 2, strain Lansing}
SVRVMQLTLGNSTITTQEAANSVVAYGRWPEYIKDSEANPVDQPTPEPDVAACRFYTLDTVTWRKES
RGWWKLPDALRDMGLFGQNMFYHYLGRAGYTVHVQCNASKFHQGALGVFAVPEMCLAGDSTT
HMF TKYENANPGEKGGFEKGSFTLDTNATNPARNFCPVDYLFSGVLAGNAFVYPHQIINLRTNNC
ATLVLPYVNSLSIDSMVKHNNWGIAILPLAPLDFATESSTEIPITLTIAPMCCEFNGLRNITVPRQT

>d1eah3_b.10.1.4 (3:) Poliovirus {Poliovirus type 2, strain Lansing}
GLPVLNTPGSNQYLTDNYQSPCAIPEFDVTPPIDIPGEVRNMMELAEIDTMIPNLNTNQRKNTMD
MYRVELNDAAHSDTPILCLSLSPASDPRLAHTMLGEILNYTHWAGSLKFTFLFCGSMMATGKLLVS
YAPPGAEAPKSRKEAMLGTHVIWDIGLQSSCTMVVPWISNTTYRQTINDSFTEGGYISMIFYQTRVVV

PLSTPRKMDILGFVSACNDFSVRLLRDTHISQEA

>d1pvc1_b.10.1.4 (1:) Poliovirus {Poliovirus type 3, strain Sabin}

QDSLPTKASGPAHSKEVPALTAVETGATNPLAPSDTVQTRHVVQRRSRSESTIESFFARGACVAIIEV
DNEQPTTRAQKLFAMWRITYKDTVQLRRKLEFFTYSRFDMEFTFVVTANFTNANNNGHALNQVYQI
MYIPPGAPTPKSWDDYTWTSSNPSIFYTYGAAPARISVPYVGLANAYSHFYDGFVPLKTDANDQ
IGDSLYSAMTVDDFGVLAVRVVNDHNPTKVTSTKVRIYMKPKHVRVWCPRPPRAVPYYPGVDYRN
NLDPLSEKGLTTY

>d1pvc2_b.10.1.4 (2:) Poliovirus {Poliovirus type 3, strain Sabin}

ACGYSDRVLQLTLGNSTITTQEAANSVVAYGRWPEFIRDDEANPVDQPTPEPDVATCRFYTLDTVMW
GKESKGWVWKLDPALRDMGLFGQNMYYHYLGRSGYTVHVQCNASKFHQALGVFAIPEYCLAGD
SDKQRYTSYANANPGERGGKFYSQFNKDNAVTSKREFCPVDYLLGCGVLLGNFVYPHQIINLRN
NSATIVLPYVNALAIDSMVKHNNWGIAILPLSPLDFAQDSSVEIPITVTIAPMCSEFNGLRNVTPAKFQ

>d1pvc3_b.10.1.4 (3:) Poliovirus {Poliovirus type 3, strain Sabin}

GLPVLNTPGSNQYLTSNDHQSPCAIPEFDVTPPIDIPGEVKNMELAEIDTMIPLNLESTKRNTMDM
YRVTLSDSADLSQPILCLSLSPAFDPRLSHTMLGEVLNYYTHWAGSLKFTFLFCGSMMATGKILVAYA
PPGAQPPTSREAMLGTHVIWDLGLQSSCTMVVVPWISNVTYRQTTQDSFTEGGYISMFYQTRIVVPL
STPKSMSMLGFVSACNDFSVRLLRDTHISQSA

>d4rhv1_b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 14}

TVASISSGPKHTQKVPILTANETGATMPVLPDSIETRTTYMHFNGSETDVECFLGRAACVHVTEIQN
KDATGIDNHREAKLFNDWKNLSSLVQLRKKLELFTYVRFDSEYITILATASQPDSANYSSNLVVQAM
YVPPGAPNPKEWDDYTWTQSASNPVFFKVGDTSRFSVPYVGLASAYNCFYDGYSHDDAETQYGITV
LNHMGSMAFRIVNEHDEHKTLLKIRVYHRAKHVEAWIPRAPRALPYTSIGRTNYPKNTEPVIKKRK
GDIKSY

>d4rhv2_b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 14}

GYSDRVQQITLGNSTITTQEAANAVVCYAEWPEYLPDVDASDVNKTSKPDTSVCRFYTLDSKTWTTG
SKGWCWKLDPALKDMGVFGQNMFFHSLGRSGYTVHVQCNATKFHSGCLLVVVIPEHQLASHEGGN
VSVKYTFTHPGERGIDLSSANEVGGPVKDVLYNMNGTLLGNLLIFPHQFINLRNNTATIVIPYINSVP
IDSMTRHNNVSLMVIAPLTVPTGATPSLPITVTIAPMCTEFSGIRSKSIVPQ

>d4rhv3_b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 14}

GLPTTTLPGSGQFLTDDRQSPSALPNYEPTPRIHIPGKVHNLLEIIQVDTLIPMNNHTHKDEVNSYL
IPLNANRQNEQVFGTNLFIGDGVFKTLLGEIVQYYTHWSGLRFSMLYTGALSSAKLILAYTPPGA
RGPQDRREAMLGTHVVDIGLQSTIVMTIPWTSGVQFRYTDPTYTSAGFLSCWYQTSILIPPETT
GQVYLLSFISACPDFKLRLMKDTQTISQTVLALTE

>d1aym1_b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 16}

NPVERYVDEVLNEVLVVPNINQSHPTTSNAAPVLDAEETGHTNKIQPEDTIETRYVQSSQTLDEMVS
ESFLGRSGCIHESVLDIVDNYNDQSFTKWNINLQEMAQIRRFEMFTYARFDSEITMVPSVAAKDGH
IGHIVMQYMYVPPGAPIPTTRDDYAWQSGTNASVFWQHGQPFPRFSLPFLSIASAYMFDYDGYDGT
YKSRYGTVVTNDMGTLCSRIVTSEQLHKVKVVTRIVYHAKHTKAWCPRPPRAVQYSHTHTTNYKLS
SEVHNDVAIRPRTNLTTV

>d1aym2_b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 16}

SDRIIQITRGDSTITSQDVANAVVGYGVWPHYLTPQDATAIDKPTQPDTSNRFYTLDSKMWNSTSK
GWWWKLPDALKDMGIFGENMFYHFLGRSGYTVHVQCNASKFHQGTLLVVMPIEHQLATVKNKGNV
NAGYKYTHPGEAGREVGTVENEKQPSDDNWLNFDTLLGNLLIFPHQFINLRNNSATLIVPYVNA
VPMDSMVRHNNWSLVIPVCQLQSNNISNIVPITVSISPMCAEFSGARAKTVVQ

>d1aym3_b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 16}
GLPVYVTPGSGQFMTTDDMQSPCALPWYHPTKEIFIPGEVKNLIEMCQVDTLIPINSTQSNIGNVSM
YTVTLSPQTKLAEEIFAIKVDIASHPLATTLIGEIASYFTHWTGSLRFSFMFCGTANTTLKVLLEYTPP
GIGKPRSRKEAMLGTHVVWDVGLQSTVSLVVPWISASQYRFTTTPDTYSSAGYITCWYQTNFVVPNT
PNTAEMLCFVSGCKDFCLRMARDTDLHKQTGPITQ

>d1r1a1_b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 1A}
NYIDEVLNEVLVVPNIKESHHTTSNSAPLLDAAETGHTSNVQPEDAIETRYVITSQTRDEMSIESFLG
RSGCVHISRIKVDYTDYNGQDINFTKWKITLQEMAQIRRFELFTYVRFDSEITLVPCIAGRGDDIGHI
VMQYMYVPPGAPIPSKRNDFSWQSGTNMSIFWQHQPFRFSIPFLSIASAYMFYDGYDGDNTSS
KYGSVVTNDMGTICSRIVTEKQKLSVITTHIYHKAKHTKAWCPRPPRAVPYTHSHVTNYMPETGD
VTTAIVRRNTITTA

>d1r1a2_b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 1A}
DRIMQITRGDSTISSDDVANAVVGYGVWPHYLTPQDATAINKPTQPDTSNRFYTLKSHWNGSSKG
WWWKLPDALKDMGIFGENMYHFLGRSGYTVHVQCNAKSFHQGTLVAMIPHEQLASAKHGSVT
AGYKLTHPGEAGRDVSRDASLRQPSDDSWLNFDGTLGNLLIFPHQFINLRSNNSATLIVPYVNA
VPMDSMLRHNWCLVIIPISPLRSETTSSNIVPITVISIPMCAEFSGARAKNIQ

>d1r1a3_b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 1A}
GLPVYITPGSGQFMTTDDMQSPCALPWYHPTKEISIPGEVKNLIEMCQVDTLIPVNNVGNVGNVS
MYTVQLGNQTMGAQKVFVSIKVDITSTPLATTLIGEIASYTHWTGSLRFSFMFCGTANTTLKLLLAYT
PPGIDEPTTRKDALMLGTHVVWDVGLQSTISLVVWVVSASHFRLTADNKYSMAGYITCWYQTNLVVP
PSTPQTADMCLFVSACKDFCLRMARDTDLHIQSGPIEQ

>d1fpn1_b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 2}
LVVPNINSSNPTTSNSAPALDAAETGHTSSVQPEDVIETRYVQTSQTRDEMSLESFLGRSGCIHESKLE
VTLANYNKENFTVWAINLQEMAQIRRFELFTYTRFDSEITLVPCISALSQDIGHITMQYMYVPPGA
PVPNSRDDYAWQSGTNASVFWQHQAAYPRFSLPFLSVASAYMFYDGYDEQDQNYGTANTNMGSL
LCSRIVTEKHIHKVHIMTRIYHKAKHVKAWCPRPPRALEYTRAHRTNFKIEDRSIQTAIVTRPIITTA

>d1fpn2_b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 2}
RIIQITRGDSTITSQDVANAIVAYGVWPHYLSSKDASAIKPSQPDTSNRFYTLRSVTWSSSSKGGWW
WKLDPDALKDMGIFGENMFYHYLGRSGYTIHVQCNAKSFHQGTLIVALIPEHQIASALHGNVNVGYNV
THPGETGREVKAETRLNPDLPTEEYWLNFDTLLGNITIFPHQFINLRSNNSATIAPYVNAVPM
SMRSHNNWSLVIIPICPLETSSAINTIPITISIPMCAEFSGARAKRQ

>d1fpn3_b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 2}
GLPVFITPGSGQFLTTDDFQSPCALPWYHPTKEISIPGEVKNLVEICQVDSLVPINNTDTYINSENMY
VVLQSSINAPDKIFSIRTDVASQPLATTLIGEISSYFTHWTGSLRFSFMFCGTANTTVKLLLAYTPPGIA
EPTTRKDALMLGTHVIWDVGLQSTISMVVPWISASHYRNTSPGRSTSGYITCWYQTRLVIPPQTPPTA
RLLCFVSGCKDFCLRMARDTNLHLQSGAIAQ

>d1rhi1_b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 3}
QTLASVSSGPKHTQSVPALANETGATLPTRPDNDVETRTTYMHFNGSETDVESFLGRAACVHVTEI
KNKNAAGLDNHRKEGLFNDWKINLSSLVQLRKKLELFTYVRFDSEYTLATASQPEASSYSSNLTVQA
MYVPPGAPNPKEWDDYTWQSASNPVFFKVGETSRFSVPFVGIASAYNCFYDGYSHDDPDPYGIT
VLNHMGSMARVNEHDVHTTIVKIRVYHRAKHVEAWIPRAPRALPYVSIGRNTYPRDSKTIVKKR
TNIKTY

>d1rhi2_b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 3}
GYSDRVQQITLGNSTITTQEARNAIVCYAEWPEYLSNDASDVNKTSKPDISVCRFYTLDSKTWKAT

SKGWCWKLDPALKDMGVFGQNMFYHSLGRTGYTIHVQCNA TKFHSGCLLVVVIPEHQLASHEGGT
VSVKYKYTHPGDRGIDLDTVEVAGGPTSDAIYNMDGTLGNLLIFPHQFINMRTNNTATIVVPYINSV
PIDSMTNRHNNVSLMVVPIAPLNAPTGSSTPLPVTVTIAPMCTEFTGIRSR SIVPQ

>d1rhi3_b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 3}

GLPTTTLPGSGQFLTDDRQSPSALPSYEPTPRIHIPGKVRNLEIIQVGT LIPMNNTGTNDNVTNYLI
PLHADRQNEQIFGTKLYIGDGVFKTLLGEIAQYYTHWSGSLRISL MYTGPALSSAKIILAYTPPGTRG
PEDKKEAMLGTHVVDIGLQSTIVMTIPWTSQVQFRYTDPTYTSAGYLSCWYLTSLILPPQTSQV
YLLSFISACPDFKLRLMKDTQTISQTDALTE

>d1bev1_b.10.1.4 (1:) Bovine enterovirus coat protein {Bovine enterovirus, VG-5-27}

QAAGALVAGTSTSTHSVATDSTPALQAAETGATSTARDESMIETRTIVPTHG IHETSVESFFGRSSLVG
MPLLATGTSITHWRIDFREFVQLRAKMSWFTYMRFDVEFTIIATSSTGQNVTT EQHTTYQVMYVPP
GAPVPSNQDSFQWQSGCNPSVFADTDGPPAQFSVPFMSSANAYSTVYDGYARFMDTDPDRYGILPS
NFLGFMYFRTLEAAHQVRFRIYAKIKHTSCWIPRAPRQAPYKKRYNLVFSGSDSDR ICNRSASLTSY

>d1bev2_b.10.1.4 (2:) Bovine enterovirus coat protein {Bovine enterovirus, VG-5-27}

EACGYSRVAQLTLGNSTITTQEAANICVAYGCWPAKLSDTDATSVDKPTEPGVSADR FYTLRSKPW
QADSKGWYWKLPDALNNTGMFGQNAQFHLYRGGWAVHVQCNA TKFHQGTLLVLA IPEHQIATQE
QPAFDRTMPGSEGGTFQEPFWLEDGTSLGNSLIYPHQWINLR TNNSATLILPYVNAIPMDSAIRHSN
WTLAIIPVAPLKYAAETPLVPITVTIAPMETEYNGLRRAIASNQ

>d1bev3_b.10.1.4 (3:) Bovine enterovirus coat protein {Bovine enterovirus, VG-5-27}

GLPTKPGPGSYQFMTTDED CSPCILPDFQPTPEIFIPGKVN NLEIAQVESILEANNREGVEGVERYVI
PVSVDALDAQIYALRLELGGSGPLSSLLGTLAKHYTQWSGSVEITCMFTGTFMTTGKVL LAYTPPG
GDMPRNREEAMLGTHVIWDFGLQSSITLVIPWISASHFRGVSND DVLNYQYAAAGHVTIWYQTNMV
IPPGFPNTAGIIMMIAAQPNFSFRIQKDREDMTQTALQ

>d2mev1_b.10.1.4 (1:) Mengo virus {Host: monkey brain; middle size plaque variant}

GVENAEKGV TENDATADFVAQPVYLPENQTKVAFFYDRSSPIGAF AVKSGSLES GFAPFSNKACPN S
VILTPGPQFDPAYDQLRQLRTEIWGNNGNEETSEVFPLKTKQDYSFCLFSPFVYYKCDLEVTLSPTS
GAHGLLVRWCPTGTPTKPTTQVLHEVSSLSEGRTPQVYSAGPGTSNQISFVVPYNSPLSVLPAVWYN
GHKRFDNTGDLGIAPNSDFGTLFFAGTKPDIKFTVYLYRYKNMRVFCRPTVFFPWPTSGDKIDMT

>d2mev2_b.10.1.4 (2:) Mengo virus {Host: monkey brain; middle size plaque variant}

ENLSDRVSQDTAGNTVTNTQSTVGRVLVGYGTVHDGEHPASCADTASEKILAVERY YTFKVN DWTST
QKPFYIRIPLPHVLSGEDGGVFGATLRRHYLVKTGWRVQVQCNASQFHAGSLLVFM APEYPTLDVF
AMDNRWSKDNLPNGTRTQTNRKGP FAMDHQNFQWWTLYPHQFLNLR TTTVDLEVPYVNIAPT
SSWTQHASWTLVIAVVAPLTYSTGASTSLDITASIQVPRPVFNGLRHEVLSRQ

>d2mev3_b.10.1.4 (3:) Mengo virus {Host: monkey brain; middle size plaque variant}

SPIPVTIREHAGTWYSTLPDSTVPIYGKTPVAPAN YMVGEYKDFLEIAQIPTFIGNKVPNAVPIEASN
TAVKTQPLAVYQVTLSCSCLANTFLAALSRNFAQYRGS LVTFTVFTGTAMMKGKFLIAYTPPGAGKPT
SRDQAMQATYAIWDLGLNSSYSFTVPFISPTHFRMVGTDQANITNVDGWVTVWQLTPLTYPPGCPT
SAKILTMVSAGKDFSLKMPISPAPWSPQ

>d1cov1_b.10.1.4 (1:) Coxsackievirus B3 {Host: human (Homo sapiens)}

RVADTVGTGPTNSEAIPALTA AETGHTSQVVP SDTMQTRHVKNYHSRSESTIENFLCRSACVYFTEYE
NSGAKRYAEWVITPRQAAQLRRKLEFFTYVRFDELTFVITSTQQPSTTQNQDAQILTHQIMYVPPG
GPVPDKVDSYVWQTSTNPSVFWTEGNAPPRMSVPFLSIGNAYSNFYD GWSEFSRNGVYGINTLNN
MGTLYARHVNAGSTGPIKSTIRIYFKPKHKV KAWIPRPPRLCQYEKAKNVNFQPSGVTTTRQSITMT
NT

>d1cov2_b.10.1.4 (2:) Coxsackievirus B3 {Host: human (Homo sapiens)}
GYSDRVRISITLGNSTITTQECANVVVGYGVWPDYLDKSEATAEDQPTQPDVATCRFYTLDSVQWQKT
SPGWWWKLPDALSNLGLFGQNMQYHYLGRTGYTIHVQCNASKFHQGCLLVVCVPEAEMGCATLN
NTPSSAELLGGDTAKEFADKPVASGSNKLQVRVYNAGMGVGVGNLTIFPHQWINLRTNNSATIVMP
YTNSVPMDNMFRHNNVTLMVIPFVPLDYCPGSTTYVPITVTIAPMCAEYNGLRLAGHQ

>d1cov3_b.10.1.4 (3:) Coxsackievirus B3 {Host: human (Homo sapiens)}
GLPTMNTPGSCQFLTSDDFQSPSAMPQYDVTPEMRIPGEVKNLMEIAEVDSVVPVQNVGEKVNSME
AYQIPVRSNEGSGTQVFGFPLQPGYSSVFSRTLLGEILNYYTHWSGSIKLTFMFCGSAMATGKFLAYS
PPGAGAPTKRVDAMLGTHVVDVGLQSSCVLCIPWISQTHYRYVASDEYTAGGFITCWYQTNIVVPA
DAQSSCYIMCFVSACNDFSVRLLKDTPFISQENFFQ

>d1d4m1_b.10.1.4 (1:) Coxsackievirus A9 {Host: human (Homo sapiens)}
GDVEEAIERAVVHVADTMRSGPSNSASVPALTAVETGHTSQVTPSDTMQTRHVKNYHSRSESTVENF
LGRSACVYMEEYKTTDNDVNKKFVAWPINTKQMVQMRRKLEMFTYLRFDMEVTFVITSRQDPGTT
LAQDMPVLTHQIMYVPPGGPIPAKVDDYAWQTSTNPSIFWTEGNAPARMSIPFISIGNAYSNFYDGW
SNFDQRGSYGYNTLNNLGHYVVRHVSGSSPHPITSTIRVYFKPKHTRAWVPRPPRLCQYKKAHSVDF
TPTPITDTRKDINTVTTV

>d1d4m2_b.10.1.4 (2:) Coxsackievirus A9 {Host: human (Homo sapiens)}
SDRVRISITLGNSTITTQECANVVVGYGRWPTYLRDDEATAEDQPTQPDVATCRFYTLDSIKWEKGSV
GWWWKFPALSDMGLFGQNMQYHYLGRAGYTIHVQCNASKFHQGCLLVVCVPEAEMGGAVVGQA
FSATAMANGDKAYEFTSATQSDQTKVQTAIHNAGMGVGVGNLTIYPHQWINLRTNNSATIVMPYINS
VPMDNMFRHYNFTLMVIPFVKLDYADTASTYVPITVTVAPMCAEYNGLRLAQAQ

>d1d4m3_b.10.1.4 (3:) Coxsackievirus A9 {Host: human (Homo sapiens)}
GLPTMNTPGSTQFLTSDDFQSPCALPQFDVTPSMNIPGEVKNLMEIAEVDSVVPVNNVQDTTDQME
MFRIPVTINAPLQQQVFLRLQPLDVSFKHTLLGEILNYYAHWSGSMKLTFFVFCGSAMATGKFLIAY
SPPGANPPKTRKDAMLGTHIWDIGLQSSCVLCVPWISQTHYRLVQQDEYTSAGYVTCWYQTMIV
PPGTPNSSSIMCFASACNDFSVRMLRDTPFISQDNKLQ

>d1ev11_b.10.1.4 (1:) Echovirus type 1 {Host: human (Homo sapiens)}
GDVQNAVEGAMVRVADTVQTSATNSERVPNLAVETGHTSQAVPGDTMQTRHVINNHRSESTIEN
FLARSACVFYLEYKTGTKEDSNSFNWVITTRRVAQLRRKLEMFTYLRFDMEITVVITSSQDQSTSQ
NQNAPVLTHQIMYVPPGGPIVSVDDYSWQTSTNPSIFWTEGNAPARMSIPFISIGNAYSNFYDGS
HFSQAGVYGFRTLNNMGQLFFRHVNKPNPAAITSVARIYFKPKHVRAWVPRPPRLCPYINSTNVNF
EPKPVTEVRTNIIT

>d1ev12_b.10.1.4 (2:) Echovirus type 1 {Host: human (Homo sapiens)}
GYSDRVRISITLGNSTITTQECANVVVGYGEWPEYLSNEATAEDQPTQPDVATCRFYTLDSVQWENG
SPGWWWKFPDALRDMGLFGQNMYYHYLGRAGYTIHVQCNASKFHQGCILVVCVPEAEMGSAQTS
GVVNYEHISKGEIASRFTTTTTAEDHGVQAAVWNAGMGVGVGNLTIFPHQWINLRTNNSATIVMPY
VNSVPMDNMYRHHNFTLMIIPFVPLDFSAGASTYVPITVTVAPMCAEYNGLRLAGHQ

>d1ev13_b.10.1.4 (3:) Echovirus type 1 {Host: human (Homo sapiens)}
GLPTMNTPGSNQFLTSDDFQSPSAMPQFDVTPEMHIPGEVRNLMEIAEVDSVMPINNDSSAAKVSSM
EAYRVELSTNTNAGTQVFGFQLNPGAESVMNRTLMGEILNYYAHWSGSIKITFFVFCGSAMTTGKFL
SYAPPGAGAPKTRKDAMLGTHVVDVGLQSSCVLCIPWISQTHYRFVEKDPYTNAGFVTCWYQTSV
VSPASNQPKCYMMCMVSACNDFSVRMLRDTKFIEQTSFYQ

>d1tme1_b.10.1.4 (1:) Theiler's murine encephalomyelitis virus {Theiler's murine
encephalomyelitis virus, strain da}

GSDNAEKGKVSNDASVDFVAEPVKLPENQTRVAFFYDRAVPIGMLRPGQNIESTFVYQENDLRLNC
LLLTPLSFCPDSTSGPVKTKAPVQWRWVRSRGGTTNFPLMTKQDYAFLCFSPFTYYKCDLEVTVSAL
GTDTVASVLRWAPTAPADVTDQLIGYTPSLGETRNPMMWLVGAGNTQISFVVPYNSPLSVLPAAW
FNGWSDFGNTKDFGVAPNADFGRLWIQGNTSASVRIRYKKMKVFCRPTLFFPWPV

>d1tme2_ b.10.1.4 (2:) Theiler's murine encephalomyelitis virus {Theiler's murine
encephalomyelitis virus, strain da}

DRVASDKAGNSATNTQSTVGRLCGYGEAHHGEHPASCADTATDKVLAAERYTIDLASWTTTQEAF
SHIRIPLPHVLAGEDGGVFGATLRRHYLCKTGWRVQVQCNASQFHAGSLLVFMapefytgkgtktg
DMEPTDPFTMDTTWRAPQGAPTGYRYDSRTGFFAMNHQNWQWTVYPHQILNLRNTTTVDLEV
PYVNIAPTSSWTQHANWTLVAVFSPLQYASGSSSDVQITASIQVNPVFNGLRHETVIA

>d1tme3_ b.10.1.4 (3:) Theiler's murine encephalomyelitis virus {Theiler's murine
encephalomyelitis virus, strain da}

SPIAVTVREHKGFYSTNPDDTTVPIYGKTISTPNDYMCGEFSDLLELCKLPTFLGNPNNSNNKRYPYFS
ATNSVPTTSLVDYQVALSCSCMCNSMLAAVARNFNQYRGSNLNLFVFTGAAMVKGKFLIAYTPPGAG
KPTTRDQAMQATYAIWDLGLNSSFVFTAPFISPTHYRQTSYTSATIASVDGWVTVWQLTPLTYPSTG
PVNSDILTVSAGDDFTLRMPISPTKWVPQ

>d1tmf1_ b.10.1.4 (1:) Theiler's murine encephalomyelitis virus {Theiler's murine
encephalomyelitis virus, strain da}

GVDNAEKGKVSNDASVDFVAEPVKLPENQTRVAFFYDRAVPIGMLRPGQNMETTFNYQENDYRL
NCLLLTPLSFCPDSSSGPQKTKAPVQWRWVRSRGGVNGANFPLMTKQDYAFLCFSPFTFYKCDLEV
TVSALGTDTVASVLRWAPTAPADVTDQLIGYTPSLGETRNPMMWLVGAGNSQVSVFVVPYNSPLSVL
PAAWFNGWSDFGNTKDFGVAPNADFGRLWIQGNTSASVRIRYKKMKVFCRPTLFFPWPPTTTTK
INADNPVPILELE

>d1tmf2_ b.10.1.4 (2:) Theiler's murine encephalomyelitis virus {Theiler's murine
encephalomyelitis virus, strain da}

DQNTEEMENLSDRVASDKAGNSATNTQSTVGRLCGYGKSHHGEHPASCADTATDKVLAAERYTID
LASWTTTQEAFSHIRIPLPHVLAGEDGGVFGATLRRHYLCKTGWRVQVQCNASQFHAGSLLVFMapefytgkgtktg
EFYTGKGTGTMEPSDPFTMDTEWRSPQGAPTGYRYDSRTGFFATNHQNWQWTVYPHQILNLR
RTNTTTVDLEVYVNVAPSSSWTQHANWTLVAVLSPLQYATGSSPDVQITASLQVNPVFNGLRHET
VIAQ

>d1sva1_ b.10.1.4 (1:) Simian virus 40 (SV40) coat protein {Simian virus 40}

PKKPKPEVQVPKLVIKGGIEVLGVKTVGVSFTEVECFLNPMGNPDEHQKGLSKSLAAEKQFTDDSP
DKEQLPCYSVARIPLPNINEDLTCGNILMWEAVTVKTEVIGVTAMLNLHSGTQKTHENGAGKPIQGS
NFHFFAVGGEPLELQGVLANRYRTKYPAQTVTPKNATVDSQQMNTDVKAVLDKDNAYPVECWVPDP
SKNENTRYFGTYTGGENVPPVLHITNTATTVLLDEQGVGPLCKADSLYSAVDICGLFTNTSGTQQW
KGLPRYFKITLRKRSVKNPYPIFLLSDLINRRTQRVDGQPMIGMSSQVEEVRVYEDTEELPGDPDMI
RYIDFEGQTTTRMQ

>d1dzla_ b.10.1.4 (A:) L1 protein {Human papillomavirus type 16}

KVVSTDEYVARTNIYYHAGTSRLLAVGHPYFPIKPNNNKILVPKVSGLQYRVFRIHLDPNKFQFPD
TSFYNPDTQRLVWACVGEVGRGQPLGVGISGHPLLNKLDDETENASAYAANAGVDNRECISMDYKQ
TQLCLIGCKPPIGEHWGKSPCTQVAVQPGDCPPLELINTVIQDGMVDTGFGAMDFTTLQANKSEV
PLDICTSICKYPDYIKMVSEPYGDSLFFYLRRREQMFVRHLFNragtvgenvpddlyiksgsgstanlass
NYFPTPSGSMVTSDAQIFNKPYWLQRAQGHNNGICWGNQLFVTVVDTRSTNMSLCAAISTSETTY
KNTNFKEYLRHGEEYDLQFIFQLCKITLTADVMTYIHSMNSTILEDWNFGLQPPPGGTLEDTYRFVT

SQAIACQKHTPPAPKEDPLKKYTFWEVNLKEKFSADLDQFPLGRKFLLQLGL
>d1ihma_b.10.1.4 (A:) Calcivirus capsid protein {Norwalk virus}
DPLAMDPVAGSSTAVATAGQVNPIDPWIINNFVQAPQGEFTISPNNTPGDVLFDSLGLPHLNPFLHL
SQMYNGWVGNMRVRIMLAGNAFTAGKIIVSCIPPGFGSHNLIAQATLFPHVIAADVRLDPIEVPLED
VRNVLFHNNDRNQQTMRLVCMLYTPLRTGGGTGDSFVAVGRVMTCPSPDFNFLVLPPTVEQKTRP
FTLPNLPLSSLSNSRAPLPISSMGISPDNVQSVQFQNGRCTLTGRLVGTTPVSLSHVAKIRGTSNGTVI
NLTELDGTPFHPFEGPAPIGFDPDLGGCDWHINMTQFGHSSQTQYDVDTPDFTVPHLGSIQANGIGS
GNYVGVLSWISPPSPSGSQVDLWKIPNYGSSITEATHLAPSVPYPPGFGEVLVFFMSKMPGPGAYNLP
CLLPQEYISHLASEQAPTVEAALLHYVDPDTGRNLGEFKAYPDGFLTCVPNGASSGPQQLPINGVVF
FVSWVSRFYQLKPVGTAS
>d1amm_1 b.11.1.1 (1-85) gamma-Crystallin {Cow (Bos taurus), isoform II (B)}
GKITFYEDRGFQGHCEYECSSDCPNLQPYFSRCNSIRVDSGCWMLYERPNIYQGHQYFLRRGDYDPDYQQ
WMGFNDSIRSCRLIPQHT
>d1amm_2 b.11.1.1 (86-174) gamma-Crystallin {Cow (Bos taurus), isoform II (B)}
GTFMRRIYERDDFRGQMSEITDDCPSLQDRFHLTEVHSLNVLEGSWVLYEMPYSYRGRQYLLRPGEY
RRYLDWGAMNAKVGSLRRVMDFY
>d1elpa1 b.11.1.1 (A:1-85) gamma-Crystallin {Cow (Bos taurus), isoform IIIb (D)}
GKITFYEDRGFQGRHYECSSDHSNLQPYLGRCSVRVDSGCWMIYEQPNYLGPQYFLRRGDYDPDYQQ
QWMGLNDSIRSCRLIPHAG
>d1elpa2 b.11.1.1 (A:87-174) gamma-Crystallin {Cow (Bos taurus), isoform IIIb (D)}
SHRLRLYEREDYRGQMIEITEDCSSLQDRFHFNEIHSNVLEGSWVLYELPNYRGRQYLLRPGEYRRY
HDWGAMNAKVGSLRRVIDIY
>d1a7ha_b.11.1.1 (A:) gamma-Crystallin {Cow (Bos taurus), isoform S}
MYKIQIFEKGFDFNGQMHEITTEDCPSIMEQFHMREVHSCVKVLEGAWIFYELPNYRGRQYLLDKKEYR
KPVWDGAASPAVQSFRRIVE
>d1ha4a_b.11.1.1 (A:) gamma-Crystallin {Human (Homo sapiens)}
GQYKIQIFEKGFDFSGQMYETTEDCPSIMEQFHMREIHSCKVLEGVWIFYELPNYRGRQYLLDKKEYR
KPIDWGAASPAVQSFRRIVE
>d1a45_1 b.11.1.1 (1-84) gamma-Crystallin {Cow (Bos taurus), isoform F}
GKITFYEDRGFQGRHYECSSDHSNLQPYFSRCNSIRVDSGCWMLYEQPNFQGPQYFLRRGDYDPDYQQ
WMGLNDSIRSCRLIPHT
>d1a45_2 b.11.1.1 (86-174) gamma-Crystallin {Cow (Bos taurus), isoform F}
GSHRLRIYEREDYRGQMVEITEDCSSLHDFHFSEIHSFNVLGWWVLYEMTNYRGRQYLLRPGDY
RRYHDWGATNARVGLRRRAVDYF
>d2bb2_1 b.11.1.1 (-2-85) beta-Crystallin {Cow (Bos taurus)}
LNPKIIIFEQENFQGHSHLNGPCPNLKETGVEKAGSVLVQAGPWVGYEQANCKGEQVFVEKGEYPR
WDSWTSSRRTDSLSSLRPIKVDS
>d2bb2_2 b.11.1.1 (86-175) beta-Crystallin {Cow (Bos taurus)}
QEHKITLYENPNFTGKKMEVIDDDVPSFHAHGYQEKVSSVRVQSGTWVGYQYPGYRGLQYLLEKGD
YKDSGDFGAPQPQVQSVRRIRDMQW
>d1a5da1 b.11.1.1 (A:1-84) beta-Crystallin {Rat (Rattus norvegicus), isoform E}
GKITFYEDRGFQGRHYECSTDHSNLQPYFSRCNSVRVDSGCWMLYEQPNFTGCQYFLRRGDYDPDYQQ
QWMGFSDSVRSCRLIPHS
>d1a5da2 b.11.1.1 (A:85-174) beta-Crystallin {Rat (Rattus norvegicus), isoform E}

SSHRIRIYEREDYRGQMVEITDDCPHLQDRFHFSDFHFSFHVMEGYWVLYEMPNYRGRQYLLRPGEY
RRYHDWGANARVGSLLRRIMDFY
>d1bd7a_b.11.1.1 (A:) beta-Crystallin {Rat (*Rattus norvegicus*), isoform E}
EHKIILYENPNFTGKKMEIVDDDDVPSFHAHGYQEKVSSVRVQSGTWVGYQYPGYRGLQYLLEKGDYK
DNSDFGAPHPQVQSVRRIRDMQGNPKIIIFEQENFQGHSHELSGPCPNLKETGMEKAGSVLVQAGP
WVGYEQANCKGEQFVFEKGEYPRWDSWTSSRRTDSLSSLRPIK
>d1npsa_b.11.1.1 (A:) Protein S {*Myxococcus xanthus*}
ANITVFYNEDEFQKGKQVDLPPGNYTRAQLAALGIENNTISSVKVPPGVKAILYQNDGFAGDQIEVVANA
EELGPLNNNVSSIRVISVPV
>d1pr_2_b.11.1.1 (91-173) Protein S {*Myxococcus xanthus*}
PRARFFYKEQFDGKEVDLPPGQYTQAELERYGIDNNTISSVKPQGLAVVLFKNDNFSGDTLPVNSDA
PTLGAMNNNTSSIRIS
>d1hdfa_b.11.1.1 (A:) Spherulin 3a (S3a) {Slime mold (*Physarum polycephalum*)}
SVCKGVSGNPAKGEVFLYKHVNFQGDSWKVTGNVYDFRSVSGLNDVSSVKVGPNTKAFIFKDDRF
NGNFIRLEESSQVTDLTTRNLNDAISSMIVATFE
>d1wkt_b.11.1.2 (-) Yeast killer toxin {*Williopsis mrakii*}
GDGYLIMCKNCDPNTGSCDWKQNWNTCVGIGANVHWMVTGGSTDGKQGCATIWEKSGCVGRSTT
MCCPANTCCNINTGFYIRSRRVE
>d1bhu_b.11.1.3 (-) *Streptomyces* metalloproteinase inhibitor, SMPI {*Streptomyces*
nigrescens}
APSCPAGSLCTYSGTGLSGARTVIPASDMEKAGTDGVKLPASARFANGTHFTLRYGPARKVTCVRF
CYQYATVGVKVPAGQALRSLPSPGATVTVGQDLGD
>d1f53a_b.11.1.4 (A:) Killer toxin-like protein SKLP {*Streptomyces* sp.}
IDHVPCRGENFLKIWSHGGQSVDCYANRGRIDFGGWVVDKISTGNNDLIYYDANGDSVRVDR
WHDITYPNRPPKVNSEIL
>d1g6ea_b.11.1.6 (A:) Antifungal protein AFP1 {*Streptomyces tendae*, tu901}
MINRTDCNENSYLEIHNNEGRDTLCFANAGTMPVAIYGVNWWVESGNNVVTLQFQRNLSDPRLTIT
LQKWGSWNPGHIHEILSIRIY
>d1c01a_b.11.1.5 (A:) Plant antimicrobial protein MIAMP1 {*Macadamia nut* (*Macadamia*
integrifolia)}
SAFTVWSGPGCNRAERYSKGCSAIHQKGGYDFSYTGQTAALYNQAGCSGVAHTRFGSSARACNPF
GWKSIFIQC
>d1f8na2_b.12.1.1 (A:6-149) Plant lipoxigenase {Soybean (*Glycine max*), isozyme L1}
HKIKGTVVLMPKNELEVNPDGSAVDNLNAFLGRSVSLQLISATKADAHGKGVKGDTFLEGINTSLP
TLGAGESAFNIHFEWDGSMGIPGAFYIKNYMQVEFFLKSLEAISNQGTTIRFVCNSWVYNTKLYKSV
RIFFANHTY
>d1ik3a2_b.12.1.1 (A:9-167) Plant lipoxigenase {Soybean (*Glycine max*), isozyme L3}
GHKIKGTVVLMRKNVLDVNSVTSVGGHIGQLDLVGSTLDTLTAFLGRSVSLQLISATKADANGKGL
GKATFLEGITSLPTLGAGQSAFKINFEDDGSIPGAFYIKNFMQTEFFLVSLTLEDIPNHGSIHFVC
NSWIYNKLFKSDRIFFANQTY
>d1lox_2_b.12.1.1 (2-112) 15-Lipoxygenase {Rabbit (*Oryctolagus cuniculus*)}
GVYRVCVSTGASIYAGSKNKVELWLVGQHGEVELGSCLRPTRNKEEFKVNVSXYLGSLLFVRLRKK
HFLKEDAWFCNWISVQALGAAEDKYWFPCYRWVVDGQSLPVG
>d1hpla1_b.12.1.2 (A:337-449) Pancreatic lipase, C-terminal domain {Horse (*Equus*

caballus})

RWRYRVDVTLGKVKVTHVLSLFGNKGNSRQYEIFQGTLPDNTYSNEFSDSDVEVGDLEKVKFIW
YNNVINLTLPKVGASKITVERNDGSVFNFCSEETVREDVLLTLTAC

>d1etha1 b.12.1.2 (A:337-448) Pancreatic lipase, C-terminal domain {Pig (*Sus scrofa*)}

ARWRYKVSVTLSGKVKVTHVLSLFGNEGNSRQYEIYKGTLPDNTHSDEFSDSDVEVGDLDQKVKFIW
YNNVINPTLPRVGASKITVERNDGKVDYDFCSQETVREEVLLTLNPC

>d1gpl_1 b.12.1.2 (337-449) Pancreatic lipase, C-terminal domain {Guinea pig (*Cavia porcellus*)}

RWRYKVSVTLSGKVKVTHVLSLFGNKGNSKQYEIFKGTLPDSTHSNEFSDSDVDVGDLDQMVKFIW
NNVINPTLPRVGASKIIVETNVGKQFNFCSPETVREEVLLTLTPC

>d1rp1_1 b.12.1.2 (337-449) Pancreatic lipase, C-terminal domain {Dog (*Canis familiaris*)}

RWRYGVSITLSGKRATGQAKVALFGSKGNTHQFNIFKILKPGSTHSNEFDDAKLDVGTIEKVKFLWN
NNNPTFPKVGAAKITVQKGEKTVHFCSESTVREDVLLTLTPC

>d1bu8a1 b.12.1.2 (A:337-449) Pancreatic lipase, C-terminal domain {Rat (*Rattus norvegicus*)}

RWRYKVSVTLSGAKKLSGYILVALYGNNGNSKQYEIFKGLKPEARHVRDIDVDINVEIQKVKFLWN
NKVINLFRPTLGASQITVQSGVDGKEYNFCSSDTVREDVLSLYPC

>d1ca1_2 b.12.1.3 (250-370) Alpha-toxin, C-terminal domain {*Clostridium perfringens*}

SVGKNVKELVAYISTSGEKDAGTDDYMYFGIKTKDGKTQEWEMDNPGNDFMTGSKDITYTFKLKDE
NLKIDDIQNMWIRKRKYTAFPDAYKPENIKVIANGKVVVDKINWISGNSTYNIK

>d1k5ja_b.13.3.1 (A:) Nucleoplasmin core {*Xenopus laevis*}

VSLIWGCELNEQNKTFEFKVEDDEEKCEHQLALRTVCLGDKAKDEFHIVEIVTQEEGAEKSVPIATL
KPSILPMATMVGIELTPPVTFRLKAGSGPLYISGQHVA

>d1pgs_1 b.13.1.1 (4-140) Peptide:N-glycosidase F, PNGase F {*Flavobacterium meningosepticum*}

DNTVNIKTFDKVKNAFGDGLSQAEGTFTFPADVTTVKTIKMFIKNECPNKTCDREWDRYANVYVKN
KTTGEWYEIGRFITPYWVGTEKLPRGLEIDVTDKSLLSGNTELKIYTETWLAKGREYSVDFDIVYGT
PDY

>d1pgs_2 b.13.1.1 (141-314) Peptide:N-glycosidase F, PNGase F {*Flavobacterium meningosepticum*}

KYSAVVPVIQYNKSSIDGVPYGAHTLGLKKNLQPTNTEKAYLRTTISGWGHAKPYDAGSRGCAEW
CFRTHTHIANNANTFQHLGALGCSANPINNQSPGNWTPDRAGWCPGMAVPTRIDVLNNSLTGSTF
SYEYKFSQSWTNGTNGDAFYAISSFVIAKSNTPIAPVVTN

>d1phm_1 b.13.1.2 (45-198) Peptidylglycine alpha-hydroxylating monooxygenase, PHM {Rat (*Rattus norvegicus*)}

NECLGTIGPVTPLDASDFALDIRMPGVTPKESDITYFCMSMRLPVDEEAFVIDFKPRASMDTVHHML
LFGCNMPSSTGSYWFCDGCTCTDKANILYAWARNAPPTRLPKGVGFRVGGGETGSKYFVLQVHYGDIS
AFRDNHKDCSGVSVHLTRVPQ

>d1phm_2 b.13.1.2 (199-354) Peptidylglycine alpha-hydroxylating monooxygenase, PHM {Rat (*Rattus norvegicus*)}

PLIAGMYLMMSVDTVIPPGEKVVNADISCQYKMYPMHVFAYRVHTHHLGKVVSGYRVRNGQWTLI
GRQNPQLPQAFYPVEHPVDVTFGDILAARCVFTGEGRTEATHIGGTSSDEMONLYIMYYMEAKYALS
FMTCTKNVAPDMFRTIPAEANIPI

>d1hx6a1 b.13.2.1 (A:15-244) Coat protein p3 {Bacteriophage prd1}

LRNQQAMAANLQARQIVLQQSYPIQQVETQTFDPANRSVFDVTPANVGIVKGLVKVTAAITNNHA
TEAVALTDFGPANLVQRVIYYDPDNQRHTTETSGWHLHFVNTAKQGAPFLSSMVTDSPIKYGDVMNV
IDAPATIAAGATGELTMYWVPLAYSETDLTGAVLANVPQSKQRLKLEFANNNTAFAAVGANPLEAIY
QGAGAADCFEESIYTVYQSYLDQLPVGQ

>d1hx6a2 b.13.2.1 (A:245-384) Coat protein p3 {Bacteriophage prd1}

NGYILPLIDLSTLYNLENSAQAGLTPNVDFVYQYANLYRYLSTIAVFDNGGSFNAGTDINYLSQRTANF
SDTRKLDPKTWAAQTRRRIATDFPKGVYYCDNRDKPIYTLQYGNVGFVVPKTVNQARLLMGYE
YFTSRT

>d1dhx_1 b.13.2.2 (44-650) Adenovirus hexon {Human adenovirus type 2}

FRNPTVAPTHDVTDRSQRLTLRFIPVDREDTAYSYKARFTLAVGDNRVLDMASTYFDIRGVLDGRGP
TFKPYSGTAYNALAPKGAPNSCEWEQTEDSGRAVAEDEEEDEDEEEEEEQNARDQATKKTTHVYA
QAPLSGETITKSLQIGSDNAETQAKPVYADPSYQPEPQIGESQWNEADANAAGGRVLKKTTPMKPC
YGSYARPTNPFQGSVLPDEKGVPLPKVDLQFFSNTTSLNDRQGNATKPKVLYSEDVNMETPDT
HLSYKPGKGDENSKAMLGQQSMPNRPNYIAFRDNFIGLMYYNSTGNMGVLAGQASQLNAVVDLQD
RNTELSYQLLLDSIGDRTRYFSMWNQAVDSYDPDVRIENHGTEDELPNYCFPLGGIGVTDITYQAIKA
NGNGSGDNGDTTWTKDETFATRNEIGVGNNFAMEINLNANLWRNFLYSNIALYLPDKLKYNPTNV
EISDNPNYDYMNKRVVAPGLVDCYINLGARWSLDYMDNVNPNFHHRNAGLRYRSMLLGNGRYVP
FHIQVPQKFFAIKNLLLLPGSYTYEWNFRKDVNMVLQSSLGNDLRVDGASIKFDSICLYATFFPMAHN
TASTLEAMLR

>d1ruxa1 b.13.2.2 (A:5-636) Adenovirus hexon {Human adenovirus type 5}

MMPQWSYMHISGDASEYLSPLVQFARATETYFSLNNKFRNPTVAPTHDVTDRSQRLTLRFIPV
DREDTAYSYKARFTLAVGDNRVLDMASTYFDIRGVLDGRGPTFKPYSGTAYNALAPKGAPNPCEWDE
AATALEINLEEEEDDNEDEVDEQAEQQKTHVFGQAPYSGINITKEGIQIGVEGQTPKYADKTFQPEP
QIGESQWYETEINHAAGRVLKKTTPMKPCYGSYAKPTNENGGQILVKQQNGKLESQVEMQFFSTT
EATAGNGDNLTPKVVLYSEDVDIETPDTHISYMPITKEGNSRELMGQQSMPNRPNYIAFRDNFIGLM
YYNSTGNMGVLAGQASQLNAVVDLQDRNTELSYQLLLDSIGDRTRYFSMWNQAVDSYDPDVRIEN
HGTEDELPNYCFPLGGVINTETLTKVKPKTGQENGWEKDATEFSDKNEIRVGNNFAMEINLNANLW
RNFLYSNIALYLPDKLKYSVSNVKISDNPNYDYMNKRVVAPGLVDCYINLGARWSLDYMDNVNPNF
NHHRNAGLRYRSMLLGNGRYVPFHIQVPQKFFAIKNLLLLPGSYTYEWNFRKDVNMVLQSSLGNDL
RVDGASIKFDSICLYATFFPMAHNTASTLEAMLRND

>d1ruxa2 b.13.2.2 (A:637-946) Adenovirus hexon {Human adenovirus type 5}

TNDQSFNDYLSAANMLYPIPANATNPVIPSISRNWAAFRGWAFTRLKTKETPSLGSYDPPYYTYSGSI
PYLDGTFYLNHTFKKVAITFDSSVSWPGNDRLLTPNEFEIKRSVDGEGYNVAQCNMTKDWFLVQML
ANYNIGYQGFYIPESYKDRMYSFFRNFPMSRQVVDVDTKYKDYQQVILGHQHNNSGFVGYLAPTMR
EGQAYPANFPYPLIGKTAVDSITQKKFLCDRTLWRIPFSSNFMMSGALTDLGQNLLYANSAHALDMT
FEVDPMDEPTLLYVLFVFDVVRVHRPHRGVIETVYLRTPFSA

>d1kful2 b.14.1.1 (L:356-514) Calpain large subunit, middle domain (domain III) {Human
(Homo sapiens)}

WKLTKMDGNWRRGSTAGGCRNYPNTFWMNPQYLIKLEEEDEDEEDGESGCTFLVGLIQKHRRRQ
RKMGEDMHTIGFGIYEVPEELSGQTNIHLSKNFFLTNRARERSDTFINLREVLNRFKLPPGEYILVPS
TFEPNKDGDGFCIRVFSEKKADYQAVDD

>d1df0a2 b.14.1.1 (A:356-514) Calpain large subunit, middle domain (domain III) {Rat
(Rattus norvegicus)}

WKLTKMDGNWRRGSTAGGCRNYPNTFWMNPQYLIKLEEEDEDEEDGERGCTFLVGLIQKHRRRQ

RKMGEDMHTIGFGIYEVPEELTGQTNIHLSKNFFLTTRARERSDTFINLREVLNRFKLPPEGEYVLVPS
TFEPHKNDFCIRVFSEKKADYQTVDD

>d1f35a_b.94.1.1 (A:) Olfactory marker protein {Mouse (*Mus musculus*)}
AEDGPQKQLEMPVLVDQDLTQQMRLRVESLKQRGEKKQDGEKLRPAESVYRLDFIQQKLQFDH
WNVVLDKPGKVTITGTSQNWTPDLTNLMTRQLLDPAEIFWRKEDSDAMDWNEADALEFGERLSD
LAKIRKVMYFLITFGEGVEPANLKASVVFNQL

>d1shsa_b.15.1.1 (A:) Small heat shock protein {Archaeon *Methanococcus jannaschii*}
TGIQISGKGFMPISIIEGDQHIKVIAWLPGVNKEDIILNAVGDLEIRAKRSPLMITESERIIYSEIPEEEEE
IYRTIKLPATVKEENASAKFENGVLVILPKAESSIKKGINIE

>d1gmea_b.15.1.1 (A:) Small heat shock protein {Wheat (*Triticum aestivum*)}
SIVRRSNVDFPFADLWADPFDFRSIVPAISGGSETAAAFANARMDWKETPEAHVFKADLPGVKKEE
VKVEVEDGNVLVSGERTKEKEDKNDKWHRVERSSGKFVRRFRLLEDAKVEEVKAGLENGVLTVT
VPKAEVKKPEVKAIQISG

>d1gmeb_b.15.1.1 (B:) Small heat shock protein {Wheat (*Triticum aestivum*)}
NARMDWKETPEAHVFKADLPGVKKEEVKVEVEDGNVLVSGERTKEKEDKNDKWHRVERSSGKF
VRRFRLLEDAKVEEVKAGLENGVLTVTVPKAEVKKPEVKAIQISG

>d1ejfa_b.15.1.2 (A:) Co-chaperone p23 {Human (*Homo sapiens*)}
MQPASAKWYDRRDYVFIIEFCVEDSKDVNVNFEKSKLTFSCGGSDNFKHLNEIDLFCIDPNDSKH
KRTDRSILCCLRKGESGQSWPRLTKERAKLNWLSVDFNNWKDWE

>d1ezsa_b.16.1.1 (A:) Ecotin, trypsin inhibitor {*Escherichia coli*}
PYPQAEKGMKRQVIQLTPQEDESTLKVLELLIGQTLVDCNLHRLGGKLENKTLEGAAAAYVFDKVS
SPVSTRMACPDGKKEKKFVTAYLGDAGMLRYNSKLPVVYTPDNVDVKYRVWKAEEKIDNAVVR

>d1slua_b.16.1.1 (A:) Ecotin, trypsin inhibitor {*Escherichia coli*}
IAPYPQAEKGMKRQVIQLTPQEDESTLKVLELLIGQTLVDCNLHRLGGKLENKTLEGWGYDYVFDK
VSSPVSTMMHCPDGKKEKKFVTAYLGDAGMLRYNSKLPVVYTPDNVDVKYRVWKAEEKIDNAV
R

>g1fi8.1 b.16.1.1 (C,D:) Ecotin, trypsin inhibitor {*Escherichia coli*}
PLEKIAPYPQAEKGMKRQVIQLTPQEDESTLKVLELLIGQTLVDCNLHRLGGKLENKTLEGWGYDY
VFDKVSSPIEPDXKFVTAYLGDAGMLRYNSKLPVVYTPDNVDVKYRVWKAEEKIDNAVVR

>d1beha_b.17.1.1 (A:) Phosphatidylethanolamine binding protein, PEBP {Human (*Homo sapiens*)}
VDLSKWSGPLSLQEVDQPHPLHVTYAGAAVDELGKVLTPQVKNRPTSISWDGLDSGKLYTLVLT
DPDAPSRKDPKYREWHHFLVNMKGNDISSGTVLSDYVGSPPKGTGLHRYVWLVEYEQDRPLKCD
EPILSNRSGDHRGKFKVASFRKKYELRAPVAGTCYQAEWDDYVPKLYEQLSG

>d1a44_b.17.1.1 (-) Phosphatidylethanolamine binding protein, PEBP {Cow (*Bos taurus*)}
PVDLSKWSGPLSLQEVDQPHPLQVKYGAEVDELGKVLTPQVKNRPTSITWDGLDPGKLYTLV
LTDPDAPSRKDPKYREWHHFLVNMKGNNISSGTVLSDYVGSPPKGTGLHRYVWLVEYEQEGPLK
DEPILSNRSGDHRGKFKVASFRKKYELGAPVAGTCYQAEWDDYVPKLYEQLSG

>d1qoua_b.17.1.1 (A:) Centroradialis protein Cen {Garden snapdragon (*Antirrhinum majus*)}
GRVIGDVVDHFTSTVKMSVIYNSNNSIKHVYNGHELFPASVTSTPRVEVHGGDMRSFFTLIMTDPDV
PGPSDPYLREHLHWIVTDIPGTTDSSFGKEVVSYEMPRPNIGIHRFVLLFKQKKRGQAMLSPPVVC
RDGFNTRKFTQENELGLPVAAVFFNCQRET

>d1fjja_b.17.1.2 (A:) Hypothetical protein YbhB {*Escherichia coli*}

AMKLISNDLRDGDKLPHRHVFNGMGYDGDNISPHLAWDDVPAGTKSFVVTTCYDPDAPTGSWWH
WVVVNLPADTRVLPQGFSGLVAMPDGLVLRTRDFGKTGYDGAAPPKGETHRYIFTVHALDIERID
VDEGASGAMVGFNVHFHSLASASITAMFS

>d1fuxa_b.17.1.2 (A:) Hypothetical protein YbcL {Escherichia coli}

EFQVTSNEIKTGEQLTTSVHVFSGFGCEGGNTSPSLTWSGVPEGTKSFAVTVYDPDAPTGSWWHWT
VVNIPATVTYLPVDAGRRDGTGLPTGAVQGRNDFGYAGFGGACPPKGDKPHHYQFKVWALKTEKIP
VDSNSSGALVGYMLNANKIATAEITPVYEIKLE

>d1g13a_b.95.1.1 (A:) Ganglioside M2 (gm2) activator {Human (Homo sapiens)}

SSFSWDNCDEGKDPVIRSLTLEPDPIIVPGNVTLVSMGSTSVPLSSPLKVDLVLEKEVAGLWIKIPCT
DYIGSCTFEHFCDVLDMLIPTGEPCEPLRTYGLPCHCPFKEGTYSLPKSEFVVPDLELPSWLTTGNY
RIESVLSSSGKRLGCIKIAASLKGI

>d1i9ba_b.96.1.1 (A:) Acetylcholine binding protein (ACHBP) {Great pond snail (Lymnaea stagnalis)}

FDRADILYNIRQTSRPDVIPTQRDRPVAVSLSKFINILEVNEITNEVDVVFVWQQTTWSDRTLAWNS
SHSPDQVSVPISSLWVPDLAAYNAISKPEVLTPQLARVVSDGEVLYMPSIRQRFSCDVSGVDTESGATC
RIKIGSWTHHSREISVDPTTENSDDSEYFSQYSRFEILDVTQKKNVSVTYSCPEAYEDVEVSLNFRKK
G

>d1k3ia2_b.18.1.1 (A:-12-150) Galactose oxidase, N-terminal domain {Fungi (Fusarium spp)}

IPEGSLQFLSLRASAPIGSAISRNNWAVTCDSAQSGNECNKAIDGNKDTFWHTFYGGANGDPKPPHTY
TIDMKTTQNVNGLSMLPRQDGNQNGWIGRHEVYLLSSDGTNWGSPVAGSFWFADSTTKYSNFETRP
ARYVRLVAITEANGQPWTSIAEINVFQASS

>d1eut_2_b.18.1.1 (506-647) Sialidase, C-terminal domain {Micromonospora viridifaciens}

QARMSIADVDSEETAREDGRASNVIDGNPSTFWHTEWSRADAPGYPHRISLDLGGTHTISGLQYTR
RQNSANEQVADYEIYTSLNGTTWGDPVASGRFTTSLAPQRAVFPARDARYIRLVALSEQTGHKYAAV
AELEVEGQR

>d1czsa_b.18.1.2 (A:) C2 domain of factor V {Human (Homo sapiens)}

GCSTPLGMENKIKQITASSFKKSWWGDYWEPPFRARLNAQGRVNAWQAKANNKQWLEIDLL
KIKKITAHTQGCKSLSEMYVKSytiHYSEQVWKPYPRLKSSMVDKIFEGNTNTKGHVKNFFNPPII
SRFIRVIPKTWNQSITLRLLEFGCDIY

>d1d7pm_b.18.1.2 (M:) C2 domain of factor VIII {Human (Homo sapiens)}

LNCSMPLGMESKAISDAQITASSYFTNMFATWSPSKARLHLQGRSNAWRPQVNNPKEWLQVDFQ
KTMKVTGVTTQGVKSLTSMYVKEFLISSQDGHQWTLFFQNGKVKVFQGNQDSFTPVVNCCLDPPL
LTRYLRIHPQSWVHQIALRMEVLGCEAQ

>d1jhja_b.18.1.9 (A:) APC10/DOC1 subunit of the anaphase-promoting complex {Human (Homo sapiens)}

ATPNKTTPPGADPKQLERTGTVREIGSQAVWSLSSCKPFGVDQLRDDNLETYWQSDGSQPHLVNIQ
FRRKTTVKTLCIYADYKSDSYTPSKISVRVGNFHNLQEIRQLELVEPSGWIHVPLTDNHHKPTRTF
MIQIAVLANHQNGRDTHMRQIKIYTPV

>d1dlc_1_b.18.1.3 (500-644) delta-Endotoxin, C-terminal domain {Bacillus thuringiensis tenebrionis, CRYIIIA (BT13)}

FFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQCTENGSAATYVTPDVSYSQKYRARIHYA
STSQITFTLSLDGAPFNQYYFDKTINKGDTLTYNFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDK
IEFIPVN

>d1ji6a1_b.18.1.3 (A:503-652) delta-Endotoxin, C-terminal domain {Bacillus thuringiensis,

CRY3bb1}
FFNTIDAEKITQLPVVKAYALSSGASIIIEGPGFTGGNLLFLKESSNSIAKFKVTLNSAALLQRYRVRIRY
ASTTNLRLRFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESFVSNEKI
YIDKIEFIPVQL
>d1ciy_1 b.18.1.3 (462-609) delta-Endotoxin, C-terminal domain {Bacillus thuringiensis,
CRYIA (A)}
NNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVRIRYASTT
NLQFHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFSTPFNFSNGSSVFTLSAHVFNSGNEVYIDRI
EFVPAEVT
>d1i5pa1 b.18.1.3 (A:473-633) delta-Endotoxin, C-terminal domain {Bacillus thuringiensis
subsp. kurstaki, CRY2AA}
NIYAANENGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNTTARYTLRGNG
NSYNYLRLVSSIGNSTIRVTINGRVYTVSNVNTTNDGVDNDGARFSDINIGNIVASDNTNVTLTDIN
VTLNSGTPFDLMNIMFVPTNLPLY
>d1nuka_b.18.1.4 (A:) Ligand-binding domain of the ephb2 receptor tyrosine kinase {Mouse
(Mus musculus)}
EETLMDSTTATAELGWMVHPPSGWEEVSGYDENMNTIRTYQVCNVFESSQNNWLRTKFIRRRGAH
RIHVEMKFSVRDCSSIPVPGSCKETFNLYYYEADFDLTKTFPNWMENPWVKVDTIAADESFSQV
DLGGRVMKINTEVRSFGPVS RNGFYLAFAQDYGGCMSLIAVRVVFYR
>d1jz8a3 b.18.1.5 (A:13-219) beta-Galactosidase {Escherichia coli}
RRDWENPGVTQLNRLAAHPPFASWRNSEEARTDRPSQQLRSLNGEWRFAWFPAPEAVPESWLEC
DLPEADTVVPSNWQMHGYDAPIYTNVTYPITVNPPFVPTENPTGCYSLTFNVDESWLQEGQTRIIF
DGVNSAFHLWCNGRWVGYGQDSRLPSEFDLSAFLRAGENRLAVMVLRWSDGSYLEDQDMWRMSG
IFRDVSLHKPT
>d1bhga2 b.18.1.5 (A:22-225) beta-Glucuronidase {Human (Homo sapiens)}
GLQGGMLYPQESPRECKELDGLWSFRADFSDNRRRGFEEQWYRRPLWESGPTVDMVPVSSFNDIS
QDWRLRHVFGVWVYEREVILPERWTQDLRTRVVLRIGSAHSYAIVWVNGVDTLEHEGGYLPFEAD
ISNLVQVGPLPSRLRITIAINNTLTPTTLPPGTIYQLTDTSKYPKGYFVQNTYFDFFNAGLQRSVLLYT
TPT
>d1cx1a_b.18.1.6 (A:) Cellulose-binding domain {Cellulomonas fimi}
ASLDSEVELLPHTSFAESLGPWSLYGTSEPVFADGRMCVDLPGGQGNPW DAGLVYNGVPVGEGESY
VLSFTASATPDMPVRVLVGE GGGAYRTAFEQGSAPLTGEPATREYAFTSNLTFPPDGDAPGQVAFHLG
KAGAYEFCISQVSLTTSAT
>d1ulo_b.18.1.6 (-) Cellulose-binding domain {Cellulomonas fimi}
ASPIGEGTFDDGPEGWVAYGTDGPLDTSTGALCVAVPAGSAQYGVGVVLNGVAIEEGTTYTLRYTATA
STDVTVRALVGQNGAPYGTVLDTSPALTSEPRQVTETFTASATYPATPAADDPEGQIAFQLGGFSADA
WTLCLDDVALDSEVEL
>d1gamma_b.18.1.10 (A:) Carbohydrate binding module from xylanase U {Clostridium
thermocellum}
FSKIESEEYNSLKSSTIQTIGTSDGGSGIGYIESGDYLVFNKINFGNGANSFKARVASGADTPTNIQLRL
GSPTGTLIGTLTVASTGGWNNYEEKSCSITNTTGQHDLYLVFSGPVNIDYFIFDSN
>d1gnya_b.18.1.11 (A:) Xylan-binding module from xylanase 10c {Pseudomonas cellulosa}
GNVVIEVDMANGWRGNASGSTSHSGITYSADGVTFAALGDGAVFDIARPTTLEDAVIAMVVNVSA
EFKASEANLQIFAQLKEDWSKGEWDCLAGSSELTADTDLTLTCTIDEDDDKFNQTARDVQVGIQAKG

TPAGTITIKSVTITLAQEA

>d1j83a_b.18.1.12 (A:) Endo-1,4-beta glucanase EngF {Clostridium cellulovorans}
QPTAPKDFSSGFWDNDGTTQGFVNPDPSPITAINVENANNALKISNLNSKGSNDLSEGNFWANVRI
SADIWQSQSINIYGDTKLTMDVIAPTPVNVSIAAIPQSSTHGWGNPTRAIRVWTFNVAQTDGTYKAT
LTISTNDSPNFNTIATDAADSVVTNMILFVGSNSDNISLDNIKFTK

>d1dyoa_b.18.1.7 (A:) Xylan-binding domain {Clostridium thermocellum}
PDAGYYYHDTFEGSVGQWTARGPAEVLVLSGRTAYKGSESLVLRNRRTAAWNGAQRALNPRTFVPGNT
YCFSVVASFIEGASSTTFMCKLQYVDGSGTQRYDTIDMKTVGPNQWVHLYNPQYRIPSDATDMYVYV
ETADDTINFYIDEAIGAVAGTVI

>d1xnaa_b.18.1.8 (A:) N-terminal domain of xrcc1 {Human (Homo sapiens)}
MPEIRLRHVSCSSQDSTHCAENLLKADTYRKWRAAKAGEKTISVVLQLEKEEQIHSVDIGNDGSAF
VEVLVGSAGGAGEQDYEVLLVTSSFMSPSESRSGSNPNRVRMFGPDKLVRAAAEKRWDRVKIVCSQ
PYSKDSPFGLSFVRFHS

>d1ju3a1_b.18.1.13 (A:352-574) Bacterial cocaine esterase C-terminal domain {Rhodococcus
sp. mb1}
PLPDTAYTPFYLGSGAANTSTGGGTLSTSISGTESADTYLYDPADPVPSLGGTLLFHNGDNGPADQR
PIHDRDDVLCYSTEVLTDPEVETGTVSARLTVSSAVDFTAKLVDFPDGRAIALCDGIVRMRYRE
TLVNPTLIEAGEIYVAIDMLATSNVFLPGRHIMVQVSSSNFPKYDRNSNTGGVIAREQLEEMCTAVN
RIHRGPEHPSHIVLPIIKR

>d1bvp12_b.19.1.1 (1:121-254) Virus capsid protein vp7 (BTV-10 vp7), central (top) domain
{Bluetongue virus}
PARQPYGFFLETEETFQPGRWFMRAAQAVTAVVCGPDMIQVSLNAGARGDVQQIFQGRNDPMMIYL
VWRIENFAMAQNSQQTQAGVTVSVGGVDMRAGRIIAWDQQAALHVNPTQQNAMVQIQVVFYI
SMD

>d1ahsa_b.19.1.1 (A:) Virus capsid protein vp7 (BTV-10 vp7), central (top) domain {African
horse sickness virus}
TGPYAGAVEVQQSGRYVYPQGRTRGGYINSNIAEVCMDAGAAGQVNALLAPRRGDAMIYFVWRPL
RIFCDPQGASLESAPGTFVTVDGVNVAAGDVVAWNTIAPVNVGNPGARRSILQFEVLWYT

>d1qhda2_b.19.1.1 (A:149-332) vp6, the major capsid protein of group A rotavirus {Bovine
rotavirus}
GFTFHKNPFIYPYASFTLNRSQPAHDNLMGTMWLNAGSEIQVAGFDYSCAINAPANTQQFEHIVQLR
RVLTTATITLLPDAERFSFPRVITSADGATTWYFNPVILRPNNVEIEFLLNGQIINTYQARFGTIIARNF
DTIRLSFQLMRPPNMTPAVAALFPNAQPFHHATVGLTLRIESAVCE

>d1jsda_b.19.1.2 (A:) Hemagglutinin {Influenza A virus, different strains}
DKICIGYQSTNSTETVDTLTETNVPVTHAKELLHTSHNGMLCATNLGHPLILDCTIEGLIYGNPSCD
LLGGREWSYIVERPSAVNGMCYPGNVENLEELRSLFSSASSYQRIQIFPDTIWNVSYSGTSSACSDSF
YRSMRWLTQKNNAYPIQDAQYTNNRGSILFMWGINHPPTDTVQTNLYTRTDTTTSVTTEDINRTF
KPVIGRPLVNLHGRIDYYWSVLKPGQTLRVRNNGNLIAPWYGHILSGESHGRILKTDLNSGNCVV
QCQTERGGLNTTLPFHNVSXYAFGNCPKYVGVKSLKLAVGLRNVPAR

>d1jsma_b.19.1.2 (A:) Hemagglutinin {Influenza A virus, different strains}
DQICIGYHANNSTEQVDTIMEKNVTVTHAQDILEKTHNGKCLDLNGVKPLILRDCSVAGWLLGNPM
CDEFLNVPEWSYIVEKDNPNVGLCYPENFNDYEELKHLSSSTNHFEKIRIIPRSSWSNHDASSGVSSA
CPYNGRSSFFRNWVWLIKNNAYPTIKRSYNNNTNQEDLLILWGIHHPNDAAEQTKLYQNPTTYVSVG
TSTLNQRSVPEIATRPKVNGQSGRMEFFWTILKPNDAINFESNGNFIAPEYAYKIVKKGSAIMKSGL

EYGNCNTKQCQTPMGAINSSMPFHNIHPLTIGECPKYVKSGRLVLATGLRNVP
>d2visc_b.19.1.2 (C:) Hemagglutinin {Influenza A virus, different strains}
VQSSSTGKICNNPHRILDGIDCTLIDALLGDPHCDVFQNETWDLFVERSKAFSNCYPYDVPDYASLRS
LVASSGTLEFITEGFTWTGVIQNGGSNACKRGPSSGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKL
YIWGIHHPSTNQEQTSLYVQASGRVTVSTRRSQQTIIIPNIGSRPWVRGLSSRISYWTIVKPGDVLVINS
NGNLIAPRGYFKMRTGKSSIMRSDAPIDTCISECITPNGSIPNDKPFQNVNKITYGACPKYV
>d2viua_b.19.1.2 (A:) Hemagglutinin {Influenza A virus, different strains}
STATLCLGHHAVPNGTLVKTITDDQIEVTNATELVQSSSTGKICNNPHRILDGIDCTLIDALLGDPHCD
VFQNETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFITEGFTWTGVIQNGGSNACKRGPSS
GFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYIWGIHHPSTNQEQTSLYVQASGRVTVSTRRSQQT
IIIPNIGSRPWVRGLSSRISYWTIVKPGDVLVINSNGNLIAPRGYFKMRTGKSSIMRSDAPIDTCISECI
TPNGSIPNDKPFQNVNKITYGACPKYVKQNTLKLATGMRNVPEKQT
>d1flca1_b.19.1.3 (A:151-306) Hemagglutinin domain of haemagglutinin-esterase-fusion
glycoprotein HEF1 {Influenza C virus}
CMSLVNALDKTIPLQVTAGTAGNCNNSFLKNPALYTQEVKPSENKCGKENLAFFTLPTQFGTYECKL
HLVASCYFIYDSKEVYNKRGCDFYQVIYDSFGKVVGGLDNRVSPYTGNSGDTPMQCDMLQLKPGR
YSVRSSPRFLLMPERSYCFDMK
>d1aol_b.20.1.1 (-) F-MuLV receptor-binding domain {Friend murine leukemia virus}
QVYNITWEVTNGDRETVWASGNHPLWTWWPVLTPDLCMLALSGPPHWGLEYQAPYSSPPGPPC
CSGSSGSSAGCSRDCDEPLTSLTPRCNTAWNRLKLDQVTHKSSEGFYVCPGSHRPREAKSCGGPDSFY
CASWGCETTGRVYWKPSSWDYITVDNNLTTSQAVQVCKDNKWCNPLAIQFTNAGKQVTSWTTGH
YWGLRLYVSGRDPGLTFGIRLRYQNLGPRVP
>d1knb_b.21.1.1 (-) Adenovirus fiber protein head domain (knob domain) {Human
adenovirus type 5}
NDKLTWTTTPAPSPNCRLNAEKDAKLTLLVLTCKGSQILATVSVLAVKGLAPISGTVQSAHLIIRFDEN
GVLLNNSFLDPEYWNFRNGDLTEGTAYTNAVGFMPNLSAYPKSHGKTAKSNIVSQVYLNKDGTKPV
TLTITLNGTQETGDTTSPAYSMSFSWDWSGHNYINEIFATSSYTFSYIAQE
>d1qhva_b.21.1.1 (A:) Adenovirus fiber protein head domain (knob domain) {Human
adenovirus type 2}
AITIGNKNDKLTWTTTPDPSPCRIHSDNDCKFTLVLTCKGSQVLATVAALAVSGDLSSMTGTVASV
SIFLRFDQNGVLMENSSLKKHYNFRNGNSTNANPYTNAVGFMPNLLAYPKTQSQTAKNNIVSQVY
LHGDKTKPMILTITLNGTSESTETSEVSTYSMSFTWSWESGKYTTETFATNSYTFSYIAQE
>d1h7za_b.21.1.1 (A:) Adenovirus fiber protein head domain (knob domain) {Human
adenovirus type 3}
KNNTLWTGPKPEANCIIEYGKQNPDSKLTLLILVKNNGGIVNGYVTLMGASDYVNTLTKNKNVSNINVEL
YFDATGHILPDSSSLKTDLELKYKQTADFSARGFMPSTTAYPFVLPNAGTHNENYIFGQCYKASDGA
LFPLEVTVMNLKRLPDSRTSYVMTFLWSL NAGLAPETTQATLITSPFTFSYIREDDD
>d1kaca_b.21.1.1 (A:) Adenovirus fiber protein head domain (knob domain) {Human
adenovirus type 12}
TPYDPLTLWTTTPDPPNCSLIQELDAKLTLLCLTKNGSIVNGIVSLVGKGNLLNIQSTTTTTVGVHLVFD
EQGRLITSTPTALVPQASWGYRQGQSVSTNTVTNGLGFMPNV SAYPRPNASEAKSQMVSLTYLQGDT
SKPITMKVAFNGITSLNGYSLTFMWSGLSNYINQPFSTPSCSFSYITQE
>d1kkea1_b.21.1.2 (A:250-312) Reovirus attachment protein sigma 1 {Reovirus}
EQSYVASAVTPLRLNSSTKVLDM LIDSSTLEINSSGQLTVRSTSPNLRYP IADVSGGIGMSPN

>d1aly_ b.22.1.1 (-) Extracellular domain of CD40 ligand {Human (Homo sapiens)}
GDQNPQIAAHVISEASSKTTSVLQWAEKGYTMSNNLVLENGKQLTVKRQGLYYIYAQVTFCSNRE
ASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHLGGVFELQPGASVFNVTDPQVSHGT
GFTSFGLLKL

>d1c28a_ b.22.1.1 (A:) 30 kd adipocyte complement-related protein {Mouse (Mus musculus)}
MYRSAFSVGLTRVTVPNVPIRFTKIFYNQNHYDGGSTGKFCNIPGLYYFSYHITVYMKDVKVSLFK
KDKAVLFTYDQYQEKVNDQASGSVLLHLEVDQVWLQVYGDGDHNGLYADNVNDSTFTGFLLYHD
T

>d1tnra_ b.22.1.1 (A:) Tumor necrosis factor (TNF) {Human (Homo sapiens)}
KPAAHLIGDPSKQNSLLWRANTDRAFLQDGFSLNNSLLVPTSGIYFVYSQVVFSGKAYS PKATSSPLY
LAHEVQLFSSQYPFHVPLSSQKMVYPGLQEPWLHSMYHGAAAFQLTQGDQLSTHTDGIPHLVLSPT
VFFGAFAL

>d4tsva_ b.22.1.1 (A:) Tumor necrosis factor (TNF) {Human (Homo sapiens)}
DKPVAHVANPQAEGQLQWSNRRANALLANGVELRDNLVVPPIEGLFLIYSQVLFKGGCPSTHVL
THTISRIAVSYQTKVNLSSAIKSPCQRETPEGAEAKPWYEPIYLGGVFQLEKGDRLSAEINRPDYLDFA
ESGQVYFGIHAL

>d2tnfa_ b.22.1.1 (A:) Tumor necrosis factor (TNF) {Mouse (Mus musculus)}
SDKPVAHVANHQVEEQLEWLSQRANALLANGMDLKDNLVVPADGLYLVSQVLFKGGCPDYV
LLTHTVSRFAISYQEKVNLSSAVKSPCKDTPEGAELKPWYEPIYLGGVFQLEKGDQLSAEVNLPKYL
DFAESGQVYFGVIAL

>d1dg6a_ b.22.1.1 (A:) Apoptosis-2 ligand, apo2l/TRAIL {Human (Homo sapiens)}
QRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNLHLRNGELVIHEKGFYIYSQ
TYFRFQEEIKENTKNDKQMVQYIYKYTSYPAPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDR
IFVSVTNEHLIDMDHEASFFGAFLVG

>d1jtzx_ b.22.1.1 (X:) TRANCE/RANKL cytokine {Mouse (Mus musculus)}
QPFAHLTINAASIPSGSHKVTLSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSG
SVPTDYLQLMVYVVKTSIKIPSSHNLKGGSTKNWGSNSEHFYSINVGFFKLRAGEEISIQVSNPS
LLDPDQDATYFGAFKVQDID

>d1jh5a_ b.22.1.1 (A:) Soluble part of TALL-1, sTALL-1 {Human (Homo sapiens)}
VTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKILVKETGYFFIYQVLYTDKTYAMG
HLIQRKKVHVFGDELSLVTFRCIQNPETLPNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVT
FFGALKLL

>d1gr3a_ b.22.1.1 (A:) Collagen X NC1 trimerisation domain {Human (Homo sapiens)}
MPVSAFTVILSKAYPAIGTPIPFDKILYNRQQHYDPRGTGIFTQCIPGIYFSYHVHVKGTHVWVGLYKN
GTPVMYTYDEYTKGYLDQASGSAIIDLTENDQVWLQLPNAESNGLYSSEYVHSSFSGLVAPM

>d1sfp_ b.23.1.1 (-) Acidic seminal fluid protein (ASFP) {Cow (Bos taurus)}
LPRNTNCGGILKEESGVIATYYGPKTNCVWTIQMPPEYHVRVSIQYLQLNCNKESLEIIDGLPGSPVL
GKICEGSLMDYRSSGSIMTVKYIREPEHPASFYEVLYFQDPQA

>d1sppa_ b.23.1.1 (A:) Major seminal plasma glycoprotein PSP-I {Pig (Sus scrofa)}
LDYHACGGRLTDDYGTIFTYKGPKECVWTLQVDPKYKLLVSIPTLNLTGCKEYVEVLEGAPGSKSLG
KFCEGLSILNRGSSGMTVKYKRDSGHPASPYEIIFLRDSQG

>d1sppb_ b.23.1.1 (B:) Major seminal plasma glycoprotein PSP-II {Pig (Sus scrofa)}
ARINGPDECGRVIKDTSGSISNTDRQKNLCTWTILMKPDQKVRMAIPYLNACGKEYVEVFDGLLSG

PSYGKLCAGAAIVFLSTANTMTIKYNRISGNSSSPFLIYFYGSSP
>d1cb8a2_b.24.1.1 (A:600-700) Chondroitinase AC {*Pedobacter heparinus* (*Flavobacterium heparinum*)}
PKVLANTNQLQAVYHQQLDMVQAIIFYTAGKLSVAGIEIETDKPCAVLIKHINGKQVIWAADPLQKEK
TAVLSIRDLKTGKTNRVKIDFPQQEFAGATVELK
>d1egua2_b.24.1.1 (A:815-893) Hyaluronate lyase {*Streptococcus pneumoniae*}
SSLIENNETLQSVYDAKQGVWVIVKYDDSVSTISNQFQVLKRGVYTIRKEGDEYKAIAYNPETQESAP
DQEVFKKLEQH
>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*)}
AGAVIDGASLSFDILKTVLEALGNVKRKIAVGVNDNESGKTWTALNTYFRSGTSDIVLPHKVPHGKALL
YNGQKDRGPVATGAVGVLAYLMSDGNTLAVLFSVPYDYNWYSNWWNVRIYKGRRADQRMYEEL
YYNLSPFRGDNGWHTRNLGYGLKSRGFMNSSGHAILEIHVSKA
>d1aun__b.25.1.1 (-) Pathogenesis-related protein 5d {Common tobacco (*Nicotiana tabacum*)}
SGVFEVHNNCPYTVWAAATPVGGRRRLERQSWWFVAPPGTKMARIWGRNTCNFDGAGRGWCQ
TGDCGGVLECKGWGKPPNTLAEYALNQFSNLDFWDISVIDGFNIPMSFGPTKPGPGKCHGIQCTANI
NGECPGSLRVPGGCNPCTTFGGQQYCCTQGPGPTELSRWFKQRCPDAYSYPQDDPTSTFTCTSW
TTDYKVMFCPYG
>d1du5a_b.25.1.1 (A:) Zeamatin {Maize (*Zea mays*)}
AVFTVVNQCPFTVWAAASVPVGGGRQLNRGESWRITAPAGTTAARIWARTGCKFDASGRGSCRTGDC
GGVLQCTGYGRAPNTLAEYALKQFNLDFFDISLIDGFNVPMDFSPTRGCRGVRCAADIVGQCP
AELRQDGVCCNACPVFKKDEYCCVGSAAANDCHPTNYSRYFKGQCPDAYSYPKDDATSTFTCPAGTN
YKVVFCP
>d1thw__b.25.1.1 (-) Thaumatin {*Ketemfe* (*Thaumatococcus daniellii*)}
ATFEIVNRCSTVWAAASKGDAALDAGGRQLNSGESWTINVEPGTKGGKIWARTDCYFDDSGSGICK
TGDCGGLLRCKRFRPPTTLAEFSLNQYGKDYIDISNIKGFNVPMDFSPTRGCRGVRCAADIVGQCP
AKLKAPGGCNDACTVFTSEYCCTTGKCGPTEYSRFFKRLCPDAFSYVLDKPTTVTCPGSSNYRVT
FCPTA
>d1dd1a_b.26.1.1 (A:) Smad4 tumor suppressor C-terminal domain {Human (*Homo sapiens*)}
NGHLQHPPMPHPGHYWPVHNELAFQPPISNHPAPEYWCSIAYFEMDVQVGETFKVPSSCPIVTV
DGYVDPSGGDRFCLGQLSNVHRTEAIERARLHIGKGVQLECKGEGDVVVRCLSDHAVFVQSYLDR
EAGRAPGDAVHKIYPSAYIKVFDLRQCHRQMQQAAATAQAAAAAAQAAAVAGNIPGPGSVGGIAPAI
SLSAAAGIGVDDLRLRLCILRMSFVKGWGPDYPRQSIKETPCWIEIHLHRALQLLDEVLHTMPI
>d1ygs__b.26.1.1 (-) Smad4 tumor suppressor C-terminal domain {Human (*Homo sapiens*)}
APEYWCSIAYFEMDVQVGETFKVPSSCPIVTVDGYVDPSGGDRFCLGQLSNVHRTEAIERARLHIGK
VQLECKGEGDVVVRCLSDHAVFVQSYLDREAGRAPGDAVHKIYPSAYIKVFDLRQCHRQMQQAA
TAQAAAAAAQAAAVAGNIPGPGSVGGIAPAISSAAAGIGVDDLRLRLCILRMSFVKGWGPDYPRQ
SIKETPCWIEIHLHRALQLLDEVLHTM
>d1khxa_b.26.1.1 (A:) Smad2 MH2 domain {Human (*Homo sapiens*)}
PVTYSEPAFWCSIAYYELNQRVGETFHASQPSLTVDGFTDPSNSERFCLGLLSNVNRNATVEMTRRH

IGRGVRLYYIGGEVFAECLSDSAIFVQSPNCNQRYGWHPATVCKIPPGCNLKIFNNQEFAALLAQSVN
QGF EAVYQLTRMCTIRMSFVKGWGAEYRRQTVTSTPCWIELHLNGPLQWLDKVLTMGSPSVRCSS
MS

>d1khua_ b.26.1.1 (A:) Smad1 {Human (Homo sapiens)}

PKHWCSIVYYELNNRVGEAFHASSTSVLVDGFTDPSNNKNRFCLGLLSNVNRNSTIENTRRRHIGKGV
HLYYVGGEVYAECLSDSSIFVQSRNCNYHHGFHPTTVCKIPSGCSLKIFNNQEFAQLLAQSVNHGFET
VYELTKMCTIRMSFVKGWGAEYHRQDVTSTPCWIEIHLHGPLQWLDKVLTMGSPHNPISVS

>d1dmza_ b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53 {Baker's yeast
(Saccharomyces cerevisiae)}

GNGRFLTLKPLPDSIIQESLEIQQGVNPFIFGRSEDCNCKIEDNRLSRVHCFIFKKRHAVGKSMYESPA
QGLDDIWYCHTGTNVSYLNNRMIQGTKFLLQDGEIKIWDKNNKFVIGFKVEINDTTGLFNEGL
GMLQEQRVVLKQTAEKDLVKKL

>d1g6ga_ b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53 {Baker's yeast
(Saccharomyces cerevisiae)}

GENIVCRVICTTGQIPIRDLSDISQVLKEKRSIKKVWTFGRNPACDYHLGNISRLSNKHFQILLGEDG
NLLNDISTNGTWLNGQKVEKNSNQLLSQGDEITVGVGVESDILSLVIFINDKFKQCL

>d1k3ja_ b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53 {Baker's yeast
(Saccharomyces cerevisiae)}

ATQRFLIEKFSQEQIGENIVCRVICTTGQIPIRDLSDISQVLKEKRSIKKVWTFGRNPACDYHLGNISR
LSNKHFQILLGEDGNLLNDISTNGTWLNGQKVEKNSNQLLSQGDEITVGVGVESDILSLVIFINDKF
KQCLEQNKVDRIR

>d1qu5a_ b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53 {Baker's yeast
(Saccharomyces cerevisiae)}

EAETREQKLLHSNNTENVKSSKKKGNRFLTLKPLPDSIIQESLEIQQGVNPFIFGRSEDCNCKIEDN
RLSRVHCFIFKKRHAVGKSMYESPAQGLDDIWYCHTGTNVSYLNNRMIQGTKFLLQDGEIKIWD
KNNKFVIGFKVEINDTTGLFNEGLGMLQEQRVVLKQTAEKDLVKKL

>d1cq3a_ b.27.1.1 (A:) Soluble secreted chemokine inhibitor, VCCI {Cowpox virus}

SFSSSSCSTEENKHHMGIDVIKVKQDQPTNDKICQSVTEVTESEDESEEVVKGDPTTYTVVGG
GLTMDFGFTKCPKISSISEYSDGNTVNARLSSVSPGQKDSPAITREEALSMIKDCEMSINIKCSEEEK
DSNIKTHPVLGNSHKKVSYEDIIGSTIVDTKCVKNLEISVRIGDMCKESSELEVKGDFKYVDGSASE
DAADDTSLINSAKLIACV

>d1p35a_ b.28.1.1 (A:) Paculovirus p35 {Nuclear polyhedrosis virus (Autographa californica),
ACMNPV}

CVIFPVEIDVSQTIIRDQCQVDKQTRRELVYINKIMNTQLTKPVLMMFNISGPIRSVTRKNNNLRDRIKSK
VDEQFDQLERDYSQMDGFHDSIKYFKDEHYSVSCQNGSVLKSFAKILKSHDYTDKKSIEAYEKYC
LPKLVDERNDYYVAVCVLPGFENGSNQVLSFEYNPIGNKVIVPFAHEINDTGLYEYDVVAYVDSVQF
DGEQFEFVQSLILPSSFKNSEKVLVYNEASKNKSMIYKALEFTTESSWGKSEKYNWKIFCNGFIYDK
KSKVLYVKLHNVTALNKNVILNTIKA

>d1nls_ b.29.1.1 (-) Concanavalin A {Jack bean (Canavalia ensiformis)}

ADTIVAVELDTYPNTDIGDPSYPHIGIDIKSVRSKKTAKWNMQNGKVGTAHIYNSVDKRLSAVVSYP
NADSATVSYDVLDNLPEWVRVGLSASTGLYKETNTILSWSFTSKLKSNTHETNALHFMFNQFS
KDQKDLILQGDATTGTDGNLELTRVSSNGSPQGSSVGRALFYAPVHIWESSAVVASFEATFTFLIKSPD
SHPADGIAFFISNIDSSIPSGSTGRLLGLFPDAN

>d2cna_ b.29.1.1 (-) Concanavalin A {Jack bean (Canavalia ensiformis)}

ADTIVAVELDTYPNTDIGDPSYPHIGIDIKSVRSKKTAKWNMQDGKVGTAHIIYNSVDKRLSAVVSYP
NADATSVSYDVLNDVLPWVVRVGLSASTGLYKETNTILSWSFTSKLKSNSTHQTDALHFMFNQFS
KDQKDLILQGDATTGTDGNLELTRVSSNGSPEGSSVGRALFYAPVHIWESSATVSAFEATFAFLIKSPD
SHPADGIAFFISNIDSSIPSGSTGRLLGLFPDAN

>g2ltn.1 b.29.1.1 (A;,B:) Legume lectin {Garden pea (*Pisum sativum*)}

TETTSFLITKFSPDQQLNLIQGDGYTTKEKLTLTAKVKNVGRALYSSPIHIWDRETGNVANFVTSFT
FVINAPNSYNVADGFTFFIAPVDTKPQTGGGYLGVFNSEAEDKTTQTVAVEFDTFYNAAWDPSNRD
RHIGIDVNSIKSVNTKSWKLQNGEEANVVIAFNAATNVLTVSLTYPNXVTSYTLSDVVSLKDVVPEW
VRIGFSATTGAEYAAHEVLSWSFHSELSG

>g1len.1 b.29.1.1 (A;,B:) Legume lectin {Common lentil (*Lens culinaris*)}

TETTSFSITKFSPDQQLNLIQGDGYTTKGLTTLKAVKSTVGRALYSTPIHIWDRDTGNVANFVTSFTF
VIDAPSSYNVADGFTFFIAPVDTKPQTGGGYLGVFNSKEYDKTSQTVAVEFDTFYNAAWDPSNKERH
IGIDVNSIKSVNTKSWNLQNGERANVVIAFNAATNVLTVTLTYPNXVTSYTLNEVVPLKDVVPEWVR
IGFSATTGAEEAAQEVHSWSFNSQLG

>d1led_ b.29.1.1 (-) Legume lectin {West-central african legume (*Griffonia simplicifolia*)}

ENTVNFTYPDFWSYSLKNGTEITFLGDATRIPGALQLTKTDANGNPVRSSAGQASYSEPVFLWDSTG
KAASFYTSFTFLLKNYGAPTADGLAFLAPVDSSVKDYGGFLGLFRHETAADPSKNQVVAVEFDTWI
NKDWNDDPPYPHIGIDVNSIVSVATTRWENDDAYGSSIATAHITYDARSKILTVLVLSYEHGRDYILSHV
DLAKVLPQKVRIGFSAGVGYDEVYILSWHFFSTLDGTNK

>d1hqla_ b.29.1.1 (A;) Legume lectin {*Griffonia simplicifolia*, lectin I-b4}

SVSFTFPNFWSVEDSIIQGDANTTAGTLQLCKTNQYGTPLQWSAGRALYSDPVQLWDNKTESVAS
FYTEFTFFLKITGNGPADGLAFLAPPDSDVKDAGEYLGLFNKSTATQPSKNQVVAVEFDTWTPNF
PEPSYRHIGINVNSIVSVATKRWEDSDIFSGKIATARISYDGSAEILTVVLSYDPGSDYILSHSVDMRQN
LPESVRVGISASTGNNQFLTYYILSWRFSSNL

>d1ax0_ b.29.1.1 (-) Legume lectin {Coral tree (*Erythrina corallodendron*)}

VETISFSFSEFEPGNDNLTLQGAALITQSGVLQLTKINQNGMPAWDSTGRTLYAKPVHIWDMTTGTV
ASFETRFSFSIEQPYTRPLPADGLVFFMGPTKSKPAQGYGLGIFNNSKQDNSYQTLGVEFDTFSPNW
DPPQVPHIGIDVNSIRSITQPFQLDNGQVANVVIKYDASSKILHAVLVYPSSGAIYTIIEIVDKQVLP
EWVDVGLSGATGAQRDAAETHDVYSWSFQASLPE

>d1wbfa_ b.29.1.1 (A;) Legume lectin {Winged bean (*Psophocarpus tetragonolobus*), basic agglutinin}

KTISFNFNQFHQNEEQKLQRDARISSNSVLELTKVNVGVPTWNSTGRALYAKPVQVWDSTTGNVA
SFETRFSFSIRQPFPRHPADGLVFFIAPPNTQTGEGGGYFGIYNPLSPYPFAVEFDTFRNTWDPQIP
HIGIDVNSVISTKTVPFTLDNGGIANVVIKYDASTKILHVVLVFPVSLGTIYTIADIVDLKQVLPESVNVG
FSAATGDPGSKQRNATETHDILSWSFSASLPG

>d1f9ka_ b.29.1.1 (A;) Legume lectin {Winged bean (*Psophocarpus tetragonolobus*), acidic lectin}

ETQSFNFDHFEENSKELNLQRQASIKSNGVLELTKLTKNGVPVWKSTGRALYAEPKIWDSTTGNVA
SFETRFSFNITQPYAYPEPADGLTFFMVPPNSPQGEDGGNLGVFKPPEGDNAFAVEFDTFQNTWDPQ
VPHIGIDVNSIVSSKTLHFQLENGGVANVVIKYDSPTKILNVVLAHFSVGTVYTLNIVDLKQEFNSE
WVNVGLSATTGYQKNAVETHEIISWSFTSSL

>g1loe.1 b.29.1.1 (A;,B:) Legume lectin {*Lathyrus ochrus*, isolectin I}

TETTSFSITKFSPDQQLNLIQGDGYTTKERLTTLKAVRNTVGRALYSSPIHIWDSKTGNVANFVTSFT
FVIDAPNSYNVADGFTFFIAPVDTKPQTGGGYLGVFNPKDYDKTSQTVAVEFDTFYNTAWDPSNGDR

HIGIDVNSIKSINTKSWALQNGKEANVVI AFNAATNVLT VSLTYPXTSYTLNEVVPLKEFVPEWVRIG
FSATTGAEEFAAHEVLSWYFHSELA

>d2pela_b.29.1.1 (A:) Legume lectin {Peanut (*Arachis hypogaea*)}

AETVSFNFNFSFSEGNPAINFQGDVTVLSNGNIQLTNLNKVN SVGRVLYAMPVRIWSSATGNVASFLTS
FSFEMKDIKDYDPADGIIFFIAPEDTQIPAGSIGGGTLGVSDTKGAGHFVGVFEDTYSNSEYNDPPTDH
VGIDVNSVDSVKTVPWNSVSGAVVKVTVIYDSSTKTL SVAVTNDNGDITITIAQVVDL KAKLPERVKF
GFSASGSLGGRQIHLIRSWSTLIT

>d1g9fa_b.29.1.1 (A:) Legume lectin {Soybean (*Glycine max*)}

AETVSFSWNKFVPKQPNMILQGD AIVTSSGKLQLNKVDENGT PKPSSLGRALYSTPIHIWDKETGSV
ASFAASFNFTFYAPDTKRLADGLAFFLAPIDTKPQTHAGYLG LFNENESGDQVVAVEFDTRNSWDP
PNPHIGINVNSIRSIKTTSWDLANNKVAKVLITYDASTLLV ASLVYPSQRTSNILSDVVDLKTSLPEW
VRIGFSAATGLDIPGESHDVLSWSFASNLPHASSNIDPLDLTSFVLHE

>g1qmo.1_b.29.1.1 (A,E:) Legume lectin {Field bean (*Dolichos lab lab*), Fril}

AQSLSFSTKFDPNQEDLIFQGHATSTNNV LQVTKLDSAGNPVSSAGRVLYSAPLRLWEDSAVLT SF
DTIINFEISTPYTSRIADGLAFFIAPPDSVISYHGGFLGLFPNANXSNVVAVEFDTYLNP DYGDPNYIHI
GIDVNSIRSKVTAKWDWQNGKIATAHISYNSVSKRLSVTSYYAGSKPATLSYDIELHTV LPEWVRVGL
SASTGQDKERNTVHSWSFTSSLWTN

>d1g7ya_b.29.1.1 (A:) Legume lectin {Horse gram (*Dolichos biflorus*), different isoforms}

ADIQSF SFKNFNSSSFI LQGDATVSSSKLRLTKVKGNGLPTLSSLGRAFYSSPIQIYDKSTGAVASWATS
FTANIFAPNKSSSADGIAFALVPVGSEPKSNSGFLGVFDSVDNSAQTVAVEFDTF SNTDWDPTSRH
IGIDVNSIKSIRTASWGLANGQNAEILITYNAATSLLVASLVHPSRRTSYIVSERVDITNELPEYVSIGFS
ATTGLSEGYTETHDVLSWSFASKLPDDSTTEPLDIASYLVRNVL

>d1lu1_b.29.1.1 (-) Legume lectin {Horse gram (*Dolichos biflorus*), different isoforms}

ANIQSF SFKNFNSPSFI LQGDATVSSGKLQLTKVKENGIPTSSLGRAFYSSPIQIYDKSTGAVASWATS
FTVKISAPSKASFADGIAFALVPVGSEPRRNGGYLGVFDSVDYNNNSAQTVAVEFDTL SNSGWDPSMK
HIGIDVNSIKSIATVSWDLANGENAEILITYNAATSLLVASLVHPSRRTSYILSERVDITNELPEYVSVGF
SATTGLSEGYIETHDVLSWSFASKLPDDSTAEPDLASYLVRNVL

>d1h9wa_b.29.1.1 (A:) Legume lectin {Duke (*Dioclea guianensis*)}

ADTIVAVELDSYPNTDIGDPSYPHIGIDIKSIRSKSTARWNMQTGKVGTAHISYNSVAKRLSAVVSYTG
SSSTTVSYDVLNNVLP EWVRVGLSATTGLYKETNTILSWSFTSKLKTNSIADANSLHFSFNQFSQNP
KDLILQGDATTDSGNLELTKVSSSGDPQGSSVGRALFYAPVHIWEKSAVVASFDATFTFLIKSPDRDP
ADGITFFIANTDTSIPSGSGRLLGLFPDAN

>d1fx5a_b.29.1.1 (A:) Legume lectin {Furze (*Ulex europaeus*), UEA-I}

SDDL SFKFNFSQNGKDL SFQGNASVIETGVLQLNKVGNL PDETGGIARYIAPIHIWNCNTGELASF
ITSFSFFMETSANPKAATDGLTFFLAPPD SPLRRAGGYFLFN DTKCDSSYQTVAVEFDTIGSPVNFW
DPGFPHIGIDVNCVKSINAERWNKRYGLNNVANVEIIEASSKTLTASLTYP SDQTSISVTSIVDLKEIL
PEWVSVGFSGSTYIGRQATHEVLN WYFTSTFINT

>d1qnwa_b.29.1.1 (A:) Legume lectin {Furze (*Ulex europaeus*), UEA-II}

SDDL SFNFDK FVPNQKNII FQGDASVSTTGVLQVTKVSKPTTTSIGRALYAAPIQI WDSITGKVASFAT
SFSFVVKADKSDGVDGLAFFLAPANSQIPSGSSAGMFLGFSSSDSKSSNQIIAVEFDTYFGKAYNPWD
PDFKHIGIDVNSIKSIKTVKWDWRNGEVADV VITYRAPTKSLTVCLSYPSDGT SNII TASVDL KAILPE
WVSVGFSGGVGNAAEFETHDVLSWYFTSNLE

>d1dbna_b.29.1.1 (A:) Legume lectin {Maackia amurensis, leukoagglutinin}

SDELSFTINNFV PNEADLLFQGEASVSSTGVLQLTKVENGQPQKYSVGRALYAAPVRIWGNTTG SVAS

FSTSFTFVVKAPNPDITSDGLAFYLAPPDSQIPSGSVSKYLGLFNNSNSDSSNQIVAVEFDITYFAHSYD
PWDPNYRHIGIDVNGIESIKTVQWDWINGGVAFATITYLAPNKTLIASLVYPSNQTTFSVAASVDLKE
ILPEWVRVGFSAATGYPTVEVDVLSWSFTSTL

>d1fnya_b.29.1.1 (A:) Legume lectin {Black locust (*Robinia pseudoacacia*)}

TGSLSFSPKFPAPNPYLNQGDALVTSTGVLQLTNNVNGVPSKSLGRALYAAPFQIWDSTTGNVASF
VTSFTFIIQAPNPATTADGLAFFLAPVDTQPLDLGGMLGIFKDG YFNKSNQIVAVEFDTF SNGDWDPK
GRHLGINVNSIESIKTVPW NWTNGEVANVFISYEASTKSLTASLVYPSLET SFIIDAIVDVKIVLPEWV
RFGFSATTGIDKGYVQTNDVLSWSFESNLPG

>d1avba_b.29.1.1 (A:) Phytohemagglutinin-L, PHA-L, also arcelin {Kidney bean (*Phaseolus vulgaris*)}

SNDASFNVETFNKTNLILQGDATVSSEGHLLLTNVKGNEEDSMGRAFYSAPIQINDRTIDNLASFSTN
FTFRINAKNIENSAYGLAFALVPVGSRPKLGKRYLGLFNNTNYDRDAHTVAVVFDTVSNRIEIDVNSIR
PIATESCNFGHNNGEKAEV RITYDSPKNDLRVSLLYPSSEEKCHVSATVPLEKEVEDWVSVGF SATSG
SKKETTETHNVLSWSFSSNFI

>d1dhkb_b.29.1.1 (B:) Phytohemagglutinin-L, PHA-L, also arcelin {Kidney bean (*Phaseolus vulgaris*)}

ATETSFIIDAFNKTNLILQGDATVSSNGNLQLSYNSYDSMSRAFYSAPIQIRDSTTGNVASFDTNFTM
NIRTHRQANSVGLDFVLVPVQPESKGDVTVEFDTFLSRISIDVNNNDIKSVPWDVHDYDQNAEV
RITYNSSTKVFSVLSNPSTGKSNNVSTTVELEKEVYDWVSVGF SATSGAYQWSYETHDVLWSFSS
KF

>d1g8wa_b.29.1.1 (A:) Phytohemagglutinin-L, PHA-L, also arcelin {Kidney bean (*Phaseolus vulgaris*)}

SNDIYFNFRFNETNLILQRDASVSSGQLRLTNLNGNGEPRVGLGRAFYSAPIQIWDNTTGTVASF
ATSFTFNIQVPNNAGPADGLAFALVPVGSQPKDKGGFLGLFDG SNSNFHTVAVEFD TLYNKDWDPT E
RHIGIDVNSIRSIKTTRWDFVNGENAEVLITYDSSTNLLVASLVYPSQKTSFIVSDTVDLKSVLPEWVS
VGFSATTGINKGNVETNDVLSWSFASKLS

>d1ioaa_b.29.1.1 (A:) Phytohemagglutinin-L, PHA-L, also arcelin {Kidney bean (*Phaseolus vulgaris*), G02771, arcelin-5a}

ATETSFNFPNFHTDDKLILQGNATISSKGQLQLTGVSNELPRVDSLGRAFYSAPIQIKDSNNVASFNT
NFTFIIRAKNQSSISAYGLAFALVPVNSPPQKKQEF LGIFNTNPEPNARTVAVVFN TFKNRIDFDKNFI
KPYVNENCDFHKYNGEKT DVQITYDSSNNDLRVFLHFTVSQVKCSVSATVHLEKEVDEWVSVGFSP
TSGLTEDTTETHDVLWSFSSKFR

>d1gbg_b.29.1.2 (-) Bacillus 1-3,1-4-beta-glucanase {*Bacillus licheniformis*}

QTGGSFYEPFNNTGLWQKADGYSNGNMFNCTWRANNVSM TSLGEMRLSLTSPSYNKFD CGEN
RSVQTYGYGLYEVNMKPAKNV GIVSSFFTYTGPTDGT PWDEIDIEFLGKDTTKVQFNYYTNGVGNHE
KIVNLGFDAANSYHTYAFDWQPN SIKWYVDGQLKHTATTQIPQTPGKIMMNLWNGAGVDEWLGSY
NGVTPLYAHYNWVRYTKR

>d2ayh_b.29.1.2 (-) Bacillus 1-3,1-4-beta-glucanase {Hybrid protein: residues 1-16 from *Bacillus amyloliquefaciens* and *Bacillus macerans*}

QTGGSFFEPFNNSYNSGTWEKADGYSNGGVFNCTWRANNVNF TNDGKLGKLTSSAYNKFDCAEYR
STNIYGYGLYEVSMKPAKN TGIVSSFFTYTGPAGHTQWDEIDIEFLGKDTTKVQFNYYTNGVGGHEK
VISLGF DASKGFHTYAFDWQPGYIKWYVDGVLKHTATANIPSTPGKIMMNLWNGTGVD DWLGSYN
GANPLYAEYDWVKYTSN

>d1ajka_b.29.1.2 (A:) Bacillus 1-3,1-4-beta-glucanase {*Bacillus macerans*}

NTGIVSSFFTYTTPAHGTQWDEIDIEFLGKDTTKVQFNYYTNGVGGHEKVISLGF DASKGFHTYA F DWQPGYIKWYVDGVLKHTATANIPSTPGKIMMNLWNGTGVDWDLG SYNGANPLYAEYD WVKYTSNQTGGSFFEPFN SYNSGTWEKADGYSNGGVFNCTWRANNVNF TNDGK LKLG LTSSAYNKFDCAEYRSTNIYGYGLYEVSMKPAK

>d1ajoa_b.29.1.2 (A:) Bacillus 1-3,1-4-beta-glucanase {Bacillus macerans}

GHEKVISLGF DASKGFHTYA F DWQPGYIKWYVDGVLKHTATANIPSTPGKIMMNLWNGTGVDWDLG SYNGANPLYAEYD WVKYTSNQTGGSFFEPFN SYNSGTWEKADGYSNGGVFNCTWRANNVNF TNDGK LKLG LTSSAYNKFDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTTPAHGTQWDEIDIEFLGKDTTKVQFNYYTNG

>d1cpm_b.29.1.2 (-) Bacillus 1-3,1-4-beta-glucanase {Bacillus macerans}

FDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTTPAHGTQWDEIDIEFLGKDTTKVQFNYYTNG VGGHEKVISLGF DASKGFHTYA F DWQPGYIKWYVDGVLKHTATANIPSTPGKIMMNLWNGTGVDWDLG SYNGANPLYAEYD WVKYTSNQTGGSFFEPFN SYNSGTWEKADGYSNGGVFNCTWRANNVNF TNDGK LKLG LTSSAYNA

>d1cpn_b.29.1.2 (-) Bacillus 1-3,1-4-beta-glucanase {Bacillus macerans}

FDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTTPAHGTQWDEIDIEFLGKDTTKVQFNYYTNG VGGHEKVISLGF DASKGFHTYA F DWQPGYIKWYVDGVLKHTATANIPSTPGKIMMNLWNGTGVDWDLG SYNGANPLYAEYD WVKYTSNGSVFWEPKSYFNPSTWEKADGYSNGGVFNCTWRANNVNF TNDGK LKLG LTSS

>d1dypa_b.29.1.2 (A:) kappa-Carrageenase, catalytic {Pseudoalteromonas carrageenovora}

SMQPPIAKPGETWILQAKRSEDFNVKDATKWNFQTENYGVWSWKNENATVSKGKLLTKRESH QRTFWDGCNQQVANYPLYTSGVAKSRATGNYGYEARIKGASTFPGVSPAFWMYSTIDRSLTKEG DVQYSEIDVVELTQKSAVRESHDHLHNIVVKNKPTWMRPGSFPQTNHNGYHLPDFPRNDFHTYG VNVTKDKITWYVDGEIVGEKDNLWHRQMNLTLSQLRAPHTQWKCQNQFYPSANKSAEGFPTSM EVDYVRTWVKV

>d1slta_b.29.1.3 (A:) S-lectin, different isoforms {Cow (Bos taurus)}

CGLVASNLNLKPGECLEVRGEVAADAKSFLNLGKDDNNLCLHFNPRFNAHGDVNTIVCNSKDAGA WGAEQRESAFPFPQGSVVEVCISFNQTDLTIKLPDGYEFKFPNRLNLEAINYLSAGGDFKIKCVAFE

>d1bkza_b.29.1.3 (A:) S-lectin, different isoforms {Human (Homo sapiens)}

SNVPHKSSLPEGIRPGTVLRIRGLVPPNASRFHVNLLCGEEQGS DAALHFNPRLD TSEVVFNSKEQGS WGREERPGVPFQRQPFEVLIIASDDGFKAVVGDAQYHHRHRLPLARVRLVEVGGDVQLDSVRIF

>d1hlca_b.29.1.3 (A:) S-lectin, different isoforms {Human (Homo sapiens)}

ELEVKNMDMKPGSTLKITGSIADGTDGFVINLQGQTDKLNLFNPRFSESTIVCNSLDGSNWGQEQ REDHLCFSPGSEVKFTVTFESDKFKVKLPDGHELTFPNRLGHSLSYLSVRGGFNMSSFKLKE

>d1qmja_b.29.1.3 (A:) S-lectin, different isoforms {Chicken (Gallus gallus)}

QGLVVTQLDVQPGECKVKVKILSDAKGFSVNVGKDSSTLMLHFNPRFDCHGDVNTVVCNSKEDGT WGEEDRKADFPFQQGDKVEICISFDAAEVKVKVPEVEFEFPNRLGMEKIQYLAVEGDFKVKAIKFS

>d1a78a_b.29.1.3 (A:) S-lectin, different isoforms {Toad (Bufo arenarum)}

ASAGVAVTNLNLKPGHCVEIKSIPDCKGFAVNLGEDASNFLHFNARFDLHGDVNVKIVCNSKEAD AWGSEQREEVFPFQQGAEMVCFEYQTQKIIKFSSGDQFSFPVRKVLPSIPFLSLEGLAFKSITTE

>d1hdka_b.29.1.3 (A:) Charcot-Leyden crystal (CLC) protein {Human (Homo sapiens)}

SLLPVPTYEAASLSTGSTVTIKRPLVCFLNEPYLQVDFHTEMKEESDIVFHFQVCFGRVVMNSREY GAWKQQVESKNMPFQDQGEFELSISVLPDKYQVMVNGQSSYTFDHRIKPEAVKMVQVWRDISLTKF NVSYL

>d1a3k_b.29.1.3 (-) Galectin-3 CRD {Human (Homo sapiens)}
LIVPYNLPLPGGVVPRMLITILGTVKPNANRIALDFQRGNDVAFHFNPRFNENNRRRVIVCNTKLDNN
WGREERQSVFPFESGKPFKIQVLVEPDHFKVAVNDAHLLQYNHRVKKLNEISKLGISGDIDLTSASYT
MI

>d1c1la_b.29.1.3 (A:) Congerin I {Conger eel (Conger myriaster)}
GGLQVKNFDFTVGKFLTVGGFINNSPQRFSVNVGEMNSLSLHLDHRFNYGADQNTIVMNSTLKGD
NGWETEQRSTNFTLSAGQYFEITLSYDINKFYIDILDGPNLEFPNRYKEFLPFLSLAGDARLTLVKLE

>d1d2sa_b.29.1.4 (A:) Sex hormone-binding globulin {Human (Homo sapiens)}
PPAVHLSNGPGQEPIAVMTFDLTKITKTSSEFEVRTWDPEGVIFYGDTNPKDDWFMLGLRDGRPEIQ
LHNHWAQLTVGAGPRLLDGRWHQVEVKMEGDSVLEVDGEEVLRRLRQVSGHPIMRIALGGLLPA
SNLRLPLVPALDGCLRRDSWLDKQAEISASAPTSLRSC

>d1dyka1_b.29.1.4 (A:2744-2932) Laminin alpha2 chain {Mouse (Mus musculus)}
HGPCVAESEPALLTGSKQFGLSRNSHIAIAFDDTKVKNRLTIELEVRTEAESGLLFYMARINHADFATV
QLRNGFPYFSYDLGSGDTSTMIPTKINDGQWHKIKIVRVKQEGILYVDDASSQTISPCKADILDVVGIL
YVGGLPINYTTTRRIGPVTYSLDGCVRNLHMEQAPVLDLQPTSSFHVGTCEA

>d1dyka2_b.29.1.4 (A:2933-3117) Laminin alpha2 chain {Mouse (Mus musculus)}
NAESGTYFDGTGFAKAVGGFKVGLDLLVEFEFRTTRPTGVLLGVSSQKMDGMGIEMIDEKLMFHVD
NGAGRFTAIYDAEIPGHMCNGQWHKVTAKKIKNRLELVVDGNQVDAQSPNSASTSADTNDPVFVGG
FPGGLNQFGLTTNIRFRGCIRSLKLTGKTGKPLEVNFAKALELRGVQPVSCPT

>d1c4ra_b.29.1.4 (A:) Ligand-binding domain of neuexin 1beta {Rat (Rattus norvegicus)}
HAGTTYIFSKGGGQITYKWPPNDRPSTRADRLAIGFSTVQKEAVLVRVDSSSGLGDYLELHIHQGKIG
VKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPAGRQLTIFNSQATIIGGK
EQGQPFQGLSGLYNGLKVLNMAAENDANIAIVGNVRLVGEV

>d1saca_b.29.1.5 (A:) Serum amyloid P component (SAP) {Human (Homo sapiens)}
HTDLSGKVFVFPRESVTDHVNLIPTLEKPLQNFTLCFRAYSLSLFSYNTQGRDNELLVYKERV
GEYSLYIGRHKVTSKVIEKFPAPVHICVSWESSGIAEFWINGTPLVKKGLRQGYFVEAQPKIVLGGQEQ
DSYGGKFDRSQSFVGEIGDLYMWDVLPPENILSAYQGTPLPANILDWQALNYEIRGYVIIKPLVWV

>d1b09a_b.29.1.5 (A:) C-reactive protein (CRP) {Human (Homo sapiens)}
QTDMSRKAFVFPKESDTSYVSLKAPLTKPLKAFTVCLHFYTELSSTRGYSIFSATKRQDNEILIFWSK
DIGYSFTVGGSEILFEVPEVTVAPVHICTSWESASGIVEFWVDGKPRVRKSLKKGTYVGAESIILGQE
QDSFGGNFEQSLSVGDIGNVMWDFVLSPEINTIYLGPFSPNVLNWRALKYEVQGEVFTKPQL
WP

>d1jhna1_b.29.1.12 (A:61-262) Calnexin {Dog (Canis familiaris)}
YKAPVPSGEVYFADSFDRGTLGWLKAKKDDTDDEIAKYDGKWEVDEMKETKLPDGKGLVMS
RAKHHAISAKLNKPLFDTKPLIVQYEVNFQNGIECGGAYVKLLSKTPELNLDQFHDKTPYTIMFGP
DKCGEDYKLFHIFRHKNPKTGVYEEKHAKRPDADLKYFTDKKTHLYTLILNPDNSFEILVDQSIVN
SGN

>d1jhna2_b.29.1.12 (A:412-458) Calnexin {Dog (Canis familiaris)}
LEPFKMTFSAIGLELWSMTSDIFFDNFIVCGDRRVDDWANDGWGL

>d1a8d_1_b.29.1.6 (1-247) Tetanus neurotoxin {Clostridium tetani}
MKNLDCWVDNEEDIDVILKSTILNLDINNDIISDISGFNSSVITYPDAQLVPGINGKAIHLVNNESSE
VIVHKAMDIEYNDMFNNFTVSFWLRVPKVSASHLEQYGTNEYSIISMKKHLSIGSGWSVSLKGNN
LIWTLKDSAGEVRQITFRDLDPDKFNAYLANKWVFITITNDRLSSANLYINGVLMGSAEITGLGAIRD
NNITLKLDRCNNNNQYVSIDKFRIFCKALNPKEIEKLYTSYLS

>d3btaa1 b.29.1.6 (A:872-1078) Botulinum neurotoxin {Clostridium botulinum, serotype A}
IINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQQLFNLESSKIEVILKNAIVYNSMYENFST
SFWIRIPKYFNSISLNNEYTIINCMENNSGWKVS LN YGEIHWTLQDTQEIKQRVVFYKYSQMINISDYIN
RWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKEL

>d1epwa1 b.29.1.6 (A:862-1079) Botulinum neurotoxin {Clostridium botulinum, serotype B}
NIILNLRKDNLDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIFNSVFLDFSVSF
WIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIHWTLIDINGKTKSVFFEYNIREDISEYIN
RWFVVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQS
NIEERYKIQSY

>d1ikpa1 b.29.1.7 (A:2-251) Exotoxin A, N-terminal domain {Pseudomonas aeruginosa}
EEAFDLWNECAKACVLDLKDGVRSRMSVDPADTNGQGV LHYSMVLEGGNDALKLAIDNALSIT
SDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTI
EMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVSVVMAQAQPRREKRWSEWASGKVLCLLD
QLDGVYNYLAQRCNLDDTWEGKIYRVLAGNPAKHDLDIKPTVISHRLHFP

>d1kit_1 b.29.1.8 (25-216) Vibrio cholerae sialidase, N-terminal and insertion domains
{Vibrio cholerae}
ALFDYNATGDTEFDSPAKQGWMQDNTNNGSGVLTNADGMPAWLVQGIGGRAQWTYSLSTNQHAQ
ASSFGWRMTTEMKVLSSGMITNYYANGTQRVLPISLSDSSGNLVVEFEGQTGRTVLATGTAATEYHK
FELVFLPGSNPSASFYFDGKLIRDNIQPTASKQNMIVWGNSSNTDGVAAYRDIKFEIQGD

>d1kit_2 b.29.1.8 (347-543) Vibrio cholerae sialidase, N-terminal and insertion domains
{Vibrio cholerae}
DVTDQVKERSFQIAGWGGSELYRRNTSLNSQQDWQSNKIRIVDGAANQIQVADGSRKYVVTLSIDE
SGGLVANLNGVSAPIILQSEHAKVHSFHDYELQYSALNHTTTTLFVDGQQITTWAGEVQS ENNIQFGN
ADAQIDGRLHVQKIVLTQQGHNLVEFD AFYLAQQTPEVEKDLEKLGWTKIKTGNTMSLYGNAS

>d2sli_1 b.29.1.9 (81-276) Leech intramolecular trans-sialidase, N-terminal domain {North
american leech (Macrobdelella decora)}
IPEGILMEKNNVDIAEGQGYSLDQEAGAKYVKAMTQGTIILSYKSTSENGIQSLFSVGNSTAGNQDRH
FHIYITNSGGIGIELRNTDGVFN YTLDRPASVRALYKGERVFNTVALKADAANKQCRLFANGELLATL
DKDAFKFISDITGVDNVTLLGGTKRQKIAYPFGGTIGDIKVYSNALSDEELIQATGVTTY

>d6cel_ b.29.1.10 (-) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {Trichoderma
reesei, Cel7A}
ESACTLQSETHPPLTWQKCSSGGTCTQQTGVSVIDANWRWTHATNSSTNCYDGN TWSSTLCPDNE
TCAKNCCLDGAAYASTYGVTTSGNSLSIDFVTQSAQKNV GARLYLMASDTTYQEFLLGNEFSFDVD
VSQLPCGLNGALYFVSMADGGVSKYPTNTAGAKYGTGYCDSQCPRDLKFINGQANVEGWEPSSNN
ANTGIGGHGSCCSQMDIWEANSISEALTPHPCTTVGQEICEGDGCGGTYS DNRYGGTCDPDGCDWN
PYRLGNTSFYGPSSFTLDTTKKLTVVVTQFETSGAINRYVQNGVTFQQPNAELGSYSGNELNDYCT
AEEAEFGSSFSKDKGLTQFKKATSGGMVLMVSLWDDYANMLWLDSTYPTNETSSTPGAVRGSCS
TSSGVPAQVESQSPNAKVTF SNIKFGPIGSTGNPSG

>d1eg1a_ b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1)
{Trichoderma reesei, Endoglucanase I}
EQPGTSTPEVHPKLT TYKCTKSGGCVAQDTSVVL DWNYRWMHDANYNSCTVNGGVNTTLCPEAT
CGKNCFIEGVDYAASGVTTSGSSLTMNQYMPSSSGGYSSVSPRLLYLLDSDGEYVMLKLNQELSFDVD
LSALPCGENGLYLSQMDENGGANQYNTAGANYGSGYCDACPVQ TWRNGLNTSHQGFCCEMND
ILEGNSRANALTPHSCTATAACDSAGCGFN PYGSGYKSYYPGDTVDTSKTFTIITQFN TDNGSPSNLV

SITRKYQQNGVDIPSAQPGGDTISSCPSASAYGGLATMGKALSSGMVLVFSIWNDNSQYMNWLDSGN
AGPCSSTEGNPSNILANNPNTHVVFSNIRWGDIGSTT

>d3ovwa_ b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {*Fusarium oxysporum*}

ETPDKAKEQHPKLETYRCKASGCKKQTNIVADAGIHGIRQKNGAGCGDWGQKPNATAACPDDEASC
AKNCILSGMDSNAYKNAGITTSNGNKLRLQLINQLVSPRVYLLEENKKKYEMLHLTGTEFSFDVEM
EKLPCGMNGALYLSEMPQDGGKSTSRNSKAGAYYGAGYCDACQYVTPFINGVGNKQGVCCNELDI
WEANSRATHIAPHPCSKPGLYGCTGDECGSSGICDKAGCGWNHNRINVTDFYGRGKQYKVDSTRKF
TVTSQFVANKQGDLELHRHYIQDNKVIESAVVNISGPPKINFINDKYCAATGANEYMRGGTKQMG
DAMSRGMVLAWSVWWSEGDFMAWLDQGVAGPCDATEGDPKNIVKVQPNPEVTFNSNIRIGEIGSTS
SV

>d1dyma_ b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {*Humicola insolens*, Cel7b}

EKPGETKEVHPQLTFRCTKRGGCKPATNFIVLDSLPHIARAEGLGPGGCGDWGNPPPKDVC PDVE
SCAKNCIMEGIPDYSQYGVTTNGTSLRLQHILPDGRVPSRVYLLDKTKRRYEMLHLTGFEFTFDVDA
TKLPCGMNSALYLSEMHPTGAKSKYNPGGAYYGTGYCDAQCFVTPFINGLGNIEGKSGCCNAMDIWE
ANSRASHVAPHTCNKKGLYLCEGEECAFEGVCDKNGCGWNNYRVNVTDYGRGEEFKVNTLKPFT
VVTQFLANRRGKLEKIHRFYVQDGKVIESFYTNKEGVPYTNMIDDEFCEATGSRKYMELGATQGMG
EALTRGMVLAWSIWWQGGNMEWLDHGEAGPCA KEGGAPSNIVQVEPFPEVTTYTNLRWGEIGST
Y

>d1gpia_ b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1)
{*Phanerochaete chrysosporium*, Cel7d}

EQAGTNTAENHPQLQSQQCTTSGGCKPLSTKVVLDNWRWVHSTSGYTNCYTGNEWDTS LCPDGK
TCAANCALDGADYSGTYGITSTGTALTLKFVTGSNVGSRVYLMADDTHYQLLLNQEFTFDVDM
NLPCGLNGALYLSAMDADGGMSKYPGNKAGAKYGTGYCDSQCPKDIKFINGEANVGNWTETGSNT
GTGSYGTCCSEMDIWEANNDAAAFTHPCTTTGQTRCSGDDCARNTGLCDGDGDFNSFRMGDKT
FLGKGMTVDTSKPFTVVTQFLTNDNTSTGTLSEIRRIYIQNGKVIQNSVANIPGVDPVNSITDNFCAQ
QKTAFGDTNWFAQKGLKQMG EALGNGMVLALS IWDHHAANMLWLDSDYPTDKDPSAPGVARGT
CATTSGVPSDVESQVPNSQVVFVSNIFGDI GSTFSGTS

>d1xnb_ b.29.1.11 (-) Xylanase II {*Bacillus circulans*}

ASTDYWQNWT DGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGWTTGSPFRTINY NAGVWAPNGNG
YLTLYGWTRSPLIEYYVVD SWGTYRPTGTYKGT VKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSV
RQSKRPTGSNATITFTNHVNAWKSHGMNLG SNWAYQVMATEGYQSSGSSNVTVW

>d1qh7a_ b.29.1.11 (A:) Xylanase II {*Bacillus agaradhaerens*}

EIVTDNSIGNHDGYDYEFWKDSGGSGTMILNHGGTFSAQWNNVNNILFRKGKFFNETQTHQVGN
MSINYGANFQPNGNAYLCVYGWTV DPLVEYYIVDSWGNWRPPGATPKGTITVDGGTYDIYETLRVN
QPSIKGIATFKQYWSVRRSRKRTSGTISVSNHFRAWENLGMNMGKMYEVALTVEGYQSSGSANVYSNT
LRINGNPLS

>d1hixa_ b.29.1.11 (A:) Xylanase II {*Streptomyces* sp. s38, xyl1}

ITTNQTGTNNGYYSFWTDGGGVS MNLASGGSYGTSWTNCGNFVAGKGWANGARRTVNYSGSFN
PSGNAYLTLYGWTANPLVEYYIVDNWGTYRPTGTYKGTVTS DGGTYDVYQTTRVNAPSVEGKTFN
QYWSVRQSKRTGGSITAGNHFD AWARYGMPLGSFNYYMIMATEGYQSSGSSSIS

>d1xnd_ b.29.1.11 (-) Xylanase II {*Trichoderma harzianum*}

QTIGPGTGYSNYYSYWNWDGHAGVTTYNGGGGSFTVNWSNSGNFVAGKGWQPGTKNKVINFSGS

YNPNGNSYLSIYGWSRNPLIEYYIVENFGTYNPSTGATKLGEVTS DGSVYDIYRTQRVNQPSIIGTATF
YQYWSVRRNHRSSGSVNTANHFNAWASHGLTLGTM DYQIVAVEGYFSSGSASITVS
>d1xyn_ b.29.1.11 (-) Xylanase II {Trichoderma reesei, xynI}
ASINYDQNYQTGGQVSYSNTGFSVNWNTQDDFVVGWTTGSSAPINFGGSFVNSGTGLLSVYG
WSTNPLVEYYIMEDNHNYPAQGTVKGTVTS D GATYTIWENTRVNEPSIQGTATFNQYISVRNSPRTS
GTVTVQNHFNAWASLGLHLGQMNYQVVAVEGWGGSGSASQSVSN
>d1enxa_ b.29.1.11 (A:) Xylanase II {Trichoderma reesei, xynII}
ETIQPGTGYNNGYFYSYWNDGHGGVTYTNGPGGQFSVNWNSNGNFVGGKGWQPGTKNKVINFGSG
YNPNGNSYLSVYGWSRNPLIEYYIVENFGTYNPSTGATKLGEVTS DGSVYDIYRTQRVNQPSIIGTATF
YQYWSVRRNHRSSGSVNTANHFNAWAQQGLTLGTM DYQIVAVEGYFSSGSASITVS
>d1yna_ b.29.1.11 (-) Xylanase II {Thermomyces lanuginosus}
ETTPNSEGWHDGYYYSWWS D GGAQATYTNLEGGTYEISWGDGGLVGGKGNPGLNARAIHFEG
VYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTV ECDGSIYRLGKTTRVNAPSIDGTQ
TFDQYWSVRQDKRTSGTVQTGCHFD AWARAGLNVNGDHYYQIVATEGYFSSGYARITVADVG
>d1bk1_ b.29.1.11 (-) Xylanase II {Aspergillus kawachii}
AGINYVQNYNGNLGDFTYDESAGTFSMYWEDGVSSDFVVGWTTGSSNAITYSAEYSASGSSSYLA
VYGWVNYPQAEYYIVEDYGDYNPCSSATSLGTVYSDGSTYQVCTDTRTNEPSITGTSTFTQYFSVRES
TRTSGTVTVANHFNFWAQHGFNSDFNYQVMAVEAWSGAGSASVTIS
>d1pvxa_ b.29.1.11 (A:) Xylanase II {Paecilomyces variotii bainier}
GTPNSEGWHDGYYYSWWS D GGGDSTYTNNSGGTYEITWNGGNL VGGKGNPGLNARAIHFTG
VYQPNGTSYLSVYGWTRNPLVEYYIVENFGSSNPSSGSTD LGTVSCDGSTYTLGQSTRYNAPSIDGTQ
TFNQYWSVRQDKRSSGTVQTGCHFD AWASAGLNVTDHYYQIVATEGYFSSGYARITVADVG
>d1f5ja_ b.29.1.11 (A:) Xylanase II {Dictyoglomus thermophilum}
ALTSNASGTFDGYYYELWKDTGNTTMTVYTQGRFSCQWSNINNALFRTGKKYNQNWQSLGTIRITY
SATYNPNGNSYLCIYGWSTNPLVEFYIVESWGNWRPPGATSLGQVTIDGGTYDIYRTTRVNQPSIVGT
ATFDQYWSVRTSKRTSGTVTVDHFRWANRGLNLGTIDQITLCVEGYQSSGSANITQNTFSQSS
>d2nlra_ b.29.1.11 (A:) Endo-1,4-beta-glucanase (cellulase) catalytic domain {Streptomyces
lividans, CelB2}
DTTICEPFGTTTTIQGRYVVQNNRWGSTAPQCVTATDTGFRVTQADGSAPTNGAPKSYPSVFNGCHYT
NCSPGTDLPVRLD TVSAAPSSISYGFVDGAVYNASYDIWLDPTARTDGVNQTEIMIWFNRVGP IQPIG
SPVGTASVGGRTWEVWVSGGNGSNDVLSFVAPSAISGWSFDVMDVFRATVARGLAENDWYLT SVQAG
FEPWQNGAGLAVNSFSSTVET
>d1h8va_ b.29.1.11 (A:) Endo-1,4-beta-glucanase (cellulase) catalytic domain {Trichoderma
reesei, Cel12A}
ETSCDQWATFTGNGYTVSNNLWGASAGSGFCVTA VSLSGGASWHADWQWSGGQNNVKS YQNSQI
AIPQKRTVNSISSMPTTASWSYSGSNIRANVAYDLFTAANPNHVYTS GDYELMIWLKYGDIGPIGSS
QGTVNVGGQSWTLYYGYNGAMQVYSFVAQTNTTNYSGDVKNFFNYLRDNKGYNAAGQYVLSYQFG
TEPFTGSGTLNVASWTASIN
>d1jz8a4 b.30.1.1 (A:731-1023) beta-Galactosidase, domain 5 {Escherichia coli}
PAASHAIPHLTTSEMDFCIELGNKRWQFN RQSGFLSQMWIGDKKQLLTPLRDQFTRAPLDNDIGVSE
ATRIPNAWVERWKAAGHYQAE AALLQCTADTLADAVLITTAHAWQHQGKTLFISRKTYRIDGSGQ
MAITVDVEVASDTPH PARIGLNCQLAQAERVNWLGLGPQENY PDRLT AACFDRWDLPLSDMYTPY
VFPSENLRCGTRELNYGPHQWRGDFQFNISRYSQQLMETSHRLLHAE EGTWLNIDGFHMGIG
GDDSWSPSVSAEFQLSAGRYHYQLVWCQK

>d1oaca1 b.30.2.1 (A:301-724) Copper amine oxidase, domain 3 (catalytic) {Escherichia coli}

PAVKPMQIIEPEGKNYTITGDMIHWRNWDFHLSMNSRVGPMISTVITYNDNGTKRKVMYEGSLGGM
IVPYGDPDIGWYFKAYLDSGDYGMGTLSPIARGKDAPSNVLLNETIADYTGVPMEIPRAIAVFERV
AGPEYKHQEMGQPNVSTERRELVVRWISTVGNADYIFDWIFHENGITIGIDAGATGIEAVKGVKAKTM
HDETAKDDTRYGTLIDHNIVGTTTHQHIYNFRLDLVDGENNSLVAMDPVVKPNTAGGPRTSTMQVN
QYNIGNEQDAAQKFDPGTIRLLSNPNKENRMGNPVSYQIIPYAGGTHPVAKGAQFAPDEWIYHRLSF
MDKQLWVTRYHPGERFPEGKYPNRSTHDTGLGQYSKDNESLDNTDAVVWMTTGTTHVARAEW
PIMPTEWVHTLLKPWNFFDETPTLGALK

>d1ksia1 b.30.2.1 (A:207-647) Copper amine oxidase, domain 3 (catalytic) {Pea seedling (Pisum sativum)}

VSKQSPFFGPKQHSLSLTHQPGQPGFQINGHSVSWANWKFHIGFDVRAGIVISLASIYDLEKHKSRRLV
YKGYISELFPVYQDPTEEFYFKTFFDSGEFGFLSTVSLIPNRDCPPHAQFIDTYVHSANGTPILLKNAI
CVFEQYGNIMWRHTENGIPNESIEESRTEVNLIVRTIVTVGNADNVIDWEFKASGSIKPSIALSGILEI
KGTNIKHKDEIKEDLHGKLVANSIGIYHDHFYIYYLDFDIDGTHNSFEKTSKTVRIKDGSSKRKSY
WTTETQTAKTESDAKITIGLAPAELVVNPNIKTAVGNVEGYRLIPAIPAHPLLEDYDYPQIRGAFTNY
NVVWTAYNRTEKWAGGLYVDHSRGDDTLAVWTKQREIVNKDIVMWHVVGIIHVPAQEDFPIMP
LLSTSFELRPTNFFERNPVLKTLSPRDVAWPGC

>d1av4_1 b.30.2.1 (212-628) Copper amine oxidase, domain 3 (catalytic) {Arthrobacter globiformis}

PLRTTQKPSITQPEGPSFTVTGGNHIEWEKWSLDVGFVREGVVLHNIAFRDGDLRPIINRASIAE
MVPYGDPSPIRSWQNYFDTGEYLVGQYANSLELGCDCLDITYLSPVISDAFGNPREIRNGICMHEE
DWGILAKHSDLWSGINYTRRNRRMVISFFTIGNADYGFYWYLYLDGTIEFEAKATGVVFTSAFPEG
GSDNISQLAPGLGAPFHQHIFSARLDMAIDGFTNRVEEEDVVRQTMGPGNERGNAFSRKRTVLTRES
EAVREADARTGRTWIISNPESKNRLNEPVGKYLHAHNQPTLLADPGSSIARRAAFATKDLWVTRYA
DDERYPTGDFVNQHSAGLPSYIAQDRDIDGQDIVVWHTFGLTHFPRVEDWPIMPVDTVGFKLRLP
EGFFDRSPVLDVPAN

>d1a2va1 b.30.2.1 (A:237-672) Copper amine oxidase, domain 3 (catalytic) {Yeast (Hansenula polymorpha)}

PEAPPINVTQPEGVSFKMTGNVMEWSNFKFHIGFNYREGIVLSDVSYNDHGNVRPIFHRISLSEMIV
PYGSPEFPHQRKHALDIGEYAGYMTNPLSLGDCCKGVIHYLDAHFSDRAGDPITVKNVCIHEEDD
GLLFKHSDFRDNFATSLVTRATKLVVSQIFTAANAAYCLYWVFMQDGAIRLDIRLTGILNTYILGDDEE
AGPWGTRVYPNVNAHNHQLFSLRIDPRIDGDGNSAAACDAKSSPYPLGSPENMYGNAFYSEKTTF
KTVKDSLTYESATGRSWDIFNPNKVNPNYSKPPSYKLVSTQCPPLLAKEGSLVAKRAPWASHSVNV
VPYKDNRLYPSGDHVPQWSGDGVRGMREWIGDSENIDNTDILFFHTFGITHFPAPEDFPLMPAEP
ITLMLRPRHFFTENPGLDIQPSYAMTTSEAKRAV

>d1cb8a3 b.30.3.1 (A:336-599) Chondroitinase AC {Pedobacter heparinus (Flavobacterium heparinum)}

IEPYHHQFWNGDYVQHLPAYSFNVRMVSKRTRRSESGNKENLLGRYLSDGATNIQLRGPEYYNIM
PVWEWDKIPGITSRDYLTDRPLTKLWGEQGSNDFAGGVSDGVYGASAYALDYDSLQAKKAWFFFDK
EIVCLGAGINSNAPENITTTLNQSWLNGPVISTAGKTGRGKITTFKAQQQFWLLHDAIGYFFPEGANL
SLSTQSQKGNWFHINNSHSHKDEVSGDVFKLWINHGARPENAQYAYIVLPGINKPEEIKKYNGTA

>d1egua3 b.30.3.1 (A:541-814) Hyaluronate lyase {Streptococcus pneumoniae}

TSYLSAFNKMDKTAMYNAEKGFGLSLFSSRTLNYEHMKNENKRGWYTSDGMFYLYNGDLSHYS

DGYWPTVNPYKMPGTTETDAKRADSDTGKVLPSAFVGTSKLDDANATATMDFTNWNQTLTAHKS
WFMLKDKIAFLGSNIQNTSTDTAATTIDQRKLESSNPYKVYVNDKEASLTEQEKDYPETQSVFLESS
DSKKNIGYFFFKSSISMSKALQKGAWKDINEGQSDKEVENEFLTISQAHKQNGDSYGYMLIPNVDR
ATFNQMIKELE

>d1f1sa4 b.30.3.1 (A:620-919) Hyaluronate lyase {*Streptococcus agalactiae*}

LKSNLSTFNSMDRLAYNAKKDFGFALSLSKRTLNIEGMNDENTRGWYTGDMFYIYNSDQSHY
SNHFWPTVNPYKMAGTTEKDAKREDTTKEFMSKHSKDAKEKTGQVTGTSDFVGSVKLNDHFALA
AMDFTNWDRTLAQKGWVILNDKIVFLGSNIKNTNGIGNVSTTIDQRKDDSKTPYTTYVNGKTIDL
KQASSQQFTDTKSVFLESKEPGRNIGYIFFKNSTIDIERKEQTGTWNSINRTSKNTSIVSNPFITISQKH
DNKGDYGYMMVNPIDRTSFDKLANKEVELLENS

>d1h54a2 b.30.4.1 (A:1-268) Lactobacillus maltose phosphorylase, N-terminal domain
{*Lactobacillus brevis*}

MKRIFEVQPWNVITHTFDPKDKRLQESMTSLGNGYMGMRGDFEEGYSGDSLQGIYLGGVWYPDKT
RVGWWKNGYPKYFGKVVNAVNFILKPIEINGEPVDLAKDKISDFTLDLMDHQVNLNRSFVVERGAV
RVALNFQRFLSVAQPELSVQKVTVKNLSDAEVDVTLKPSIDADMNEEANYDERFWDVLATDQQA
DRGSIVAKTTPNPFGTFRFTSGMEMRLVTDLKNVAITQPNEKEVTTAYTGKLAPQASAELEKRVIVV
TSRDY

>d1hs6a2 b.98.1.1 (A:1-208) Leukotriene A4 hydrolase N-terminal domain {Human (*Homo sapiens*)}

PEIVDTCSLSPASVCRTKHLHLRCSVDFTRRRLTGTAALTVQSQEDNLRSLVLDTKDLTIEKVVINGQ
EVKYALGERQSYKSPMEISLPIALSKNQEIVIEISFETSPKSSALQWLTPEQTSKGHEPHYLSQCQAIH
CRAILPCQDTPSVKLTYYAEVSVPKELVALMSAIRDGETPDPEPDRKIYKFIQKVPIPCYLIALVVGVA

>d1es6a b.31.1.1 (A:) EV matrix protein {Ebola virus}

GDTPSNPLRPIADDTIDHASHTPGSVSSAFIEMVNVISGPKVLMKQIPIWLPLGVADQKTYSFST
TAAIMLASYTITHFGKATNPLVRVNLGPGIPDHPLRLLRIGNQAFLQEFVLPVQLPQYFTFDLTAL
KLITQPLPAATWTDPTGSGALRPGISFHPKLRPILLPNKSGKKGNSADLTSPEKIQAIMTSLQDF
KIVPIDPTKNIMGIEVPETLVLKLTKGKVTSKNGQPIIPVLLPKYIGLDPVAPGDLTMVITQDCDCHS
PASLP

>d1qexa_ b.32.1.1 (A:) gp9 {Bacteriophage T4}

MFIQEPKKLIDTGEIGNASTGDILFDGGNKINSDFNAIYNAFGDQRKMAVANGTGADGQIIHATGYIQ
KHSITEYATPVKVGTRHDIDTSTVGKVIIEERGELGDCVEFINSNGSISVTNPLTIQAIDSIGVSGNLVV
TSPYSKVTLCISSDNSTSVWNYSIESMFGQKESPAEGTWNISTSGSVDIPLFHRTEYNMAKLLVTCQ
SVDGRKIKTAEINILVDTVNSEVISSEYAVMRVGNETEEDIEANIAFSIKENYVTATISSSTVGMRAAVK
VIATQKIGVAQ

>d1rie_ b.33.1.1 (-) ISP subunit of the mitochondrial cytochrome bc1-complex, watersoluble
domain {Cow (*Bos taurus*)}

AMSKIEIKLSDIPEGKNMAFKWRGKPLFVRHRTKKEIDQEAAVEVSQLRDPQHDLERVKKPEWVILI
GVCTHLGCVPIANAGDFGGYCPCHGSHYDASGRIRKGPAPLNLEVPSYEFTSDDMVIVG

>d1ezve1 b.33.1.1 (E:87-215) ISP subunit of the mitochondrial cytochrome bc1-complex,
watersoluble domain {Baker's yeast (*Saccharomyces cerevisiae*)}

DVLAMAKVEVNLAAPLGLKNNVVKWQKPVFIRHRTPHEIQEANSVDMSALKDPQTDADRVKDPQ
WLIMLGICTHLGCVPIGEAGDFGGWFCPCCHGSHYDISGRIRKGPAPLNLEIPAYEFDGDKVIVG

>d1rfs_ b.33.1.1 (-) ISP subunit from chloroplast cytochrome bf complex {Spinach (*Spinacia oleracea*)}

TIAKDALGNDVIAAEWLKTHAPGDRTLTQGLKGDPTYLVVESDKTLATFGINAVCTHLGCVVPFNAA
ENKFICPCHGSQYNNQGRVVRGPAPLSLALAHCDVDDGKVVFPWTETDFRTGEAPWWSA
>d1g8kb_b.33.1.1 (B:) Arsenite oxidase Rieske subunit {Alcaligenes faecalis}
RTTLAYPATAVSVAKNLAANEPVSFTYPTDSSPCVAVKLGAPVPGGVPDDDDIVAYSVLCTHMGCPST
YDSSSKTFSCPCHFTEFDAEKAGQMICGEATADLPRVLLRYDAASDALAVGVDGLIYGRQANVI
>d1fqta_b.33.1.1 (A:) Rieske-type ferredoxin associated with biphenyl dioxygenase
{Burkholderia cepacia}
MKFTRVCDRRDVPEGEALKVESGGTSVAIFNVDGELFATQDRCTHGDWLSLSDGGYLEGDVVECSLH
MGKFCVRTGKVKSPPPCEALKIFPIRIEDNDVLVDFEAGYLAP
>d1eg9a1_b.33.1.2 (A:1-154) Naphthalene 1,2-dioxygenase alpha subunit, N-domain
{Pseudomonas putida}
MNYNNKILVSEGLSQKHLIHGDEELFQHELKTI FARNWFLTHDSLIPAGDYVTAKMGIDEVIVSR
QNDGSIRAFLNVCRRHGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFKDLYGESLNKKCLGL
KEVARVESFHGFYGCDFDQ
>d1bia_2_b.34.1.1 (271-317) Biotin repressor/biotin holoenzyme synthetase, C-terminal
domain {Escherichia coli}
FINRPVKLIIGDKEIFGISRGIDKQGALLLEQDGIKPWMGGEISLR
>d1byma_b.34.1.2 (A:) Diphtheria toxin repressor (DtxR) {Corynebacterium diphtheriae}
NPIPGLDELGVGNSDAAAPGTRVIDAATSMRKRVRIVQINEIFQVETDQFTQLLDADIRVGSEVEIVD
RDGHITLSHNGKDVVELLDDLAHTIRIEEL
>d1c0wa3_b.34.1.2 (A:165-223) Diphtheria toxin repressor (DtxR) {Corynebacterium
diphtheriae}
IVQINEIFQVETDQFTQLLDADIRVGSEVEIVDRDGHITLSHNGKDVVELLDDLAHTIRI
>d1g3sa3_b.34.1.2 (A:148-225) Diphtheria toxin repressor (DtxR) {Corynebacterium
diphtheriae}
PGTRVIDAATSMRKRVRIVQINEIFQVETDQFTQLLDADIRVGSEVEIVDRDGHITLSHNGKDVVELL
DLAHTIRIEE
>d1fx7a3_b.34.1.2 (A:145-230) Iron-dependent regulator IdeR {Mycobacterium
tuberculosis}
GADDANLVRLTELPAGSPVAVVVRQLTEHVQGDIDLITRLKDAGVVPNARVTVETTPGGGVTIVIPGH
ENVTLPHEMAHAVKVEKV
>d1igqa_b.34.1.3 (A:) Transcriptional repressor protein KorB {Escherichia coli}
KKAIVQVEHDERPARLILNRRPPAEGYAWLKYEDDGQEFANLADV KLVALIEG
>d1igub_b.34.1.3 (B:) Transcriptional repressor protein KorB {Escherichia coli}
PDPDKLKKAI VQVEHDERPARLILNRRPPAEGYAWLKYEDDGQEFANLADV KLVALIEG
>d1ckaa_b.34.2.1 (A:) C-Crk, N-terminal SH3 domain {Mouse (Mus musculus)}
AEYVRALFD FNGNDEEDLPFKKGDILRIRDKPEEQWNAEDSEGKRG MIPVPYVEKY
>d1efna_b.34.2.1 (A:) Fyn proto-oncogene tyrosine kinase, SH3 domain {Human (Homo
sapiens)}
ALFVALYDYEAITEDDLSFHKG EK FQILNSSEG DWWEARSLTTGETGYIPS NYVAPV
>d1shfa_b.34.2.1 (A:) Fyn proto-oncogene tyrosine kinase, SH3 domain {Human (Homo
sapiens)}
VTLFVALYDYEARTEDDLSFHKG EK FQILNSSEG DWWEARSLTTGETGYIPS NYVAPVD
>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)}
NLFVALYDFVASGDNTLSITKGEKLRVLGYNHNGEWCEAQTKNQGQWVPSNYITPVNS
>d2abl_1_b.34.2.1 (75-139) Abl tyrosine kinase, SH3 domain {Human (Homo sapiens)}
MGPSNDPNLFVALYDFVASGDNTLSITKGEKLRVLGYNHNGEWCEAQTKNQGQWVPSNYITPVN
>d1pht__b.34.2.1 (-) Phosphatidylinositol 3-kinase (p85-alpha subunit, pi3k), SH3 domain
{Human (Homo sapiens)}
AEGYQYRALYDYKKEREEDIDLHLGDILTVNKGSLVALGFSGQEARPEEIGWLNNGYNETTGERGDF
PGTYVEYIGRKKISPP
>d1g2ba_b.34.2.1 (A:) alpha-Spectrin, SH3 domain {Chicken (Gallus gallus)}
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)}
KKPLPPTPEDNRRSFQEPEETLVIALYDYQTNDPQELALRCDEEYLLDSSEIHWWRVQDKNGHEG
YAPSSYLVEKS
>d1bu1a_b.34.2.1 (A:) Hemapoetic cell kinase Hck {Human (Homo sapiens)}
IIVVALYDYEAIIHEDLSFQKGDQMVVLEESGEWWKARSLATRKEGYIPSNYVARVD
>d1qcfa1_b.34.2.1 (A:80-145) Hemapoetic cell kinase Hck {Human (Homo sapiens)}
SGIRIIVVALYDYEAIIHEDLSFQKGDQMVVLEESGEWWKARSLATRKEGYIPSNYVARVDSLET
>d1cska_b.34.2.1 (A:) c-src tyrosine kinase {Human (Homo sapiens)}
GTECIAKYNFHGTAEQDLPFCKGDVLTIVAVTKDPNWKAKNKVGREGIIPANYVQKR
>d1fmk_1_b.34.2.1 (82-145) c-src tyrosine kinase {Human (Homo sapiens)}
MVTTFVALYDYESRTETDLSFKKGERLQIVNNTTEGDWWLAHSLSTGQTGYIPSNYVAPSDSIQA
>d1nloc_b.34.2.1 (C:) c-src tyrosine kinase {Chicken (Gallus gallus)}
TFVALYDYESRTETDLSFKKGERLQIVNNTTEGDWWLAHSLTTGQTGYIPSNYVAPS
>d1awx__b.34.2.1 (-) Bruton's tyrosine kinase {Human (Homo sapiens)}
GSMSTSELKKVVALYDYMPMNANDLQLRKGDEYFILEESNLPWWRARDKNGQEGYIPSNYVTEAE
DS
>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)}
GSEIVVAMYDFQATEAHDRLRLERLQEQEYIILEKNDLHWWWRARDKYGSEGYIPSNYVTGKKSNNLDQY
D
>d1gcqa_b.34.2.1 (A:) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal
domains {Human (Homo sapiens)}
STYVQALFDFDPQEDGELGFRGDFIHVMDNSDPNWWKGACHGQTGMFPRNYVTPV
>d1gria1_b.34.2.1 (A:1-56) Growth factor receptor-bound protein 2 (GRB2), N- and
C-terminal domains {Human (Homo sapiens)}
MEAIKAYDFKATADDELSFKRGDILKVLNEECDQNWYKAELNGKDGFIKPNYIEMK

>d1gria2 b.34.2.1 (A:157-217) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal domains {Human (Homo sapiens)}
QPTYVQALFDFDPQEDGELGFRRGDFIHVMDNSDPNWWKGACHGQTGMFPRNYVTPVNRNV

>d1gbra_ b.34.2.1 (A:) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal domains {Mouse (Mus musculus)}
GSRRASVGSMEAIKDYDFKATADDELSFKRGDILKVLNEECDQNWYKAELNGKDGFIKPNYIEMKP
HPEFIVTD

>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)}
GSPTFKCAVKALFDYKAQREDELTFIKSAHQNVEKQEGGWWRGDYGGKKQLWFPSNYVEEMVNPE
GIHRD

>d1h92a_ b.34.2.1 (A:) p56-lck tyrosine kinase, SH3 domain {Human (Homo sapiens)}
GSPLQDNLVIALHSYEPSHDGDLGFKEGELRILEQSGEWWKAQSLTTGQEGFIPFNFAKAN

>d1lcka1 b.34.2.1 (A:63-116) p56-lck tyrosine kinase, SH3 domain {Human (Homo sapiens)}
DNLVIALHSYEPSHDGDLGFKEGELRILEQSGEWWKAQSLTTGQEGFIPFNFA

>d1ycsb2 b.34.2.1 (B:457-519) 53BP2 {Human (Homo sapiens)}
IMNKGVIYALWDYEPQNDDELPMKEGDCMTIIHREDEDEIEWWARLNDKEGYVPRNLLGLYP

>d1bb9_ b.34.2.1 (-) Amphiphysin 2 {Rat (Rattus norvegicus)}
TTGRLDLPPGFMFVKVQAQHDYATDDELQKAGDVVLVIFQNPQEEQDEGWLMGVKESDWNQH
KELEKCRGVFPENFTEVQ

>d1i07a_ b.34.2.1 (A:) EPS8 SH3 domain {Mouse (Mus musculus)}
KKYAKSKYDFVARNSELVSMKDDVLEILDDRRQWWKVRNASGDSGFVPPNNILDIMRTP

>d1gcqc_ b.34.2.1 (C:) Vav N-terminal SH3 domain {Mouse (Mus musculus)}
GSHMPKMEVFQEYYGIPPPGAFGPFRLNPGDVELTKAEAEHNWWEGRNTATNEVGWFCNVRV
HPYV

>d1k1za_ b.34.2.1 (A:) Vav N-terminal SH3 domain {Mouse (Mus musculus)}
RAQDKKRNELGLPKMEVFQEYYGIPPPGAFGGFLRLNPGDVELTKAEAEHNWWEGRNTATNEV
GWFCNVRVHPYVH

>d1i1ja_ b.34.2.1 (A:) Melanoma inhibitory activity protein {Human (Homo sapiens)}
GPMPKLADRKLCADQECSPISMAVALQDYMAPDCRFLTIHRGQVVVYVFSKLGKGRGLFWGGSVQG
DYYGDLAARLGYFPSSIVREDQTLKPGKVDVKTDKWDFYC

>d1kjwa1 b.34.2.1 (A:430-525) Pcd-95 {Rat (Rattus norvegicus)}
GFYIRALFDYDKTKDCGFLSQALSFRFGDVLHVIDAGDEEWWQARRVHSDSETDDIGFIPSKRRVER
REWSRLKAKDWGSSSGSQGREDSVLSYET

>d1br2a1 b.34.3.1 (A:34-79) Myosin S1 fragment, N-terminal domain {Chicken (Gallus gallus), pectoral muscle}
LVWVPSSEKHGFEEAASIKKEEGDEVTVLQENGKKTLSKDDIQKMN

>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 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)}
QQWKVGDKCSAIWSEGDGCIYPATIASIDFKRETCVVVYTYGYNREEQNLSDLLSPI
>d1khca_ b.34.9.2 (A:) DNA methyltransferase DNMT3B {Mouse (Mus musculus)}
TEYQDDKEFGIGDLVWGKIKGFSWWPAMVVSWKATSKRQAMPGMRWVQWFGDGKFSEISADKLV
ALGLFSQHFNLATFNKLVSYRKAMYHTLEKARVRAGKTFSSSPGESLEDQLKPMLEWAHGGFKPTG
IEGLKPN
>d1vie_ b.34.4.1 (-) R67 dihydrofolate reductase {Escherichia coli, plasmid PLZ1}
PSNATFGMGDRVRKKSAAWQGGQIVGWYCTNLTPEGYAVESEAHPGSVQIYPVAALERIN
>d1psf_ b.34.4.2 (-) Photosystem I accessory protein E (PsaE) {Cyanobacterium (Synechococcus sp.), pcc 7002}
AIERGSKVKILRKESYWYGDVGTVASIDKSGIIPVIVRFNKVNYNGFSGSAGGLNTNNFAEHELEVVG
>d1qp2a_ b.34.4.2 (A:) Photosystem I accessory protein E (PsaE) {Cyanobacterium (Nostoc sp.), strain pcc8009}
MVQRGSKVRLRPESYWFQDVGTVASVDQSGIKYPVIVRFKVNYSGINTNNFAEDELVEVEAPKAK
PKK
>d1jb0e_ b.34.4.2 (E:) Photosystem I accessory protein E (PsaE) {Synechococcus elongatus}
VQRGSKVKILRPESYWYNEVGTVASVDQTPGVKYPVIVRFKVNYSGINTNNFAEDELVEVEAPKAK
VA
>d1dj7b_ b.34.4.3 (B:) Ferredoxin thioredoxin reductase (FTR), alpha (variable) chain {Synechocystis sp.}
MNVGDRVRVTSSVVVYHHPEHKKTAFDLQGMGEVAAVLTEWQGRPISANLPVLVKFEQRFKAHF
RPDEVTLI
>d2ahjb_ b.34.4.4 (B:) Nitrile hydratase beta chain {Rhodococcus erythropolis}
MDGVHDLAGVQGFQKVPHTVNADIGPTFHAWEHLPYSLMFAGVAELGAFVDEVRVYVVERMEPR
HYMMTPYYERYVIGVATLMVEKGILTQDELESAGGPFPLSRPSESEGRPAPVETTTFEVQQRVVRD
EYVPGHIRMPAYCRGRVGTISHRTTEKWPFPDAIGHGRNDAGEEPTYHVKFAAEELFGSDTDGGSVV
VDLFEGYLEPA
>d1jj2s_ b.34.5.1 (S:) Ribosomal proteins L24 (L24p) {Archaeon Haloarcula marismortui}
SKQPDKQRKSQRRAPLHERHKQVRATLSADLREEYQQRNVVRNAGDTVEVLRGDFAGEEVEVINVD
LDKAVIHVEDVTLEKTDGEEVPRPLDTSNVRVTDLDLEDEKREARLESEDDSA
>d1jj2p_ b.34.5.1 (P:) Ribosomal proteins L21e {Archaeon Haloarcula marismortui}
PSSNGPLEGTRGKLNKPRDRGTSPQRAVEEFDDGKVKHLKIDPSVPNGRFHPRFDGQTGTVEGK
QGDAYKVDIVDGGKEKTIIVTAAHLRRQE
>d2eifa1 b.34.5.2 (A:1-73) N-terminal domain of eukaryotic initiation translation factor 5a {Archaeon Methanococcus jannaschii}
VIIMPGTKQVNVGSLKVGQYVMIDGVPCEIVDISVSKPGKHGGAKARVVGIGIFEKVKKEFVAPTSSKV
EVPI

>d1bkb_1 b.34.5.2 (4-74) N-terminal domain of eukaryotic initiation translation factor 5a {Archaeon Pyrobaculum aerophilum}

KWVMSTKYVEAGELKEGSYVVIDGEPGRVVEIEKSKTGKHGSAKARIVAVGVFDGGKRTLSLPVDAQ
VEVP

>d1rl2a1 b.34.5.3 (A:126-195) C-terminal domain of ribosomal protein L2 {Bacillus stearothermophilus}

GNALPLENIPVGTLVHNIELKPGRGGQLVRAAGTSAQVLGKEGKYVIVRLASGEVRMILGKCRATVGE
VG

>d1jj2a1 b.34.5.3 (A:91-237) C-terminal domain of ribosomal protein L2 {Archaeon Haloarcula marismortui}

GNTLPLAEIPEGVPCNVESPPGDGGKFARASGVNAQLLTHDRNVAVVKLPSGEMKRLDPQCRATIG
VVGGGGRTDKPFVKAGNKHKMKARGTKWPNVRGVAMNAVDHPFGGGGRQHHPGPKSISRNAPP
GRKVGDIASKRTGRGG

>d3vub_ b.34.6.1 (-) CcdB {Escherichia coli}

MQFKVYTYKRESRYRLFVDVQSDIIDTPGRRMVIPLASARLLSDKVSRELYPVVHIGDESWRMMTT
DMASVPVSVIGEEVADLSHRENDIKNAINLMFWGI

>d1hyoa1 b.34.8.1 (A:1-118) Fumarylacetoacetate hydrolase, FAH, N-terminal domain {Mouse (Mus musculus)}

MSFIPVAEDSDFPIQNLPGYVFSTQSNPKPRIGVAIGDQILDLSVIKHLFTGPALSKHQHVFDETTLNN
FMGLGQAAWKEARSLQNLSSASQARLRDDKELRQRAFTSQASATMHL

>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}

MIQNFVYYRDSRDPVWKGPAKLLWKGEGAVVIQDNSDIKVVPRRKAKIIRD

>d1c0ma1 b.34.7.1 (A:217-269) DNA-binding domain of retroviral integrase {Rous sarcoma virus (RSV, avian sarcoma virus)}

VLTEGPPVKIRIETGEWEKGNVWVWGRGYAAVKNRDTDKVIWVPSRKKVPDI

>d1c6vx_ b.34.7.1 (X:) DNA-binding domain of retroviral integrase {Simian immunodeficiency virus}

KNSKFKNFRVYYREGDQLWKGPGELLWKGEGAVLLKVGTDIKVVPRRKAKIIRD

>d1aono_ b.35.1.1 (O:) Chaperonin-10 (GroES) {Escherichia coli}

MNIRPLHDRVIVKRKEVETKSAGGIVLTGSAAAKSTRGEVLAVGNRILENGEVKPLDVKVGDIVIFN
DGYGVKSEKIDNEEVLIMSESDILAIVEA

>d1jh2a_ b.35.1.1 (A:) Chaperonin-10 (GroES) {Mycobacterium tuberculosis}

AKVNIKPLEDKILVQANEAETTTASGLVIPDTAKEKPQEGTVVAVGPRWDEDEKRIPLDVAEGDT
VIYSKYGGTEIKYNGEYLLSARDVLAVVSK

>d1lepa_ b.35.1.1 (A:) Chaperonin-10 (GroES) {Mycobacterium leprae}

AKVKIKPLEDKILVQAGEAETMTPSGLVIPENAKEKPQEGTVVAVGPRWDEDEGAKRIPVDVSEGDI
VIYSKYGGTEIKYNGEYLLSARDVLAVVSK

>d1g31a_ b.35.1.1 (A:) GP31 co-chaperonin {Bacteriophage T4}

QQLPIRAVGEYVILVSEPAQAGDEEVTESGLIIGKRVQGEVPELVCVHVSVPDVEGFCVGDLSLPV
GQIRNVPHPPFVALGLKQPKEIKQKFVTCHYKAIPCLYK

>d1heta1 b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Horse (Equus caballus)}
STAGKVIKCKAAVLWEEKKPFSEIEVEVAPPKAHEVRIKMOVATGICRSDDHVVSGLTVPPLVVIAGHE
AAGIVESIGEGVTTVRPGDKVIPLFTPQCCKRVCCKHPEGNFCLKNDLSMPRGTMQDGTSRFTCRGK
PIHHFLGTSTFSQYTVVDEISVAKIDAASPLEKVCLIGCXKDSVPKLVADFMMAKKFALDPLITHVLPFE
KINEGFDLLRSGESIRTILTF

>d1d1ta1 b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Human (Homo sapiens),
different isozymes}
GTAGKVIKCKAAVLWEQKQPFSEIEIEVAPPKTKEVRIKILATGICRTDDHVVIKGTMVSKFPVIVGHEA
TGIVESIGEGVTTVKPGDKVIPLFLPQCRECNACRNPDPGNLCIRSDITGRGVLADGTTFRFTCKGKPVH
HFLNTSTFTFEYTVVDESSVAKIDDAAPPEKVCLIGCXRDDVVKLVTEFLAKKFDLDQLITHVLPFKKIS
EGFELLNSGQSIRTVLTF

>d1hsoa1 b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Human (Homo sapiens),
different isozymes}
STAGKVIKCKAAVLWELKKPFSEIEVEVAPPKAHEVRIKMOVAVGICGTDDHVVSGLTVPPLVILGHE
AAGIVESVGEVTTVKPGDKVIPLAIPQCCKRICKNPESNYCLKNDVSNPQGTLDGTSRFTCRRKP
IHHFLGISTFSQYTVVDENAVAKIDAASPLEKVCLIGCXKECVKLVADFMMAKKFSLDALITHVLPFEK
INEGFDLLHSGKSIRTILMF

>d1hsza1 b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Human (Homo sapiens),
different isozymes}
STAGKVIKCKAAVLWEVKKPFSEIEDVEVAPPKAYEVRIKMOVAVGICGTDDHVVSGLNLTVPPLVILGHE
AAGIVESVGEVTTVKPGDKVIPLFTPQCCKRICKNPESNYCLKNDLGNPRGTLQDGTTRFTCRGK
PIHHFLGTSTFSQYTVVDENAVAKIDAASPLEKVCLIGCXKEGIPKLVADFMMAKKFSLDALITHVLPFE
KINEGFDLLHSGKSIRTILMF

>d1ht0a1 b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Human (Homo sapiens),
different isozymes}
STAGKVIKCKAAVLWELKKPFSEIEVEVAPPKAHEVRIKMOVAAAGICRSDEHVVSGLNLTVPPLVILGHE
AAGIVESVGEVTTVKPGDKVIPLFTPQCCKRICKNPESNYCLKNDLGNPRGTLQDGTTRFTCSGKP
IHHFVGVSTFSQYTVVDENAVAKIDAASPLEKVCLIGCXKESVPKLVADFMMAKKFSLDALITNVLPFEK
INEGFDLLRSGKSIRTILTF

>d1teha1 b.35.1.2 (A:3-174,A:325-374) Alcohol dehydrogenase {Human (Homo sapiens),
different isozymes}
ANEVIKCKAAVAWEAGKPLSIEIEVAPPKAHEVRIKIIATAVCHTDAYTLGADPEGCFPVILGHEGA
GIVESVGEVTKLKAGDTVIPLYIPQCCKRCKLCLSPNLNLCQKIRVTQGGKGLMPDGTSRFTCKGKTIL
HYMGTSTFSEYTVVADISVAKIDPLAPLDKVCLLGCXVESVPKLVSEYMSKKIKVDEFVTHNLSFDEI
NKAFELMHSGKSIRTVVKI

>d1e3ia1 b.35.1.2 (A:1-174,A:325-376) Alcohol dehydrogenase {Mouse (Mus musculus),
class II}
GTQGVKVIKCKAAIAWKTGSPLCIEIEVSPPKACEVRIQVIATCVCPTDINATDPKKKALFPVVLGHEC
AGIVESVGPVNTNFKPGDKVIPFFAPQCCKRCKLCLSPNLNLCGKLRNFKYPTIDQELMEDRTSRFTCK
GRSIYHFMGVSSFSQYTVVSEANLARVDDEANLERVCXKSVSDSVPNLVSDYKNKKFDLDDLVTALP
FESINDAIDLMKEGKSIRTILTF

>d1cdoa1 b.35.1.2 (A:1-175,A:325-374) Alcohol dehydrogenase {Cod (Gadus callarias)}
ATVGVKVIKCKAAVAWEANKPLVIEIEVDVPHANEIRIKIIATGVCHTDLYHLFEGKHKDGFVVLGH
EGAGIVESVGPVTEFQPGKVIPLFISQCGECRQCSPKTNQCVKGWANESPDVMSPKETRFCTCKG

RKVLQFLGTSTFSQYTVVNQIAVAKIDPSAPLDTVCLLGCKDGVPKMVKAYLDDKKVKLDEFITHRM
PLESVNDAIDLKMGKHCIRTVLSL

>d1keva1 b.35.1.2 (A:1-150,A:315-351) Bacterial secondary alcohol dehydrogenase
{Clostridium beijerinckii}
MKGFAMLGINKLWIEKERPVAGSYDAIVRPLAVSPCTSDIHTVFEGALGDRKNMILGHEAVGEVVE
VGSEVKDFKPGDRVIVPCTTPDWRSLEVQAGFQQHNSGMLAGWKFSNFKDGVFGEYFHVNDADM
NLAILPKDMPLNAVMITDXDLSKLVTHVYHGFHDHIEEALLMKDKPKDLIKAVVIL

>d1ykfa1 b.35.1.2 (A:1-150,A:315-352) Bacterial secondary alcohol dehydrogenase
{Thermoanaerobacter brockii}
MKGFAMLSIGKVGWIEKEKPAPGPFDAIVRPLAVAPCTSDIHTVFEGAIGERHNMILGHEAVGEVVEV
GSEVKDFKPGDRVVPAITPDWRTSEVQRGYHQHSGGMLAGWKFSNVKDGVFGEFFHVNDADMN
LAHLPKEIPLEAAVMIPDXDPSKLVTHVFRGFDNIEKAFMLMKDKPKDLIKPVVILA

>d1e3ja1 b.35.1.2 (A:4-150,A:314-351) Ketose reductase (sorbitol dehydrogenase)
{Silverleaf whitefly (Bemisia argentifolii)}
DNLSAVLYKQNDLRLEQRPIPEPKEDEVLLQMAYVIGCGSDVHYEHGRIADFIKDPMPVIGHEASGT
VVKVGKNVKHLKKGDRVAVEPGVPCRRQCFCKEGKYNLCPDLTFCATPPDDGNLARYVVAADFCH
KLPDVSLEEGALXNVKQLVTHSFKLEQTVDAFEAARKKADNTIKVMISCRQ

>d1qora1 b.35.1.2 (A:2-135,A:266-327) Quinone oxidoreductase {Escherichia coli}
ATRIEFHKHGGPEVLQAVEFTPADPAENEIQVENKAIGINFIDTYIRSGLYPPPSLPSGLGTEAAGIVSK
VGSGVKHIKAGDRVVAQALGAYSSVHNIADKAAILPAAISFEQAAASFLKGLTVYYLLRKTXLQGYI
TTREELTEASNELFSLIASGVIKVDVAEQKYPLKDAQRAHEILES RATQGSSLLIP

>d1auua_b.35.2.1 (A:) SacY {Bacillus subtilis}
MKIKRILNHNAIVVKDQNEEKILLGAGIAFNKKKNDIVDPSKIEKTFIRKDTDPDY

>d1pdr_b.36.1.1 (-) Discs large protein homolog {Human (Homo sapiens)}
ITREPRKVVLRHGSTGLGFNIVGGEDGEGIFISFILAGGPADLSGELRKGDRISVNSVDLRAASHEQAA
AALKNAGQAVTIVAQYRPEEYSRQHA

>d1kwaab.36.1.1 (A:) Cask/Lin-2 {Human (Homo sapiens)}
RSRLVQFQKNTDEPMGITLKMNELNHCIVARIMHGGMIHRQGTLVHVGDEIREINGISVANQTVEQLQ
KMLREMRGSITFKIVPSYREF

>d1be9a_b.36.1.1 (A:) Synaptic protein PSD-95 {Rat (Rattus norvegicus)}
FLGEEDIPREPRRIVHRGSTGLGFNIIGGEDGEGIFISFILAGGPADLSGELRKGDKILSVNGVDLRNAS
HEQAAIALKNAGQVTIIAQYKPEEYSRFEANSRVNSSGRIVTN

>d1qlcab.36.1.1 (A:) Synaptic protein PSD-95 {Rat (Rattus norvegicus)}
AEKVMEIKLIKPKGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAHKDGRQLQIGDKILAVNSVGLQDV
MHEDAVAALKNTYDVVYLKVAKPSNA

>d1qavab.36.1.1 (A:) Syntrophin {Mouse (Mus musculus)}
GSLQRRRVTVRKADAGGLGISIKGGRENKMPILISKIFKGLAADQTEALFVGDAILSVNGEDLSSATHD
EAVQALKKTGKEVVLEVKYMK

>d1b8qab.36.1.1 (A:) Neuronal nitric oxide synthase, NNOS {Rat (Rattus norvegicus)}
GSHMIEPNVISVRLFKRKVGGGLFLVKERVSKPPVIISDLIRGGAAEQSGLIQAGDIILAVNDRPLVDLS
YDSALEVLRGIAETHVVLILRGPEGFTTHLETTFTGDGTPKTIRVTQPLGPPTKAV

>d1qauab.36.1.1 (A:) Neuronal nitric oxide synthase, NNOS {Rat (Rattus norvegicus)}
NVISVRLFKRKVGGGLFLVKERVSKPPVIISDLIRGGAAEQSGLIQAGDIILAVNDRPLVDLSYDSALEV
LRGIAETHVVLILRGPEGFTTHLETTFTGDGTPKTIRVTQP

>d3pdza_b.36.1.1 (A:) Phosphatase hPTP1e {Human (Homo sapiens)}
PKPGDIFEVELAKNDNSLGISVTGGVNTSVRHGGIYVKAVIPQGAESDGRHKGDRVLAVNGVSLEG
ATHKQAVETLRNTGQVVHLLLEKQSQPT

>d1g9oa_b.36.1.1 (A:) Na⁺/H⁺ exchanger regulatory factor, NHERF {Human (Homo sapiens)}
RMLPRLCCLEKGPNGYGFHLHGEKGLGQYIRLVEPGSPAEEKAGLLAGDRLVEVNGENVEKETHQQ
VVSRIIRAALNAVRLLVVDPETDEQL

>d1ihja_b.36.1.1 (A:) Inad {Fruit fly (Drosophila melanogaster)}
GELIHMVTLDKTGKKSFGICIVRGEVKDSPNTKTTGIFIKGIVPDSPAHLGRLKVGDRILSLNGKDVR
NSTEQAVIDLKIEADFKIELEIQTF

>d1fc6a3_b.36.1.3 (A:157-248) Photosystem II D1 C-terminal processing protease {Algae (Scenedesmus obliquus)}
AGSVTGVGLEITYDGGSGKDVVVLTPAPGGPAEKAGARAGDVIVTVDTAVKGMPLYDVSDDLQGEA
DSQVEVVLHAPGAPSNTRTLQLTRQ

>d1k32a1_b.36.1.3 (A:763-853) Tricorn protease {Archaeon Thermoplasma acidophilum}
GRIACDFKLDGDHYVAKAYAGDYSNEGEKSPIFEYGIDPTGYLIEDIDGETVAGSNIYRVLSEKAGT
SARIRLSGKGGDKRDLMDILD

>d1i16_b.36.1.2 (-) Interleukin 16 {Human (Homo sapiens)}
MPDLNSSTDSAASASAASDVSVESTAEATVCTVTLEKMSAGLGFSLGKSLHGDKPLTINRIFKGA
ASEQSETVQPGDEILQLGGTAMQGLTRFEAWNIIKALPDGPVTIVIRKSLQSKETTAAGDS

>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 g3p {Bacteriophage M13}
EYGDTPIPGYTYINPLDGTYPGTEQNPANPNPSLEESQPLNTFMFQNNRFRNRQGALTVYTGTVTQ
GTDVPKTYTYQYTPVSSKAMYDAYWNGKFRDCAFHSGFNEDIFVCEYQGQSSDLPQPPVNA

>d1fgp_b.37.1.1 (-) N-terminal domains of the minor coat protein g3p {Bacteriophage fd}
ETVESCLAKPHTENSFTNVWKDDKTLDRYANYEGCLWNATGVVVCTGDETQCYGTWVPIGLAIP
NAAAH

>d1b34a_b.38.1.1 (A:) D1 core SNRNP protein {Human (Homo sapiens)}
KLVRFMLKLSHETVTIELKNGTQVHGTTGVDVSMNTHLKAVKMTLKNREPVQLETLSIRGNNIRYF
ILPDSLPLDTLLV

>d1b34b_b.38.1.1 (B:) D2 core SNRNP protein {Human (Homo sapiens)}
TGPLSVLTQSVKNNTQVLINCRNKKLLGRVKAFDRHCNMVLENVKEMWTEVPKSGKGGKSKPV
NKDRYISKMFLRGDSVIVVLRNPLIAGK

>d1d3ba_b.38.1.1 (A:) D3 core SNRNP protein {Human (Homo sapiens)}
GVPIKVLHEAEGHIVTCETNTGEVYRGKLEAEDNMNCQMSNITVTYRDGRVAQLEQVYIRGCKIRF
LILPD

>d1d3bb_b.38.1.1 (B:) B core SNRNP protein {Human (Homo sapiens)}
SKMLQHIDYRMRCILQDGRIFIGTFKAFDKHMNLILCDCDEFKIKPKNSKQAEREKRVLGLVLLRG
ENLVSMTVEGPPP

>d1d3bl_b.38.1.1 (L:) B core SNRNP protein {Human (Homo sapiens)}
TVGKSSKMLQHIDYRMRCILQDGRIFIGTFKAFDKHMNLILCDCDEFKIKPKNSKQAEREKRVLGL

VLLRGENLVSM TVEGPPPKDTG

>d1i81a_ b.38.1.1 (A:) Archaeal homoheptameric Sm protein {Archaeon Methanobacterium thermoautotrophicum}

RVNVQRPLDALGNSLNSPVIIKLGKDREFRGLKSFDLHMNLVLNDAEELEDGEVTRRLGTVLIRGD
NIVYISP

>d1jria_ b.38.1.1 (A:) Archaeal homoheptameric Sm protein {Archaeon Methanobacterium thermoautotrophicum}

QRPLDALGNSLNSPVIIKLGKDREFRGLKSFDLHMNLVLNDAEELEDGEVTRRLGTVLIRGDNIVYI
SRGK

>d1i8fa_ b.38.1.1 (A:) Archaeal homoheptameric Sm protein {Archaeon Pyrobaculum aerophilum}

ATLGATLQDSIGKQVLVKL RDSHEIRGILRSFDQHVNLLLEDAEEIIDGNVYKRGTMVVRGENVLFISP
VP

>d1i4k1_ b.38.1.1 (1:) Archaeal homoheptameric Sm protein {Archaeon Archaeoglobus fulgidus}

PPRPLDVLN RSLKSPVIVRLKGGREFRGLDGYDIHMNLVLLDAEEIQNGEVVRKVGSSVIRGDTVVF
VSPA

>d1h5pa_ b.99.1.1 (A:) Nuclear autoantigen Sp100b {Human (Homo sapiens)}

MDENINFKQSEL PVTTCGEVKGTLYKERFKQGTSKKCIQSEDKKWFTPREFEIEGDRGASKNWKLSIR
CGGYTLKVL MENKFLPEPPSTRKKVTIK

>d1whi_ b.39.1.1 (-) Ribosomal protein L14 {Bacillus stearothermophilus}

MIQQESRLKVADNSGAREVLVIKVLGGSGRRYANIGDVVVATVKDATPGGVVKKGQVVKAVVVRTKR
GVRRPDGSYIRFDENACVIIRD DKS PRGTRIFGVPARELRDKDFMKIISLAPEVI

>d1jj2j_ b.39.1.1 (J:) Ribosomal protein L14 {Archaeon Haloarcula marismortui}

MEALGADV TQGLEKGLITCADNTGARELKVISVHGYSGTKNRHPKAGLGDKITVSVTKGTPEMRR
QVLEAVVVRQRKPIRRPDGTRVKFEDNAAVVDENEDPRGTELKGP IAREVAQRFGSVASAATMIV

>d1ez6a_ b.40.1.1 (A:) Staphylococcal nuclease {Staphylococcus aureus}

LHKEPATLIKAIDGDTVKL MYKGQPMVFRLLLVDIPETKHPKKGVEKYGPEAAAF TKKMVENAKKIE
VEFDKGQRTDKYGRGLAYIYADGKMVNEALVRQGLAKVAYVYKGNNTHEQLLRKAE AQAKKEKLN
WS

>d1joqa_ b.40.1.1 (A:) Staphylococcal nuclease {Staphylococcus aureus}

ATSTKKLHKEPATLIKAIDGDTVKL MYKGQPMTFRLLLVDPETKHPKKGVEKYGPEASAFTKKMV
ENAKKIEVEFDKGQRTDKYGRGLAYIYADGKMVNEALVRQGLAKVAYVYKPNNTHEQLLRKSEAQA
KKEKLN I WSEDNADSGQ

>d1sty_ b.40.1.1 (-) Staphylococcal nuclease {Staphylococcus aureus}

KLHKEPATLIKAIDGDTVKL MYKGQPMTFRLLLVDPETKHPKKGVEKYGPEASAFTKKMVENAKK
IEVEFDKGQRTDKYGRGLAYIYADGKMVNEALVRQGLAKVAYVYKPNNTHEQHLRGKSEAQA KKEK
LN I WS

>d2sob_ b.40.1.1 (-) Staphylococcal nuclease {Staphylococcus aureus}

ATSTKKLHKEPATLIKAIDGDTVKL MYKGQPMTFRLLLVDPETKHPKKGVEKYGPEASAFTKKML
ENAKKIEVEFDKGQRTDKYGRV LAYIYADGKMVNEAL

>d1djrd_ b.40.2.1 (D:) Heat-labile toxin {Escherichia coli, type IB}

APQTITELCSEYRNTQIYTINDKILSYTESMAGKREMVIIITFKSGETFQVEVPGSQHIDSQKKA IERMK
DTLRITYLTETKIDKLCVWNNKTPNSIAAISMKN

>d1ltrd_b.40.2.1 (D:) Heat-labile toxin {Escherichia coli, type IB}
APQSITELCSEYHNTQIYTINDKILSYTESMAGKREMVIIITFKSGATFQVEVPGSQHIDSQKKAIERMK
DTLRITYLTETKIDKLCVWNNKTPNSIAAISMEKLYAGA

>d1tiid_b.40.2.1 (D:) Heat-labile toxin {Escherichia coli, type IIB}
GASQFFKDNCRRTASLVEGVELTKYISDINNNTDGMVVSSTGGVWRISRAKDYPDNVMTAEMRK
IAMA AVLSGMRVNM CASPASSPNVIWAIELEA

>d3chbd_b.40.2.1 (D:) Cholera toxin {Vibrio cholerae}
TPQNITDLCAEYHNTQIHTLNDKIFS YTESLAGKREMAITFKNGATFQVEVPGSQHIDSQKKAIERM
KDTLR IAYL TEAKVEKLCVWNNKTPRAIAAISMAN

>d1c4qa_b.40.2.1 (A:) Verotoxin-1/shiga-toxin, B-pentamer {Escherichia coli}
TPDCVTGKVEYTKYND DDTFTVKVGDKELATNRANLQSLLSAQITGMTVTIKTNACHNGGGFSEV
IFR

>d2bosa_b.40.2.1 (A:) Verotoxin-1/shiga-toxin, B-pentamer {Escherichia coli}
ADCAKGKIEFSKYNE DNTFTVKVSGREYWTNRWNLQPLLQSAQLTGMTVTIISNTCSSGSGFAEVQF
N

>d1prtb1_b.40.2.1 (B:90-199) Pertussis toxin S2/S3 subunits, C-terminal domain {Bordetella
pertussis}
TTRNTGQPATDHYYSNVTATRLSSTNSRLCAVFVRSGQPVIGACTSPYDGKYWSMYSRLRKMLYLI
YVAGISVRVHVSKEEQYYDYEDATFETYALTGISICNPGSSLC

>d1prtc1_b.40.2.1 (C:90-199) Pertussis toxin S2/S3 subunits, C-terminal domain {Bordetella
pertussis}
TIYKTGQPAADHYYSKVTATRLLASTNSRLCAVFVRDQSVIGACASPYEGRYRDMYDALRRLLYMIY
MSGLA VRVHVSKEEQYYDYEDATFQTYALTGISLCNPAASIC

>d1prtd_b.40.2.1 (D:) Pertussis toxin S4 subunit {Bordetella pertussis}
DVPYVLVKTNMVVTSVAMKPYEVTPT RMLVCGIAAKLGAAASSPDAHVPFCFGKDLKRP GSSPMEV
MLRAVFMQQRPLRMFLGPKQLTFEGKPALELIRMVECSGKQDCP

>d1prtf_b.40.2.1 (F:) Pertussis toxin S5 subunit {Bordetella pertussis}
LPTHLYKNFTVQELALKLGKNQEFCLTAFMSGRSLVRACLSDAGHEHDTWFDTMLGFAISAYALKS
RIALTVEDSPYPGTPGD LLELQICPLNGYCE

>d1esfa1_b.40.2.2 (A:1-120) Staphylococcal enterotoxin A, SEA {Staphylococcus aureus}
SEKSEEINEKDLRKKSELQGTALGNLQIYYNEKAKTENKESH DQFLQHTILFKGFFTDHSWYNDL
LVDFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNK TACMYGGVTLHDNNRLT

>d1i4pa1_b.40.2.2 (A:1-120) Staphylococcal enterotoxin C2, SEC2 {Staphylococcus aureus}
ESQPDPTPDELHKSSEFTGMTGMNMKYLYDDHYVSATKVM SVDKFLAHDLIYNISDKKLNKYDKVKT
ELLNEDLAKKYKDEVVDVYGSNYVNCYFSSKDNVGVKVTGGKTCMYGGITKHEG

>d3tss_1_b.40.2.2 (5-93) Toxic shock syndrome toxin-1 (TSST-1) {Staphylococcus aureus}
NIKDLLDWYSSGSDTFTNSEVLDNSLGS MRIKNTDGSISLIIFSPYSPAFTKGEKVDLNTKRIKKSQ
HTSEG TWIHFQISGVTNTEK

>d1sebd1_b.40.2.2 (D:2-121) Staphylococcal enterotoxin B, SEB {Staphylococcus aureus}
SQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKD TYDNVRVEFKNKD
LADKYKDKYVDVFGANYYYQCYFSKKTTCMYGGVTEH

>d3seb_1_b.40.2.2 (1-121) Staphylococcal enterotoxin B, SEB {Staphylococcus aureus}
ESQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKD TKLGNYDNVRVE
FKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTCMYGGVTEH

>d1jckb1 b.40.2.2 (B:1-121) Staphylococcal enterotoxin C3, SEC3 {Staphylococcus aureus}
ESQPDPMPDDLHKSSEFTGTMGNMKYLYDDHYVSATKVKSVDKFLAHDLIYNINDKKLNNYDKVK
TELLNEDLANKYKDEVVDVYGSNYVNCYFSSKDNVGVKVTSGKTCMYGGITKHEGN

>d1enfa1 b.40.2.2 (A:2-101) Staphylococcal enterotoxin H, SEH {Staphylococcus aureus}
DLHDKSELTDLALANAYGQYNHPFIKENIKSDEISGEKDLIFRNQGDGNDLRVKFATADLAQKFKN
KNVDIYGASFYKCEKISENISECLYGGTTLNS

>d1an8_1 b.40.2.2 (3-95) Streptococcal superantigen Spe-C {Streptococcus pyogenes}
KKDISNVKSDLLAYTITPYDYKDCRVNFSTHTLNIDTQKYRGKDYISSEMSYEASQKFKRDDHVD
VFGLFYILNSHTGEYIYGGITPAQN

>d1et9a1 b.40.2.2 (A:1-95) Streptococcal superantigen Spe-H {Streptococcus pyogenes}
NSYNTNRHNLKHSNLIEADSIKNSPDIVTSMLKYSVKDKNLSVFFEKDWISQEFKDKKEVD
IYALSAQEVCECPGKRYEAFGGITLNS

>d1eu3a1 b.40.2.2 (A:2A-96) Streptococcal superantigen Smez-2 {Streptococcus pyogenes}
GLEVDNNSLLRNIYSTIVYEYSIDIVIDFKTSHNLVTKKLDVRDARDFINSEMDEYAANDFKTGDKIA
VFSVPFDWNYLSKGKVTAYTYGGITPYQK

>d1bxta1 b.40.2.2 (A:1-119) Streptococcal superantigen SSA {Streptococcus pyogenes}
SSQPDPTPEQLNKSSQFTGVMGNLRCLYDNHFVEGTNVRSTGQLLQHDLIFPIKDLKLNYSVSKTE
FNSKDLATKYKNKDVIDIFGSNYYYNCYSEGNCKNAKKTTCMYGGVTEHHRN

>d1fnua1 b.40.2.2 (A:1-107) Streptococcal pyrogenic exotoxin A1 {Streptococcus pyogenes}
QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHEENVKSVDQLLSDLIYNVSGPNYDKLKLTELKNQE
MATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHE

>d1d2ba_ b.40.3.1 (A:) TIMP-1 {Human (Homo sapiens)}
CTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDAADIRFVYTPAME
SVCGYFHRSHNRSEEFLLIAGKLQDGLLHITTCFVAPWNSLSLAQRRGFTKTYTVGCEE

>d1ueab_ b.40.3.1 (B:) TIMP-1 {Human (Homo sapiens)}
CTCVPPHPQTAFCNSDLVIRAKFVGTPEVAQTTLYQRYEIKMTKMYKGFQALGDAADIRFVYTPAME
SVCGYFHRSHARSEEFLLIAGKLQDGLLHITTCFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSI
CKLQSGTHCLWTDQLLQGSEKGFQSRHLACLPREPGLCTWQSLRS

>d1br9_ b.40.3.1 (-) TIMP-2 {Human (Homo sapiens)}
CSCSPVHPQQAFCNADVVIRAKAVSEKEVDSGNDIYGNPIKRIQYEIKQIKMFKGPEKDIEFIYTAPSSA
VCGVSLDVGKKEYLIAGKAEGDGKMHITLCDFIVPWDTLSTTQKSLNHRYQMGCECKITRCPMIP
CYISSPDECLWMDWVTEKNINGHQAKFFACIKRSDGSCAWYRGAA

>d2tmp_ b.40.3.1 (-) TIMP-2 {Human (Homo sapiens)}
CSCSPVHPQQAFCNADVVIRAKAVSEKEVDSGNDIYGNPIKRIQYEIKQIKMFKGPEKDIEFIYTAPSSA
VCGVSLDVGKKEYLIAGKAEGDGKMHITLCDFIVPWDTLSTTQKSLNHRYQMGCE

>d1bqqt_ b.40.3.1 (T:) TIMP-2 {Cow (Bos taurus)}
CSCSPVHPQQAFCNADIVIRAKAVNKKEVDSGNDIYGNPIKRIQYEIKQIKMFKGPDQDIEFIYTAPAA
AVCGVSLDIGKKEYLIAGKAEGNGMHITLCDFIVPWDTLSATQKSLNHRYQMGCECKITRCPMI
PCYISSPDECLWMDWVTEKNINGHQAKFFACIKRSDGSCAWYRGAAAPP

>d1jb3a_ b.40.3.2 (A:) The laminin-binding domain of agrin {Chicken (Gallus gallus)}
ELQRREEEANVVLGTVEEIMNVDPVHHTYSCKVRVWRYLKGKDIVTHEILLDGGNKVVIGGFDP
LICDNQVSTGDTRIFFVNPAPQYMWPAHRNELMLNSSLMRITLRNLEEVEHCVEEHRKLLA

>d1k28a1 b.40.8.1 (A:6-129) Tail-associated lysozyme gp5, N-terminal domain
{Bacteriophage T4}

NNLNWVFGVVEDRMDPLKLRVVRVVGVLHPPQRAQGDVMGIPTEKLPWMSVIQPITSAAMSGIG
GSVTGPVEGTRVYGHFLDKWKTNGIVLGTYYGGIVREKPNRLEGFSDPTGQYPRRLGNDT
>d1eova1 b.40.4.1 (A:71-204) Aspartyl-tRNA synthetase (AspRS) {Baker's yeast
{Saccharomyces cerevisiae}}
AKDNYGKLP LIQSRSDRTGQKRVKFVDLDEAKSDKEVLFRRARVHNTRQQGATLAFLTLRQQASLI
QGLVKANKEGTISKNMVKWAGSLNLESIVLVRGIVKKVDEPIKSATVQNLEIHITKIYTISETPEAL
>d1b8aa1 b.40.4.1 (A:1-103) Aspartyl-tRNA synthetase (AspRS) {Archaeon Pyrococcus
kodakaraensis}
MYRTHYSSEITEELNGQVKVAGWVWEVKDLGGIKFLWIRDRDGIVQITAPKKKVDPELFLKIPKLR
SEVVAVEGVVNFNTPKAKLGFELPEKIVVLNRAET
>d1c0aa1 b.40.4.1 (A:1-106) Aspartyl-tRNA synthetase (AspRS) {Escherichia coli}
MRTEYCGQLRLSHVQGVTLGCGWVNRRLDLGSLIFIDMRDREGIVQVFFDPDRADALKLASELRNE
FCIQVTGTVRARDEKNINRDMATGEIEVLASSLTIINRAD
>d1g51a1 b.40.4.1 (A:1-104) Aspartyl-tRNA synthetase (AspRS) {Thermus thermophilus}
MRRTHYAGSLRETHVGEEVVELEGWVNRRLDLGGLIFLDLRDREGLVQLVAHPASPAYATAERVRPE
WVVRAGKLVRLRPEPNRLATGRVEVELSAEVLAEAK
>d1bbua1 b.40.4.1 (A:11-154) Lysyl-tRNA synthetase (LysRS) {Escherichia coli, gene lysS}
VVDLNNELKTRREKLANLREQGIAPNDFRRDHTSDQLHAEFDGKENELEALNIEVAVAGRMMT
RRIMGKASFVTLQDVGGRIQLYVARDDLPEGVYNEQFKKWDLGDILGAKGKLFKTKTGELSIHCTEL
RLLTKALRPLPD
>d1krs_ b.40.4.1 (-) Lysyl-tRNA synthetase (LysRS) {Escherichia coli, gene lysS}
FRRDHTSDQLHAEFDGKENELEALNIEVAVAGRMMTRRIMGKASFVTLQDVGGRIQLYVARDDL
EGVYNEQFKKWDLGDILGAKGKLFKTKTGELSIHCTELRLLTKA
>d1e1oa1 b.40.4.1 (A:11-153) Lysyl-tRNA synthetase (LysRS) {Escherichia coli, gene lysU}
AIDFNDELNRNREKLAALRQQGVAFPNDFRRDHTSDQLHEEFDAKDNQEESLNIEVAVAGRMMT
RRIMGKASFVTLQDVGGRIQLYVARDSLPEGVYNDQFKKWDLGDIIGARGTLFKTQTGELSIHCTELR
LLTKALRPLP
>d1gm5a2 b.40.4.9 (A:106-285) RecG "wedge" domain {Thermotoga maritima}
CSGEEVDLSTDIYAKGVGPNRKKKLLKLGIEFLRDLLEFFPRDYEDRRKIFKLNLLPGEKVTTQGK
IVSVETKKFQNMNILTAVLSDGLVHVPLKWFNQDYLQTYLQKLTGKEVFVTGTVKSNAITGQYEIHN
AEVTPKEGEYVRRILPIYRLTSGISQKQMRKIFEENIPSLCCSLK
>d1cuk_3 b.40.4.2 (1-64) DNA helicase RuvA subunit, N-terminal domain {Escherichia coli}
MIGRLRGIIEKQPPLVLIIEVGGVGYEVHMPMTCFYELPEAGQEAIIVFTHFVVREDAQLLYGFN
>d1bvsa3 b.40.4.2 (A:1-63) DNA helicase RuvA subunit, N-terminal domain {Mycobacterium
leprae}
MIFSVRGEVLEVALDHAVIEAAGIGYRVNATPSALATLNQGSQARLVTAMVVREDSMTLYGFS
>d3ulla_ b.40.4.3 (A:) ssDNA-binding protein {Human (Homo sapiens), mitochondria}
LERSLNVRHLLGRVQDPVLRQVEGKNPVTIFSLATNEMWRSGDSEVYQLGDVSQKTTWHRISVFR
PGLRDVAYQYVKKGSRIYLEGKIDYGEYMDKNNVRRQATTIADNIIFL
>d1kawa_ b.40.4.3 (A:) ssDNA-binding protein {Escherichia coli}
RGNVNVILVGNLQDPEVRYMPNGGAVANITLATSESWRDKATGEMKEQTEWHRVVLFGKLAEVA
SEYLRKGSQVYIEGQLRTRKWTDQSGQDRYTTEVVVNVGGTMQML
>d1qvca_ b.40.4.3 (A:) ssDNA-binding protein {Escherichia coli}
ASRGNVNVILVGNLQDPEVRYMPNGGAVANITLATSESWRDKATGEMKEQTEWHRVVLFGKLAE

VASEYLRKGSQVYIEGQLRTRKWTQSGQDRYTTEVVVNVGGTMQMLGGRQGGGAPAGGNIGGGQ
PQGGWGQPQPQGGN

>d1ewia_ b.40.4.3 (A:) Replication protein A 70 KDa subunit (RPA70) fragment {Human (Homo sapiens)}

MVGQLSEGAIAAIMQKGDNIKPIQVINIRPITGNPPRYRLLMSDGLNLTSSFMLATQLNPLVEEE
QLSSNCVCQIHRFIVNTLKDGRRVILMELEVLKSAEAVGVKIGN

>d1fgua1 b.40.4.3 (A:181-298) Replication protein A 70 KDa subunit (RPA70) fragment {Human (Homo sapiens)}

MSKVVPASLTPYQSKWTICARVTNKSQIRTWSNSRGGKLSLELVDESGEIRATAFNEQVDKFFPL
IEVNKVYFYSKGLKIANKQFTAVKNDYEMTFNNETSVMPCEDDHHLPTV

>d1fgua2 b.40.4.3 (A:299-426) Replication protein A 70 KDa subunit (RPA70) fragment {Human (Homo sapiens)}

QFDFGTGIDLENKSKDSLVDIIGICKSYEDATKITVRSNNREVAKRNIYLMDTSGKVVTATLWGEDAD
KFDGSRQPVLAIKGARVSDFGGRSLSVLSSTHIANPDIPEAYKLRGWFDAGQALDGVS

>d1quqa_ b.40.4.3 (A:) Replication protein A 32 KDa subunit (RPA32) fragment {Human (Homo sapiens)}

HIVPCTISQLSATLVDEVFRIGNVEISQVTIVGIIRHAEKAPTNIYKIDDMTAAAPMDVRQWVDTDD
TSENTVVPPEYVVKVAGHLRSFQNKSLVAFKIMPLEDMNEFTTHILEVINAHMVLK

>d1quqb_ b.40.4.3 (B:) Replication protein A 14 KDa (RPA14) subunit {Human (Homo sapiens)}

DMMDLPRSRINAGMLAQFIDKPVCFVGRLEKIHPTGKMFILSDGEGKNGTIELMEPLDEEISGIVEVV
GRVTAKATILCTSYVQFKEDSHPFDLGLYNEAVKIIHDFPQFYPLG

>d1jb7a1 b.40.4.3 (A:36-204) Telomere end binding protein alpha subunit {Oxytricha nova}

YEYVELAKASLTSAPQHFAVVIDATFPYKTNQERYICSLKIVDPTLYLKQKQKAGDASDYATLVLYA
KRFEDLPIIHRAGDIIRVHRATLRLYNGQRQFNANVFYSSSWALFSTDKRSVTQEINNQDAVSDTTPF
SFSSKHATIEKNEISILQNLRKWANQYFSSYS

>d1jb7a2 b.40.4.3 (A:205-328) Telomere end binding protein alpha subunit {Oxytricha nova}

VISSDMYTALNKAQAQKGFDFVAKILQVHELDEYTNELKLDASGQVFYTLSLKLFPHVRTGEVV
RIRSATYDETSTQKKVLILSHYSNIITFIQSSKLAKELRAKIQDDHSVEVASLKKNV

>d1jb7a3 b.40.4.3 (A:329-495) Telomere end binding protein alpha subunit {Oxytricha nova}

SLNAVVLTEVDKHAALPSTSLQDLFHHADSDKELQAQDTFRTQFYVTKIEPSDVKEWVKGYDRKT
KKSSSLKGASGKGNIFVQVFLVKDASTQLNNTYRVLTYQDGLGANFFNVKADNLHKNADARKK
LEDSAELLTKFNSYVDAVVERRNGFYLIKDTKLIY

>d1k8ga2 b.40.4.3 (A:205-315) Telomere end binding protein alpha subunit {Oxytricha nova}

VISSDMYTALNKAQAQKGFDFVAKILQVHELDEYTNELKLDASGQVFYTLSLKLFPHVRTGEVV
RIRSATYDETSTQKKVLILSHYSNIITFIQSSKLAKELRAKIQD

>d1jb7b_ b.40.4.3 (B:) Core domain of telomere end binding protein beta subunit {Oxytricha nova}

QQQSFAFKQLYTELFNNEGDFSKVSSNLKPLKCYVKESYPHFLVTDGYFFVAPYFTKEAVNEFHAKF
PNVNIVDLTDKIVINNWSLELRRVNSAEVFTSYANLEARLIVHSFKPNLQERLNPTRYPVNLFRRDD
EFKTTIQHFRHTALQAANKTVKGDNLVDISKVADAAGKKGKVDAGIVKASASKGDEFSDFSFKEGNT

ATLKIADIFVQKEG

>d1jjcb3 b.40.4.4 (B:39-151) Domain B2 of PheRS-beta, PheT {*Thermus thermophilus* (*Thermus aquaticus*)}

FPIPRGVVFARVLEAHPIPGTRLKRLVLDAGRTVEVVSQAENARKGIGVALALPGTELPGLGQKVGGER
VIQGVRSFGMALSPRELGVGEYGGGLLEFPEDALPPGTPLSEAWP

>d1f0a_ b.40.4.4 (A:) EMAP II {Human (*Homo sapiens*)}

IDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNHVPLEQMQRNMVILLCNLKPAK
MRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAFPGEPAKELNPKKKIWEQIQPDLHTNDEC
VATYKGVPPFEVKGKGCRAQTMSNSGIKL

>d1gd7a_ b.40.4.4 (A:) CsaA {*Thermus thermophilus*}

MTPLEAFQILDLRVGRVLRAPHEKARKPSYKLWVDLGLGPKQSSAQITELYRPEDLVGRLVCAV
NLGAKRVAGFLSEVLVLPDEAGRVLLAPDREVPLGGKVF

>d1mjc_ b.40.4.5 (-) Major cold shock protein {*Escherichia coli*}

SGKMTGIVKWFNADKGFITPDDGSKDVFVHFSAIQNDGYKSLDEGQKVSFTIESGAKGPAAGNVT
SL

>d1csp_ b.40.4.5 (-) Major cold shock protein {*Bacillus subtilis*}

MLEGKVKWFNSEKGFIEVEGQDDVVFHFSAIQEGFKTLEEGQAVSFEIVEGNRGPQAANVTKE
A

>d1c9oa_ b.40.4.5 (A:) Major cold shock protein {*Bacillus caldolyticus*}

MQRGKVKWFNNEKGYGFIEVEGSDVVFHFTAIQEGFKTLEEGQEVSEIVQGNRGPQAANVVKL

>d1g6pa_ b.40.4.5 (A:) Major cold shock protein {*Thermotoga maritima*}

MRGKVKWFDSKKGYGFITKDEGGDVVFHWSAIEGFKTLKEGQVVEFEIQEGKKGPQAAHVKVV
E

>d1h95a_ b.40.4.5 (A:) Y-box protein 1 cold shock domain (YB1-CSD) {Human (*Homo sapiens*)}

MKKVIATKVLGTVKWFNVRNGYGFINRNDTKEDVVFHQTAIKKNNPRKYLRVGDGETVEFDVVE
GEKGAEAAANVTGPG

>d1sro_ b.40.4.5 (-) S1 RNA-binding domain of polyribonucleotide phosphorylase, PNPase {*Escherichia coli*}

AEIEVGRVYTGKVTTRIVDFGAFVAIGGGKEGLVHISQIADKRVEKVTDYLMGQEVPPVKVLEVDROG
RIRLSIKEA

>d1e3pa2 b.40.4.5 (A:656-717) S1 RNA-binding domain of polyribonucleotide phosphorylase, PNPase {*Streptomyces antibioticus*}

GSVVKTTFGAFVSLPGKDGLLHISQIRKLAGGKRVENVEDVLGVGQKQVQVEIAEIDSRGK

>d1hh2p1 b.40.4.5 (P:127-198) S1 domain of NusA {*Thermotoga maritima*}

FEKyselKGTVTTAEVIRVMGEWADIRIGKLETRLPKKEWIPGEEIKAGDLVKVYIIDVVKTTKGPKIL
VSR

>d1k0ra1 b.40.4.5 (A:108-183) S1 domain of NusA {*Mycobacterium tuberculosis*}

STREGEIVAGVIQRDSRANARGLVVVRIGTETKASEGVIPAAEQVPGESYEHGNRLRCYVVGVTTRGAR
EPLITLSR

>d1go3e_ b.40.4.5 (E:) RNA polymerase II subunit RBP4 (RpoE) {Archaeon *Methanococcus jannaschii*}

MYKILEIADVVKVPPEEFGKDLKETVKKILMEKYEGRLDKDVGFLSIVDVKDIGEGKVVHGDGSAY
HPVVFETLVYIPEMYELIEGEVVDVVEFGSFVRLGPLDGLIHVSQIMDDYVSYDPKREAIHGKETGKVL

EIGDYVRARIVAISLKAERKRGSKIALTMRQPYLKLEWIEEEKAKKQ
>d1ah9_ b.40.4.5 (-) Translational initiation factor 1, IF1 {Escherichia coli}
AKEDNIEMQGTVLETLPNTMFRVELENGHVVTAHISGKMRKNYIRILTGDKVTVELTPYDLSKGRIV
FRSR
>d1hr0w_ b.40.4.5 (W:) Translational initiation factor 1, IF1 {Escherichia coli}
AKEKDTIRTEGVVTEALPNATFRVKLDSGPEILAYISGKMRMHYIRILPGDRVVVEITPYDPTRGRIVY
RK
>d1jt8a_ b.40.4.5 (A:) Archaeal initiation factor-1a, aIF1a {Archaeon Methanococcus
jannaschii}
MAEQQQEQQIRVRIPRKEENEILGIEQMLGASRVVRCLDGKTRLGRIPGRLKNRIWVREGDVVIVK
PWEVQGDQKCDIWRYTQVEWLKRKGYLDELL
>d1d7qa_ b.40.4.5 (A:) Translation initiation factor-1a, eIF1a {Human (Homo sapiens)}
PKNKGKGGKRRRRGKNENESEKRELVFKEDGQEYAQVIKMLGNGRLEAMCFDGVKRLCHIRGKLR
KKVWINTSDIILVGLRDYQDNKADVILKYNADARSCLKAYGELPEHAKINETDTFGPGDDDEIQFDDI
GDDDEDIDDI
>d1a62_2 b.40.4.5 (48-125) Rho termination factor, RNA-binding domain {Escherichia coli}
DIFGDGVLEILQDGFGLRSADSSYLGPDDIYVSPSQIRRFNLRTGDTISGKIRPPKEGERYFALLKVN
EVNFDKPE
>d2eifa2 b.40.4.5 (A:74-132) C-terminal domain of eukaryotic initiation translation factor 5a
{Archaeon Methanococcus jannaschii}
IDRRKQVLAIMGDMVQIMDLQTYETLELPIPEGIEGLEPGGEVEYIEAVGQYKITRVI
>d1bkb_2 b.40.4.5 (75-139) C-terminal domain of eukaryotic initiation translation factor 5a
{Archaeon Pyrobaculum aerophilum}
IIEKFTAQILSVSGDVIQLMDMRDYKTIEVPMKYVEEEAKGRLAPGAEVEVWQILDYKIIRVKG
>d1rl2a2 b.40.4.5 (A:60-125) N-terminal domain of ribosomal protein L2 {Bacillus
stearothermophilus}
QYRIIDFKRDKDGIPGRVATIEYDPNRSANIALINYADGEKRYIIAPKNLKVGMIEIMSGPDADIKI
>d1jj2a2 b.40.4.5 (A:1-90) N-terminal domain of ribosomal protein L2 {Archaeon Haloarcula
marismortui}
GRRIQQRRGRGTSTFRAPSHRYKADLEHRKVEDGDVIAGTVVDIEHDPARSAPVAAVEFEDGDRRL
ILAPEGVGVGDELQVGVDAEIAP
>d1fjgl_ b.40.4.5 (L:) Ribosomal protein S12 {Thermus thermophilus}
PTINQLVRKGREKVRKSKVPALKGAPFRRGVCTVVRTVTPKKPNSALRKVAVRLTSGYEVTAYIPG
EGHNLQEHSVVLIRGGRVKDLPGVRYHIVRGVYDAAGVKDRKKSRSKYGTKKPKAAA
>d1fjgq_ b.40.4.5 (Q:) Ribosomal protein S17 {Thermus thermophilus}
PKKVLTVGVVSDKMQKTVTVLVERQFPHPYLYGKVIKRSKLYLAHDPEEKYKLGDVVEIIESRPISKRK
RFRVLRVLESGRMDLVEKYLIRRQNYQSLSKRGGKA
>d1i94q_ b.40.4.5 (Q:) Ribosomal protein S17 {Thermus thermophilus}
PKKVLTVGVVSDKMQKTVTVLVERQFPHPYLYGKVIKRSKLYLAHDPEERYKVGDVVEIIEARPISKRK
RFRVLRVLEEGRLDLVEKYLVRQNYASLSKRGGKA
>d1rip_ b.40.4.5 (-) Ribosomal protein S17 {Bacillus stearothermophilus}
QRKVYVGRVSDKMDKTITVLVETYYKHPYLYGKRVKYSKLYKAHDEHNEAKVGDIVKIMETRPLSA
TKRFRVLEIVEKAVR
>d1ckma1 b.40.4.6 (A:239-327) RNA guanylyltransferase (mRNA capping enzyme)

{Chlorella virus, PBCV-1}
THHTIDFIIMSEDGTIGIFDPNLRKNVPVVGKLDGYYNKGSIVECGFADGTWKYIQRSDKNQANDRL
TYEKTLLNIEENITIDELDLF
>d1a0i_1 b.40.4.6 (241-349) ATP-dependent DNA ligase {Bacteriophage T7}
PENEADGIIQGLVWGTKGLANEGKVIGFEVLLESGRLVNATNISRALMDEFTETVKEATLSQWGFPS
PYGIGDNDACTINPYDGWACQISYMEETPDGSLRHPSFVMFR
>d1fvia1 b.40.4.6 (A:190-293) ATP-dependent DNA ligase {Chlorella virus, PBCV-1}
FKDAEATIISMTALFKNTNTKTKDNFGYSKRSTHKSQVEEDVMGSIEVDYDGVVFSIGTGFDADQR
RDFWQNKESYIGKMKVFKYFEMGSKDCPRFPVFIGIR
>d1dgsa2 b.40.4.6 (A:315-400) NAD+-dependent DNA ligase {Thermus filiformis}
AEEKETRLLDVVFQVGRTPVGVLEPVFIEGSESVRTLHNESYIEELDIRIGDWVLVHKAGGVI
PEVLRVLKERRTGKERPI
>d1gvp_ b.40.4.7 (-) Gene V protein {Filamentous bacteriophage (f1, M13)}
MIKVEIKPSQAQFTTRSGVSRQKPYSLNEQLCYVDLNEYPVLVKITLDEGQPAYAPGLYTVHLSSFK
VGQFGSLMIDRLRLVPAK
>d1pfsa_ b.40.4.7 (A:) Gene V protein {Pseudomonas bacteriophage pf3}
MNIQITFTDSVRQGTSAGNPYTFQEGFLHLEDKPHPLQCQFFVESVIPAGSYQVPYRINVNNGRPEL
AFDFKAMKRA
>d1gpc_ b.40.4.7 (-) Gene 32 protein (gp32) core {Bacteriophage T4}
GFSSSEDKGEWKLKLDNAGNGQAVIRFLPSKNDEQAPFAILVNHGFKKNGKWIETCSSTHGDYDSCP
VCQYISKNDLYNTDNKEYSLVKRKTSYWANILVVKDPAAPENEGKVFYRFGKKIWDKINAMIAVDV
EMGETPVDVTCPWEGANFVLKVKQVSGFSNYDESKFLNQSAIPNIDDESFKELFEQMVDLSEMTS
KDKFKSFEELNTKFGQVM
>d1je5a_ b.40.4.7 (A:) gp2.5 {Bacteriophage T7}
MAKKIFTSALGTAEPYAYIAKPDYGNNEERGFNPRGVYKVDLTIPNKDPRCQRMVDEIVKCHEEAYA
AAVEEYEANPPAVARGKKPLKPYEGDMPFFDNGDGTTFKFKCYASFQDKKTKETKHINLVVVDK
GKKMEDVPIIGGSGSLKLVKYSVLPYKWNTAVGASVKLQLESVMLVELATFGGGEDDWADEVEEN
>d1i50h_ b.40.4.8 (H:) RNA polymerase subunit RBP8 {Baker's yeast (Saccharomyces
cerevisiae)}
SNTLFDDIFQVSEVDPGRYNKVCRIEAASTTQDQCKLTLINVELFPVAAQDSLTVTIASSLNLEDTPA
NDSSATRWRPPQAGDRSLADDYDYVMYGTAYKFEVSKDLIAVYYSFGLLMRLEGNYRNLNLLK
QENAYLLIRR
>d1e9ga_ b.40.5.1 (A:) Inorganic pyrophosphatase {Baker's yeast (Saccharomyces
cerevisiae)}
TYTTRQIGAKNTLEYKVYIEKDGKPVSAFHDIPLYADKENNIFNMVVEIPRWTNAKLEITKEETLNPI
IQDTKKGKLRFRNCFPHHGYIHNYGAFPQTWEDPNVSHPETKAVGDNDPIDVLEIGETIAYTGQVK
QVKALGIMALLDEGETDWKVIADINDPLAPKLN DIEDVEKYFPGLLRATNEWFRYKIPDGKPENQ
FAFSGEAKNKYALDIHKETHDSWKQLIAGKSSDSKIDLTNTVTLPTPTYSKAASDAIPPASLKADAP
IDKSIDKWFFISG
>d1qeza_ b.40.5.1 (A:) Inorganic pyrophosphatase {Archaeon Sulfolobus acidocaldarius}
KLSPGKNAPDVVNVLVEIPQGSNIKYEYDDEEGVIKVDRLVLYTSMNYPFNYGFIPGTLEEDGDPLDVL
VITNYQLYPGSVIEVRPIGILYMKDEEGEDAKIVAVPKDKTDPSFSNIKDINDLPQATKNKIVHFFEYH
KELEPGKYVKISGWGSATEAKNRIQLAIKRVS
>d1i40a_ b.40.5.1 (A:) Inorganic pyrophosphatase {Escherichia coli}

SLLNVPAGKDLPEDIYVVIEIPANADPIKYEIDKESGALFVDRFMSTAMFYPCNYGYINHTLSLDGDPV
DVLVPTPYPLQPGSVTRCRPVGVLKMTDEAGEDAKLVAVPHSKLSKEYDHIKDVNDLPELLKAQIAH
FFEHYKDLEKGGKVVVEGWENAEAAKAEIVASFERAANK

>d2prd_ b.40.5.1 (-) Inorganic pyrophosphatase {*Thermus thermophilus*}
ANLKSPLVGDKAPEVVMVIEVPRGSGNKYEYDPLGAIKLDRLPGAQFYFPGDYGFIPSTLAEDGD
PLDGLVLTSTYPLLPGVVVEVRVVGLLLMEDEKGGDAKIVIGVVAEDQRLDHIQDIGDVPEGVKQEIQH
FFETYKALEAKKGGKVVVTGWRDRKAALVEVRACIARYKG

>d1fr3a_ b.40.6.1 (A:) Molybdate/tungstate binding protein MOP {*Sporomusa ovata*}
MKISGRNKLEATVKEIVKGTVMKIVMDYKGTTELVAAITIDSVADLDLVPGDKVTLVKATEMEVLK

>d1guta_ b.40.6.1 (A:) Molybdate/tungstate binding protein MOP {*Clostridium pasteurianum*,
MOP II}
SISARNQLKGGKVVGLKGGVVTAEVVLEIAGGNKITSIISLDSVEELGVKEGAELTAVVKSTDVMILA

>d1h9ma1 b.40.6.2 (A:1-73) Cytoplasmic molybdate-binding protein ModG {*Azotobacter
vinelandii*}
MKISARNVFKGTVSALKEGAVNAEVDILLGGGDKLAAVVTLESARSLQAAGKEVVAVVKAPWVLL
MTDSSGY

>d1h9ma2 b.40.6.2 (A:74-141) Cytoplasmic molybdate-binding protein ModG {*Azotobacter
vinelandii*}
RLSARNILGTVKTIETGAVNAEVTALQGGTEITSMVTKEAVAELGLKPGASASAVIKASNVILGVP

>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*}
DNQLPGIISHIERGAEQCEVLMALPDGQTLCATVPVNEATSLQQGQNVTAIFYNADSVIIATL

>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*}
VRVPGENLVRAVVEIVENLGSERIVRLRVGGVTFVGSFRSESRVREGVEVDVVFDMKKIHIFDKTTGK
AIF

>d1b3qa2 b.40.7.1 (A:540-671) Histidine kinase CheA, C-terminal domain {*Thermotoga
maritima*}
TLAICALLVKVNNLVYAIPIANIDTILSISKEDIQRVQDRDVIVIRGEVIPVYRLWEVLQIEHKEELEEM
EAVIVRVGNRKYGIVVDDLLGQDDIVIKSLGKVFSEVKEFSGAAILGDGSIALIINVSGIV

>d1k0sa_ b.40.7.1 (A:) Chemotaxis protein CheW {*Thermotoga maritima*}
MKTLADALKEFEVLSFEIDEQALAFDVDNIEMVIEKSDITPVPKSRHFVEGVINLRGRIIPVNLAKIL
GISFDEQKMSIIVARTKDVEVGLVDRVLGVLRLITENQLDLTNVSDKFGKKSGLVKTDGRLIYLDI
DKIIEEITVKEGV

>d1dxrh1 b.41.1.1 (H:37-258) Photosynthetic reaction centre {*Rhodospseudomonas viridis*}
RREGYPLVEPLGLVKLAPEDGQVYELPYPKTFVLPHGTVTVPRRRPETRELKLAQTDGFEGAPLQP
TGNPLVDAVGPAHYAERADEVVDTVDGKAKIVPLRVATDFSIAEGDVPDPRGLPVVAADGVEAGTVTD

LWVDRSEHYFRYLELSVAGSARTALIPLGFCDVKDKIVVTSILSEQFANVPRLQSRDQITLREEDKVS
AYYAGGLLYATPERAESLL

>d1qovh1 b.41.1.1 (H:36-250) Photosynthetic reaction centre {Rhodobacter sphaeroides}
MREGYPLENEDGTPAANQGPFLPKPKTFILPHGRGTLTVPGPESEDRPIALARTAVSEGFPHAPTG
DPMKDGVPASWVARRDLPELDGHGHNKIKPMKAAAGFHVSAGKNPIGLPVRGCDLEIAGKVVDI
WVDIPEQMARFLEVELKDGSTRLLPMQMVQVSNRVHVNALSSDLFAGIPTIKSPTEVTLLEEDKIC
GYVAGGLMYAAPKRKS

>d1eysh1 b.41.1.1 (H:59-259) Photosynthetic reaction centre {Thermochromatium
tepidum}

PDLDPKTFVLPHNGGTVVAPRVEAPVAVNATPFSPAPGSPLVPNGDPMLSGFGPAASDRPKHCDL
TFEGLPKIVPMRVAKEFSIAEGDPDPRGMTVVGLDGEVAGTVSDVWVDRSEPIRYLEVEVAANKKK
VLLPIGFSRFDKARKVKVDAIKAAHFANVPTLSNPDQVTLYEEDKVCAYYAGGKLYATAERAGPLL

>d1bfg_ b.42.1.1 (-) Basic FGF (FGF2) {Human (Homo sapiens)}

DPKRLYCKNGGFFLRIHPDGRVDGVREKSDPHIKLQLQAEERGVSISIKGVSANRYLAMKEDGRLLAS
KSVTDECFFFERLESNNYNTYRSRKYTSWYVALKRTGQYKLGSKTGPGQKAILFLPMSA

>d1bla_ b.42.1.1 (-) Basic FGF (FGF2) {Human (Homo sapiens)}

MAEGEITLTPALPEDGGSGAFPPGHFKDPKRLYCKNGGFFLRIHPDGRVDGVREKSDPHIKLQLQAE
ERGVSISIKGVSANRYLAMKEDGRLLASKSVTDECFFFERLESNNYNTYRSRKYTSWYVALKRTGQYK
LGSKTGPGQKAILFLPMSAKS

>d1bara_ b.42.1.1 (A:) Acidic FGF (FGF1) {Cow (Bos taurus)}

PKLLYCSNGGYFLRILPDGTVDGTDRSDQHIQLQLAAESIGEVYIKSTETGQFLAMDTDGLLYGSQT
PNEECLFLERLEENGYNTYISKKHAEKHWVGLKKNGRSKLGPRTTHFGQKAILFLPLPV

>d1jqza_ b.42.1.1 (A:) Acidic FGF (FGF1) {Human (Homo sapiens)}

HHHHFNLPNGYKPKLLYCSNGGHFLRILPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTETGQ
YLAMDTDGLLYGSQTPNEECLFLERLEENHYNTYISKKHAEKWVGLKKNGSCKRGPRTHYGQKA
ILFLPLPV

>d2afga_ b.42.1.1 (A:) Acidic FGF (FGF1) {Human (Homo sapiens)}

KPKLLYCSNGGHFLRILPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTETGQYLAMDTDGLLYGSQ
TPNEECLFLERLEENHYNTYISKKHAEKWVGLKKNGSCKRGPRTHYGQKAILFLPLPVS

>d1fmms_ b.42.1.1 (S:) Acidic FGF (FGF1) {Eastern newt (Notophthalmus viridescens)}

QKPKLLYCSNGGYFLRIFPDGKVDGTRDRSDPYIQLQFYAESVGEVYIKSLETGQYLAMDSGQLYAS
QSPSECLFLERLEENNYNTYKSKVHADKDWVFGIKKNGKTKPGSRTHFGQKAILFLPLPVSSD

>d1ijta_ b.42.1.1 (A:) Fibroblast growth factor 4 (FGF4) {Human (Homo sapiens)}

GIKRLRRLYCNVIGIFHLQALPDGRIGGAHADTRDSLELSPVERGVVSIFGVASRFFVAMSSKGKLYG
SPFFTDECTFKEILLPNYAYESYKYPGMFIALGKNGKTKKGNRVSPMKVTHFLPRL

>d1qqka_ b.42.1.1 (A:) Keratinocyte growth factor, FGF7 {Rat (Rattus norvegicus)}

DIRVRRFLFCRTQWYLRLIDKRGKVKGTQEMRNSYNIMEIRTVAVGIVAIGVESEYLLAMNKEGKLYAK
KECNEDCNFKELILENHYNTYASAKWTHSGGEMFVALNQGLPVKGGKTKKEQKTAHFLPMAIT

>d1qqla_ b.42.1.1 (A:) Keratinocyte growth factor, FGF7 {Rat (Rattus norvegicus)}

DIRVRRFLFCRTQWYLRLIDKRGKVKGTQEMRNSYNIMEIRTVAVGIVAIGVESEYLLAMNKEGKLYAK
QTPNEECLFLERLEENHYNTYISKKHAEKWVGLKKNGSCKRGPRTHYGQKAILFLPLPVSS

>d1ihka_ b.42.1.1 (A:) Fibroblast growth factor 9, FGF9 {Human (Homo sapiens)}

TDLDHKGLRRRQLYCRGTFHLEIFPNGTIQGTRKDHSRFGILEFISIAVGLVSIRGVDSGLYLMNEK
GELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTREGTRTRKRHQKFTHF

LPRPVDPKVPELYKDILSQS

>d1i1b_ b.42.1.2 (-) Interleukin-1beta {Human (Homo sapiens)}

VRSLNCTLRDSQQKSLVMSGPYELKALHLQGQDMEQQVVFMSFVQGEESNDKIPVALGLKEKNLY
LSCVLKDDKPTLQLESVDPKNYPKKKMEKRFVFNKIEINNKFESAQFPNWWYISTSQAENMPVFL
GGTKGGQDITDFTMQFVSS

>d8i1b_ b.42.1.2 (-) Interleukin-1beta {Mouse (Mus musculus)}

QLHYRLRDEQQKSLVLSDPYELKALHLNGQINQQVIFMSFVQGEPSNDKIPVALGLKGNLYLSCV
MKDGTPTLQLESVDPKQYPKKKMEKRFVFNKIEVKSKVEFESAEPNWWYISTSQAEHKPVFLGNNS
GQDIIDFTMESV

>d1ilr1_ b.42.1.2 (1:) Interleukin-1 receptor antagonist protein {Human (Homo sapiens)}

SKMQAFRIWDVNQKTFYLRNNQLVAGYLQGPVNVLEEKIDVPIEPHALFLGIHGGMCLSCVKSG
DETRLQLEAVNITDLSNRKQDKRFAFIRSDSGPTTSFESAACPGWFLCTAMEADQPVSLTNMPDEG
VMVTKFYFQEDE

>d2ila_ b.42.1.2 (-) Interleukin-1alpha {Human (Homo sapiens)}

NVKYNFMRIIKYEFILNDALNQSIRANAQYLTAALHNLDEAVKFDMGAYKSSKDDAKITVILRISK
QLYVTAQDEDQPVLKEMPEIPKTITGSETNLLFFWETHGTKNYFTVAHPNLFIATKQDYWVCLAG
GPPSITDFQILE

>d2aai1 b.42.2.1 (B:1-135) Plant cytotoxin B-chain (lectin) {Castor bean (Ricinus communis), Ricin}

ADVCMDEPIVIRVGRNGLCVDVDRGRFHNGNAIQLWPCKSNTDANQLWTLKRDNTIRSNGKCLTT
YGYSPGVVMIYDCNTAATDTRWQIWDNGTIINPRSSLVLAATSGNSGTTTLVQTNIYAVSQWLPT
N

>d2aai2 b.42.2.1 (B:136-262) Plant cytotoxin B-chain (lectin) {Castor bean (Ricinus communis), Ricin}

NTQPFVTTIVGLYGLCLQANSQVWIEDCSSEKAEQQWALYADGSIRPQQNRDNCCLTSDSNIRETVV
KILSCGPASSQRWFMKNDGTILNLYSGLVLDVRASDPSLKQIILYPLHGDPNQIWLPLF

>d1abrb1 b.42.2.1 (B:1-140) Plant cytotoxin B-chain (lectin) {Abrus precatorius}

IVEKSKICSSRYEPTVRIGGRDGMCDVDVYDNGYHNGNRIIMWKCKDRLEENQLWTLKSDKTIRSNGK
CLTTYGYAPGSYVMIYDCTSAVAEATYWEIWDNGTIINPKSALVLSAESSMGGTTLVQTNIEYLMRQG
WRTGN

>d1abrb2 b.42.2.1 (B:141-267) Plant cytotoxin B-chain (lectin) {Abrus precatorius}

NTSPFVTSISGYSDLCMQAQSNNVWVWADCDNSNKEQQWALYTDGSIRSVQNTNCLTSKDHKQGST
ILLMGCSNGWASQRWVFNKNDGSIYSYDDMVMDVKGSDPSLKQIILWPYTGKPNQIWLTLF

>d1ce7b1 b.42.2.1 (B:1-133) Plant cytotoxin B-chain (lectin) {European mistletoe (Viscum album)}

CSASEPTVRIVGRNGMNVDRDDDFHDGNQIQLWPSKSNNDPNQLWTIKRDGTIRSNGSCLTTYGY
TAGVYVMIFDCATAVGEATVWQIWGNGTIINPRSNLVLAASSGIKGTTLVQTLDYTLGQGWLAGND

>d1ce7b2 b.42.2.1 (B:134-255) Plant cytotoxin B-chain (lectin) {European mistletoe (Viscum album)}

TAPREVTIYGFNDLCMESGGGSVTVETCSSGKADKWALYGDGSIRPEQNQAQCLTSGGDSVAGVNIVS
CSGAASGQRWVFTNEGAILNLKNGLAMDVANPGGGRIIYPATGKPNQMWLPLF

>d1hwmb1 b.42.2.1 (B:3-135) Plant cytotoxin B-chain (lectin) {Sambucus ebulus, ebulin}

ETCAIPAPFTRRIVGRDGLCVDRNGYDTDGTPIQLWPCGTQRNQQWTFYNDKTIRSMGKCMTAN
GLNSGSYIMITDCSTAAEDATKWEVLIDGSIINPSSGLVMTAPSGASRTTLLENNIHAASQGWTVSN

>d1hwmb2 b.42.2.1 (B:136-266) Plant cytotoxin B-chain (lectin) {Sambucus ebulus, ebulin}
DVQPIATLIVGYNEMCLQANGENNNVWMECDVTSVQQWALFDDRTIRVNNRGLCVTSNGYVS
KDLIVIRKQCGLATQRWFFNSDGSVVLKSTRVMDVKESDVSLEVIIFPATGNPNQQWRTQVPQI
>d1xyfa1 b.42.2.1 (A:313-436) Endo-1,4-beta-xylanase C-terminal domain {Streptomyces
olivaceoviridis}
GQIKGVGSGRCLDVPNASTTDGTQVQLYDCHSATNQQWTYTDAGELRVYGDKCLDAAGTGNGTKVQ
IYSCWGGDNQKWRLNSDGSIVGVQSGLCCLDAVGGGTANGTLIQLYSCSNGSNQRWTRT
>d1dqga_b.42.2.2 (A:) Mannose receptor {Mouse (Mus musculus)}
DARQFLIYNEDHKRCVDALSASVQTATCNPEAESQKFRWVSDSQIMSVAFKLCGLVPSKTDWASVT
LYACDSKSEYQKWECKNDTLFGIKGTLYFYNGNRQEKNIKLYKGSGLWSRWKVYGTDDLCRSGYE
>d1jlx1 b.42.3.1 (A:1-153) Agglutinin {Love-lies-bleeding (Amaranthus caudatus)}
AGLPVIMCLKSNNHQYLRYQSDNIQYGLLQFSADKILDPLAQFEVEPSKTYDGLVHIKSRYTNKYL
VRWSPNHYWITASANEPDENKSNWACTLFLKPLYVEEGNMKKVRLHLVQLGHYTNQNYTVGGSFVSY
LFAESSQIDTGSKDVFHVID
>d1jlx2 b.42.3.1 (A:154-299) Agglutinin {Love-lies-bleeding (Amaranthus caudatus)}
WKSIFQFPKGYVTFKGNNGKYLGVITINQLPCLQFGYDNLNDPKVAHQMFVTSNGTICIKSNYMNKF
WRLSTDDWILVDGNDPRETNEAAALFRSDVHDFNVISLLNMQKTWFIKRFTSGKPGFINCMNAAT
QNVDETAILEIHEL
>d1wba_b.42.4.1 (-) Winged bean albumin 1 {Goa bean (Psophocarpus tetragonolobus)}
DDPVYDAEGNKLVRNGKYTIVSFDGAGIDVVATGNENPEDPLSIVKSTRNIMYATSISSEDKTPPQP
RNILENMRLKINFATDPHKGDVWSVDFQPDGQQLKLAGRYPNQVKGAFITQKGSNTPRTYKLLFC
PVGSPCKNIGISTDPEGKKRLVVSQSDPLVVKFHRH
>d1tie_b.42.4.1 (-) Erythrina cafra trypsin inhibitor {Erythrina caffra}
VLLDNGEVVQNGGTYLLPQVWAQGGVQLAKTGEETCPLTVVQSPNELSDGKPIRIESRLRSFIP
DDDKVRIGFAYAPKCAPSPWWTVVEDEQEGLSVKLESEDESTQFDYPFKFEQVSDQLHSYKLLYCEGK
HEKCASIGINRDQKGYRRLVVTEDYPLTVVLLKDE
>d1eyla_b.42.4.1 (A:) chymotrypsin inhibitor WCI {Winged bean (Psophocarpus
tetragonolobus)}
EFDDDLVDAEGLVENGTYLLPHIWAHGGGIETAKTGNPCPLTVVRSNEVSKGEPRISSQFLS
LFIPRGSVALGFANPPSCAASPWWTVVDSQPQPAVKLSQQKLEPKDILVFKFEKVSHSNIHVYKLLY
CQHDEEDVKCDQYIGIHRDRNGNRRLVVTENPLELVLLKAKS
>d1avwb_b.42.4.1 (B:) Soybean trypsin inhibitor {Soybean (Glycine max)}
DFVLDNEGNPLENGGTYILSDITAFGGIRAAPTGNERCPLTVVQSRNELDKGIGTHISSPYRIRFIAEG
HPLSLKFDSFAVIMLCVGIPTWVSVVDELPEGPAVKIGENKDAMDGWFRLERVSEFNKYLVFCPQD
KCGDIGISIDHDDGTRRLVVSKNKPLVVQFQKLD
>d1avac_b.42.4.1 (C:) Amylase/subtilisin inhibitor {Barley (Hordeum vulgare), seed}
ADPPPVHDTDGHELADANYVLSANRAHGGGLTMAPGHRHCPLFVSQDPNGQHDGFPVRITPY
GVAPSDKIIRLSTDVRIFRAYTTCLQSTEWHLSELAAGRHRVITGPVKDPSPSGRENAFRIEKYSGA
EVHEYKLMSCGDWCQDLGVFRDLKGGAWFLGATEPYHVVVFKKAPPA
>d1a8d_2 b.42.4.2 (248-452) Tetanus neurotoxin {Clostridium tetani}
ITFLRDFWGNPLRYDTEYYLIPVASSSKDVQLKNITDYMYLTNAPSNTGKLNIIYRRLYNGLKFIKR
YTPNNEIDSFVKSGDFIKLYVSYNNNEHIVGYPKDGNAFNLDLRLRVGYNAPGIPLYKKMEAVKLRD
LKTYSVQLKLYDDKNASLGLVGTHTNGQIGNDPNRDILIASNWFNHLKDKILGCDWYFVPTDEGWT
ND

>d3btaa2 b.42.4.2 (A:1079-1295) Botulinum neurotoxin {Clostridium botulinum, serotype A}

NEKEIKDLYDNQNSGILKDFWGDYLYQDKPYMLNLYDPNKYVDVNNVVGIRGYMYLKGPRGSVMT
TNIYLNSSLYRGTKFKIHKYASGNKDNIVRNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDV
GNLSQVVVMKSKNDQGITNKCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWYNRQIERSRTLGC
SWEFIPVDDGWERPL

>d1epwa2 b.42.4.2 (A:1080-1290) Botulinum neurotoxin {Clostridium botulinum, serotype B}

SEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIR
RKSNSQSINDDIVRKEDIYILDFFNLNQEWVYTYKYFKKEEKLFLAPISDSDEFYNTIQIKEYDEQ
PTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKKRKPYNLKLGCNWQFIPK
DEGWTE

>d1dfca1 b.42.5.1 (A:1008-1140) Fascin {Human (Homo sapiens)}

EAVQIQFGLINCGNKYLTAFAFGFKVNASASSLKKKQIWTLEQPPDEAGSAAVCLRSHLGRYLAADKD
GNVTCEREVPGPDCRFLIVAHDGGRWSLQSEAHRRYFGGTEDRLSCFAQTVSPAEEKWSVHIAMHP

>d1dfca2 b.42.5.1 (A:1141-1259) Fascin {Human (Homo sapiens)}

QVNIYSVTRKRYAHLARPADAIAVDRDVPWGVDSLITLAFQDQRYSVQTADHRFLRHDGRLVARPE
PATGYTLEFRSGKVAFRDCEGRYLAPSGPSGTLKAGKATKVGKDELFALEQS

>d1dfca3 b.42.5.1 (A:1260-1382) Fascin {Human (Homo sapiens)}

CAQVVLQAANERNVSTRQGMDSLQNDQETDQETQLEIDRDTKKCAFRTHTGKYWTLTATGGVQ
STASSKNASCYFDIEWRDRRITLRASNGKFVTSKKNQLAASVETAGDSEFLMKLIN

>d1dfca4 b.42.5.1 (A:1383-1493) Fascin {Human (Homo sapiens)}

RPIIVFRGEHGFICRKYVTGTLNANSSYDVFQLEFNDGAYNIKDSTGKYWTVGSDSAVTSSGDTVPD
FFFEFCDYNKVAIKVGGRYLKGDHAGVLKASAETVDPASLWEY

>d1hcd_ b.42.5.2 (-) Histidine-rich actin-binding protein (hisactophilin) {Dictyostelium discoideum}

MGNRAFKSHHGHFLSAEGEAVKTHHGHHDHHTHFHVENHGGKVALKTHCGKYLSIGDHKQVYLS
HHLHGDHSLFHLHGGKVSIGHHHHYISADHHGHVSTKEHHDHDTTFEEIII

>d1i8da1 b.43.4.3 (A:1-93) Riboflavin synthase {Escherichia coli}

MFTGIVQGTAKLVSIDEKPNFRTHVVELPDHMLDGLGTGASVAHNGCCLTVTEINGNHVSFDLMKET
LRITNLGDLKVGDWVNERAAKFSDE

>d1i8da2 b.43.4.3 (A:94-206) Riboflavin synthase {Escherichia coli}

IGGHLMSGHIMTTAEVAKILTSENNRQIWFVKVQDSQLMKYIYKGFIDGISTVGEVTPTRFCVHLI
PETLERTTLGKKLGLARVNIEIDPQTQAVVDTVERVLAARENAM

>d1fnc_1 b.43.4.2 (19-154) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Spinach (Spinacia oleracea)}

HSKMEEGITVNKFKPKTPYVGRCLLNTKITGDDAPGETWHMVFSEGEIPYREGQSVGVIPDGED
KNGKPHKLRLYSIASSALGDFGDAKSVSLCVKRLIYTNDAGETIKGVCSNFLCDLKPGEVVKLTGPVKG
E

>d1qfza1 b.43.4.2 (A:1-153) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Garden pea (Pisum sativum)}

QVTTEAPAKVVKHSKKQDENIVVNKFKPKPEYVGRCLLNTKITGDDAPGETWHMVFSTEGEVYPYRE
GQSIGIVPDGIDKNGKPHKLRLYSIASSAIGDFGDSKTVSLCVKRLVYTNDAGEVVKGVCSNFLCDLKP
GSEVKITGPVKGKEMLMPK

>d1fb3a1 b.43.4.2 (A:67-207) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Paprika (*Capsicum annum*)}
 ISKKQDEGVVVNFKFRPKPEYIGRCLLNTKITGDDAPGETWHMVFSTEGEIPIYREGQSIGVIADGVDA
 NGKPHKRLRYSIASSALGDFGDSKTVSLCVKRLVYTNDKGEEVKGVCNFCDLKPGADVKITGPVVGK
 EMLMPK

>d1gawa1 b.43.4.2 (A:11-156) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Maize (*Zea mays*), leaf isoform}
 PATAKAKKESKKQEEGVVNTLYKPKPEYVGRCLLNTKITGDDAPGETWHMVFSTEGKIPYREGQSIG
 VIADGVDKNGKPHKVRLYSIASSAIGDFGDSKTVSLCVKRLIYTNDAGEIVKGVCNFCDLQPGDNV
 QITGPVKGEML

>d1jb9a1 b.43.4.2 (A:6-162) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Maize (*Zea mays*), root isoform}
 SRSKVSVAPLHLESAKEPPLNTYKPKPEFTATIVSVESLVGPKAPGETCHIVIDHGGNVPYWEGQSYG
 VIPPGENPKKPGAPQNVRLYSIASTRYGDNFDGRTGSLCVRRAVYYDPETGKEDPSKNGVCNFCNS
 KPGDKIQLTGPSGKIMLLPEE

>d1que_1 b.43.4.2 (1-141) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Cyanobacterium (*Anabaena* sp.), pcc 7119}
 TQAKAKHADVPVNLVYRPNAPFIGKVISNEPLVKEGGIGIVQHIKFDLTGGNLKYIEGQSIGIIPPGVDKN
 GKPEKLRYSIASTRHGDDVDDKTISLCVRQLEYKHPESGETVYGVCSYTLTHIEPGSEVKITGPVVGKE
 ML

>d1fdr_1 b.43.4.2 (2-100) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Escherichia coli}
 ADWVTGKVTKVQNWTDALFSLTVHAPVLPFTAGQFTKLGLEIDGERVQRAYSYVNSPDNPDLEFYL
 VTVPDGKLSPRLAALKPGDEVQVSEAGFFVL

>d1a8p_1 b.43.4.2 (2-100) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Azotobacter vinelandii}
 SNLNVERVLSVHHWNTLFSFKTTRNPSLRFENGQFVMIGLEVDGRPLMRAYSIASPNYEEHLEFFS
 IKVQNGPLTSRLQHLKEGDELMVSRKPTGTLV

>d1qfja1 b.43.4.2 (A:1-97) NAD(P)H:flavin oxidoreductase {Escherichia coli}
 TTLCKVTSVEAITDVTYRVRIVPDAAFSFRAGQYLMVVMDEKRPFSMASTPDEKGFIELHIGASE
 INLYAKAVMDRILKDHQIVVDIPHGEAWL

>d2cnd_1 b.43.4.2 (11-124) Nitrate reductase core domain {Corn (*Zea mays*)}
 GRIHCRLVAKKELSRDVRLFRFSLPSPDQVLGLPIGKHIFVCATIEGKLCMRAYTPTSMVDEIGHFDLL
 VKVYFKNEHPKFPNGGLMTQYLDLSPVGSYIDVKGPLGHVEYTGR

>d1ndh_1 b.43.4.2 (3-125) cytochrome b5 reductase {Pig (*Sus scrofa*), liver}
 PAITLENPDIKYPLRLIDKEVVNHDTRRRFRFALPSPEHILGLPVGQHIYLSARIDGNLVIRPYTPVSSDD
 DKGFVDLVIKVYFKDTHPKFPAGGKMSQYLESKIGDTIEFRGNGLLVYQGK

>d1i7pa1 b.43.4.2 (A:29-153) cytochrome b5 reductase {Rat (*Rattus norvegicus*)}
 HHHMITLENPDIKYPLRLIDKEILSHDTRRRFRFALPSPQHILGLPIGQHIYLSRIDGNLVIRPYTPVSS
 DDDKGFVDLVVVKVYFKETHPKFPAGGKMSQYLENMNIGDTIEFRGNGLLVYQGK

>d2pia_1 b.43.4.2 (1-103) Phthalate dioxygenase reductase {Pseudomonas cepacia, db01}
 TTPQEDGFLRLKIASKEKIARDIWSFELTDPQGAPLPPFEAGANLTVAVPNGSRRTYSLCNDQSQRNR
 YVIAVKRDSNGRGGSSIFIDDTSEGDAVEVSLPRN

>d1ep3b1 b.43.4.2 (B:2-102) Dihydroorotate dehydrogenase B, PyrK subunit {Lactococcus

lactis, isozyme B}

SQLQEMMTVVVSQREVAYNIFEMVLKGTLVDEMDDLPGQFLHLAVPNGAMLLRRPISISSWDKRAKTC
TILYRIGDETTGTGYKLSKLESGAKVDVMGPLGNF

>d1cqa2 b.43.4.2 (A:151-261) Flavohemoglobin, central domain {Alcaligenes eutrophus}
WKGWRTFVIREKRPESDVITSFILPADGGPVVNFEPGQYTSVAIDVPALGLQIRQYSLSDMPNGRT
YRISVKREGGGPQPPGYVSNLLHDHVNVDQVKLAAPYGSFHI

>d1ja1a1 b.43.4.1 (A:240-518) NADPH-cytochrome p450 reductase {Rat (Rattus norvegicus)}

SSIRQYELVVHEDMDVAKVYTGEMGRKLSYENQKPPFDAKNPFLAAVTANRKLNGQTERHLMHLE
LDISDSKIRYESGDHVAVYPANDSALVNQIGEILGADLDVIMSLNNLDEESNKKHPFCPTTYRTALTY
YLDITNPPRTNVLYELAQYASEPSEQEHLHKMASSSGEGKELYLSWVVEARRHILAILQDYP SLRPPI
DHLCELLPRLQARYYAIASSSKVHPNSVHICAVAVEYEAKSGRVNKGVATSWLRAKEPAGENGGRALV
PMFVRKSQF

>d1dda1 b.43.4.1 (A:226-446) Sulfite reductase flavoprotein {Escherichia coli}

IHTSPYSKDAPLVAASLVNQTGRNSEKDVRHIEIDLGDSGLRYQPGDALGVVYQNDPALVKELVEL
LWLKGDEPVTVEGKTLPLNEALQWHFELTVNTANIVENYATLTRSETLLPLVGDKAKLQHYAATPI
VDMVRFSPAQLDAEALINLLRPLTPRLYSIASSQAEEVENEVHVTVGVVRYDVEGRARAGGASSFLADR
VEEEGEVRFVIEHNDNFR

>d1f20a1 b.43.4.1 (A:963-1232) Neuronal nitric-oxide synthase FAD/NADP+ domain {Rat (Rattus norvegicus)}

SWKRNKFRITYVAEAPDLTQGLSNVHKKRVSAARLLSRQNLQSPKSSRSTIFVRLHTNGNQELQYQP
GDHLGVFPGNHEDLVNALIERLEDAPPANHVVKEMLEERNALGVISNWKDESRLPPCTIFQAFK
YYLDITTPPTPLQLQQFASLATNEKEKQRLVLVSKGLQEYEEWKWGKNPTMVEVLEEFPSIQMPATL
LLTQLSLLQPRYYSISSPDMYPDEVHLTVAIVSYHTRDGEGPVHVGVCSSWLNRIQADDVVPCFVRG
AP

>d1fua1 b.43.2.1 (A:356-591) L-fucose isomerase, C-terminal domain {Escherichia coli}

AQVFADVRTYWSPEAIERTVGHKLDGLAEHGHILNSGSAALDGCKQRDSEGNPTMKPHWEISQQ
EADACLAATEWCPAIHEYFRGGYSSRFLTEGGVPFTMTRVNIKGLGPVLQIAEGWSVELPKDVHDI
LNKRTNSTWPTTWFAPRLTGKGPFTDVYSVMANWGANHGVLTIHVGADFITLASMLRIPVCMHN
VEETKVYRPSAWAAHGMDIEGQDYRACQNYGPLYKR

>d1efca1 b.43.3.1 (A:205-296) Elongation factor Tu (EF-Tu), domain 2 {Escherichia coli}

AIDKPFLPIEDVFSISGRGTVVTGRVERGIIKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGEN
VGVLLRGIKREEIERGQVLAKPG

>d1exma1 b.43.3.1 (A:213-312) Elongation factor Tu (EF-Tu), domain 2 {Thermus thermophilus}

PVRDVKPFLMPVEDVFTITGRGTVATGRIERGKVKVGDEVEIVGLAPETRKT VVTGVEMHRKTLQ
EGIAGDNVGVLLRGVSREEVERGQVLAKPGSITP

>d1d2ea1 b.43.3.1 (A:251-348) Elongation factor Tu (EF-Tu), domain 2 {Cow (Bos taurus), mitochondrial}

TRDLEKPFLLPVESVYSIPGRGTVVTGTLERGIKKGDECEFLGHSKNIRTVVTGIEMFHKSLDRAEA
GDNL GALVRGLKREDLRRGLVMAKPGSIQP

>d1f60a1 b.43.3.1 (A:241-334) Elongation factor eEF-1alpha, domain 2 {Baker's yeast (Saccharomyces cerevisiae)}

DKPLRLPLQDVYKIGGIGTVPVGRVETGVIKPGMVVTFAPAGVTTEVKSVMHHEQLEQGVPGDNV

GFNVKNVSVKEIRRGVCGDAKNDPPKG

>d1jnya1 b.43.3.1 (A:228-322) Elongation factor eEF-1alpha, domain 2 {Archaeon Sulfolobus solfataricus}

PVDKPLRIPIQDVYSISGVGTVPVGRVESGVLKVGDKIVFMPAGKVGEVRSIETHHTKMDKAEPGDNI
GFNVRGVEKKDIKRGDVGHPNNPPTV

>d1dar_1 b.43.3.1 (283-400) Elongation factor G (EF-G), domain II {Thermus thermophilus}

PLDIPPIKGTTPEGEVVEIHPDPNGPLAALAFKIMADPYVGRLLTFIRVYSGTLTSGSYVYNTTKGRKER
VARLLRMHANHREEVEELKAGDLGAVVGLKETITGDTLVGEDAPRVILE

>d1g7sa1 b.43.3.1 (A:228-328) Initiation factor IF2/eIF5b, domains 2 and 4 {Archaeon Methanobacterium thermoautotrophicum}

EDSPARGTILEVKEETGLGMTIDAVIYDGLRKDDTIAMMTSKDVISTRIRSLKPRPLEEMRESRKK
FQKVDEVVAAAGIKIVAPGIDDMAGSPLRVVT

>d1g7sa2 b.43.3.1 (A:460-587) Initiation factor IF2/eIF5b, domains 2 and 4 {Archaeon Methanobacterium thermoautotrophicum}

IIKPASIRLIPKLVFRQSKPAIGGVEVLTGVIRQGYPLMNDGGETVGTVESMQDKGENLKSASRGQKVA
MAIKDAVYGKTIHEGDTLYVDIPENHYHILKEQLSGDLTDEELDLMDKIAEIKRKKNP

>d1d1na_ b.43.3.1 (A:) Initiation factor IF2/eIF5b, domains 2 and 4 {Bacillus stearothermophilus}

YEEKVIGQAEVRQTFKVSXVGTIAGCYVTDGKITRDSKVRLLIRQGIVVYEGEIDSLKRYKDDVREVAQ
GYEGLTIKFNFDIKEGDVIEAYVMQEVARA

>d1jj2b_ b.43.3.2 (B:) Ribosomal protein L3 {Archaeon Haloarcula marismortui}

PQPSRPRKGLGFGPRKRSTSETPRFNSWPSDDGQPGVQGFAGYKAGMTHVVLVNDPNSPREGM
EETVPVTVIETPPMRAVALRAYEDTPYGQRPLTEVWTDEFHSELDRTLDVPEDHDPDAAEEQIRDA
HEAGDLGDLRLITHVTPDAVPSVPKKPDVMEVTRVGGSVSDRLDHALDIVEDGGEHAMNDIFRAG
EYADVAGVTKGKGTQGPVKRWGVQKRKKGKHARQGWRRRIGNLGPWNPSRVRSTVPQQGQTYHQ
RTELNKRLLIDIGEGDEPTVDGGFVNYGEVDGPYTLVKGSVPGPKRLVRFRAVRPNDQPRLDPEVR
YVSNESNQG

>d1efca2 b.44.1.1 (A:297-393) Elongation factor Tu (EF-Tu) {Escherichia coli}

TIKPHTKFESEVYILSKDEGGRHTPFFKGYRQPQFYFRITDVTGTIELPEGVEMVMPGDNIKMVVTLI
HPIAMDDGLRFAIREGGRTVGAGVVAKVLS

>d1exma2 b.44.1.1 (A:313-405) Elongation factor Tu (EF-Tu) {Thermus thermophilus}

HTKFEASVYVLKKEEGGRHTGFFSGYRQPQFYFRITDVTGVVQLPPGVEMVMPGDNVFTVELIKPV
ALEEGLRFAIREGGRTVGAGVVTKILE

>d1d2ea2 b.44.1.1 (A:349-451) Elongation factor Tu (EF-Tu) {Cow (Bos taurus), mitochondrial}

HQKVEAQVYILTKEEGGRHKPFVSHFMPVMFSLTWDMACRIILPPGKELAMPGEDLKLTLILRQPMI
LEKQQRFTLRDGNRTIGTGLVTDTPAMTEEDKNIKW

>d1f60a2 b.44.1.1 (A:335-441) Elongation factor eEF-1alpha, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

CASFNATVIVLNHGQISAGYSPVLDCHTAHIACRFDELLEKNDRRSGKKLEDHPKFLKSGDAALVKF
VPSKPMCVEAFSEYPPPLGRFAVRDMRQTVAVGVIKSVDK

>d1jnya2 b.44.1.1 (A:323-429) Elongation factor eEF-1alpha, C-terminal domain {Archaeon Sulfolobus solfataricus}

ADEFTARIIVVWHPTALANGYTPVLHVHTASVACRVSELVSKLDPRTGQEAENPQFLKQGDVAIVK

FKPIKPLCVEKYNEFPPLGRFAMRDMGKTVGVGIIVDVKP

>d1flma_b.45.1.1 (A:) FMN-binding protein {Desulfovibrio vulgaris, strain Miyazaki F}
MLPGTFFEVLKNEGVAIATQGEDGPHLVNTWNSYLKVLVDGNRIVVPPVGGMMHKTEANVARDERVL
MTLGSRKVAGRNGPGTGLIRGSAAFRTDGPEFEAIARFKWARAALVITVVSAEQTL

>d1ci0a_b.45.1.1 (A:) Pyridoxine 5'-phosphate oxidase (PNP oxidase) {Baker's yeast
{Saccharomyces cerevisiae}}

FTLNEKQLTDDPIDLFTKWFNEAKEDPRETLPEAITFSSAELPSGRVSSRILLFKELDHRGFTIYSNW
GTSRKAHDIATNPNAIIVFFWKDLQRQVRVEGITEHVNRSETSERYFKTRPRGSKIGAWASRQSDVIK
NREELDELTKQKNTERFKDAEDIPCPDYWGGLRIVPLEIEFWQGRPSRLHDFVYRRKTENDPWKV
VRLAP

>d1dnla_b.45.1.1 (A:) Pyridoxine 5'-phosphate oxidase (PNP oxidase) {Escherichia coli}
GGLRRRDLPADPLTLFERWLSQACEAKLADPTAMVVATVDEHGQPYQRIVLLKHYDEKGMVFYTNL
GSRKAHQIENNPVSLFPWHTLERQVMVIGKAERLSTLEVMKYFHSRPRDSQIGAWVSKQSSRISA
RGILESKFLELKQKFQGEVPLPSFWGGFRVSLEQIEFWQGGHRLHDFLYQRENDWKIDRLAP

>d1eja_b.45.1.2 (A:) FMN-binding protein MTH152 {Archaeon Methanobacterium
thermoautotrophicum}

GSQAAHMMSMDFEDFPVESAHRLTPRPTVMVTTVDEEGNINAAPFSFTMPVPSIDPPVAFASAPD
HHTARNIESTHEFVINITPADIIERMWVTARDIPAGENELEAAGLAWTSSRRVKPPRIVEAPGHLECE
LLRMFEVGDHNLITGSVVSASVRSVAVKEGLLDVESVKPVLHVGGNKFFVVDHVRHVE

>d1i0ra_b.45.1.2 (A:) Ferric reductase {Archaeon Archaeoglobus fulgidus}
MDVEAFYKISYGLYIVTSESNGRCKGQIANTVFQLTSKPVQIACVCLNKENDTHNAVKESGAFGVSVLE
LETPMEFIGRFGFRKSSEFEKFDGVEYKTKTGVPLVTQHAVAVIEAKVVKECDVGTHTLVGEAVD
AEVLKDAEVLTYADYHLMKKGKTPRT

>d1k28d1_b.106.1.1 (D:4-200) Baseplate structural protein gp27 {Bacteriophage T4}
LQRPGYPNLSVKLFDSDAWSNNRFVELAATITTLTMRDSLYGRNEGMLQFYDSKNIHTKMDGNEII
QISVANANDINNVTRIYGGCKHFSVSVDSKGDNIIEIELGTIHSIENLKFGRPFFPDAGESIKEMLVYIY
QDRTLTPAINAINAYVPDIPWTSTFENYLSYVREVALAVGSDKFVFWQDIMGVNMMDY

>d1k28d2_b.106.1.1 (D:201-376) Baseplate structural protein gp27 {Bacteriophage T4}
DMMINQEPYPMIVGEPQLIGQFIQELKYPLAYDFVWLTKSNPHKRDPMKNATIYAHSFLDSSIPMITT
GKGENSIVVSRSGAYSEMRYNGYEEAIRLQTMAYQDYAKCSTIGNFNLTGPKIIFNDSKNQFKTE
FYVDEVIHELNNNSVTHLYMFTNATKLETIDPVKVKNEF

>d1fma1_b.46.1.1 (A:207-314) Methionyl-tRNA^{met} formyltransferase, C-terminal domain
{Escherichia coli}

LSKEEARIDWSLSAAQLERCIRAFNPWPMSWLEIEGQPVKVKASVIDTATNAAPGTILEANKQGIQ
VATGDGILNLLSLQAGKKAMSAQDLLNSRREWFVPGNRLV

>d1ewna_b.46.1.2 (A:) 3-methyladenine DNA glycosylase (AAG, ANPG, MPG) {Human (Homo
sapiens)}

HLTRLGLEFFDQPAVPLARAFGLQVLVRRPLNGTELGRIVETQAYLGPEDAAHSRGGRTPRNRG
MFMKPGTLYVYIYGYFCMNISSQGDGACVLLRALEPLEGLETMRQLRSTLRKGTASRVLKDRELC
SGPSKLCQALAINKSFQDRDLAQDEAVWLERGPLEPSEPAVVAARVGVGHAGEWARKPLRFYVRG
SPWVSVDRAEQD

>d1arb_b.47.1.1 (-) Achromobacter protease {Achromobacter lyticus, strain m497-1}
GVSGSCNIDVVCPEGDGRRDIIIRAVGAYSKSGTLACTGSLVNNTANDRKMFLTAHHCGMGTASTAAS
IVVYWNQNSTCRAPNTPASGANGDGSMSQTQSGSTVKATYATSDFTLLELNNAANPAFNLFWAG

WDRRDQNYPGAIAIHPNVAEKRISNSTSPTSFWAWGGGAGTTHLNVQWQPSGGVTEPGSSGSPYIS
PEKRVLGQLHGGPSSCSATGTNRSDQYGRVFTSWTGGGAAASRLSDWLDPASTGAQFIDGLDS
>d1qq4a_b.47.1.1 (A:) alpha-Lytic protease {Lysobacter enzymogenes, 495}
ANIVGGIEYSINNASLCSVGFVTRGATKGFVTAGHCCTVNATARIGGAVVGTFAARVFPNDRAWVS
LTSAQTLPRVANGSSFVTVRGSTEAAVGAACHSGRTTGYQCGTITAKNVTANYAEGAVRGLTQSNA
CMGRGDSGGSWITSAGQAQGVMSGGNVQSNNGNCGIPASQRSSLFERLQPILSQYGLSLVTG
>d2sga_b.47.1.1 (-) Protease A {Streptomyces griseus, strain k1}
IAGGEAITTGGSRCSLGFNVSVNGVAHALTAGHCTNISASWSIGTRTGTSPFNNDYGIIRHSNPAAADG
RVYLYNGSYQDITTAGNAFVGQAVQRSSTGLRSGSVTGLNATVNYGSSGIVYGMQTNVCAQPGDS
GGSLFAGSTALGLTSGGSGNCRTGGTTFYQPVTEALSAYGATVL
>d1hpga_b.47.1.1 (A:) Glutamic acid-specific protease {Streptomyces griseus}
VLGGGAIYGGGSRCSAAFNVTKGGARYFVTAGHCTNISANWSASSGGSVVGVREGTSFPTNDYGIIVRY
TDGSSPAGTVLDLYNGSTQDISSAANAVVGQAIIKKSSTTKVTSGTVTAVNVTVNYGDGPVYMNVRTT
ACSAGGDSGGAHFAGSVALGIHSGSSGCSGTAGSAIHQPVTEALSAYGVTVY
>d1sgt_b.47.1.1 (-) Trypsin {Streptomyces griseus, strain k1}
VVGGTAAQGEFFPMVRLSMGCCGALYAQDIVLTAHCVSGSGNNTSITATGGVVDLQSGAAVKVRS
TKVLQAPGYNGTGKDWALIKLAQPINQPTLKIATTTAYNQGTFTVAGWGANREGGSQRYLLKANV
PFVSDAACRSAYGNELVANEEICAGYPDTGGVDTCQGDSSGPMFRKDNADEWIQVIVSWGYGCAR
PGYPGVYTEVSTFASAIASAARTL
>d2sfa_b.47.1.1 (-) Serine proteinase {Streptomyces fradiae}
IAGGEAIYAAGGRCSLGFNVRSSSGATYALTAGHCTEIASTWYTNSGQTSLLGTRAGTSFPGNDYGLI
RHSNASAADGRVYLYNGSYRDITGAGNAYVQTVQRSSTGLHSGRVTGLNATVNYGGDIVSGLIQ
TNVCAEPGDSGGALFAGSTALGLTSGGSGNCRTGGTTFQPVTEALSAYGVSIL
>d1sgpe_b.47.1.1 (E:) Protease B {Streptomyces griseus, strain k1}
ISGGDAIYSSSTGRCSLGFNVRSGSTYYFLTAGHCTDGATTTWANSARTTVLGTTSGSSFPNNDYGIVR
YTNTTIPKDGTVGGQDITSAANATVGMATVRRGSTTGTTHSGSVTALNATVNYGGGDVVYGMIRTNV
CAEPGDSGGPLYSGTRAIGLTSGGSGNCSSGGTTFQPVTEALVAYGVSIVY
>d1agja_b.47.1.1 (A:) Epidermolytic (exfoliative) toxin A {Staphylococcus aureus}
EVSAAEIKKHEEKWNKYYGVNAFNLPKELFSKVDEKDRQKYPYNTIGNVFVKGQTSATGVLIGKNT
VLTNRHIAKFANGDPSKVSFRPSINTDDNGNTETPYGEYEVKEILQEPFGAGVDLALIRLKPQNGVS
LGDKISPAKIGTNDLKDGDKLELIGYPFDHKVNQMHRSEIELTTLRGLRYYGFTVPGNSGSGIFNSN
GELVGIHSSKVSHLDREHQINYGVGIGNYVKRIINEKNE
>d1qtfa_b.47.1.1 (A:) Exfoliative toxin B {Staphylococcus aureus}
KEYSAEEIRKLKQKFEVPPPTDKELYTHITDNARSPYNSVGTVFVKGSTLATGVLIGKNTIVTNYHVAR
EAAKNPSNIIFTPAQNRDAEKNEFPTPYGKFEAEIKESPYGQGLDLAIKLPNEKGESAGDLIQPAN
IPDHIDIAKGDKYSLGYPYNSAYSLSYQSIEMFNDSQYFGYTEVGNSSGIFNLKGELIGHSGKGGQ
HNLPIGVFFNRKISSLYVDNTFGDTLGNLKKRAKLDK
>d1ezxc_b.47.1.2 (C:) Trypsin(ogen) {Cow (Bos taurus)}
CGGSLINSQWVVSAAHCYKSGIQVRLGEDNINVEGNEQFISASKSIVHPSYNSNTLNNDIMLIKLS
AASLNSRVASISLPTSCASAGTQCLISGWGNTKSSGTSYDPVLKCLKAPILSDSSCKSAYPGQITSNMFC
AGYLEGGKDSCQGDSSGPPVCSGKLQGIVSWGSGCAQKNKPGVYTKVCNYVSWIKQTIASN
>d1hj9a_b.47.1.2 (A:) Trypsin(ogen) {Cow (Bos taurus)}
IVGGYTCCGANTVPYQVSLNSGYHFCGGSLINSQWVVSAAHCYKSGIQVRLGEDNINVEGNEQFISAS
KSIVHPSYNSNTLNNDIMLIKLSAASLNSRVASISLPTSCASAGTQCLISGWGNTKSSGTSYDPVLKLC

LKAPILSDSSCKSAYPGQITSNMFCAGYLEGGKDSCQGDSSGGPVVCSGKLGIVSWGSGCAQKNKPGV
YTKVCNYVSWIKQTIASN

>d1mcta_b.47.1.2 (A:) Trypsin(ogen) {Pig (Sus scrofa)}

IVGGYTCAANSIPYQVSLNSGSHFCGGSLNSQWVVSAAHCYKSRIQVRLGEHNIDVLEGNEQFINAA
KIITHPNFNGNTLDNDIMLIKLSPPATLNSRVATVSLPRSCAAAGTECLISGWGNTKSSGSSYPSLLQC
LKAPVLSNSSCKSSYPGQITGNMICVGFLOGGKDSCQGDSSGGPVVCSGKLGIVSWGSGCAQKNKPG
VYTKVCNYVNWIIQQTIAAN

>d1f7za_b.47.1.2 (A:) Trypsin(ogen) {Rat (Rattus norvegicus)}

IVGGYTQENSVPYQVSLNSGYHFCGGSLINDQWVVSAAHCYKSRIQVRLGEHNINVLGNEQFVNA
AKIHKHPNDRKTLNNDIMLIKLSPPVKNARVATVALPSSCAPAGTQCLISGWGNTLSSGVNEPDL
QCLDAPLLPQADCEASYPGKITDNMVCVGFLEGGKDSCQGDSSGGPVVCSGKLGIVSWGSGCALPD
NPGVYTKVCNYVDWIQDTIAAN

>d1trna_b.47.1.2 (A:) Trypsin(ogen) {Human (Homo sapiens)}

IVGGYNCEENSVPYQVSLNSGYHFCGGSLINEQWVVSAGHCYKSRIQVRLGEHNIEVLGNEQFINAA
KIIRHPQYDRKTLNNDIMLIKLSRAVINARVSTISLPTAPPATGKCLISGWGNTASSGADYPDELQC
LDAPVLSQAKCEASYPGKITSNMFCVGFLEGGKDSCQGDSSGGPVVCSGKLGIVSWGSGCAQKNK
GVYTKVYNYVKWIKNTIAANS

>d1h4wa_b.47.1.2 (A:) Trypsin(ogen) {Human (Homo sapiens), trypsin IV (brain isoform)}

IVGGYTCEENSLPYQVSLNSGSHFCGGSLISEQWVVSAAHCYKTRIQVRLGEHNIKVLGNEQFINAV
KIIRHPKYNRDLDNDIMLIKLSPPAVINARVSTISLPTAPPAAGTECLISGWGNTLSFGADYPDELKC
LDAPVLTQAECKASYPGKITNSMFCVGFLEGGKDSCQRDSGGPVVCSGKLGIVSWGSGCAWKNR
PGVYTKVYNYVDWIKDTIAANS

>d1a0ja_b.47.1.2 (A:) Trypsin(ogen) {North atlantic salmon (Salmo salar)}

IVGGYECRKNASYSYQASLQSGYHFCGGSLISSTWVVSAAHCYKSRIQVRLGEHNIAVNEGTEQFIDSVK
VIMHPSYNSRNLNNDIMLIKLSKPSLNSYVSTVALPSSCASSGTRCLVSGWGNLSGSSSNYPDLRCL
DLPISSSSCNSAYPGQITSNMFCAGFMEGGKDSCQGDSSGGPVVCSGKLGIVSWGSGCAQRNKPGV
YTKVCNYRSWISSTMSSN

>d1hj8a_b.47.1.2 (A:) Trypsin(ogen) {North atlantic salmon (Salmo salar)}

IVGGYECKAYSQPHQVSLNSGYHFCGGSLVNNWVVSAAHCYKSRVEVRLGEHNIKVTEGSEQFISS
RVIRHPNYSSYNIDNDIMLIKLSKPATLNTYVQPVALPTSCAPAGTMCTVSGWGNLMSSTADSNKLQ
CLNIPILSYSDCNSYPMITNAMFCAGYLEGGKDSCQGDSSGGPVVCSGKLGIVSWGSGCAEPGNP
GVYAKVCIFNDWLTSTMASY

>d1gdna_b.47.1.2 (A:) Trypsin(ogen) {Mold (Fusarium oxysporum)}

IVGGTSASAGDFPFIVSISRNGGPWCGSLLNANTVLTAACHCVSGYAQSGFQIRAGSLRSTSGGITSSLS
SVRVHPSYSGNNNDLAILKLSSTIPSGGNIGYARLAASGSDPVAGSSATVAGWGATSEGGSSTPVNLK
VTVPIVSRATCRAQYGTSAITNQMFCAVSSGGKDSCQGDSSGGPIVDSNTLIGAVSWGNGCARPNYS
GVYASV GALRSFIDTYA

>d1pytd_b.47.1.2 (D:) (alpha,gamma)-chymotrypsin(ogen) {Cow (Bos taurus)}

CGAPIFQPNLSARVVGEDAIPHSWPWQISLQYLRDNTWRHTCGGTLITPNHVLTAACHISNTLT
VALGKNNLEVEDEAGSLYGVDTIFVHEKWNFLVRNDIALIKLAETVELGDTIQVACLPSGSLLPQ
DYPCFVTGWGRLYTNGPIAAELQQLQPVVDYATCSQRDWWGTTVKETMVCAGGDGVISACNGDS
GGPLNCQADGQWDVRGIVSFGSGLSCNTFKKPTVFTRVSAIDWINQKLQL

>g1gg6.1 b.47.1.2 (A,B,C:) (alpha,gamma)-chymotrypsin(ogen) {Cow (Bos taurus)}

CGVPAIQPVLXIVNGEEAVPGSWPWQVSLQDKTGFHFCGGSLINENWVVTAAHCGVTTSDVVVAGE

FDQGSSEKIQKLIKIAKVFKNKYNLSLTINNDITLLKLSTAASFSQTVSAVCLPSASDDFAAGTTCVTTG
WGLTRYXANTPDRLQQASLPLLSNTNCKKYWGTKIKDAMICAGASGVSSCMGDSGGPLVCKKNGA
WTLVGIVSWGSSTCSTSTPGVYARVTALVNWVQQTLAAN

>d1eq9a_ b.47.1.2 (A:) (alpha,gamma)-chymotrypsin(ogen) {Red fire ant (Solenopsis
invicta)}

IVGGKDAPVGKYPYQVSLRLSGSHRCGASILDNNNVLTAAHCVDGLSNLNRKLVHVGNTNYLSESGDV
YDVEDAVVNKNYDDFLLRNDVALVHLTNPIKFNDLVQPIKLNSTNDEDELESNPCTLTGWGSTRLLGGNT
PNALQEIELIVHPQKQCERDQWRVIDSHICTLTKRGEACHGDSGGPLVANGAQIGIVSFGSPCALGE
PDVYTRVSSFVSWINANLKK

>d1npma_ b.47.1.2 (A:) Neuropsin {Mouse (Mus musculus)}

ILEGRECIPHSQPWQAALFQGERLICGGVLVGDWRVLTAAHCKKQKYSVRLGDHLSQRSRQPEQEIQ
VAQSIQHPCYNNNSNPEDHSHDIMLIRLQNSANLGDVKVPVQLANLCPKVGQKCIISGWGTVTSPQEN
FPNTLNCAEVKIYSQNK CERAYPGKITEGMVCAGSSNGADTCQGDSGGPLVCDGMLQGITSWGS DPC
GKPEKPGVYTKICRYTTWIKKTM

>d1azza_ b.47.1.2 (A:) Crab collagenase {Atlantic sand fiddler crab (Uca pugilator)}

IVGGVEAVPNSWPHQAALFIDDMYFCGGSLISPEWILTAAHCMDGAGFVDVVLGAHNIREDEATQVT
IQSTDFTVHENYNSFVISNDIAVIRLPVPVTLTAAIATVGLPSTDVGVGTVVPTPTGWGLPSDSALGISD
VLRQVDVPIMSNADCAVYIVTDGNICIDSTGGKGTGNGDSGGPLNYNGLTYGITSFGAAAGCEAGY
PDAFTRVTYFLDWIQTQTGITP

>d2hlca_ b.47.1.2 (A:) HL collagenase {Common cattle grub (Hypoderma lineatum)}

IINGYEAYTGLFPYQAGLDITLQDQRRVWCGGSLIDNKWILTAAHCVHDAVSVVVYLGSAVQYEGEAV
VNSERIISHSMFNPDTYLNDVALIKIPHVEYTDNIQPIRLPSGEELNNKFENIWATVSGWQSN TDTV
ILQYTYNLVIDNDRCAQEYPPGIIVESTICGDTSDGKSPCFGDSGGPFVLSDKNLLIGVVSFVSGAGCES
GKPVGFSRVTSYMDWIQNTGIKF

>g1h8d.1 b.47.1.2 (L:,H:) Thrombin {Human (Homo sapiens)}

EADCGLRPLFEKKSLEDKTERELLESYISXIVEGSDAEIGMSPWQVMLFRKSPQELLCGASLISDRWV
LTAAHCLLYPPWDKNFTENDLLVRIGKHSRTRYERNIEKISMLEKIYIHPRYNWRENLDRDIALMKL
KKPVAFSDYIHPVCLPDRETAASLLQAGYKGRVTGWGNLKETGQPSVLQVVNLPIVERPVCKDSTRIR
ITDNMFCAGYKPDEGKRGDACEGDSGGPFV MKSPFNRRWYQMGIVSWGEGCDRDGKYGFYTHVF
RLKKWIKVIDQFGCSSVLIVVC

>g1jou.1 b.47.1.2 (A:,B:) Thrombin {Human (Homo sapiens)}

SEYQTFNPRFTFGSGEADCGLRPLFEKKSLEDKTERELLESYIDGXIVEGSDAEIGMSPWQVMLFRKS
PQELLCGASLISDRWVLTAAHCLLYPPWDKNFTENDLLVRIGKHSRTRYERNIEKISMLEKIYIHPRY
NWRENLDRDIALMKLKKPVAFSDYIHPVCLPDRETAASLLQAGYKGRVTGWGNLKETWTANVKGK
QPSVLQVVNLPIVERPVCKDSTRIRITDNMFCAGYKPDEGKRGDACEGDAGGPFV MKSPFNRRWYQ
MGIVSWGEGCDRDGKYGFYTHVFRLKKWIKVIDQFGE

>g1vr1.1 b.47.1.2 (L:,H:) Thrombin {Human (Homo sapiens)}

ADCGLRPLFEKKSLEDKTERELLESYIXIVEGSDAEIGMSPWQVMLFAKHRRSPGERFLCGASLISDR
WVLTAAHCLLYPPWDKNFTENDLLVRIGKHSRTRYERNIEKISMLEKIYIHPRYNWRENLDRDIALM
KLKKPVAFSDYIHPVCLPDRETAASLLQAGYKGRVTGWGNLKETWTANVKGKQPSVLQVVNLPIVE
RPVCKDSTRIRITDNMFCAYYKPDEGKRGDACEGDSGGPFV MKSPFNRRWYQMGIVSWGEGCDRD
GKYGFYTHVFRLKKWIKVID

>g2hnt.1 b.47.1.2 (L:,C:,E:,F:) Thrombin {Human (Homo sapiens)}

ADCGLRPLFEKKSLEDKTERELLESYIDXIVEGSDAEIGMSPWQVMLFRKSPQELLCGASLISDRWV

TAAHCLLYPPWDKNFTENDLLVRIGKHSXEKISMLEKIYIHPRYNWRENLDRDIALMKLKKPVAFSD
YIHPVCLPDRETAASLLQAGYKGRVTGWGXPSVLQVVNLPIVERPVCKDSTRIRITDNMFCAGYKPDE
GKRGDACEGDSGGPFVMKSPFNRRWYQMGIVSWGEGCDRDGKYGFYTHVFRLKKWIQKVIDQ
>g1etr.1_b.47.1.2 (L,H:) Thrombin {Cow (Bos taurus)}
TFGAGEADCGLRPLFEKKQVQDQTEKELFESYIEGRXIVEGQDAEVGLSPWQVMLFRKSPQELLCGA
SLISDRWVLTAAHCLLYPPWDKNFTVDDLLVRIGKHSRTRYERKVEKISMLDKIYIHPRYNWKENLD
RDIALLLKLRPIELSDYIHPVCLPDKQTAAKLLHAGFKGRVTGWGNRRETWTTSVAEVQPSVLQVVN
LPLVERPVCKASTRIRITDNMFCAGYKPGEGKRGDACEGDSGGPFVMKSPYNNRWYQMGIVSWGEG
CDRDGKYGFYTHVFRLKKWIQKVIDRLGS
>d1fona_b.47.1.2 (A:) Procarboxypeptidase A-S6 subunit III (zymogen E) {Cow (Bos
taurus)}
SWSWQVSLQYEKDGAFHHTCGGSLIAPDWVVTAGHCISTSRTYQVVLGEYDRSVLEGSEQVIPINAG
DLFVHPLWNSNCVACGNLALVKLSRSAQLGDKVQLANLPPAGDILPNEAPCYISGWGRLYTGGPLP
DKLQQLPTVDYEHCSQWDWWGITVKKTMVCAGGDTRSGCNGDSGGPLNCPAADGSWQVHGV
TSFVSAFGCNTIKKPTVFTRVSAFIDWIDETIASN
>d1pytc_b.47.1.2 (C:) Procarboxypeptidase A-S6 subunit III (zymogen E) {Cow (Bos taurus)}
SRPSSRVVNGEDAVPYSWSWQVSLQYEKDGAFHHTCGGSLIAPDWVVTAGHCISTSRTYQVVLGEY
DRSVLQGSEQVIPINAGDLFVHPLWNSNCVACGNLALVKLSRSAQLGDKVQLANLPPAGDILPNEAP
CYISGWGRLYTGGPLPDKLQEQALLPVVDYEHCSQYDWWGITVKKTMVCAGGDTRSGCDGDSGGPL
NCPAADGSWQVHGVTSFVSAFGCNTIKKPTVFTRVSAFIDWINETIASN
>d1ppfe_b.47.1.2 (E:) Elastase {Human (Homo sapiens)}
IVGGRRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNLSRREPT
RQVFAVQRIFENGYDPVNLNDIVILQLNGSATINANVQVAQLPAQGRRLGNGVQCLAMGWLLGRN
RGIASVLQELNVTVVTSLCRRSNVCTLVRGRQAGVCFGDSGSPLVCNGLIHGIASFVRGGCASGLYPDA
FAPVAQFVNWIDSIIQ
>d1brup_b.47.1.2 (P:) Elastase {Pig (Sus scrofa)}
VVGGEDARPNWPWQVSLQYDSSGQWRHTCGGTLVDQSWVLTAAHCISSRTRYRVVLGRHSLSTNE
PGSLAVKVKLVVHQDWNNSQLSNGNDIALLLKASPVSITDKIQLGCLPAAGTILPNNYVCYVTGWG
RLQTNGASPDILQQGQLLVVDYATCSKPGWWGSTVKTNMICAGGDGISSCNGDSGGPLNQCQANG
QWQVHGVISFGSSLGCNYYHKPSVFTVRSNYIDWINSVIANN
>d1qnja_b.47.1.2 (A:) Elastase {Pig (Sus scrofa)}
VVGTEAQRNSWPSQISLQYRSGSSWAHTCGGTLIRQNWVMTAAHCVDRELTFRVVVEHNLNQN
DGTEQYVGVQKIVVHPYWNDDVAAGYDIALRLAQSVTLNSYVQLGVLPRAGTILANNSPCYITGW
GLTRTNGQLAQLTQQAYLPTVDYAICSSSYWGSTVKNSMVCAGGDGVRSGCQGDSSGGLHCLVNGQ
YAVHGVTSFVSRLGCNVTRKPTVFTRVSAYISWINNVIASN
>d1elt_b.47.1.2 (-) Elastase {Salmon (Salmo salar)}
VVGGRVAQPNWPWQISLQYKSGSSYHTCGGSLIRQGWVMTAAHCVDARSARTWRVVLGEHNLNTN
EGKEQIMTVNSVFIHSGWNSDDVAGGYDIALRLNTQASLNSAVQLAALPPSNQILPNNNPCYITGW
GKTSTGGPLSDSLKQAWLPSVDHATCSSSGWWGSTVKTTMVCAGGGANSGCNGDSGGPLNQCQVNG
SYYVHGVTSFVSSGCNASKKPTVFTRVSAYISWMNGIM
>d1ekbb_b.47.1.2 (B:) Enteropeptidase (enterokinase light chain) {Cow (Bos taurus)}
IVGGSDSREGAWPWVVALYFDDQVCGASLVSRLVLSAAHCVYGRNMEPSKWKAVLGLHMASNL
TSPQIETRLIDQIVINPHYNKRRKNNDIAMMHLEMKVNYTDYIPICLPEENQVFPFGRICSIAGWG
ALIYQGSTADVLQEADVPLLSNEKCCQQMPEYNITENMVCAGYEAGGVDSQCQGDSSGGLMCQENNR

WLLAGVTSFGYQCALPNRPGVYARVPRFTEWISFLH

>d1a7s_ b.47.1.2 (-) Heparin binding protein, HBP {Human (Homo sapiens)}

IVGGRKARPRQFPFLASIQNQRHFCCGALIHARFVMTAASCFFPGVSTVVLGAYDLRRRERQSRQTFSSMSSENGYDPPQNLNDLMLLQLDREANLTSSVTILPLPLQATVEAGTRCQVAGWGSQRSGGRLSRFPRFVNVTVTPEDQCRPNVCTGVLTRRGGICNGDGGTPLVCEGLAHGVASFSLGPCGRGPDFFTRVALFRDWIDGVLNNPGPGA

>d1a0la_ b.47.1.2 (A:) beta-Tryptase {Human (Homo sapiens)}

IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGSLIHPQWVLTAAHCVGPDKDLAALRVQLREQHLYYQDQLLPVSRIVHPQFYTAQIGADIALLEEPVKVSSHVHTVTLPPASETFFPPGMPCWVTGWGDVDNDERLPPFPFLKQVKVPIMENHICDAKYHLGAYTGDDVVRIVRDDMLCAGNTRRSDSCQGDSSGPLVCKVNGTWLQAGVVSWECAQPNRPGIYTRVYTYLDWIHHYVPPK

>d1cgha_ b.47.1.2 (A:) Cathepsin G {Human (Homo sapiens)}

IIGGRESRPHSRPYMAYLQIQSPAGQSRCCGFLVREDFVLTAAHCWGSNINVTLGAHNIQRRENTQQHITARRAIRHPQYNQRTIQNDIMLLQLSRRVRRNRNPNVALPRAQEGLRPGTLCTVAGWGRVSMRRGTDTLREVQLRVQRDRQCLRIFGSYDPRRQICVGDRRERKAFAFKGDSGGPLLCNNVAHGIVSYGKSSGVPPEVFTRVSSFLPWIRTTMRS

>d1danh_ b.47.1.2 (H:) Coagulation factor VIIa {Human (Homo sapiens)}

IVGGKVCPCGECPWQVLLLVNGAQLCGGTLINTIWWVSAAHCFDKIKNWRNLIAVLGEHDLSEHDGDEQSRRVAQVIIPSTYVPGTTNHDIALLRHLHQPVVLTDHVVPLCLPERTFSERTLAFVRFSLVSGWQQLLDRGATALELMVLNVPRLMTQDCLQSRKVGDSNPITEYMFCAQYSDGSKDCKGDSGGPHATHYRGTWYLTGIVSWGQCATVGHFGVYTRVSQYIEWLQKLMRSEPRPGVLLRAPFP

>d3rp2a_ b.47.1.2 (A:) Chymase (Proteinase II) {Rat (Rattus rattus)}

IIGGVESIPHSRPMAYLHDIVTEKGLRVICGGFLISRQFVLTAAHCCKGREITVILGAHDVRKRESTQQKIKVEKQIIHESYNSVNLHDIMLLKLEKKVELTAVNVVPLPSPSDFIHPGAMCWAAGWGKTGVRDPTSYTLREVELRIMDEKACVDYRYEYKFQVCVGSPTTLRAAFMGDSGGPLLCAGVAHGIVSYGHPDAKPPAIFTRVSTYVPWINAVIN

>d1klt_ b.47.1.2 (-) Chymase (Proteinase II) {Human (Homo sapiens)}

IIGGTESKPHSRPYMAYLEIVTSNGPSKFCGGFLIRRFVLTAAHCAGRSITVTLGAHNITEEEDTWQKLEVIKQFRHPKYNTSTLHHDIMLLKLEKASLTLAVGTLFPFSQFNFPVPPGRMCRVAGWGRTGVLKPGSDTLQEVLRLMDPQACSHFRDFDHLQLCVGNPRKTKSAFKGDSGGPLLCAGVAQGIVSYGRSDAKPPAVFTRISHYRPWINQILQAN

>g2pka.1 b.47.1.2 (A:,B:) Kallikrein A {Pig (Sus scrofa)}

IIGGRECEKNSHPWQVAIYHYSSFQCGGVLVNPKWVLTAAHCCKNDNYEVWLGRHNLFENENTAQFFGVTADFPHPGFNLXADGKDYSHDLMLLRLQSPAKITDAVKVLELPTQEPELGSTCEASGWGSIEPGPDDFEFPDEIQCVQLTLLQNTFCADAHDPKVTESMLCAGYLPGGKDTMCGDSGGPLICNGMWQGITSWGHTPCGSANKPSIYTKLIFYLDWIDDTITENP

>d1ton_ b.47.1.2 (-) Tonin {Rat (Rattus rattus)}

IVGGYKCEKNSQPWQVAVINEYLCGGVLIDPSWVITAHCYSNNYQVLLGRNNLFKDEPFQARRLVRQSFRRHPDYIPLIVTNDTEQPVHDHSDNLMLLHLSEPADITGGVKVIDLPTKEPKVGSTCLASGWGSTNPSEMVVSHDLQCVNIHLLSNEKCIETYKDNVTDVMLCAGEMEGGKDTACAGDSGGPLICDGVLQGITSGGATPCAKPKTPAIYAKLIKFTSWIKKVMKENP

>d1sgfa_ b.47.1.2 (A:) 7S NGF protease subunits {Mouse (Mus musculus)}

NSQPWHVAVYRFNKYQCGGVLLDRNWVLTAAHCYNDKYQVWLKNNFLEDEPSDQHRLVSKAIPHPDFNMSLLNEHTPQPEDDYSNDLMLLRLSKPADITDVVKPITLPTTEPKLSTCLASGWGSTTPIK

YPDDLQCVNLKLLPNEDCDKAHEMKVTDAMLCAGEMDGGSYTCEHDSGGPLICDGILQGITSWGPE
PCGEPTEPSVYTKLIKFSSWIRETMANNP

>d1sgfg_b.47.1.2 (G:) 7S NGF protease subunits {Mouse (Mus musculus)}

IVGGFKCEKNSQPWHVAVYRYTQYLCGGVLLDPNWWLTAACHCYDDNYKVWLGKNNLFKDEPSAQH
RFVSKAIPHPGFNMSLMRFLEYDYSNDLMLLRLSKPADITDTVKPITLPTTEPKLGSTCLASGWGSIT
PTKFQFTDDLYCVNLKLLPNEDCAKAHIEKVTDAMLCAGEMDGGKDTCKGDSGGPLICDGVLQGITS
WGHTPCGEPDMPGVYTKLNKFTSWIKDTMAKNP

>d1dlea_b.47.1.2 (A:) Factor B {Human (Homo sapiens)}

ADPDESQSLSLCGMVWEHRKGTDYHKQPWQAKISVIRPSKGHESCMGAVVSEYFVLTAACHCFTVDD
KEHSIKVSVGGEKRDLEIEVVLVFNPNYINGKKEAGIPEFYDYDVALIKLNKLYGQTIRPICLPCTE
GTTTRALRLPPTTTCQQKEELLPAQDIKALFVSEEEKLTRKEVYIKNGDKKGCERDAQYAPGYDK
VKDISEVVTPRFLCTGGVSPYADPNTCRGDSGGPLIVHKRSRFIQGVISWGVVDVCKNQKRQKQVPA
HARDFHINLFQVLPWLKEKLQDEDLGF

>d1bio_b.47.1.2 (-) Factor D {Human (Homo sapiens)}

ILGGREAEAHARPYMASVQLNGAHLCCGGVLAEQWVLSAAHCLEDAADGKVQVLLGAHLSQPEPS
KRLYDVLRAVPHPDSQPDTIDHDLQLLQSEKATLGPVLRPLPWQRVDRDVAPGTLCDVAGWGIVN
HAGRRPDSLQHVLLPVLDRATCNRRTHHDGAITERLMCAESNRRDSCKGDSGGPLVCGGVLEGVVT
SGSRVCGNRKKPGIYTRVASYAAWIDSVLA

>g1rtf.1_b.47.1.2 (A;B:) Two-chain tissue plasminogen activator (TC)-T-PA {Human (Homo sapiens)}

TCGLRQYSXIKGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAACHCFQERFPPHHLTV
ILGRTYRVVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALQLKSDSSRCAQESSVVRTVCLPPADLQL
PDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQAN
LHDACQGDGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNMRP

>d1a5ia_b.47.1.2 (A:) Single chain tissue plasminogen activator {Vampire bat (Desmodus rotundus)}

TCGLRKYKEPQLHSTGGLFTDITSHPWQAAIFAQNRSSGERFLCGGILISSCWVLTAAHCFQESYLP
DQLKVVLGRTYRVKPGEEEQTFKVKYIVHKEFDDDTYNNDIALQLKSDSPQCAQESDSVRAICLP
EANLQLPDWTECELSGYGKHKSSSPFYSEQLKEGHVRLYPSSRCAPKFLFNKTVTNMLCAGDTRS
GEIYPNVHDACQGDGGPLVCMNDNHMTLLGIISWGVGCGEKDVPVYTKVTNYLWIRDNMHL

>d1bqya_b.47.1.2 (A:) Plasminogen activator from snake venom, TSV-PA {Chinese green tree viper (Trimeresurus stejnegeri)}

VFGGDECNINEHRSLVFLFNSNGFLCGGTLINQDWVVTAAHCDSNNFQLLFGVHSHKILNEDEQTR
DPKEKFFCPNRKKDDEVDKDIMLIKLDSSVSNSEHIAPLSLPPSSVSVCRIMGWGKTIPTKEIYP
DVPHCANINILDHAVCRTAYSWRQVANTTLCAGILQGGRTCHFDSGGPLICNGIFQGIVSWGPHPC
GQPGEVYTKVFDYLDWIKSIIAGNKDATCPP

>d1ao5a_b.47.1.2 (A:) Kallikrein-13 {Mouse (Mus musculus)}

VVGGFNCEKNSQPWQVAVYYQKEHICGGVLLDRNWWLTAACHCYVDQYEVWLGKNNLFQEEPSAQH
RLVSKSFPHPGFNMSLLMLQTIPPGADFSDDLMLLRLSKPADITDVVKPIALPTKEPKPGSKCLASG
WGSITPTRWQKPDDLQCVFITLLPNENCAKVYLQKVTDVMLCAGEMGGKDTCRDDSGGPLICDGI
LQGTTSYGPVPCGKPGVPAIYTNLIKFNKDTMMKNA

>d1pfxc_b.47.1.2 (C:) Coagulation factor IXa, protease domain {Pig (Sus scrofa)}

IVGGENAKPGQFPWQVLLNGKIDAFCCGSIINEKVVVTAACHCIEPGVKITVVAGEYNTTEETEPTEQR
RNVIRAIPHHSYNATVNKYSHDIALLELDEPLTNSYVTPICIADKEYTNIFLKFSGSYVSWGVRVNR

GRSATILQYLKVLVDRATCLRSTKFTIYSNMFCAGFHEGGKDCSCQGDSSGGPHVTEVEGTSFLTGIIS
WGECAVKGKYGIYTKVSRYVNWIKETKLT

>d1rfna_b.47.1.2 (A:) Coagulation factor IXa, protease domain {Human (Homo sapiens)}
VVGGEDAKPGQFPWQVVLNGKVDAFCGGSIVNEKWIVTAAHCVETGVKITVVAGEHNIEETEHETEQ
KRNVIIRIIPHHNYNAAINKYNHDIALLELDEPLVLSYVTPICIADKEYTNIFLKFSGSYVSGWGRVFIH
KGRSALVQLYLRVPLVDRATCLRSTKFTIYNMFCAGFHEGGRDSCQGDSSGGPHVTEVEGTSFLTGIIS
SWGEECAMKGYGIYTKVSRYVNWIKETKLT

>d1fjsa_b.47.1.2 (A:) Coagulation factor Xa (Christmas factor), protease domain {Human (Homo sapiens)}
IVGGQECKDGECPWQALLINEENEGFCGGTILSEFYILTAACHCLYQAKRFKVRVGDNRNTEQEEGGAEAV
HEVEVVIKHNRFKETYDFDI AVLRLKTPITFRMNVAPACLPERDWAESTLMTQKTGIVSGFGRTHE
KGRQSTRKMLLEVPYVDRNSCKLSSSFITQNMFCAGYDTKQEDACQGDSSGGPHVTRFKDITYFVTGI
VSWGEGCARKGKYGIYTKVTAFLKWIDRSMKT

>d1kigh_b.47.1.2 (H:) Coagulation factor Xa (Christmas factor), protease domain {Cow (Bos taurus)}
IVGGRDCAEGECPWQALLVNEENEGFCGGTILNEFYVLTAACHLHQAQRFTVRVGDNRNTEQEEGNE
MAHEVEMTVKHSRFBKETYDFDI AVLRLKTPIRFRNVAPACLPEKDWAESTLMTQKTGIVSGFGR
THEKGRSSTLKMLEVPYVDRSTCKLSSSFITPNMFCAGYDTQPEDACQGDSSGGPHVTRFKDITYFV
TGIVSWGEGCARKGKFGVYTKVSNFLKWIDKIMKARAGAAGS

>d1fxya_b.47.1.2 (A:) Coagulation factor Xa-trypsin chimera {Synthetic, based on Homo sapiens sequence}
IVGGYNCKDGEVPWQALLINEENEGFCGGTILSEFYILTAACHCLYQAKRFKVRVGDNRNTEQEEGGAEAV
HEVEVVIKHNRFKETYDFDI AVLRLKTPITFRMNVAPASLPTAPPATGKCLISGWGNTASSGADYP
DELQCLDAPVLSQAKCEASYPGKITSNMFCVGFLEGGKDCSCQGDSSGGPVVCNGQLQGVVSWGDCGA
QKNKPGVYTKVYNYVKWIKNTIAANS

>d1elva1_b.47.1.2 (A:410-668) Complement C1s protease, catalytic domain {Human (Homo sapiens)}
CGVPREPFEKQRIIGSDADIKNFPWQVFFDNPWAGGALINEYWVLTAACHVVEGNREPTMYVVGST
SVQTSRLAKSKMLTPEHVFIHPGWKLLAVPEGRTNFDNDIALVRLKDPVKMGPTVSPICLPGTSSDY
NLMDGDLGLISGWGRTEKRDRAVRLKAARLPVAPLRKCKEVKVEKPTADAEAYVFTPNMICAGGEK
GMDSCKGDSSGGAFAVQDPNDKTKFYAAGLSVWGPQCGTYGLYTRVKNYVDWIMKTMQENS

>d1autc_b.47.1.2 (C:) Activated protein c (autoprothrombin IIa) {Human (Homo sapiens)}
LIDGKMTRRGDSPWQVVLDSKKKLACGAVLIHPSWVLTAAHCMDESKLLVRLGEYDLRRWEKW
ELDLDIKEVFFVHPNYSKSTTDNDIALHQAQATLSQTIVPICLPDGLAERELNQAQETLVTGWGY
HSSREKEAKRNRFTVLFNFIKIPVPHNECSEVMNSMSENMLCAGILGDRQDACEGDSGGPMVASF
HGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRD

>d1fuja_b.47.1.2 (A:) Myeloblastin, PR3 {Human (Homo sapiens)}
IVGGHEAQPHSRPYMASLQMRGNPQSHFCGGTLIHPFVLTAAHCLRDIPQRLVNVVLGAHNVRTQE
PTQQHFSVAQVFLNNYDAENKLNLDILLIQLSSPANLSASVATVQLPQQDQPVPHGTQCLAMGWGRV
GAHDPPAQLVQLNVTVVTFPCRPHNICTFVPRRKAGICFGDSSGGPLICDGIHQGIDSFVIWGCATRLF
PDFFTRVLYVDWIRSTLR

>g1c5y.1_b.47.1.2 (A,B:) Urokinase-type plasminogen activator (LMW U-PA), catalytic domain {Human (Homo sapiens)}
LKFQCGQKTXIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLMSPCWVISATHCFIDYPPKEDYI

VYLGSRSLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMY
NDPQFGTSCEITGFGKEASTDYLYPEQLKMTVVVKLISHRECQPHYGSEVTTKMLCAADPQWKTD
SCQGDSSGGLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHSTKEE

>d1ddja_b.47.1.2 (A:) Plasmin(ogen), catalytic domain {Human (Homo sapiens)}

SFDCGKQPVEPKKCPGRVVGCVAPHSWPWQVSLRTRFRGMHFCGGTLISPEWVLTAAHCLEKSPR
PSSYKVLGAHQEVNLEPHVQEIEVSRLFLEPTRKDIALKLSPPAVITDKVIPACLSPSNYVVADRTEC
FITGWGETQGTGAGLLKEAQLPVIENTKVCNRYEFLNGRVQSTELCAGHLAGGTDSCQGDAGGPLVC
FEKDXYILQGVTSWGLGCARPKNKPGVYVRVSRFVTWIEGVMRNN

>d1fi8a_b.47.1.2 (A:) Granzyme B {Rat (Rattus norvegicus)}

IIGGHEAKPHSRPYMAYLQIMDEYSGSKKCGGLIREDFVLTAHCSGSKIQVTLGAHNIKEQEKMQQ
IIPVVKIIPHPAYNSKTISNDIMLLKLSKAKRSSAVKPLNLP RRNVKVKPGDVCYVAGWGKLGPMGK
YSDTLQEVELTVQEDQKCESYLKNYFDKANEICAGDPKIKRASFRGDSGGPLVCKKVAAGIVSYGQND
GSTPRAFTKVSTFLSWIKKTMKK

>d1iaua_b.47.1.2 (A:) Granzyme B {Human (Homo sapiens)}

IIGGHEAKPHSRPYMAYLMIWDQKSLKRCGGFLIRDDFVLTAHCSGSSINVTLGAHNIKEQEPTQQ
FIPVKRPIPHPAYNPKNFSNDIMLLQLERKAKRTRAVQPLRLPSNKAQVKPGQTCVAGWGQTAPLG
KHSHTLQEVKMTVQEDRKCESDLRHYYDSTIELCVGDPEIKKTSFKGDSGGPLVCNKVAQGIVSYGR
NNGMPRACTKVSSFVHWIKKTMKR

>d1eufa_b.47.1.2 (A:) Duodenase {Cow (Bos taurus)}

IIGGHEAKPHSRPYMAFLLFKTSKGSHICGGFLVREDFVLTAHCLGSSINVTLGAHNIMERERTQQVI
PVRRIPIHPDYNDETLANDIMLLKLTRKADITDKVSPINLPRSLAEVKPGMMCSVAGWGRLGVNMP
STDKLQEVLDLEVQSEEKCIARFKNYIPFTQICAGDPSKRKNSFSGDSGGPLVCNGVAQGIVSYGRNDG
TTPDVYTRISSFLSWIHSTMR

>g1fiw.1 b.47.1.2 (L:,A:) Beta-acrosin {Sheep (Ovis aries)}

TTCDGPCGVRFRQNXIIGGQDAAHGAWPVMVSLQIFTYHNNRRYHVCGGSLLNSQWLLTAAHCFRI
KKKVTDWRLIFGAKEVEWGTNKPVKPPLQERYVEKIIIHEKYSASSEANDIALMKITPPVTCGHFIGP
GCLPQFRAGPPRPVQTCWVAGWGFLQENARRTSPMLQEARVDLIDLGLCNSTRWYNGRIRSTNVC
AGYPEGKIDTCQGDSSGGLMCKDSAENSYVVVGITSWGVCARAKRPGVYTSTWSYLNWIASKIGST
AVHMIQLPT

>g1fiz.1 b.47.1.2 (L:,A:) Beta-acrosin {Pig (Sus scrofa)}

ATCDGPCGLRFRQXVVGMSAEPGAWPVMVSLQIFMYHNNRRYHTCGGILLNSHWVLTAAHCFKN
KKKVTDWRLIFGANEVVWGSNKPVKPPLQERFVEEIIIHEKYVSGLEINDIALIKITPPVPCGPFIPG
CLPQFKAGPPRAPQTCWVTGWGYLKEKGPRTSPTLQEARVALIDLELCNSTRWYNGRIRSTNVCAG
YPRGKIDTCQGDSSGGLMCRDRAENTFVVVGITSWGVCARAKRPGVYTSTWPYLNWIASKIGSNA
LQMVQLGTPPR

>d1eaxa_b.47.1.2 (A:) Matriptase MTSP1 {Human (Homo sapiens)}

VVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHD
QSQRSAPGVQERRLKRIISHPPFNDFTFDYDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVT
GWGHTQYGGTGALILQKGEIRVINQTTENLLPQQITPRMMCVGFLSGGVDSCQGDSSGGLSSVEAD
GRIFQAGVSWGDGCAQRNKPGVYTRLPLFRDWIKENTGV

>d1svpa_b.47.1.3 (A:) Viral capsid protein {Sindbis virus}

ALKLEADRLFDVKNEDGDVIGHALAMEGKVMKPLHVKGTIDHPVLSKLKFTKSSAYDMEFAQLPVN
MRSEAFYTYSEHPEGFYNNWHHGAVQYSGGRFTIPRGVGGRGDAGRPIMDNSGRVVAIVLGGADEGT
RTALSVVTTWNSKGTIKTTPEGTEEWSA

>d1vcpa_b.47.1.3 (A:) Viral capsid protein {Semliki forest virus}
CIFEVKHEGKVTGYACLVGDKVMKPAHVKGVIDNADLAKLAFKKSSKYDLECAQIPVHMRS DASKYT
HEKPEGHYNWHHGAVQYSGGRFTIPTGAGKPGDSGRPIFDNKGRVVAIVLGGANEGSRTALSVVTTW
NKDMVTRVTPPEGSEEW

>d1a1qa_b.47.1.3 (A:) NS3 protease {Human hepatitis C virus (HCV), different isolates}
PITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAGSKTLAGPKG
PITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKG
SSGGPLLCPGSHAVGIFRAAVCTRGVAKAVDFVPVESMETTMRSPVF

>d1cu1a1_b.47.1.3 (A:705-720,A:3-186) NS3 protease {Human hepatitis C virus (HCV),
different isolates}
GSVVIVGRIILSGSGSXIITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTV
YHGAGSKTLAGPKGIPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRGDS
RGSLLSPRPVSYLKGSSGGPLLCPGSHAVGIFRAAVCTRGVAKAVDFVPVESMETTMRSPVFTD

>d1dxwa_b.47.1.3 (A:) NS3 protease {Human hepatitis C virus (HCV), different isolates}
TGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAGSKTLAGPKGIPITQMYTNVDQDLVGWQ
APPGARSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPGSHAVGIFR
AAVCTRGVAKAVDFVPVESMETTMRASKKKK

>g1a1r.1_b.47.1.3 (A:,C:) NS3 protease {Human hepatitis C virus (HCV), different isolates}
VEGEVQIVSTATQTFLATCINGVCWTVYHGAGTRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS
LTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISYLKGS
SSGGPLLCPGSHAVGLFRAAVCTRGVAKAVDFIPVENLETTMRXGSSVVIVGRIVLSGKPA

>g1a1r.2_b.47.1.3 (B:,D:) NS3 protease {Human hepatitis C virus (HCV), different isolates}
PITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTATQTFLATCINGVCWTVYHGAGTRTIASPKGP
VIQMYTNVDQDLVGWPAPQGSRS
LTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISYLKGS
SSGGPLLCPGSHAVGLFRAAVCTRGVAKAVDFIPVENLETTMRXKGSVVIVGRIVLSGKPAIIPK

>g1dy9.1_b.47.1.3 (A:,C:) NS3 protease {Human hepatitis C virus (HCV), different isolates}
APITAYSQQTRGLLGCIITSLTGRDKNQVDGEVQVLSTATQSFLATCVNGVCWTVYHGAGSKTLAGPK
GPITQMYTNVDQDLVGWPAPPGARSMTPTCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYL
KGS
SSGGPLLCPGSHVVGIFRAAVCTRGVAKAVDFIPVESMXGSSVVIVGRIILS

>g1ns3.1_b.47.1.3 (A:,C:) NS3 protease {Human hepatitis C virus (HCV), different isolates}
ITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAGSKTLAGPKGPI
TQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGS
SSGGPLLCPGSHAVGIFRAAVCTRGVAKAVDFVPVESMETTMRXKGSVVIVGRIILS

>d1befa_b.47.1.3 (A:) NS3 protease {Dengue virus serotype 2}
WDVPSPPVVGKAELEDGAYRIKQKGLGYSQIGAGVYKEGTFHTMWHVTRGAVLMHKGKRIEPSWA
DVKKDLVSCGGGWKLEGEWKEGEEVQLALEPGKNPRAVQTKPGLFKTNAGTIGAVSLDFSPGTSG
SPIIDKKGKVVGIYNGVVTTRSGAYVSAIAQTEKSIEDNPEIEDD

>d1cqqa_b.47.1.4 (A:) 3C cysteine protease (picornain 3C) {Human rhinovirus type 2}
GPEEEFGMSLIKHNSCVITTENGKFTGLGVYDRFVVVPTHADPGKEIQVDGITTKVIDSYDLYNKNGI
KLEITVLKLDREKFRDIRRYIPNNEDDYPNCNLALLANQPEPTIINVGDVVSYGNILLSGNQTARML
KYSYPTKSGYCGGVLYKIGQVLGIHVGNGRDFGFSAMLLRSYFT

>d1hava_b.47.1.4 (A:) 3C cysteine protease (picornain 3C) {Human hepatitis A virus}
STLEIAGLVRKNLVQFGVGEKNGSVRWVMNALGVKDDWLLVPSHAYKFEKDYEMMEFYFNRRGGTY
YSISAGNVVIQSLDVGFDVVLKVPVPTIPKFRDITQHFIIKGDVPRALNRLATLVTTVNGTPMLISEG

PLKMEEKATYVHKKNDGTTVDLTVDQAWRGKGEGLPGMCGGALVSSNQSIQNAILGIHVAGGNSILV
AKLVTQEMFQNIIDKKI
>d2hrva_b.47.1.4 (A:) 2A cysteine proteinase {Human rhinovirus 2}
GPSDMYVHVGNIYRNLHLFNSEMHE SILVSYSSDLIIYRTNTVGGDDYIPSCDCTQATYYCKHKRNRYF
PITVTSHDWYEIQESEYYPKHIQYNLLIGEGPCEPGDCGGKLLCKHGVIGIVTAGGDNHVAFIDLRHF
HCA
>d1bco_1 b.48.1.1 (481-560) mu transposase, C-terminal domain {Bacteriophage mu}
TEEQKRMLLLPAEAVNVSARKGEFTLVGGSLKGAKNVYYNMALMNAGVKKVVVRFDPQQLHSTVY
CYTLDGRFICEAECL
>d1e79a2 b.49.1.1 (A:19-94) N-terminal domain of alpha and beta subunits of F1 ATP
synthase {Cow (Bos taurus)}
ADTSVDLEETGRVLSIGDGIARVHGLRNVQAEEMVEFSSGLKGMSLNLEPDNVGVVVVFGNDKLIKEG
DIVKRTGAI
>d1e79d2 b.49.1.1 (D:9-81) N-terminal domain of alpha and beta subunits of F1 ATP
synthase {Cow (Bos taurus)}
TTGRIVAVIGAVVDVQFDEGLPPILNALEVQGRETRLVLEVAQHLGESTVRTIAMDGTEGLVRGQKVL
DSGAP
>d1maba2 b.49.1.1 (A:10-94) N-terminal domain of alpha and beta subunits of F1 ATP
synthase {Rat (Rattus norvegicus)}
SSILEERILGADTSVDLEETGRVLSIGDGIARVHGLRNVQAEEMVEFSSGLKGMSLNLEPDNVGVVVV
GNDKLIKEGDIVKRTGAI
>d1mabb2 b.49.1.1 (B:1-81) N-terminal domain of alpha and beta subunits of F1 ATP
synthase {Rat (Rattus norvegicus)}
SAAPKAGTATGQIVAVIGAVVDVQFDEGLPPILNALEVQGRESRLVLEVAQHLGESTVRTIAMDGTEG
LVRGQKVLDSGAP
>d1skyb2 b.49.1.1 (B:21-95) N-terminal domain of alpha and beta subunits of F1 ATP
synthase {Bacillus sp., strain ps3}
SQIQVSDVGTVIQVGDGIARAHGLDNVMSGEAVEFANAVMGMALNLEENNVGIVILGPYTGKEGDE
VRRTRGRIM
>d1skye2 b.49.1.1 (E:1-82) N-terminal domain of alpha and beta subunits of F1 ATP
synthase {Bacillus sp., strain ps3}
MTRGRVIQVMGPVVDVKFENGHLPAIYNALKIQHKARNENEVDIDLTLEVALHLGDDTVRTIAMAS
TDGLIRGMEVIDTGAP
>d1fx0a2 b.49.1.1 (A:25-96) N-terminal domain of alpha and beta subunits of F1 ATP
synthase {Spinach (Spinacia oleracea), chloroplast}
KVVNTGTVLQVGDGIARIHGLDEV MAGELVEFEETIGIALNLESNNVGVVLMGDGLMIQEGSSVKA
TGRIA
>d1fx0b2 b.49.1.1 (B:19-97) N-terminal domain of alpha and beta subunits of F1 ATP
synthase {Spinach (Spinacia oleracea), chloroplast}
NLGRIAQIIGPVLNVAFPPGKMPNIYNALIVKGRDTAGQPMNVTCEVQQLGNNRVRVAVAMSATDGL
TRGMEVIDTGAP
>d1bd0a1 b.49.2.1 (A:2-11,A:245-382) Alanine racemase {Bacillus stearothermophilus}
NDFHRDTWAEXFSLHSRLVHVKKLQPGKVSYGATYTAQTEEWIGTIPIGYADGWLRRQLQHFHVLV
DGQKAPIVGRICMDQCMIRLPGPLPVGTKVTLIGRQGDDEVISIDDVARHLETINYEVPCTISYRVPRIF

FRHKRIMEVRNAIG

>d1d7ka1 b.49.2.1 (A:7-43,A:284-427) Eukaryotic ornithine decarboxylase {Human (Homo sapiens)}

EEFDCHFLEDEGFTAKDILDQKINEVSSDDKDAFYVAXFTLAVNIIAKKIVLKEQTGSDDDESESEQTF
MYVNDGVYGSFNCILYDHAHVKPLLQKRPKPDERYYSSSIWGPTCDGLDRIVERCDLPEMHVGDW
MLFENMGAYTVAAASTFNGFQRPTIYYVMSGPAWQLMQQFQNPDFPP

>d7odca1 b.49.2.1 (A:2-43,A:284-418) Eukaryotic ornithine decarboxylase {Mouse (Mus musculus)}

SSFTKDEFDCHILDEGFTAKDILDQKINEVSSDDKDAFYVAXFTLAVNIIAKKTVWKEQPGSDDDEDE
SNEQTFMYVNDGVYGSFNCILYDHAHVKALLQKRPKPDEKYYSSSIWGPTCDGLDRIVERCNLPE
MHVGDWMLFENMGAYTVAAASTFNGFQRPNIIYYVMSRPMWQLMK

>d1f3ta1 b.49.2.1 (A:14-43,A:284-422) Eukaryotic ornithine decarboxylase {Trypanosoma brucei}

RFLEGFNTRDALCKISMNTCDEGDPFFVAXFTLAVNVIKKVTPGVQTDVGAHAESNAQSFMYV
NDGVYGSFNCILYDHAVRPLPQREPIPNKLYPSSVWGPTCDGLDQIVERYLPEMQVGEWLLFED
MGAYTVVGTSSFNGFQSPTIYYVVSGLPDHVRELKS

>d2toda1 b.49.2.1 (A:37-43,A:284-410) Eukaryotic ornithine decarboxylase {Trypanosoma brucei}

GDPFFVAXFTLAVNVIKKVTPGVQTDVGAHAESNAQSFMYVNDGVYGSFNCILYDHAVRPLPQR
EPIPNKLYPSSVWGPTCDGLDQIVERYLPEMQVGEWLLFEDMGAYTVVGTSSFNGFQSPTIYYV
S

>d1b6la_ b.50.1.1 (A:) Human immunodeficiency virus type 1 protease {Human immunodeficiency virus type 1}

PQITLWKRPLVTIRIGGQLKEALLDTGADDTVIEEMNLPGKWKPKMIGGIGGFIVRQYDQIPVEIXG
HKAIGTVLVGPTPVNIIGRNLLTQIGXTLNF

>d1bdqa_ b.50.1.1 (A:) Human immunodeficiency virus type 1 protease {Human immunodeficiency virus type 1}

PQITLWQRPLVTIKIGGQLKEALLDTGADDSIVAGIELPGRWPKMVGIGGFIKVRQYDQILIEICGH
KAIGTVLVGPTPNIIGRNLLTQIGCTLNF

>d1c6ya_ b.50.1.1 (A:) Human immunodeficiency virus type 1 protease {Human immunodeficiency virus type 1}

PQITLWQRPVVTIKIGGQLMEALIDTGADDTVLEEMDLGRWPKIIGGIGGFVVRQYDQIPIEICG
HKVIGTVLVGPTPTNIIGRNLLTQIGCTLNF

>d1dazc_ b.50.1.1 (C:) Human immunodeficiency virus type 1 protease {Human immunodeficiency virus type 1}

PQITLWKRPLVTIKIGGQLKEALLDTGADDTVIEEMSLPGRWPKMIGGIGGFIVRQYDQIIEIAGH
KAIGTVLVGPTPVNIIGRNLLTQIGATLNF

>d1difa_ b.50.1.1 (A:) Human immunodeficiency virus type 1 protease {Human immunodeficiency virus type 1}

PQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWPKMIGGIGGFIVRQYDQILIEICG
HKAIGTVLVGPTPVNIIGRNLLTQIGCTLNF

>d1hvc_ b.50.1.1 (-) Human immunodeficiency virus type 1 protease {Human immunodeficiency virus type 1}

PQITLWQRPLVTIRIGGQLKEALLDTGADDTVLEEMNLPGKWKPKMIGGIGGFIVRQYDQILIEICG

HKAIGTVLVGPTPVNIIGRNLLTQIGCTLNFGGSSGPQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWPKMIGGIGGFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNF

>d1idaa_ b.50.1.1 (A:) Human immunodeficiency virus type 2 (HIV-2) protease {Human immunodeficiency virus type 2}
PQFSLWKRPPVVTAYIEGQPVEVLLDTGADDSIVAGIELGNNYSPKIVGGIGGFINTKEYKNVEIEVLNK
KVRATIMTGDTPINIFGRNLLTALGMSLNL

>d1az5_ b.50.1.1 (-) Simian immunodeficiency virus (SIV) protease {Simian immunodeficiency virus, different strains}
PQFHLWKRPPVTAHIEGQPVEVLLDTGADDSIVTGIELGPHYTPKIVGGIGGFINTKEYKNVEVEVLG
KRIKGTIMTGDTPINIFGRNLLTALGMSLNF

>d1k6va_ b.50.1.1 (A:) Simian immunodeficiency virus (SIV) protease {Simian immunodeficiency virus, different strains}
PQITLWKRPLVTIRIGGQLKEALLDTGADDTVLEEMNLPGRWPKMIGGIGGFIKVRQYDQIPIEICG
HKAIGTVLVGPTPTNVIGRNLLTQIGCTLNF

>d1siva_ b.50.1.1 (A:) Simian immunodeficiency virus (SIV) protease {Simian immunodeficiency virus, different strains}
PQFSLWRRPPVTAHIEGQPVEVLLDTGADDSIVTGIELGPHYTPKIVGGIGGFINTKEYKNVKIEVLGK
RIKGTIMTGDTPINIFGRNLLTALGMSLNL

>d4fiv_ b.50.1.1 (-) Feline immunodeficiency virus (FIV) protease {Feline immunodeficiency virus}
VGTTTTLEKRPEILIFVNGYPIKFLLDTGADITILNRRDFQVKNSIENGRQNMIGVGGGKRGNTYINV
HLEIRDENYKTQCIFGNVCVLEDNSLIQPLLGRDNMIKFNIRLVM

>d1baia_ b.50.1.1 (A:) Rous sarcoma virus protease {Rous sarcoma virus, strain pr-C}
LAMTMEHKDRPLVRVILTNTGSHPVKQRSVYITALLDTGADDTVISEEDWPTDWPVMEANPQIHG
IGGGIPVRKSRDMIELGVINRDGSLERPLLLFPLVAMTPVNILGRDCLQGLGLRLTNL

>d2rspa_ b.50.1.1 (A:) Rous sarcoma virus protease {Rous sarcoma virus, strain pr-C}
LAMTMEHKDRPLVRVILTNTGSHPVKQRSVYITALLDSGADITIISEEDWPTDWPVMEANPQIHGI
GGGIPMRKSRDMIELGVINRDGSLERPLLLFPAVAMVRGSILGRDCLQGLGLRLTNL

>d1fmb_ b.50.1.1 (-) EIAV protease {Equine infectious anemia virus}
VTYNLEKRPTTIVLINDTPLNVLLDTGADTSVLTTHAHYNRLKYRGRKYQGTGIGGVGGNVETFSTPV
TIKKKGRHIKTRMLVADIPVTILGRDILQDLGAKLVL

>d2er7e_ b.50.1.2 (E:) Endothiapepsin {Chestnut blight fungus (Endothia parasitica)}
STGSATTPIDSLDDAYITPVQIGTPAQTLLNDFDTGSSDLWVFSSETTASEVDGQTIYTPSKSTTAKL
LSGATWSISYGDGSSSSGDVYTDTVSVGGLTVTGQAVESAKKVSSFTEDSTIDGLLGLAFSTLNTVSP
TQQKTFFDNAKASLDSPVFTADLGYHAPGTYNFGFIDTTAYTGSITYTAVSTKQGFWEWTSTGYAVG
SGTFKSTSIDGIADTGTTLLYLPATVVSAYWAQVSGAKSSSSVGGYVPCSATLPSFTFGVGSARIVIPG
DYIDFGPISTGSSSCFGGIQSSAGIGINIFGDVALKAAFVVFNGATTPTLGFASK

>d1bxa_ b.50.1.2 (A:) Acid protease {Fungus (Penicillium janthinellum), penicillopepsin}
AASGVATNTPTANDEEYITPVTIGGTTLNLFDTGSADLWVFSSTELPASQQSGHVSYNPSATGKELSG
YTWSISYGDGSSASGNVFTDSVTVGGVTAHQAVQAAQQISAQFQQTNNNDGLLGLAFSSINTVQPQ
SQTTFFDQTVKSSLAQPLFAVALKHQQPGVYDFGFIDSSKYTGSLTYTGVDNSQGFWSFNVDSYTAGSQ
SGDGFSGIADTGTTLLLLDDSVVSQYYSQVSGAQQDSNAGGYVFDCTNLPDFSVSISGYTATVPGSLI
NYGPSGDGSTCLGGIQSNSGIGFSIFGDIFLKSQYVVFSDGPGQLGFAPQA

>d1ibqa_ b.50.1.2 (A:) Acid protease {Fungus (Aspergillus phoenicis), aspergillopepsin}

SKGSAVTPPQNNDEEYLTPVTVGKSTLHLDFDTGSADLWVFSDELPSSEQTGHDLTPSSSATKLSGY
SWDISYGDGSSASGDVYRDTVTVGGVTTNKQAVEAASKISSEFVQDTANDGLLGLAFSSINTVQPKAQ
TTFFDVTVKSQLDSPFAVQLKHDAPGVYDFGYIDDSKYTGSTYTDADSSQGYWGFSTDGYSIGDGSS
SSSGFSAIADTGTTLLILLDDDEIVSAYYEQVSGAQESYEAGGYVFCSTDLPDFTVVIGDYKAVVPGKYIN
YAPVSTGSSTCYGGIQSNSGLGLSILGDVFLKSQYVVFNSEGPKLGFAAQA

>d2apr_ b.50.1.2 (-) Acid protease {Bread mold (*Rhizopus chinensis*)}

AGVGTVPMTDYGNDIEYYGQVTIGTPGKKFNLDFTGSSDLWIASTLCTNCGSGQTKYDPNQSSTYQ
ADGRTWSISYGDGSSASGILAKDNVNLLGGLIKGQTIELAKREAAAFASGPNDGLLGLGFDITITVRG
VKTPMDNLISQGLISRPIFGVYLGKAKNGGGGEYIFGGYDSTKFKGSLTTVPIDNSRGWWGITVDRAT
VGTSTVASSFDGILDTGTTLLLPNNIAASVARAYGASDNGDGTYTISCDTSAFKPLVFSINGASFQVSP
DSLVEEFQGGCIAGFGYGNWGFHIGDTFLKNNYVVFNQGVPEVQIAPVAE

>d2asi_ b.50.1.2 (-) Acid protease {*Rhizomucor miehei*}

GSVDTPGYDFDLEEYAI PVSIGTPGQDFLLFDTGSSDTPVPHKGCTKSEGCVGSRRFFDPSASSTFK
ATNYNLNITYGTGANGLYFEDSIAIGDITVTKQILAYVDNVRGPTAEQSPNADIFLDGLFGAAYPDNTA
MEAEYGSTYNTVHVNLKQGLISSPLFSVYMNTNSGTGEVVFGGVNNTLLGGDIAYTDVMSRYGGYY
FWDAPVTGITVDGSAAVRFSRPAFTIDTGTNFFIMPSSAASKIVKAALPDATETQQGWVPCASYQ
NSKSTISIVMQSGSSDTEISVPVSKMLLPVDQSNETCMFIIIPDGGNQYIVGNLFLRFFVNVYDFG
NNRIGFAPLASAYENE

>d1eaga_ b.50.1.2 (A:) Acid protease {Yeast (*Candida albicans*)}

QAVPVTLHNEQVTYAADITVGSNNQKLNIVVDTGSSDLWVPDVNVDCQVTYSQDTADFCQKQGTYD
PSGSSASQDLNTPFKIGYGDGSSSQGTLYKDTVGFGGVSIKNQVLADVDSTSIDQGILGVGYKTNEAGG
SYDNVPVTLKKQGVIAKNAYSLYLNSPDAATGQIIFGGVDNAKYSGSLIALPVTSDRELRLSLSVEVSG
KTINTDNVDVLLDSGTTITYLQQLADQIIFKAFNGKLTQDSNGNSFYEVDCNLSGDVVFNFNSKNAKIS
VPASEFAASLQDDGQPYDKCQLLFDVNDANILGDNFLRSAYIVYDLDDNEISLAQVKYTSASSISALT

>d1j71a_ b.50.1.2 (A:) Acid protease {Yeast (*Candida tropicalis*)}

SDVPTTLINEGPSYAADIVVGSNQQKQTVVIDTGSSDLWVVDTDAECQVTYSGQTNNFCKQEGTFDP
SSSSSAQNLNQDFSIEYGLTSSQGSFYKDTVGFGGISIKNQFADVTTTSDVQDQIMGIGFTADEAGYN
LYDNVPVTLKKQGIINKNAYSLYLNSSEDASTGKIIFGGVDNAKYTGTLTALPVTSSVELRVHLGSINFD
GTSVSTNADVLDSTTITYFSQSTADK FARIVGATWDSRNEIYRLPSCDLSGDAVFNFDQGVKITVP
LSELILKDS DSSICYFGISRNDANILGDNFLRRAYIVYDLDDKTISLAQVKYTSSSDISAL

>d1dpja_ b.50.1.2 (A:) Acid protease {Baker's yeast (*Saccharomyces cerevisiae*), proteinase A}

GGHDVPLTNYLNAQYYTDITLGTTPPQNFKVILDTGSSNLWVPSNECGSLACFLHISKYDHEASSSYKA
NGTEFAIQYGTGSLEGYISQDTLSIGDLTIPKQDFAEATSEPGLTFAGKFDGILGLGYDTISVDKVVPPF
YNAIQDQLLDEKRFAFYLGDTSKDTENGGEATFGGIDESKFKGDITWLPVRRKAYWEVKFEGIGLGD
EYAELESHGAAIDTGTSLITLPSGLAEMINAEIGAKKGWGTGQYTLDCNTRDNLPLIFNFNGYNFTIG
PYDYTLEVSGSCISAITPMDPEPVGPLAIVGDAFLRKYYSIYDLGNNAVGLAKAI

>g1b5f.1 b.50.1.2 (A;B:) Plant acid proteinase, phytepsin {*Cynara cardunculus*}

GSAVVALTNRDRTSYFGEIGTTPPKFTVIFDTGSSVLWVPSKCKINAKACRAHSMYESSDSSTYKEN
GTFGAIYGTGSITGFFSQSVTIGDLVVKEQDFIEATDEADNVFLHRLFDGILGLSFGTISVPVWYNM
LNQGLVKERRFSFWLNRNVDEEEGGELVFGGLDPNHFRGDHTYVPVPTYQYYWQFGIGDVLIGDKST
GFCAPGCQAFADSGTSLLSGPTAIVTQINHAIGANXEELQVDCNTLSSMPNVSFTIGGKFKGLTPEQYI
LKVGKGEATQCISGFTAMDATLLGPLWILGDVFMRPYHTVFDYGNLLVGFAEAA

>d1qdma2 b.50.1.2 (A:2-247,A:248-338) Plant acid proteinase, phytepsin {Barley (*Hordeum*)}

vulgare}}

EEEGDIVALKNYMNAQYFGEIGVGTTPQKFTVIFDTGSSNLWVPSAKCYFSIACYLHSRYKAGASSTY
KKNKGPAAIQYGTGSIAGYFSEDSVTVGDLVVKDQEFIEATKEPGITFLVAKFDGILGLGFKEISVGVKAV
PVWYKMI EQGLVSDPVFSFWLNRHVDEGEGGEIIFGGMDPKHYVGEHTYVPVTQKGYWQFDMGD
VLVGGKSTGFCAGGCAAIADSGTSLLAGPTAIITEINEKIGAAGXSPMGESAVDCGSLGSMPIEFTIGG
KKFALKPEEYILKVGEGAAAQCISGFTAMDIPPRGPLWILGDVFMGPYHTVFDYGLRIGFAKAA

>d3psg_ b.50.1.2 (-) Pepsin(ogen) {Pig (Sus scrofa)}

LVKVPLVRKKSLRQNLKDGKLDKDFLTKHKHNPASKYFPEAAALIGDEPLENYLDTEYFGTIGIGTPA
QDFTVIFDTGSSNLWVPSVYCSSLACSDHNQFNPDDSSSTFEATSQELSITYGTGSMTGILGYDTVQVG
GISDTNQIFGLSETEPGSFLYAPFDGILGLAYPSISASGATPVFDNLWDQGLVSQDLFSVYLSNDDSG
SVVLLGGIDSSYYTGSLNWWVPVSVVEGYWQITLDSITMDGETIACSGGCQAIVDTGTSLLTGPTSAIANI
QSDIGASENSDGMVISCSSIDSLPDIVFTIDGVQYPLSPSAYILQDDDSCTSGFEGMDVPTSSGELWIL
GDVFIRQYYTVFDRANNKVGLAPVA

>d4pep_ b.50.1.2 (-) Pepsin(ogen) {Pig (Sus scrofa)}

IGDEPLENYLDTEYFGTIGIGTPAQDFTVIFDTGSSNLWVPSVYCSSLACSDHNQFNPDDSSSTFEATSQ
ELSITYGTGSMTGILGYDTVQVGGISDTNQIFGLSETEPGSFLYAPFDGILGLAYPSISASGATPVFDNL
WDQGLVSQDLFSVYLSNDDSGSVVLLGGIDSSYYTGSLNWWVPVSVVEGYWQITLDSITMDGETIACSG
GCQAIVDTGTSLLTGPTSAIANIQSDIGASENSDGMVISCSSIDSLPDIVFTIDGVQYPLSPSAYILQDD
DSCTSGFEGMDVPTSSGELWILGDVFIRQYYTVFDRANNKVGLAPVA

>d1psoe_ b.50.1.2 (E:) Pepsin(ogen) {Human (Homo sapiens), 3A}

VDEQPLENYLDMEYFGTIGIGTPAQDFTVIFDTGSSNLWVPSVYCSSLACTNHNRFNPEDSSTYQST
SETVSITYGTGSMTGILGYDTVQVGGISDTNQIFGLSETEPGSFLYAPFDGILGLAYPSISSGATPVFD
NIWNQGLVSQDLFSVYLSADDQSGSVVIFGGIDSSYYTGSLNWWVPVTVEGYWQITVDSITMNGEAIAC
AEGCQAIVDTGTSLLTGPTSPIANIQSDIGASENSDGMVSVCSAISSLPDIVFTINGVQYPPPSAYILQ
SEGSCISGFQGMNLPTESGELWILGDVFIRQYYTVFDRANNQVGLAPVA

>g1htr.1 b.50.1.2 (P;.B:) Pepsin(ogen) {Human (Homo sapiens), progastricsin (pepsinogen C)}

AVVKVPLKKFKSIRETMKEKLLGEFLRTHKYDPAWKYRFGDLXSVTYEPMAYMDAAAYFGEISIGTP
PQNFLVLFDTGSSNLWVPSVYCQSQACTSHSRFNPSESSTYSTNGQTFSLQYGSGLTGFFGYDTLTVQ
SIQVPNQEFGLSENEPNTNFVYAQFDGIMGLAYPALSVDEATTAMQGMVQEGALTSVFSVYLSNQQ
GSSGAVVFGGVDSSLYTGQIYWAPVTQELYWQIGIEEFLIGGQASGWCSEGCQAIVDTGTSLTVPQ
YMSALLQATGAQEDEYQFLVNCNSIQNLPSLTFIINGVEFPLPPSSYILSNNGYCTVGVEPTYLSSQN
GQPLWILGDVFLRSYYSVYDLGNNRVGFATAA

>d1am5_ b.50.1.2 (-) Pepsin(ogen) {Atlantic cod (Gadus morhua)}

RVTEQMKN EADTEYYGVISIGTPPESFKVIFDTGSSNLWVSSSHCSAQACSNHNKFKPRQSSTYVETG
KTVDLTYGTGGMRGILQDQTVSVGGGSDPNQELGESQTEPGPFQAAAPFDGILGLAYPSIAAAGAVPV
FDNMGSQLVEKDLFSFYLSGGGANGSEVMLGGVDNSHYTGSIHWPVTAEKYWQVALDGITVNGQ
TAACEGCQAIVDTGTSKIVAPVSALANIMKDIGASENQGEMMGNCASVQSLPDITFTINGVKQPLPPS
AYIEGDQAFCTSGLGSSGVPSNTSELWIFGDVFLRNYTYIYDRTNKNKVGFPAA

>d1mpp_ b.50.1.2 (-) Pepsin {Mucor pusillus}

GSVDTPGLYDFDLEEYAI PVSIGTPGQDFYLLFDTGSSDTWVPHKGCNSEGCVGKRFFDPSSSTFK
ETDYNLNITYGTGGANGIYFRDSITVGGATVKQQT LAYVDNVSGPTAEQSPDSELFLDGIFGAAYPDN
TAMEAEYGDYNTVHVNLKQGLISSPVFSVYMNNTNDGGGQVVFVGGVNTLLGGDIQYTDVLKSRG
GYFFWDAPVTGKIDGSDAVSFDGAQAFTIDTGTNFFIAPSSFAEKVVKAALPDATESQQGYTVPCSK

YQDSKTTFSLVLQKSGSSSDTIDVSVPIKMLLPVDKSGETCMFIVLPDGGNQFIVGNLFLRFFVNVYD
FGKNRIGFAPLASGYEND

>g1yb.1 b.50.1.2 (A;B:) Cathepsin D {Human (Homo sapiens)}

GPIPEVLKNYMDAQYYGEIGIGTPPQCFTVVFDTGSSNLWVPSIHCKLLDIACWIHHKYNSDKSSTYV
KNGTSFDIHYGSGSLSGYLSQDTSVPCQXGGVKVERQVFGEATKQPGITFIAAKFDGILGMAYPRISV
NNVLPVFDNLMQQKLVQDNIFSFYLSRDPDAQPGGELMLGGTDSKYYKGSLSYLVNTRKAYWQVHL
DQVEVASGLTLCKEGCEAIVDTGTSLMVGVPDEVRELQKAIGAVPLIQGEYMIPCEKVSTLPAITLKLK
GKGKYLSPEDYTLKVSQAGKTLCLSGFMGMDIPPPSGPLWILGDVFIGRYTTFDRDNNRVGFAEAA

>d3cms_ b.50.1.2 (-) Chymosin (synonym: renin) {Cow (Bos taurus)}

GEVASVPLTNYLDSQYFGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQN
LGKPLSIHYGTGSMQGILGYDVTVSNIVDIQQTIVGLSTQEPGDFFTYAEFDGILGMAYPSLASEYSIPV
FDNMMNRHLVAQDLFSVYMDRNGQESMLTLGAIDPSYYTGSLSHWVPVTVQYQWQFTVDSVTISGV
VVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYMPVTVFEINGKMYPLTP
SAYTSQDQGFCTSGFQSENHSQKWILGDVFIREFYYSVDFRANNLVGLAKAI

>d1hrna_ b.50.1.2 (A:) Chymosin (synonym: renin) {Human (Homo sapiens)}

GNTTSSVILTNYMDTQYYGEIGIGTPPQTFKVVFDTGSSNVWVPSKCSRLYTACVYHKLFDASDSSSY
KHNGTELTLRYSTGTVSGFLSQDIITVGGITVTQMFGEVTEMPALPFMLAEFDGVVGMGFIEQAIGRV
TPIFDNIISQGVKEDVFSFYNRDSENSQSLGGQIVLGGSDPQHYEGNFHYINLIKTGVWQIQMKGV
SVGSSTLLCEDGCLALVDTGASYISGSTSSIEKLMEALGAKKRLFDYVVKCNEGPTLPDISFHLGGKEY
TLTSADYVVFQESYSSKCLCTLAIHAMDIPPTGPTWALGATFIRKIFYTEFDRRNNRIGFALAR

>d1smra_ b.50.1.2 (A:) Chymosin (synonym: renin) {Mouse (Mus musculus)}

TDLISPVVLTNYLNSQYYGEIGIGTPPQTFKVFVFDTGSSANLWVPSKCSRLYLACGIHSLYESSDSSSYM
ENGDDFTIHYGSGRKGFLSQDSVTVGGITVTQTFGEVTQLPLIPFMLAQFDGVLGMGFPAAQAVGGV
TPVFDHILSQGVKKEKVFVYVNRGPHLLGGEVVLGGSDPQHYQGDFHYVSLSKTDSWQITMKGVS
GSSTLLCEECEVVVDTGSSFISAPTSSLKIMQALGAKEKRLHEYVVVSCSQVPTLPDISFNLGGRAYT
LSSTDYVLQYPNRRDKLCTVALHAMDIPPTGPVWVLGATFIRKIFYTEFDRHNNRIGFALAR

>d1fkna_ b.50.1.2 (A:) beta-secretase (memapsin) {Human (Homo sapiens)}

RRGSFVEMVDNLRGKSGQGYVEMTVGSPQTLNILVDTGSSNFAVGAAPHPFLHRYRQQLSSTYR
DLRKGVYVPTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWEGLGLAYAEIARP
DDSLEPFDSLKQTHVPLFSLQLCGAGPLNQSEVLASVGGSMIIGIDHSLYTGSLWYTPIRREW
YYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRPKKVFEEAVKSIKAASSTEKFPDGFWLGE
QLVCWQAGTTPWNIFPVISLYLMGEVTNQSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVM
GAVIMEGFYVDFRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYN

>d1pfza_ b.50.1.2 (A:) Plasmepsin ii (a hemoglobin-degrading enzyme) {Plasmodium falciparum}

HLTIGFKVENAHDRLKTIKTHKLKNIKESVNFLNSGLTKTNYLGSSNDNIELVDFQNMIFYGDAEV
GDNQQPFTFILDTGSANLWVPSVKCTTAGCLTKHLYDSSKSRTYEKDGTKVEMNYVSGTVSGFFSKD
LVTVGNLSLPYKFIEVIDTNGFEPTYTASTFDGILGLGWKDLSIGSDPIVVELKNQNKIENALFTFY
PVHDKHTGFLTIGGIEERFYEGPLTYEKLNHDLWQITLDAHVG NIMLEKANCIVDSGTSAITVPTDF
LNKMLQNLQNDVIKVPFLPFYVTLNNSKLPTEFTSENGKYTLEPEYYLQHIEDVGPGLCMLNIIGLDF
PVPTFILGDPFMRKYFTVFDYDNHSGIALAKKNL

>d1smea_ b.50.1.2 (A:) Plasmepsin ii (a hemoglobin-degrading enzyme) {Plasmodium falciparum}

SSNDNIELVDFQNMIFYGDAEVGDNQQPFTFILDTGSANLWVPSVKCTTAGCLTKHLYDSSKSRTYEK

DGTKVEMNYVSGTVSGFFSKDLVTVGNLSLPYKFIEVIDTNGFEPTYTASTFDGILGLGWKDLSIGSV
DPIVVELKNQNKIENALFTFYLPVHDKHTGFLTIGGIEERFYEGPLTYEKLNHDLYWQITLDAHVGNI
MLEKANCIVDSGTSAITVPTDFLNKMLQNLVDVIKVPFLPFYVTLNNSKLPTEFTESENGKYTLEPE
YYLQHIEDVGPGLCMLNIIGLDFPVPTFILGDPFMRKYFTVFDYDNHNSVGIALLAKKNL
>d1qs8a_ b.50.1.2 (A:) Plasmepsin ii (a hemoglobin-degrading enzyme) {Plasmodium vivax}
SENDVIELDDVANIMFYGEVEVDGNHQQFMLIFDTGSANLWVPSKCCNSGCSIKNLYDSSKSKSYEK
DGTKVDITYGSGTVKGFSSKDLVTLGHLSMPYKFIEVIDTDDLEPIYSSVEFDGILGLGWKDLSIGSIDP
IVVELKNQNKIDNALFTFYLPVHDLVHAGYLTIGGIEEKFYEGNITYEKLNHDLYWQIDLVDVHFGKQT
MEKANVIVDSGTTTTITAPSEFLNKFFANLNVIKVPFLPFYVTTCDNKEMPTLEFKSANNTYTLPEY
YMNPILEVDDTLCMITMLPVDIDSNTFILGDPFMRKYFTVFDYDKESVGFIAIKN
>d1ile_2 b.51.1.1 (198-386) Isoleucyl-tRNA synthetase (IleRS) {Thermus thermophilus}
KEIQDPSVYVRFPLKEPKKLGLEKASLLIWTTPWTLPGNVAAAVHPEYTYAAFQVGDEALILEEGL
GRKLLGEGTQVLKTFPGKALEGLPYTPPYPALEKGYFVVLADYVSQEDGTGIVHQAPAFGAEDLET
ARVYGLPLLKTVDEEGKLLVEPFKGLYFREANRAILRDLRGRGLLFKEESYLHSY
>d1ffya2 b.51.1.1 (A:201-394) Isoleucyl-tRNA synthetase (IleRS) {Staphylococcus aureus}
HDKRSASIYVAFNVKDDKGVVDADAKFIIWTTTPWTIPSNVAITVHPELKYGQYNVNGEKYIIAEALS
DAVAEALDWDKASIKLEKEYTGKELEWVVAQHPFLDRESLVINGDHVTTDAGTGCVHTAPGHGEDD
YIVGQQYELPVISPIDDKGVFTEEGGFEGMFDKANKAVTDLLTEKGALLKLDIFITHSY
>d1gaxa2 b.51.1.1 (A:190-342) Valyl-tRNA synthetase (ValRS) {Thermus thermophilus}
TEPTPGKLYTLRYEVEGGGFIEIATVRPETVFADQAIAVHPEDERYRHLLGKRARIPLTEVWIPILADP
AVEKDFGTGALKVTPAHDPLDYEIGERHGLKPVSVINLEGRMEGERVPEALRGLDRFEARRKAVELF
REAGHLVKEEDYTIALA
>d1gmua1 b.107.1.1 (A:1-70) Urease metallochaperone UreE, N-terminal domain {Klebsiella
aerogenes}
MLYLTQRLEIPAAATASVTLPIDVRVKSrvKVTLNDRDAGLLLPRGLLLRGGDVLNSNEEGTEFVQVI
AA
>d1eara1 b.107.1.1 (A:1-74) Urease metallochaperone UreE, N-terminal domain {Bacillus
pasteurii}
MVITKIVGHIDDLSHQIKKVDWLEVEWEDLNKRILRKETENGTDIAIKLENSGTLRYGDVLYESDDT
LIAIRTK
>d2eng_ b.52.1.1 (-) Endoglucanase V {Humicola insolens}
ADGRSTRYWDCKPSCGWAKKAPVNQPVFSCNANFQRITDFDAKSGCEPGGVAYSCADQTPWAVN
DDFALGFAATSIAGSNEAGWCCACYELFTSGPVAGKKMVVQSTSTGGDLGSNHFDLNIPIGGVGFID
GCTPQFGGLPGQRYGGISSRNECDRFPDALKPGCYWRFDWFKNADNPSFSFRQVQCPAELVARTGC
RRNDDGNFPAV
>d1bw3_ b.52.1.2 (-) Barwin {Barley (Hordeum vulgare)}
EQANDVRATYHYRPAQNNWDLGAPAVSAYCATWDASKPLSWRSKYGWTAFCGPAGPRGQAACGK
CLRVTNPATGAQITARIVDQCANGGLDLWDVFTKIDTNGIGYQQGHLNVNYQFVDCRD
>g1aw8.1 b.52.2.1 (A;B:) Pyruvyl dependent aspartate decarboxylase, ADC {Escherichia
coli}
MIRTMLQGKLRVKTTHADLHYEGXSCAIDQDFLDAAGILENEAIDIWNVTNGKRFSTYIAIAAERGS
RIISVNGAAAHCASVGDIVIIASFVTMPDEEARTWRPNVAYFEGDNEMK
>d1eu1a1 b.52.2.2 (A:626-780) Dimethylsulfoxide reductase (DMSO reductase)
{Rhodobacter sphaeroides}

ERLGGAGAKYPLHVVASHPKSRLHSQLNGTSLRDLYAVAGHEPCLINPADAAARGIADGDVLRVFNDRGQILVGAKVSDAVMPGAIQIYEGGWYDPLDPSEEGTLDKYGDVNVLSLDVGTSKLAQGNCGQTLADVEKYAGAPVTVTVFDTPKGA

>d1dmr_1 b.52.2.2 (626-781) Dimethylsulfoxide reductase (DMSO reductase) {Rhodobacter capsulatus}

ERLDGPGAKYPLHIAASHPFNRLHSQLNGTVLREGYAVQGHEPCLMHPDDAAARGIADGDVVRVHNRGQILTGVKVTDAVMKGVIIQIYEGGWYDPSDVTEPGTLDKYGDVNVLSADIGTSKLAQGNCGQTVLAEVEKYTGPAVTLTGTFVAPKAAE

>d1aa6_1 b.52.2.2 (565-715) Formate dehydrogenase H {Escherichia coli}

PIDKLTDEYPMVLSTVREVGHYSCRSMGTGNCAALAADEPGYAQINTEDAKRLGIEDEALVWVHSRKGKIITRAQVSDRPNKGAIYMTYQWWIGACNELVTENLSPITKTPEYKYCAVRVEPIADQRAAEQYVIDEYNKLRRLREAALA

>d1tmo_1 b.52.2.2 (632-798) Trimethylamine N-oxide reductase {Shewanella massilia}

ERSHGGPGSDKHPIWLQSCHPDKRLHSQMCESEYRETYAVNGREPVIYISPVDAKARGIKDGDIVRVFNDRGQLLAGAVVSDNFPKGIVRIHEGAWYGPVKGKDGSTEGGAEVGALCSYGDPTLTLTDIGTSKLAQACSAYTCLVEFEKYQGGKVPKVSSFDGPIEVEI

>d1g8ka1 b.52.2.2 (A:683-825) Arsenite oxidase large subunit {Alcaligenes faecalis}

LPATVQQKDKYRFWLNNGRNNEVWQTAYHDQYNSLMQERYPMAYIEMNPDDCKQLDVTGGDIVEVYNDFGSTFAMVYPVAEIKRGQTFMLFGYVNGIQGDVTTDWTDRDIIPYYKGTWGDIRKVGSMSEFKRTVSFKSRRFG

>d2napa1 b.52.2.2 (A:601-723) Dissimilatory nitrate reductase (NAP) {Desulfovibrio desulfuricans}

AAEPPDAEYPLYLTSMRVIDHWHTATMTGKVPPELQKANPIAFVEINEEDAARTGIKHGDSVIVETRRDAMELPARVSDVCRPGLIAPFFDPKLVNKLFLDATDPVSREPEYKICAAVRKA

>d1qcsa1 b.52.2.3 (A:0-85) N-terminal domain of NSF-N, NSF-Nn {Hamster (Cricetulus griseus)}

NMAGRSMQAARCPDELSSNCAVVSEKDYQSGQHVVIVRTSPNHKYIFTLRTHPSVVPVGSVAFSLPQRKWAGLSIGQEIEVALYSF

>d1cr5a1 b.52.2.3 (A:26-107) N-terminal domain of NSF-N, NSF-Nn {Baker's yeast (Saccharomyces cerevisiae), sec18p}

TRHLKVSNCNNSYALANVAAVSPNDFPNNIYIIIDNLFVFTTRHSNDIPPGTIGFNGNQRTWGGWSLNQDVQAKAFDLFKY

>d1cz4a1 b.52.2.3 (A:1-91) N-terminal domain of VAT-N, VAT-Nn {Archaeon Thermoplasma acidophilum}

MESNNGIILRVAEANSTDPGMSRVRLDESSRRLDAAEIGDVVEIEKVRKTVGRVYRARPEDENKGIIVRIDSVMRNCCGASIGDKVKVRKVR

>d1e32a1 b.52.2.3 (A:21-106) Membrane fusion atpase p97 N-terminal domain , P97-Nn {Mouse (Mus musculus)}

NRPNRLIVDEAINEDNSVVSLSQPKMDELQLFRGDTVLLKGGKRREAVCIVLSDDTCSDEKIRMNRVVRNNLRVRLGDVISIQPCP

>d1dfup_ b.53.1.1 (P:) Ribosomal protein L25 {Escherichia coli}

MFTINAEVRKEQGGASRRLRAANKFPPIIYGGKEAPLAIELDHDKVMNMQAKAEFYSEVLTIVVDGKEIKVKAQDVQRHPYKPKLQHIDFVRA

>d1feua_ b.53.1.1 (A:) Ribosomal protein TL5 (general stress protein CTC) {Thermus

thermophilus}
MEYRLKAYYREGEKPSALRRAGKLPGLMYNRHLNRKVYVDLVEFDKVFQRQASIIHHVIVLELPDGQS
LPTLVRQVNLDKRRRPEHVDFFVLSDEPVEMYVPLRFVGTGTPAGVRRAGGVLQEIHRDILVKVSPRNI
PEFIEVDVSGLEIGDSLHASDLKLPGLVAVSPEETIAAVVPPEDVEKLAE
>d1gtra1 b.53.1.2 (A:339-547) Gln-tRNA synthetase (GlnRS), C-terminal (anticodon-binding)
domain {Escherichia coli}
APRAMAVIDPVKLVNIENYQGEEMVTMPNHPNKPENGRSRQVPFSGEIWIDRADFREEANKQYKRL
VLGKEVRLRNAYVIKAERVEKDAEGNITTFCTYDADTLSKDPADGRKVKGVHWSAAHALPVEIRL
YDRLFSVPNPGAADDFLSVINPESLVIKQGAEPKDAVAGKAFQFEREGYFCLDSRHSTAEPVFN
RTVGLRDT
>d1h9db_ b.54.1.1 (B:) Core binding factor beta, CBF {Human (Homo sapiens)}
PRVVPDQRSKFENEEFFRKLRSRECEIKYTGFDRDPHEERQARFQNAACRDGRSEIAFVATGTNLSLQFF
PASWQGEQRQTPSREYVDLEREAGKVYLKAPMILNGVCVIWKGWIDLQRLDGMGCLEFDEERAQQ
E
>d1mai_ b.55.1.1 (-) Phospholipase C delta-1 {Rat (Rattus norvegicus)}
GLQDDPDLQALLKGSQLLKVKSSSWRRERFYKLQEDCKTIWQESRKVMRSPESQLFSIEDIQEVRM
GHRTEGLEKFARDIPEDRCFSIVFKDQRNTLDLIAPSPADAQHWVQGLRKIIH
>d1btn_ b.55.1.1 (-) beta-spectrin {Mouse (Mus musculus), brain}
MEGFLNRKHEWEAHNKKASSRSWHNVYCVINNQEMGFYKDAKSAASGIPYHSEVPVSLKEAICEVA
LDYKKKKHVFKLRLSDGNEYLFQAKDDEEMNTWIQAISSA
>d1dro_ b.55.1.1 (-) beta-spectrin {Fruit fly (Drosophila melanogaster)}
GSGTGAGEGHEGYVTRKHEWDSTTKKASNRSDKVYMAAKAGRISFYKDQKGYKSNPELTFRGEF
SYDLQNAIEIASDYTKKKHVLRVLANGALFLLQAHDDEMSQWVTSLKAQSDSTA
>d1dyna_ b.55.1.1 (A:) Dynamin {Human (Homo sapiens)}
ILVIRKGWLTINNIGIMKGGKEYWVFLTAENLSWYKDDEEKEKKYMLSVDNLKLRDVEKGFMSK
HIFALFNTEQRNVYKDYRQLELACETQEEVDSWKASFLRAGVYPERV
>d1btk_ b.55.1.1 (A:) Bruton's tyrosine kinase {Human (Homo sapiens)}
AAVILESIFLKRQQKKKTSPLNFKKCLFLLTVHKLSYIEYDFERGRGSKKGSIDVEKITCVETVVPE
KNPPPERQIPRRGEESSEMEQISIIERFPYPFQVVYDEGPLYVFSPTTEELRKRWIHQLKNVIRYNSDLV
QKYHPCFWIDGQYLCCSQTAKNAMGCQILEN
>d1pls_ b.55.1.1 (-) Pleckstrin, N-terminal domain {Human (Homo sapiens)}
MEPKRIREGYLVKKGVSFNTWKPMWVVLLEDGIEFYKKS DNSPKGMIPLKGSTLTSPCQDFGKRM
FVFKITTTKQDHFQAAFLEERDAWVRDINKAIKICIEGLEHHHHHH
>d1dbha2 b.55.1.1 (A:418-550) Son of sevenless-1 (sos-1) {Human (Homo sapiens)}
AIKKMNEIQKNIDGWEGKDIGQCCNEFIMEGTLTRVGAKHERHIFLFDGLMICCKSNHGQPRLP GAS
NAEYRLKEKFFMRKVQINDKDDTNEYKHA FEIILKDENS VIFSAKSAEEKNNWMAALISLQYRSTL
>d1foea2 b.55.1.1 (A:1240-1401) GEF of TIAM1 (T-Lymphoma invasion and metastasis
inducing protein 1) {Mouse (Mus musculus)}
EFGAVFDQLIAEQTGEKKEVADLSMGDLLLLHTSVIWLNPPASLGKWKKEPELAAAFVFKTAVVLVYKD
GSKQKKKLVGSHRLSIYEEWDPFRFRHMIPTEALQVRALPSADAEANAVCEIVHVKSESEGRPERVF
HLCCSSPESRKDFLKSIVHSILRDKHRRQ
>d1bak_ b.55.1.1 (-) G-protein coupled receptor kinase 2 (beta-adrenergic receptor kinase 1)
{Human (Homo sapiens)}
GSHMGKDCIMHGYMSKMGNPFLTQWQRRYFYLPNRLEWRGEGEAPQSLTMEEIQSVEETQIKE

RKCLLLKIRGGKQFILQCSDPELVQWKELRDAYREAQQLVQRVPMKNKPRS
>d1faoa_ b.55.1.1 (A:) Dual adaptor of phosphotyrosine and 3-phosphoinositides
DAPP1/PHISH {Human (Homo sapiens)}
PSLGTKEGYLTKQGGLVKTWKTRWFTLHRNELKYFKDQMSPEPIRILDLTECSAVQFDYSQERVNCF
CLVFPFRTFYLCAKTGVEADEWIKILRWKLSQI
>d1fgya_ b.55.1.1 (A:) Grp1 {Mouse (Mus musculus)}
TFFNPDREGWLLKLGGRVKTWKRRWFILTDNCLYFYEYTTDKEPRGIIPLENLSIREVLDPRKPNCF
ELYNPSHKGQVIKACKTEADGRVVEGNHVYRISAPSPEEKEEWMKSIKASISRDPFYDM
>d1fhoa_ b.55.1.1 (A:) UNC-89 {Nematode (Caenorhabditis elegans)}
MGDTGKLGRIIRHDAFQVWEGDEPPKLRVYVFLFRNKIMFTEQDASTSPPSYTHYSSIRLDKYNIRQH
TTDEDIVLQPQEPGLPSFRIKPKDFETSEYVRKAWLRDIAEEQEKYAAERD
>d1aqca_ b.55.1.2 (A:) X11 {Human (Homo sapiens)}
MEDLIDGIIFAANYLGSTQLLSDKTPSKNVRMMQAQEAVSRIKMAQKLAKSRRKKAPEGESQPMTEV
DLFILTQRIKVLNADTQETMMDHPLRTISYIADIGNIVVLMARRRIPRSNSQENVEASHPSQDGKRQY
KMICHVFESEDAQLIAQSIGQAFSVAYQEFLR
>d1qqga1 b.55.1.2 (A:12-114) Insulin receptor substrate 1, IRS-1 {Human (Homo sapiens)}
DVRKVGYLKPKSMHKRFFVLRAASEAGGPAREYYENEKKWRHKSSAPKRSIPLESCFNINKRAD
SKNKHLVALYTRDEHFAIAADSEAEQDSWYQALLQLH
>d1qqga2 b.55.1.2 (A:159-262) Insulin receptor substrate 1, IRS-1 {Human (Homo sapiens)}
AFKEVWQVILKPKGLGQTKNLIGIYRLCLTSKTISFVKLNSEAAAVVLQLMNIRRCGHSENFVIEVGR
SAVTGPGEFWMQVDDSVVAQNMHETILEAMRAMSD
>d1shca_ b.55.1.2 (A:) Shc adaptor protein {Human (Homo sapiens)}
GSHMGQLGGEWTRHGSFVNKPTRGWLHPNDKVMGPGVSYLVRYMGCVEVLQSMRALDFNTRT
QVTREAISLVCEAVPGAKGATRRRKPCSRPLSSILGRSNLKFAGMPITLTVSTSSLNLMAADCKQIIAN
HHMQSISFASGGDPDTAEYVAYVAKDPVNQRACHILECPEGLAQDVISTIGQAFELRFKQYLR
>d1ddma_ b.55.1.2 (A:) Numb {Fruit fly (Drosophila melanogaster)}
HQWQADEEAVRSATCSFSVKYLGCVFVFESEALKVLQRSSRRPVRGLLHVSGDGLRVVD
DETKGLIVDQTIEKVSFCAPDRNHERGFSYICRDGTTRRWCMCHGFLACKDSGERLSHAVGCAFAVCL
ER
>d1rrpb_ b.55.1.3 (B:) Nuclear pore complex protein Nup358 {Human (Homo sapiens)}
HFEPVPLPKIEVKTEGEDEEEFFCNRAKLFKRFVDESKEWKERGIGNVKILRHKTSKIRLLMRRE
QVLKICANHYISPDMLTPNAGSDRSFVWHALDYADELPKPEQLAIRFKTPEEAALFKCKFEEAQSI
>d1k5db_ b.55.1.3 (B:) Ran-binding protein 1, Ranbp1 {Human (Homo sapiens)}
NHDPQFEPVSLPEQEIKTLEEDDEEELFKMRAKLFRAFASNDLPEWKERGTGDVKLLKHKEKGAIRL
LMRRDKTLKICANHYITPMMELKPNAGSDRAWVWNTHADFADECPELLAIRFLNAENAQKFKT
KFEECRKEIEEREK
>d1evha_ b.55.1.4 (A:) Enabled {Mouse (Mus musculus)}
SEQSICQARAAMVYDDANKKWPAGGSTGFSRVHIYHHTGNNTFRVVGKIQDHQVVINCAIPKG
LKYNQATQTFHQWRDARQVYGLNFGSKEDANVFASAMMHALEVLN
>d1qc6a_ b.55.1.4 (A:) Ena/vasp-like protein {Mouse (Mus musculus)}
MSEQSICQARASVMYDDTSKKWVPIKPGQGGFSRINIYHNTASSTFRVVGKLDQDQVINYIVKQ
LKYNQATPTFHQWRDARQVYGLNFASKEEATTFSNAMLFALNIMN
>d1legxa_ b.55.1.4 (A:) Vasodilator-stimulated phosphoprotein (VASP) {Human (Homo
sapiens)}

MSETVICSSRATVMLYDDGNKRWLPAGTGPQAFSRVQIYHNPTANSFRVVGGRKMOPDQQVVINCAI
VRGVKYNQATPNFHQWRDARQVWGLNFGSKEDAAQFAAGMASALEALEG
>d1ddwa_b.55.1.4 (A:) Homer {Rat (Rattus norvegicus)}
MGEQPIFSTRAHVQIDPNTKKNWVPTSKHAVTVSYFYDSTRNVYRIISLDGSKAIINSTITPNMTFT
KTSQKFGQWADSRANTVYGLGFSSEHLSKFAEKFQEFKEAAR
>d1i7aa_b.55.1.4 (A:) Homer {Mouse (Mus musculus), 2b/vesl 2}
EQPIFTTRAHVQIDPSTKKNWVPASKQAVTVSYFYDVTRNSYRIISVDGAKVIINSTITPNMTFTKTS
QKFGQWADSRANTVYGLGFSSELQTKFAEKFQEVREAAR
>d1e5wa2_b.55.1.5 (A:199-346) Moesin {Human (Homo sapiens)}
EMYGVNYFSIKNKKGSELWLGVDALGLNIYEQNDRLTPKIGFPWSEIRNISFNDKKFVIKPIDKKAPD
FVFYAPRLRINKRILALCMGNHELYMRRRKPDTIEVQMQKAQAREEKHQKQMERAMLENEKKKRE
MAEKEKEKIEREKEE
>d1ef1a2_b.55.1.5 (A:199-297) Moesin {Human (Homo sapiens)}
EMYGVNYFSIKNKKGSELWLGVDALGLNIYEQNDRLTPKIGFPWSEIRNISFNDKKFVIKPIDKKAPD
FVFYAPRLRINKRILALCMGNHELYMRRRKP
>d1gc7a2_b.55.1.5 (A:199-297) Radixin {Mouse (Mus musculus)}
EMYGVNYFEIKNKKGTELWLGVDALGLNIYEHDDKLTTPKIGFPWSEIRNISFNDKKFVIKPIDKKAPD
FVFYAPRLRINKRILALCMGNHELYMRRRKP
>d1gg3a2_b.55.1.5 (A:188-279) Erythroid membrane protein 4.1R {Human (Homo sapiens)}
GVDLHKAKDLEGVDIILGVCSSGLLVYKDKLRINRFPWPVKLKISYKRSSFIFIKIRPGEQEYESTIGFK
LPSYRAAKKLWKCVEHHTFFR
>d1h4ra2_b.55.1.5 (A:215-313) Merlin {Human (Homo sapiens)}
EMYGVNYFAIRNKKGTELLGVDALGLHIYDPENRLTPKISFPWNEIRNISYSDKEFTIKPLDKKIDVF
KFNSSKLRVNLKILQLCIGNHDLFMRRRKA
>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)}
NTQSKLTVKGNLDTYGFCDVWTFIVKNCQVTVEDSHRDASQNGSGDSQSVISVDKLRIVACNSK
>d1iega_b.57.1.1 (A:) Human cytomegalovirus protease {Human cytomegalovirus}
QAVAPVYVGGFLARYDQSPDEAELLPRDVVEHWLHAQGQGQPSLSVALPLNINHDDTAVVGHVAA
MQSVRDGLFCLGCVTSPRFLEIVRRASEKSELVSRGPVSPLQPKVVEFLSGSYAGLSLASRRCDDVEQ
ATSLSGSETTPFKAVALCSVGRRRGTLAVYGRDPEWVTQRFDPDLTAARDGLRAQWQRCGSTAVDA
SGDPFRSDSYGLLGNSVDALYIRERLPKLRDYDKQLVGVTERESYVKA
>d1jq6a_b.57.1.1 (A:) Human cytomegalovirus protease {Human cytomegalovirus}
VAPVYVGGFLARYDQSPDEAELLPRDVVEHWLHAQGQGQPSLSVALPLNINHDDTAVVGHVAA
SVRDGLFCLGCVTSPRFLEIVRRASEKSELVSRGPVSPLQPKVVEFLSGSYAGLSLSSRRCDDVEQAT
SLSGSETTPFKHVALCSVGRRRGTLAVYGRDPEWVTQRFDPDLTAARDGLRAQWQRCGSTAVDASG
DPFRSDSYGLLGNYVDALY
>d1at3a_b.57.1.1 (A:) HSV-2 protease {Herpes simplex virus type 2}
RAVPIYVAGFLALYDSGDPGELALDPDTVRAALPPENPLPINVDHRARCEVGRVLAVVNDPRGPFV
GLIACVQLERVLETAASAAIFERRGPALSREERLLYLITNYLPSVSLSTKRRGDEVPPDRTLFAHVALCA
IGRRLGTIVTYDTSLDAAIAPFRHLDPATREGVRREAAEALALAGRTWAPGVEALTHLSTAVNN

MMLRDRWSLVAERRRQAGIAGHTYLQA

>d1fl1a_b.57.1.1 (A:) KSHV protease {Kaposi's sarcoma-associated herpes virus}

AQGLYVGGFVDVVSCKPLEQELYLDPDQVTDYLPVTEPLPITIEHLPETEVGWTGLGLFQVSHGIFCTG
AITSPAFLELASRLADTSHVARAPVKNLKPKEPLLEILHTWLPGLSLSSIHPRELSQTPSGPVFQHVSCL
ALGRRRGTVAVYGHDAEWVVSFRFSSVSKSERAHILQHVSSCRLEDLSTPNFVSPLETLMAKAIDAGFI
RDRLDLLKTDRGVASILSPVYLKA

>d1vzv__ b.57.1.1 (-) VZV protease {Varicella-Zoster virus}

EALYVAGYLALYSKDEGELNITPEIVRSALPPTSKIPINIDHRKDCVVGEVIAIIEDIRGPFFLGIVRCPQL
HAVLFEEAHSNFFGNRDSVLSPLERALYLVNTYLPVSLSSKRLFTHVVALCVVGRRVGTVVNYDCTPE
SSIEPFRVLSMESKARLLSLVKDYAGLNKVVWVSEDKLAKVLLSTAVNNMMLLRDRWDVVAKRREA
GIMGH

>d1a49a1 b.58.1.1 (A:116-217) Pyruvate kinase (PK) {Rabbit (*Oryctolagus cuniculus*)}

PEIRTGLIKSGTAEVELKKGATLKITLDNAYMEKCDENILWLDYKNICKVVVDVGSKVYVDDGLISLQ
VKQKGPFLVTEVENGGFLGSKKGVNLPGAAVDL

>d1pkm_1 b.58.1.1 (116-217) Pyruvate kinase (PK) {Cat (*Felis domestica*)}

PEIRTGLIKSGTAEVELKKGATLKITLDNAYMEKCDENLVLDYKNICKVVEVGSKVYVDDGLISLL
VKEKGADFLVTEVENGGSLGSKKGVNLPGAAVDL

>d1pkla1 b.58.1.1 (A:88-186) Pyruvate kinase (PK) {*Leishmania mexicana*}

EIRTGQFVGDAVMERGATCYVTTDPAFADKGTDKDFYIDYQNLKVVVRPGNYIYIDDGILILQVQSH
EDEQTLLECTVTNSHTISDRRGVNLPGCDVDL

>d1a3wa1 b.58.1.1 (A:88-188) Pyruvate kinase (PK) {Baker's yeast (*Saccharomyces cerevisiae*)}

PEIRGTTTTNDVDYPIPPNHEMIFTTDDKYAKACDDKIMYVDYKNITKVISAGRIIYVDDGVLSFQVL
EVDVDDKTLKVKALNAGKICSHKGVNLPGTDVDL

>d1e0ta1 b.58.1.1 (A:70-167) Pyruvate kinase (PK) {*Escherichia coli*}

PEIRTMKLEGGNDVSLKAGQTFTFTTDSVIGNSEMVAVTYEGFTTDLVSGNTVLVDDGLIGMEVTA
IEGNKVICVLNNGDLGENKGVNLPGVSIAL

>d1g8fa1 b.58.1.2 (A:2-168) ATP sulfurylase N-terminal domain {Baker's yeast (*Saccharomyces cerevisiae*)}

PAPHGILQDLIARDALKKNELLSEAQSSDILVWNLTTPRQLCDIELILNNGGFSPLTGFLNENDYSSVVT
DSRLADGTLWTIPITLDVDEAFANQIKPDTRIALFQDDEIPIAILTVQDVYKPNKTIEAERVFRGDPEH
PAISYLFNVAGDYVYVGGSLAIQLPQHYD

>d1i2da1 b.58.1.2 (A:2-170) ATP sulfurylase N-terminal domain {Fungus (*Penicillium chrysogenum*)}

ANAPHGGVLKDLLARDAPRQAELAAEAESLPAVTLTERQLCDLELIMNGGFSPLGFMNQADYDRV
CEDNRLADGNVFSMPITLDASQEVIDEKKLQAGSRITLDRFRDDRNLAILTIDDIYRPDKTKEAKLVF
GGDPEHPAIVYLNNTVKEFYIGGKIEAVNKLNHVD

>d1jhda1 b.58.1.2 (A:1-173) ATP sulfurylase N-terminal domain {unnamed symbiont of *Riftia pachyptila*}

MIKPVGSDELKPLFVYDPEEHHKLSHEAESLPSVVISSQAAGNAVMMGAGYFSPQLGFMNVADAMG
AAEKMTLSDGSFFPVPVLCLENTDAIGDAKRIALRDPNVEGNPVLAVMDIEAIEEVSDEQMAVMT
DKVYRRTDMDHIGVKTFFNSQGRVAVSGPIQVLNFSYFQADF

>d1ik9a1 b.59.1.1 (A:1-117) XRCC4, N-terminal domain {Human (*Homo sapiens*)}

MERKISRHLVSEPSITHFLQVSWEKTLESQVITLTDGHSAWTGTVSESEISQEADDMAKMKGYVG

ELRKALLSGAGPADVYTFNFSKESAYFFFEKNLKDVSFRLGFSFNLEKVE
>d1hbq_ b.60.1.1 (-) Retinol binding protein {Cow (Bos taurus)}
ERDCRVSSFRVKENFDKARFAGTWYAMAKKDPEGLFLQDNVAEFSVDENGQMSATAKGRVRLN
WDVCADMVGTFTDTEPAKFKMKYWGVASFLQKGNDDHWIIDTDYETFAVQYSCRLNLDGTCAD
SYSFVFARDPSGFSPEVQKIVRQRQEELCLARQYRLIPHNGYCNK
>d1aqb_ b.60.1.1 (-) Retinol binding protein {Pig (Sus scrofa domestica)}
ERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNVAEFSVDENGHMSATAKGRVRLN
WDVCADMVGTFTDTEPAKFKMKYWGVASFLQKGNDDHWIIDTDYDYAVQYSCRLQNLDTGCA
DSYSFVFARDPHGFSPEVQKIVRQRQEELCLARQYRIITHNGYCD
>d1rbp_ b.60.1.1 (-) Retinol binding protein {Human (Homo sapiens)}
ERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNVAEFSVDETGQMSATAKGRVRLN
WDVCADMVGTFTDTEPAKFKMKYWGVASFLQKGNDDHWIVD TDYDYAVQYSCRLNLDGTCAD
DSYSFVFSRDPNGLPPEAQKIVRQRQEELCLARQYRLIVHNGYCD
>d1iua_ b.60.1.1 (A:) Retinol binding protein {Chicken (Gallus gallus), plasma isoform}
MDCRVSSFKVKENFDKNRYSGTWYAMAKKDPEGLFLQDNVVAQFTVDENGQMSATAKGRVRLFN
NWDVCADMIGSFTDTEPAKFKMKYWGVASFLQKGNDDHWVVD TDYDYALHYSRELNEDGTC
ADSYSFVFSRDPKGLPPEAQKIVRQRQIDLCLDRKYRVIVHNGFCS
>d1hn2a_ b.60.1.1 (A:) Odorant-binding protein {Cow (Bos taurus)}
AQEEEEAEQNLSELSPWRTVYIGSTNPEKIQENGFRTYFRELVDDEKGTVDYFYSVKRDGKWK
VHVKATKQDDGTYVADYEGQNVFKIVSLSRTHLVAHNINVDKHKQTTELTELTVKLNVEDELEK
WKLTEKIDKKNVNFLENENHPHPE
>d1dzka_ b.60.1.1 (A:) Odorant-binding protein {Pig (Sus scrofa)}
FELSGKWITSYIGSSDLEKIGENAPFQVFMRSIEFDDKESKYYLNFFSKENGICEEFLIGTKQEGNTY
DVNYAGNNKFVVSYASETALISNINVDEEGDKTIMTGLLGKGTDIEDQDLEKFKEVTRENGIPEENIV
NIERDDCPA
>d1bj7_ b.60.1.1 (-) Lipocalin allergen {Cow (Bos taurus), bos d 2}
IDPSKIPGEWRIIAAADNKDKIVEGGPLRNYRRIECINDCESLSITFYLKDQGTCLLLTEVAKRQEGY
VYVLEFYGTNTLEVIHVSENMLVTVYVENYDGERITKMTEGLAKGTSFTPEELEKYQQLNSERGV
NIENLIKTDNCP
>d1ew3a_ b.60.1.1 (A:) Lipocalin allergen {Horse (Equus caballus), equ c 1}
VAIRNFDISKISGEWYSIFLASDVKEKIEENGSMRVFVDVIRALDNSSLYAEYQTKVNGECTEFPMV
KTEEDGVYSLNYDGYNVFRISEFENDEHIILYLVNFDKDRPFQLFEFYAREPDVSPEIKEEFV
KIVQKR
GIVKENIIDLTKIDRCFQLRG
>d1e5pa_ b.60.1.1 (A:) Aphrodisin, a sex pheromone {Golden hamster (Mesocricetus
auratus)}
FAELQGWYTIIVIAADNLEKIEEGPLRFYFRHIDCYKNCSEMEITFYVITNNQCSKTTVIGYLKNG
TYETQFEGNNIFQPLYITSDKIFFTNKNMDRAGQETNMIVVAGKGNALTPPEENEILVQFAHEKIPVE
NILNILATDTCPE
>d1beba_ b.60.1.1 (A:) beta-Lactoglobulin {Cow (Bos taurus)}
QTMKGLDIQKVAGTWYSLAMAASDISLLDAQSAPLRVYVEELKPTPEGDLEILLQKWENGECAQKKI
IAEKTKIPAVFKIDALNENKVLVLD TDYKYYLLFCMENSAPPEQSLVCQCLVRTPEVDDEALEKFDKA
LKALPMHIRLSFNPTQLEEQ
>d1exsa_ b.60.1.1 (A:) beta-Lactoglobulin {Pig (Sus scrofa)}
VEVTPIMTELDTQKVAGTWHTVAMAVSDVSLLDKSSPLKAYVEGLKPTPEGDLEILLQKRENDKC

AQEVLLAKKTDIPAVFKINALDENQLFLLD TDYD SHLLLCMENSASPEHSLVCQSLARTLEVDDQIRE
KFEDALKTLSVPMRILPAQLEEQCRV

>d1epba_b.60.1.1 (A:) Retinoic acid-binding protein {Rat (Rattus norvegicus), albino}
VKDFDISKFLGFWYEIAFASKMGTPGLAHKEEKMGAMVVELKENLLALTTTYSEDHCVLEKVTAT
EGDGPAPKFQVTRLSGKKEVVVEATDYLYTIAIIDITSLVAGAVHRTMKLYSRSLDDNGEALYNFRKITS
D HGFSETDLYILKHDLT CVKVLQSA A

>d1jv4a_b.60.1.1 (A:) Major urinary protein/alpha-2u-globulin {Mouse (Mus musculus)}
EEASSTGRNFNVEKINGEWHITILASDKREKIEDNGNFRLFLEQIHVLEKSLVLKFHTVRDEECSELS
MVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLIN EKDGETFQLMGLYGREPDLSSDIKERFA
QLCEEHGILRENIIDLSNANRC

>d2a2ua_b.60.1.1 (A:) Major urinary protein/alpha-2u-globulin {Rat (Rattus norvegicus)}
EEASSTRGNLDVAKLNGDWFSIVVASNKREKIEENGSMRVFMQHIDVLENSLGFKFRIKENGECREL
YLVA YKTPEDGEYFVEYDGGNTFTILKTDYDRYVMFH LINFKNGETFQLMVLYGR TKDLSSDIKEKFA
KLCEAHGITRDNIIDLT KTDRCL

>d1qgsa_b.60.1.1 (A:) Neutrophil gelatinase-associated lipocalin (NGAL) {Human (Homo sapiens)}
TSDLIPAPPLSKVPLQQNFQDNQFQGK WYVGLAGNAILREDKDPQKMYATIYEEKEDASYNVTSVL
FRKKKCDYAIRTFVPGCQPG EFTLGNIKSYPLTSYLVRVSTNYNQHAMVFFKKV SQNREYFKITLY
GR TKELTSELKNNFIRFSKSLGLPENHIVFPVPIDQCID

>d1bbpa_b.60.1.1 (A:) Bilin-binding protein {Cabbage butterfly (Pieris brassicae)}
NVYHDGACPEVKPVDNFDWSNYHGKWW EVAKYPNSVEKYGKCGWAEYTP EGKSVKVS NYHVIHG
KEYFIEGTAYPVGDSKIGKIYHKLTYGGVTKENVFNVLSTDNKNYIIGYYCKYDEDDKKGHQDFVWVLS
RSKVL TGEAKTAVENYLIGSPV VDSQKL VYSDFSEAAACKVN

>d1i4ua_b.60.1.1 (A:) Alpha-crustacyanin {European lobster (Homarus gammarus)}
DKIPDFVVP GK CASVDRNKLWAEQTPNRNSYAGVWYQFALTNNPYQLIEKCVRNEYSFDGKQFVIES
TGIAYDGNLLKRNGKLYPNPFGEPHLSIDYENSFAAPLVILETDYSNYACLYSCIDY NFGYHSDFSFIFS
RSANLADQYVKKCEAAFKNINVD TTRFVKTVQGSSCPYDTQKTL

>d1qfta_b.60.1.1 (A:) Histamine binding protein {Brown ear tick (Rhipicephalus appendiculatus)}
NQPDWADEAANGAHQDAWKS LKADVENVYYMVKATYKNDP VWGNDFTCVGVMANDVNEDEKS
IQAEFLFMNADTNMQFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAYSDDNCDVIYVPGTD
GNEEGYELWTTDYDNIPANCLNKFNEYAVGRETRDVFTSACLEIAAA

>d1np1a_b.60.1.1 (A:) Nitrophorin 1 {Rhodnius prolixus}
KCTKNALAQ TGFNKDKYFNGDVWYVTDYLDLEPDDV PKRYCAAL AAGTASGKLKEALYHYDPKTQ
DTFYDVSELQEESPGKYTANFKKVEKNGNVKVDV TSGNYTFTVMYADDSSALIHTCLHKG NKDLG
DLYAVLNRNKDTNAGDKVKGAVTAASLKFSDFISTKDNKCEYDNVSLKSL LTK

>d1euoa_b.60.1.1 (A:) Nitrophorin 2 (prolixin-s) {Rhodnius prolixus}
MDCSTNISPKQLDKAKYFSGK WYVTHFLDKDPQVTDQYCSSFTPRES DGTVKEALYHYNANKKTS
FYNIGEGKLESSGLQYTAKYKTVDKKAVLKEADEKNSYTLTVLEADDSSALVHICLREGSKDLGDLY
TVLTHQKDAEPSAKVKS AVTQAGLQLSQFVGT KDLGCCYDDQFTSL

>d1koia_b.60.1.1 (A:) Nitrophorin 4 {Rhodnius prolixus}
ACTKNAIAQTGFNKDKYFNGDVWYVTDYLDLEPDDV PKRYCAAL AAGTASGKLKEALYHYDPKTQ
DTFYDVSELQVESLGKYTANFKKVDKNGNVKVAVTAGNYTFTVMYADDSSALIHTCLHKG NKDLG
DLYAVLNRNKDAAAGDKVKS AVSAATLEFSKFISTKENNCAYDNDSLKSL LTK

>d1hms_ b.60.1.2 (-) Muscle fatty acid binding protein (m-fabp) {Human (Homo sapiens)}
VDAFLGTWKLVDKSNFDDYMKSLGVGFATRQVASMTKPTTIIKNGDILTLKTHSTFKNTEISFKLGV
EFDETTADDRKVKSIIVTLDGGKLVHLQKWDGQETTLVRELIDGKLILTLHGTAVCTRTRTYEKE

>d1bwya_ b.60.1.2 (A:) Muscle fatty acid binding protein (m-fabp) {Cow (Bos taurus)}
VDAFVGTWKLVDKSNFDDYMKSLGVGFATRQVGNMTKPTTIIENVNGDTVIIKTQSTFKNTEISFKLG
VEFDETTADDRKVKSIIVTLDGGKLVHVQKWNGQETSLVREMVDGKLILTLHGTAVCTRTRTYEKQA

>d1a57_ b.60.1.2 (-) Intestinal fatty acid binding protein {Rat (Rattus norvegicus)}
AFDGTWKVDRNENYSGAHDNLKLTITQEGNKFTVKESSNFRNIDVVFELGVDFAYSADGTELTGT
WTMEGNKLVGKFKRVDNGKELIAVREISGNELIQTYTYEGVEAKRIFKKE

>d1ifc_ b.60.1.2 (-) Intestinal fatty acid binding protein {Rat (Rattus norvegicus)}
AFDGTWKVDRNENYEKFMKMGINVVKRKLAGHDNLKLTITQEGNKFTVKESSNFRNIDVVFELG
VDFAYSADGTELTGTWTMEGNKLVGKFKRVDNGKELIAVREISGNELIQTYTYEGVEAKRIFKKE

>d3ifba_ b.60.1.2 (A:) Intestinal fatty acid binding protein {Human (Homo sapiens)}
AFDSTWKVDRSENYDKFMEKMGVNIVKRKLAHDNLKLTITQEGNKFTVKESSAFRNIEVVFELGV
TFNYNLADGTELRGTWSLEGNKLIGKFKRTDNGNELNTVREIIGDELVQTYVYEGVEAKRIFKKE

>d1fdqa_ b.60.1.2 (A:) Brain fatty acid binding protein {Human (Homo sapiens)}
VEAFCATWKLNSQNFDEYMKALGVGFATRQVGNVTKPTVVISQEGDKVVIRTSTFKNTEISFQLGE
EFDETTADDRNCKSVVSLDGDGLVHIQKWDGKETNFRVREIKDGKMMVMTLTFGDVVAVRHYEKA

>d1b56_ b.60.1.2 (-) Epidermal fatty acid binding protein {Human (Homo sapiens)}
TVQQLEGRWRLVDSKGFDEYMKELGVGIALRKMAMAKPDCIITCDGKNLTIKTESTLKTQFSCCTL
GEKFEETTADGRKTQTVCNFTD GALVQHQEWDGKESTITRKLKDGKLVVECVMMNVTCTRIYEKVE

>d1lid_ b.60.1.2 (-) Adipocyte lipid-binding protein, ALBP {Mouse (Mus musculus)}
CDAFVGTWKLVSSENFDDYMKVGVGFATRQVAGMAKPNMIISVNGDLVTIRSESTFKNTEISFKLG
VEFDEITADDRKVKSIITLDGGALVQVQKWDGKSTTIKRRKRDGDKLVVECVMKGVSTSTRVYERA

>d1mdc_ b.60.1.2 (-) Fatty acid-binding protein {Tobacco hornworm (Manduca sexta)}
SYLGKVVYSLVKQENFDGFLKSAGLSDDKIQALVSDKPTQKMEANGDSYSNTSTGGGGAKTVSFKSGV
EFDDVIGAGDSVSKSMYTVDGNVVTHVVKGDAGVATFKKEYNGDDLVTITSSNWDGVARRYKA

>d1ftpa_ b.60.1.2 (A:) Fatty acid-binding protein {Desert locust (Schistocerca gregaria)}
VKEFAGIKYKLDSTNFEEYMKAIQVGAIERKAGLALSPVIELEILDGDKFKLTSKTAIKNTEFTFKLG
EEFDEETLDGRKVKSTITQDGPKNLVHEQKGDHPTIIREFSKEQCVITIKLGDVATRIYKAQ

>d1cbs_ b.60.1.2 (-) Cellular retinoic-acid-binding protein (CRABP) {Human (Homo sapiens), CRABP-II}
PNFSGNWKIIRSENFEEELKVLGVNVMLRKiAVAAASKPAVEIKQEGDTFYIKTSTTVRTTEINFKVG
EEFEEQTVDGRPCKSLVKWESENKMVCEQKLLKGEKPKTSWTRELTNDGELILMTADDVVCTRVY
VRE

>d1cbia_ b.60.1.2 (A:) Cellular retinoic-acid-binding protein (CRABP) {Cow and mouse (Bos taurus) and (Mus musculus), CRABP-I, identical sequences}
PNFAGTWKMRSENFDELLKALGVNAMLKRVAVAAASKPHVEIRQDGDQFYIKTSTTVRTTEINFK
VGEGFEEETVDGRKCRSLPTWENENKIHCTQTLLEGDPKTYWTRELANDELILTFGADDVVCTRI
YVRE

>d1crb_ b.60.1.2 (-) Cellular retinol-binding protein II (CRBP) {Rat (Rattus norvegicus)}
PVDFNGYWKMLSNENFEEYLRALDVNVALRKIANLLKPDKEIVQGDHMIIRTLSTFRNYIMDFQV
GKEFEEDLTGIDDRKCMTTVSWDGDKLQCVQKGEKEGRGWTQWIEGDELHLEMRAEAVTCKQVF
KKVH

>d1opaa_b.60.1.2 (A:) Cellular retinol-binding protein II (CRBP) {Rat (Rattus norvegicus)}
TKDQNGTWEMESNENFEGYMKALDIDFATRKiAVRLTQTKIIVQDGDNFKTKTNSTFRNYDLDFTV
GVEFDEHTKGLDGRNVKTLVTWEGNTLVCVQKGEKENRGWKQWVEGDKLYLELTCGDQVCRQVF
KKK

>d1ggla_b.60.1.2 (A:) Cellular retinol-binding protein III {Human (Homo sapiens)}
PPNLTGYRfVFSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRNYTVQFDVG
VEFEEDLRSVDGRKQCQTIVTWEEHLLVCVQKGEVPNRGWRHWLEGEMLYLELTARDAVCEQVFRK
VH

>d1lfo_b.60.1.2 (-) Liver fatty acid binding protein {Rat (Rattus norvegicus)}
MNFSGKYQVQSQENFEPFMKAMGLPEDLIQKGDIKGVSEIVHEGKVKLTITYGSKVIHNEFTLGE
ECELETMTGEKVKAVVKMEGDNKMVTTFKGIKSVTEFNQDTITNTMTLGDIVYKRVSKRI

>d1pmpa_b.60.1.2 (A:) P2 myelin protein {Cow (Bos taurus), caudal spinal root myelin}
SNKFLGTWKLVSSENFDEYMKALGVGLATRKLGNLAKPRVIISKKGDIIITIRTESPFKNTEISFKLGQE
FEETTADNRKTKSTVTLARGSLNQVQKWNGNETTIKRKLVDGKMVVECKMKDVVCTRIYEKV

>d1eal_b.60.1.2 (-) Ileal lipid binding protein {Pig (Sus scrofa)}
AFTGKYEIESEKNYDEFMKRLALPSDAIDKARNLKIISEVKQDGNFTWSQQYPGGHSITNTFTIGKE
CDIETIGGKFKFATVQMEGGKVVVNSPNYHHTAEIVDGKLVVSTVGGVSYERVSKKLA

>d1avgi_b.60.1.3 (I:) Thrombin inhibitor {Triatomine bug (Triatoma pallidipennis)}
AEGDDCSIEKAMGDFKPEEFFNGTWYLAHGPGVTSPAVCQKFTTSGSKGFTQIVEIGYNKFESNVKF
QCNQVDNKNGEQYSFKCKSSDNTEFEADFTFISVSYDNFALVCRSITFTSQPKEDRYLVFERTKSDTD
PDAKEIC

>d1swga_b.61.1.1 (A:) Streptavidin {Streptomyces avidinii}
SRYVLTGRYDSAPATDGSALTGWTVAWKNNYRNAHSATTWSGQYVGGAEARINTQWLLTSGTTE
ANAWKSTLVGHDTFTKVKPSAASGGGSAEAGITGTWYNQLGSTFIVTAGADGALTGTYESA

>d1swua_b.61.1.1 (A:) Streptavidin {Streptomyces avidinii}
GITGTWYNQLGSTFIVTAGADGALTGTfESAVGNAESRYVLTGRYDSAPATDGSALTGWTVAWKNN
YRNAHSATTWSGQYVGGAEARINTQWLLTSGTTEANAWKSTLVGHDTFTKVKP

>d1ij8a_b.61.1.1 (A:) Avidin {Chicken (Gallus gallus)}
KCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYTTAVTATSNEIKESPLHGTENTINKRTQPTFGFTVN
WKfSESTTVFTGQCfIDRNGKEVLKTMWLLRSSVNDIGDDWKATRVGINIFTRL

>d1smpi_b.61.2.1 (I:) Metalloprotease inhibitor {Erwinia chrysanthemi}
SSLRLPSAAELSGQWVLSGAEQHCDIRLNTDVLDTWKLAGDTACLQKLLPEAPVGWRPTPDGLT
LTQADGSAVAFFSRNRDRYEHLKLVDSVRTLKKK

>d1jiwi_b.61.2.1 (I:) Metalloprotease inhibitor {Pseudomonas aeruginosa, aprin}
SSLILLSASDLAQWTLQQDEAPAICHLELRDSEVAEASGYDLGGDTACLTRWLPSEPRAWRPTPAGI
ALLERGGLTMLLGRQGEgDYRVQKGDGGQLVLRAT

>d1ei5a1_b.61.3.1 (A:336-417) D-aminopeptidase, middle and C-terminal domains
{Ochrobactrum anthropi}
EVSrVEADSAWFGSWLDDDETGLVLSLEDAGHGRMKARFGTSPeMMDVVSANEARSAVTTIRRDGE
TIELVRASENLRLSMKR

>d1ei5a2_b.61.3.1 (A:418-520) D-aminopeptidase, middle and C-terminal domains
{Ochrobactrum anthropi}
VKGEAKHDIIGRYHSDELADLLLVSSEGGAiYGAFEGFLGKSDMYPLYSVGSDVWLLPVQRSMDAPSP
GEWKLVRFRDDKGEITGLSVGCWLARGVEYRRVQP

>d1jua5 b.61.4.1 (A:166-273) Quinohemoprotein amine dehydrogenase A chain, domain 3 {Paracoccus denitrificans}

PDAYADDASGAYVLAGRQPGRGDYTGRLVLKKGEDYEVTMTLDFADGSRFSFGTGRILGAGEWRA
TLSDGTVTIRQIFALQDGRFSGRWHDADSDVIGGRLAAVKAD

>d1jmx5 b.61.4.1 (A:163-281) Quinohemoprotein amine dehydrogenase A chain, domain 3 {Pseudomonas putida}

ESAAWAEWQKARPKADALPGQWAFSGHMLAKGDVRGVMSVTPDQGDTFKVEVKGAYADGTPFNG
SGSAILYNGYEWGRNVKVGDNLRQVFAALDGEMKGRMFEAHDERGLDFTAVKE

>d2cpl_ b.62.1.1 (-) Cyclophilin (eukaryotic) {Human (Homo sapiens), variant A}

VNPTVFFDIAVDGEPLGRVSFELFADKVPKTAENFRALSTGEKGFYKGSCHFRIIPGFMCQGGDFTR
HNGTGGKSIYGEKFEDEFILKHTGPGILSMANAGPNTNGSQFFICTAKTEWLDGKHVVFGKVKEG
MNIVEAMERFGSRNGKTSKKITIADCGQLE

>d1cyna_ b.62.1.1 (A:) Cyclophilin (eukaryotic) {Human (Homo sapiens), variant B}

GPKVTVKVYFDLRIGDEDVGRVIFGLFGKTVPKTVDNFVALATGEKGFYKNSKFHRVIKDFMIQGG
DFTRGDGTGGKSIYGERFPDENFKLKHYGPGWVSMANAGKDTNGSQFFITTVKTAWLDGKHVVFG
KVLEGMEEVVRKVESTKTDSDRKPLKDVIIADCGKIEVEKPFIAIAKE

>d1qoia_ b.62.1.1 (A:) Cyclophilin (eukaryotic) {Human (Homo sapiens), U4/U6 snRNP-specific cyclophilin snucyp-20}

NSSPVNPVFFDVSIQGEVGRMKIELFADVVPKTAENFRQFCTGEFRKDGVPYGYKGFHHRVIKDF
MIQGGDFVNGDGTGVASIRGPFADENFKLRHSAPGLLSMANSRSTNGCQFFITCSKCDWLDGKH
VVFVKIIDGLLVMRKIENVPTGPNNKPKLPVVISQCGEM

>d2rmca_ b.62.1.1 (A:) Cyclophilin (eukaryotic) {Mouse (Mus musculus), variant C}

KRGPSTVDKVFVDVIRIGDKDVGRIVIGLFGNVVPKTVENFVALATGEKGYGYKGSIFHRVIKDFMIQG
GDFTARDGTGGMSIYGETFPDENFKLKHYGIGWVSMANAGPDTNGSQFFITLTKPTWLDGKHVVFG
KVLDMGMTVVHSIELQATDGHDRPLTDCTIVNSGKIDVKTPFVVEVPDW

>d1a33_ b.62.1.1 (-) Cyclophilin (eukaryotic) {Nematode (Brugia malayi)}

KDRRRVFLDVTIDGNLAGRIVMELYNDIAPRTCNNFLMLCTGMAGTGKISGKPLHYKGFHHRVIKN
FMIQGGDFTKGDGTGGESIYGGMFDEEFVMKHDEPFVSMANKGPNTNGSQFFITTTAPHLNNI
HVVFGKVVSGQEVVTKIEYLKTNKSKNRPLADVILNCGELV

>d1dywa_ b.62.1.1 (A:) Cyclophilin (eukaryotic) {Caenorhabditis elegans, isoform 3}

MSRSKVFFDITIGGKASGRIVMELYDDVVPKTAGNFRALCTGENGIGKSGKPLHFKGSKFHRIPNFMI
QGGDFTRGNGTGGESIYGEKFPDENFKEKHTGPGVLSMANAGPNTNGSQFFLCTVKTEWLDGKHV
VFRGVVEGLDVVKAVESNGSQSGKPVKDCMIADCGQLK

>d1qnga_ b.62.1.1 (A:) Cyclophilin (eukaryotic) {Plasmodium falciparum}

SKRSKVFFDISIDNSNAGRIIFELFSDITPRTCENFRALCTGEKIGSRGKNLHYKNSIFHRIPQFMCQG
GDITNGNGSGGESIYGRSFTDENFMKHDQPGLLSMANAGPNTNSSQFFITLVPCPWLDGKHVVFG
KVIEGMNVVREMEKEGAKSGYVKRSVVITDCGEL

>d1ihga2 b.62.1.1 (A:2-196) Cyclophilin 40 isomerase domain {Cow (Bos taurus)}

SHPSQAKPSNPSNPRVFFVDVIGGERVGRIVLELFADIVPKTAENFRALCTGEKIGIPTTGKPLHFKG
CPFHRIKKFMIQGGDFSNQNGTGGESIYGEKFEDEFHYKHDKEGLLSMANAGSNTNGSQFFITTV
PTPHLDGKHVVFGQVIKGMGVAKILENVEVKGEKPAKLCVIAECGELKEGDDWGIFPKD

>d1clh_ b.62.1.1 (-) Bacterial cyclophilin {Escherichia coli}

AKGDPHVLLTTSAGNIELELDKQKAPVSVQNFVDYVNSGFYNNTTFHRVIPGFMIQGGGFTEQMQQ
KKPNPPIKNEADNGLRNTRGTIAMARTADKDSATSQFFINVADNAFLDHGQRDFGYAVFGKVVKGM

DVADKISQVPTHDVGPYQNVPSKPVVILSAKVLP
>d1lopa_ b.62.1.1 (A:) Bacterial cyclophilin {Escherichia coli}
MVTFHTNHGDIVIKTFDDKAPETVKNFLDYCREGFYNNITIFHRVINGFMIQGGGFEPGMKQKATKE
PIKNEANGLKNTGRGLAMARTQAPHSATAQFFINVVDNDFLNFSGESLQGWGYCVFAEVVDGMD
EVDKIKGVATGRSGMHQDVPKEDVIIESVTVSE
>d1jsg_ b.63.1.1 (-) p14-TCL1 {Human (Homo sapiens)}
CPTLGEAVTDHPDRLWAWEKFVYLDEKQHAWLPLTIEIKDRLQLRVLLRREDVVLGRPMTPTQIGP
SLLPIMWQLYPDGRYRSSDSSFWRVLVYHIKIDGVEDMLLELLPDD
>d1jnpa_ b.63.1.1 (A:) p14-TCL1 {Mouse (Mus musculus)}
RAETPAHPNRLWIWEKHVYLDEFRRSWLPVVIKSNEKFQVILRQEDVTLGEAMSPSQLVPYELPLM
WQLYPKDRYSADSMYWQILYHIKFRDVEDMLLEL
>d1a1x_ b.63.1.1 (-) p13-MTCP1 {Human (Homo sapiens)}
AGEDVGAPPDHLWVHQEGIYRDEYQRTWVAVVEEETSFLRARVQQIQVPLGDAARPSHLLTSQLPL
MWQLYPEERYMDNNSRLWQIQHMLMVRGVQELLLKLLPDD
>d1ijaa_ b.100.1.1 (A:) Sortase {Staphylococcus aureus}
MQAKPQIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENESLDDQNISIAGHTFIDRPN
YQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRDVKPTDVGVLDEQKGDQKQLTLITCDDYNEKTGV
WEKRKIFVATEVK
>d1c39a_ b.64.1.1 (A:) Cation-dependent mannose 6-phosphate receptor, extracytoplasmic
domain {Cow (Bos taurus)}
EKTCDLVGEKGESEKELALLKRLTPLFQKSFESTVGGQSPDMYSYVFRVCREAGQHSSGAGLVQIQKS
NGKETVVGRFNETQIFQGSNWIMLIYKGGDEYDNHCGREQRRAVVMISCNRHTLADNFPVSEERG
KVQDCFYLFEMDSSLACS
>d1e6fa_ b.64.1.1 (A:) Cation-independent mannose-6-phosphate receptor (MIR-receptor)
{Human (Homo sapiens)}
DDCQVTNPSTGHFLDSSLGRAGFTAAYSEKGLVYMSICGENENCPPGVGACFGQTRISVGKANKRL
RYVDQVLQLVYKDGSPCPSKGLSYKSVISFVCRPEAGPTNRPMLISLDKQCTLFFSWHTPLACE
>d1f3ua_ b.65.1.1 (A:) TFIIF beta subunit, Rap30 {Human (Homo sapiens)}
AERGELDLTGAKQNTGVWLKVPKYLSSQWAKASGRGEVGLRIAKTQGRTEVSFTLNEDLANIHD
IGGKPASVSAPREHPFVLQSVGGQTLTVFTESSDKLSLEGIVVQRAECRPA
>d1f3ub_ b.65.1.1 (B:) TFIIF alpha subunit, Rap74 {Human (Homo sapiens)}
GPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVN FATWNQARLERDLSNKKIYQEEEMPESGAGS
EFNRKLREEARRKKYGIVLKEFRPEDQPWLLRVNGKSGRKFKGIKKGGVTENTSYYIFTQCPDGAFE
AFPVHNWYNFTPLARHR
>d1f3ud_ b.65.1.1 (D:) TFIIF alpha subunit, Rap74 {Human (Homo sapiens)}
SSQNVTEYVVRVPKNTTKKYNIMAFNAADKVN FATWNQARLERDLSNKKIYQEEEMPESGAGSEF
NRKLREEARRKKYGIVLKEFRPEDQPWLLRVNGKSGRKFKGIKKGGVTENTSYYIFTQCPDGAFEAF
PVHNWYNFTPLARHRTLTAEEAEEEWERRN
>d1hxn_ b.66.1.1 (-) Hemopexin {Rabbit (Oryctolagus cuniculus)}
ESTRCDPDLVLSAMVSDNHGATYVFSGSHYWRLDTNRDGWHSWPIAHQWPQGPSTVDAAFSWED
KLYLIQDTKVYVFLTKGGYTLVNGYPKRLEKELGSPVISLEAVDAAFVCPGSSRLHIMAGRRLWWLD
LKSGAQATWTELPWPHEKVDGALCMEKPLGPNSCSTSGPNLYLIHGPPLYCYRHVDKLNAAKNLPQ
PQRVSRLGCTH
>d1qhua1 b.66.1.1 (A:24-215) Hemopexin {Rabbit (Oryctolagus cuniculus)}

IEQCSDGWSFDATTLDDNGTMLFFKDEFVWVKSHRGIRELISERWKNFIGPVDAAFRHGHTSVYLIK
DKVWVYTSEKNEKVYPKSLQDEFPGIPFLDAAVECHRGEQDEGILFFQGNRKWFWDLTGTGKK
ERSWPAVGNCTSLARWLGRYYCFQGNQFLRFNPVSGEVPPGYPLDVRDYFLSCPRGRHRS
>d1gen_ b.66.1.1 (-) Gelatinase A (MMP-2), C-terminal domain {Human (Homo sapiens)}
LGPVTPEICKQDIVFDGIAQIRGEIFFFKDRFIWRTVTPRDKPMGPLLVAATFWPELPEKIDAVYEAPQ
EEKAVFFAGNEYWIYSASTLERGYPKPLTSLGLPPDVQRVDAAFNWSKNKKTIFAGDKFWRYNEV
KKKMDPGFPKLIADAWNAIPDNLDAVVDLQGGGHSYFFKGAYLKLENQSLKSVKFGSIKSDWLGC
>d1fbl_1 b.66.1.1 (272-466) Collagenase, C-terminal domain {Pig (Sus scrofa)}
PQTPQVCDSKLTFAITTLRGELMFFKDRFYMRTNSFYPEVELNFISVFWPQVPNGLQAAYEIADRD
EVRFFKGNKYWAVRGQDVLYGYPKDIHRSFGFPSTVKNIDAAVFEEDTGKTYFFVAHECWRYDEYK
QSMDTGYPKMIAEEFPGIGNKVDVAVFQKDGFLYFFHGTRQYQFDFKTKRILTQKANSWFNC
>d1pex_ b.66.1.1 (-) Collagenase-3 (MMP-13), C-terminal domain {Human (Homo sapiens)}
TPDKCDPSLSLDAITSLRGETMIFKDRFFWRLHPQQVDAELFLTksfwPELPNRIDAAAYEHPSHDLI
FIFRGRKFWALNGYDILEGYPKKISELGLPKEVKKISA AVHFEDTGKTLFSGNQVWRYDDTNHIMD
KDYPRLIEEDFPGIGDKVDAVYEKNGYIYFFNGPIQFEYSIWSNRIVRVMPANSILWC
>d1tl2a_ b.67.1.1 (A:) Tachylectin-2 {Japanese horseshoe crab (Tachypleus tridentatus)}
GGESMLRGVYQDKFYQGTYPQNKNDNWLARATLIGKGGWSNFKFLFLSPGGELYGLVNDKIYKGT
PTHNDNDNMGRAKKIGNGGWNQFQFLFFDPNGYLYAVSKDKLYKASPPQSDTDNWIARATEVGS
GWSGFKFLFFHPNGYLYAVHGQQFYKALPPVSNQDNWLARATKIGQGGWDTFKLFFSSVGTFLG
VGGKfyedyPPSYAYDNWLARAKLIGNGGWDDFRFLFF
>d3sil_ b.68.1.1 (-) Salmonella sialidase {Salmonella typhimurium, strain lt2}
EKSVVFKAEGEHFTDQKGNITVGS GSGGTTKYFRIPAMCTTSKGTIVVFADARHNTASDQSFIDTAAA
RSTDGGKTWNKIAIYNDRVNSKLSRVMPTCIVANIQGREILVMVGKWNNDKTWGAIRDKAP
DTDWDLVLYKSTDDGVTFSKVETNIHDIVTKNGTISAMLG GVGSLQLNDGKLVFPVQMVRTKNITT
VLNTSFIYSTDGITWLSLPSGYCEGFGSENNIIEFNASLVNNIRNSGLRRSFETKDFGKTWTEFPPMDK
KVDNRNHGVQGSTITIPSGNKLVAHSSAQNKNDYTRSDISLYAHNLYS GEVKLIDDFYPKVGNASG
AGYSCLSYRKNVDKETLYVVYEANGSIEFQDLSRHLPIKSYN
>d1f8ea_ b.68.1.1 (A:) Influenza neuraminidase {Influenza A virus, different strains}
RDFNLTGKLCITNSWHIYGKDNAVRIGEDSDVLVTREPYVSCDPDECRFYALSQGT TIRGKHSNGTI
HDRSQYRALISWPLSSPPTVYNSRVECIGWSSTSCHD GKTRMSICISGPNNNASAVIWNRRPVTEIN
TWARNILRTQESECVCHNGVCPVFTDGSATGPAETRIYYFKEGKILKWEPLAGTAKHIEECSCYGER
AEITCTCRDNWQGSNRPVIRIDPVAMTHTSQYICSPVLTDNPRPNDPTVGKCNDPYPGN NNGVKG
FSYLDGVNTWLGRTISIASRSGYEMLKVPNALTD DSKSPTQGGTIVLNTDWSGYSGSFMDYWAEGE
CYRACFYVELIRGRPKEDKVVWTSNSIVSMCSSTEF LGQWDWPDGAKIEYFL
>d2bat_ b.68.1.1 (-) Influenza neuraminidase {Influenza A virus, different strains}
VEYRNWSKPPCQITGFAPFSKDNSIRLSAGGDIWVTREPYVSCDPVKCYQFALGQGTTLDNKHSNDT
VHDRIHRTLLMNELGVPFHLGTRQVCIAWSSSSCHD GKAWLHVCITGDDKNATASFIYDGR LVDSI
GSWSQNILRTQESECVCHNGVCPVFTDGSATGPAETRIYYFKEGKILKWEPLAGTAKHIEECSCYPRY
PGVRCICRDNWQGSNRPVVDINMEDYSIDSSYVCSGLVGDTPRNDRSSNSNCRPNPNERGTQGVK
GWA FDNNDLW MGR TISKDLRSGYETFKVIGGWSTPNSKSQINRQVIVDSDNRSYSGIFSVEGKSC
INRCFYVELIRGRKQETRVWWTNSIVVFCGTS GTYGTGSWPDGANINFMPI
>d1inv_ b.68.1.1 (-) Influenza neuraminidase {Influenza B virus, different strains}
EPEWTPRLSCQGSTFQKALLISPHRFGEIKGNSAPLIIREPFVACGPKECRHFALHYAAQPGGYNG
TRKDRNKLRLHLSVKLGKIPTVENSIFHMAAWSGSACHD GREWTYIGVDGPDNDALVKIKYGEAYT

DTYHSYAHNILRTQESACNCIGGDCYLMITDGSASGISKRFLKIREGRIIKEILPTGRVEHTEECTCGF
ASNKTIEACRDNSYTAKRPFVKLVNVEDTAEIRLMCTKTYLDTPRPDDGSIAGPCESNGDKWLGGI
KGGFVHQRMASKIGRWYSRTMSKTNRMGMELYVRYDGDPTDSDALTLSGVMVMSIEEPGWYSFGF
EIKDKKCDVPCIGIEMVHDGGKDTWWSAATAIYCLMGSGQLLWDTVTGVDMAL

>d1nsca_b.68.1.1 (A:) Influenza neuraminidase {Influenza B virus, different strains}

EPEWTPRLSCQGSTFQKALLISPHRFGARGNSAPLIIREPFIACGPKECKHFALTHYAAQPGGYNN
GTREDRNLRLHLSVKLGKIPTVENSIFHMAAWSGSACHDGREWYIYIGVDGPDNSALIKIKYGEAYT
DTYHSYANNILRTQESACNCIGGDCYLMITDGSASGISKRFLKIREGRIIKEIFPTGRVEHTEECTCGF
ASNKTIEACRDNSYTAKRPFVKLVNVEDTAEIRLMCTETTYLDTPRPDDGSITGPCESNGDKGRGGIK
GGFVHQRMASKIGRWYSRTMSKTERMGMEELYVRYDGDPTDSDALAHSGVMVSMKEPGWYSFG
FEIKDKKCDVPCIGIEMVHDGGKDTWWSAATAIYCLMGSGQLLWDTVTGVDMAL

>d1e8ua_b.68.1.1 (A:) Paramyxovirus hemagglutinin-neuraminidase head domain
{Newcastle disease virus}

GAPIHDPDFIGGIGKELIVDNASDVTSFYPSAFQEHLNFIPAPTTGSGCTRIPSFDMASATHYCYTHNVI
LSGCRDHSLSHQYLALGVLRTTATGRIFSTLRSISLDDTQNRKSCSVSATPLGCDMLCSKVTETEEE
DYNSAVPTLMAHGRLGFDGQYHEKDLDTLFEWVANYPGVGGGSFIDGRVWFSVYGGKLPNSPS
DTVQEGKYVIYKRYNDTCPDEQDYQIRMAKSSYKPGFRGGKRIQQAILSIVKSTSLGEDPVLTPPNT
VTLMGAEGRILTVGTSHFLYQRGSSYFSPALLYPMTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPN
SCVTGVYTDYPLIFYRNHTLRGVFGTMLDSEQARLNPASAVFDSTSRSRITRVSSSSTKAAYTTSTCF
KVVKTNKTYCLSAEISNTLFGFRIVPLLVEILKND

>d1eur_b.68.1.1 (-) Micromonospora sialidase, N-terminal domain {Micromonospora
viridifaciens}

GEPLYTEQDLAVNGREGFPNYRIPALTVTPDGDLLASYDGRPTGIDAPGPNLQRRSTDGGRTWGE
QQVVSAGQTTAPIKGFSDPSYLVRETGTIFNFHVYSQRQGFAGSRPGTDPADPNVLHANVATSTDG
GLTWSHRTITADITPDGWRSRFAASGEGIQLRYGPHAGRLIQYTIINAAGAFQAVSVYSDDHGRT
WRAGEAVGVGMENKTVELSDGRVLLNSRDSARSGYRKVAVSTDGGHSYGPVTIDRDLDPPTNNAS
IIRAFDPAGSARAKVLLFSNAASQTSRSQGTIRMSCDDGQTPVSKVFQPGSMSYSTLTALPDGTY
GLLYEPGTGIRYANFNLAWLGGICAP

>d2sli_2 b.68.1.1 (277-759) Leech intramolecular trans-sialidase, C-terminal domain {North
american leech (Macrobdeella decora)}

GENIFYAGDVTESNYFRIPSLTLSTGTVISAADARYGGTHDSKSKINIAFAKSTDGGNTWSEPTLPLK
FDDYIAKNIDWPRDSVGKNVQIQGSASYIDPVLEDKLTKRIFLFDLMPAGIGSSNASVSGSFKEVN
GKKYLKLRWHKDAGRAYDYTIKREKVIYNDATNQPTFEFRVDGEYNLYQHDTNLTCKQYDYNFSGNN
LIESKTDVDVNMNIFYKNSVFKAFPTNYLAMRYSDEGASWSDLDIVSSFKPEVSKFLVVGPGIGKQI
STGENAGRLLVPLYSKSSAELGFMYSDDHGDNWYVEADNLTGGATAEAQIVEMPDGSLKTYLRTGS
NCIAEVTSIDGGETWSDRVPLQGISTTSYGTQLSVINYSQPIDGKPAILSSPNATNGRKNKGIWIGLVN
DTGNTGIDKYSVEWKYSYAVDTPQMGSYSCLAELPDGQVGLLYEKYDSWSRNELHLKDLKFEKYS
ISELTGQA

>d1kit_3 b.68.1.1 (217-346,544-781) Vibrio cholerae sialidase {Vibrio cholerae}

VIFRGPDRIPSIVASSVTPGVVTAFAEKRVGGDPGALSNTNDIITRTRSDGGITWDTELNLTEQINVS
DEFDFSDPRPIYDPSNNTVLVSYARWPTDAAQNGDRIKPWMPNGIFYSVYDVASGNWQAPIXVNP
PGHGITLTRQQNISGSQNGRLIYPAIVLDRFFLNVMSIYSDDGGSNWQTGSTLPIPFWRKSSSILETLE
PSEADMVELQNGDLLLTLARLDFNQIVNGVNYSPRQQFLSKDGGITWSLLEANNANVFSNISTGTVDA
SITRFEQSDGSHFLFTNPQGNPAGTNGRQNLGLWFSFDEGVTWKGPQLVNGASAYSIDIYQLDSEN

AIVIVETDNSNMRLRMPITLLKQKLTLSQN

>d1crua_ b.68.2.1 (A:) Soluble quinoprotein glucose dehydrogenase {Acinetobacter calcoaceticus}

DVPLTPSQFAKAKSENFDDKVVLSNLNKPBALLWGPDPNQIWLTERATGKILRVNPESGSVKTVFQVP
EIVNDADGQNGLLGFAPDFKNNPYIYISGTFKNPKSTDKELPNQTIIRRYTYNKSTDTLEKPVDLL
AGLPSSKDHQSGRLVIGPDQKIYYTIGDQGRNQLAYLFLPNQAQHTPTQQELNGKDYHTYMGKVLRL
LNLDGSIPKDNPSFNGVSHIYTLGHRNPQGLAFTPNGKLLQSEQGPNSDDEINLIVKGGNYGWPNV
AGYKDDSGYAYANYSAAANKSIKDLAQNGVKVAAGVPVTKESEWTGKNFVPPKLTLYTVQDTYNYN
DPTCGEMTYICWPTVAPSSAYVYKGGKAITGWENTLLVPSLKRGVIFRIKLDPTYSTTYDDAVPMF
KSNRRYRDVIASPDGNVLYVLTDTAGNVQKDDGSVTNTLENPGSLIKFT

>d1h6la_ b.68.3.1 (A:) Thermostable phytase (3-phytase) {Bacillus amyloliquefaciens}

KLSDPYHFTVNAAAETEPVDTAGDAADDPAIWLDPKNPQNSKLITTNKKSGLAVYSLEGKMLHSYH
TGKLNNDIRYDFPLNGKKVDAIAASNRSEGNKNTIEIYIDGKNGTLQSITDPNRPIASAIDEVYGFSL
YHSQKTGKYYAMVTGKEGEFEQYELNADKNGYISGKVKRAFKNMSQTEGMAADDEYGSYIAEED
AIWKFSAEPDGGSNGTVIDRADGRHLTPDIEGLTIYYAADGKGYLLASSQGNSSYAIYERQGQNKYVA
DFQITDGPETDGTSDTDGIDVLGFLGPEYFGLFVAQNGENIDHGQKANQNFKMVPWERIADKIG
FHPQVVKQVDPKMTDRS

>d1crza1 b.68.4.1 (A:141-409) TolB, C-terminal domain {Escherichia coli}

AFRTRIAVYVQTNGGQFPYELRVSDYDGYNQFVVHRSPQPLMSPAUSPDGSKLAYVTFESGRSALVI
QTLANGAVRQVASFPRHNGAPAFSPDGSKLAFALSKTGSLNLYVMDLASGQIRQVTDGRSNNTPT
WFPDSQNLAFSTQAGRPQVYKVNINGGAPQRITWEGSQNDADVSSDGKFMVMVSSNGGQQHIA
KQDLATGGVQVLSSTFLDETPSLAPNGTMVIYSSSQGMGSVNLNVSTDGRFKARLPATDGQVKFPAW
SPYL

>d1ijqa1 b.68.5.1 (A:377-642) Low density lipoprotein (LDL) reseptor YWTD domain {Human (Homo sapiens)}

IAYLFFTRHEVRKMTLDRSEYTSVIPNLRNVVALDTEVASNRIYWSDLSQRMICSTQLDRAHGVSSY
DTVISRDIQAPDGLAVDWIHSNIYWTDSVLGTVSVADTKGVKRRKTLFRENGSKPRAIVVDPVHGFMY
WTDWGTPAKIKKGGVLDIYSLVTENIQWPNGITLDDLGRLYWVDSKLSISSIDVNGGNRKTIL
EDEKRLAHPFSLAVFEDKVFWDIINEAIFSANRLTGSDVNLLAENLLSPEDMVLFHNLTPRG

>d1e1aa_ b.68.6.1 (A:) Diisopropylfluorophosphatase (phosphotriesterase, DFP) {Squid (Loligo vulgaris)}

IPVIEPLFTKVTEDIPGAEGPVFDKNGDFYIVAPEVEVNGKPAGEILRIDLKTGKKTIVICKPEVNGYGGI
PAGCQCDRDANQLFVADMRLGLLVVQTDGTFEEIAKKDSEGRMQGCNDCAFDEYNLWITAPAGE
VAPADYTRSMQEKFGSIYCFITDGMQIQVDTAFQFPNGIAVRHMNDGRPYQLIVAETPTKKLWSYDI
KGPAPIENKKVWGHIPGTHEGGADGMDFEEDNLLVANWGSSEHIEVFGPDGGQPKMRIRCPFEKP
SNLHFKPQTKTIFVTEHENNAVWKFQWQRNGKQYCETLKFQIF

>d1k32a2 b.68.7.1 (A:39-319) Tricorn protease N-terminal domain {Archaeon Thermoplasma acidophilum}

MPNLLLNPDIHGDRIFVCCDDLWEHDLKSGSTRKIVSNLGVINNARFFPDGRKIAIRVMRGSSLNTA
DLYFYNGENGEIKRITYFSGKSTGRRMFTDVAGFDPDGNLIISTDAMQPFSSMTCLYRVENDGINFVP
LNLGPATHILFADGRRVIGRNTFELPHWKGYRGGTRGKIWIEVNSGAFKKIVDMSTHVSSPVIHGHRI
YFITDIDGFGQIYSTDLGKDLRKHTSFTDYPRHLNTDGRRILFSKGGSIYIFNPDTEKIEKIEIGDLE
SPEDRII

>d1k3ia3 b.69.1.1 (A:151-537) Galactose oxidase, central domain {Fungi (Fusarium spp)}

YTAPQPGLGRWGPTIDLPIVAAAAIEPTSGRVLWSSYRNDAFGGSPGGITLTSSWDPSTGIVSDRT
VTVTKHDMFCPGISMDGNGQIVVTGGNDAKKTSLYDSSSDSWIPGPDMPVARGYQSSATMSDGRVF
TIGGSWSGGVFEKNGEVYSPSSKTWTSLPNAKVNPMPLTADKQGLYRSDNHAWLFGWKKGSVFAQG
PSTAMNWWYTSVSGSDVKSAGKRQSNRGVAPDAMCGNAVMYDAVKGKILTFGGSPDYQDSDATTNA
HIITLGEPTSPNTVFASNGLYFARTFHTSVVLPDGGSTFITGGQRRGIPFEDSTPVFTPEIYVPEQDTFY
KQNPNSIVRVYHSISLLLPDGRVFNNGGGGLCGDCTTNHFDAQIFTPNYLYNSN

>d1mdah_ b.69.2.1 (H:) Methylamine dehydrogenase, H-chain {Paracoccus denitrificans}

EKSKVAGSAAAASAAAASDGSSCDHGPAGISRRSHITLPAYFAGTTENWVSCAGCGVTLGHSLGAFLS
LAVAGHSGSDFALASTSFARSAGKRTDYVEVDFPVTFLPIADIELPDAPRFSVGPVHIIINCASSACL
LFFLFGSSAAAGLSVPGASDDQLTKSASCFFHIHPGAAATHYLGSCPASLAASDLAAAPAAAGIVGAQCT
GAQNCSSQAAQANYPGMLVWAVASSILQGDIPAAGATMKAADGNESGRKADNFRSAGFQMVAKLK
NTDGIMILTVEHSRSLAAEAENTSSVTASVGTSGPISNGHSDAIIAAQDGASDNYANSAGTEVLDIY
DAASDQDQSSVELDKGPESLSVQNEA

>d2bbkh_ b.69.2.1 (H:) Methylamine dehydrogenase, H-chain {Paracoccus denitrificans}

DEPRILEAPAPDARRVYVNDPAHFAAVTQQFVIDGEAGRVIGMIDGGFLPNPVVADDGSFIAHASTVF
SRIARGERTDYVEVDFPVTLLPTADIELPDAPRFLVGTYPWMTSLTPDGGKTLFFYQFSPAPAVGVVDL
EGKAFKRMLDVPDCYHIFPTAPDTFFMHCRDGLAKVAFGTEGTPEITHTEVFHPEDEFLINHPAYS
QKAGRLVWPTYTGKIHQIDLSSGDAKFLPAVEALTEAERADGWRPQGWQVAYHRALDRIYLLVDQ
RDEWRHKTASRFVVLDKATGERLAKFEMGHEIDSINVSQDEKPLLYALSTGDKTLYIHDAESGEEL
RSVNQLGHGPQVITTADMG

>d2madh_ b.69.2.1 (H:) Methylamine dehydrogenase, H-chain {Gram negative
methylophilic bacteria (Thiobacillus versutus)}

SSASAAAAAAAAAALAGAADGPTNDEAPGADGRRSYINLPAHHSIIQQWVLDAGSGSILGHVNGGF
LPNPVAAHSGSEFALASTSFSAIAKGRRTDYVEVDFPVTFLPIADIELPDAPRFDVGPYSWMMNANTP
NNADLLFFQFAAGPAVGLVVQGGSSDDQLLSSPTCYHIHPGAPSTFYLLCAQGGAKTDHAGGAAGA
GLVGAMLTAAQNLTPAQANKSGRIVWPVYSGKILQADISAAGATNKAPIDALSGGRKADTWRPQG
WQQVAYLKSSDGIYLLTSEQSAWKLHAAAKEVTSVTGLVGTSSQISLGHVDVAISVAQDGGPDLYAL
SAGTEVLHIYDAGAGDQDQSTVELGSGPQVLSVMNEA

>d1jjub_ b.69.2.2 (B:) Quinohemoprotein amine dehydrogenase B chain {Paracoccus
denitrificans}

RDYILAPARPDKLVIDTEKMAVDKVITIADAGPTMPVPMVAPGGRIAYATVNKSESLVKIDLVTGET
LGRIDLSTPEERVKSLFGAALSPDGKTLAIYESPVRLLETHFEVQPTRVALYDAETLSRRKAFAEAPRQI
TMLAWARDGSKLYGLGRDLHVMDPEAGTLVEDKPIQSWEAETYAQPDLAVWNQHESGVMATPF
YTARKDIDPADPTAYRTGLLTMDLETGEMAMREVRIMDVFFYFSTAVNPAKTRAFGAYNVLESFDLEK
NASIKRVPLPHSYYSVNVSTDGSTVWLGGALGDLAAYDAETLEKKGQVDLPGNASMSLASVRLFTRD
E

>d1jmx_ b.69.2.2 (B:) Quinohemoprotein amine dehydrogenase B chain {Pseudomonas
putida}

GPALKAGHEYMIVTNYPNLHVVDVASDTVYKSCVMPDKFGPGTAMMAPDNRTAYVLNNHYGDIY
GIDLDTCKNTFHANLSSVPGVGRSMYSFAISPDGKEVYATVNPTQRLNDHYVVKPPRLEVFSTADG
LEAKPVRTFPMPRQVYLMRAADDGSLYVAGPDIYKMDVKTGKYTVLPLRNWNRKYSAPDVLVYF
WPHQSPRHEFSMLYTIARFKDDKQDPATADLLYGYLSVDLKTGKTHHTQEFADLTELYFTGLRSPKDP
NQIYGVNLRLAKYDLKQRKLIKAANLDHTYYCVAFDKKGDKLYLGGTFNDLAVFNPDTLEKVKNIKL
PGGDMSTTTPQVFIR

>d1qnia2_b.69.3.1 (A:10-450) Nitrous oxide reductase, N-terminal domain {Pseudomonas nautica}

AHVAPGELDEYYGFWSGGHQGEVRLVGVPSMRELMRIPVFNVDSATGWGITNESKEILGGDQQYLN
GDCHHPHISMTDGRYDGYLFINDKANTRVARIRLDIMKTDKITHIPNVQAIHGLRLQKVPKTNVVF
CNAEFVIPQPDGTFDFSLDNSYTMFTAIDAETMDVAWQVVDGNLNDTDADYTGKYATSTCYNSER
AVDLAGTMRNDRDWWVFNVERIAAAVKAGNFKTIGDSKVPVVDGRGESEFTRYIPVPPKNPHGLNT
SPDGKYFIANGKLSPTVSIVIAIDKLDLDFEDKIELRDTIVAEPGLGLPLHTTFDGRGNAYTTLFIDSQ
VCKWNIADAIKHYNGDRVNYIRQKLDVQYQPGHNHASLTERDADGKWLVLVLSKFSKDRFLPVGPL
HPENDQLIDISGEEMKLVHDGPTYAEPHDCILVRRDQIKTK

>d1fwa2_b.69.3.1 (A:8-451) Nitrous oxide reductase, N-terminal domain {Paracoccus denitrificans}

ADGSVAPGQLDDYYGFWSGGQSGEMRILGIPSMRELMRVPVFNRCATGWGQTNESVRIHERTMSE
RTKKFLAANGKRIHDNGDLHHVHMSFTEGKYDGRFLFMNDKANTRVARVRCDVMKCDAILIPNA
KGIHGLRPQKWPRSNYVFCNGEDETPLVNDGTNEMEDVANYVNVFTAVDADKWEVAWQVLVSGNL
DNCADADYEGKWAFSTSYNSEKGMTLPEMTAAEMDHIVVFNIAEIEKAIAAGDYQELNGVKVVDGRK
EASSLFTRYIPIANNPHGCNMAPDKKHLCVAGKLSPTVTVLVDVTRFDVAVFYENADPRSAVVAEPELG
LGPLHTAFDGRGNAYTSLFLDSQVVKWNIEDAIRAYAGEKVDPIKDKLDVHYQPGHLKTVMGETLD
ATNDWLVLCKSKDRFLNVGPLKPENDQLIDISGDKMVLVHDGPTFAEPHDAIAVHPSILSDIK

>d1tbga_b.69.4.1 (A:) beta1-subunit of the signal-transducing G protein heterotrimer {Cow (Bos taurus)}

MSELDQLRQEAQLKNQIRDARKACADATLSQITNNIDPVGRIQMTRRRTLGRHLAKIYAMHWGTD
SRLVLSASQDGKLIWDSYTTNKVHAIPLRSSWVMTCAAYAPSGNYVACGGLDNICSIYNLKTREGNVR
VSRELAGHTGYLSCCRFLDDNQIVTSSGD'TTCALWDIETGQQT'TTFTGHTGDVMSLSLAPDTRLFVS
GACDASAKLWDVREGMCRQFTTGHESDINAICFFPNGNAFATGSDDATCRLFDLRADQELMTYSHD
NIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRAGVLAGHDNRVSLGVTDDGMAVATGSWD
SFLKIWN

>d1erja_b.69.4.1 (A:) Tup1, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

HYLVYPYNQRANHSKPIPPFLDLDSQSPDALKKQTNDDYIILYNPALPREIDVELHKSLDHTSVVCCV
KFSNDGEYLATGCNKTTQVYRVSDGSLVARLSDDSAANKDPENLNTSSSPSSDLYIRSVCFSPDGKFL
ATGAEDRLIRIWDIENRKIVMILQGHEQDIYSLDYFSPGDKLVSGSGDRTVRIWDLRTGQCSLTLIED
GVTTVAVSPGDGKYIAAGSLDRAVRVWVWSETGFLVERLDSENEGTGHKDSVYSVVFTRDGQSVVSG
SLDRSVKLWNLQNANNKSDSKTPNSGTCEVTYIGHKDFVLSVATTQNDYILSGSKDRGVLFWDKK
SGNPLMLQGHRNSVISVAVANGSSLGPEYNVFATGSGDCKARIWKYKKI

>d1k8kc_b.69.4.1 (C:) Arp2/3 complex 41 kDa subunit ARPC1 {Cow (Bos taurus)}

AYHSFLVEPISCHAWNKDRTQIAICPNNHEVHIYEKSGNKWVQVHELKEHNGQVTGVDWAPDSNRI
VTGGTDRNAYVWTLKGRTWKPTLVILRINRAARCVRWAPNEKKFAVGSGSRVISICYFEQENDWWV
CKHIKKPIRSTVLSLDWHPNSVLLAAGSCDFKCRIFSAIYEVEERPAPTPWGSKMPFGELMFESSSS
CGVWHGVCFSANGSRVAWVSHDSTVCLADADKMAVATLASETLPLLAVTFITESSLVAAGHDCFPV
LFTYDSAAGKLSFGGRLDVPKQSSQRGLTARERFQNLDDKASSEGSAAAGAGLDSLHKNVSVQISVLS
GGKAKCSQFCTTGMDGMSIWDVRSLESALKDLKIV

>d1a12a_b.69.5.1 (A:) Regulator of chromosome condensation RCC1 {Human (Homo sapiens)}

KKVKVSHRSHSTEPGLVLTGLGQGDVGLGLGENVMERKKPALVSIPEDVVQAEAGGMHTVCLSKSGQ
VYSGFCNDEGALGRDTSVEGSEMVPKVELQEKVVQVSAGDSHTAALTDDGRVFLWGSFRDNGVI

GLLEPMKKSMPVQVQLDVPVVKVASGNDHLVMLTADGDLYTLGCGEQQQLGRVPELFANRGGRRQG
LERLLVPKCVMLKSRGSRGHVRFQDAFCGAYFTFAISHEGHVYGFGLSNYHQLGTPGTESCIFPQNLT
SFKNSTKSWVGFSGGQHHTVCMDESEGKAYSLGRAEYGRLLGLGEGAEKSIPTLISRLPAVSSVACGAS
VGYAVTKDGRVFAWGMGTNYQLGTGQDEDAWSPVEMMGKQLENRVVLSVSSGGQHTVLLVKDKE
QS

>d1jtdb_ b.69.5.2 (B:) of beta-lactamase inhibitor protein-II, BLIP-II {Streptomyces
exfoliatus}

VAATSVVAWGGNNDWGEATVPAAEQSGVDAIAGGYFHGLLALKGGKVLGWGANLNGQLTMPAATQS
GVDAIAAGNYHSLALKDGEVIAWGGNEDGQTTVPAEARSGVDAIAAGAWASYALKDGVIAWGGDS
DGQTTVPAAEQSGVTALDGGVYALAVKNGGVIAWGDNYFGQTTVPAAEQSGVDDVAGGIFHSLAL
KDGKVIWGDNRKQTTVPTEALSGVSAIASGEWYSLALKNGKVIWGGSSRTAPSSVQSGVSSIEAGP
NAAYALKG

>d1c9la2 b.69.6.1 (A:3-330) Clathrin heavy-chain terminal domain {Rat (Rattus norvegicus)}

QILPIRFQEHLQLQNLGINPANIGFSTLTMESDKFICIREKVGEQAQVVIIDMNDPSNPIRRPISADSAI
MNPASKVIALKAGKTLQIFNIEMKSKMKAHTMTDDVTFWKWISLNTVALVTDNAVYHWSMEGES
QPVKMFDHRSSLAGCQIINYRTDAKQKWLLLTGISAQQNRVVGAMQLYSVDRKVSQPIEGHAASFAQ
FKMEGNAEESTLFCFAVRGQAGGKLHIEVGTPTGNQPFPPKAVDVFFPPEAQNDFPVAMQISEKH
DVVFLITKYGYIHLYDLETGTCIYMNRISGETIFVTAPHEATAGIIGVNRKQVLSVCVE

>d1jv2a4 b.69.8.1 (A:1-438) Integrin alpha N-terminal domain {Human (Homo sapiens)}

FNLDVDSPAEYSGPEGSYFGFAVDFFVPSASSRMFLVVGAPKANTTQPGIVEGGQVLKCDWSSTRRC
QPIEFDATGNRDYAKDDPLEFKSHQWFGASVRSKQDKILACAPLYHWRTMKEQEREPVGTGCFDQDQ
TKTVEYAPCRSQDIDADGQGFQCGGFSIDFTKADRVLLGGPGSFYWQQLISDQVAEIVSKYDPNVYS
IKYNNQLATRTAQAIFFDSDYLGYSVAVGDFNGDGDIDFVSGVPRAARTLGMVYIYDGNMSSLYNFTG
EQMAAYFGFSVAATDINGDDYADVFIGAPLFMDRGSQGLQEVGQVSVSLQRASGDFQTTKLNQFV
FARFGSAIAPLGLDLDQDGFNDIAIAAPYGGEDKKGIVYIFNGRSTGLNAVPSQILEGQWAARSMPPSF
GYSMKGATDIDKNGYPLIVGAFGVDRAILYRAR

>d1qfma1 b.69.7.1 (A:1-430) Prolyl oligopeptidase, N-terminal domain {Pig (Sus scrofa)}

MLSFQYQPDVYRDETAIQDYHGHKVCOPYAWLEDPDSEQTKAFVEAQNKITVPFLEQCPIRGLYKER
MTELYDYPKYSCHFCKGKRYFYFYNTGLQNQRVLYVQDSLEGEARVFLDPNLSDDGTVALRGYAFSE
DGEYFAYGLSASGSDWVTIKFMKVDGAKELPDVLERVKFSCMAWTHDGKGMFYNAYPQQDGKSDG
TETSTNLHQKLYYHVLGTDQSEDILCAEFPDEPKWMGGAELSDDGRYVLLSIREGCDPVNRLWYCD
LQQESNGITGILKWWKLIDNFEGEYDYVTNEGTVFTFKTNRHSPNYRLINIDFTDPEESKWKVLVPE
HEKDVLEWVACVRSNFLVLCYLHDVKNTLQLHDLATGALLKIFPLEVGSVVGYSQKQKDEIFYQFT
SFLSPGIYHCDLTKEELEPRVFREVTVKGI

>d1k32a3 b.69.9.1 (A:320-679) Tricorn protease N-terminal domain {Archaeon
Thermoplasma acidophilum}

SIPSKFAEDFSPDLGDLIAFVSRGQAFIQDVSQTYVLKVPEPLRIRYVRRGGDTKVAFIHGTREGDFLGI
YDYRTGKAEKFEENLGNVFAMGVDRNGKFAVVANDRFEIMTVDLETGKPTVIERSREAMITDFTISD
NSRFIAYGFPLKHGETDGYVMQAIHVYDMEGRKIFAATTENSHDYAPAFDADSKNLYLSYRSLDPSP
DRVVLFNSFEVSKPFVIPLIPGSPNPTKLVPRSMTSEAGEYDLNDMYKRSSPINVDPGDYRMIIPLES
SILIYSVPVHGEFAAYYQGAPEKGVLLKYDVKTRKVTVEKNNLTLRLSADRKTVMVRKDDGKIYTF
PLEKPEDERTVETDKRPLV

>d1g72a_ b.70.1.1 (A:) Methanol dehydrogenase, heavy chain {Methylophilus
methylotrophus, w3a1}

DADLDKQVNTAGAWPIATGGYYSQHNSPLAQINKSNVKNVKAAWSFSTGVLNGHEGAPLVIGDMM
YVHSAFPNNTYALNLDNPGKIVWQHKKPKQDASTKAVMCCDVVDRGLAYGAGQIVKKQANGHLLAL
DAKTGKINWEVEVCDPKVGSTLTQAPFVAKDTVLMGCSGAELGVRGAVNAFDLKTGELKWRAFATG
SDDSVRLAKDFNSANPHYGQFGLGKTWEGDAWKIGGGTNWGWYAYDPKLNLFYYGSGNPAPWN
ETMRPGDNKWTMTIWGRDLDTGMAKWGYQKTPHDEWDFAGVNMVLTQPVNGKMTPLLSHI
DRNGILYTLNRENGNLIVAEEKVDPVAVNVFKKVDLKTGTPVRDPEFATRMDHKGNTNCPMSAMGFHNQ
GVDSYDPESRTLYAGLNHICMDWEPFMLPYRAGQFFVGATLAMYPGPNPPTKKEMGQIRAFDLTTG
KAKWTKWEKFAAWGGTLYTKGGLVWYATLDGYLKALDNKDGKELWNFKMPSGGIGSPMTYSFKG
KQYIGSMYGVGGWPGVGLVFDLTDPSAGLGAVGAFRELQNHTQMGGGLMVFSL

>d1h4ia_b.70.1.1 (A:) Methanol dehydrogenase, heavy chain {Methylobacterium
extorquens}

NDKLVELSKSDDNWVMPGKNYDSNNFSDLKQINKGNVQLRPAWTFSTGLLNGHEGAPLVVDGK
MYIHSTFPNNTFALGLDDPGTILWQDKPKQNPAAARAVACCDLVNRLAYWPGDGKTPALILKTQLD
GNVAALNAETGETVWQVENS DIKVGSTLTIAPIYVVKDKVIIGSSGAELGVRGYLTAYDVKTGEQVWR
AYATGPKDLLASDFNIKNPHYGQKGLGTWEGDAWKIGGGTNWGWYAYDPGTNLIYFGTGNP
APWNETMRPGDNKWTMTIFGRDADTGEAKFGYQKTPHDEWDYAGVNMMLSEQKDKDGKARK
LLTHPDRNGIVYTLDRDGDALVSANKLDDTVNVFKSVDLKTGQPVRDPEYGTMRMDHLAKDICPSAM
GYHNQGHDSYDPKRELFMGINHICMDWEPFMLPYRAGQFFVGATLNMYPGPKGDRQNYEGLGQI
KAYNAITGDYKWEKMERFAVWGGTMATAGDLVFGYGLDGYLKARDSDTGDLLWFKIPSGAIGYP
MTYTHKGTQYVAIYGVGGWPGVGLVFDLADPTAGLGAVGAFKLLANYTQMGGGVVVFSLDGKGPY
DDPNVGEWK

>d1flga_b.70.1.1 (A:) Ethanol dehydrogenase {Pseudomonas aeruginosa}

KDVTWEDIANDDKTTGDVLQYGMGTHAQRWSPKQVNADNVFKLTPAWSYSFGDEKQRGQESQAI
VSDGVIYVTASYSRLFALDAKTGKRLWTYNHRLPDDIRPCCDVVNRGAAYGDKVFFGTLDASVVAL
NKNTGKVVWKKKFADHGAGYTMTGAPTIVKDGTGKVLIIHGSSGDEFGVVGRFLFARDPDTGEEI
WMRPFVEGHMGRNLNGKSTVTGDVKAPSWPDDRNSPTGKVESWSHGGAAPWQSASFDAETNTII
VGAGNPGPWNTWARTAKGGNPHDYDSLYTSGQVGVDPSSGEVKWQFYQHTPNDAWDFSGNNEVLV
FDYKAKDGKIVKATAHADRNFFYVVDNRNGKLQNAFPFVDNITWASHIDLKTGRPVEREQRPPL
PEPGQKHGKAVEVSPFLGGKNWNPMAYSQDTGLFYVPANHWKEDYWTEEVSYTKGSAYLGMGF
RIKRMYYDDHVGLRAMDPVSGKVVWEHKEHLPLWAGVLATAGNLVFTGTGDGYFKAFDAKSGKEL
WKFKQTGSGIVSPITWEQDGEQYLGVTVGYGGAVPLWGGDMADLTRPVAQGGSFVWFKLPSW

>d1kb0a2_b.70.1.1 (A:1-573) Quinoprotein alcohol dehydrogenase, N-terminal domain
{Comamonas testosteroni}

TGPAAQAAAQVRVDGDFIRANAARTPDWPTIGVDYAETRYSRDLQINAANVKDLGLAWSYNLEST
RGVEATPVVVDGIMYVSASWSVHAIIDTRTGNRIWYDTPQIDRSTGFKGCCDVVNRGVALWKGKQVY
VGAWDGRLLIALDAATGKEVWHQNTFEGQKGLTITGAPRVFKGKVIIGNGGAEYGVRYITAYDAET
GERKWRWFSPGDPSPKPFEDESMKRAARTWDPGKWWWEAGGGTMWDSMTFDAELNTMYVGT
GNGSPWSHKVRSKGGDNLASIVALDPDTGKYKWHYQETPGDNWDYTSTQPMILADIKIAGKPR
KVILHAPKNGFFFVLDRTNGKFISAKNFVNVNWSAGYDKHGKPIGIAAARDGSKPQDAVPGPYGAH
NWHPMFSNPQTGLVYLPAQNVVNLMDKKWFEFNQAGPGKQSGTGWNTAKFFNAEPPKSKPFG
RLLAWDPAQAASVEHVSPWNGGTLTTAGNVVFGQTADGRLVAYHAATGEKLWEAPTGTGVVA
APSTYMDGRQYVSAVGGVYGLAARATERQGPVTYTFVVGKARMPE

>d1nira2_b.70.2.1 (A:118-543) C-terminal (heme d1) domain of cytochrome cd1-nitrite
reductase {Pseudomonas aeruginosa}

EWGMPEMRESWKVLVLPEDRPPKQLNDLDPNLFVSVTLRDAGQIALVDGDSKKIVKVIDTGYAVHI
SRMSASGRYLLVIGRDARIDMIDLWAKEPTKVAEIKIGIEARSVESSKFKGYEDRYTIAGAYWPPQFAI
MDGETLEPKQIVSTRGMTVDTQTYHPEPRVAIIASHEHPEFIVNVKETGKVLVNYKDIDNLTVTSI
GAAPFLHDGGWSSSHRYFMTAANNSNKVAVIDSKDRRLSALVDVGKTPHPGRGANFVHPKYGPVW
STSHLGDGSISLIGTDPKNHPQYAWKKVAELQGQGGSLFIKTHPKSSHLYVDTTFNPDARISQSVAV
FDLKNLDAKYQVLPPIAEWADLGEAKRVVQPEYNKRKRGDEVWFSVWNGKNDSSALVVVDDKTLKLLK
AVVKDPRRLITPTGKFNVTYNTQHDVY

>d1qksa2 b.70.2.1 (A:136-567) C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase {Paracoccus denitrificans}

EFGMKEMRESWKVHVAPEDRPTQQMNDWDLENLFSVTLRDAGQIALIDGSTYEIKTVLDTGYAVHI
SRLSASGRYLFVIGRDGKVNLMIDLWMKEPTTVAEIKIGSEARSIEFSKMEGWEDKYAAGAYWPPQY
VIMDGETLEPKKIQSTRGMTYDEQEYHPEPRVAAILASHYRPEFIVNVKETGKILLVDYTDLNNLKT
EISAERFLHDGGLDGSRYFITAANARNKLVIDTKEGKLVAIEDTGGQTPHPGRGANFVHPTFGPV
WATSHMGDDSDVALIGTDPGHPDPAWILDSFPALGGSLFIKTHPNSQYLYVDATLNPEAEISGSVA
VFDIKAMTGDGSDPEFKTLPIAEWAGITEGQPRVVQGEFNKDGTEVWFSVWNGKDQESALVVVDD
KTLELKHVIKDERLVTPTGKFNVTYNTMTDTY

>d1e43a1 b.71.1.1 (A:394-483) Bacterial alpha-Amylase {Bacillus licheniformis}

YAYGAQHDFDHHDIVGWTREGDSSVANSGLAALITDGGGAKRMYVGRQNAGETWHDITGNRSE
PVINSEGWGEFHVNGGSVSIYVQR

>d1g94a1 b.71.1.1 (A:355-448) Bacterial alpha-Amylase {Pseudoalteromonas haloplanctis (Alteromonas haloplanctis)}

NWAVTNWWDNTNNQISFGRGSSGHMAINKESTLTATVQTDMASGQYCNVLKGELSADAKSCSGE
VITVNSDGTINLNIGAWDAMAIHKNKLN

>d1bag_1 b.71.1.1 (348-425) Bacterial alpha-Amylase {Bacillus subtilis}

QPEELSNPNGNNQIFMNQRGSHGVLANAGSSSVSINTATKLPDGRYDNKAGAGSFQVNDGKLTGTI
NARSAVLYPD

>d1hvxa1 b.71.1.1 (A:394-483) Bacterial alpha-Amylase {Bacillus stearothermophilus}

YAYGTQHDYLDHSDIIGWTREGVTEKPGSGLAALITDGGGSKWYVVGKQHAGKVFYDLTGNRSDT
VTINSDGWGEFKVNGGSVSVWVPR

>d1gjwa1 b.71.1.1 (A:573-636) Maltosyltransferase {Thermotoga maritima}

GKFENLTKDLVMSYKNGQKIVIAANVGKEPKEITGGRVWNGKWSDEEKVVLKPLEFALVVQ

>d1cgt_3 b.71.1.1 (407-494) Cyclodextrin glycosyltransferase {Bacillus circulans, different strains}

GSTQQRWINNDVYVYERKFGKSVAVVAVNRNLSTASITGLSTSLPTGSYTDVLGGVLLNGNNITSTNG
SINNFTLAAGATAVWQYTAA

>d1kcla3 b.71.1.1 (A:407-495) Cyclodextrin glycosyltransferase {Bacillus circulans, different strains}

GSTQERWINNDVLIYERKFGSNVAVVAVNRNLNAPASISGLVTSLPQGSYNDVLGGLLNGNTLSVGSG
GAASNFTLAAGGTAVWQYTAA

>d1cyg_3 b.71.1.1 (403-491) Cyclodextrin glycosyltransferase {Bacillus stearothermophilus}

GDTEQRWINGDVYVYERQFGKDVVLVAVNRSSSSNYSITGLFTALPAGTYTDQLGGLLDGNTIQVGSN
GSVNAFDLGPGEVGVWAYSAT

>d1qhoa3 b.71.1.1 (A:408-495) Cyclodextrin glycosyltransferase {Bacillus stearothermophilus, maltogenic alpha-amylase}

GTTTQRWINNDVYIYERKFFNDVVLVAINRNTQSSYSISGLQTALPNGSYADYLSGLLGNGISVSNGS
VASFTLAPGAVSVWQYSTS
>d1pama3 b.71.1.1 (A:407-496) Cyclodextrin glycosyltransferase {Bacillus sp., strain 1011}
GSTHERWINNDVYIYERKFGNNVAVVAINRNMNTPASITGLVTSPLRGSYNDVLLGGILNGNTLTVGAG
GAASNFTLAPGGTAVWQYTTDA
>d1ciu_3 b.71.1.1 (407-495) Cyclodextrin glycosyltransferase {Thermoanaerobacterium
thermosulfurigenes, EM1}
GTTQQRWINNDVYIYERKFGNNVALVAINRNLSTSYNITGLYTALPAGTYTDVLLGGLLNGNSISVASD
GSVTPFTLSAGEVAVWQYVSS
>d1hx0a1 b.71.1.1 (A:404-496) Animal alpha-amylase {Pig (Sus scrofa)}
QPANWWDNGSNQVAFGRGNRGFIVFNDDWQLSSTLQTGLPGGTYCDVISGDKVGNSTGKIVVY
SSDGTAFSISNSAEDPFIAIHAESKL
>d1smd_1 b.71.1.1 (404-496) Animal alpha-amylase {Human (Homo sapiens)}
QPFTNWDNGSNQVAFGRGNRGFIVFNDDWTFSLTLQTGLPAGTYCDVISGDKINGNCTGIKIYVS
DDGKAHFSISNSAEDPFIAIHAESKL
>d1jae_1 b.71.1.1 (379-471) Animal alpha-amylase {Yellow mealworm (Tenebrio molitor),
larva}
GTQVENWWSNDDNQIAFSRGSQGFVAFTNGGDLNQNLTGLPAGTYCDVISGELSGGSCTGKSVTV
GDNGSADISLGAEDDGVLAHVNAKL
>d2aaa_1 b.71.1.1 (382-476) Fungal alpha-amylase {Aspergillus niger, acid amylase}
YANDAFYTDSENTIAMAKGTSGSQVITVLSNKGSSGSSYTLTSLSGSYTAGQQLTEVIGCTTVTVGSDGDI
PVPMASGLPRVLLPASVVDSSSLCG
>d2taa1 b.71.1.1 (A:382-478) Fungal alpha-amylase {Aspergillus oryzae, Taka-amylase}
YKNPYIKDDTTIAMRKGTDGSQIVTILSNKGASGDSYTLTSLGASYTAGQQLTEVIGCTTVTVGSDGNV
PVPMAGGLPRVLYPTEKLAGSKICSDSS
>d7taa_1 b.71.1.1 (382-476) Fungal alpha-amylase {Aspergillus oryzae, Taka-amylase}
YKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYTLTSLGAGYTAGQQLTEVIGCTTVTVGSDG
NVPVPMAGGLPRVLYPTEKLAGSKICS
>d1smaa2 b.71.1.1 (A:506-588) Maltogenic amylase {Thermus sp.}
GDVAFLTADDEVNHLVYAKTDGNETVMIINRSNEAAEIPMPIDARGKWLVNLLTGERFAAEAETLC
VSLPPYGFVLYAVESW
>d1bvza2 b.71.1.1 (A:503-585) Maltogenic amylase {Thermoactinomyces vulgaris, TVAII}
GNVRSWHADKQANLYAFVRTVQDQHVGVVLLNRRGEKQTVLLQVPESGGKTWLDCLTGEEVHGKQ
GQLKLTLRPYQGMILWNGR
>d1eh9a2 b.71.1.1 (A:491-557) Glycosyltrehalose trehalohydrolase {Archaeon Sulfolobus
solfataricus, km1}
CDRRVNVVNGENWLIKGREYFSLYVFSKSSIEVKYSGTLLSSNNSFPQHIEEGKYEFDKGFALYK
>d1bf2_2 b.71.1.1 (638-750) Isoamylase {Pseudomonas amyloclavata}
YSGSQLTWYQPSGAVADSNYWNNTSNYAIYAINGPSLGDNSNIYVAYNGWSSSVTFTLPAPPSGTQ
WYRVTDTCWWDGASTFVAPGSETLIGGAGTTYGQCGQSLLLISK
>d1gcy1 b.71.1.1 (A:358-418) G4-amylase (1,4-alpha-D-glucan maltotetrahydrolase)
{Pseudomonas stutzeri}
RADSAISFHSGYSLVATVSGSQQLVVALNSDLGNPGQVAGSFSEAVNASNGQVRVWRS
>d1avaa1 b.71.1.1 (A:347-403) Plant alpha-amylase {Barley (Hordeum vulgare), seeds,

AMY2 isozyme}

HNESKLQIIEADADLYLAEIDGKIVIVKLGPRYDVGNLIPGGFKVAAHGNDYAVWEKI

>d1uok_1 b.71.1.1 (480-558) Oligo-1,6-glucosidase {*Bacillus cereus*}

GSYDLILENNPSIFAYVRTYGVKLLVIANFTAEECIFELPEDISYSEVELLIHNYDVENGPIENITLRPY
EAMVFKLK

>d1g5aa1 b.71.1.1 (A:555-628) Amylosucrase {*Neisseria polysaccharea*}

RLVTFNTNKNHIIIGYIRNNALLAFGNFSEYPQTVTAHTLQAMPFKAHDLIGGKTVSLNQDLTLQPYQ
VMWLEIA

>d1f8ab1 b.72.1.1 (B:1-42) Mitotic rotamase PIN1 {Human (*Homo sapiens*)}

GSHGMADEEKLPPEGWEKRMSRSSGRVYYFNHITNASQWERPS

>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 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*)}

PASQHFLSTSVQGPWERAISPKNKVPYYINHETQTTTCWD

>d1i5hw_ b.72.1.1 (W:) Ubiquitin ligase NEDD4 WWIII domain {Rat (*Rattus norvegicus*)}

GSPVDSNDLGLPLPPGWEERTHTDGRVFFINHNKKTQWEDPRMQNVAITG

>d1e0na_ b.72.1.1 (A:) Hypothetical protein Yjq8 (Set2p) {Baker's yeast (*Saccharomyces cerevisiae*)}

PGWEIIHENGRPLYNAEQKTKLHYPP

>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*}

MGDCANANVYPNWWVKDWAGGQPTHNEAGQSIVYKGNLYTANWYTASVPGSDSSWTQVGSCN

>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
ASDGQHLGSFDPKTNQLKGPDPKRNKIKYL

>d1hcb_ b.74.1.1 (-) Carbonic anhydrase {Human (*Homo sapiens*), erythrocytes, isozyme I}

PDWGYDDKNGPEQWSKLYPIANGNNQSPVDIKTSETKHDTSLKPISVSYNPATAKEIINVGHSHFVN
FEDNDNRSVLKGGPFSDSYRLFQHFHFWGSTNEHGSEHTVDGVKYS AELHVAHWNSAKYSSLAEA
ASKADGLAVIGVLMKVGEANPKLQKVLDALQAIKTKGRAPFTNFD PSTLLPSSLDFTYTPGSLTHP

PLYESVTWIICKESISVSSEQLAQFRSLLSNVEGDNAVPMQHNNRPTQPLKGRTVRASF
>d2cba_ b.74.1.1 (-) Carbonic anhydrase {Human (Homo sapiens), erythrocytes, isozyme II}
HHWGYGKHNGPEHWHKDFPIAKGERQSPVDIDHTAKYDPSLKPLSVSYDQATSLRILNNGHAFNV
EFDDSQDKAVLKGGLDGTYRLIQFHFHWGSLDGGSEHTVDKYYAAELHLVHWNTKYGDFGKA
VQQPDGLAVLGIKLVGSAKPLQKVVDVLSIKTKGKSADFTNFDPRGLLPESLDYWTYPGSLTTP
LLECVTWIVLKEPISVSSEQVLKFRKLNFNNGEPEELMVDNWRPAQPLKNRQIKASFK
>d1flja_ b.74.1.1 (A:) Carbonic anhydrase {Rat (Rattus norvegicus), isozyme III}
AKEWGYASHNGPEHWHELYPIAKGDNQSPIELHTKDIRHDPQLPWSVSYDPSAKTILNNGKTCR
VVFDDTFDRSMLRGGPLSGPYRLRQFHLHWGSSDDHGSEHTVDGVKYYAAELHLVHWNPKYNTFGE
ALKQPDGIQVAVGIFLKGREKGEFQILLDALDKIKTKGKEAPFNHFDPSCLFPACRDYWTYHGSFTTP
PCEECIVWLLLKEPMTVSSDQMAKLRSLFASAENEPVPLVGNWRPPQPIKGRVVRASF
>d1znca_ b.74.1.1 (A:) Carbonic anhydrase {Human (Homo sapiens), isozyme IV}
WCYEVQAESSNYPCLVPVKWGGNCQKDRQSPINIVTTKAKVDKLGRRFFSGYDKKQTTWTVQNG
HVMMLLENKASISGGPLPAPYQAKQLHLHWSLDLPYKGEHSLDGEHFAMEMHIVHEKEKGTSRN
VKEAQDPEDEIAVLAFLVEAGTQVNEGFQPLVEALSNIKPEMSTTMAESSLLDLLPKEEKLRYFRY
LGLSTTPCDEKVVWTVFREPIQLHREQILAFSQKLYYDKEQTVSMKDNVRPLQQLGQRTVIKS
>d2znc_ b.74.1.1 (-) Carbonic anhydrase {Mouse (Mus musculus), isozyme IV}
WCYEIQTEDPRSSCLGPEKWPGACKENQSPINIVTARTKVNPRLTPFILVGYDQKQWPIKNNQHT
VEMTLGGGACIIGDLARYEAVQLHLHWSNGNDNGSEHSIDGRHFAMEMHIVHKKLTSSKEDSKD
KFAVLAFMIEVGDKNKGFQPLVEALPSISKPHSTSTVRESSLQDMLPPSTKMYTYFRYNGSLTTPNC
DETVIWTVYKQPIKIHKNQFLEFSKNLYDEDQKLNMKDNVRPLQPLGKRQVFKSHA
>d1dmxa_ b.74.1.1 (A:) Carbonic anhydrase {Mouse (Mus musculus), liver, isozyme V}
GTRQSPINIWKDSVYDPLAPLRVSYDAASCRLWNTGYFFQVEFDDSCEDSGISGGPLGNHYRLK
QFHFHWGATDEWGSEHAVDGHTYPAELHLVHWNSTKYENYKKASVGENGLAVIGVFLKLGAAHQ
ALQKLVLDLPEVRHKDTQVAMGPFDPACRDYWTYPGSLTTPPLAESVTWIVQKTPVEVSPS
QLSMFRTLLFSGRGEEEDVMVNNYRPLQPLRDRKLRSSFR
>d1jd0a_ b.74.1.1 (A:) Carbonic anhydrase {Human (Homo sapiens), isozyme XII}
KWTFYFGPDGENSWSKKYPSCGGLLQSPIDLHSDILQYDASLTPLFQGYNLSANKQFLLTNNGHSVK
LNLPSDMHIQGLQSRYSATQLHLHWGNPNDPHGSEHTVSGQHFAAELHIVHYNSDLYPDASTASNK
SEGLAVLAVLIEMGSFNPSYDKIFSHLQHVYKQGEAFVPGFNIEELLPERTAEYYRYRGSLLTTPCNP
TVLWTVFRNPVQISQEQLLALETALYCTHMDDPSPREMINNFRQVQKFDERLVYTSFS
>d1kopa_ b.74.1.1 (A:) Carbonic anhydrase {Neisseria gonorrhoeae}
HTHWGYTGHDSPESWGNLSEEFRLCSTGKNQSPVNITETVSGKLPKLVNYKPSMVDVENNGHTIQ
VNYPEGNTLTVNGRITYTLKQFHFHVPSENQIKGRTPMEAHFVHLDENKQPLVLAVLYEAGKTNG
RLSSIWNVMPMTAGKVKLNQPFDASTLLPKRLKYRFAAGSLTTPCTEGVSWLVKTYDHIDQAQA
EKFTRAVGSENNRPVQPLNARVVIE
>d1koqa_ b.74.1.1 (A:) Carbonic anhydrase {Neisseria gonorrhoeae}
THWGYTGHDSPESWGNLSEEFRLCSTGKNQSPVNITETVSGKLPKLVNYKPSMVDVENNGHTIQV
NYPEGNTLTVNGRITYTLKQFHFHVPSENQIKGRTPMEAHFVHLDENKQPLVLAVLYEAGKTNG
LVLAVLYEAGKTNGRLSLAVLYEAGKTNGRLSSIWNVMPMTAGKVKLNQPFDASTLLPKRLKYRFA
GSLTTPCTEGVSWLVKTYDHIDQAQA EKFTAVGSENNRPVQPLNARVVIE
>d4bcl_ b.75.1.1 (-) Bacteriochlorophyll A protein {Prosthecochloris aestuarii, strain 2k}
TTTAHSDYEIILEGGSSSWGQVKGRAKVNVPAAIPLPTDCNIRIDAKPLDAQKGVVRFRTTKIESVVD
VKNTLNVEVDIANETKDRRIAVGEGSLVSGDFSHSFSFEQSVVNMYYYYRSDAVRRNIPNPIYMQGRQ

FHDILMKVPLDNNDLVDTWEGFQQSISGGGANFGDWIREFWFIGPAFAAINEGGQRISPIVVNSSNV
EGGEKGPVGVTRWKFSSHAGSGVDSISRWTELPVEQLNKPASIEGGFRSDSQGIEVKVDGNLPGVS
RDAGGLRRILNHPLIPLVHHGMVGGKFNDFVDTQLKIVLPKGYKIRYAAPQFRSQNLLEEYRWSSGA
YARWVEHVCKGGTGQFEVLYAQ

>d1ksaa_b.75.1.1 (A:) Bacteriochlorophyll A protein {Green sulfur bacterium (Chlorobium tepidum)}

TTAHSDEYIVLEGGSSSWGKVKARAKVNAPPASPLLPADCDVKNLNVKPLDPAKGFVRISAVFESIVDS
TKNKLTIADIANETKERRISVGEVMVSGDFSHTFSFEGSVNLFYRSDAVRRNVNPIYMQGRQ
FHDILMKVPLDNNDLIDTWEGTVKAIGSTGAFNDWIRDFWFIGPAFTALNEGGQRISRIEVNGLNTE
SGPKGPVGVSRWRFSHGGSGMVDSISRWAELFPSDKLNRPAQVEAGFRSDSQGIEVKVDGEFPGVSV
DAGGLRRILNHPLIPLVHHGMVGGKFNDFVDAQLKVLPKGYKIRYAAPQYRSQNLLEEYRWSSGAY
ARWVEHVCKGGVGQFEILYAQ

>d1ospo_b.76.1.1 (O:) Outer surface protein A {Lyme disease spirochete (Borrelia burgdorferi)}

SLDEKNSVSVLDLPGEMKVLVSKEKNKDGKYDLIATVDKLELKGTSKNNNGSGVLEGVKADKCKVKL
TISDDLQTTLEVFKEGDKTLVSKKVTSKDKSSTEEKFNEKGEVSEKIIIRADGTRLEYTGIKSDGSGK
AKEVLKGYVLEGLTAEKTTLVVKEGTVTLSKNISKSGEVSVELNDTDSSAATKKTAAWNSGTSTLTI
TVNSKKTDLVFTKENTITVQQYDSNGTKLEGSAREITKLDEIKNALK

>d1vmoa_b.77.1.1 (A:) Vitelline membrane outer protein-I (VMO-I) {Hen (Gallus gallus)}

RTREYTSVITVPNGGHWGKWGIRQFCHSGYANGFALKVEPSQFGRDDTALNGIRLRLCDGSVIESLV
GKWGTWTSFLVCPTGYLVSFSLRSEKSQGGDDTAANNIQFRCSDEAVLVGDGLSWGFRGFPWSKRC
KICGLQTKVESPOGLRDDTALNNVRFCCCK

>d1dlc_2_b.77.2.1 (290-499) delta-Endotoxin (insectocide), middle domain {Bacillus thuringiensis tenebrionis, CRYIIIA (BT13)}

LYPKEVKTELTRDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLRHRIQFHTRFQPGYYGNDSFN
YWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLFEKGVYRAVANTNLAVWPSAVYSGVTKVEFS
QYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPETTDEPLEKGYSHQLNYVMCFMQGSRGTIPVL
TWTHTKSVD

>d1ji6a2_b.77.2.1 (A:291-502) delta-Endotoxin (insectocide), middle domain {Bacillus thuringiensis, CRY3bb1}

LYSKGVKTELTRDIFTDPIFSLNTLQEYGPFTLSIENSIRKPHLFDYLRGIEFHTRLQPGYFGKDSFNY
WSGNYVETRPSIGSSTITSPFYGDKSTEPVQKLSFDGQKVYRTIANTDVAAWPNGKVYLVGVTKVDF
SQYDDQKNETSTQTYDSKRNNGHVSAQDSIDQLPETTDEPLEKAYSHQLNYAECFLMQDRRGITP
FFTWTHTRSVD

>d1ciy_2_b.77.2.1 (256-461) delta-Endotoxin (insectocide), middle domain {Bacillus thuringiensis, CRYIA (A)}

PIRTVSQLTREIYTNPVLENFDGSFRGMAQRIEQNIRQPHLMDILNSITIYTDVHRGFNYWSGHQITA
SPVGFSGPEFAFPLFGNAGNAAPPVLVSLTGLGIFRTLSSPLYRRIILGSGPNNQELFVLDGTEFSASLT
TNLPSTIYRQRGTVDSDLVIPPQDNSVPPRAGFSHRLSHVTMLSQAAGAVYTLRAPTFSWQHRSAEF

>d1i5pa2_b.77.2.1 (A:264-472) delta-Endotoxin (insectocide), middle domain {Bacillus thuringiensis subsp. kurstaki, CRY2AA}

YQSLMVSSGANLYASGSGPQQTQSFTAQNWPFYLSLFQVNSNYILSGISGTRLSITFPNIGGLPGSTTT
HLSNSARVNYSGGVSSGLIGATNLNHNFCSTVLPPLSTPFVRSWLDSTDRAGVATSTNWQTESFQ
TTLSLRCCGAFSARGNSNYFPDYFIRNISGVPLVIRNEDLTRPLHYNQIRNIESPSGTPGGARAYLVSVH

NRKN

>g1jac.5 b.77.3.1 (B:,A:) Jacalin {Jackfruit (*Artocarpus integrifolia*)}
SGKSQTVIVGSWGAKXGKAFDDGAF TGIREINLSYNKETAIGDFQVVYDLNGSPYVQNHKSFITGFT
PVKISLDFPSEYIMEVSGYTG NVSGYVVVRS LTFKTNKKTYGPGVTS GTPFNLPIENGLIVGFKGSIGY
WLDYFSMYLSL

>g1jot.2 b.77.3.1 (B:,A:) Lectin MPA {Osage orange (*Maclura pomifera*)}
RNGKSQSIIVGPWGDRXGVT FDDGAYTGIREINFEYNSETAIGGLRVTYDLNGMPFVAEDHKSFITGF
KPKVISLEFPSEYIVEVSGYV GKVVEGYTVIRSLTFKTNKQTYGPGV TNGTPFSLPIENGLIVGFKGSIGY
WLDYFSIYLSL

>d1c3ma_ b.77.3.1 (A:) Heltuba lectin {Jerusalem artishoke (*Helianthus tuberosus*)}
ASDIAVQAGPWGGNGGKRWLQTAHG GKITSIIKGGTCIFSIQFVYKDKDNIEYHSGKFGVLGDKAETI
TFAEDEDIT AISGTFGAYYHMTVV TSLTFQTNKKVYGPFGTVASSFS LPLTKGKFAGFFGNSGDVLDS
IGGVVVP

>d1jpc_ b.78.1.1 (-) Lectin (agglutinin) {Snowdrop (*Galanthus nivalis*)}
DNILYSGETLSTGEFLNYGSFV FIMQEDCNLVLYDVKPIWATNTGGLSRSCFLSMQTDGNLVVYNPS
NKPIWASNTGGQNGNYVCILQKDRNVVIYGTDRWATGTHT

>d1bwua_ b.78.1.1 (A:) Lectin (agglutinin) {Garlic (*Allium sativum*)}
RNILRNDEGLYGGQSLDVN PYHFIMQEDCNLVLYDHSTSVWASNTGILGKKGCRAVLQSDGNFVVYD
AEGRSLWASHSVRGNGNYV LVLQEDGNVVIYRSDIWSTN

>d1bwud_ b.78.1.1 (D:) Lectin (agglutinin) {Garlic (*Allium sativum*)}
RNILTND EGLYGGQSLDVN PYHLIMQEDCNLVLYDHSTAVWSSNTDIPGKKGCKAVLQSDGNFVVYD
AEGASLWASHSVRGNGNYV LVLQEDGNVVIYRSDIWSTNTYR

>d1kj1a_ b.78.1.1 (A:) Lectin (agglutinin) {Garlic (*Allium sativum*)}
RNLLTNGEGLYAGQSLDVEPYHFIMQEDCNLVLYDHSTSVWASNTGILGKKGCKAVLQSDGNFVVYD
AEGRSLWASHSVRGNGNYV LVLQEDGNVVIYGS DIWSTGTYK

>d1kj1d_ b.78.1.1 (D:) Lectin (agglutinin) {Garlic (*Allium sativum*)}
RNILMNDEGLYAGQSLDVEPYH LIMQEDCNLVLYDHSTAVWTTNTDIPGKKGCKAVLQSDGNFVVY
DAEGRSLWASHSVRGNGNYV LVLQEDGNVVIYGS DIWSTNTYK

>d1npla_ b.78.1.1 (A:) Lectin (agglutinin) {Daffodil (*Narcissus pseudonarcissus*)}
DNILYSGETLSPGEFLNNGRYV FIMQEDCNLVLYDVKPIWATNTGGLDRRCHLSMQSDGNLVVYSP
RNNPIWASNTGGENGNYV CVLQKDRNVVIYGTARWATGTNIH

>d1b2pa_ b.78.1.1 (A:) Lectin (agglutinin) {Bluebell (*Scilla campanulata*)}
NNIIFSKQPDDNHPQILHATESLEILFGTHVYRFIMQ TDCNLVLYDNNNPIWATNTGGLGNGCRAVL
QPDGVLVITNENVTVWQSPVAGKAGHYV LVLQPDRNVVIYGDALWATQTVR

>d1dlpa1 b.78.1.1 (A:1-115) Fetuin-binding protein Scafet precursor {Bluebell (*Scilla campanulata*)}
NNILFGLSHEGSHPQTLHAAQSLELSSFRFTMQSDCNLVLFDS DVRVWASNTAGATGCRAVLQSDGL
LVILTAQNTIRWSSGTKGSIGNYV LVLQPDRVTIYGPGLWDSGTSNK

>d1dlpa2 b.78.1.1 (A:116-235) Fetuin-binding protein Scafet precursor {Bluebell (*Scilla campanulata*)}
GSVVVANNGNSILYSTQGNDNHPQTLHATQSLQLSPYRLSMETDCNLVLFDRDDR VSTNTAGKGT
GCRAVLQPNGRMDVLTNQNIAVW TSGNSRSAGRYVFLQPDRNLAIYGGALWTT

>d1kapp1 b.79.1.1 (P:247-470) Metalloprotease, C-terminal domain {*Pseudomonas aeruginosa*, alkaline protease}

GANLTTTRTGDTVYGFNSNTERDFYSATSSSSKLVFSVWDAGGNDTLDFSGFSQNQKINLNEKALSDV
GGLKGNVSIAGVTVENAIGGSGDLLIGNDVANVLKGGAGNDILYGGADQLWGGAGADTFVYGDI
AESSAAPDTRLRDFVSGQDKIDLSGLDAFVNGGLVLQYVDAFAGKAGQAILSYDAASKAGSLAIDFSG
DAHADFAINLIGQATQADIVV

>d1sat_1 b.79.1.1 (247-471) Metalloprotease, C-terminal domain {*Serratia marcescens*}

GANLSTRTGDTVYGFNSNTGRDFLSTTSNSQKVIFAAWDAGGNDTFDFSGYTANQRINLNEKSFSDV
GGLKGNVSIAGVTVIENAIGGSGNDVIVGNAANNVLKGGAGNDVLFGGGGADELWGGAGKDIFVFS
ASDSAPGASDWIRDFQKIDKIDLSFFDKEANSSSFIHFVDHFSGTAGEALLSYNASSNVTDLSVNIGG
HAAPDFLVKIVGQVDVATDFIV

>d1air_ b.80.1.1 (-) Pectate lyase {*Erwinia chrysanthemi*, type C}

ATDTGGYAATAGGNVTGAVSKTATSMQDIVNIIDAARLDANGKKVKGAYPLVITYTGNEDSLINAAA
ANICGQWSKDPRGVEIKEFTKGITIGANGSSANFGIWKSSDVVVQNMRIYLPGGAKDGMIRVD
DSPNVVVDHNEFANHECDGTPDNDTTFESAVIDIKASNTVTVSYNYIHGVKVKVGLDGSSSSDTG
RNITYHHNYNDVNARLPLQRGGLVHAYNNLYTNITGSLNVRQNGQALIENNWFKAINPVTSRY
DGKNFGTWVLKGNITKPADFSTYSITWTADTKPYVNADSWTSTGTFTVAYNYSVSAQCCKDKL
PGYAGVGKNLATLTSTAC

>d1pcl_ b.80.1.1 (-) Pectate lyase {*Erwinia chrysanthemi*, type E}

AVETDAATTGWATQNGGTTGGAKAAKAVEVKNISDFKKALNGTDSSAKIIVTGPIDISGGKAYTSFD
DQKARSQISIPSNTHIGVGSNGKFTNGSLVIKGVKNVILRNLYIETPVDVAPHYESGDGWNAEWDAA
VIDNSTNVVVDHVTISDGSFTDDKYTTKDGKEYVQHDGALDIKKSVDYVTISYSR FELHDKTILIGHS
DSNGSQDSGKLRVTFHNNVDFRATERAPRVRFGSIHAYNNVYLGDKHSVYPYLSFGLGTSGSILSE
SNSFTLSNLKSIDGNPECSIVKQFNSKVFSDKGSVNGSTTTKLDTCGLTAYKPTLPYKYSAQTMSS
LATSINNNAGYGKL

>d1bn8a_ b.80.1.1 (A:) Pectate lyase {*Bacillus subtilis*}

ADLGHQTLGSNDGWGAYSTGTTGGSKASSNVYTVSNRNQLVSALGKETNTTPKIIYIKGTIDMNVD
DNLKPLGLNDYKDPEYDLKYLKAYDPSTWGKKEPSGTQEEARARSQKNQKARVMVDIPANTTIV
GSGTNAKVVGNGFQIKSDNVIIRNIEFQDAYDYFPQWDPTDGSSGNWNSQYDNITINGGTHIWIDHC
TFNDGSRPDSTSPKYYGRKYQHHDGQTDASNGANYITMSYNYHDHDKSSIFGSSDSTSDGKDKI
TLHHNRYKNIVQRAPRVRFGQVHVYNNYEGSTSSSYPFYAWGIGKSSKIYAQNNVIDVPGLSAAK
TISVFGGTALYDSGTLNLTQINASAANGLSSVWTPSLHGSIDASANVKSNNVINQAGAGKLN

>d1ee6a_ b.80.1.1 (A:) Pectate lyase {*Bacillus* sp., strain ksmp15}

APTVVHETIRVPAGQTFDQKQTYVANPNTLGDGSAENQKPIFRLEAGASLKNVIGAPAADGVHC
YGDCTITNVIWEDVGEDALTLKSSGTVNISGGAAYKAYDKVFQINAAGTINIRNFRADDIGKLRQNG
GTTYKVMNVENCNISRVKDAILRTDSSTSTGRIVNTRYSNVPTLFKGFKSGNTTASGNTQY

>d1idk_ b.80.1.2 (-) Pectin lyase {*Aspergillus niger*, type A}

VGVSGSAEGFAKGVTTGGGSAFPVYPTIDELVSYLGDDEARVIVLTKTFDFTDSEGTGTCAPWGT
ASACQVAIDQDDWCENYEPDAPSVSVEYYNAGTLGITVTSNKSLIGEGSSGAIKGKLRIVSGAENIIQ
NIAVTDINPKYVWGGDAITLDDCDLVWIDHVTARIGRQHYVLGTSADNRVSLTNNYIDGVSDYSAT
CDGYHYWAIYLDGDADLVMTKGNYYHTSGRSPKVQDNTLLHAVNNYWDISGHAFEIGEGGYVLA
EGNVFQNVDTVLETYEGEAFTVPSSTAGEVCSTYLGRDCVINGFGSSGTFSEDSTSFLSDFEGKNIASA
SAYTSVASRVVANAGQGNL

>d1qcx_ b.80.1.2 (A:) Pectin lyase {*Aspergillus niger*, type B}

AGVVGAAEGFAHGVTTGGGASPVYPTTTDELVSYLGDNEPRVILDTQTFDFTGTEGTTTTGCAPWG
TASQCQVAINLHSCDNYQASAPKVSVTYDKAGILPITVNSNKSIVGQGTGKGVKGLRVVSGAKNV

IIQNIAVTDINPKYVWGGDAITVDDSDLVWIDHVTTARIGRQHIVLGTSAADNRVTISYSLIDGRSDYSA
TCNGHHYWGCVYLDGSNDMVTLKGNFYNLGRMPKVQGNLLHAVNNLFHNFDFGHAFFEIGTGGY
VLAEGNVFQDVNVVETPISGQLFSSPDANTNQQCASVFRSCQLNAFGNSGSMGSDTSSIISKFAGK
TIAAAHPPGAIAQWTMKNAGQGK

>d1rmg_ b.80.1.3 (-) Rhamnogalacturonase A {*Aspergillus aculeatus*}

QLSGSVGPLTSASTKGATKTCNLSYGAVADNSTDVGPAITSAWAACKSGGLVYIPSGNYALNTWVTLT
GGATAIQLDGIIYRTGTASGNMIAVTDTTDFELFSSTSKGAVQGFYVYHAEGTYGARILRLTDVTHF
SVHDIILVDAPAFHFTMDTCSDEYVYMAIRGGNEGGLDGDVWGSNIWVHDVEVTNKDECVTVKS
PANNILVESIYCNWSGGCAMSGLGADTDVTDIVYRNVYTWSSNQMYMIKSNGGSGTVSNVLENFIG
HGNAYSLDIDGYWSSMTAVAGDGVQLNNTVKNWKGTEANGATRPPIRVVCSDTAPCTDLTLEDIAI
WTEGSSSELYLCRSAYSGYCLKDSSSHTSYTTTSTVTAAPSGYSATTMAADLATAFGLTASIPIPTIPT
SFYPGLTPYSALAG

>d1bhe_ b.80.1.3 (-) Polygalacturonase {*Erwinia carotovora*, subsp. *carotovora*}

SDSRTVSEPKTPSSCTTLKADSSTATSTIQKALNNCDQKAVRLSAGSTSVFLSGPLSLPSGVSLLDKG
VTLRAVNNAKSFENAPSSCGVVDKNGKGCDAFITAVSTTNSGIYGPIDGQGGVQLQDKKVSWE
LAADAKVKKLQNTPRLIQINKSKNFTLYNVSLINSPNFHVVFSDGDGFTAWKTTIKTPSTARNTDGI
DPMSSKNITIAYSNIATGDDNVAIKAYKGRAETRNISILHNDFGTGHGMSIGSETMGVYVNTVDDLK
MNGTTNGLRIKSDKSAAGVNVGVRYSNVVMKNVAKPIVIDTVYEKKEGSNVPDWSITFKDVTSET
KGVVVLNGENAKKPIEVTMKNVKLSDSTWQIKNVVKK

>d1ia5a_ b.80.1.3 (A:) Polygalacturonase {Fungus (*Aspergillus aculeatus*)}

ATTCTFSGSNGASSASKTSCSTIVLSNVAVPSGTTDLTKLNDGTHVIFSGETTFGYKEWGPLISVS
GSDLTITGASGHSINGDGRWWDGEGNGGKTKPKFFAAHSLTNSVISGLKIVNSPVQVFSVAGSDYL
TLKDITIDNSDGDNDGGHNTDAFDIGTSTYVTISGATVYNQDDCVAVNSGENIYFSGGYCSGGHGLSI
GSVGGRSNDTVKNVTFVDSTIINSNDNGVRIKTNIDTTGSVSDVYKIDITLSIAKYGIVVQNYGDTSS
TPTTGPITDFVLDNVHGSVSSGTNILISCGSGSCSDWTWTDVSVSGGKTSSKCTNVPSGASC

>d1czfa_ b.80.1.3 (A:) Polygalacturonase {Fungus (*Aspergillus niger*),
endo-polygalacturonase II}

DSCTFTTAAAKAGKAKCSTITLNNIEVPAGTTLDLTGLTSGTKVIFEGTTTFQYEEWAGPLISMGE
HITVTGASGHLINCDGARWWDGKGTSGKKPKFFYAHGLDSSITGLNIKNTPLMAFSVQANDITFT
DVTINNADGDTQGGHNTDAFDVGNVSVGNIIKPVVHNQDDCLAVNSGENIWFTEGGTCIGGHGLSIG
SVGDRSNVKNVTIEHSTVSNSENAVRIKTISGATGSVSEITYSNIVMSGISDYGVVIQDYEDGKPT
GKPTNGVTIQDVKLESVTGSVDSGATEIYLLCGSGSCSDWTWDDVKVTGGKKSTACKNFPSVASC

>d1hg8a_ b.80.1.3 (A:) Polygalacturonase {*Fusarium moniliforme*}

DPCSVTEYSGLATAVSSCKNIVLNGFQVPTGKQLDLSSLQNDSTVTFKGTTFATTADNDFNPVIVSGS
NITITGASGHVIDGNGQAYWDGKGSNSNSNQPDHFIVVQKTTGNSKITNLNIQNWVHCFDITGSS
QLTISGLILDNRAGDKPNAKSGSLPAAHNTDGFDISSDHVTLNHNHVYNQDDCVAVTSGTNIVVSN
MYCSGGHGLSIGSVGGKSDNVVDGVQFLSSQVNSQNGCRIKSNSGATGTINNVTYQNIALTNIITYG
VDVQQDYLNNGGPTGKPTNGVKISNIKFIKVTGTVASSAQDWFILCGDGSCSGFTFSGNAITGGGKTSS
CNYPTNTCPS

>d1dbga_ b.80.1.4 (A:) Chondroitinase B {*Flavobacterium heparinum*}

QVVASNETLYQVVKEVKPGGLVQIADGTYKDVQLIVNSGKSLPITIKALNPGKVFFTGDAKVELRG
EHLILEGIWFKDGNRAIQAWKSHGPLVAIYGSYNRITACVFDCFDEANSAYITSLTEDGKVPQHCR
DHCSFTDKITFDQVINLNNNTARAIDKGSVGGPGMYHRVDHCFFSNPQKPGNAGGGIRIGYYRNDIGR
CLVDSNLFMRQDSEAEIITSKSQENVVYGNLYLNCQGTMMFRHGDHQAIVNNFYIGNDQRFYGGM

FVWGSRHVIACNYFELSETIKSRGNAALYLNPGAMASEHALAFDMLIANNAFINVNGYAIHFNPLDE
RRKEYCAANRLKFETPHQLMLKGNLFFKDKPYVYPPFFKDDYFIAGKNSWTGNVALGVEKGIPVNISA
NRSAYKPVKIKDIQPIEGIALDLNALISKGITGKPLSWDEVPRPYWLKEMPGTYALTARLSADRAAKFK
AVIKRNKEH

>d1h80a_b.80.1.8 (A:) iota-carrageenase {Alteromonas sp., atcc 43554}

VSPKTYKDADFVYVAPTQQDVNYDLVDDFGANGNDTSSDSNALQRAINAISRKPNGGTLIPNGTYH
FLGIQMKSINVHIRVESDVIIKPTWNGDGKNHRLFVGVNNIVRNFSFQGLGNGFLVDFKDSRDKNLA
VFKLGDVRNYKISNFTIDDNKTIFASILVDVTERNRGLHWSRNGIIERIKQNNALFGYGLIQTYGADNI
LFRNLHSEGGIALRMETDNLMMKNYKQGGIRNIFADNIRCSKGLAAVMFGPHFMKNGDVQVTNVSS
VSCGSAVRSDSGFVELFSPTDEVHTRQSWKQAVESKLGRCQAQTPYARGNGGTRWAARVTQKDA
DKAKLEYGIEPGSFGTVKVFDTARFGYNADLKQDQLDYFSTSNPMCKRVCLPTKEQWSKQGQIYIG
PSLAAVIDTTPETSKYDYDVKTFNVKRINFPVNSHKTIDTNTTESSRVCNYYGMSECSRRWER

>d1qja_b.80.1.5 (A:) Pectin methylesterase PemA {Erwinia chrysanthemi}

ATTYNAVVSKESSDGKTFKTIADAIASAPAGSTPFVILIKNGVYNERLTITRNNLHLKGESRNGAVIAA
ATAAGTLKSDGSKWGTAGSSTITISAKDFSASQLTIRNDFDFPANQAKSDSDSSKIKDTQAVLYVTKS
GDRAYFKDVS LVGYQDTLYVSGGRSFFSDCRISGTVDFIFGDGTALFNCDLVSRYRADVKSGNVSGYL
TAPSTNINQKYGLVITNSRVIRESDSVPKASYGLGRPWHPTTTFSDGRYADPNAIGQTVFLNTSMDN
HIYGWDKMSGKDKNGNTIWFNPEDSRFFEYKSYGAGAAVSKDRRQLTDAQAAEYTSKVLGDWTP
TLP

>d1qq1a_b.80.1.6 (A:) P22 tailspike protein {Salmonella phage P22}

YSIEADKKFKYSVKLSDYPTLQDAASAAVDGLLIDRDYNYFGGETVDFGGKVLTIIECKAKFIGDGNLIF
TKLGKGSRIAGVFMESTTTPWVIKPWTDNQNWLTDAAAVVATLKQSKTDGYQPTVSDYVKFPGIET
LLPPNAKQONITSTLEIRECIGVEVHRASGLMAGFLFRGCHFCMKVDANNPSGGKDGITFENLSGD
WGKGNVYVIGGRTSYGSVSSAQFLRNNGGFERDGGVIGFTSYRAGGSGVKTWQGTVGSTSRNYNLQ
FRDSVVIYPVWDGFDLADTDMNPELDRPGDYPTQYPLHQLPLNHLIDNLLVRGALGVGFGMDGK
GMYVSNITVEDCAGSGAYLLTHESVFTNIAIIDTNTKDFQANQIYISGACRVNGLRLIGIRSTDQSLTI
DAPNSTVSGITGMVDPSRINVANLAEELGNIRANSFGYDSAAIKLRIHKLKSKTLDGALYSHINGGAG
SGSAYTQLTAISGSTPDAVSLKVNHKDCRGAIEPFPDIASDDFIKSSCFLPYWENNSTSLKALVKKP
NGELVRLTLATL

>d1daba_b.80.1.7 (A:) Virulence factor P.69 pertactin {Bordetella pertussis}

DWNNQSIVKTGERQHGIHIQSDPGGVRTASGTTIKVSGRQAQGILLENPAAELQFRNGSVTSSGQLS
DDGIRRFGLGTVTKAGKLVADHATLANVGDWDDDGIALYVAGEQAQASIADSTLQAGGVQIERGA
NVTVQRSAIVDGGHLHIGALQSLQPEDLPPSRVLRDNTVAVPASGAPAAVSVLGASELTDGGHITG
GRAAGVAAMQGAHVHLQRATIRRGDALAGGAVPGGAVPGGAVPGGFGPVGFDGWYGVDSVGS
SVELAQSIVEAPELGAIRVGRGARVTVPGGSLSAPHGNVIETGGARRFAPQAAPLSITLQAGAHAQG
KALLYRVLPEPVKLTLTGGADAQGDIVATELPSIPGTSIGPLDVALASQARWTGATRAVDLSIDNATW
VMTDNSNVGALRLASDGSVDFQPAEAGRFKVLTVNTLAGSGLFRMNVFADLGLSDKLVVMQDASG
QHRLWVRNSGSEPASANTLLLVQTPLGSAATFTLANKDGKVDIGTYRYRLAANGNGQWSLVGAKAP
P

>d1ezga_b.80.2.1 (A:) Insect cysteine-rich antifreeze protein {Yellow mealworm (Tenebrio molitor)}

QCTGGADCTSGTACTGCGNCPNAVCTCTNSQHCVKANTCTGSTDCNTAQTCTNSKDCFEANTCTDS
TNCYKATACTNSSGCP

>d1hf2a1_b.80.3.1 (A:100-206) Cell-division inhibitor MinC, C-terminal domain {Thermotoga

maritima}

TGKVIKRNIRSGQTVVHSGDVIVFGNVNKGAEILAGGSVVVFGKAQGNIRAGLNEGGQAVVAALDLQ
TSLIQIAGFITHSKGEENVPSIAHVKGNRIVIEPFDKVSF

>d1ea0a1 b.80.4.1 (A:1203-1472) Alpha subunit of glutamate synthase, C-terminal domain
{Azospirillum brasilense}

GRNEVPDTLDARIVADARPLFEEGEKMQLAYNARNTQRAIGTRLSSMVTRKFGMFGQLQPGHITIRLR
GTAGQSLGAFVQGIKLEVMGDANDYVVGKLSGGTIVVRPTTSSPLETNKNTIIGNTVLYGATAGKLF
AAGQAGERFAVRNSGATVVVEGCGSNGCEYMTGGTAVILGRVGDNFAAGMTGGMAYVYDLDDSLPL
YINDESVIFQRIEVGHYESQLKHLIEEHVTETQSRFAAEILNDWAREVTKFWQVVPKEMLNRLVLPV
HL

>d1kq5a_ b.80.5.1 (A:) C-terminal domain of adenylcyclase associated protein {Baker's
yeast (*Saccharomyces cerevisiae*)}

MPPRKELVGNKWFNIENYENETESLVIDANKDESIFIGKCSQVLVQIKGKVNALSETESCSVVLDDSSIS
GMDVIKSNKFGIQVNHSLPQISIDKSDGGNIYLSKESLNTEIYTSCTAINVNLPIGEDDDYVEFPISEQ
MKHSFADGKFKSAVFE

>d1lxa_ b.81.1.1 (-) UDP N-acetylglucosamine acyltransferase {*Escherichia coli*, gene lpxA}

MIDKSAFVHPTAIVEEGASIGANAHIGPFCIVGPHVEIGEGTVLKSHVVVNGHTKIGRDNEIYQFASIG
EVNQDLKYAGEPTRVEIGDRNRIRESVTIHRGTVQGGGLTKVGSNLLMINAHIAHDCTVGNRCILA
NNATLAGHVSVDFAIIGGMTAVHQFCIIGAHVMVGGCSGVAQDVPPYVIAQGNHATPFGVNIEGLK
RRGFSREAITAIRNAYKLIYRSGKTLDEVKPEIAELAETYPVKAFTDFFARSTRGLIR

>d3tdt_ b.81.1.2 (-) Tetrahydrodipicolinate-N-succinyltransferase,
THDP-succinyltransferase, DapD {*Mycobacterium bovis*}

MQQLQNVIESAFERRADITPANVDTVTREAVNQVIGLLDSGALRVAEKIDGQWVTHQWLKKAVALLS
FRINDNKVMDGAETRYYDKVPMKFADYDEARFQKEGFRVVPATVRQGAFIARNTVLMPSYVNIGA
YVDEGTMVDTWATVGSCAQIGKNVHLSGGVGGVLEPLQANPTIIEDNCFIGARSEVVEGVIVEEGS
VISMGVYLGQSTRIYDRETGEIHYGRVPAGSVVVSIGNLPSKDGYSYLYCAVIVKKVDAKTRGKVGINEL
LRTID

>d1xat_ b.81.1.3 (-) Xenobiotic acetyltransferase {*Pseudomonas aeruginosa*}

NYFESPFRGKLLSEQVSNPNIRVGRYSYSGYYHGHSFDDCARYLMPDRDDVDKLVIGSFCSIGSGAA
FIMAGNQGHRAEWASTFPFHFHHEEPAFAGAVNGYQAGDTLIGHEVWIGTEAMFMPGVRVGHGA
IIGSRALVTGDVEPYAIVGGNPARTIRKRFSDDGIQNLLEMAWWDWPLADIEAAMPLCTGDIPALY
QHWKQRQA

>d1kk6a_ b.81.1.3 (A:) Xenobiotic acetyltransferase {*Enterococcus faecium*, VAT(D)}

MGNPNMKMYPIEGNKSVQFIKPILEKLENVEVGEYSYDSKNGETFDKQILYHYPILNDKLGKIGKFCSI
GPGVTIIMNGANHRMDGSTYPFNLFNGWEKHMPKLDQLPIKGDTHGNDVWIGKDVVIMPGVKIG
DGAIVAANSVVVKDIAPYMLAGGNPANEIKQRFDDQDTINQLLDIKWVWNPIDIINENIDKILDNSIIR
EVIW

>d1fxja1 b.81.1.4 (A:252-329) N-acetylglucosamine 1-phosphate uridyltransferase GlmU,
C-terminal domain {*Escherichia coli*}

VMLRDPARFDLRGTLTHGRDVEIDTNVHIEGNVTLGHRVKIGTGCVIKNSVIGDDCEISPYTVVEDAN
LAAACTIGPF

>d1hv9a1 b.81.1.4 (A:252-452) N-acetylglucosamine 1-phosphate uridyltransferase GlmU,
C-terminal domain {*Escherichia coli*}

VMLRDPARFDLRGTLTHGRDVEIDTNVHIEGNVTLGHRVKIGTGCVIKNSVIGDDCEISPYTVVEDAN

LAAACTIGPFARLRPGAELLEGAHVGNFVEMKKARLGKGSKAGHLTYLGDAEIGDENVNIGAGTITCN
YDGANKFKTIIGDDVFGSDTQLVAPVTVGKGATIAAGTTVTRNVGENALAIRVPQTQKEGWRRP
>d1hm9a1 b.81.1.4 (A:252-459) N-acetylglucosamine 1-phosphate uridyltransferase GlmU,
C-terminal domain {Streptococcus pneumoniae}
VSFVNPEATYIDIDVEIAPEVQIEANVILKGQTKIGAETVLTNGTYVVDSTIGAGAVITNSMIEESSVAD
GVTVGPYAHIRPNSSLGAQVHIGNFVEVKGSSIGENTKAGHLTYIGNCEVGSNVNFGAGTITVNYDGGK
NKYKTVIGDENVFVGSNSTIIPVELGDNSLVGAGSTITKDVPAIAIGRGRQINKDEYATRLPHHPKN
Q

>d1qrea_ b.81.1.5 (A:) Carbonic anhydrase {Archaeon Methanosarcina thermophila}
TVDEFSNIRENPVTPWNPEPSAPVIDPTAYIDPQASVIGEVITGANVMVSPMASIRSDEGMPIFVGD
SNVQDGVVLAHALETINEEGEPIEDNIVEVDGKEYAVYIGNNVSLAHQSQVHGPAAVGDDTFIGMQAF
VFKSKVGNNCVLEPRSAAGVTIPDGRYIPAGMVVTSQAEADKLPEVTDDYAYSHTNEAVVYVNVHL
AEGYKETS

>d1ewwa_ b.81.2.1 (A:) An insect antifreeze protein {Spruce budworm (Choristoneura
fumiferana)}
DGSTNTNSQLSANSKCEKSTLTNCYVDKSEVYGTCTGSRFDGVTITTTSTSTGSRISGPGCKISTCIIT
GGVPAPSAACKISGCTFSAN

>d1dzra_ b.82.1.1 (A:) dTDP-4-dehydrorhamnose 3,5-epimerase RmlC {Salmonella
typhimurium}
MMIVIKTAIPDVLILEPKVFGDERGFFESYNQQTFEELIGRKVTFVQDNHSSKKNVLRGLHFQERGE
NAQGKLVRCVGEVFDVAVDIRKESPTFGQWVGNLSAENKRQLWIPEGFAHGFVTLSEYAEFLYKA
TNYYSPPSEGSILWNDEAIGIEWPFSQLPELSAKDAAAPLLDQALLTE

>d1ep0a_ b.82.1.1 (A:) dTDP-4-dehydrorhamnose 3,5-epimerase RmlC {Archaeon
Methanobacterium thermoautotrophicum}
EFRFIKTSLDGAIIEPEVYTDERGYFMETFNEAIFQENGLVRFVQDNESMSVIRGVLRLHFQREKP
QGKLVIRGEIFDVAVDLRKNSDTYGEWTGVRLSDENRREFPIPEGFAHGFLALSDECIVNYKCTEL
YHPEYDSGIPWDDPDIGIDWPLEMVDDLISEKDRNWKPLRENPVYL

>d1fi2a_ b.82.1.2 (A:) Germin {Barley (Hordeum vulgare)}
TDPDPLQDFCVADLDGKAVSVNGHTCKPMSEAGDDFLFSSKLTKAGNTSTPNGSAVTELDVAEWPG
TNTLGVSMNRVDFAPGGTNPPIHIPRATEIGMVMKCELLVGLGSLDSGNKLYSRVVRAGETFVPIRG
LMHFQFNVGKTEAYMVVSFNSQNPQIVFVPLTLFGSDPPIPTPVLTKALRVEAGVVELLKSFKFAGGS

>d2phla1 b.82.1.2 (A:11-210) Seed storage 7S protein {French bean (Phaseolus vulgaris),
phaseolin}
DNPFFYFNSDNSWNTLFKNQYGHIRVLQRFDQQSKRLQNLEDYRLVEFRSKPETLLLPQQADAELL
VVRSGSAILVLVKPDDRREYFFLTSDNPIFSDHQIPAGTIFYLVNPDPKEDLRRIQLAMPVNNPQIHE
FFLSSTEAQQSYLQEFKSKHILEASFNSKFEEINRVLFEEEGQQEGVIVNIDSEQIKELSKHAKSS

>d2phla2 b.82.1.2 (A:220-381) Seed storage 7S protein {French bean (Phaseolus vulgaris),
phaseolin}
NTIGNEFGNLTERTDNSLNVLISSIEEMEEGALFVPHYYSKAIVILVVNEGEAHVELVGPKNKETLEYE
SYRAELSKDDVFVIPAAYPVAIKATSNVNFTGFGINANNNRNLLAGKTDNVISSIGRALDGKDVGL
TFSGSGDEVMLINKQSGSYFVDAH

>d1dgwa_ b.82.1.2 (A:) Seed storage 7S protein {Jack bean (Canavalia ensiformis),
canavalin/vinculin}
NNPYLFRSNKFLTLFKNQHGLRLLQRFNEDTEKLENLRDYRVLEYCSKPNTLLPHHSDSDLLVLV

LEGQAILVLVNPDRDQTYKLDQGDAIKIQAGTPFYLINPDNNQNLRLKFAITFRRPGTVEDFFLSSTK
RLPSYLSAFSKNFLEASYDSPYDEIEQTLQEEQEGVIVKMP

>g1dgr.3 b.82.1.2 (M;N:) Seed storage 7S protein {Jack bean (*Canavalia ensiformis*),
canavalin/vinculin}

QLRRYAATLSEGDIIVIPSSFPVALKAASDLNMVGIGVNAENNERNFLAGHKENVIRQIPRQVSDLTFP
GSGEEVEELLENQKESYFVDGQPXDKPFNLRSDPIYSNNYGKLYEITPEKNSQLRDLILLNCLQM
NEGALFVPHYNSRATVILVANEGRAEVELVLE

>g1dgw.1 b.82.1.2 (X;Y:) Seed storage 7S protein {Jack bean (*Canavalia ensiformis*),
canavalin/vinculin}

DKPFNLRSDPIYSNNYGKLYEITPEKNSQLRDLILLNCLQMNEGALFVPHYNSRATVILVANEGRA
EVELVLEQLRRYAATLSEGDIIVIPSSFPVALKAASDLNMVGIGVNAENNERNFLAGHKENVIRQIP
RQVSDLTFPQSGEEVEELLENQKESYFVDGQP

>d1fxza1 b.82.1.2 (A:10-248) Seed storage 7S protein {Soybean (*Glycine max*), proglycinin}
NECQIQKLNALKPDNRIESEGLIETWNPNNKPFQAGVALSRCTLNRNALRRPSYTNQGPQEIYIQQ
GKGIFGMIYPCPSTFEPPQPPQQRGQSSRPQDRHQKIYNFREGDLIAVPTGVAAWWMYNNEDTPVV
AVSIIDTNSLENQLDQMPRRFYLAGNQEFLKYQQEQGGHQSQKQKQEEENEGGSILSGFTLEF
LEHAFSVDKQIAKNLQGENEGEDKGAIVTVKGLSVIKP

>d1fxza2 b.82.1.2 (A:297-470) Seed storage 7S protein {Soybean (*Glycine max*), proglycinin}
ICTMRLRHNIQTSSPDIYNPQAGSVTTATSLDFPALSRLSAEFGSLRKNAMFVPHYLNANSIY
ALNGRALIQVNCNGERVFQDQEGRLVLPQNFVVAARSQSDNFEYVSFKTNDTPMIGTLAGANS
LLNALPEEVIQHTFNLKSQARQIKNNNPFKFLVPPQES

>d1pmi_ b.82.1.3 (-) Phosphomannose isomerase {Yeast (*Candida albicans*)}

SSEKLFRIQCGYQNYDWGKIGSSSAVAQFVHNSDPSITIDETKPYAELWMGTHPSVPSKAIDLNNQTL
RDLVTAKPQEYLGESIITKFGSSKELPFLFKVLSIEKVLSIAHPDKKLGALHAADPKNYPDDNHKP
EMAIAVTDFEGFCGFKPLDQLAKTLATVPELNEIIGQELVDEFISGIKLPAEVGSQDDVNNRKLQKV
FGKLMNTDDDVIKQQTAKLLERTDREPQVFKDIDSRLPELIQRLNKQFPNDIGLFCGCLLNHVGLN
KGEAMFLQAKDPHAYISGDIECMAASDNVVRAGFTPKFKDVKNLVEMLTYSYESVEKQKMPLEFP
RSKGDVKSVLDPPIAEFVSLQTFDKSKGGKQVIEGLNGPSIVIATNGKGTIQTGDDSTKQKIDTGY
VFFVAPGSSIELTADSANQDQDFTTYRAFVEA

>d1eyba_ b.82.1.4 (A:) Homogentisate dioxygenase {Human (*Homo sapiens*)}

AELKYISGFGNECSSEDPKCPGLPEGQNNPQVCPYNLYAEQLSGSAFTCPRSTNKRSWLYRILPSVSH
KPFESIDEGHVTHNWDEVDPDPNQLRWKPFEPKASQKKVDFVSGLHTLCGAGDIKSNNGLAIHIFL
CNTSMENRCFYNSDGDFLVLPQKGNLLIYTEFGKMLVQPNEICVIQRGMRFSDVFEETRKYILEVYG
VHFELPDLGPIGANLANPRDFLIPIAWYEDRQVPGGYTVINKYQKGLFAAKQDVSPFNVAWHGN
YTPYKYNLKNFMVINSVAFDHADPSIFTVLTAKSVRPGVAIADFVIFPPRWGVADKTFRPPYYHRNC
MSEFMGLIRGHYEAQGGFLPGGSLHSTMPHGPADCFEKASKVKLAPERIADGTMAFMFESSL
SLAVTKWGLKASRCLDENYHKWEPLKSHFTPNSRN

>d1qjea_ b.82.2.1 (A:) Isopenicillin N synthase {*Emericella nidulans*}

SKANVPKIDVSPLFGDDQAAKMRVAQQIDAASRDGFFYAVNHGINVQRLSQKTEFHMSITPEEK
WDLAIRAYNKEHQDQVRAGYLSIPGKKAVESFCYLNPNFTPDHPRIQAKTPTHEVNVWPDETKH
PGFQDFAEQYYWDVFLSSALLKGYALALGKEENFFARHFKPDDTLASVVLIRYPYLDPYPEAAIKTA
ADGTKLSFEWHEDVSLITVLYQSNVQNLQVETAAGYQDIEADDTGYLINCOSYMAHLTNNYYKAPIH
RVKWWNAERQSLPFFVNLGYDSVIDPFDPREPNGKSDREPLSYGDYLNGLVSLINKNGQT

>d1dcs_ b.82.2.1 (-) Deacetoxycephalosporin C synthase {*Streptomyces clavuligerus*}

MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTTELKSAKDLVIDFFEHGSEAEKRAVT
SPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFERIWTQYFDRQYTASRAVA
REVL RATGTEPDGGVEAFLDCEPLLRFYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANG
FVSLQAEVGGAFDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPN
ADFTFSVPLARECGFDVSLDGETATFQDWIGGNYVNIRRTSKA

>d1gp6a_b.82.2.1 (A:) Anthocyanidin synthase {Mouse-ear cress (*Arabidopsis thaliana*)}
VAVERVESLAKSGIISIPKEYIRPKEELESINDVFLEEKEDGPVPTIDLKNIESDDEKIRENCIEELKK
ASLDWGMHLINHGIPADLMERVKKAGEEFFSLSVEEKEYANDQATGKIQGYGSKLANNASGQLE
WEDYFFHLAYPEEKRDLSIWPKTPSDYIEATSEYAKCLRLLATKVFKALSVGLGLEPDRLEKEVGGLE
ELLQMKINYYPKCPQPELALGVEAHTDVSALTFILHNMVPGQLFYEGKWVTAKVPSIVMHIGD
TLEILSNGKYKSILHRGLVNKEKVRISWAVFCEPPKDKIVLKLPEMVSVESPAKFPPTFAQHIEHKL
FGKEQEEL

>d1ds1a_b.82.2.2 (A:) Clavaminic acid synthase {*Streptomyces clavuligerus*}
TSVDCTAYGPELRALAAARLPRTPRADLYAFLDAAHTAAASLPGALATALDTFNAEGSEDGHLRLGLP
VEADADLPTTSPSTPAPEDRSLTMEAMLGLVGRRLGLHTGYRELRSQTVYHDVYPSGAAHLSSET
SETLLEFHTMAYHRLQPNYVMLACSRADHERTAATLVASVRKALPLLDERTRARLLDRRMPCCVD
VAFRGGVDDPGAIAQVKPLYGDADDPFLGYDRELLAPEDPADKEAVAALS KALDEVTEAVYLEPGDL
LIVDNFRTHARTPFSPRWGDKDRWLHRVYIRTDRNGQLSGGERAGDVVAFTPRG

>d1jr7a_b.82.2.3 (A:) Gab protein (hypothetical protein YgaT) {*Escherichia coli*}
GQDYSGFTLTPSAQSPRLLELTFTEQTTKQFLEQVAEWPVQALEYKSFLRFRVAKILDDL CANQLQLL
LLKTLNRAEGALLINAVGVDDVKQADEMVKLATAVAHLIGRSNFDAMSGQYYARFVVKNDNSDS
YLRQPHRMELHNDGTYVEEITDYVLMMKIDEQNMQGGNSLLHLDDWEHLDNFRHPLARRPM
RFAAPPSKNVSKDVFHPVFDVDQGRPVMRYIDQFVQPKDFEEGVWSELSDAIETSKGILSVPVPV
GKFLINNLFWLHGRDRFTPHPDLRRELMRQRGYFAYASNHYQTHQ

>d1e5sa_b.82.2.4 (A:) Type II Proline 3-hydroxylase (proline oxidase) {*Streptomyces* sp.}
MRSHILGKIELDQTRLAPDLAYLAAVPTVEEYDEFSNGFWKHVPLWNASGDSEDRLYRDLKDA
QPTAHVEHVPYLKEIVTTFVFDGTHLQMARSRLKNAIVIPHRDFVELDREVDRYFRFMVLEDSPL
AFHSNEDTVIHM RPGEIWF LDAATVHSAVNFSEISRQSLCVDFAFDGPFDEKEIFADATLYAPG
LPERRPFTA EHRRLSLGQVIERENFRDILFLLSKVHYKYDVHPSETYDWLIEISKQAGDEK
EQIRDFAVEARALSERFSLTSW

>d1ft9a2_b.82.3.1 (A:2-133) CO-sensing protein CooA, N-terminal domain {*Rhodospirillum rubrum*}

PPRFNIANVLLSPDGETFFRGRFSKIHKGLVCTGEGDENG VVVVDGRLRVYLVGEEREISLFYLT
GDMFCMHSGLVEATERTEVRFADIRTFEQKLQTCPSMAWGLIAILGRALTSCMRTIEDLMFH

>d1hw5a2_b.82.3.2 (A:1-137) Catabolite gene activator protein, N-terminal domain {*Escherichia coli*}

VLGKQPQTDPTLEWFLSHCHIHKYPKSTLIHQGEKAETLYYIVKGSVAVLIKDEEGKEMILSYLNQGD
FIGELGLFEEGQERSAWVRAKTACEVAEISYKKFRQLIQVNPDI MLRLSAQMARRLQVLAEKVGNLA
FL

>d1rgs_1_b.82.3.2 (113-244) Regulatory subunit of Protein kinase A {Cow (*Bos taurus*)}
RKVIPKDYKTMALAKAIEKNVLFSLDDNERSDIFDAMFPVSFIAGETVIQGGDEGDNFYVIDQGE
MDVYVNNNEWATSVGEGGSFGELALIYGT PRAATVKAKTNVKLWGIDRDSYRRILMGSTLRKRKMY

>d1rgs_2_b.82.3.2 (245-376) Regulatory subunit of Protein kinase A {Cow (*Bos taurus*)}
EEFLSKVSILES LDKWERLTVADALEPVQFEDGQKIVVQGEFGDEFFIILEGSAAVLQRRSENEEFVEV

GRLGPSDYFGEIALLMNRPRAATVVARGPLKCVKLDPRPRFERVLGPCSDILKRNIQQYNSFVS
>d1cx4a1 b.82.3.2 (A:130-265) Regulatory subunit of Protein kinase A {Rat (Rattus norvegicus)}
RIIHPKTDDQRNRLQEACKDILLFKNLDPEQMSQVLDAMFEKLVKEGEHVIDQGDDGDNFYVIDRG
TFDIYVKCDGVGRCVGNVDNRGSFGELALMYNTPRAATITATSPGALWGLDRVTFRRRIIVKNNAKKR
KMY
>d1cx4a2 b.82.3.2 (A:266-412) Regulatory subunit of Protein kinase A {Rat (Rattus norvegicus)}
ESFIESLPFLKSLEVSERLKVVVDVIGTKVYNDGEQIIAQGDSADSFVIVESGEVRITMKRKGKSDIEENG
AVEIARCLRGQYFGEALVTNKPRAASAHAGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLV
ALFGTNMDIV
>d2arca_b.82.4.1 (A:) Regulatory protein AraC {Escherichia coli}
DPLLPGYSFNAHLVAGLTPIEANGYLDFIDRPLGMKGYILNLTIRGQGVVKNQGREFVCRPGDILLFP
PGEIHYYGRHPEAREWYHQVVYFRPRAYWHEWLNWPSIFANTGFFRPDEAHQPHFSDLFGQIINA
GQGEGRYSELLAINLLEQLLLRRMEAI
>d1ig3a1 b.82.6.1 (A:179-263) Thiamin pyrophosphokinase, substrate-binding domain
{Mouse (Mus musculus)}
DSLIIYLLQPGKHLRHVDTGMEGSWCGLIPVGQPCNQVTTTGLKWNLNDVVGFGTLVSTSNTYDGS
GLVTVETDHPLLWTMAIKS
>d1ig0a1 b.82.6.1 (A:224-319) Thiamin pyrophosphokinase, substrate-binding domain
{Baker's yeast (Saccharomyces cerevisiae)}
TDLIFLIKNGTLIEYDPQFRNTCIGNCGLLPIGEATLVKETRGLKWDVKNWPTSVVTGRVSSSNRFV
GDNCCFIDTKDDIILNVEIFVDKLIDFL
>d1wapa_b.82.5.1 (A:) Trp RNA-binding attenuation protein (TRAP) {Bacillus subtilis}
DFVVIKAVEDGVNVIGLTRGTDTKFHHSEKLDKGEVIAQFTEHTSAIKVRGEALIQTAYGEMKSEKK
>d1c9sa_b.82.5.1 (A:) Trp RNA-binding attenuation protein (TRAP) {Bacillus
stearothermophilus}
SDFVVIKALEDGVNVIGLTRGADTRFHHSEKLDKGEVLIAQFTEHTSAIKVRGKAYIQTRHGVIESEG
K
>g1h6w.1 b.108.1.1 (A,B:) Heat- and protease-stable fragment of the short fibre
{Bacteriophage T4}
TGATLNGRGSTTSMRGVVKLTTTAGSQSGGDASSALAWNADVHQGGQTINGTLRINNTLTIASGG
ANITGTVNMTGGYIQGKRVVTQNEIDRTIPVGAIMMWAADSLPSDAWRWFCHGGTVSASDCPLYASRI
GTRYGGSSSNPGLPDMRXSLNYIIVKVE
>d1k28a2 b.108.1.2 (A:362-584) Tail-associated lysozyme gp5, C-terminal domain
{Bacteriophage T4}
DPADPPIPNDSRILFKEPVSSYKGEYPYVHTMETESGHIQEFDDTPGQERYRLVHPTGTYYEEVSPSGR
RTRKTVDNLYDITNADGNFLVAGDKKTNVGGSEIYNNMDNRLHQIDGSNTIFVRGDETKTVEGNGTI
LVKGNVTIIEGNADITVKGDATTLVEGNQNTNTVNGNLSWKVAGTVDWDVGGDWTEKMASMSSIS
SGQYTIDGSRIDIGSVDHHHHHH
>d1qiu2 b.83.1.1 (A:319-395) Adenovirus {Human adenovirus type 2}
VSIKSSGLNFDNTAIAINAGKGLEFDTNTSESPDINPIKTKIGSGIDYNENGAMITKLGAGLSFDNSG
AITIGNKN
>d1kke2 b.83.1.2 (A:313-455) Reovirus attachment protein sigma 1 {Reovirus}

YRFRQSMWIGIVSYSGSLNWRVQVNSDIFIVDDYIHICLPAFDGFSIADGGDLSLNFVTGLLPPLLTG
DTEPAFHNDVVTYGAQTVAIGLSSGGAPQYMSKNLWVEQWQDGVLRRLRVEGGGSITHSNSKWPAM
TVSYPRSF

>d1h8ga_ b.109.1.1 (A:) Choline binding domain of autolysin C-LytA {Streptococcus pneumoniae}
TDGNWYWFDNSGEMATGWKKIADKWYFNEEGAMKTGWVKYKDTWYYLDAKEGAMVSNAFIQ
SADGTGWYYLKPDLADRPEFTVEPDGLITVK

>d1hcxa_ b.109.1.1 (A:) Choline binding domain of autolysin C-LytA {Streptococcus pneumoniae}
GSYPKDKFEKINGTWYFDFSSGYMLADRWRKHTDGNWYWFDNSGEMATGWKKIADKWYFNEE
GAMKTGWVKYKDTWYYLDAKEGAMVSNAFIQSADGTGWYYLKPDLADRPEFTVEPDGLITVK

>d1bdo_ b.84.1.1 (-) Biotinyl domain of acetyl-CoA carboxylase {Escherichia coli}
EISGHIVRSPMVGTFYRTPSPDAKAFIEVGQKVNVDGLCIVEAMKMMNQIEADKSGTVKAILVESG
QPVEFDEPLVVIE

>d1dd2a_ b.84.1.1 (A:) Biotin carboxyl carrier domain of transcarboxylase (TC 1.3S)
{Propionibacterium freudenreichii, subsp. shermanii}
AGAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV
QGGQGLIKIG

>d1htp_ b.84.1.1 (-) Protein H of glycine cleavage system {Pea (Pisum sativum)}
SNVLDGLKYAPSHWVVKHEGVSATIGITDHAQDHLGEVVFVELPEPGVSVTKGKGFVAVESVKATSD
VNSPISGEVIEVNTGLTGKPLINSSPYEDGWMIKIKPTSPDELESLLGAKEYTKFCEEEEDAAH

>d1lac_ b.84.1.1 (-) Ipoyl domain of dihydrolipoamide acetyltransferase {Bacillus stearothermophilus}
AFEFKLPDIGINHEGEIVKWFVKPGDEVNEDDVLCEVQNDKAVVEIPSPVKGKVLVLEILVPEGTVATV
GQTLITLDAPGY

>d1iyu_ b.84.1.1 (-) Ipoyl domain of dihydrolipoamide acetyltransferase {Azotobacter vinelandii}
SEIIRVPDIGGDGEVIELLVKTGDLIEVEQGLVVLESKASMEVPSPKAGVVKSVSVKLGDKLKEGDII
ELEPAAGAR

>d1qjoa_ b.84.1.1 (A:) Ipoyl domain of dihydrolipoamide acetyltransferase {Escherichia coli}
MVKEVNPDIGGDEVEVTEVMVVKVGDVAAEQSLITVEGDKASMEVPAPFAGVVKELKVNVDGKV
KTGSLIMIFEVEGAA

>d1gxa_ b.84.1.1 (A:) Ipoyl domain of dihydrolipoamide acetyltransferase {Neisseria meningitidis}
ALVELKVPDIGGHENVDIIAVEVNVGDTIAVDDTLITLETDKATMDVPAEVAGVVKEVKVKGDKISE
GGLIVVVEAEGTA

>d1fyc_ b.84.1.1 (-) Ipoyl domain of dihydrolipoamide acetyltransferase {Human (Homo sapiens)}
GSNMSYPPHMVLLPALSPTMTMGTVQRWEKKVGEKLGSEGDLLAEIETDKATIGFEVQEEGYLAKIL
VPEGTRDVPDLGTPLCIIVEKEADISAFADYRPTVTDLK

>d1ghk_ b.84.1.1 (-) Lipoyl domain of the 2-oxoglutarate dehydrogenase complex
{Azotobacter vinelandii}
AIDIKAPTFPESADGTVATWHKKPGEAVKRDELIVDIETDKVMEVLAEADGVIAEIVKNEGDTVLS
GELGKLTEGG

>d1pmr_ b.84.1.1 (-) Lipoyl domain of the 2-oxoglutarate dehydrogenase complex {Escherichia coli}

SSVDILVDPDPESVADATVATWHKKPGDAVVRDEVLVEIETDKVVLEVPASADGILDAVLEDEGTTVT
SRQILGRLREGN

>d1k8ma_ b.84.1.1 (A:) Lipoyl domain of the mitochondrial branched-chain alpha-ketoacid dehydrogenase {Human (Homo sapiens)}

MGQVVQFKLSDIGEGIREVTVKEWYVKEGDTVSQFDSICEVQSDKASVTITSRYDGVIKKLYYNLDDI
AYVGKPLVDIETEALKDLE

>d1dv1a1 b.84.2.1 (A:331-446) Biotin carboxylase subunit of acetyl-CoA carboxylase, C-terminal domain {Escherichia coli}

RGHAVECRINAEDPNTFLPSPGKITRFHAPGGFGVRWESHYAGYVPPYYDSMIGKLICYGENRDVA
IARMKNALQELIIDGIKTNVDLQIRIMNDENFQHGGTNIHYLEKKLGL

>d1gsoa1 b.84.2.1 (A:328-426) Glycinamide ribonucleotide synthetase (GAR-syn). {Escherichia coli}

ERASLGVVMAAGGYPGDYRTGDVIHGLPLEEVAGGKVFHAGTKLADDEQVVTNGGRVLCVTALGHT
VAEAQKRAYALMTDIHWDDCFCKRDIGWRAIER

>d1b6ra1 b.84.2.1 (A:277-355) N5-carboxyaminoimidazole ribonucleotide synthetase, AIRC, PurK {Escherichia coli}

NNPSVMINLIGSDVNYDWLKLPLVHLHWYDKEVRPGRKVGHLNLTSDTSRLTATLEALIPLLPPEY
ASGVIWAQSKFG

>d1eyza1 b.84.2.1 (A:319-392) Glycinamide ribonucleotide transformylase PurT {Escherichia coli}

GPAASAVILPQLTSQNVTFDNVQNAVGADLQIRLFGKPEIDGSRRLGVALATAESVVDIAIERAKHAAG
QVKVQG

>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}

TIYNASAAGKIVAITALSEKKGFEVSIEKANGEVVVDKIPAGPDLIVKEGQTVQADQPLTNNP

>d1ci3m2 b.84.2.2 (M:170-231) Cytochrome f, small domain {Phormidium laminosum}

AVYNASAAGVITAIKADDDGSAEVKIRTEDGTTIVDKIPAGPELIVSEGEVAAGAALNNP

>d1gpr_ b.84.3.1 (-) Glucose permease IIa domain, IIa-glc {Bacillus subtilis}

EPLQNEIGEEVFPVSPITGEIHPITDVPDQVFSGKMMGDGFAILPSEGIVVSPVRGKILNVFPTKHAIGL
QSDGGREILIHFGIDTVSLKGEFTSFVSEGDRVEPGQKLEVDLDAVKPNVPSLMTPIVFTNLAEGE
TVSIKASGSVNREQEDIVKIE

>d2gpr_ b.84.3.1 (-) Glucose permease IIa domain, IIa-glc {Mycoplasma capricolum}

MWFFNKNLKVLPACDGTIITLDEVEDEVFKERMLGDGFAINPKSNDFHAPVSGKLVTAFTPKHAFGI
QTKSGVEILLHIGLDTVSLDGNFESFVTQDQEVNAGDKLVTVDLKSVAKKVPSIKSPIIFTNNGGKTL
EIVKMGEVQGDVVAILK

>d1glaf_ b.84.3.1 (F:) Glucose-specific factor III (glsIII) {Escherichia coli}

GLFDKLSLVSDDKKDTGTIEIAPLSGEIVNIEDVDPVVFVFAEKIVGDGIAIKPTGNKMOVAPVDGTIGKI
FETNHAFSIESDSGVELFVHFGIDTVLKGEGFKRIAEQGQRVKVGDVIEFDLPLEEKAKSTLTPVV
ISNMDEIKELIKLSGSVTVGETPVIRIKK

>d2f3ga_ b.84.3.1 (A:) Glucose-specific factor III (glsIII) {Escherichia coli}

TIEIAPLSGEIVNIEDVDPVVFVFAEKIVGDGIAIKPTGNKMOVAPVDGTIGKIFETNHAFSIESDSGVELFV

HFGITVELKGEFKRIAEEGQRVKVGDVIEFDLPLLEEKAKSTLTPVVISNMDEIKELIKLSGSVTV
GETPVIRIKK
>d1hg7a_b.85.1.1 (A:) Type III antifreeze protein {Ocean pout (*Macrozoarces americanus*),
different isoforms}
MNQASVVANQLIPINTALTLVMMRSEVVTPVGIPAEDIPRLVSMQVNRAVPLGTTLMPDMVKGYAA
>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*)}
SPGLKSVVANQLIPINTALTLVMMKAEVSPKIPSEEISKLVGMQVNRAVYLDQTLMPDMVKNYE
>d3rdn_b.85.1.1 (-) Type III antifreeze protein {Antarctic eel pout (*Austrolycichthys*
brachycephalus) and (*Lycodichthys dearborni*)}
NKASVVANQLIPINTALTLIMMKAEEVTPMGIPAEIIPNLVGMQVNRAVPLGTTLMPDMVKNYEDG
TTSPGLK
>d1c5ea_b.85.2.1 (A:) Head decoration protein D (gpD, major capsid protein D)
{Bacteriophage lambda}
SDPAHTATAPGGLSAKAPAMTPLMLDTSRKLVAWDGTTDGAAVGILAVAADQTSTTLTFYKSGTFR
YEDVLWPEAASDETKKRTAFAGTAISIV
>d1ejrb_b.85.3.1 (B:) Urease, beta-subunit {*Klebsiella aerogenes*}
MIPGEYHVKPGQIALNTGRATCRVVVENHGDRPIQVGSYHFAEVNPALKFDRQQAAGYRLNIPAGT
AVRFEPGQKREVELVAFAGHRAVFGFRGEVMGPL
>d4ubpb_b.85.3.1 (B:) Urease, beta-subunit {*Bacillus pasteurii*}
NYIVPGEYRVAEAGEIEINAGREKTTIRVSNTGDRPIQVGSYHIFVEVNKELLDRAEGIGRRLNIPSGT
AARFEPGEEMEVELTELGGNREVFISDLTNGSVDNKEILQRAKELGYKGV
>d1e9ya1_b.85.3.1 (A:106-238) Urease, beta-subunit {*Helicobacter pylori*}
LVPGELFLKNEDITINEGKKAVSVKKNVGDPRVQIGSHFHFVEVNRCLDFDREKTFGKRLDIAAGTA
VRFEPGEEKSVELIDIGNRRIFGFNALVDRQADNESKIALHRAKERGFHGAKSSDNYVKTIKE
>d1g8la1_b.85.6.1 (A:327-409) Molybdenum cofactor biosynthesis protein MoeA, C-terminal
domain {*Escherichia coli*}
LPARQRVRTASRLKKTTPGRLDFQRGVLQRNADGELEVTGHHGQSHIFSSFLGNCFIVLERDRGNV
EVGEWVEVEPFNALFG
>d1euwa_b.85.4.1 (A:) Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase)
{*Escherichia coli*}
MMKKIDVKILDPRVGKEFPLPTYATSGSAGLDLRACLNDAVELAPGDTTLVPTGLAIHIADPSLAAM
MLPRSGLGHKHGIVLGNLVGLIDSDYQGQLMISVWNRGQDSFTIQPGERIAQMIFVPVQAEFNLVE
DF
>d1f7da_b.85.4.1 (A:) Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase) {Feline
immunodeficiency virus}
MIIEGDGILDKRSEDAGYDLLAAKEIHLPLGEVKVIPTGVKLMPLPKGYWGLIIGKSSIGSKGLDVLGGVI
DEGYRGEIGVIMINVSRSITLMERQKIAQLIILPCKHEVLEQGKVV
>d1f7ra_b.85.4.1 (A:) Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase) {Feline
immunodeficiency virus}
MIIEGDGILDKRSEDAGYDLLAAKEIHLPLGEVKVIPTGVKLMPLPKGYWGLIIGKSSIGSKGLDVLGGVI

DEGYRGEIGVIMINVSRSITLMERQKIAQLLILPCKHEVLEQGKVVMDSERGDNGYGSTGVF
>d1dun_ b.85.4.1 (-) Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase) {Equine infectious anemia virus}
MLAYQGTQIKEKRDEDAGFDLCVPYDIMIPVSDTKIIPTDVKIQVPPNSFGWVVTGKSSMAKQGLLING
GIIDEGYTGEIQVICTNIGKSNIKLIEGQKFAQLLILQHHSNSRQPWDENKI
>d1tul_ b.85.5.1 (-) ACMNPV telokin-like protein {Baculovirus (Autographa californica), nuclear polyhedrosis virus}
GTPDIIVNAQINSEDENVLDFIIEDEYYLKKRGVGAHIIKVASSPQLRLLYKNAYSTVSCGNYGVLCLNV
QNGEYDLNAIMFNCAEIKLNKGQMLFQTKIWR
>d1at0_ b.86.1.1 (-) Hedgehog {Fruit fly (Drosophila melanogaster)}
CFTPESTALLESVVRKPLGELSIGDRVLSMTANGQAVYSEVILFMDRNLEQMNFVQLHTDGGAVLT
VTPAHLVSVWQPESQKLTFFVADRIEKNQVLVRDVETGELRPQRVVKVGSVRSKGVVAPLTREGTIV
VNSVAASCYA
>d1dfaa1 b.86.1.2 (A:1-180,A:416-454) PI-Scei intein {Baker's yeast (Saccharomyces cerevisiae)}
CFAKGTNVLMADGSIECIENIEVGNKVMGKDGRPREVIKLPREGRETMYSVVQKSQHRAHKSDSSREV
PELLKFTCNATHELVVRTPRSVRRLSRTIKGVEYFEVITFEMGQKKAPDGRIVELVKEVSKSYPISSEGP
ERANELVESYRKASNKAYFEWTIEARDLSLLGSHVRKATYQTYAXCRGFYFELQELKEDDYGITLSD
DSDHQFLLANQVVVHN
>d1dq3a1 b.86.1.2 (A:1-128,A:415-454) PI-Pfui intein {Archaeon Pyrococcus furiosus}
CIDGKAKIIFENEGEEHLTTMEEMYERYKHLGEFYDEEYNRWGIDVSNVPIYVKSFDPEKRVVKGK
VNVIWKYELGKDVTKYEIITNKGTKILTSPWHPFFVLTPDFKIVEKRADELKEGDILIGGMXGLEVVR
HITTTNEPRTFYDLTVENYQNYLAGENGMIFVHN
>d1am2_ b.86.1.2 (-) GyrA intein {Mycobacterium xenopi}
ASITGDALVALPEGESVRIADIVPGARPNSDNAIDLKVLDRHGNPVLADRLFHSGEHPVYAVRTVEGL
RVTGTANHPLLCVLDVAGVPTLLWKLIDEIKPGDYAVIQRSAFSVDCAGFARGKPEFAPTTYTVGVPG
LVRFLEAHRDPDAKAIADELTDGRFYAKVASVTDAGVQPVYSLRVDTADHAFITNGFVSHN
>d1umua_ b.87.1.1 (A:) UmuD' {Escherichia coli}
DYVEQRIDLNQLLIQHPSATYFVKASGDSMIDGGISDGDLLIVDSAITASHGDIVIAAVDGEFTVKKLQ
LRPTVQLIPMNSAYSPLITISSEDTLDVFGVVIHVVK
>d1jhfa2 b.87.1.1 (A:73-198) LexA C-terminal domain {Escherichia coli}
EEGLPLVGRVAADPELLAQHIEGHYQVDPSLFPKNADFLLRVSGMSMKDIGIMDGDLLAVHKTQD
VRNGQVVVARIDDEVTVKRLKKQGNKVPELLPENSEFKPIVVDLRQQSFTIEGLAVGVIRN
>d1f39a_ b.87.1.1 (A:) lambda repressor C-terminal domain {Bacteriophage lambda virus}
ASASAFWLEVEGNSMTAPTGSKPSFPDGMILLVDPEQAVEPGDFCIARLGGDEFTFKKLIRDSGQVFL
QPLNPQYPMIPCNESCSVVGKVIASQWPEETFG
>d1b12a_ b.87.1.2 (A:) Type 1 signal peptidase {Escherichia coli}
RSFIYEPFQIPSGSMPTLLIGDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRA
VGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSTRNGGEATSGFFEVPKNE
TKENGIRLSERKETLGDVTHRILTVPIAQDQVGMYYQPGQQLATWIVPPGQYFMMGDNRDNSADS
RYWGFVPEANLVGRATAIWMSFDKQEGEWPTGLRLSRIGGIH
>d1jcha2 b.110.1.1 (A:84-315) Colicin E3 translocation domain {Escherichia coli}
VAAPVAFGFPALSTPGAGGLAVSISAGALSAAIADIMAALKGPFKFLWGVALYGVLPQIAKDDPNM
MSKIVTSLPADDITESPVSSLPLDKATVNVNVRVDDVKDERQNISSVSGVPMSVPVDDAKPTERPG

VFTASIPGAPVLNISVNNSTPAVQTLSPGVTNNTDKDVRPAFGTQGGNTRDAVIRFPKDSGHNAVYVS
VSDVLSPDQVKQRQDEENRRQEWDATEHP
>d1hxra_b.88.1.1 (A:) RabGEF Mss4 {Rat (Rattus norvegicus)}
ELVSAEGRNRKAVLCQRCSRVLQPGTALFSRRQLFLPSMRKKPDLVDGSNPDGDVLEEHWLVNDM
FIFENVGFTKDVGNVFLVCADCEIGPIGWHLCLDDKNSFYVALERSHE
>d1fwqa_b.88.1.1 (A:) RabGEF Mss4 {Human (Homo sapiens)}
ELVSAEGRNRKAVLCQRCSRVLQPGTALFSRRQLFLPSMRKKPALSDGSNPDGDLLQEHWLVEDM
FIFENVGFTKDVGNKFLVCADCEIGPIGWHLCLDDKNSFYVALERSHE
>d1h6qa_b.88.1.2 (A:) Translationally controlled tumor-associated protein tctp, p23fyp
{Fission yeast (Schizosaccharomyces pombe)}
MLLYKDVISGDELVSDAYDLKEVDDIVYEADCQMVTVKQGGDVIDIGANPSAEDAEENAEETETVN
NLVYSFRLSPTSFDKKSYSYIKGYMKAIKARLQESNPERVPVFEKNAIGFVKKILANFKDYDFYIGES
MDPDAMVVLMNYREDGITPYMIFFKDGLVSEKF
>d3ezma_b.89.1.1 (A:) Cyanovirin-N {Cyanobacterium (Nostoc ellipsosporum)}
LGKFSQTCYNSAIQGSVLTSTCERTNGGYNTSSIDLNSVIENVDSGLKWQPSNFIETCRNTQLAGSSEL
AAECKTRAQQFVSTKINLDDHIANIDGTLKYE
>d1fjra_b.102.1.1 (A:) Methuselah ectodomain {Fruit fly (Drosophila melanogaster)}
DILECDYFDTVDISAAQKLQNGSYLFEGLLPAILTGEYDFRILPDDSKQKVARHIRGCVCKLKPCVRF
CCPHDHIMDNGVCYDNMSDEELAELDPFLNVTLDDGSVSRRHFKNELIVQWDLPMPCDGMFYLD
NREEQDKYTLFENGTFRRHFDRVTLRKREYCLQHLTFADGNATSIRIAPHNCLIV
>d1lkta_b.90.1.1 (A:) Head-binding domain of phage P22 tailspike protein {Salmonella
bacteriophage P22}
ANVVVSNPRPIFTESRSFKAVANGKIYIGQIDTDPVN PANQIPVYIENEDGSHVQITQPLIINAAGKIVY
NGQLVKIVTVQGHSMAIYDANGSQVDYIANVLKY
>d1qqha_b.91.1.1 (A:) E2 regulatory, transactivation domain {Human papillomavirus type
18}
KSKAHKAIELQMALQGLAQSAKYKTEDWTLQDTCEELWNTEPTHCFFKGGQTVQVYFDGNKDNM
TYVAWDSVYYMTDAGTWDKTATCVSHRGLYYVKEGYNTFYIEFKSECEKYGNTGTWEVHFGNNVI
DCNDSMCSTSDDTVS
>d1dtoa_b.91.1.1 (A:) E2 regulatory, transactivation domain {Human papillomavirus type
16}
HMETLCQRLNVCQDKILTHYENDSTDLRDHIDYWKHMRLECAIYYKAREMGFKHINHQVVPTLAV
SKNKALQAIELQLTLETIYNSQYSNEKWTLQDVSLEVYLTAPTGCIKKHGYTVEVQFDGDICNTMHY
TNWTHIYICEEASVTVEGQVDYYGLYYVHEGIRTYFVQFKDDAEKYSKNKVWEVHAGGQVILCPTS
VFS
>d1g8la2_b.103.1.1 (A:7-177) Molybdenum cofactor biosynthesis protein MoeA, N-terminal
and linker domains {Escherichia coli}
LMSLDTALNEMLSRVTPPLTAQETLPLVQCFGRILASDVVSPLDVPFGDNSAMDGYAVRLDIASGQPL
PVAGKSFAGQPYHGEWPAGTCIRIMTGAPVPEGCEAVVMQEQTQMDNGVRFTA EVRSGQNIRRRG
EDISAGAVVFPAGTRLTTAELPVIASLGIAEVPVIRK
>d1k6wa1_b.92.1.2 (A:4-55,A:376-426) Cytosine deaminase {Escherichia coli}
ALQTIINARLPGEGLWQIHLQDQKISIDAQSGVMPITENSLDAEQGLVIPXLIILPAENGF DALRRQ
VPVRYSVRGGKVIASQPAQT TVYLEQPEAIDYKR
>d1ejrc1_b.92.1.1 (C:1002-1129,C:1423-1475) alpha-Subunit of urease {Klebsiella

aerogenes}

SNISRQAYADMFGPTVGDVRLADTELWIEVEDDLTTYGEEVKFGGGKVIRDGMGQQLAADCVD
LVLTNALIVDHWGIVKADIGVKDGRIFAIGKAGNPDIQPNVTIPIGAATEVIAAEGKIVTAGXSIEVGKL
ADLVVWSPAFFGVKPVATVIKGGMIAIAPMGDINASIPTQPVHYRP

>d4ubpc1 b.92.1.1 (C:1-131,C:435-483) alpha-Subunit of urease {*Bacillus pasteurii*}

MKINRQQYAESYGPTVGDVRLADTLWIEVEKDYTTYGDEVNFGGGKVLREGMGENGTYTRTEN
VLDLLLTNALILDYTGIIKADIGVKDGYIVGIGKGGNPDIMDGVTPNMIVGTATEVIAAEGKIVTAXLVL
WEPKFFGVKADRVIKGGIIAYAQIGDPSASIPTQPVMGRRMYGTV

>d1e9yb1 b.92.1.1 (B:1-131,B:432-480) alpha-Subunit of urease {*Helicobacter pylori*}

MKKISRKEYVSMYGPTTGDVRLGDTDLIAEVEHDYTIYGEELKFGGGKTLREGMSQSNPSKEELD
LIITNALIVDYTGIIKADIGIKDGIAGIGKGGNKDMQDGVKNNLSVGPATEALAGEGLIVTAGXADLV
LWSPAFFGVKPNMIIKGGFIALSQMGDANASIPTQPVYYREMFA

>d1aqt_2 b.93.1.1 (2-86) Epsilon subunit of F1F0-ATP synthase N-terminal domain
{*Escherichia coli*}

STYHLDVVSAAEQMFSGLVEKIQVTGSEGELGIYPGHAPLLTAIKPGMIRIVKQHGHEEFIYLSGGILEV
QPGNVTVLADTAIRG

>d1e79h2 b.93.1.1 (H:15-100) Epsilon subunit of F1F0-ATP synthase N-terminal domain
{*Cow (Bos taurus)*}

QMSFTFASPTQVFFNSANVRQVDVPTQTGAFGILAAHVPTLQVLRPGLVVVHAEDGTTSKYFVSSGS
VTVNADSSVQLLAEAVTL

>d1hhna_b.104.1.1 (A:) Calreticulin {*Rat (Rattus norvegicus)*}

SKKIKDPDAKPEDWDERAKIDDPTDSKPEDWDKPEHIPDPDAKKPEDWDEEMDGEWEPPVIQN
PEYKGEWKPRQIDNPDYKGTWIHPEIDNPEYSPDANI

>d1jhna3 b.104.1.1 (A:270-411) Calnexin {*Dog (Canis familiaris)*}

PVNPSREIEDPEDQKPEDWDERPKIPDPDAVKPDDWNEDAPAKIPDEEATKPDGWLDDPEYVVD
PDAEKPEDWDEDMDGEWEAPQIANPKCESAPGCGVWQRPMIDNPNYKKGKWKPPMIDNPNYQGI
WKPRKIPNPDFFED

>d1tph1_c.1.1.1 (1:) Triosephosphate isomerase {*Chicken (Gallus gallus)*}

RKFFVGGNWKMNKSLGELIHTLNGAKLSADTEVVCAPSILDFARQKLDKIGVAAQNCYKV
PKGAFTEISPAMIKDIGAAWVILGHSERRHVFGESEDELIGQKVAHALAEGLGVIACIGEKLDEREAGI
TEKVVFEQTKAIADNVKDWSKVVLAYEPVWAIGTGKTATPQQAQEVHEKLRGWLKTHVSDAVAQS
TRIIYGGSVTGGNCKELASQHDVDGFLVGGASLKPEFVDIINAKH

>d1htia_c.1.1.1 (A:) Triosephosphate isomerase {*Human (Homo sapiens)*}

APSRKFFVGGNWKMNKQSLGELIGTLNAAKVPADTEVVCAPPTAYIDFARQKLDPKIAVAAQNCY
KVTNGAFTGEISPMIKDCGATWVVLGHSERRHVFGESEDELIGQKVAHALAEGLGVIACIGEKLDER
EAGITEKVVFEQTKVIADNVKDWSKVVLAYEPVWAIGTGKTATPQQAQEVHEKLRGWLKSNVSDAV
AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPEFVDIINAKQ

>d1i45a_c.1.1.1 (A:) Triosephosphate isomerase {*Baker's yeast (Saccharomyces cerevisiae)*}

ARTFFVGGNFKLNGSKQSIKEIVERLNTASIPENVEVVICPPATYLDYSVSLVKKPQVTVGAQNAYLKA
SGAFTGENSVQIKDVGAKYVILGHSERRSYFHEDDKFIADKTKFALGQGVGVLICIGETLEEKAGK
TLDVVERQLNAVLEEVKDFTNVVVAYEPVWAIGTGLAATPEDAQDIHASIRKFLASKLGDKAASELRI
LYGGSANGSNAVTFKDKADVDGFLVGGASLKPEFVDIINSRN

>d1ttj_c.1.1.1 (-) Triosephosphate isomerase {*Trypanosoma brucei*}

SKPQPIAAANWKCNGSQSLSELIDLFNSTSINHVDVQCVVASTSSHLAMTKERLSHPKFVIAAQNAG

NADALASLKDFGVNWIVLGHSEARRAYYGETNEIVADKVAAAVASGFMVIACIGETLQERESGRTAVVV
LTQIAAIAKLLKADWAKVVIAYEPVWAIGTGKVATPQQAQEAHALIRSWVSSKIGADVAGELRILYG
GSVNGKNARTLYQQRDVNGFLVGGASLKPEFVDIIKATQ

>d5tima_ c.1.1.1 (A:) Triosephosphate isomerase {Trypanosoma brucei}

SKPQPIAAANWKCNGSQSLSELIDLFNSTSINHVDVQCVVASTFVHLAMTKERLSHPKFVIAAQNAIA
KSGAFTGEVSLPILKDFGVNWIVLGHSEARRAYYGETNEIVADKVAAAVASGFMVIACIGETLQERESG
RTAVVVLTQIAAIAKLLKADWAKVVIAYEPVWAIGTGKVATPQQAQEAHALIRSWVSSKIGADVAG
ELRILYGGSVNGKNARTLYQQRDVNGFLVGGASLKPEFVDIIKATQ

>d1tcda_ c.1.1.1 (A:) Triosephosphate isomerase {Trypanosoma cruzi}

KPQPIAAANWKCNGSESLVPLIETLNAATFDHDVQCVVAPTFLHIPMTKARLTNPKFQIAAQNAIT
RSGAFTGEVSLQILKDYGISWVVLGHSERRLLYGETNEIVA EKVAQACAAGFHVIVCVGETNEEREAG
RTAAVVLTQLAAVAQKLSKEAWSRVVIAYEPVWAIGTGKVATPQQAQEVHELLRRWVRSKLGTDIAA
QLRILYGGSVTAKNARTLYQMRDINGFLVGGASLKPEFVEIIEATK

>d1ydva_ c.1.1.1 (A:) Triosephosphate isomerase {Plasmodium falciparum}

RKYFVAANWKCNGTLESIKSLTNSFNLDLDFPSKLDVVFPVSVHYDHTRKLQSKFSTGIQNVSKF
NGSYTGEVSAEIAKDLNIEYVIIGHFERRKYFHETDEDVREKLQASLKNLKA VVCFGESLEQREQN
KTIEVITKQVKAFVDLIDNFDNVILVYEPLWAIGTGKTATPEQAQLVHKEIRKIVKDTTCGEKQANQIRI
LYGGSVNTENCSSLIQEDIDGFLVGNASLKESFVDIISAM

>d1amk_ c.1.1.1 (-) Triosephosphate isomerase {Leishmania mexicana}

SAKPQPIAAANWKCNGTTASIEKLVQVFNEHTISHDVQCVVAPTFFVHIPLVQAKLRNPKYVISAENAI
AKSGAFTGEVSMPIKDIGVHWVILGHSERRTYGETDEIVAQKVSEACKQGMVIACIGETLQQREA
NQTA KVLSQTSIAAAKLT KDAWNQVVLAYEPVWAIGTGKVATPEQAQEVHLLLRKVVSENIGTDV
AAKL RILYGGSVNAANAATLYAKPDINGFLVGGASLKPEFRDIIDATR

>d1trea_ c.1.1.1 (A:) Triosephosphate isomerase {Escherichia coli}

MRHPLVMGNWKLNGSRHMVHELVSNLRELKELAGVAGCAVAIAPPEMYIDMAKREAEGSHIMLGAQN
VNLNLSGAFTGETSAAMLKDIGAQYIIHGHSERRTYHKESEDELI AKKFVAVLKEQGLTPVLCIGETEAE
EAGKTEEV CARQIDAVLKTQGA AFEGAVIAYEPVWAIGTGKSATPAQAQAVHKFIRDHIAKVDANIA
EQVIIQYGGSVNASNAELFAQPDIDGALVGGASLKADAFVIVKAAEAAKQA

>d2btma_ c.1.1.1 (A:) Triosephosphate isomerase {Bacillus stearothermophilus}

RKPIIAGNWKMNGTLAEAVQFVEDVKGHVPPADEVISVVCAPFLFLDRLVQAADGTDL KIGAQTMH
FADQGAYTGEVSPVMLKDLGVTYVILGHSERRQMFAETDET VNKVLA AFTRGLIPIICCGESLEERE
AGQTN AVVASQVEKALAGLTPEQVKQAVIAYEPIWAIGTGKSSTPEDANSVCGHIRSVSRLFGPEAAE
AIRIQYGGSVKPDNIRDFLAQQQIDGALVGGASLEPASFLQLVEAGRH

>d1aw1a_ c.1.1.1 (A:) Triosephosphate isomerase {Vibrio marinus}

RHPVVMGNWKLNGSKEMVVDLLNGLNAELEGVTGVDVAVAPPALFVDLAERTLTEAGSAILGAQN
TDLNNSGAFTGDMSPAMLKEFGATHIIHGHSERRREYHAESDEFVAKKF AFLKENG LTPVLCIGESDAQ
NEAGETMAV CARQLDAVINTQGV EALEGAI IAYEPIWAIGTGKAATAEDAQR IHAQIRAHIAEKSEAV
AKNVVIQYGGSVKPENAAAYFAQPDIDGALVGGAAALDAKSFAAIAKAAAEAKA

>d1b9ba_ c.1.1.1 (A:) Triosephosphate isomerase {Thermotoga maritima}

TRKLILAGNWKMHKTI SEAKKFVSLLVNELHDVKEFEIVVCPPTAL SEVGEILSGRNIKLG AQNVFY
EDQGAFTGEISPLMLQEIGVEYVIVGHSERRIFKEDDEFINR KVKAVLEKGMT PILCVGETLEEREK
GLTFCVVEKQVREGFYGLDKEEAKRVVIAYEPVWAIGTG RVATPQQAQEVHAFIRKLLSEMYDEETA
GSIRILYGGSIKPDNFLGLIVQKDIDGGLVGGASLKESFIELARIMRGV

>d1hg3a_ c.1.1.1 (A:) Triosephosphate isomerase {Archaeon Pyrococcus woesei}

AKLKEPIIAINFKTYIEATGKRALEIAKAAEKVYKETGVTIVVAPQLVDLRMIAESVEIPVFAQHIDPIK
PGSHTGHVLP EAVKEAGAVG TLLNHS ENRMILADLEAAIRRAEEVGLMTMVC SNNPAVSAVAALN
PDYVAVEPELIGTGIPVSKAKPEVITNTVELVKKNVPEVKVLCGAGISTGEDVKKAIELGTGVLLAS
GVTKAKDPEKAIWDLVSGI

>d1qo2a_ c.1.2.1 (A:) Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide
isomerase HisA {Thermotoga maritima}

MLVVP AIDLFRGKVARMIKGRKENTIFYEKDPVELVEK LIEEGFTLIHVVDLSNAIENSGENLPVLEKL
SEFAEHIQIGGGIRSLDYAEKLRKLG YRRQIVSSK VLEDPSFLKSLREIDVEPVFSLDTRGGRVAFKGW
LAEEEIDPV SLLKRLKEYGLEEIVHTEIEKDGTLQEHDFSLTKKIAIEAEVKVLAAGGISSENSLKT AQK
VHTETNGLLKG VIVGRAFLLEGILTVEVMKRYAR

>d1thfd_ c.1.2.1 (D:) Cyclase subunit (or domain) of imidazoleglycerolphosphate synthase
HisF {Thermotoga maritima}

MLAKRIIACLDVKGRVVKGSNFENLRDSGDPVELGKFYSEIGIDELVFLDITASVEKRKTMLELVEKV
AEQIDIPFTVGGGIHDFETASELILRGADKVSINTAAVENPSLITQIAQTFGSQAVVVAIDAKRVDGFEFM
VFTYSGKKN TGILLRDWVVEVEKRGAGEILLTSIDRDGTKSGYDTEMIRFVRPLTTLPIIASGGAGKM
EHFLEAFLAGADAALAASVFHFREIDVRELKEYLKKHG VNVRLLEGL

>d1jvna1 c.1.2.1 (A:230-552) Cyclase subunit (or domain) of imidazoleglycerolphosphate
synthase HisF {Baker's yeast (Saccharomyces cerevisiae), His7}

DYSNYGLTRRIIACLDVRTNDQGD LVVTKGDQYDVREKSDGKGV RNLGKPVQLAQKYYQQGADEV T
FLNITSFRDCPLKDT PMLV LKQA AKTVFVPLTVGGG IKDIVDVGTKIPALEVASLYFRSGADKVSIG
TDAVYAAEKYYELGNRGDGTSP IETISKAYGAQAVVISVDPKRVVNSQADTKNKVFETEYPPNGEK
YCWYQCTIKGGRESRDLGVWELTRACEALGAGEILLNCIDKDG SNSGYDLELIEHVKDAVKIPVIASS
GAGVPEHFEEAFLKTRADACLGAGMFHRGEFTVNDVKEYLLEHGLKVRMDEE

>d1h5ya_ c.1.2.1 (A:) Cyclase subunit (or domain) of imidazoleglycerolphosphate synthase
HisF {Archaeon Pyrobaculum aerophilum}

HMALRIIPCLDIDGGAKVVVKGVNFQGIREVGPVEMAVRYEEEGADEIAILDITAAPEGRATFIDSVK
RVAEAVSIPVLVGGGVRSLEDATTLFRAGADKVS VNTAAVRNPQLVALLAREFGSQSTVVAIDAKWNG
EYEVYVVKGGREATGLDAVKWAKEVEELGAGEILLTSIDRDGTGLGYDVELIRR VADSVRIPVIASGGA
GRVEHFY EAAAAGADAVLAASLFHFRVLSIAQVKRYLKERGVEVRI

>d1rpxa_ c.1.2.2 (A:) D-ribulose-5-phosphate 3-epimerase {Potato (Solanum tuberosum)}

SRVDKFSKSDIIVSPSILSANF SKLGEQVKAIEQAGCDWIHVDVMDGRFV PNTITIGPLVVD SLRPITDL
PLDVHLMIV EPDQRVPDFIKAGADIVSVHCEQSSTIHLHRTINQIKSLGAKAGVVLNPGTPLTAIEYVL
DAVDLVLIMSVNPGFGGQSFIESQVKKISDLRKICAERGLNPWIEVDGGVGPKNAYKVIEAGANALVA
GSAVFGAPDYAEAIKGIKTSKRPE

>d1dbta_ c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase)
{Bacillus subtilis}

MKNNLPIIALDFASAEETLAFLAPFQQEPLFVKVGMELFYQEGPSIVKQLKERNCELFLDLKLHDIPT
TVNKAMKRLASLGVDLVNVHAAGGKMMQAALEGLEEGTPAGKKRPSLIAVTQLTSTSEQIMKDEL
LIEKSLIDTVVHYSKQAEESGLDGVVCSVHEAKAIYQAVSPSFLT VTPGIRMSEDAANDQVRVATPAIA
REKGSSAIVVGRSITKAEDPVKAYKAVRLEWEGI

>d1eixa_ c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase)
{Escherichia coli}

VTNSPVVVALDYHNRDDALAFVDKIDPRDCRLKVGKEMFTLFGPQFVRELQQRGFDIFLDLKFHDIP
NTAAHAAAAADLGVMVNVHASGGARMMTAAREALVPFGKDAPLLIAVTVLTSMEASDLVDLGM

TLSPADYAERLAALTQKCGLDGVVCSAQEAVRFKQVFGQEFKLVTPGIRPQGSEAGDQRRIMTPEQAL
SAGVDYMVIGRPVTQSVDPAQTLKAINASLQ

>d1dvja_ c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase)
{Archaeon Methanobacterium thermoautotrophicum}

MDVMNRLILAMDLMNRDDALRVGTGEVREYIDTVKIGYPLVLSEGMDIIAEFRKRFGCRIIADFKVADI
PETNEKICRATFKAGADAIIVHGFPGADSVRACLNVAEEMGREVFLLTEMShPGAEMFIQGADEIA
RMGVDLGVKNYVGPSTRPERLSRLREIIGQDSFLISPGVGAQGGDPGETLRFADAIIVGRSIYLADNPA
AAAAGIIESIKDLLIPEDPAANKARKEAELAAATA

>d1dvjb_ c.1.2.3 (B:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase)
{Archaeon Methanobacterium thermoautotrophicum}

RLILAMDLMNRDDALRVGTGEVREYIDTVKIGYPLVLSEGMDIIAEFRKRFGCRIIADFKVADIPETNE
KICRATFKAGADAIIVHGFPGADSVRACLNVAEEMGREVFLLTEMShPGAEMFIQGADEIARMGVD
LGVKNYVGPSTRPERLSRLREIIGQDSFLISPGVGAQGGDPGETLRFADAIIVGRSIYLADNPA
AAAAAGIIESIKD

>d1dqwa_ c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase)
{Baker's yeast (Saccharomyces cerevisiae)}

MHKATYKERAATHPSVAAKLFNIMHEKQTNLCASLDVRTTKELLELVEALGPKICLLKTHVDILTD
FSMEGTVKPLKALSAYNFFLFEDRKFADIGNTVKLQYSAGVYRIA EWADITNAHG VVGPGIVSGLK
QAAEEVTKEPRGLLMLAELSCKGSLSTGEYTKGTVDIAKSDKDFVIGFIAQRDMGGRDEGYDWLIMT
PGVGLDDKGDALGQQYRTVDDVSTGSDIIIVGRGLFAKGRDAKVEGERYRKAGWEAYLRRCGQQD

>d1pii_2 c.1.2.4 (255-452) N-(5'phosphoribosyl)antranilate isomerase, PRAI {Escherichia coli}

GENKVCGLTRGQDAKAAAYDAGAIYGGIFVATSPRCVNVEQAQEVMAAAPLQYVGVFRNHDIADVVD
KAKVLSLAAVQLHGNEEQLYIDTLREALPAHVAIWKALSVGETLPAREFQHVDKYVLDNGQGGSGQ
RFDWSLLNGQSLGNVLLAGGLGADNCVEAAQTGCAGLDFNSAVESQPGIKDARLLASVFQTLRAY

>d1nsj_ c.1.2.4 (-) N-(5'phosphoribosyl)antranilate isomerase, PRAI {Thermotoga maritima}

MVRVKICGITNLEDALFSVESGADAVGFVFPKSKRYISPEDARRISVELPPFVFRVGVFVNEEPEKIL
DVASYVQLNAVQLHGEEPIELCRKIAERILVIKAVGVSNERDMERALNYREFPILLDTKTPEYGGSGKT
FDWSLILPYRDRFRYLVLSSGLNPENVRSAIDVVRPFADVSSGVEAFPGKDHDSIKMFIKNAKGL

>d1pii_1 c.1.2.4 (1-254) Indole-3-glycerophosphate synthase, IPGS {Escherichia coli}

MQTVLAKIVADKAIWVEARKQQQPLASFQNEVQPSTRHFYDALQGARTAFIECKKASPSKGVIRDD
FDPARIAAIKYHAYASISVLTDEKYFQGSFNFLPIVSQIAPQPILCKDFIIDPYQIYLARYYQADACLLML
SVLDDDQYRQLAAVAHSLEMGLTEVSNEEQERAIALGAKVVGINNRDLRDLSDLNRTRELAPKL
GHNVTVISESGINTYAQVRELSHFANGFLIGSALMAHDDLHAAVRRVLL

>d1a53_ c.1.2.4 (-) Indole-3-glycerophosphate synthase, IPGS {Archaeon Sulfolobus solfataricus}

PRYLKGLWKDQVQLSLRRPSFRASRQRPIISLNERILEFNKRNITAIIEYKRKSPSGLDVERDPIEYSK
FMERYAVGLSILTEEKYFNQSYETLRKIASSVSIPILMKDFIVKESQIDDAYNLGADTVLLIVKILTEREL
ESLLEYARSYGMEPLIEINDENDLDIALRIGARFIGINSRDLLETLEINKENQRKLISMIPSNVVKVAESG
ISERNEIEELRKLGVNAFLIGSSLMRNPEKIKEFIL

>d1qopa_ c.1.2.4 (A:) Trp synthase alpha-subunit {Salmonella typhimurium}

MERYENLFAQLNDRREGAFVFPVTLGDPGIEQSLKIIDLIDAGADALELGVPFSDPLADGPTIQNAN
LRAFAAGVTPAQCFEMLAIIREKHPTIPIGLLMYANLVFNNGIDAFYARCEQVGVDSVLVADVPVEESA

PFRQAALRHNIAPIFICPPNADDDLLRQVASYGRGYTYLLSRSGVTGAENRGALPLHHLIEKLKEYHA
APALQGFGISSPEQVSAAVRAGAAGAISGSAIVKIIKLNLASPKQMLAELRSFVSAMKAASR
>d1geqa_c.1.2.4 (A:) Trp synthase alpha-subunit {Archaeon Pyrococcus furiosus}
MFKDGLIPYLTAGDPDKQSTLNFLLALDEYAGAIELGIPFSDPIADGKTIQESHYRALKNGFKLREAF
WIVKEFRRHSSSTPIVLMTYYNPIYRAGVRNFLAEAKASGVDGILVVDLPVFHAKFTEIAREEGIKTV
FLAAPNTPDERLKVIDDMTTGFVYLVSLYGTGAREEIPKTAYDLLRRAKRICRNKVAVGFGVSKREH
VVSLLKEGANGVVGSALVKIIGEKGREATEFLKKKVEELLGI
>d2tpsa_c.1.3.1 (A:) Thiamin phosphate synthase {Bacillus subtilis}
HGIRMTRISREMMKELLSVYFIMGSNNTKADPVTVVQKALKGGATLYQFREKGGDALTEGARIKFAE
KAQAACREAGVPFIVNDDVELALNLKADGIHIGQEDANAKEVRAAIGDMILGVSAMTSEVKAEE
DGADYVGLGPIYPTETKKDTRAVQGVSLIEAVRRQGISIPIVGIGGITIDNAAPVIQAGADGVSMISAISQ
AEDPESAARKFREEIQTYKTGR
>d1ho1a_c.1.24.1 (A:) Pyridoxine 5'-phosphate synthase {Escherichia coli}
AELLGVIDHIATLRNARGTAYDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRILRQTLDR
MNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDACKRLADAGIQVSLFI
DADEEQIKAAAIEVGAFFIEIHTGCYADAKTDAEQAQELARIAKAATFAASLGLKVNAGHGLTYHNVK
AIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLEARG
>d2dora_c.1.4.1 (A:) Dihydroorotate dehydrogenase {Lactococcus lactis, isozyme A}
MLNTTFANAKFANPFMNASGVHCMTIEDLEELKASQAGAYITKSSTLEKREGNPLPRYVDLELGSIN
SMGLPNLGFYLDYLVKNQKENAQEGPIFFSIAGMSAAENIAMLKKIQESDFSGITELNLSCPNVPG
KPQLAYDFEATEKLLKEVFTFFTKPLGVKLPYFDLVHFDIMAEILNQFPLTYVNSVNSIGNGLFIDPE
AESVVIKPKDGFGGIGGAYIKPTALANVRAFYTRLKPEIQIIGTGGIETGQDAFEHLLCGATMLQIGTAL
HKEGPAIFDRIIKELEEIMNQKGYQSIADFHGKLSL
>d1ep3a_c.1.4.1 (A:) Dihydroorotate dehydrogenase {Lactococcus lactis, isozyme B}
MTENNRLSVKLPGLDLKNPIIPASGCFGFGEYAKYDLNKLGSIMVKATTLHPRFGNPTPRVAETAS
GMLNAIGLQNPGLVIMTEKLPWLNENFPELPIIANVAGSEEDYVAVCAKIGDAANVKAIELNISCP
NVKHGGQAFGTDPEVAALVKACKAVSKVPLYVKLSPNVTDIVPIAKAVEAAGADGLTMINTLMGVR
FDLKRQPILANITGGLSGPAIKPVALKLIHQVAQDVIDIPIIGMGGVANAQDVLEMYMAGASAVAVGT
ANFADPFVCPKIIDKLPPELMDQYRIESLESLEIQEVKEGKK
>d1d3ga_c.1.4.1 (A:) Dihydroorotate dehydrogenase {Human (Homo sapiens)}
MATGDERFYAEHLMP TLQGLDPESAHLAVRFTSLGLLPRARFQDSMDEVRLVGHKFRNPVGVIA
AGFDKHGEAVDGLYKMGFGFVEIGSVTPKPEGNPRPRVFRFPEDQAVINRYGFNSHGLSVVEHRLR
ARQQKQAKLTEDGLPLGVNLGKNKTSVDAEDYAEGVRVLGPLADYLVVNVSSPNTAGLRLSLQGKAE
LRRLLTKVLQERDGLRRVHRPAVLVKIAPDLTSQDKEDIASVVKELGIDGLIVTNTTVSRPAGLQAL
RSETGGLSGKPLRDLSTQTIREMYALTQGRVPIIGVGGVSSQDALEKIRAGASLVQLYTALTFWGPV
VGKVKRELEALLKEQFGGVTD AIGADHRR
>d1oyb_c.1.4.1 (-) Old yellow enzyme (OYE) {Brewer's yeast (Saccharomyces
carlsbergensis)}
SFVKDFKPKQALGDTNLFKPIKIGNNELLHRAVIPPLTRMRALHPGNIPNRD WAVEYYTQRAQRPGT
MIITEGAFISQAGGYDNAPGVWSEEQMVWTKIFNAIHEKKSFWVWQLWVLGWAAFPDNLARDG
LRYDSASDNVFMDAEQEAKAKANNPQHSLTKDEIKQYIKEYVQAAKNSIAAGADGVEIHSANGYLL
NQFLDPHSNTRTDEYGGSIENRARFTLEVVDALVEAIGHEKVGLRLSPYGVFNSMSGGAETGIVAQYA
YVAGELEKRAKAGKRLAFVHLVEPRVTNPFLETEGEGEYEGGSNDFVYSIWKGVPVIRAGNFALHPEVV
REEVKDKRTLIGYGRFFISNPDLDVDRLEKGLPLNKYDRDTFYQMSAHGYIDYPTYEEALKLGDWKK

>d1icpa_ c.1.4.1 (A:) 12-oxophytodienoate reductase 1 (OYE homolog) {Tomato (Lycopersicon esculentum)}

QVDKIPLMSPCKMGKFELCHRVVLAFLTRQRSYGYIPQPHAILHYSQRSTNGLLIGEATVISETGIGY
KDVPGIWTKQEVAWKPIVDAVHAKGGIFCQIWHVGRVSNKDFQPNGEDPISCTDRGLTPQIMSN
GIDIAHFTRPRRLTTDEIPQIVNEFRVAARNAIEAGFDGVEIHGAHGYLIDQFMKDQVNDKSDKYGGS
LENRCRFALEIVEAVANEIGSDRVGIRISPFAYHNEAGDTNPTALGLYMVESLNKYDLAYCHVVEPRM
KTAWEKIECTESLVPMRKAYKGTFFIVAGGYDREDGNRALIEDRADLVAYGRLFISNPDLPKRFELNAP
LNKYNRDTFYTSDPVGYTDYPFLE

>d1gox_ c.1.4.1 (-) Glycolate oxidase {Spinach (Spinacia oleracea)}

MEITNVNEYEAIKQKLPKMVYDYASGAEDQWTLAENRNAFSRILFRPRILIDVTNIDMTTTLILGF
KISMPIMIAPTAMQKMAHPEGEYATARAASAAGTIMTLSSWATSSVEEVASTGPGIRFFQLYVYKDRN
VVAQLVRRRAERAGFKAIALTVDTPRLGRREADIKNRFVLPFFLTKNFEGIDLGKMDKANDSGLSSYV
AGQIDRSLSWKDVAVLQTTITSLPILVKGVITAEDARLAVQHGAAGIIVSNHGARQLDYVPATIMALEE
VVKAAQGRIPVFLDGGVRRGTDVFKALALGAAGVFIGRPVVFSLAAEGEAGVKKVLQMMRDEFELT
MALSGCRSLKEISRSHIAADWD

>d1huva_ c.1.4.1 (A:) Membrane-associated (S)-mandelate dehydrogenase {Pseudomonas putida}

NLFNVEDYRKLAKRLPKMVYDYLEGGAEDEYGVKHNDRDVFQQWRFKPKRLVDVSRSLQAEVLG
KRQSMPLLIGPTGLNGALWPKGDLALARAATKAGIPFVLSTASNMSIEDLARQCDGLWFQLYVIHR
EIAQGMVLKALHTGYTTLVLTDDVAVNGYRERDLHNRFKIPPFLTKNFEGIDLGKMDKANLEMQA
ALMSRQMDASFNWEALRWLRDLWPHKLLVKGLLSAEDADRCIAEGADGVILSNHGGRQLDCAISP
MEVLAQSVAKTGKPVLDVSGFRGSDIVKALALGAEAVLLGRATLYGLAARGETGVDEVLTLLKADID
RTLAQIGCPDITSLSPDYLQNE

>d1h61a_ c.1.4.1 (A:) Pentaerythritol tetranirate reductase {Enterobacter cloacae}

SAEKLFTPLKVGAVTAPNRVFMAPLRLRSIEPGDIPTPLMGEYYRQRASAGLIISEATQISAQAKGYA
GAPGLHSPEQIAAWKKITAGVHAEDGRIAVQLWHTGRISHSSIQPGGQAPVSASALNANTRTSLRDE
NGNAIRVDTTTTPRALELDEIPGIVNDFRQAVANAREAGFDLVELHSAHGYLLHQFLSPSSNQRTDQY
GGSVENRARLVLEVVDVAVCNESADRIGIRVSPIGTFQNVNNGPNEEADALYLIEELAKRGIAYLHMS
ETDLAGGKPYSEAFRQKVRERFHGVIIGAGAYTAEKAEDLIGKGLIDAVAFGRDYIANPDLVARLQKK
AELNPQRPESEFYGGGAEGYTDYPSL

>d1djna1 c.1.4.1 (A:1-340) Trimethylamine dehydrogenase, N-terminal domain {Methylophilus methylotrophus, w3a1}

ARDPKHDILFEPIQIGPKTLRNRFYQVPHCIGAGSDKPGFQSAHRSVKAEGGWAALNTEYCSINPESD
DTHRLSARIWDEGDVRNLKAMTDEVHKGALAGVELWYGGAHAPNMESRATPRGPSQYASEFETL
SYCKEMDLSDIAQVQQFYVDAAKRSRDAGFDIVVYGAHSYLPQLFNPYYNKRTDKYGGSLNRRAR
FWLETLEKVKHAVGSDCAIATRFVDTVYGGPQIEAEVDGQKFVEMADSLVDMWDITIGDIAEWGE
DAGPSRFYQQGHTIPWVKLVKQVSKKPVLVGGRYTDPEKMIEIVTKGYADIIGCARPSIADPFLPQKV
EQGRYD

>d1ltda1 c.1.4.1 (A:98-511) Flavocytochrome b2, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

APGETKEDIARKEQLKSLPLDNIINLYDFEYLASQTLTKQAWAYYSSGANDEVTHREHNHAYHRIF
FKPKILVDVRKVDISTDMLGSHVDVPFYVSATALCKLGNPLEGEKDVARGCGQGVTKVPQMISTLASC
SPEEIIAAPSDKQIQWYQLYVNSDRKITDDLKVNVEKLGKALFVTVDAPSLGQREKDMKLFKFSNT
KAGPKAMKKTNVEESQGASRALSKFIDPSLTWKDIEELKKTCLPIVIKGVQRTEDVIKAAEIGVSGV

VLSNHGGRQLDFSRAPIEVLAETMPILEQRNLKDKLEVFVDGGVRRGTDVLKALCLGAKGVGLGRPF
LYANSCYGRNGVEKAIEILRDEIEMSMRLLGVTSAIELKPDLLDLSTLKARTVGPNDVLYNEVEYEGP
TLTEFEDA

>d1h7wa2 c.1.4.1 (A:533-844) Dihydropyrimidine dehydrogenase, domain 4 {Pig (Sus
scrofa)}

ISVEMAGLKFINPFGLASAAPTTSSSMIRRAFEAGWGFALTKTFLDKDIVTNSPRIVRGTTSGPMY
GPGQSSFLNIELISEKTAAYWCQSVTELKADFPDNIVIASIMCSYNKNDWMELSRKAEEASGADALEL
NLSCPHGMGERGMGLACGQDPELVRNICRWVRQAVQIPFFAKLTPNVTDIVSIARAAKEGGADGVTA
TNTVSGLMGLKADGTPWPAVGAGKRTTYGGVSGTAIRPIALRAVTTIARALPGFPILATGGIDSAESG
LQFLHSGASVLQVCSAVQNQDFTVIQDYCTGLKALLYLKSIE

>d1ea0a2 c.1.4.1 (A:423-1193) Alpha subunit of glutamate synthase, central and FMN
domains {Azospirillum brasilense}

TTHLDELVKTASLKGEPDMDKAELRRRQAFGLTMEDMELILHPMVEDGKEAIGSMGDDSPIAVL
SDKYRGLHHFFRQNFQVTPNPPIDSLRERRVMSLKTRLGNLGNLDEDETQTRLLQLESPVLTAAEF
RAMRDYMGDTAAEIDATFPVDGGPEALRDALRRIRQETEDAVRGGATHVILTDEAMGPAAAAIPAIL
ATGAVHHTLIRSNLRTFTSLNVRTAEGLDTHYFAVLIGVGATTVNAYLAQEIAAERHRRGLFGSMPL
KGMANYKKAIDDGLLKIMSKMGISVISSYRGGNFEAIGLSRALVAEHFPAMVSRISIGLNGIQKKVL
EQHATAYNEEVVALPVGGFYFRKSGDRHGWEGVIHTLQQAQVTDNSYTTFKKYSEQVNKRPPMQ
LRDLLELRSTKAPVPVDEVESITAIRKRFITPGMSMGALSPEAHGTLNVAMNRIGAKSDSGEGGEDP
ARFRPKNGDNWNSAIKQVASGRFGVTAEYLNQCRELEIKVAQGAQKPGEGGQLPGFKVTEMIARLR
HSTPGVMLISPPPHDIYSIEDLAQLIYDLKQINPDAKVTVKLVSRSGIGTIAAGVAKANADIILISGNS
GGTGASPQTSIKFAGLPWEMGLSEVHQVLTNRLRHRVRLRTDGGKLTGRDIVIAAMLGAEEFGIGT
ASLIAMGCIMVRQCHSNTCPVGVCVQDDKLRQKQFVGTPEKVVNLFVFLAAEEVREILAGLGRSLNEVI
GRTDLLHQVSRGAEHLDDLNPRLAQVDPG

>d1eepa_ c.1.5.1 (A:) Inosine monophosphate dehydrogenase (IMPDH) {Lyme disease
spirochete (Borrelia burgdorferi)}

NKITKEALTFDDVSLIPRKSSVLPSEVSLKTQLTKNISLNIPFLSSAMDTVTESQMAIAIAKEGGIGIHK
NMSIEAQRKEIEKVTKYKFQKTINTNGDTNEQKPEIFTAKQHLEKSDAYKNAEHKEDFPNACKDLN
NKLRVGAASIDIDTIERVEELVKAHVLDILVIDSAHGHSTRIELIKKIKTKYPNLDLIAGNIVTKEAALD
LISVGADCLKVIGPGSICTRIVAGVGVQITAICDVYEACNNTNICIADGGIRFSGDGVVKAIAAGADS
VMIGNLFAGTKESPSEIIYNGKKFKSYVGMGSISAMKRGSKSRFYQLENNEPKKLVEGIEGMVPYS
GKLDILTQLKGGLMSGMGLGAATISDLKINSKFKVISHS

>d1zfja1 c.1.5.1 (A:2-94,A:221-492) Inosine monophosphate dehydrogenase (IMPDH)
{Streptococcus pyogenes}

SNWDTKFLKKGTYFDDVLLIPAESHVLPNEVDLKTKLADNLTNIPITAAMDVTGSKMAIAIARAG
GLGVIHKNMSITEQAEEVRKVKRSEXGRLLVAAAVGVTSDTFERAEALFEAGADAVIDTAHGHSAGV
LRKIAEIRAHFPNRTLIAGNIATAEGARALYDAGVDVVKVIGIGPGSICTRRVAGVGVQVTAIYDAAA
VAREYGKTIADGGIKYSGDIVKALAAGGNAVMLGSMFAGTDEAPGETEIQGRKYKTYRGMGSIAA
MKKGSSDRYFQGSVNEANKLVPEGIEGRVAYKAASDIVFQMLGGIRSGMGYVAGAGDIQELHENAQF
VEMSGAGLIESHPHDVQITNEAPNYSV

>d1ak5_1 c.1.5.1 (2-101,222-483) Inosine monophosphate dehydrogenase (IMPDH)
{Trichomonas foetus}

AKYYNEPCHTFNEYLLIPGLSTVDCIPSNVNLSTPLVKFQKGQQSEINLKIPLVSAIMQSVSGEKMAIA
LAREGGISFIFGSQSIESTAAMVHAVKNFKAXHNELVDSQKRYLVGAGINTRDFRERVPALVEAGADV

LCIDSSDGFSEWQKITIGWIREKYGDVKVKGAGNIVDGEFRYLADAGADFIKIGIGGGSICITREQKGI
GRGQATAVIDVVAERNKYFEETGIYIPVCSDDGIVYDYHMTLALAMGADFIMLGRYFARFEESPTRKV
TINGSVMKEYWGEGSSRARNWQRYDLGGKQKLSFEEGVDSYVPYAGKLDKNVEASLNKVKSTMCN
CGALTIPQLQSKAKITLVSSVSI

>d1jr1a1 c.1.5.1 (A:17-112,A:233-514) Inosine monophosphate dehydrogenase (IMPDH)
{Chinese hamster (*Cricetulus griseus*)}

GLTAQQLFNCGDGLTYNDFLILPGYIDFTADQVDLTSALTKKITLKTPLVSSPMDTVTEAGMAIAMAL
TGGIGFIHNNCTPEFQANEVRKVKKYEQXYPLASKDAKKQLLGGAAIGTHEDDKYRLDLLALAGVDV
VVLDSQGNISIFQINMIKYMKEKYPNLQVIGGNVVTAAQAKNLIDAGVDALRVGMGCGSICITQEVLA
CGRPQATAVYKVFSEYARRFGVPVIADGGIQNVGHIKALALGASTVMMGSLAATTEAPGEYFFSDGI
RLKKYRGMGSLDAMDKHLSSQNRVFSEADKIKVAQGVSGAVQDKGSIHKFVPPYLIAGIQHSCQDIGA
KSLTQVRAMMYSGELKFEKRTSSAQVEGGVHSLHSYKRLF

>d1bd0a2 c.1.6.1 (A:12-244) Alanine racemase {*Bacillus stearothermophilus*}

VDLDAIYDNVENLRLLPDDTHIMAVVKANAYGHGDVQVARTALEAGASRLAVAFLEALALREKGI
EAPILVLGASRPADAALAAQRIALTVFRSDWLEASALYSGPFPIHFHLKMDTGMGRLGVKDEEET
KRIVALIERHPHFVLEGLYTHFATADEVNTDYFSYQYTRFLHMLEWLPSRPLVHCANSAASLRFPD
RTFNMVRFGIAMYGLAPSPGIKPLLPYPLKEA

>d1d7ka2 c.1.6.1 (A:44-283) Eukaryotic ornithine decarboxylase {Human (*Homo sapiens*)}

DLGDILKKHLRWLKALPRVTPFYAVKCNDSKAIVKTLAATGTGFDCASKTEIQLVQSLGVPPERIIYAN
PCKQVSQIKYAANNGVQMMTFDSEVELMKVARAHPKAKLVLRIATDDSKAVCRLSVKFGATLRTSRL
LLERAKELNIDVVGVSFHVSGCTDPETFVQAISSARCVFDMGAEVGFMSYLLDIGGGFPGSEDEVKL
KFEEITGVINPALDKYFPSDSGVRIIAEPGRYYVASA

>d7odca2 c.1.6.1 (A:44-283) Eukaryotic ornithine decarboxylase {Mouse (*Mus musculus*)}

DLGDILKKHLRWLKALPRVTPFYAVKCNDSRAIVSTLAAIGTGFDCASKTEIQLVQGLVPAERVIYAN
PCKQVSQIKYAASNGVQMMTFDSEIELMKVARAHPKAKLVLRIATDDSKAVCRLSVKFGATLRTSRL
LLERAKELNIDVIGVSFHVSGCTDPDTFVQAVSDARCVFDMATEVGFMSHLLDIGGGFPGSEDTKL
KFEEITSVINPALDKYFPSDSGVRIIAEPGRYYVASA

>d2toda2 c.1.6.1 (A:44-283) Eukaryotic ornithine decarboxylase {*Trypanosoma brucei*}

DLGDIVRKHETWKKCLPRVTPFYAVACNDDWRVLGTLAALGTGFDCASNTEIQRVGRIGVPPKEIIYA
NPCKQISHIRYARDSGVDVMTFDCVDELEKVAKTHPKAKMVLRIATDDSLARCRLSVKFGAKVEDCR
FILEQAKKLNIDVTGVSFHVSGSTDASTFAQAISSSRFVDMGTELGFNMHILDIGGGFPGTRDAPL
KFEEIAGVINNALEKHFPPDLKLTIVAEPGRYYVASA

>d1ct5a_ c.1.6.2 (A:) "Hypothetical" protein ybl036c {Baker's yeast (*Saccharomyces cerevisiae*)}

TGITYDEDRKTQLIAQYESVREVVNAEAKNVHVNENASKILLVVSCLKPASDIQILYDHGVREFGEN
YVQELIEKAKLLPDDIKWHFIGGLQTNKCKDLAKVPNLYSVETIDSLKKAKKLNESRAKFPDCNPIL
CNVQINTSHEDQKSGLNNEAEIFEVIDFFLSEECKYIKLNGLMTIGSWNVSHEDSKENRDFATLVEW
KKKIDAKFGTSLKLSMGMSADFREAIRQGTAEVRIGTDIFG

>d1frb_ c.1.7.1 (-) FR-1 (fibroblast growth factor-induced) protein {Mouse (*Mus musculus*)}

ATFVELSTKAKMPIVGLGTWKSPPNQVKEAVKAAIDAGYRHIDCAYAYCNENEVGEAIQEKIKEKAV
QREDLFIVSKLWPTCFEKLLKEAFQKTLTDLKLDYLDLYLIHWPQGLQPGKELFPKDDQGRILT
TTFLEAWEGMEELVDQGLVKALGVSFNHNFQIERLLNKPGLKHKPVTNQVECHPYLTQEKLQYCH
SKGISVTAYSPLGSPDRPSAKPEDPSLLEDPKIKEIAAKHEKTSAQVLRFHQRNVVPIKSVTPSRIQ
ENIQVDFDQLSDEEMATILSFNRNWRACLLPETVNMEEYPYDAEY

>d1exba_ c.1.7.1 (A:) Voltage-dependent K⁺ channel beta subunit {Rat (*Rattus norvegicus*)}
LQFYRNLGKSLRVSLGLGTWVTFGGQITDEMAEHLMTLAYDNGINLFDTAEVYAAGKAEVVLGNI
IKKKGWRRSSLVITTKIFWGGKAETERGLSRKHIIIEGLKASLERLQLEYVDVVFANRPDPNTPMEET
VRAMTHVINQGMAMYWGTSRWSSMEIMEAYSVARQFNLIPPICEQAEYHMFQREKVEVQLPELFH
KIGVGAMTWSPLACGIVSGKYDSGIPPYSRASLKGQWLKDKILSEEGRRQAKLQELQAI AERLGCT
LPQLAIAWCLRNEGVSLLGASNAEQLMENIGAIQVLPKLSSSIVHEIDSILGNKPYS

>d1ads_ c.1.7.1 (-) Aldose reductase (aldehyde reductase) {Human (*Homo sapiens*)}
ASRLLNNGAKMPILGLGTWKSPPGQVTEAVKVAIDVGYRHIDCAHVYQNEVEGVAIQEKLREQVV
KREELFIVSKLWCTYHEKGLVKGACQKTLSDLKLDYLDLYLIHWPTGFKPGKEFFPLDESGNVVPSD
TNILDTWAAMEELVDEGLVKAIGISNFNHLQVEMILNKPGLKYKPAVNQIECHPYLTQEKLQYCQSK
GIVVTAYSPLGSPDRPWAKPEDPSLLEDPRIKAI AAKHNKTTAQVLRIFPMQRNLVVPKSVTPERIA
ENFKVDFELSSQDMTLLSYNRNWRVCALLSCTSHKDYPFHEEF

>d2alr_ c.1.7.1 (-) Aldose reductase (aldehyde reductase) {Human (*Homo sapiens*)}
AASCVLLHTGQKMPILGLGTWKSEPGQVKA AVKYALSVGYRHIDCAA IYGNPEIGEALKEVDVGP GK
AVPREELFVTSKLWNTKHHPEDVEPALRKT LADLQLEYLDLYLMHWPYAFERGDNPFPKNADGTIC
YDSTHYKETWKALEALVAKGLVQALGLSNFNSRQIDDL SVASVRPAVLQVECHPYLAQNELIAHCQA
RGLEVTAYSPLGSSDRAWRPDEPVLL EEPVVLALAEKYGRSPAQILLRWVQVRKVICIPKSITPSRIL
QNIKVFDFTFSP EEMKQLNALNKNWRYIVPMLTV D GKRVPRDAGHPLYPFNDPY

>d1ah4_ c.1.7.1 (-) Aldose reductase (aldehyde reductase) {Pig (*Sus scrofa*)}
ASHLVLYTGAKMPILGLGTWKSPPGKVTEAVKVAIDLGYRHIDCAHVYQNEVEGLGLQEKLQGGVV
KREDLFIVSKLWCTDHEKNLVKGACQTTLRDLKLDYLDLYLIHWPTGFKPGKDPFPLDGDGNVVPD
ESDFVETWEAMEELVDEGLVKAIGVSNFNHLQVEKILNKPGLKYKPAVNQIEVHPYLTQEKLIEYCKS
KGIVVTAYSPLGSPDRPWAKPEDPSLLEDPRIKAI AAKYKNTTAQVLRIFPMQRNLVVPKSVTPERIA
ENFQVDFELSPEDMNTLLSYNRNWRVCALMSCASHKDYPFHEEY

>d1hqta_ c.1.7.1 (A:) Aldose reductase (aldehyde reductase) {Pig (*Sus scrofa*)}
AASCVLLHTGQKMPILGLGTWKSEPGQVKA AIKYALTVGYRHIDCAAIFGNELEIGEALQETVGP GK
VPREELFVTSKLWNTKHHPEDVEPALRKT LADLQLEYLDLYLMHWPYAFERGDNPFPKNADGTIR
YDATHYKDTWKALEALVAKGLVRLALGLSNFSSRQID DVLSVASVRPAVLQVECHPYLAQNELIAHCQ
ARGLEVTAYSPLGSSDRAWRPNEPVLL EEPVVQALAEKYNRSPAQILLRWVQVRKVICIPKSVTPSR
IPQNIQVDFTFSP EEMKQLDALNKNLRFIVPMLTV D GKRVPRDAGHPLYPFNDPY

>d1afsa_ c.1.7.1 (A:) 3-alpha-hydroxysteroid dehydrogenase {Rat (*Rattus norvegicus*)}
MDSISLRVALNDGNFIPVLGFGTTVPEKVAKDEVIKATKIAIDNGFRHFDSAYLYEVEEEVGQAIRSKI
EDGTVKREDIFYTSKLWSTFHRPELVRTCLEKTLKSTQLDYVDLYIIHFPMALQPGDIFFPRDEHGKL
LFETVDICDTWEAMEKCKDAGLAKSIGVSNFNCRQLERILNKPGLKYKPCVNQVECHLYLNQSKML
DYCKSKDIILVSYCTLGSSRDKTWVDQKSPVLLDDPVLCAIAKKYKQTPALVALRYQLQRGVVPLIRSF
NAKRIKELTQVFEFQLASEDMKALDGLNRNFRYNNAKYFDDHPNHPF

>d1ihia_ c.1.7.1 (A:) 3-alpha-hydroxysteroid dehydrogenase {Human (*Homo sapiens*), type III}
SKYQCVKLNDGHFMPVLGFGTYAPAEVPSKALEAVKLAIEAGFHHIDSAHVYNNEEQVGLAIRSKIA
DGSVKREDIFYTSKLWNSHRPELVRPALERSLKNLQLDYVDLYLIHFVSVKPGEEVIPKDENGKILF
DTVDL CATWEAMEKCKDAGLAKSIGVSNFNHRLLEMILNKPGLKYKPCVNQVECHPYFNQRKLLDF
CKSKDIVLVAYSALGSHREEPWVDPNSPVLL EDPVLCALAKKHKRTPALIALRYQLQRGVVVLAKSY
NEQRIRQNVQVFEFQLTSEEMKAIDGLNRNVRYLTL DIFAGPPNYPFSD E

>d1c9wa_ c.1.7.1 (A:) CHO reductase {Chinese hamster (*Cricetulus griseus*)}

STFVELSTKAKMPIVGLGTWQSPPGQVKEAVKVAIDAGYRHIDCAYAYNEHEVGEAIQEKIKEKAVR
REDLFIVSKLWPTCFERKLLKEAFQKTLTDLKLDYLDLYLIHWPPQGLQPGKELFPKDDQGNVLTSKI
TFLDAWEVMEELVDEGLVKALGVSNNFHFQIERILNKPLKHKPVTNQVECHPYLTQEKLIEYCHSK
GITVTAYSPLGSPNRPWAKPEDPSLLEDPKIKEIAAKHKKTSAQVLIRFHIQRNVVVIPKSVTPARIHE
NFQVFDLQSDQEMATILGFNRNWRACLLPETVNMEEYPYDAEY

>d1hw6a_c.1.7.1 (A:) 2,5-diketo-D-gluconic acid reductase A {Corynebacterium sp.}

TVPSIVLNDGNSIPQLGYGVFKVPPADTQRAVEEAEVGYRHIDTAAIYGNEEGVGAAIAASGIARDDL
FITTKLWNRDHDGDEPAAIAESLAKLALDQVDLYLVHWPTPAADNYVHAWEKMIELRAAGLTRSI
GVSNNHLVPHLERIVAATGVVPAVNQIELHPAYQQREITDWAHAHDVKIESWGPLGQGGKYDLFGAEPV
TAAAAAHGKTPAQAVLRWHLQKGFVVPKSVRRERLEENLDVDFDLTDTEIAAIDAMP

>d1bli_2 c.1.8.1 (3-393) Bacterial alpha-amylase {Bacillus licheniformis}

LNGTLMQYFEWYMPNDGQHWKRLQNDSAYLAEHGITAVWIPPAYKGTSDVGYGAYDLYDLGEF
HQKGTVRTKYGKTELQSAIKSLHSRDINVYGDVVINHKGADATEDVTAVEVDPADRNRVISGEHLI
KAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYKFGKAWDWEVSNEFGNYDLYMY
ADIDYDHPDVA AEIKRWGTWYANELQLDGFRLDAVKHIKFSFLRDWVNHVREKTGKEMFTVAEY
WSYDLGALENYLNKTNFNHNSVFDVPLHYQFHAASTQGGGYDMRKLNGTVVSKHPLKSVTFVDNH
DTQPGQSLESTVQTFWKPLAYAFILTRESGYPQVFGDMYGTGKDSQREIPALKHKIEPILKARKQ

>d1e43a2 c.1.8.1 (A:1-393) Bacterial alpha-amylase {Bacillus amyloliquefaciens/Bacillus licheniformis chimera}

VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLYDLGEFQ
QKGTVRTKYGKTELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNPANRNQETSEEQI
KAWTDFRFPGRGNTYSDFKWHWYHFDGADWDESRKISRIFKFRGEGKAWDWEVSSENGNYDYL
MYADVDYDHPDVAAETKKWGIWYANELSLDGFRIAAKHKFSFLRDWVQAVRQATGKEMFTVAE
YWQNNAGKLENYLNKTSFNQSVFDVPLHFNLAASSQGGGYDMRKLNGTVVSKHPLKSVTFVDN
HDTQPGQSLESTVQTFWKPLAYAFILTRESGYPQVFGDMYGTGKDSQREIPALKHKIEPILKARKQ

>d1g94a2 c.1.8.1 (A:1-354) Bacterial alpha-amylase {Pseudoalteromonas haloplanctis (Alteromonas haloplanctis)}

TPPTTFVHLFEWNWQDVAQECEQYLGPKGYAAVQVSPNEHITGSQWWTRYQPVSYELQSRGGNRA
QFIDMVNRCSAAGVDIYVDTLINHMAAGSGTGTAGNSFGNKSFPYIYSPQDFHESCTINNSDYGNDRY
RVQNCGLVGLADLTASNYVQNTIAAYINDLQAIQVKGFRFDASKHVAASDIQSLMAKVNQSPVVFQE
VIDQGGAEVAVGASEYLSGLVTEFKYSTEELGNTFRNGSLAWLSNFGEGWGFMPSSSAVVFVDNHDNQ
RGHGGAGNVITFEDGRLYDLANVFMLAYPYGYPKVMSSYDFHGD TDAGGPNVPVHNNGNLECFAS
NWKCEHRWSYIAGGVDFRNNTAD

>d1bag_2 c.1.8.1 (1-347) Bacterial alpha-amylase {Bacillus subtilis}

LTAPSIKSGTILHAWNWSFN TLKHNMKDIHDAGYTAIQTSPINQVKEGNQGDKMSMNWYWLYQPTS
YQIGNRYLGTEQEFKEMCAAEEYGIKVIQVDAVINHTTFDYAAISNEVKSIPNWTGNTQIKNWSDR
WDVTQNSLLGLYDWNTQNTQVQSYLKRFLERALNDGADGFRFDAAKHIELPDDGSYGSQFWPNIT
NTSAEFQYQQLQDSASRDAAYANYMDVTASNYGHSIRSALKNRNLGVSNIHYASDVADKLVTVW
ESHDTYANDDEESTWMSDDDIRLWAVIASRSGSTPLFFSRPEGGGNGVRFPGKSQIGDRGSALFED
QAITAVNRFHNV MAG

>d1hvxa2 c.1.8.1 (A:1-393) Bacterial alpha-amylase {Bacillus stearothermophilus}

AAPFNGTMMQYFEWYLPDDGTLWTKVANEANLSSLGITALWLPPAYKGTSDVGYGVYDLYDLG
EFNQKGAVRTKYGKTAQYLQAIQAAHAAGMQVYADVDFDHKGGADGTEWVDAVEVNPSPDRNQEIS
GTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRGIGKAWDWEVDTENGN

YDYLMYADLMDHPEVVTELKSWGKWYVNTTNIDGFRLDAVKHIKFSFFPDWLSYVRSQTGKPLF
TVGEYWSYDINKLHNYIMKTNGTMSLFDAPLHNKFYTASKSGGTFDMRTLMTNTLMKDQPTLAVT
FVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEGYPCVFGDYGIPQYNIPSLKSKIDPLLIARRD
>d1gja2 c.1.8.1 (A:1-572) Maltosyltransferase {Thermotoga maritima}
MLLREINRYCKEKATGKRIYAVPKLWIPGFFKFKFDEKSGRCFVDPYELGAEITDWILNQSREWDYSQ
PLSFLKGEKTPDWIKRSVVYGSPLRRTAAYNHKGSGYEEENDVLGFREAGTFFKMMLLLPFVKSLGA
DAIYLLPVSMSDLFKKGDAPSPYSVKNPMELDERYHDPLLEPFKVDEEFKAFVEACHILGIRVILDFI
PRTAARDSDLIREHPDWFYVIKVEELADYTPPRAEELPFKVPDEDELEIYNKENVKRHLKFKFTLPP
NLIDPQKWEKIKREEGNILELIVKEFGIITPPGFSDLINDPQPTWDDVTFLRLYLDHPEASKRFLDPN
QPPYVLYDVIKASKFPGKEPNRELWEYLAGVIPHYQKKYGIDGARLDMGHALPKELLDLIKNVKEY
DPAFVMIAEELMEKDKASKEAGYDVLGSSWYFAGRVEEIGKLPDIAEELVLPFLASVETPDTPRIA
TRKYASKMKKLAPFVTYFLPNSIPYVNTGQEIGEKQPMNLGLDTPNLRKVLSPTEFFGKLAFFDH
YVLHWDSRDRGVLNFIKKLIKVRHEFLDFVLN

>d1cgt_4 c.1.8.1 (1-406) Cyclodextrin glycosyltransferase {Bacillus circulans, different strains}
DPDTAVTNKQSFSTDVIYQVFTDRFLDGNPSNNPTGAAAYDATCSNLKLYCGGDWQGLINKINDNYFS
DLGVTALWISQPVENIFATINYSVNTAYHGYWARDFKKTNPYFGTMADFQNLITTAHAKGKIVID
FAPNHTSPAMETDTSFAENGRLYDNGTLVGGYTNDTNGYFHHNGGSDFSLENGIYKNLYDLADFN
HNNATIDKYFKDAIKLWLDMGVDGIRVDAVKHMPLGWQKSWMSSIAHKPVFTFGWFLGSAASD
ADNTDFANKSGMSLLDFRNSAVRNVRDNTSNMYALDSMINSTATDYNQVNDQVTFIDNHMDR
FKTSAVNNRRLEQALAFTLTSLRGVPAIYYGTEQYLTGNGDPDNRAKMPFSKSTTAFNVISKLAPLRK
SNPAIAY

>d1kcla4 c.1.8.1 (A:1-406) Cyclodextrin glycosyltransferase {Bacillus circulans, different strains}
APDTSVSNKQNFSTDVIYQVFTDRFSDGNPANNPTGAAFDGTCTNLRLYCGGDWQGIINKINDGYLTG
MGVTAIWISQPVENIYSIINYSVNTAYHGYWARDFKKTNPAYGTIADFQNLIAAAHAKNIKVIIDFA
PNHTSPASSDQPSFAENGRLYDNGTLLGGYTNDTQNLFHHNLGTDFTTENG IYKNLYDLADLNHN
NSTVDVYLKDAIKMWLDLGDGIRMDAVKHMPPFGWQKSFMAAVNNYKPVFTFGWFLGVNEVSP
ENHKFANESGMSLLDFRFAQKVRQVFRDNTDNMYGLKAMLEGSAAQVDDQVTFIDNHDMER
FHASNANRRKLEQALAFTLTSLRGVPAIYYGTEQYMSGGTPDNRRARIPSFSTSTAYQVIQKLAPLRK
CNPAIAY

>d1cyg_4 c.1.8.1 (1-402) Cyclodextrin glycosyltransferase {Bacillus stearothermophilus}
AGNLNKNVFTSDVVYQIVVDRFVDGNTSNNPSGALFSSGCTNLRKYCGGDWQGIINKINDGYLTDM
GVTAIWISQPVENVFSVMNDASGSASYHGYWARDFKKPNPFFGTLSDFQRLVDAAHAKGKVIIDFA
PNHTSPASETNPSYMEGRLYDNGTLLGGYTNDANMYFHHNGGTTFSLEDEGIYRNLFDLADLNH
QNPVIDRYLKDAVKMWIDMGIDGIRMDAVKHMPPFGWQKSLMDEIDNYRPVFTFGWFLSENEVD
ANNHYFANESGMSLLDFRFGQKLRQVLRNNSDNWYGFNQMIQDTASAYDEVLDQVTFIDNHDM
RFMIDGGDPRKVDLAVLLTSLRGVPAIYYGTEQYMTGNGDPNRRKMMSSFNKNTRAYQVIQKLSS
LRRNNPALAY

>d1qhoa4 c.1.8.1 (A:1-407) Cyclodextrin glycosyltransferase {Bacillus stearothermophilus, maltogenic alpha-amylase}
SSSASVKGDVIYQIIIDRFYDGDTTNNNPAKSYGLYDPTKSKWKMYWGGDLEGVRQKLPYLKQLGVT
TIWLSPLVDNLDTLAGTDNTGYHGYWTRDFKQIEEHFGNWTTFDFTLVNDAHQNGIKVIVDFVPH
STPFKANDSTFAEGGALYNGTYMGNYFDDATKGYFHHNGDISNWDDRYEAQWKNFTDPAGFSLA

DLSQENGTIAQYLTDAAVQLVAHGADGLRIDAVKHFNSGFSKSLADKLYQKKDIFLVGEWYGDDPGT
ANHLEKVRVYANNVSGVNVLDLDFLNTVIRNVFGTFTQTMVDLNNMVNQGTGNEYKYKENLITFIDNHD
MSRFLSVNSNKANLHQALAFILTSRGTPSIYYGTEQYMAGGNDPYNRGMMPAFDTTTTAFKEVSTL
AGLRRNNAAIQY

>d1pama4 c.1.8.1 (A:1-406) Cyclodextrin glycosyltransferase {Alkalophilic bacillus sp., strain 1011}

APDTSVSNKQNFSTDVIYQIFTDRFSDGNPANNPTGAAFDGSCNTNLRLYCGGDWQGIINKINDGYLTG
MGITAIWISQPVENIYSVINYSVNVNTAYHGYWARDFKKTNPAYGTMQDFKNLIDTAHAHNKVIIDF
APNHTSPASSDDPSFAENGRLYDNGNLLGGYTNDTQNLFHHYGGTDFSTIENGIYKNLYDLADLNHN
NSSVDVYLKDAIKMWLDLGVGDGIRVDAVKHMPFGWQKSFMATINNYKPVFTFGWFLGVNEISPE
YHQFANESGMSLLDFRFAQKARQVFRDNTDNMYGLKAMLEGSEVDYAQVNDQVTFIDNHDMERF
HTSNGDRRKLEQALAFTLTSRGVPAIYYGSEQYMSGGNDPDRARLPSFSTTTTAYQVIQKLAPLRKS
NPAIAY

>d1ciu_4 c.1.8.1 (1-406) Cyclodextrin glycosyltransferase {Thermoanaerobacterium thermosulfurigenes, EM1}

ASDTAVSNVNYSTVDVIYQIVTDRFVDGNTSNNPTGDLYDPTHTSLKKYFGGDWQGIINKINDGYLT
GMGVTAIWISQPVENIYAVLPDSTFGGSTSYPHYWARDFKRTNPFYGSFTDFQNLINTAHAHNKVII
DFAPNHTSPASETDPTYAENGRLYDNGTLLGGYTNDTNGYFHHYGGTDFSSYEDGIYRNLFDLADLN
QQNSTIDSYLKSAIKVWLDMGIDGIRLDAVKHMPFGWQKNFMDSILSYRPVFTFGWFLGTNEIDV
NNTYFANESGMSLLDFRFSQKVRQVFRDNTDTMYGLDSMIQSTASDYNFINDMVTFIDNHDMDRF
YNGGSTRPVEQALAFTLTSRGVPAIYYGTEQYMTGNPYNRAMMTSFNTSTTAYNVIKKLAPLRKS
NPAIAY

>d1hx0a2 c.1.8.1 (A:1-403) Animal alpha-amylase {Pig (Sus scrofa)}

EYAPQTQSGRTSIVHLFEWRWVDIALECERYLGPKGFGGVQVSPNENIVVTNPSRPWWERYQPVS
YKLCTRSGNENEFDRDMVTRCANNVGVRIYVDAVINHMCAGSAAAGTGTTCGSYCNPGNREFPAVPYS
AWDFNDGKCKTASGGIESYNOPYQVRDCQLVGLLDLALDKDYVRSKIAEYMNHLIDIGVAGFRIDASK
HMWPGDIKAVLDKHLNLTNWFPAWSRPFIFQEVIDLGGEAIKSSEYFGNGRVTEFKYGAKLGTVV
RKWSGEKMSYLKNWGEWGFMPDRALVFDNHDNQRGHGAGGSSILTFWDARLYKIAVGFMLA
HPYGFTRVMSSYRWARNFVNGEDVNDWIGPPNNGVIKEVTINADTTGNDWVCEHRWREIRNM
VWFRNVVDG

>d1smd_2 c.1.8.1 (1-403) Animal alpha-amylase {Human (Homo sapiens)}

EYSSNTQQGRTSIVHLFEWRWVDIALECERYLAPKGFQVSPNENVAIHNPFPPWWERYQPVS
YKLCTRSGNEDEFNMVTRCANNVGVRIYVDAVINHMCNAVSAGTSSTCGSYFNPGSRDFPAVPYSG
WDFNDGKCKTGSVDIENYNDATQVRDCRLSGLLDLALGKDYVRSKIAEYMNHLIDIGVAGFRIDASK
HMWPGDIKAILDKHLNLSNWFPEGSKPFYQEVIDLGGEPIKSSDYFGNGRVTEFKYGAKLGTVIR
KWNGEKMSYLKNWGEWGFMPDRALVFDNHDNQRGHGAGGASILTFWDARLYKMAVGFMLA
HPYGFTRVMSSYRWPRYFENGKDVNDWVGPPNDNGVTKEVTINPDTTGNDWVCEHRWRQIRN
MVNFRNVVDG

>d1jae_2 c.1.8.1 (1-378) Animal alpha-amylase {Yellow mealworm (Tenebrio molitor), larva}

EKDANFASGRNSIVHLFEWKWNDIADECERFLQPQGFQVQISPPNEYLVADGRPWWERYQPVSYII
NTRSGDESAFTDMTRRCNDAGVRIYVDAVINHMTGMNGVGTSGSSADHDGMNYPVPYSGDFHS
PCEVNNYQDADNVRNCELVGLRDLNQGSDYVRGVLIDYMNHMIDLVAGFRVDAAKHMSPGDLSVI
FSGLKNLNTDYGFADGARPFYQEVIDLGGEAISKEYTGFVGVLEFQFGVSLGNAFQGGNQLKNLAN
WGPEWGLLEGLDAVFDNHDNQRGTGGSQILTYKNPKPYKMAIAFMLAHPYGTTRIMSSFDFTDN

DQGPPQDGSGNLISPGINDDNTCSNGYVCEHRWRQVYGMVGFRAVE

>d2aaa_2 c.1.8.1 (1-381) Fungal alpha-amylases {*Aspergillus niger*, acid amylase}

LSAASWRTQSIYFLLTDRFGRTDNSTTATCNTGNEIYCGGSWQGIIDHLDYIEGMGFTAIWISPITEQL
PQDTADGEAYHGYWQQKIYDVNSNFGTADNLKSLSDALHARGMYLMVDVVPDHMGYAGNGNDVD
YSVFDPFSSSYFHPYCLITDWDNLTMVEDCWEGDTIVSLPDLDTTETAVRTIWDVWADLVSNYS
VDGLRIDSVLEVQPDFFFPGYNKASGVYCVGEIDNGNPASDCPYQKVLGDVNLNYPIYWQLLYAFESSG
SISNLNMIKSVASDCSDPTLLGNFIENHDNPRFAKYTSDYSQAKNVLSYIFLSDGIPIVYAGEEQHYAG
GKVPYNREATWLSGYDTSAELYTWIATTNAIRKLAIAADSAYIT

>d7taa_2 c.1.8.1 (1-381) Fungal alpha-amylases {*Aspergillus oryzae*, Taka-amylase}

ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAIWITPVTAQ
LPQTTAYGDAYHGYWQQDIYSLNENYGTADDLALSSALHERGMYLMVDVVANHMGYDGAGSSVD
YSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNVSLPDLDTTKDVVKNEWYDWVGSLSVSNYS
IDGLRIDTVKXHVQKDFWPGYNKAAGVYICIGEVLDGDPAYTCPYQNVMDGVLNYPYIYPLLNAFKSTS
GSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEYH
YAGGNDPANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVT

>d1smaa3 c.1.8.1 (A:124-505) Maltogenic amylase, central domain {*Thermus sp.*}

DLFQAPDWVKDVTWVYQIFPERFANGNPAISPKGARPWGSEDPPTTSFFGGDLQGIIDHLDYLADLGI
TGIYLTPIFRAPSNHKYDTADYFEIDPHFGDKETLKTTLVKRCHEKGIRVMLDAVFNHCGYEFAPFQDV
LKNGAASRYKDWFHIREFPLQTEPRPNYDTFAFVPHMPKLNTHPEVKRYLLDVATYWIREFDIDG
WRLDVANEIDHQFWREFRQAVKALKPDVYILGEIWHDAMPWLRGDQFDVAVMNYPLADAALRFFA
KEDMSASEFADRLMHVLSYKQVNEAAFNLLGSHDTPRLLTVCGGDVVRKVKLLFLFQLTFTGSPCI
YYGDEIGMTGGNDPECRKCMVWDPEKQNKELYEHVKQLIALRKQYRALRR

>d1bvza3 c.1.8.1 (A:121-502) Maltogenic amylase, central domain {*Thermoactinomyces vulgaris*, TVAII}

VFTTPEWAKEAVIYQIFPERFANGDPSNDPPGTEQWAKDARPRHDSFYGGDLKGVIDRLPYLEELGV
TALYFTPIFASPSHHKYDTADYLAIDPQFGDLPTFRRLVDEAHRGKIILDAVFNHAGDQFFAFRDVL
QKGEQSRYKDWFFIEDFPVSKTSRTNYETFAVQVPAMPKLRNENPEVKEYLFDVARFWMEQGIDG
WRLDVANEVDHAFWREFRRLVKSINPDALIVGEIWHDASGWLMGDQFDSVMNYLFRFVIRFFAT
GEIHAERFDAELTRARMLYPEQAAQGLWNLLDSDTERFLTSCGGNEAKFRLAVLFQMTYLGTPLIY
YGDEIGMAGATDPDCRRPMIWEKEQNRLFEFYKELIRLRHRLASLTR

>d1eh9a3 c.1.8.1 (A:91-490) Glycosyltrehalose trehalohydrolase, central domain {*Archaeon Sulfolobus solfataricus*, km1}

FNNETFLKKEDLIYEIHVGTFTPEGTFEGVIRKLDYLDKLGITAIEIMPIAQFPGKRDWGYDGVVLYA
VQNSYGGPEGFRKLVDEAHKKGLGVILDVVYNHVGPEGNMVKLGPYFSQKYKTPWGLTFNFDDAE
SDEVKRFLENVEYWIKEYNVDGFRLDAVHAIIDTSPKHILEEIAADVHKYNRIVIAESDLNDPRVVN
PKEKCGYNIDAQWVDDFHHSIHAYLTGERQGYTDFGNLDDIVKSYKDVVYDYGKYSNFRKTHGE
PVGELDGCNFVVIYQNHQVGNRKGGERIIKLVDRYSKIAAALYLLSPYIPMIFMGEEYGEENPFYFF
SDFSLSKLIQVREGRKKENGQDTPQDESTFNASKLSWKIDEEIFSFKILIKMRKELSIA

>d1bf2_3 c.1.8.1 (163-637) Isoamylase, central domain {*Pseudomonas amyloclavata*}

PSTQSTGKPTRAQKDDVIYEVHVRGFTEQDTSIPAQYRGTYGAGLKASYLASLGVTAVEFLPVQET
QNDANDVVPNSDANQNYWGYMTENYFSPDRRYAYNKAAGGPTAEFQAMVQAFHNAGIKVYMDVV
YNHTAEGGTWTSSDPTTATIYSWRGLDNATYYELTSGNQYFYDNTGIGANFNTYNTVAQNLIVDSLA
YWANTMGVDGFRFDLASVLGNSCLNGAYTASAPNCPNGGYNFADAADSNVAINRILREFTVPAAGG
SGLDLFAEPWAIGGNSYQLGGFPQGWSEWNLFRDSLRLQAQNELGSMTIYVTQDANDFSGSSNLFQ

SSGRSPWNSINFIDVHDGMTLKDVSVCNGANNSQAWPYGPSDDGGTSTNYSWDQGMSAGTGAAVDQ
RRAARTGMAFEMLSAGTPLMQGGDEYLRTLQCNNNAYNLDSSANWLTYSWTTDQSNFYTFAQRLL
AFRKAHPALRPSSW

>d1gcy2 c.1.8.1 (A:1-357) G4-amylase (1,4-alpha-D-glucan maltotetrahydrolase)
{Pseudomonas stutzeri}

DQAGKSPNAVRYHGGDEIILQGFHWNVVREAPNDWYNILRQQAATIAADGFSAIWMPVWRDFSS
WSDGSKSGGEGYFWHDFNKNRGYGSQAQLRQAASALGGAGVKVLYDVVPHMNRGYPDKEINLP
AGQGFWRNDCADPGNYPNDCDDGDRFIGGDADLNTGHPQVYGMFRDEFNLRSQYGAGGFRFDF
VRGYAPERVNSWMTDSADNSFCVWELWKGPEYPNWDWRNTASWQIHKDWSRAKCPVDFDAL
KERMQNGSIADWKHGLNGNPDPRWREAVTFVDNHDTGYSQNGGQHHWALQDGLIRQAYAYIL
TSPGTPVVYWDHMYDWGYGDFIRQLIQVRRRAAGV

>d1avaa2 c.1.8.1 (A:1-346) Plant alpha-amylase {Barley (Hordeum vulgare), seeds, AMY2
isozyme}

QVLFQGFNWESWKHNGGWYNFLMGKVDIAAAGITHVWLPPASQSVAEQGYMPGRLYDLDDASKY
GNKAQLKSLIGALHGKGVKAIADIVINHRTAEHKDGRGIYCFEGGTPDARLDWGPHEMICRDRPYA
DGTGNPDTGADFGAAPPDIDHLNLRVQKELVEWLNWLKADIGFDGWRFDFAKYSADVAKIYDRSE
PSFAVAEIWTSLAYGGDGKPNLNQDQHRQELVNVVDKVGKGPATTFDFTTKGILNVAVEGELWRL
RGTGDKAPGMIGWPAKAVTFVDNHDTGSTQHMWPFPSDRVMQGYAYILTHPGTPCIFYDHFFD
WGLKEEIDRLVSVRTRHGI

>d1uok_2 c.1.8.1 (1-479) Oligo-1,6, glucosidase {Bacillus cereus}

MEKQWWKESVVYQIYPRSFMSNGDGGDLRGIISKLDYLKELGIDVIWLSPVYESPNDNGYDISD
YCKIMNEFGTMEDWDELLHEMHERNMKLMMDLVVNHTSDEHNWFIESRKSNDKRYDYIWRP
GKEGKEPNWGAAFSGSAWQYDEMTDEYLLHLFSKKQPDNLWDNEKVRQDVYEMMKFWLEKGI
DGRMDVINFISKEEGLPTVETEEGYVSGHKHFMNGPNHKLHEMNEEVLSHYDITVGEPMGV
TTEEAKLYTGEERKELQMVVFQFEHMDLDSGEGGKWDVKPCSLTLKENLTKWQKALEHTGWNSLY
WNNHDQPRVVSFRGNDGMYRIESAKMLATVLHMMKGTPIYQGEI GMTNVRFESIDEYRDIETL
NMYKEKVMERGEDIEKVMQSIYIKGRDNARTPMQWDDQNHAGFTTGEPWITVNPYKEINVKQAI
QNKDSIFYYYKKLIELRKNNEIVVY

>d1g5aa2 c.1.8.1 (A:1-554) Amylosucrase {Neisseria polysaccharea}

SPNSQYLKTRILDIYTPEQRAGIEKSEDWRQFSRRMDTHFPKLMNELDSVYGNNEALLPMLEMLLA
QAWQSYSQRNSSLKIDIDIARENPDWILSNKQVGGVCYVDLAFAGDLKGLKDKIPYFQELGLTYLHLM
PLFKCPEGKSDGGYAVSSYRDVNPALGTIGDLREVIAALHEAGISAVVDFIFNHTSNEHEWAQRCAAG
DPLFDNFYIFPDRRMPDQYDRTLREIFPDQHPGGFSQLEDGRVWVWTTFNSFQWDLNYSNPWVF
RAMAGEMFLANLGVLDILRMDAVAFIWKQMGTSCEENLPQAHALIRAFNAVMIAPAVFFKSEAIV
HPDQVVQYIGQDECQIGYNPLQ MALLWNTLATREVNLLHQALTYRHNLPHTAWVNYVRSHDDIG
WTFADEDAAAYLGISGYDHRQFLNRFFVNRFDGSGFARGVPPFQYNPSTGDCRVSGTAAALVGLAQDDP
HAVDRIKLLYSIALSTGGLPLIYLGDEVGTLNDDDWSQDSNKSDDSRWAHRPRYNEALYAQRNDPST
AAGQIYQDLRHMIAVRQSNPRFDGG

>d1eswa_ c.1.8.1 (A:) Amylomaltase MalQ {Thermus aquaticus}

MELPRAFGLLLHPTSLPGYGVGLGREARDFLRFLKEAGGRYWQVPLPGPTGYGDSPTYQSFSAFAG
NPYLIDLRPLAERGVRLDPGFPQGRVDYGLLYAWKWPALKEAFRGFKEKASPEEREAFAAFRERE
AWWLEDYALFMALKGAHGLPWNRWPLPLRKREEKALREAKSALAEVAFHAFTQWLFFRQWG
ALKAEEALGIRIIGDMPIFVAEDSAEVWAHPEWFHLDEEGRPTVVAGVPPDYFSETGQRWGNPLY
RWDVLEREGFSFWIRLEKALELFLVLRIDHFRGFAYWEIPASCP TAVEGRWVKAPGEKLFQKIQE

VFGEVPVLAEDLGVITPEVEALRDRFGLPGMKVLQFAFDDGMENPFLPHNYPAHGRVVVYTGTHD
NDTTLGWYRTATPHEKAFMARYLADWGITFREEEVPWALMHLGMKSVARLAVYPVQDVLALGSE
ARMNYPGRPSGNWAWRLLPGELSPEHGARLRAMAEATERL

>d1byb_ c.1.8.2 (-) beta-Amylase {Soybean (Glycine max)}

SNMLLNYPVYVMLPLGVVNVDFEDPDGLKEQLLQLRAAGVDGVMVDVWWGIIELKGPQYD
WRAYRSLFQLVQECGLTLQAIMSFHQCGGNVGDIVNIPIQWVLDIGESNHDIFYTNRSGTRNKEYLT
VGVDNEPIFHGRTAIEIYSDYMKSFRENMSDFLESGLIIDIEVGLGPAGELRYPSPYQSQGWFEPRIGE
FQCYDKYLKADFKAAVARAGHPEWELPDDAGKYNDVPESTGFFKSNGTYVTEKGFLLTWYSNKL
NHGDQILDEANKAFLGCKVKLAIKVSGIHWYKVENHAAELTAGYYNLNDRDGYRPIARMLSRHH
AILNFTCLEMRDSEQPSDAKSGPQELVQQVLSGGWREDIRVAGENALPRYDATAYNQIILNAKPQGV
NNNGPPKLSMFGVTYLRSLDQLKSNFNIFKFFVLKMHADQDYCANPQKYNHAITPLKPSAPKIPI
EVLLEATKPTLPPFWLPETDMKVDG

>d1b1ya_ c.1.8.2 (A:) beta-Amylase {Barley (Hordeum vulgare)}

MKGNYVQVYVMLPLDAVSVNRRFEKGDDELRAQLRKLVEAGVDGVMVDVWWGLVEGKGPAYDWS
AYKQLFELVQKAGLKLQAIMSFHQCGGNVGDVNIPIQWVRDVGTRDPDIFYTDGHGTRNIEYTL
GVDNQPLFHGRSAVQMYADYMTSFRENKDFLDAGVIVDIEVGLGPAGELRYPSPYQSHGWSFPGI
GEFICYDKYLQADFKAAAAVGHPEWEPNDAGQYNDTPERTQFFRDNGTYLSEKGRFFLAWYSN
NLIKHGDRILDEANKVFLGYKVQLAIKIAGVHWWYKVPASHAAELTAGYYNLHHRDGYRTIARMLKR
HRASINFTCAEMRDSEQPPDAMSAPEELVQQVLSAGWREGLNVSCENALPRYDPTAYNTILRNARP
HGINQSGPPEHKLFGFTYLRSLNQLVEGQNYVNFKTFVDRMHANLPRDPYVDPMAPLPRSGPEISIE
MILQAAQPKIQPFQEHDTLPGPTGGMGGQAEGPTCG

>d1fa2a_ c.1.8.2 (A:) beta-Amylase {Sweet potato (Ipomoea batatas)}

APIPGVMPIGNVSLYVMLPLGVVNVADNVFPDKEKVEDELKQVKAGGCDGVMVDVWWGIIKAKGP
KQYDWSAYRELQVKKCGLKIQAIMSFHQCGGNVGDVFIPIQWILQIGDKNPDIYTNRAGNRN
QEYLSLGVNDQRLFQGRTALEMYRDFMESFRDNMADFLKAGDIVDIEVGCGAAGELRYPSPYQSQ
WVFPGIGEFQCYDKYMWADWKEAVKQAGNADWEMPGKAGTYNDTPDKTEFFRPNNGTYKTDMG
KFFLTWYSNKLIIHGDQVLEEANKVFLVGLRVNIAAKVSGIHWYVNHVSHAAELTAGFYNVAGRDGY
RPIARMLARHHATLNFTCLEMRDSEQPAEAKSAPQELVQQVLSGGWKEYIDVAGENALPRYDATAY
NQMLLKLRPNGVNLNGPPKLMKSGLTYLRLSDDLQTDNFELFKKFVKKMHADLDPSNAISPAVL
ERSNSAITIDELMEATKGSRPFVYDVTMPVDGSPNPF

>d1b9za2 c.1.8.2 (A:1-417) Bacterial beta-amylase, catalytic domain {Bacillus cereus}

AVNGKGMNPDYKAYLMAPLKKIPEVTNWETFENDLRWAKQNGFYAITVDFWWGDMEKNGDQQF
DFSYAQRFAQSVKNAGMKMIPISTHQCGGNVGDVNIPIQWVLDIGESNHDIFYTNRSGTRNKEYLT
LNPLASDVIRKEYGELYTAFAAAMKPYKDVIKIYLSGGPAGELRYPSPYQSQGWFEPRIGE
AKSKFRLWVLNKGSLNEVNKAWGTKLISELAILPPSDGEQFLMNGYLSMYGKDYLEWYQGILENH
TKLIGELAHNAFDTTFQVPIGAKIAGVHWQYNNPTIPHGAEKPAYNDYSHLLDAFKSAKLDVTFTC
LEMTDKGSYPEYSMPKTLVQNIATLANEKGIVLNGENALSIGNEEYKRAEMAFNYNFAGFTLLRY
QDVMYNNLSLGMGFKDLLGV

>d1xyza_ c.1.8.3 (A:) Xylanase {Clostridium thermocellum, XynZ}

NALRDYAEARGIKIGTCVNYPFYNNSDPTYNSILQREFSMVVCENEMKFDALQPRQNVDFDFSKGDQL
LAFERNGMQMRGHTLIWHNQNPVLTNGNWNDRSLLAVMKNHITVMTHEYKGVKIVEWDVANE
CMDDSGNGLRSSIWRNVIGQDYLDYAFRYAREADPDALLFYNDYNIEDLGPKSNAVFNMKSMKER
GVPIDGVGFQCHFINGMSPEYASIDQNIKRYAEIGVIVSFTEIDIRIPQSENPAATAFVQVQANNYKELMK
ICLANPNCNTFVMWGFDTKYTWIPGTFPGYGNPLIYDSNYNPKPAYNAIKEALM

>d1hiza_ c.1.8.3 (A:) Xylanase {*Bacillus stearothermophilus*, Xt6}

SYAKKPHISALNAPQLDQRYKNEFTIGAAVEPYQLQNEKDVQMLKRHFNSIVAENVMKPISIQPEEG
KFNFEQADRIVKFAKANGMDIRFHTLVWHSQVPQWFFLDKEGKPMVNETDPVKREQNKQLLLKR
LETHIKTIVERYKDDIKYWDVVNEVVGDDGKLNRSPWYQIAGIDYIKVAFQAARKYGGDNKLYMND
YNTEVEPKRTALYNLVKQLKEEGVPIDGIGHQSHIQIGWPSEAEIEKTINMFAALGLDNQITELDVSM
YGWPPRAYPTYDAIPKQKFLDQAARYDRLFKLYEKLSDKISNVTFWGIADNHTWLDSDRADVYYDAN
GNVVDPNAPYAKVEKGGKGDAPFVFGPDYKVKPAYWAIIDHK

>d1bg4_ c.1.8.3 (-) Xylanase {*Penicillium simplicissimum*}

EASVSIDAKFKAHGKYLGTIGDQYTLTKNTKNPAIIKADFGQLTPENSMKWDATEPNRGQFTFSGS
DYLVNFAQSNGKLIRGHTLVWHSQLPGWVSSITDKNTLISVLKNHITVMTRYKGIYAWDVLNEIF
NEDGSLRNSVFYNVIGEDYVRIAFETARSVDPAKLYINDYNLDSAGYSKVNGMVSHVKKWLAAGIP
IDGIGSQTHLGAGAGSAVAGALNALASAGTKEIAITELDIAGASSTDYVNVVNAACLNQAKCVGITVWG
VADPDSWRSSSSPLFDGNYNPKAAYNAIANAL

>d1edg_ c.1.8.3 (-) Endoglucanase CelA {*Clostridium cellulolyticum*}

MYDASLIPNLQIPQKNIPNNDGMNFVKGLRLGWNLGNTFDFANGTNTNELDYETSWSGIKTTKQ
MIDAIKQKGFNTVRIPVSWHPHVSGSDYKISDVWMNRVQEVVNYCIDNKMYVILNTHHDVVKVKG
YFPSSQYMASSKKYITSVWAQIAARFANYDEHLIFEGMNEPRLVGHANEWWPELTNSDVVDSINCIN
QLNQDFVNTVRATGGKNASRYLMCPGYVASPDGATNDYFRMPNDISGNNNKIIVSVHAYCPWNFAG
LAMADGGTNAWNINDSKDQSEVTWFMNINNYKTSRGIPVIIGECGAVDKNNLKTREYMSYYVA
QAKARGILCILWNNNFSGTGELFGFFDRRSCQFKFPEIIDGMVKYAFGLIN

>d1ceo_ c.1.8.3 (-) Endoglucanase CelC {*Clostridium thermocellum*}

MVSFKAGINLGGWISQYQVFSKEHFDTFITEKDIETIAEAGFDHVRLPFDYPIIESDDNVGEYKEDGLS
YIDRCLEWCKYNLGLVLDMMHAPGYRFQDFKTSTLFEDPNQKRFVDIWRFLAKRYINEREHIAF
ELLNQVVEPDSTRWNKLMLECIKAIREIDSTMWLYIGGNNYNSPDELKNLADIDDDYIVYNFHFYNP
FFFTHQKAHWSESAMAYNRTVKYPGQYEGIEEFVKNNPKYSFMMELNNLKNKELLRKDLKPAIEF
REKKKCKLYCGEFGVIAIADLESRIKWHEDEYISLLEEYDIGGAVWNYKKMDFEINYEDRKPVSQELVN
ILAR

>d1cz1a_ c.1.8.3 (A:) Exo-beta-(1,3)-glucanase {*Yeast (Candida albicans)*}

AWDYDNNVIRGVNLGGWFVLEPYMTPSLFEPFQNGNDQSGVPVDEYHWTQTLGKEAALRILQKH
WSTWITEQDFKQISNLGLNFVRIPIGYWAFQLLDNDPYVQGVQYLEKALGWARKNNIRVWIDLHG
APGSQNGFDNSGLRDSYNFQNGDNTQVTLNVLNITFKKYGGNEYSVVIGIELLNEPLGPVLNMDK
LKQFFLDGYNSLRQTGSVTPVIIHDAFQVFGYWNFLTVAEGQWNVVVDHHHYQVFSGGELSRNIN
DHISVACNWGWDAKKESHWNVAGEWSAALTDCAKWLNGVNRGARYEGAYDNAPYIGSCQPLLDIS
QWSDEHKTDTRRYIEAQLDAFEYTGGWVFWWSKTENAPEWSFQTLTYNGLFPQPVTDRQFPNQC
GFH

>d1ecea_ c.1.8.3 (A:) Endocellulase E1 {*Acidothermus cellulolyticus*}

AGGGYWHTSGREILDANNVPVRIAGINWFGFETCNVYVHGLWSRDYRSMLDQIKSLGYNTIRLPYS
DDILKPGTMPNSINFYQMNQDLQGLTSLQVMDKIVAYAGQIGLRIILDRHRPDCSGQSALWYTSSVSE
ATWISDLQALAQRYKGNPTVVGFDLHNEPHDPACWGGDPSIDWRLAAERAGNAVLSVNPPLLIFV
EGVQSYNGDSYWWGGNLQGAGQYPVVLNVPNRLVYSAHDYATSVYPQTFWSDPTFPNNMPGIWN
KNWGYLFNQNIAPVWLGEFGTTLQSTTDQTLWKTTLVQYLRPTAQYGADSFQWTFWSWNPDSGDT
GGILKDDWQTVDTVKGYLAPIKSSIFDPV

>d7a3ha_ c.1.8.3 (A:) Endoglucanase Cel5a {*Bacillus agaradhaerens*}

SVVEEHGQLSISNGELVNERGEQVQLKGMSSHGLQWYQGQFVNYESMKWLRDDWGINVFRAAMYTS

SGGYIDDPSVKEKVKAEVEAAIDLDIYVIIDWHILSDNDPNYKKEAKDFFDEMSELYGDYPNVIYEIA
NEPNGSDVTWGNQIKPYAEEVPIIRNNDPNIIIVGTGTWSQDVHHAADNQLADPNVMYAFHFYA
GTHGQNLRDQVDYALDQGAIFVSEWGTSAATGDGGVFLDEAQVWIDFMDERNLSWANWSLTHK
DESSAALMPGANPTGGWTEAELSPSGTFVREKIRE

>d1egza_ c.1.8.3 (A:) Endoglucanase Cel5a {*Erwinia chrysanthemi*}

SVEPLSVNGNKIYAGEKAKSFAGNSLFWSSNNGWGGEKFYTADTVASLKKDWKSSIVRAAMGVQESG
GYLQDPAGNKAKVERVVDAAIANDMYAIIGWHSASHAENNRSEAIRFFQEMARKYGNKPNVIYEIYN
EPLQVSWSENTIKPYAEAVISAIRAIDPDNLIIVGTSPWSQNVDEASRDPINAKNIAATLHFYAGTHGES
LRNKARQALNNGIALFVTEWGTVNADGNGGVNQTETDAWVTFMRDNNISNANWALNDKNEGAS
TYYPDSKNLTESGKKVKSIIQSWPYKA

>d1g0ca_ c.1.8.3 (A:) Alkaline cellulase K catalytic domain {*Bacillus* sp.}

PAGMQAVKSPSEAGALQLVELNGQLTLAGEDGTPVQLRGMSTHGLQWFGFGEIVNENAFVALSNDWGS
NMIRLAMYIGENGYATNPEVKDLVYEGIELAFEHDMYVIVDWHVHAPGDPRADVYSYGAYDFFEEIA
DHYKDHPKNHYIHWELANEPSPNNGGPGLTNDEKGEAVKEYAEPIVEMLREKGDNMILVGNPN
WSQRPDLSADNPIDAENIMYSVHFYTGSHGASHIGYPEGTPSSERSNVMANVRYALDNGVAVFATE
WGTSQLANGDGGPYFDEADVWLNFLNKHNSWANWSLTKNEISGAFTPFELGRDATDLDPGAN
QVWAPEELSLSGEYVRARIKIEYTPIDRTK

>d1bqca_ c.1.8.3 (A:) Beta-mannanase {*Thermomonospora fusca*}

ATGLHVKNRGLYEANGQEFIRGVSHPHNWYPQHTQAFADIKSHGANTVRVVLNSGVRWSKNGPSD
VANVISLCKQNRLICMLEVHDTTGYGEQSGASTLDQAVDYWIELKSVLQGEEDYVLINIGNEPYGNDS
ATVAAWATDTSAAIQLRAAGFEHTLVVDAPNWGQDWTNTMRNNADQVYASDPTGNTVFSIHMY
GVYSQASTITSYLEHFVNAGLPLIIGEFHGDHSDGNPDEDTIMAEAERLKLGYIGWSWSGNGGGVEY
LDMVYNFDGDNLSPWGERIFYGPNGIASTAKEAVIFG

>d1qnra_ c.1.8.3 (A:) Beta-mannanase {*Trichoderma reesei*}

ASSFVTISGTQFNIDGKVGYFAGTNCYWCFLTNHADVDSTFSHISSGLKVVVRVWGFNDVNTQPS
GQIWFQKLSATGSTINTGADGLQTLDYVVQSAEQHNKLIIPFVNNWSDYGGINAYVNAFGGNATT
WYTNTAAQTQYRKYVQAVVSRYANSTAIFAWELGNPRCNGCSTDVIVQWATSVSQQVKSLSNHLV
TLGDEGLGLSTGDGAYPYTYGEGTDFAKNVQIKSLDFGTFLHLYPDSWGTNYTWGNGWIQTHAAACL
AAGKPCVFEEYGAQQNPCTNEAPWQTTSLTRGMGGDMFWQWGDTFANGAQSNSDPYTVWYNS
SNWQCLVKNHVDAIN

>d1j9ya_ c.1.8.3 (A:) Mannanase 26A {*Pseudomonas fluorescens*, subsp. *cellulosa*}

PVTVKLVDSQATMETRSLFAFMQEQRHSIMFGHQHETTQGLTITRTDGTQSDTFNAVGDFAAVYG
WDTLSIVAPKAEGDIVAQVKKAYARGGIITVSSHFDNPKTDTQKGVWPVGTSDWQTPAVVDSLPGGA
YNPVLNGYLDQVAEWANLKDQGRLLIPVIFRLYHENTGSWFWWGDKQSTPEQYKQLFRYSVEYL
RDVKGVRNFLYAYSPNNFWDVTEANYLERYPGDEWVDVLGFDTYGPVADNADWFRNVVANAALVA
RMAEARGKIPVISEIGIRAPDIEAGLYDNQWYRKLISGLKADPDAREIAFLLVWRNAPQGVPGPNT
QVPHYWVPANRPENINNGTLEDFQAFYADEFTAFNRDIEQVYQRPT

>d1ghsa_ c.1.8.3 (A:) Plant beta-glucanases {Barley (*Hordeum vulgare*), 1,3-beta-glucanase}

IGVCYGVIGNLPSRSDVVQLYRSKINGMRIYFADGQALSALRNSGIGLILDIGNDQLANIAASTSNA
SWVQNNVRPYPAVNIKYIAAGNEVQGGATQSILPAMRNLAALSAAGLGAIKVSTSIRFDEVANSFP
PSAGVFKNAYMTDVARLLASTGAPLLANVYPYFAYRDNPGSISLNYATFQPGTTVRDQNNGLTYTSL
FDAMVDAVYAALEKAGAPAVKVVVSESGWPSAGGFAASAGNARTYNQGLINHVGGGTPKKREALET
YIFAMFNENQKTGDATERSFGLFNPDKSPAYNIQF

>d1aq0a_ c.1.8.3 (A:) Plant beta-glucanases {Barley (*Hordeum vulgare*)}

1,3-1,4-beta-glucanase}

IGVCYGMSANNLPAASTVVSFMFKSNGIKSMRLYAPNQAALQAVGGTGINVVVGAPNDVLSNLAASPA
AAASWVKSNIQAYPKVSFRYVVCVNEVAGGATRNLVLPAMKNVHGALVAAGLGHIVTTSVVSQAILGV
FSPPSAGSFTGEAAAFMGPVVQFLARTNAPLMANIYPYLAWAYNPSAMDMGYALFNASGTVVRDGA
YGYQNLFDTTVDAFYTAMGKHGGSSVKLVVSESGWPSGGTAATPANARFYNQHNLINHVGRGTPRH
PGAIETYIFAMFNENQKDSGVEQNWGLFYPNMQHVYPINF

>d1jz8a5 c.1.8.3 (A:334-625) beta-Galactosidase, domain 3 {Escherichia coli}

EVRIENGLLLLNGKPLLIRGVNRHEHHPLHGQVMDEQTMVQDILLMKQNNFNAVRCSHYPNHPLW
YTLCDRYGLYVVDEANIETHGMVPMNRLTDDPRWLPAMSERVTRMVQRDRNHPSVIIWSLGNESG
HGANDALYRWIKSVDPSPRPVQYEGGGADTTATDIICPMYARVDEDQPFPAVPKWSIKKWLSPGE
TRPLILCQYAHAMGNSLGGFAKYWQAFRQYPRLQGGFVWDWVDQSLIKYDENGNPWSAYGGDFGD
TPNDRQFCMNGLVFADRTPHPALTEAKHQQQ

>d1bhga3 c.1.8.3 (A:329-632) beta-Glucuronidase, domain 3 {Human (Homo sapiens)}

VAVTKSQFLINGKPFYFHGVNKHEDADIRGKGFDPVLLKDFNLLRWLGANAFRTSHYPYAEVVMQ
MCDRYGIVVIDECPGVGLALPQFFNNVSLHHHMQVMEEVRRDKNHPAVVMWSVANEPASHLESA
GYLKMVIAHTKSLDPSRPVTFVSNNSYAADKGAPYVDVICLSYYSWYHDYGHLELIQLQLATQFE
NWKYKQKPIIQSEYGAETIAGFHQDPPLMFTTEEQKSLLEQYHLGLDQKRRKYVVGELIWNFADF
MTEQSPTRVLGNKKGIFTRQRPKSAAFLLRERYWKIANE

>d1e0wa_ c.1.8.3 (A:) Xylanase A, catalytic core {Streptomyces lividans}

AESTLGAAAAQSGRYFGTAIASGRLSDSTYTSIAGREFNMVTAENEMKIDATEPQRGQFNFSADR
VYVAVQNGKQVRGHTLAWHSQQPGWMQSLSGSALRQAMIDHINGVMAHYKQKIVQWDVVNEAFA
DGSSGARRDSNLQRSGNDWIEVAFRTARAADPSAKLCYNDYNVENWWTWAKTQAMYNMVRDFKQR
GVPIDCVGFQSHFNSGSPYNSNFRTTLQNFALGVDVAITELDIQGAPASTYANVTNDCLAVSRCLGIT
VWGVVSDSWRSEQTPLLFNNDGSKKAAAYTAVLDALNG

>d1clxa_ c.1.8.3 (A:) Xylanase A, catalytic core {Pseudomonas fluorescens}

GLASLADFPIGVAVAASGGNADIFTSSARQNVRAEFNQITAENIMKMSYMYSGSNFSFTNSDRLVSW
AAQNGQTVHGHALVWHPYQLPNWASDSNANFRQDFARHIDTVAHFAGQVKSVDVVNEALFDS
ADDPDGRGSANGYRQSVFYRQFGGPEYIDEAFRRARAADPTAELYNDNFNTEENGAKTALVNLVQ
RLLNNGVPIDGVGFQMHVMNDYPSIANIRQAMQKIVALSPMLKIKITELDVRLNPNYDGNSSNDYTN
RNDCAVSCAGLDRQKARYKEIVQAYLEVPPGRRGGITVWGIADPDSWLYTHQNLDPWPLLFNDNL
QPKPAYQGVVEALS

>d1fxma_ c.1.8.3 (A:) Xylanase A, catalytic core {Thermoascus aurantiacus}

QAAQSVQDLIKARGKVYFGVATDQNRLTTGKNAIIQADFGQVTPENSMKWDATEPSQGNFNFAGA
DYLNVWAQQNGKLIRGHTLVWHSQVPSWVSSITDKNTLTNVMKNHITTLMTRYKQKIRAWDVVNE
AFNEDGSLRQTVFLNVIGEDIYPIAFQTARAADPNAKLYINDYNLDSASYPKTQAIVNRVKQWRAAG
VPIDGIGSQTHLSAGQAGVLQALPLLASAGTPEVAITELDVAGASPTDYVNVVNAACLVQSCVGITV
WGVADPDSWRASTTPLLFDGNFNPKPAYNAIVQDLQ

>d1tux_ c.1.8.3 (-) Xylanase A, catalytic core {Thermoascus aurantiacus}

AAAQSVQDLIDARGKVYFGVATDQNRLTTGKNAIIQADFGQVTPENSMKWDATEPSQGNFNFAGA
DYLNVWAQQNGKLIRGHTLVWHSQVPSWVSSITDKNTLTNVMKNHITTIMTRYKQKIRAWDVVNE
AFNEDGSLRQTVFNNVIGEDIYPIAFRTARAADPNAKLYINDYNLDSASKPKTSAIVKRVKKWRAAG
VPIDGIGSQTHLSAGQASIDAALPNLASAGTPEVAITELDIAGATSTDYVDVVNAACLDVDSIGITVW
GVADPDSWRASTTPLLFDGNFNPKPAYNAIVQLL

>d1xyfa2 c.1.8.3 (A:1-303) Xylanase A, catalytic core {Streptomyces olivaceoviridis}

AESTLGAAAAQSGRYFGTAIASGKLGDSAYTTIASREFNMVTAENEMKIDATEPQRGQFNFSAGDRV
YNWAVQNGKQVRGHTLAWHSQQPGWMQSLSGSTLRQAMIDHINGVMGHYKKGKIAQWDVVNEAF
SDDGSGRRDNLQRTGNDWIEVAFRTARAADPAAKLCYNDYNIENWTWAKTQGVYNNMVRDFKQ
RGVPIDCVGFQSHFNSGSPYNSNFRTTLQNFALGVDVAITELDIQGASSSTYAAVTNDCLAVSRCLGI
TVWGVDRDTSWRSGDTPLLFNGDGSKKAAAYTAVLNALNGG

>d1fh9a_ c.1.8.3 (A:) Xylanase A, catalytic core {Cellulomonas fimi}

ATTLKEAADGAGRDFGFALDPNRLSEAQYKAIADSEFNLVVAENAMKWDATEPSQNSFSFGAGDRV
ASYAADTGKELYGHTLVWHSQLPDWAKNLNGSAFESAMVNHVTKVADHFEGKVASWDVVNEAFA
DGGGRRQDSAFQKLGNGYIETAFAARAADPTAKLCINDYNVEGINAKSNSLYDLVKDFKARGVPL
DCVGFQSHLIVGQVPGDFRQNLQRFADLGVDRITELDIRMRTPSDATKLATQAADYKVVQACMQ
VTRCQGVTVWGITDKYSWVPDVPFGEAALVWDASYAKKPAYAAMVEAF

>d1e4mm_ c.1.8.4 (M:) Plant beta-glucosidase (myrosinase) {White mustard (Sinapis alba)}

EITCQENLPFTCGNTDALNSSSFSSDFIFGVASSAYQIEGTIGRGLNIWDGFTHRYPNKSGPDHNGD
TTCDSEFSYWKDIDVLDLDELNATGYRFSIAWSRIIPRGKRSRGVNEKGIDYYHGLISGLIKKGITPFVTLF
HWDLPQTLQDEYEGFLDPQIIDDFKDYADLCEFEFGDSVKYWLTINQLYSVPTRGYGSALDAPGRCS
PTVDPSCYAGNSSTEPYIVAHQLLAHAKVVDLYRKNYTHQGGKIGPTMITRWFLPYNDTRHSIAA
TERMKEFFLGWFMGLTNGTYPQIMIDTVGERLPSFSPEESNLVKGSYDFLGLNYYFTQYAQPSPNP
VNSTNHTAMMDAGAKLTYINASGHYIGPLFEKDKADSTDNIYYYPKGIYSVMDFKNKYNNPLIYVT
ENGISTPGDENRNQSM LDYTRIDYLCSHLCFLNKVIKEKDVNVKGYLAWALGDNYEFNKGFTVRFGL
LSYIDWNNVTDRDLKKSQWYQSFISP

>d1cbg_ c.1.8.4 (-) Plant beta-glucosidase (myrosinase) {Creeping white clover (Trifolium repens)}

FKPLPISFDDFSDLNRSCFAPGFVFGTASSAFQYEGAAFEDGKGPSIWDTFTHKYPEKIKDRTNGDVA
IDEYHRYKEDIGIMKDMNLDAYRFSISWPRVLPKGGKLSGGVNRGINYYNNLINEVLANGMQPYVTL
FHWDVPQALEDEYRGFLGRNIVDDFRDYAELCFKEFGDRVKHWITLNEPWGVMNAYAYGTFAPG
RCSDWLKLNCTGGDSGREPYLAAHYQLLAHAARLYKTKYQASQNGIIGITLVSHWFEPASKEKAD
VDAAKRGLDFMLGWFMHPLTKGRYPESMRYLVRKRLPKFSTEEKELTGSDFLGLNYYSSYAAKA
PRIPNARPAIQTDSLINATFEHNGKPLGPMMASSWLCIYPQGIRKLLLYVKNHYNNPVIYITENGRNE
FNDPTLSLQESLLDTPRIDYYRHLYYVLTALIGDGVNVKGYFAWSLFDNMEWDSGYTVRFGLVFVDF
KNNLKRHPKLSAHWFKSFLKK

>d1e55a_ c.1.8.4 (A:) Plant beta-glucosidase (myrosinase) {Maize (Zea mays), zmglu1}

VQMLSPSEIPQRDWFPSDFTFGAATSAYQIEGAWNEDGKGESNWDHFCHNHPERILDGSNSDIGAN
SYHMYKTDVRLKEMGMDAYRFSISWPRILPKGTKEGGINPDGIKYRNLINLLENGIEPYVTIFH
WDVPQALEEKYGGFLDKSHKSIVEDYTYFAKVCDFNFGDKVKNWLTFNDPQFTSFSYGTGVFAPG
RCSPGLDCAYPTGNSLVEPYTAGHNILLAHAEAVDLYNKHYKRDDTRIGLAFDVMGRVPYGTSLDK
QAEERSWDINLGWFLPVRGDYPPFSMRSLARERLPFFKDEQKEKLAGSYNMLGLNYYTSRFSKNI
DISPNYSVPLNTDDAYASQEVNGPDGKPIGPPMGNPWIMYPEGLKDLLMIMKNKYGNPPIYITENG
IGDVDTKETPLPMEAALNDYKRLDYIQRHIATLKESIDLSNVQGYFAWSLLDNFEWFAGFTERYGI
VYVDRNNNCTRYMKESAKWLKEFN TA

>d1pbga_ c.1.8.4 (A:) 6-phospho-beta-D-galactosidase, PGAL {Lactococcus lactis}

MTKTLPKDFIFGGATAAYQAEATHTDGKGPVAWDKYLEDNWYTAEPASDFYHKYPVDLELAEEY
GVNGIRISIAWSRIFPTGYGEVNEKGVFEYHKLFAECHKRHVPEFVTLHHFDTPEALHSNGDFLNRE
NIEHFIDYAAFCFEFPEVNYWTTFNEIGPIGDQYLVGKFPPIKYDLAKVQSHHNMVSHARAV
KLYKDKGYKGEIGVVHALPTKYPYDPENPADVRAAELEDIHKNKFI LDATYLGHYSDKTMEGVNHIL

AENGGELDLRDEDFQALDAAKDLNDFLGINYYMSDWMQAFDGETEIIHNGKGEKGSKYQIKGVGR
RVAPDYVPRTDWDWIIYPEGLYDQIMRVKNDYPNYKKIYITENGLGYKDEFVDNTVYDDGRIDYVK
QHLEVLSDAIADGANVKGYFIWLSLMDVFSWSNGYEKRYGLFYVDFDTQERYPKKSAHWYKLAET
QVIE

>d1e4ia_ c.1.8.4 (A:) Beta-glucosidase A {*Bacillus polymyxa*}

TIFQFPQDFMWTATAAYQIEGAYQEDGRGLSIWDTFAHTPGKVFNGDNGNVACDSYHRYEEDIRL
MKELGIRTYRFSVSWPRIFPNGDGEVNDKGLDYYHRVVDLLNDNGIEPFCTLYHWDLPQALQDAGG
WGNRRTIQAFVQFAETMFREFHGKIQHWLTFNEPWCIAFLSNMLGVHAPGLTNLQTAIDVGHLLLV
AHGLSVRRFRELGTSGQIGIAPNVSWAVPYSTSEEDKAACARTISLHSDWFLQPIYQGSYPQFLVDWF
AEQGATVPIQDGDMDIIGEPIDMIGINYSSMSVNRNFNEAGFLQSEEINMGLPVTDIGWPVESRGLYE
VLHYLQKYGNIDIYITENGACINDEVVNGKVQDDRRISYMQQHLVQVHRTIHDGLHVKGYMAWSLL
DNFEWAEGYNMRFGMIVHDFRTQVTRTPKQSYWYRNVVSNWLETRR

>d1qoxa_ c.1.8.4 (A:) Beta-glucosidase A {*Bacillus circulans*, subsp. *alkalophilus*}

SIHMFPSDFKVGWATAAYQIEGAYNEDGRGMSIWDTFAHTPGKVKNGDNGNVACDSYHRYEEDVQL
LKDLGVKVVYRFSISWPRVLPQGTGEVNRAGLDYYHRLVDELLANGIEPFCTLYHWDLPQALQDQGG
WGSRTIDAFAYEALMFKELGGKIKQWITFNEPWCMAFLSNYLGVHAPGNKDLQLAIDVSHLLVA
HGRAVTLFRELGISGEIGIAPNTSWAVPYRRTKEDMEACLVRNGWSDWYLDPIYFGEYPKFMLDW
YENLGYPPIVDGDMELIHQPIDFIGINYYTSSMNRYNPGEAGGMLSSEAISM GAPKTDIGWEIYAEG
LYDLLRYTADKYGNPTLYITENGACYNDGLSLDGRIHDQRRIDYLAMHLIQASRAIEDGINLKGME
WSLMDNFEWAEGYGMRFGLVHVDYDTLVRTPKDSFYWYKGVISRGWLDL

>d1gowa_ c.1.8.4 (A:) beta-Glycosidase {*Archaeon Sulfolobus solfataricus*}

MYSFPNSFRFGWSQAGFQSEMGTGSEDPNTDWYKWVHDPENMAAGLVSGDLPENGPYWGNY
KTFHDNAQKMGLKIARLNSEWSRQFPNPLPRPQNFEDESKQDVTEVEINENELKRLDEYANKDALN
HYREIFKDLKSRGLYFIQNMYYHWPLPLWLHDPVRRGDFTGPSGWLSTRTVYEFARFSAITAWKF
DDLVDYESTMNEPNVVGGLGYVGVKSGFPPGYLSFELSRRAMYNIQA HARAYDGIKSVSKKPVGIY
ANSSFPQLTDKMEAVEMAENDNRWWFFDAIIRGEITRGNEKIVRDDLKGRDLWIGVNYTTRTVV
KRTEKGYVSLGGYGHGCERNVSLAGLPTSDFGWEFFPEGLYDVLTKYWNRYHLYMYVTENGIADD
ADYQRPYYLVSHVYQVHRAINSGADVRYLHWSLADNYEWASGFMSRFGLLKVDYNTKRLYWRPS
ALVYREIATNGAITDEIEHLNSVPPVKPLRH

>d1qvba_ c.1.8.4 (A:) beta-Glycosidase {*Archaeon Thermosphaera aggregans*}

MKFPKDFMIGYSSSPFQFEAGIPGSEDPNSDWWWVHDPENTAAGLVSGDFPENGPYWNLNQN
DHDLAEKLVNTIRVGVESRIFPKPTFNVKVPVERDENGSIHVVDVDDKAVERLDELANKEAVNH
YVEMYKDWVERGRKLILNLYHWPLPLWLHNPIMVRRMGPDRAPSGWLNESVVEFAKYAAYIAW
KMGELPVMWSTMNEPNVVEYEQGYMFVKGGFPPGYLSLEAADKARRNMIQA HARAYDNIKRFSKK
PVGLIYAFQWFELLEGAEVFDKFKSSKLYYFTDIVSKGSSIINVEYRRDLANRLDWLGVNYYSRLVYK
IVDDKPIILHGYGFLCTPGGISPAENPCSDFGWEVYPEGLYLLKELYNRYGVDLIVTENGVS DSRDAL
RPAYLVSHVYSVWKAANEGIPVKGYLHWSLTDNYEWAQGFQKFGVLMVDFKTKKRYLRPSALVFR
EIATHNGIPDELQHLT LIQ

>d2hvm_ c.1.8.5 (-) Hevamine A (chitinase/lysozyme) {*Para rubber tree (Hevea brasiliensis)*}

GGIAIYWQNGNEGTLTQTCSTRKYSYVNIAFLNKFGNGQTPQINLAGHCNPAAGGCTIVSNGIRSCQ
IQGIKVMLSLGGGIGSYTLASQADAKNVADYLWNNFLGGKSSSRPLGDAVLGDIDFDIEHGSTLYWDD
LARYLSAYSKQGGKVVYLTAAAPQCPFPDRYLGTALNTGLFDYVWVQFYNNPPCQYSSGNINNIINSWN
RWTTTSINAGKIFLGLPAAPEAAGSGYVPPDVLISRILPEIKKSPKYGGVMLWSKFYDDKNGYSSSILDS

V

>d1nar_ c.1.8.5 (-) Seed storage protein {*Vicia narbonensis*, Narbonin}

PKPIFREYIGVKPNSTTLHDFPTEIINTETLEFHYILGFAIESYYESGKGTGTFEESWDVELFGPEKVK
NLKRRHPEVKVVISIGRGNVNTPFDPAEENVVWSNAKESLKLIIQKYSDDSGNLDGIDIHYEHRSDE
PFATLMGQLITELKKDDDLNINVVSIAPSENNSSHQKLYNAKKDYINWVDYQFSNQKQPVSTDDAF
VEIFKSLEKDYHPHKVLPGFSTDPLDTKHNKITRDIFIGGCTRLVQTFSLPGVFFWNANDSVIPKRDG
DKPFIVELTLQQLLAA

>d1cnv_ c.1.8.5 (-) Seed storage protein {Jack bean (*Canavalia ensiformis*), Concanavalin B}

DISSTEIAVYWGQREDGLLRDTCKTNNYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQI
KECQRMGVKVFLLALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVALDGIHFDIQKPVDE
LNWDNLLEELYQIKDVYQSTFLLSAAPGCLSPDEYLDNAIQTRHFDYIFVRFYNDRSCQYSTGNIQRI
RNAWLSWTKSVYPRDKNLFLELPASQATAPGGGYIPPSALIGQVLPYLPDLQTRYAGIALWNRQADK
ETGYSTNIIRYL

>d2ebn_ c.1.8.5 (-) Endo-beta-N-acetylglucosaminidase {*Flavobacterium meningosepticum*,
endoglycosidase F1}

TTKANIKLFSFTEVNDTNPLNNLNFTLNKNSGKPLVDMVVLFSANINYDAANDKVFSNPNVQHLL
TNRAYLKLPLQDKGIKIVLSILGNHDSRGIANLSTARAKAFAQELKNTCDLYNLDGVFFDDEYSAYQT
PPPSGFVTPSNNAARLAYETKQAMPNKLTVVYVSRSSFPATAVDGVNAGSYVDYAIHDIYGGSYDL
ATNYPGLAKSGMVMSSQEFNQGRYATAQALRNIVTKGYGGHMIFAMDPNRSNFTSGQLPALKLIAKE
LYGDELVYSNTPYSKDW

>d1eoka_ c.1.8.5 (A:) Endo-beta-N-acetylglucosaminidase {*Flavobacterium*
meningosepticum, endoglycosidase F3}

NGVCIAYYITDGRNPTFKLKDIPDKVDMVILFGLKYWSLQDTTKLPGGTGMMGSFKSYKDLDTQIRS
LQSRGIKVLQNIDDDVSWQSSKPGGFASAAAYGDAIKSIVIDKWKLDGISLDIEHSGAKPNPIPTFPGY
AATGYNGWYSGSMAATPAFLNVISELTKYFGTTAPNNKQLQIASGIDVYAWNKIMENFRNPNFYIQL
QSYGANVSRTQLMMNYATGTNKIPASKMVFYGAYAEGGTNQANDVEVAKWTPQTQGAKGGMMIYTYN
SNVSYANAVRDAVK

>d1edt_ c.1.8.5 (-) Endo-beta-N-acetylglucosaminidase {*Streptomyces plicatus*,
endoglycosidase H}

KQGPTSVAYVEVNNNSMLNVGKYTLADGGGNAFDVAVIFAANINYDTGKTAYLHFNENVQRVLDN
AVTQIRPLQQQGIVLVLGNHQQAGFANFSPQAASAFKQLSDAVAKYGLDGVDFDDEYAEYGN
NGTAQPNSSFVHLVTALRANMPDKIISLYNIGPAASRLSYGGVDVSDKFDYAWNPPYGTWQVPGIA
LPKAQLSPAAVEIGRTSRSTVADLARRTVDEGYGVYLYNLGGDRTADVSAFTRELYGSEAVRT

>d1edqa2 c.1.8.5 (A:133-443,A:517-563) Chitinase A, catalytic domain {*Serratia*
marcescens}

TDGSHLAPLKEPLLEKNKPYKQNSGKVVGSYFVEWGVYGRNFTVVKIPAQNLTHLLYGFIPICGGNGI
NDSLKEIEGSFQALQRSCQGREDFKVSIHDPFAALQKAQKGVTAWDDPYKGNFGQLMALKQAHPDL
KILPSIGGWTLSDPFFFMGDKVKRDRFVGSVKEFLQTKWFFDGDIDWEPGGKGANPNLGSPODQ
ETYVLLMKELRAMLDQLSVETGRKYELTSASAGKDKIDKVAYNVAQNSMDHIFLMSYDFYGAFDLK
NLGHQTALNAPAWKPDATYTTVNGVNALLAQGVKPGKIVVGTAMXDARSVQAKGKYVLDKQLGGL
FSWEIDADNGDILNSMNASLGNSAGVQ

>d1goia2 c.1.8.5 (A:3-291,A:380-446) Chitinase B, catalytic domain {*Serratia marcescens*}

TRKAVIGYFIPTNQINNYTETDTSVVPFVSNITPAKAKQLTHINFSFLDINSNLECAWDPATNDAK
ARDVVRNLTALKAHNPSLRIMFSIGGWYYSNDLGVSHANYVNAVKTASRAKFAQSCVRIMKDYGF

DGVNIDWEYPQAAEVDGFIAALQEIRTLNQQTITDGRQALPYQLTIAGAGGAFFLSRYYSKLAQIVA
PLDYINLMTYDLAGPWEKVTNHQAALFGDAAGPTFYNALREANLGWSWEELTRAFSPFSLTVDA
AVQQHLMMEGVPSAKIVMGVVPFXDDAESFKYKAKYIKQQQLGGVMFWHLGQDNRNGDLLAALDR
YFNAADYDDSQLDMGTGLRYTGVGPG

>d1d2ka1 c.1.8.5 (A:36-292,A:355-427) Chitinase 1 {Fungus (*Coccidioides immitis*)}
GGFRSVVYFVNWAIYGRGHNPQDLKADQFTHILYAFANIRPSGEVYLSDTWADTDKHYPGDKWDEP
GNNVYGCIKQMYLLKKNRNLKTLISIGGWYTPNFKTPASTEGRKKFADTSLKLMKDLGFDGIDI
DWEYPEDEKQANDFVLLKACREALDAYSAKHPNGKFKLLTIASPAGPQNYNKLKLAEMDKYLDF
WNLMAVDFSGSWDKVSGHMSNVFPSTTKPESTPFSSDKAVKDYIKAGVPANKIVLGMPLXDTVIA
GKKAHEYITKNGMGGGMWWESSDKTGNESLVGTVVNGLGGTGKLEQRENELSYPEVYDNLKNG
MPS

>d1e9la1 c.1.8.5 (A:22-266,A:337-393) Chitinase-like lectin ym1, saccharide binding domain
{Mouse (*Mus musculus*)}

YQLMCYYTSWAKDRPIEGSFKPGNIDPCLCTHLIYAFAGMQNNEITYTHEQDLRDYEALNGLKDN
TELKTLAIGGWKFGPAPFSAMVSTPQNRQIFIQSVIRFLRQYNFDGLNLDWQYPGSRGSPKDKHL
FSVLVKEMRKAFFEEESVEKDIPRLLTSTGAGIIVIKSGYKIPELSQSLDYIQVMTYDLHDPKDGTYG
ENSPLYKSPYDIGKSADLNVDISIYWKDHGAASEKLIVGFPAXDNVRSFKLKAQWLKDNNGGAVV
WPLDMDDFSGSFCHQRHFPLTSTLKGDLNIHSAS

>d1jfxa_ c.1.8.8 (A:) *Streptomyces lysozyme* {*Streptomyces coelicolor*, "mueller" dsm3030}
DTSGVQGIDVSHWQGSINWSSVKSAGMSFAYIKATEGTNYKDDRFSANYTNAYNAGIIRGAYHFARP
NASSGTAQADYFASNGGWSRDNRTPGVLDIEHNPSGAMCYGLSTTQMRTWINDFHARYKARTT
RDVVIYTTASWWNTCTGSWNGMAAKSPFWVAHWGVSAPTVPSPGFPTWTFWQYSATGRVGGVSG
DVEDRNFNGSAARLLALANNTA

>d1qba_3 c.1.8.6 (338-780) Bacterial chitinase (beta-N-acetylhexosaminidase) {*Serratia marcescens*}

FPYRGIFLDVARNFHKKDAVLRLLDQMAAYKLNKFHFLSDDEGWRIEIPGLPELTEVGGQRCHDLS
ETTCLLPQYQGPDPVYGGFFSRQDYIDIKYAARQIEVIPEIDMPAHARAAVVSMEARYKLLHAAGK
EQEANEFRLVDPTDTSNTTSVQFFNRQSYLNPCLDSSQRFVDKVIQEAQMHKEAGQPIKTWHFGG
DEAKNIRLGAGYTDKAKPEPGKGIIDQGNEDKPWAKSQCQTMKEGKVADMEHLPSYFGQEVSKL
VKAHGIDRMQAWQDGLKDAESSKAFATSRVGNFWDTLYWGGFDSVNDWANKGYEVVSNPDYV
YMDFPYEVNPDERGYWGTFRSDERKVFSAFDPNMPQNAETSVDNRDGNHFNKSDKPWPGAYGL
SAQLWSETQRTDPQMEYMIFPRALSVAERSWHRAGWEQDYRAGREYKG

>d1jaka1 c.1.8.6 (A:151-506) beta-N-acetylhexosaminidase {*Streptomyces plicatus*}

YAWRSAMLDVSRHFFGVDEVKRYIDRVARYKYNKLHLHLSDDQGWRIAIDSWPRLATYGGSTEVGG
GPGGYTKAKEYKEIVRYAASRHLEVVPEIDMPGHTNAALASYAELNCDGVAPPLYTGTKVGFSSLCVD
KDVTYDFVDDVIGELAALTPGRYLHIGGDEAHSTPKADFVAFMKRVQPIVAKYKGTVVGWHLAGA
EPVEGALVQYWGLDRTGDAEKAEVAAARNGTGLILSPADRTYLDMKYTKDTPGLSWAGYVEVQR
SYDWDPAGYLPGAPADAVRGVEAPLWTETLSDPDQLDYMAFPRLPGVAELGWSPASTHDWDTYKV
RLAAQAPYWEAAGIDFYRSPQVPWT

>d1iexa1 c.1.8.7 (A:1-388) Beta-D-glucan exohydrolase, N-terminal domain {Barley
(*Hordeum vulgare*)}

DYVLYKDATKPVEDRVADLLGRMTLAEKIGQMTQIERLVATPDVLRDNFIGSLLSGGGSVPRKGATAK
EWQDMVDGFQKACMSTRLGIPMIYGIDAVHGGQNNVYGATIFPHNVGLGATRDYPYLVKRIGEATALEV
RATGIQYAFAPCIAVCRDPRWGRCYESYSEDRRIVQSMTELIPGLQGDVDPKDFTSMPFVAGKNKVA

CAKHFVGDGGTVDGINENNTIINREGLMNIHMPAYKNAMDKGVSTVMISYSSWNGVKMHANQDLV
TGYLKDTLKFKGFVISDWEGIDRITTPAGSDYSYSVKASILAGLDMIMVPNKYQQFISILTGHVNGGVI
PMSRIDDAVTRILRVKFTMGLFENPYADPAMAEQLGKQEHRDLAREAARKS

>d1fcqa_ c.1.8.9 (A:) Bee venom hyaluronidase {Honeybee (*Apis mellifera*)}
EFNVYWNVPTFMCHKYGLRFEEVSEKYGILQNWMDKFRGEEIAILYDPGMFPALLKDPNGNVVAR
NGGVPQLGNLTKHLQVFRDHLINQIPDKSFPVGVGVIDFESWRPIFRQNWASLQPYKKLSVEVVRREH
PFWDDQRVEQEAKRRFEKYQLFMEETLKAAKRMRPAANWGYAYPYCYNLTPNQPSAQCEATT
MQENDKMSWLFESDVLPSVYLRWNLTSGERVGLVGGRVKEALRIARQMTTSRKKVLPYYWYKY
QDRRDTDLRADLEATLRKITDLGADGFIIWGSSDDINTKAKCLQFREYLNNELGPAVKR

>d1a4ma_ c.1.9.1 (A:) Adenosine deaminase (ADA) {Mouse (*Mus musculus*)}
TPAFNKPKVELHVHLDGAIKPETILYFGKKRGIALPADTVEELRNIIGMDKPLSLPGFLAKFDYMPV
IAGCREAIKRIAYEFVEMKAKEGVVYVEVRYSPHLLANSKVDMPMPWNQTEGDVTPDDVVLDVNQGL
QEGEQAFGIKVRSLCCMRHQPSWSLEVLELCKKYNQKTVMAMDLAGDETIEGSSLFPGHVEAYEGA
VKNGIHRTVHAGEVGSPEVVREAVDILKTERVGHGYHTIEDEALYNRLLKENMHFEVCPWSSYLTA
WDPKTTHAVVRFKNDKANYSLNTDDPLIFKSTLTDYQMTKKDMGFTEEEFKRLNINAAKSSFLP
EEEEKELLERLYREYQ

>d1j79a_ c.1.9.4 (A:) Dihydroorotase {*Escherichia coli*}
SQVLKIRRPDDWHLHLRDGDMLKTVVPTSEIYGRAIVMPNLAPPVTTVEAAVAYRQRILDAVPAP
HDFTPLMTCYLTDSLDPNELERGFNEGVFTAALY PANATTNSSHGVTSDAIMPVLERMEKIGMPL
LVHGEVTHADIDIFDREARFIESVMEPLRQRLTALKVVFEHITTKDAADYVRDGNERLAATITPQHL
MFNRNHMLVGGVRPHLYCLPILKRNIHQALRELVASGFQRVFLGTDSAPHARHRKESSCGCAGCFN
APTALGSYATVFEEMNALQHFEAFCSVNGPQFYGLPVNDTFIELVREEQQVAESIALTDDTLVPFLAG
ETVRWSVK

>d1k6wa2 c.1.9.5 (A:56-375) Cytosine deaminase catalytic domain {*Escherichia coli*}
PFVEPHIHLDTTQTAGQPNWNQSGTLFEGIERWAERKALLTHDDVKQRAWQTLKWQIANGIQHVR
THVDVSDATLTALKAMLEVKQEVAPWIDLQIVAFPQEGILSYPNGEALLEEALRLGADVGAIPHFEF
TREYGVESLHKTFALAQKYDRLIDVHCDEIDDEQSRFVETVAALAHHEGMGARVTASHTTAMHSYN
GAYTSRFLRLLKMSGINFVANPLVNIHLQGRFDYTPKRRGITRVKEMLESGINVCFGHDDVFDPWYP
LGTANMLQVLHMGLHVCQLMGYGQINDGLNLITHSARTLNLQDYGIAAGNSAN

>d1ejrc2 c.1.9.2 (C:1130-1422,C:1476-1567) alpha-subunit of urease, catalytic domain
{*Klebsiella aerogenes*}

GIDTHIHWICPQQAEEALVSGVTTMVGGGTGPAAGTHATTCTPGPWYISRMLQAADSLPVNIGLLGK
GNVSQPDALREQVAAGVIGLKIHEAWGATPAAIDCALTVADEMIDIQVALHSDTLNESGFVEDTLAAIG
GRTIHTFHTEGAGGGHAPDIITACAHPNLPSSNTPLPYTLNTIDEHLDMLMVCHHLDPDIAEDVAF
AESRIRRETIAEDVLHDLGAFSLTSSDSQAMGRVGEVILRTWQVAHRMKVQRGALAEETGDNDNF
RVKRYIAKYTINPALTHGIAHEVGXMFALGSARHHCRLTFLSQAAAANGVAERLNLRSIAIVVKGCR
TVQKADMVHNSLQPNITVDAQTYEVRVDGELITSEPADVLPMAQRYFLF

>d4ubpc2 c.1.9.2 (C:132-434,C:484-570) alpha-subunit of urease, catalytic domain {*Bacillus
pasteurii*}

GGIDTHVHFIPNDQVDVALANGITTLFGGGTGAEGSKATTVTPGPWNIEKMLKSTEGLPINVGILGK
GHGSSIAPIEQIDAGAAGLKIHEWDGATPASIDRSLTVADEADVQVAIHSDTLNEAGFLEDTLRAIN
GRVIHSFHVEGAGGGHAPDIMAMAGHPNVLPSSNTNPTRPFTVNTIDEHLDMLMVCHHLKQNIPEV
AFADSRIRPETIAAEDILHDLGIISMSTDALAMGRAGEMVLRTWQTADKMKKQRGPLAEENKNGSD
NFRLKRYVSKYTINPAIAQGIAHEVGSIEEGKFXDGLIHDTNITFMSKSSIQGVPAKLGLKRRIGT

VKNCRNIGKKDMKWNDVTTDIDINPETYEKVDGEVLTCEPVKELPMAQRYFLF
>d1e9yb2 c.1.9.2 (B:132-431,B:481-569) alpha-subunit of urease, catalytic domain {*Helicobacter pylori*}
GIDTHIHFISPPQIPTAFASGVTTMIGGGTGPADGTNATTITPGRRLKRWMLRAAEEYSMNLGFLAK
GNASNDASLADQIEAGAIGFKIHEDWGTTSPAINHALDVADKYDVQVAIHTDTLNEAGCVEDTMAAI
AGRTMHTFHTEGAGGGHAPDIKVEHNLIPASTNPTIPFTVNTEAEHMDMLMVCHHLDKSIKED
VQFADSRIRPQTIAAEDTLHDMGAFSITSSDSQAMGRVGEVITRTWQTADKNKKEFGRLKEEKGDN
DNFRIKRYLSKYTINPAIAHGISEYVGSVEVGKXHHGKAKYDANITFVSQAAYDKGIKEELGLERQVL
PVKNCRNVTKKDMQFNNTTAHIEVNPETYHVFDGKEVTSKPANKVSLAQLFSIF
>d1i0da_ c.1.9.3 (A:) Phosphotriesterase {*Pseudomonas diminuta*}
DRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRRARAAGVRTIVDVS
TFDIGRDVSLLAEVSRAADVHIVAATGLWFDPLSMRLRSVEELTQFFLREIQYGIEDTGIRAGIHKVAT
TGKATPFQELVLKAAARASLATGVPVTTHTAASQRDGEQQAIFESEGLSPSRVCIGHSDDTDDL
SYL TALAARGYLIGLDHIPHSAIGLEDNASASALLGIRSWQTRALLIKALIDQGYMKQILVSN
DWLFGFSSY VTNIMDVMDRVNPDGMAFIPLRVIPFLREKGVQPETLAGITVTNPARFLSPTLRAS
>d1bf6a_ c.1.9.3 (A:) Phosphotriesterase homology protein {*Escherichia coli*}
SFDPTGYTLAHEHLHIDLSGFKNNVDCRLDQYAFICQEMNDLMTRGVRNVIEMTNRYMGRNAQFM
LDVMRETGINVACTGYYQDAFFPEHVATRSVQELAQEMVDEIEQGIDGTELKAGIIAIEGTSE
GKITP LEEKVFIAAALAHNQTGRPISTHTSFSTMGLEQLALLQAHGVDLSRVTVGHCDLKNL
DNILKMIDL GAYVQFDTIGKNSYYPDEKRIAMHLALDRGLLRVMLSMDITRRSHLKANGGY
DYLLTTFIPQL RQSGFSQADVDVMLRENPSQFFQ
>d1jcla_ c.1.10.1 (A:) Deoxyribose-phosphate aldolase DeoC {*Escherichia coli*}
HMTDLKASSLRALKLMDLTLNDDDDTDEKVIACHQAKTPVGNTAAICYPRFIPIARKTLKEQ
GTP EIRIATVTNFPHGNDIDIALAETRAAIAYGADEVVFPYRALMAGNEQVGFDLVKACKEA
CAAAN VLLKVIETGELKDEALIRKASEISIKAGADFIKTSTGKVAVNATPESARIMMEVIR
DMGVEKTVGFKP AGGVRTAEDAQKYLAIADELFGADWADARHYRFGASSLLASLLKALGHG
>d1nal1_ c.1.10.1 (1:) N-acetylneuraminate lyase {*Escherichia coli*}
NLRGVMAALLTPFDQQALDKASLRRLVQFNQQGIDGLYVGGSTGEAFVQSLSEREQVLEI
VAEEGK GKIKLIAHVGCVTTAESQQLAASAKRYGFDAVAVTPFYYPFSFEEHCDHYRAI
IDSADGLPMVVYNIP ALSGVKLTLDQINTLVTLPGVGALKQTSGDLYQMEQIRREHPDL
VLYNGYDEIFASGLLAGADGGIGST YNIMGWRYQGIVKALKEGDIQTAQKLQTECNKVI
DLIKTG VFRGLKTVLHYMDVVSPLCRKPFPG VDEKYQPELKALAAQQLMQ
>d1f74a_ c.1.10.1 (A:) N-acetylneuraminate lyase {*Haemophilus influenzae*}
MRDLKGIFSALLVSFNEDGTINEKGLRQIIRHNIDKMKVDGLYVGGSTGENFMLSTEEKKEI
FRIAKD EAKDQIALIAQVGSVNLKEAVELGKYATELGYDCLSAVTPFYYPKFSFPEIKHY
YDTIIAETGSNMIVYSI PFLTGVNMGIEQFGELYKNPKVLGVKFTAGDFYLLERLKKAY
PNHLI WAGFDEMMLPAASLGV DGAI GSTFNVNGVRARQIFELTKAGKLKEALEIQHVT
NDLIEGILANGLYLTIKELLKLEGVDAGYCREPMTS KATAEQVAKAKDLKAKFLS
>d1dhpa_ c.1.10.1 (A:) Dihydrodipicolinate synthase {*Escherichia coli*}
MFTGSIVAIVTPMDEKGNVCRASLKKLIDYHVASGTSIVSVGTTGESATLNHDEHADVMM
TDLDA DGRIPVIAGTGANATAEAI SLTQRFNDSGIVGCLTVTPYYNRPSQEGLYQHFKAI
AEHTDLPQILYNVP SRTGCDLLPETVGR LAKVKNIIGIKEATGNLTRVNQIKELVSDDFV
LLSGDDASALDFMQLGGHGVISV TANVAARDMAQMCKLAAEGHFAEARVINQRLMPLHN
KLFVEPNPIPVKWACKELGLVATDTLRLP MTPITDSGRET VRAALKHAGLL

>d1qo5b_ c.1.10.1 (B:) Fructose-1,6-bisphosphate aldolase {Human (Homo sapiens), liver isozyme}

AHRFPALTQEKKELSEIAQSIVANGKGILAADESVMGNRLQRIKVENTEENRRQFREILFSVDSSI
NQSIGGVILFHETLYQKDSQGKLFNRNLIKKEGIVVGKLDQGGAPLAGTNKETTIGLDGLSERCAQYK
KDGVDGFKWRAVLRIADQCPSSLAIQENANALARYASICQQNGLVPIVEPEVIPDGDHDLHCQYVT
EKVLAAVYKALNDHHVYLEGTLLKPNMVTAGHACTKKYTPEQVAMATVTALHRTVPAAVPGICFLS
GGMSEEDATLNLNAINLCPLPKPWKLSFSYGRALQASALAAWGGKAANKEATQEAFMKRAMANCQ
AAKGQYVHTGSS

>d1adoa_ c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Rabbit (Oryctolagus cuniculus), muscle isozyme}

PHSHPALTPEQKKELSDIAHRIVAPGKGILAADESTGSIKRLQSIGTENTEENRRFYRQLLLTADDRV
NPCIGGVILFHETLYQKADDGRPFQVIKSKGGVVGKVDKGVVPLAGTNGETTTQGLDGLSERCAQY
KKDGADFAKWRCVLKIGEHTPSALAIMENANVLARYASICQQNGIVPIVEPEILPDGDHDLKRCQYV
TEKVLAAVYKALSDHHIYLEGTLLKPNMVTAGHACTQKYSHEEIAMATVTALRRTPPAVTVGVTFLS
GGQSEEEASINLNAINKCPLLPKWPALTFYGRALQASALKAWGGKKNLAAQEEYVKRALANSLAC
QGKYTSSGQAGAAASESLFISNHAY

>d1fdja_ c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Rabbit (Oryctolagus cuniculus), liver isozyme}

AHRFPALTPEQKKELSDIAQRIVANGKGILAADESVMGNRLQRIKVENSEENRRQFREILFTVDNS
INQSIGGVILFHETLYQKDSQGKLFNRNLIKKEGIVVGKLDQGGAPLAGTNKETTIGLDGLSERCAQY
KKDGVDGFKWRAVLRIADQCPSSLAIQENANTLARYASICQQNGLVPIVEPEVIPDGDHDLHCQYV
TEKVLAAVYKALNDHHVYLEGTLLKPNMVTAGHACTKKYTPEQVAMATVTALHRTVPAAVPGICFL
SGGMSEEDATLNLNAINLCPLPKPWKLSFSYGRALQASALAAWGGKAENKATQEAFMKRAVNC
QAAKGQYVHTGSSGAASTQSLFTASYTY

>d1fbaa_ c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Drosophila melanogaster}

TTYFNYPSELQDELREIAQKIVAPGKGILAADESVMGNRLQRIKQDQIGVENTEDNRRAYRQLLFSTDP
KLAENISGVILFHETLYQKADDGTPFAEILKKKGILGKVDKGVVPLFGSEDEVTTQGLDDLAARCAQ
YKKDGCDFAKWRCVLKIGKNTPSYQSILENANVLARYASICQSQRIVPIVEPEVLPDGDHDLDRQKQV
TETVLAAVYKALSDHHVYLEGTLLKPNMVTAGQSACKNTPEEIALATVQALRRTPPAVTVGVTFLSG
GQSEEEATVNLAINNVPLIRPWALTFYGRALQASVLRWAGKKENIAAGQNELLKRAKANGDAA
QGGYVAGSAGAGSGSLFVANHAY

>d1a5ca_ c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Plasmodium falciparum}

LPADVAEELATTAQKLVQAGKGILAADESTQTIKKRFDNIKLENTIENRASYRDLDFGTKGLKGFISGA
ILFEETLFQKNEAGVPMVNLHNNENIIPGIKVDKGLVNIPTDEEKSTQGLDGLAERCKEYKAGARF
AKWRTVLVIDTAKGKPTDLSIHETAWGLARYASICQQNRLVPIVEPEILADGPHSIEVCAVVTQKVLSC
VFKALQENGVLLEGALLKPNMVTAGYECTAKTTTQDVGFVTRTLRRTVPPALPGVVFLSGGQSEEE
ASVNLNSINALGPHPWALTFYGRALQASVLTWQGGKKNVAKAREVLLQRAEANSLATYGYKGG
AGG

>d1epxa_ c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Trypanosome (Leishmania mexicana)}

MSRVTVLQSQLPAYNRLKTPYESELIATVKKLTTPGKGLLADESIGSCTKRFQPIGLSNTEEHRRQY
RALMLEAEGFEQYISGVILHDETVGQKASNGQTFPEYLTARGVVPGIKTDMLCPLLEGAEGEQMTE
GLDGYVKRASAYYKKGCRFCKWRNVYKIQNGTVSESAVRFNAETLARYAILSQMSGLVPIVEPEVMI
DGKHDIDTCQRVSEHVWREVAALQRHGVWEGCLLKPNMVVPGAESGKTAPEQVAHYTVMTLA

RTMPAMPLPGVMFLSGGLSEVQASEYLNAINNSPLPRPYFLSFSYARALQSSALKAWGGKESGLAAGR
RAFLHRARMNSMAQLGKYKRSDD

>d1f2ja_ c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Trypanosome (Trypanosoma
brucei)}

SKRVEVLLTQLPAYNRLKTPYEALLETAKKMTAPGKLLAADESTGSCSKRFAGIGLSNTAEHRRQY
RALMLECEGFQYISGVILHDETVYQKAKTGETFPQYLRRRGVVPGIKTDCGLEPLVEGAKGEQMTA
GLDGYIKRAKKYYAMGCRFCKWRNVYKIQNGTVSEAVVRFNAETLARYAILSQCLGLVPIVEPEVMID
GTHDIETCQRVSQHVWSEVVSALHRHGCVWEGCLLKPNMVVPGAESGLKGHAEQVAEYTVKTLAR
VIPPALPGVTFLSGGLSEVMASEYLNAMNNCPLPRPWKLTFSYARALQSSAIKRWGGKESGVEAGR
AFMHRAKMNSLAQLGKYNRADD

>d1euaa_ c.1.10.1 (A:) KDPG aldolase {Escherichia coli}

MKNWKTSAESILTTGPVVPVIVVKKLEHAVPMAKALVAGGVRVLEVTLRTECAVDAIRIAKEVPEAI
VGAGTVLNPQQLAEVTEAGAQAFAISPGLTEPLLKAATEGTIPLIPGISTVSELMLGMDYGLKEFKFFPA
EANGGVKALQAIAGPFSQVRFPCPTGGISPANYRDYLALKSVLCIGGSWLVPADALEAGDYDRITKLAR
EAVEGAKL

>d1qfea_ c.1.10.1 (A:) Type I 3-dehydroquinase dehydratase {Salmonella typhi}

MKTVTVKNLIHIGEGMPKIIVSLMGRDINSVKAELAYREATFDILEWRVDHFMDIASTQSVLTAARVI
RDAMPDIPLFTFRSAKEGGEQTITTTQHYLTLNRAAIDSLVDMIDLELFTGDADV KATVDYAHAHN
VYVVMNSHDFHQTPSAEEMVSRRLRKMQUALGADIPKIAVMPQSKHDVLTLLTATLEMQQHYADRPVI
TMSMAKEGVISRLAGEVFGSAATFGAVKQASAPGQIAVNDLRSVLMILHNA

>d1i2oa_ c.1.10.1 (A:) Transaldolase {Escherichia coli}

TDKLTSLRQYTTVVADTGDIAAMKLYQPQDATTNPSLILNAAQIPEYRKLIDDAVAVAKQSNDRQA
QIVDATDKLAVNIGLEILKLVPGRISTAVDARLSYDTEASIAKAKRLIKLYNDAGISNDRILIKLASTWQ
GIRAAEQLEKEGINCNLTLLFSFAQARACAEAGVFLISPFVGRILDWYKANTDKKEYAPAEDPGVSV
SEIYQYYKEHGYESVVMGASFRNIGEILELAGCDRLTIAPALLKELAESEGAIERKLSYTGVEKARPARI
TESEFLWQHNDQPMVAVDKLAEGIRKFAIDQEKLEKMIGDLL

>d1f05a_ c.1.10.1 (A:) Transaldolase {Human (Homo sapiens)}

MESALDQLKQFTTVVADTGFHFAIDEYKQDATTNPSLILAAAQMPAYQELVEEAIAYGRKLGGSQE
DQIKNAIDKLVFLFGAEILKKIPGRVSTEVDARLSFDKAMVARARRLIELYKEAGISKDRILIKLSST
WEGIQAGKELEEQHGHCNMTLFSFAQAVACAEAGVTLISPFVGRILDWHVANTDKKSYEPLDPG
VKSVTKIYNYKKFSYKTIVMGASFRNTGEIKALAGCDFLTISP KLLGELLQDNAKLVVLSAKAAQAS
DLEKIHLDEKSFRLHNEQMAVEKLSDGIRKFAADAVKLERMLTERMFN

>d1dosa_ c.1.10.2 (A:) Fructose-bisphosphate aldolase {Escherichia coli}

SKIFDFVKPGVITGDDVQKVFQVAKENNFALPAVNCVGTDSINAVLETA AKVKAPVIVQFSNGGASFIA
GKGVKSDVPQGAAILGAISGAHHVHQMAEHYGVVILHTDHC AKKLLPWIDGLLDAGEKHFAATGK
PLFSSHMIDLSEESLQENIEICSKYLERMSKIGMTLEIELGCTGGEEDGVDNSHMDASALYTPEDVD
YAYTELSKISPRFTIAASFGNVHGVYKAGNVVLTPTILRDSQEYVSKHNLPHNSLNFVHGGSGSTA
QEIKDSVSYGVVKNIDTDTQWATWEGVLNYYKANEAYLQGQLGNPKGEDQPNKKYYDPRVWLR
AGQTSMIARLEKAFQELNAIDVL

>d1h7na_ c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
{Baker's yeast (Saccharomyces cerevisiae)}

MHTAEFLETEPTEISSVLAGGYNHPLL RQWQSERQLTKNMLIFPLFISDNPDFFTEIDSLPNINRIGV
NRLKDYKPLVAKGLRSVILFGVPLIPGKDPVGTAAADDPAGPVIQGIKFIREFPELYIICDVCLCEYTS
HGHCGLYDDGTINRERSVSRLLAAVAVNYAKAGAHCVAPSDMIDGRIRDIKRLINANLAHKTFVLSY

AAKFSGNLYGPFDAACSAPSNGDRKCYQLPPAGRGLARRALERDMSEGADGIIVKPSTFYLDIMRD
ASEICKDLPICAYHVSGEYAMLHAAAEEKGVVDLKTIAFESHQGFLRAGARLIITYLAPEFLDWLDE
>d1e51a_ c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
{Human (Homo sapiens)}

MQPQSVLHSGYFHPLLRWQTATTTLNASNLIYPIFVTDVDPDDIQPITSLPGVARYGVKRLEEMLRPL
VEEGLRCVLIFGVPSRVPKDERGSAADSEESPAIEAIHLLRKTFPNLLVACDVCLCPYTSHGHCGLLSE
NGAFRAEESRQLAEVALAYAKAGCQVVAPSDMMDGRVEAIKEALMAHGLGNRVSVMSYSKAFASC
FYGPFRDAAKSSPAFGDRRCYQLPPGARGLALRAVDRDREGADMLMVKPGMPYLDIVREVKDKH
PDLPLAVYHVSGEFAMLWHGAQAGAFDLKAAVLEAMTAFRRAGADIIITYYTPQLLQWLK

>d1b4ka_ c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
{Pseudomonas aeruginosa}

YPYTRLRRNRDDFSRRLVRENVLTVDLILPVFVLDGVDNQRRESIPSMGVERLSIDQLLIEAEWVA
LGIPALALFPVTPVEKKSLDAAEAYNPEGIAQRATRALRERFPELGIITDVALDPFTTHGQDGLDDD
GYVLNDVSDIVLRQALSHAEAGAQQVAPSDMMDGRIGAIRESAGHTNVRIMAYSAYKASAYYG
PFRDAVGSASNLGKGNKATYQMDPANSDEALHEVAADLAEGADMVMVKPGMPYLDIVRRVKDEFR
APTFFVYQVSGEYAMHMGAIQNGWLAESVILESLTAFKRAGADGILTYFAKQAAEQRLRR

>d1b4ea_ c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
{Escherichia coli}

TDLSQRPRRLRKSPALRAMFEETTLSLNDLVLPFVVEEIDDKAVEAMPGVMRIPEKHLAREIERIA
NAGIRSVMTFGISHHTDETGSDAWREDGLVARMSRICKQTVPEMIVMSDTCFCEYTSHGHCGLVKE
HGVDNDATLENLKGQAVVAAAAGADFIAPSAAMDGQVQAIRQALDAAGFKDTAIMSYSTKFASSFYG
PFREAAGSALKGDRKSYQMNPMNRREAIRESLLDEAQGADCLMVKPAYLDIVRELRETELPIGA
YQVSGEYAMIKFAALAGAIDEKVVLESLSIKRAGADLIFSIFALDLAEKKILR

>d1gg1a_ c.1.10.4 (A:) 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase (DAHPSynthase, AroG) {Escherichia coli}

DLRIKEIKELPPVALLEKFPATENAANTVAHARKAIHKILKGNDDRLLVIGPCSIHDPVAAKEYATR
LLALREELKDELEIVMRVYFEKPRTTVGWGLINDPHMNSFQINDGLRIARKLLLDINDSGLPAAG
EFLDMITPQYLADLMSWGAIGARTTESQVHRELASGLSCPVGFKNGTDGTIKVAIDAINAAGAPHCF
LSVTKWGHSAIVNTSGNGDCHIILRGGKEPNYSAKHVAEVKEGLNKAGLPAQVMIDFSHANSKQFK
KQMDVCADVCQQIAGGEKAIIGVMVESHLVEGNQSLESGEPLAYGKSITDACIGWEDTDALLRQLAN
AVKARR

>d1d9ea_ c.1.10.4 (A:) 3-deoxy-D-manno-octulosonate 8-phosphate synthase (KDO8P synthase) {Escherichia coli}

MKQKVVSIGDINVANDLPFVLFGGMNVLESRLAMRICEHYVTVTQKLGIPYVFKASFDKANRSSIH
SYRGPGLLEGMKIFQELKQTFGVKIITDVHEPSQAQPVADVVDVIQLPAFLARQTDLVEAMAKTGAVI
NVKKPQFVSPGQMGNIVDKFKEGGNEKVICDRGANFGYDNLVVDMLGFSIMKKVSGNSPVIFDVT
HALQCRDPFGAASGRRRAQVAELARAGMAVGLAGLFIEAHPDPEHAKCDGPSALPLAKLEPFLKQM
KAIDDLVKGFEELDTSK

>d1jcx_ c.1.10.4 (A:) 3-deoxy-D-manno-octulosonate 8-phosphate synthase (KDO8P synthase) {Aquifex aeolicus}

EKFLVIAGPCAIIESEELLLKVGEEIKRLSEKFKEVEFVFKSSFDKANRSSIHSFRGHGLEYGVKALRKV
KEEFLKITTDIHESWQAEPVAEVADIIQIPAFLCRQTDLLAAAKTGRAVNVKKGQFLAPWDTKNV
VEKLFKGGAKEIYLTERGTTFGYNNLVDFRSLPIMKQWAKVIYDATHSVQLPGGLGDKSGMREFI
FPLIRAAVAVGCDGVFMETHPEPEKALSASTQLPLSQLEGIIEAILEIREVASKYYETI

>d1onea1 c.1.11.1 (A:142-436) Enolase {Baker's yeast (*Saccharomyces cerevisiae*)}
SPYVLPVPFLNVLNNGGSHAGGALALQEFMIAPTGAKTFAEALRIGSEVYHNLKSLTKKRYGASAGNV
GDEGGVAPNIQTAEALDLIVDAIKAAGHDGKVKIGLDCASSEFFKDGKYDLDFKNPNSDKSKWLTG
PQLADLYHSLMKRYPIVSIEDPFAEDDWEAWSHFFKTAGIQIVADDLTVTNPKRIATAIEKKAADALL
LKVNQIGTLESSEKAAQDSFAAGWGMVSHRSGETEDTFIADLVVGLRTGQIKTGAPARSERLAKLN
QLLRIEEEELGDNAVFAGENFHHGDKL

>d1pdz_1 c.1.11.1 (140-433) Enolase {Lobster (*Homarus vulgaris*)}
DEVILPVPAFNVINGGSHAGNKLAMQEFMILPTGATSFTEAMRMGTEVYHHLKAVIKARFGLDATAV
GDEGGFAPNILNNDALDLIQEAIKKAGYTGKIEIGMDVAASEFYKQNNIYDLDFKTANNDGSQKISG
DQLRDMYMEFCKDFPIVSIEDPFDQDDWETWSKMTSGTTIQIVGDDLTVTNPKRITTAVEKKACKC
LLLKVNQIGSVTESIDAHLAKKNGWGMTVSHRSGETEDCFIADLVVGLCTGQIKTGAPCRSERLAK
YNQILRIEEELGSGAKFAGKNFRAPS

>d1e9ia1 c.1.11.1 (A:140-430) Enolase {*Escherichia coli*}
PGKYSMPVPMNIIINGGEHADNNVDIQEFMIQPVGAKTVKEAIRMGSEVFHHLAKVLKAKGMNTA
VGDEGGYAPNLGSNAEALAVIAEAVKAAGYELGKDITLAMDCAASEFYKDGKYVLAGEGNAFTSEE
FTHFLEELTKQYPIVSIEDGLDESDWDGFAYQTKVLGDKIQLVGDDLFVTNTKILKEGIEKGIANSILIK
FNQIGSLTETLAAIKMAKDAGYTAVISHRSGETEDATIADLAVGTAAGQIKTGSMRSRDRVAKYNQLIR
IEEALGEKAPYNGRKEIKGQ

>d1bqg_1 c.1.11.2 (144-422) D-glucarate dehydratase {*Pseudomonas putida*}
EGQQRDAVEMLGYLFYVGDNRKTDLGYRSEHEADNEWFRLRNKEALTPESVVALAEAAAYDRYGFK
DFKLKGGVLRGEDEIAAVTALSERFPDARITLDPNGAWSLKEAVALCRDQHHVLAEDPCGAENGY
SGREVMMAEFRRSTGLRTATNMIATDWRQMGHAIQLQSVDIPLADPHFWTMQGSVRVAQMCNEWG
LTWGSNSNNHFDISLAMFTHVAAAAPGNITADTHWIWQDQGRLTKEPLQIKGGLVEVPKPKPLGV
ELDWDALMKAHEVYKSM

>d1ec7a1 c.1.11.2 (A:138-446) D-glucarate dehydratase {*Escherichia coli*}
DGQQRSEVEMLGYLFFVGNRKATPLPYQSQPDDSCDWYRLRHEEAMTPDAVVRLAEAAAYEKYGFN
DFKLKGGVLAGEEEAESIVALAQRFPQARITLDPNGAWSLNEAIKIGKYLKGSLAYAEDPCGAEQGFS
GREVMMAEFRRATGLPTATNMIATDWRQMGHTLSLQSVDIPLADPHFWTMQGSVRVAQMCHEFGL
TWGSNSNNHFDISLAMFTHVAAAAPGKITADTHWIWQEGNQRLTKEPFEIKGGLVQVPEKPKPLGV
EIDMDQVMKAHELYQKHGLGARDAMGMQYLIPGWTFDNKRPCMV

>d1fhua1 c.1.11.2 (A:100-320) O-succinylbenzoate synthase {*Escherichia coli*}
QAANYRAAPLCNGDPDDLILKLADMPGEKVAKVKVGLYEAVRDGMVVNLLLEAIPDLHLRLDANRA
WTPLKGGQFQAKYVNPYRDRIAFLPECKTRDSDRAFARETGIAIAWDESLREPDFAFVAEEGVRAV
VIKPTLTGSLEKVREQVQAAHALGLTAVISSISSLGLTQLARIAAWLTPDTIPGLDLDLMAQQQVR
RWPGSTLPVVEVDALERLL

>d1muca1 c.1.11.2 (A:131-372) Muconate-lactonizing enzyme {*Pseudomonas putida*}
RVRDSLEVAWTLASGDTARDIAEARHMLEIRRHRVFKLKIGANPVEQDLKHVVTIKRELGDSASVRV
DVNQYWDESAIRACQVLGDNGIDLIEQPISRINRGGQVRLNQRTPAPIMADESIESVEDAFSLAADG
AASIFALKIAKNGGPRAVLRTAQIAEAAGIGLYGGTMLEGSIGTLASAHAFLTLRQLTWGTELFGLLLL
TEEIVNEPPQYRDFQLHIPRTPGLGLTLDEQLARFAR

>d2mnr_1 c.1.11.2 (133-359) Mandelate racemase {*Pseudomonas putida*}
PVQAYDSHSLDGVKLATERAVTAAELGFRAVKTIGYPALDQDLAVVRSIRQAVGDDFGIMVDYNQS
LDVPAAIKRSQALQQEGVTWIEPTLQHDYEGHQRIQSKLNVQMGENWLGPEEMFKALSIGACR
LAMPDAMKIGGVTGWIRASALAQQFGIPMSSHLFQEISAHLLAATPTAHWLERLDLAGSVIEPTLTF

EGGNAVIPDLPGVGIWREKEIGKYL

>d2chr_1 c.1.11.2 (127-370) Chlormuconate cycloisomerase {*Alcaligenes eutrophus*}
PLRSAIPIAWTLASGDTKRDLDSAVEMIERRRHNRFKVKLGFRSPQDDLHMEALSNSLGSKAYLRV
DVNQAWDEQVASVYIPELEALGVELIEQPVGRENTQALRRLSNRRVAIMADESLSTLASAFDLARD
RSVDVFLKLCNMGGVSATQKIAAAVEASGIASYGGTMLDSTIGTSVALQLYSTVPSLPGCELIGPFVL
ADTLSHEPLEIRDYELQVPTGVGHGMTLDEDEKVRQYARVS

>d1jpdx1 c.1.11.2 (X:114-321) L-Ala-D/L-Glu epimerase {*Escherichia coli*}
TLPETVITAQTVVIGTPDQMANSASTLWQAGAKLLKVLNHLISERMVAIRTAVPDATLIVDANES
WRAEGLAARCQLLADLGVAMLEQPLPAQDDAALENFIHPLPICADESCHTRS NLKALKGRYEMVNI
KLDKTGGLTEALALATEARAQGFSLMLGCMCLTSRAISAALPLVPQVSFADLDGPTWLAVDVEPALQ
FTTGELHL

>d1jpm1 c.1.11.2 (A:126-359) L-Ala-D/L-Glu epimerase {*Bacillus subtilis*}
YRDTLETDTVSVNSPEEMAADAENYLKQGFQTLKIKVGGKDDIATDIARIQEIRKRVGSVAVKLRLLDA
NQGWRPKEAVTAIRKMEDAGLIELVEQPVHKDDLGLKVTDTATDTPIMADESVFTPRQAFEVQLQ
TRSADLINIKLMKAGGISGAEKINAMAEACGVECMVGSMIETKLGITAAAHFAASKRNITRFDFDAPL
MLKTDVFNGGITYSGSTISMPGKPLGIIGAAL

>d1kcz1 c.1.11.2 (A:161-413) beta-Methylaspartase {*Clostridium tetanomorphum*}
GAEINAVPVFAQSGDDRYDNVDKMIKEADVLPALINNVEEKLGKGEKLEEVKWLDRDRIKLRV
REDYAPIFHIDVYGTIGAAFDVDIKAMADYIQTAEAAKPFHLRIEGPMDVEDRQKQMEAMRDLRA
ELDGRGVDAELVADEWCNTVEDVKFFTDNKAGHMVQIKTPDLGGVNNIADAIMYCKANGMGAYCG
GTCNETNRSAEVTTNIGMACGARQVLAKPGMGVDEGMMIVKNEMNRVLALVGRRK

>d1kko1 c.1.11.2 (A:161-411) beta-Methylaspartase {*Citrobacter amalonaticus*}
PCVPEAIPLFGQSGDDRYAVDKMILKGVVLPALINNVEEKLGFKGEKLEEVVWLSDRILSLRSS
PRYHPTLHIDVYGTIGLIFDMDPVRCAEYIASLEKEAQGLPLYIEGPVDAGNKPDQIRMLTAITKELTR
LGSVKVADEWCNTYQDIVDFTDAGSCHMVQIKTPDLGGIHNIVDAVLYCNKHGMEAYQGGTCNET
EISARTCVHVALAARPMRMLIKPGMGFDEGLNIVFEMNRTIALLQT

>d1a49a2 c.1.12.1 (A:12-115,A:218-395) Pyruvate kinase, N-terminal domain {*Rabbit (Oryctolagus cuniculus)*}
IQTQQLHAAMADTFLEHMCRLDIDSAPITARNTGICTIGPASRSVETLKEMIKSGMNVARMNFSHG
THEYHAETIKNVRTATESFASDPILYRPVAVALDTKGXPVSEKDIQDLKFGVEQDVMVFASFIRKA
ADVHEVRKILGEKGNIKIISKIENHEGVRRFDEILEASDGIMVARGDLGIEIPAEKVFLAQKMIIGRCN
RAGKPVICATQMLESMIKKPRPTRAEGSDVANAVLDGADCIMLSGETAKGDYPLEAVRMQHLIAREA
EAAMFHRKLFE

>d1pkla2 c.1.12.1 (A:1-87,A:187-357) Pyruvate kinase, N-terminal domain {*Leishmania mexicana*}
SQLAHNLTLSIFDPVANYRAARIICTIGPSTQSVEALKGLIQSGMSVARMNFSHGSHEYHQTTINNR
QAAAEELGVNIAIALDTKGPXPAVSAKDRVDLQFGVEQGVDMIFASFIRSAEQVDVRKALGPKGRDIM
IICKIENHQGVQNIDSIIIESDGIMVARGDLGVEIPAEKVVAQKILISKCNVAGKPVICATQMLESMY
NPRPTRAEVSDVANAVFNGADCVMLSGETAKGKYPNEVVQYMARICLEAQSAL

>d1a3wa2 c.1.12.1 (A:2-87,A:189-366) Pyruvate kinase, N-terminal domain {*Baker's yeast (Saccharomyces cerevisiae)*}
SRLERLTSLNVVAGSDLRRTSIIGTIGPKTNNPETLVALRKAGLNIVRMNFSHGSYEHKSVIDNARKS
EELYPRPLAIALDTKGPALSEKDKEDLRFVGNVHMFVASFIRTANDVLTIREVLGEQKDVKIIV
KIENQQGVNFDLILKVTDGVMVARGDLGIEIPAEVLAQKLIKSNLAGKPVICATQMLESMY

NPRPTRAEVSDVGNAILDGCVMLSGETAKGNYPINAVTTMAETAVIAEQAIAYLPNYD
>d1e0ta2 c.1.12.1 (A:1-69,A:168-344) Pyruvate kinase, N-terminal domain {Escherichia coli}
MKKTKIVCTIGPKTESEEMLAKMLDAGMNVMLNFSHGDYAEHGQRIQNLNRVMSKTGKTAAILL
DTKGXPALAEKDKQDLIFGCEQGVDFVAASFIRKRSVDVIEIREHLKAHGGENIHIISKIENQEGLNDFD
EILEASDGIMVARGDLGVEIPVEEVIFAQKMMIEKICIRARKVVITATMMLDMSMIKNRPTDAEAGDVA
NAILDGTDAVMLSGESAKGKYPLEAVSIMATICERTDRVMNSRLE
>d1kbla1 c.1.12.2 (A:510-873) Pyruvate phosphate dikinase, C-terminal domain
{Clostridium symbiosum}
IETQEASVSGSERIMVWADKFRTLKVRTNADTPEDTLNAVKLGAEGIGLCRTEHMFEEADRIMKIR
KMILSDSVEAREEALNELIPFQKGFKAMYKALEGRPMTVRYLDPPLHEFVPHTEEEQAELAKNMG
LTLAEVKAKVDELHEFNPMMGHRGRLAVTYPEIAKMQTRAVMEAAIEVKEETGIDIVPEIMIPLVG
EKKELKFVKDVVVEVAEQVKKEKGSMDQYHIGTMIEIPRAALTADAIAEEAEFFSFGTNDLTQMTFG
FSRDDAGKFLDSYKAKIYESDPFARLDQTVGVQLVEMAVKKGRTQTRPGLKCGICGEHGGDPSSVEF
CHKVGLNYVSCSPFRVPIARLAAAQAALNN
>d1fiy_ c.1.12.3 (-) Phosphoenolpyruvate carboxylase {Escherichia coli}
QYSALRSNVSMGLKVLGETIKDALGEHILERVETIRKLSKSSRAGNDANRQELLTTLQNLNDELPLV
ARAFSQFLNLANTAEQYHSISPKEAASNPEVIARTLRKLNQPELSEDTIKKAVESLSLELVLAHPT
EITRRTLHKMVEVNACLKQLDNKDIADYEHNLQMRRLRQLIAQSWHTDEIRKLRPSPVDEAKWGF
AVVENSLWQGVPNYLRELNEQLEENLGYPVEFVVRFTSWMGGDRDGNPNVTADITRHVLLLS
RWKATDLFLKDIQVLVSELSMVEATPELLALVGEEGAEPYRYLMKNLRSRLMATQAWLEARLKGE
ELPKPEGLLTQNEELWEPLYACYQSLQACGMGIIANGDLLDLRVRKCFGVPLVRIDIRQESTRHTEA
LGELTRYLGIGDYESWSEADKQAFILRELNSKRPLLPRNWQPSAETREVLDTQCQVIAEAPQGSIAAYV
ISMAKTPSDVLAVHLLLKEAGIGFAMPVAPLFTLDDLNNANDVMTQLLNIDWYRGLIQGKQMMVI
GYSDSAKDAGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAAHALLSQPPGSLKG
GLRVTEQGEMIRFKYGLPEITVSSLSLYTGAILEANLLPPEPKESWRRIMDELVSISCDVYRGYVREN
KDFVPYFRSATPEQELGKLPLGSRPAKRRPTGGVESLRAIPWIFAWTQNRMLPAWLGAQTALQKV
VEDGKQSELEAMCRDWPFFSTRLGMLEMVFAKADLWLAEYDQRLVDKALWPLGKELRNLQEEDI
KVVLAIANDSLHMLADLPWIAESIQLRNIYTDPLNVLQAELLHRSRQAEKEGQEPDPRVEQALMVTIA
GIAAGMRNTG
>d1pyma_ c.1.12.4 (A:) Phosphoenolpyruvate mutase {Blue mussel (Mytilus edulis)}
VKKTTQLKQMLNSKDLFIMEAHNGLSARIVQEAGFKGIWGSGLSVSAQLGVRDSNEASWTQVVEV
LEFMSDASDVPILLDADTYGNFNARRLVRKLEDRGVAGACLEDKLFPKTNSLHDGRAQPLADIEE
FALKIKACKDSQTDPDFCIVARVEAFIAGWGLDEALKRAEAYRNAGADAILMHSKKADPSDIEAFMK
AWNNQGPVVIVPTKYKTPTDHFRDMGVSMMVIWANHNLRASVSAIQTTKQIYDDQSLVNVEDKIV
SVKEIFRLQRDDELVQAEDKYLKPN
>d1dxea_ c.1.12.5 (A:) 2-dehydro-3-deoxy-galactarate aldolase {Escherichia coli}
DVFPNKFKAAALAAKQVQIGCWSALSNPISTEVLGLAGFDWLVDGEHAPNDISTFIPQLMALKGSAS
APVVRVPTNEPVIKRLLDIGFYNFLIPFVETKEEAELAVASTRYPPPEGIRGVSVSHRANMFGTVADYF
AQSNKNITILVQIESQQGVDNVDAAATEGVGIFVGPSDLAAALGHLGNASHPDVQKAIQHIFNRAS
AHGKPSGILAPVEADARRYLEWGATFVAVGSDLGVFRSATQKLADTFKK
>d1dqua_ c.1.12.6 (A:) Isocitrate lyase {Aspergillus nidulans}
SYIEEDQRYWDEVAAVKNWWKDSRWRYTKRPFTAEQIVAKRGNLKIEYPSNVQAKKLWGILERN
FKNKEASFTYGCLDPTMVTQMAKYLDTVYVSGWQSSSTASSTDEPSPDLADYPMNTVFNKVNHLW
MAQLFHDRKQREERMTTPKDQRHKVANVDYLRPIADADTGHGGLTAVMMLTKLKFVERGAAGIHIE

DQAPGTTKCGHMAGKVLVPISEHINRLVAIRAQADIMGTDLLAIARTDSEAATLITSTIDHRDHPFIIG
STNPDIQPLNDLMVMAEQAGKNGAELQAIEDEWLAKAGLKLFNDAVVDAINNSPLPNKKAIEKYL
TQSKGKSNEARAIAKEIAGTDIYFDWEAPRTREGYYRYQGGTQCAINRAVAYAPFADLIWMESKLP
DYKQAKEFADGVHAVWPEQKLAYNLSPFNWKKAMPREDEQETYIKRLGALGYAWQFITLAGLHTT
ALISDTFAKAYAKQGMRAYGELVQPEMANGVDVVTHQKWSGANYVDNMLKMITGG

>d1f8ma_c.1.12.6 (A:) Isocitrate lyase {Mycobacterium tuberculosis}

ASVVGTPKSAEQIQEWDTNPRWKDVTRTYSAEDVVALQGSVVEEHTLARRGAEVLWEQLHDLE
WVNALGALTGNMAVQQVRAGLKAIYLSGWQVAGDANLSGHTYPDQSLYPANSVPQVRRINNALQ
RADQIAKIEGDTSVENWLAPIVADGEAGFGGALNVYELQKALIAAGVAGSHWEDQLASEKKCGHLG
GKVLIPTQQHIRTLTSARLAADVADVPTVVIARTDAEAATLITSDVDERDQPFITGERTREGFYRTKN
GIEPCIRAKAYAPFADLIWMETGTPDLEAARQFSEAVKAEYPDQMLAYNCSPFNWKKHLDDATIA
KFQKELAAMGFKFQFITLAGFHALNYSMFDLAYGYAQNQMSAYVELQEREFAAEERGYTATKHQRE
VGAGYFDRIATTVPNSSTTALTGSTEEGQF

>d1igwa_c.1.12.6 (A:) Isocitrate lyase {Escherichia coli}

KTRTQQIEELQKEWTQPRWEGITRTPYSAEDVVKLKRGSVNPECTLAQLGAAKMWRLHGESKKGVI
NSLGALTGGQALQAKAGIEAVYLSGWQVAADANLAASMYPDQSLYPANSVPAVVERINNTFRAD
QIQWSAGIEPGDPRYVDYFLPIVADAEAGFGGVLNAFELMKAMIEAGAAVHFEDQLASVKKCGHM
GGKVLVPTQEAQKLVAARLCADVTGVPTLLVARTDADAADLITSDCDPYDSEFITGERTSEGFFRTH
AGIEQAISRGLAYAPYADLVWCETSTPDLELARRFAQAIHAKYPGKLLAYNCSPFNWQKNLDDKTIA
SFQQQLSDMGYKQFITLAGIHSWFMFDFLANAYAQGEKMKHYVEKVQQPEFAAAKDGYTFVSH
QQEVGTGYFDKVTTHIQG

>d1d8ca_c.1.13.1 (A:) Malate synthase G {Escherichia coli}

QTITQSRLRIDANFKRFVDEEVLPGTGLDAAAFWRNFDEIVHDLAPENRQLLAERDRIQAALDEWH
RSNPGPVKDKAAYKSFLRELGYLVPQPERVTVETTGIDSEITSQAGPQLVVPAMNARYALNAANARW
GSLYDALYGSDIIPQEGAMVSGYDPQRGEQVIAWVRRFLDESLPLENGSYQDVVAFKVVDKQLRIQLK
NGKETTLPAPQFVGYRGDAAAPTCLLKNNGLHIELQIDANGRIGKDDPAHINDVIVEAAISTILDCE
DSVAAVDAEDKILLYRNLLGLMQGTLQEKMEKNGRQIVRKLNDDRHYTAADGSEISLHGRSLLFIRN
VGHLM TIPVIWDSEGNEIPEGILDGVMGTGAIALYDLKVQKNSRTGSVYIVKPKMHGPQEVAFANKLF
TRJETMLGMAPNTLKMIMDEERTSLNLRSCIAQARNRVAFINTGFLDRTGDEMHSVMEAGPML
RKNQMKSTPWIKAYERNNVLSGLFCGLRGKAQIGKGMWAMPDLMADMYSQKGDQLRAGANTAW
VPSPTAATLHALHYHQTNVQSVQANIAQTEFNAEFELLDLLTIPVAENANWSAQEIQQELDNNV
QGILGYVVRWVEQGIGCSKVPDIHNVALMEDRATLRISSQHIANWLRHGILTKEVQASLENMAKV
DQQNAGDPAYRPMAGNFANSCAFKAASDLIFLGVKQPNQGYTEPLLHAWRLREKES

>d3rubl1_c.1.14.1 (L:148-467) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Tobacco (Nicotiana tabacum), variant turkish samsun}

FQGPPIHQVERDKLNKYGRPLLGCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMR
WRDRFLFCAEALYKAQAETGEIKGHYLNATAGTCEMIKRAVFARELGPVIMHDYLTGGFTANTSL
AHYCRDNGLLLHIHRAMHAVIDRQKNHGIHFRVLAKALRMSGGDHIHSGTVVGKLEGERDITLGFV
DLLRDDFVEQDRSRGIYFTQDWVSLPGVLPVASGGIHWHPALTEIFGDDSVLQFGGMLTGHWPWG
NAPGAVANRVALEACVKARNEGRDLAQEGNEIIREACKWSPELAAACEVWKEIVF

>d1bura1_c.1.14.1 (A:148-475) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Spinach (Spinacia oleracea)}

FQGPPIHQVERDKLNKYGRPLLGCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMR
WRDRFLFCAEALYKAQAETGEIKGHYLNATAGTCEDMMKRAVFARELGPVIMHDYLTGGFTANTT

LSHYCRDNGLLLHIHRAMHAVIDRQKNHGMHFRVLAKALRLSGGDHIHSGTVVVGKLEGERDITLGF
VDLLRDDYTEKDRSRGIYFTQSWVSTPGVLPVASGGIHVWHMPALTEIFGDDSVLQFGGGTGLGHPW
GNAPGAVANRVALEACVQARNEGRDLAREGNTIREATKWSPELAAACEVWKEIKFEFPAMDTV
>d1bwva1 c.1.14.1 (A:150-478) Ribulose 1,5-bisphosphate carboxylase-oxygenase
{Galdieria partita}

GPATGVILERERLDKFRPLLGGCTTKPKLGLSGKNYGRVVYEALKGGLDFVKDDENINSQPFMRWR
ERYLFTMEAVNKASAATGEVKGHYLNVTAAATMEEMYARANFAKELGSVIIMIDLVIQYTAIQTMKW
ARDNDMILHLHRAGNSTYSRQKNHGMNFRVICKWMRMAGVDHIHAGTVVVGKLEGDPIITRFGYKT
LLLPKLERNLQEGFFDMEWASLRKVMPPVASGGIHAGQMHQLIHYLGEDVVLQFGGGTIGHPDGIQ
AGATANRVALEAMILARNENRDYLTEGPEILREAAKTCCGALRTALDLWKDITFNYTSTDTSDFV

>d1gk8a1 c.1.14.1 (A:150-475) Ribulose 1,5-bisphosphate carboxylase-oxygenase
{Chlamydomonas reinhardtii}

GPPHGIQVERDKLNKYGRLLGCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMRWR
DRFLFVAEAIYKAQAETGEVKGHYLNATAGTCEEMMKRAVCAKELGVPIIMHDYLTGGFTANTSLAIY
CRDNGLLLHIHRAMHAVIDRQRNHGIHFRVLAKALRMSGGDHLHSGTVVVGKLEGEREVTLGFVDL
MRDDYVEKDRSRGIYFTQDWCSMPGVMPPVASGGIHVWHMPALVEIFGDDACLQFGGGTGLGHPWG
NAPGAAANRVALEACTQARNEGRDLAREGGDVIRSACKWSPELAAACEVWKEIKFEFDTIDKL

>d1bxna1 c.1.14.1 (A:151-467) Ribulose 1,5-bisphosphate carboxylase-oxygenase
{Alcaligenes eutrophus}

FAGPSTGIIVERERLDKFRPLLGATTKPKLGLSGRNYGRVVYEGLKGGLDFMKDDENINSQPFMHW
RDRFLFVMDAVNKASAATGEVKGSYLNVTAGTMEEMYRRAEFAKSLGSVIIMVDLIVGWTCIQSMS
NWCQRQNDMILHLHRAGHGTYTRQKNHGVSFVIAKWLRLAGVDHMHTGTAVGKLEGDPLTVQGY
YNVCRDAYTQTDLTRGLFFDQDWASLRKVMPPVASGGIHAGQMHQLIHLFGDDVVLQFGGGTIGHPQ
GIQAGATANRVALEAMVLARNEGRDILNEGPEILRDAARWCGPLRAALDTWGD

>d1rbla1 c.1.14.1 (A:148-475) Ribulose 1,5-bisphosphate carboxylase-oxygenase
{Synechococcus sp., strain pcc 6301}

FQGPPIHGIQVERDLLNKYGRPMLGCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENINSQPFQR
WRDRFLFVADAIHKSQAETGEIKGHYLNVTAPTCEEMMKRAEFAKELGMPIIMHDFLTAGFTANTT
LAKWCRDNGVLLHIHRAMHAVIDRQRNHGIHFRVLAKCLRLSGGDHLHSGTVVVGKLEGDKASTLGF
VDLMREDHIEADRSRGVFFFTQDWASMPGVLPPVASGGIHVWHMPALVEIFGDDSVLQFGGGTGLGHP
WGNAPGATANRVALEACVQARNEGRDLYREGGDILREAGKWSPELAAALDLWKEIKFEFETMDKL

>d5rubal c.1.14.1 (A:138-457) Ribulose 1,5-bisphosphate carboxylase-oxygenase
{Rhodospirillum rubrum}

GPSVNISALWKVLGRPEVDGGLVVGTHIIPKLGRLPKPFAEACHAFWLGGDFIKNDPQGNQPFAPL
RDTIALVADAMRRAQDETGEAKLFSANITADDPFEIARGEYVLETFGENASHVALLVDGYVAGAAAI
TTARRRFPDNFLHYHRAGHGAVTSPQSKRGYAFVHCKMARLQGASGIHTGTMGFGKMEGESSDR
AIAYMLTQDEAQGPFYRQSWGGMKACTPIISGGMNALRMPGFFENLGNANVILTAGGAFGHIDGPV
AGARSLRQAWQAWRDGVPVLDYAREHKEKELARAFESFPGDADQIYPGWRKALGV

>d1geha1 c.1.14.1 (A:137-443) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Archaeon
Thermococcus kodakaraensis}

DGPAFGIEGVRKMLEIKDRPIYGVVPPKPKVGYSPPEFEKLAYDLLSNGADYMKDDENLTSPWYNRFE
ERAEIMAKIIDKVENETGEKKTWFANITADLLEMEQRLEVLADLGLKHAMVDVVITGWGALRYIRD
LAADYGLAIHGHRAMHAAFTRNPHYGISMFLAKLYRLIGIDQLHVGTAGAGKLEGGKWDVIQNARI
LRESHYKPDENDVFHLEQKFYSIKAAPTSSGGLHPGNIQPVIEALGTDIVLQLGGGTGLGHPDGPAAAG

ARAVRQAIDAIMQGIPLDEYAKTHKELARALEKWGHVTP

>d1qtwa_ c.1.15.1 (A:) Endonuclease IV {*Escherichia coli*}

MKYIGAHVSAAGGLANAAIRAAEIDATAFALFTKNQRQWRAAPLTTQTIDEFKAAACEKYHYTSAQIL
PHDSYLINLGHVPTEALEKSRDAFIDEMQRCEQLGLSLLNFHPGSHLMQISEEDCLARIAESINIALD
KTQGVTAVENTAGQGSNLGFKFEHLAAIIDGVEDKSRVGCIDTCHAFAGAAGYDLRTPAECEKTFADF
ARTVGFKYLRGMHLNDAKSTFGSRVDRHSLGEGNIGHDAFRWIMQDDRFDGIPLILETINPDIWA
EEIAWLKAQQTEKAVA

>d1d8wa_ c.1.15.2 (A:) L-rhamnose isomerase {*Escherichia coli*}

TQLEQAWELAKQRFAAVGIDVEEALRQLDRLPVSMHCWQGDDVSGFENPEGSLTGGIQTGNYPGK
ARNASELRADLEQAMRLIPGPKRLNLHAIYLESPTVSRDQIKPEHFKNWVEWAKANQLGLDFNPS
CFSHPLSADGFTLSHADDSIRQFWIDHCASRRVSAYFGEQLGTPSVMNIWIPDGMKDITVDR LAPR
QRLAALDEWISEKLNPAHHIDAVESKLFGIGAESYTVGSNEFYMGYATSRQTALCLDAGHFHPTEVIS
DKISAAMLYVPQLLLHVS RPVRWSDHVVLLDDETQAIASEIVRHDLFDRVHIGLDFFDASINRIAA
WVIGTRNMKKALLRALLEPTAELRKLEAPGDYARLALLEEQKSLPWQAVWEMYCQRHDT PAGSE
WLESVRAYEKEILSRR

>d1dxia_ c.1.15.3 (A:) D-xylose isomerase {*Streptomyces murinus*}

MSFQPTPEDRFTFGLWTVGWQGRDPFGDATR PALDPVETVQRLAELGAYGVTFHDDDLIPFGSSDT
ERESHKFRFRQALDATGMTVPMATTNLFTHPVFKDGGFTANDRDVRRYALRKTIGNIDLAAELGAK
TYVAWGGREGAESGAKDVRDALDRMKEAFDLLGEYVTAQGYDLRFAIEPKPNEPRGDILLPTVGH
ALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGKLFHIDLNGQSGIKYDQDLRFGAGDL
RAAFWLVDLLETAGYEGPRHFDFKPPRTEDFDGVWASAAGCMRNYLILKDRAAA FRADPEVQEAL
RAARLDQLAQPTAADGLDALLADRAAFEDFDVDA AAAARGMAFEHLDQLAMDHLLGARG

>d2gyia_ c.1.15.3 (A:) D-xylose isomerase {*Streptomyces olivochromogenes*}

YQPTPEDRFTFGLWTVGWQGRDPFGDATR PALDPVETVQRLAELGAHGVTFHDDDLIPFGSSDTER
ESHKFRFRQALDATGMTVPMATTNLFTHPVFKDGGFTANDRDVRRYALRKTIRNIDLAVELGAKTYV
AWGGREGAESGA AKDVRVALDRMKEAFDLLGEYVTSQGYDTRFAIEPKPNEPRGDILLPTVGHALA
FIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGKLFHIDLNGQSGIKYDQDLRFGAGDLRAA
FWLVDLLESAGYEGPRHFDFKPPRTEDIDGVWASAAGCMRNYLILKERAAA FRADPEVQEALRASR
LDELAQPTAADGVQELLADRTAFEDFDVDA AAAARGMAFERLDQLAMDHLLGAR

>d1xis_ c.1.15.3 (-) D-xylose isomerase {*Streptomyces rubiginosus*}

NYQPTPEDRFTFGLWTVGWQGRDPFGDATRRALDPVESVRR LAELGAHGVTFHDDDLIPFGSSDSE
REEHVKRFRQALDDTG MKVPMATTNLFTHPVFKDGGFTANDRDVRRYALRKTIRNIDLAVELGAET
YVAWGGREGAESGAKDVRDALDRMKEAFDLLGEYVTSQGYDIRFAIEPKPNEPRGDILLPTVGHAL
AFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGKLFHIDLNGQNGIKYDQDLRFGAGDLR
AAFWLVDLLESAGYSGPRHFDFKPPRTEDFDGVWASAAGCMRNYLILKERAAA FRADPEVQEALRA
SRLDELARPTAADGLQALLDDRS AFEEFDVDA AAAARGMAFERLDQLAMDHLLGARG

>d1qt1a_ c.1.15.3 (A:) D-xylose isomerase {*Streptomyces diastaticus*, M1033}

SYQPTPEDKFTFGLWTVGWQGRDPFGDATRGALDPAESVRR LAELGAHGVTFHDDDLIPFGATDSE
RAEHKFRFRQGLDETGMKVP MATTNLFTHPVFKDGGFTANDRDVRRYALRKTIRNIDLAVELGAQT
YVAWGGREGAESGA AKDVRVALDRMKEAFDLLGEYVTSQGYDTPFAIEPKPNEPRGDILLPTIGHAL
AFIDGLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGKLFHIDLNGQSGIKYDQDLRFGPGDLRA
AFWLVDLLESAGYEGPRHFDFKPPRTEDFDGVWASAAGCMRNYLILKERAAA FRADPEVQEALRA
ARLDELAQPTAGDGLQALLPDRSAFEDFD PDA AAAARGMAFERLDQLAMDHLLGARG

>d4xiaa_ c.1.15.3 (A:) D-xylose isomerase {*Arthrobacter*, strain b3728}

VQPTPADHFTFGLWTVGWGTGADPFGVATRANLDPVEAVHKLAEELGAYGITFHNDLIPFDATAAER
EKILGDFNQALADTGLKVPMTTTLNLSHPVFKDGGFTSNDRSIRRFALAKVLHNIDLAAEMGAETF
VMWGGREGSEYDGSKDLAAALDRMREGVDTAAGYIKDKGYNLRIALEPKPNEPRGDIFLPTVGHGL
AFIEQLEHGDIVGLNPETGHEQMAGLNFTHGIAQALWAEKLFHIDLNGQRGIKYDQDLVFGHGDLTS
AFFTVDLLENGFPNGGPKYTGPRHFDYKPSRTDGYDGVWDSAKANMSMYLLKERALAFRADPEV
QEAMKTSGVFELGETTLNAGESAADLMNDSASFAGFDAEAAAERNFAFIRLNQLAIEHLLGSR

>d1xima_c.1.15.3 (A:) D-xylose isomerase {Actinoplanes missouriensis}

VQATREDKFSFGLWTVGWQARDAFGDATRTALDPVEAVHKLAEIGAYGITFHDDDLVFPGSDAQTR
DGIAGFKKALDETGLIVPMVTTNLFTHPVFKDGGFTSNDRSVRRYAIRKVLQMDLGAELGAKTLV
LWGGREGAEYDSAKDVSAALDRYREALNLLAQYSEDRGYGLRFAIEPKPNEPRGDILLPTAGHAIAFV
QELERPELFGINPETGHEQMSNLNFTQGIAQALWHKLLFHIDLNGQHGPKFDQDLVFGHGDLNLF
SLVDLLENGPDGAPAYDGPRHFDYKPSRTEDYDGVWESAKANIRMYLLKERAKAFRADPEVQEAL
AASKVAELKTPTLNPGEGYAELLADRSFEDYDADAVGAKGFGFVKLNQLAIEHLLGAR

>d1a0ca_c.1.15.3 (A:) D-xylose isomerase {Clostridium thermosulfurogenes, also known as
Thermoanaerobacter thermosulfurigenes}

NKYFENVSKIKYEGPKSNNPYSFKFYNPEEVIDGKTMEEHLRFSIAYWHTFTADGTDQFGKATMQR
PWNHYTDPMDIAKARVEAAFEFFDKINAPYFCFHDRDIAPEGDTLRETNNKLDTIVAMIKDYLKTS
KTKVLWGTANLFSNPRFVHGASTSCNADVFAYSAAQVKKALEITKELGGENYVFWGGREGYETLLN
TDMEFELDNFARFLHMAVDYAKEIGFEGQFLIEPKPKPEPTKHQYDFDVANVLAFLRKYDLDKYFKV
NIEANHATLAFHDFQHELRYARINGVLGSIDANTGDMLLGWDTDQFPDIRMTTLAMYEVIKMGGF
DKGGLNFDKVRRAFEPEDLFLGHIAGMDAFAKGFVAYKLVKDRVFDKFIERYASYKDGIGADIV
SGKADFRSLEKYALERSQIVNKSGRQELLESILNQYLFA

>d1a0da_c.1.15.3 (A:) D-xylose isomerase {Bacillus stearothermophilus}

PYFDNISTIAIEGPKSNPLAFKFYNPEEKVGDKTMEEHLRFSVAYWHTFTGDGSDPFGAGNMIRP
WKNYSGMDLAKARVEAAFEFFKLNIPFFCFHVDVIAPEGETLKETYKNLDIIVDMIEEYMKTSKTK
LLWNTANLFTHPRFVHGAATSCNADVFAAAAQVKKGLEIAKRLGAENYVFWGGREGYETLLNTD
MKLELDNLARFLHMAVDYAKEIGFDGQFLIEPKPKPEPTKHQYDFDVATALAFLQTYGLKDYFKFNIE
ANHATLAGHTFEHELVRARIHGMLGSVDANQGDMLLGWDTDEFPTDLYSTTLAMYEILKNGGLGR
GGLNFDKVRRAFEPEDLFYAHAGMDSFAVGLKVAHRLIEDRVFDEFIEERYKSYTEGIGREIVEGT
ADFHKLEAHALQLGEIQNSGRQERLKTLLNQYLLEVC

>d1a0ea_c.1.15.3 (A:) D-xylose isomerase {Thermotoga neapolitana}

AEFFPEIPKVQFEGKESTNPLAFKFYDPEEIIDGKPLKDLKFSVAFWHTFVNEGRDPFGDPTADRP
WNRYPMDKAFARVDALFEFCEKLNIEYFCFHDRDIAPEGKTLRETNNKILDKVVERIKERMKDSN
VKLLWGTANLFSHPRYMHGAATTCADVFAAAAQVKKALEITKELGGEGYVFWGGREGYETLLNT
DLGFELENLARFLRMAVDYAKRIGFTGQFLIEPKPKPEPTKHQYDFDVATAYAFKSHGLDEYFKFNIE
ANHATLAGHTFQHELMARILGKLSIDANQGDLLLGWDTDQFPTNVYDTTLAMYEVIKAGGFTK
GGLNFDKVRRAFEPEDLFIGHIAGMDTFALGFKVAYKLVKDGVLDFIEEKYRSFREGIGRDIVEG
KVDFEKLEEYIIDKETIELPSGKQEYLESLINSYIVKTILELR

>d1bxca_c.1.15.3 (A:) D-xylose isomerase {Thermus aquaticus, subsp. Caldophilus}

MYEPKPEHRFTFGLWTVGNVGRDPFGDAVRERLDPVYVGHKLAEELGVHGVNLHDEDLIPRGTPPQ
ERDQIVRRFKRALDETGLKVPMTGNLFSDPGFKDGGFTSRDPWVRAYAFRKSLETMDLGAELGAE
IYVVWPGREGAEVEATGKARKVWDVWREPLNFMAAYAEDQGYGYRFALEPKPNEPRGDIYFATVG
SMLALIHTLERPERFGLNPEFAHETMAGLNFVHAVAQALDAGKLLHIDLNGQRMNRFQDLRFGSE
NLKAAFLLDLLESSGYQGPRHFDHALRTEDEEGVWAFARGCMRTYLILKERAEAFREDPEVKEL

LAAYYQEDPAALPLMDPYSHEKAEALKRAELPLEAKRHRGYALERLDQLAVEYLLGVRG
>d1bxba_ c.1.15.3 (A:) D-xylose isomerase {Thermus aquaticus, subsp. Thermophilus}
MYEPKPEHRFTFGLWTVGNVGRDPFGDAVRERLDPVYVVHKLAE LGAYGVNLHDEDLIPRGTPPQE
RDQIVRRFKKALDETLGLKVPMTANLFSDFPAFKDGAFTSPDPWVRAYALRKSLETMDLGAELGAEI
YVVWPGREGAEVEATGKARKVWDWVREALNFMAAYAEDQGYGYRFALEPKPNEPRGDIYFATVGS
MLAFIHTLDRPERFGLNPEFAHETMAGLNFVHAVAQALDAGKLFHIDLNDQRMRSRFDQLRFGSE
NLKAAFFLVDLLESSGYQGPRHFDHALRTEDEEGVWAFARGCMRTYLILKERAEAFREDPEVKEL
LAAYYQEDPAALALLGPYSREKAEALKRAELPLEAKRRRGYALERLDQLAVEYLLGVRG

>d1luca_ c.1.16.1 (A:) Bacterial luciferase (alkanal monooxygenase) {Vibrio harveyi}
MKFGNFLTLYQPPELSQTEVMKRLVNLGKASEGCGFDTVWLEHHFTEFGLLGNPYVAAAHLGAT
ETLNVGTAAIVLPTAHPVRQAEDVNLLDQMSKGRFRFGICRGLYDKDFRVFGTDMDNSRALMDCW
YDLMKEGFNEGYIAADNEHIKFPKIQLNPSAYTQGGAPVYVVAESASTTEWAAERGLPMILSWIINT
HEKKAQLDLYNEVATEHGVDVTKIDHCLSYITSVDHDSNRAKDCRNFLGHWYDSYVNATKIFDDSD
QTKGYDFNKGQWRDFVLKGHKDTNRRIDYSYEINPVGTPPEECIAHQDIDATGIDNICCGFEANGSE
EIIASMKLFQSDVMPYLKEKQ

>d1lucb_ c.1.16.1 (B:) Bacterial luciferase (alkanal monooxygenase) {Vibrio harveyi}
MKFGLFFLNFNMNSKRSSDQVIEEMLDTAHYVDQLKFDTLAVYENHFSNNGVVGAPLTVAGFLLGMT
KNAKVASLNHVITTHHPVRVAEEACLLDQMSEGRFAFGFSDCEKSADMRFNRPTDSQFQLFSECH
KIINDAFTTGYCHPNDFYSFPKISVNPFAFTEGGPAQFVNATSKEVVEWAAKGLPLVFRWDDSNA
QRKEYAGLYHEVAQAAGVDVSQVRHKLTLVNQNVGDGAAARAEARVYLEEFVRESYSNTDFEQKMG
ELLSENAIGTYEESTQAARVAIECCGAADLLMSFESMEDKAQQRAVIDVNNANIV

>d1nfp_ c.1.16.2 (-) Non-fluorescent flavoprotein (luxF, FP390) {Photobacterium leiognathi}
MTKWNYGVFFLNFYHVGQEQPSLTMSNALETLRIIDEDTSIYDVVAFSEHHIDKSYNDETKLAPFVS
LGKQIHVLATSPETVVKAAKYGMPLLFKWDDSQQKRIELLNHYQAAAAKFNVDIANVRHRLMLFV
NVNDNPTQAKAELSIYLEDYLSYTAETSIDEIINSNAAGNFDCLHHVAEMAQGLNKNKVDFLFCFE
SMKDQENKKSMLINFDKRVINRKEHNLN

>d1fvpa_ c.1.16.2 (A:) Non-fluorescent flavoprotein (luxF, FP390) {Photobacterium
phosphoreum}
MNKWNYGVFFVNFYKNGQEQPSKTMNNALETLRIIDEDTSIYDVINIDDHYLVKKDSEDKKLAPFIT
LGEKLYVLATSENTVDIAAKYALPLVFKWDDINEERLKLKLSFYNASASKYNKNIDLVRHQMLHVN
NEAETVAKEELKLYIENYVACTQPSNFGSIDSIIQSNVTGSYKDCLSYVANLAGKFDNTVDFLLCFES
MQDQNKKSVMIDLNNQVIKFRQDNNLI

>d1ezwa_ c.1.16.3 (A:) Coenzyme F420 dependent tetrahydromethanopterin reductase
{Archaeon Methanopyrus kandleri}
AEVSFGIELLPDDKPTKIAHLIKVAEDNGFEYAWICDHYNNSYMGVLTAAVITSKIKLPGGITNPYT
RHPLITASNIATLDWISGGRAIIGMGPDKATFDKMGLPFPCKIPIWNPEAEDEVGPATAIREVKEVIY
QYLEGGPVEYEGKYVKTGTADVARSIQGSDIPFYMGAQGPIMLKTAGEIANGVLVNASNPKDFEVA
VPKIEEGAKEAGRSLDEIDVAAYTCFSIDKDEDKAIEATKIVVAFIVMGSPDVVLERHGIDTEKAEQIA
EAIGKGFDTAIGLVDEDMIEAFSIAGDPDVTVDKIEELLKAGVTQVVVGSPIGPDKEKAIELVGQEVI
PHFK

>d1f07a_ c.1.16.3 (A:) Coenzyme F420 dependent tetrahydromethanopterin reductase
{Archaeon Methanobacterium thermoautotrophicum}
MKFGIEFVNEPIEKIVKLVKLAEDVGFYAWITDHYNNKNVYETLALIAEGTETIKLPGVTPNPYVR
SPAITASAIATLDELNSGRATLGIGPDKATFDALGIEWVKPVSTIRDAIAMMRTLLAGEKTESGAQL

MGVKAVQEKIPIYMGAQGPMLKTAGEISDGALINASNPKDFEAAVPLIKEGAEAAGKSIADIDVAAY
TCCSIDEDAAAAANAAKIVVAFIAAGSPPVFERHGLPADTGKKFGELLGKGDFFGAIGAVDDALME
AFSVVGTPEDEFIPKIEALGEMGVTQYVAGSPIGPDKEKSIKLLGEVIASF

>d1qapa1 c.1.17.1 (A:130-296) Quinolinic acid phosphoribosyltransferase, C-terminal domain {*Salmonella typhimurium*}

VASEVRRYVGLLAGTQTQLLDTRKTLPLGLRTALKYAVLCGGGANHRLGLTDAFLIKENHIIASGVRQ
AVEKAFWLHPDVPVEVEVENLDELDDALKAGADIIMLDNFNTDQMREAVKRVNGQARLEVSGNVT
AETLREFAETGVDFISVGALTKHVRLDLSMRFC

>d1qpoa1 c.1.17.1 (A:117-285) Quinolinic acid phosphoribosyltransferase, C-terminal domain {*Mycobacterium tuberculosis*}

IATATAAWVDVAVRGTKAKIRDTRKTLPLGLRALQKYAVRTGGGVNHRLGLGDAALIKDNHVAAGSV
VDALRAVRNAAPDLPCEVEVDSLEQLDAVLPEKPELILLDNFAVWQTQTAVQRRDSRAPVMLESS
GGLSLQTAATYAETGVLDYLAVALGTHSVRLDIGLDM

>d1qasa3 c.1.18.1 (A:299-625) Phospholipase C isozyme D1 (PLC-D1) {*Rat (Rattus norvegicus)*}

DQPLSHYLVSSSHNTYLLLEDQLTGPSSTEAYIRALCKGCRCLELDCWDGPNQEPIIYHGYTFTSKILFC
DVLRAIRDYAFKASPYPVILSLENHCSLEQQRVMARHLRAILGPILLDQPLDGVTTSLSPEQLKGGKIL
LKGKLLGGLLPAGGENGSEATDVSDEVEAAEMEDEAVRSQVQHKPKEDKLLKLPESDMIIYCKSVH
FGGFSSPGTSGQAFYEMASFESRALRLLQESNGFVRHNVSCLSRIYPAGWRTDSSNYSVEMWNG
GCQIVALNFQTPGPEMDVYLGCFQDNGGCGYVLKPAFLRDPNTTFNSRALTQGPW

>d2ptd_ c.1.18.2 (-) Phosphatidylinositol-specific phospholipase C {*Bacillus cereus*}

ASSVNELENWSKWMQPIPDISIPLARISIPGTHDSGTFKLQNPQVWGMTQEYDFRYQMDHGARIF
DIRGLTDDNTIVLHHGPLYLYVTLHEFINEAKQFLKDNPSETIIMSLKKEYEDMKGAEDFSSTFEK
KYFVDPIFLKTEGNIKLGDARGKIVLLKRYSGSNEPGGYNNFYWPDNETFTTTVNQANVTVQEKY
KVSYDEKVKSIKDTMETMNSEDLNHLYINFNTSLSSGGTAWNSPYYYASYINPEIANIYIKQKNPARV
GWVIQDYINEKWSPLLYQEIVIRANKSLI

>d2plc_ c.1.18.2 (-) Phosphatidylinositol-specific phospholipase C {*Listeria monocytogenes*}

VTTKQWMSALPDTTNLAALSIPGTHDMSYNGDITWTTLTKPLAQTQMSLYQQLEAGIRYIDIRAK
DNLNIYHGPIFLNASLSGVLETITQFLKKNPKETIIMRLKDEQNSNDSFDYRIQPLINIYKDYFYTTPR
TDTSNKIPTLKDVRGKILLSENHTKKPLVINSRKFQMGAPNQVIQDDYNGPSVTKFKEIVQTAY
QASKADNKLFLNHISATSLTFTPRQYAAALNNKVEQFVLNLTSEKVRGLGILIMDFPEKQTIKNIKNN
KF

>d7reqa1 c.1.19.1 (A:4-560) Methylmalonyl-CoA mutase, alpha and beta subunits {*Propionibacterium freudenreichii*, subsp. *shermanii*}

LPRFDSVDLGNAPVPADAARRFEELAAGKAGTGEAWETAEQIPVGTFLFNEVDYKMDMDWLDTYAGIPP
FVHGYPATMYAFRPWTIRQYAGFSTAKESNAFYRRNLAAGQKGLSVAFDLPTHRYGSDSNPRVAGDV
GMAGVAIDSIYDMRELFAGIPLDQMSVSMTMNGAVLPILALYVVTAEEQGVKPEQLAGTIQNDILKEF
MVRNTYIYPPQPSMRIISEIFAYTSANMPKWNISISGYHMQEAGATADIEMAYTLADGVYIRAGES
VGLNVDQFAPRLSFFWGIGMNFMEVAKLRAARMLWAKLVHQFGPKNPKSMLRTHSQTSGWSLT
AQDVYNNVVRTCIEAMAATQGHTQSLHTNSLDEAIALPTDFSARIARNTQLFLQQESGTTTRVIDPWS
GSAYVEELTWDLARKAWGHIQEVEKVGMAKAIKGPKMRIEAAAARTQARIDSGRQPLIGVKNKYR
LEHEPPLDVLKVDNSTVLAEQKAKLVKLRAERDPEKVKAAALDKITWAAGNPDDKDPDRNLLKLCID
AGRAMATVGEMSDALEKVFGRYT

>d7reqb1 c.1.19.1 (B:16-475) Methylmalonyl-CoA mutase, alpha and beta subunits

{*Propionibacterium freudenreichii*, subsp. *shermanii*}

LTPTTSLAGDFPKATEEQWEREVEKVLNRGRPPEKQLTFAECLKRLTVHTVDGIDIVPMYRPKDAP
KKLGYPGVAPFTRGTTVRNGDMDAWDVRALHEDPDEKFTKRAILEGLERGVTSLLLVRVDPDAIAPE
HLDEVLSDVLLEMTKVEVFSRYDQGAEEALVSVYERSDKPAKDLALNLGLDPIGFAALQGTEPDLT
VLGDWVRRLAKFSPDSRAVTIDANIYHNAGAGDVAELAWALATGAEYVRALVEQGFTATEAFDTINF
RVTATHDQFLTIARLRALREAWARIGEVEFGVDEDEKRGARQNAITSWRELTREDPYVNILRGSIAFSA
SVGGAESITTLPTQALGLPEDDFPLRIARNTGIVLAEVNI GRVNDPAGGSYYVESLTRLADAAWK
EFQEVEKLGGMASKAVMTEHVTKVLDACNAERAKRLANRKPITAVSEFPMIGARSIE

>d1ccwb_ c.1.19.2 (B:) Glutamate mutase, large subunit {*Clostridium cochlearium*}

MELKNKKWTDEEFHKQREEVLQQWPTGKEVDLQEAVDYLLKIPAEKNFAEKLVLAKKKGITMAQP
RAGVALLDEHIELLRYLQDEGGADFLPSTIDAYTRQNRIDECEGKIKESKAGRSLLNGFPGVNFVGVK
GCRKVLAVNLPLQARHGTPDSRLLAEIHHAGGWTSNEGGGISYNVPYAKNVTIEKSLLDWQYCDRL
VGFYEEQGVHINREPFGLTGLVPPSMSNAVGITEALLAAEQGVKNITVGYGECGNMIQDIAALRCL
EEQTNEYLYKAYGYNDVFTVTFHQQWGGFPQDESKAFGVIVTATTIAALAGATKVVVKTPEAIGIP
TKEANAAGIKATKMALNMLEGQRMPSKELETEMAVIKAETKCILDKMFELGKGDLAGITVKAFET
GVMDIPFGPSKYNAGKMPVRDNLGCVRYLEFGVNPFTTEEIKNYNRERLQERAKFEGRDVSFQMV
DDIFAVGKGRLLGRPE

>d1eexa_ c.1.19.3 (A:) Diol dehydratase, alpha subunit {*Klebsiella oxytoca*}

MRSKRFEALAKRPVNQDGFVKEWIEEGFIAMESPNDPKPSIKIVNGAVTELDGKPVSDFDLIDHFIA
RYGINLNRAEEVMAMDSVKLANMLCDPNVNRSEIVPLTTAMTPAKIVEVVSHMNVMEMMMAMQK
MRARRTPSQAHVTNVKDNVPQIAADAAEGAWRGFDEQETTVAVARYAPFNAIALLVGSQVGRPGV
LTQCSLEEATELKLGLGHTCYAETISVYGTPEVFTDGDTPWSKGLASSYASRGLKMRFTSGSGSE
VQMGYAEKSMYLEARCIYITKAAGVQGLQNGSVSICIGVPSAVPSGIRAVLAENLICSSLDLECASN
DQTFTHSDMRRTARLLMQFLPGTDFISSGYSVNPYDNMFAGSNEDAEDFDDYNVIQRDLKVDGGL
RPVREEDVIAIRNKAARALQAVFAGMGLPPTDEEVEAATYAHGSKDMPERNIVEDIKFAQEIIKNR
NGLEVVKALAQGGFTDVAQDMLNIQKAKLTGDYLHTSAIIVGDGQVLSAVNDVNDYAGPATGYRLQG
ERWEEIKNIPGALDPN

>d1f3ea_ c.1.20.1 (A:) tRNA-guanine transglycosylase {*Zymomonas mobilis*}

RPRFSFSIAAREGKARTGTIEMKRGVIRTPAFMPVGTAAATVKALKPETVRATGADIILGNTYHMLLRP
GAERIAKLGGLHSFMGWDRLPILTDSSGGYQVMSLSSLTQSEEGVTFKSHLDGSRHMLSPERSIEIQL
LGSDIVMAFDECTPYPATPSRAASSMERSMRWAKRSRDAFDSRKEQAENAALFGIQGSVFENLRQ
QSADALAEIGFDGYAVGGLAVGEGQDEMFRVLDFSVPMPLPDDKPHYLMGVGKPDIVGAVERGIDM
FDCVLPTRSGRNGQAFWTWGPINIRNARFSEDLKPLDSECHCAVCQKWSRAYIHHLIRAGEILGAML
MTEHNIAFYQQLMQKIRDSISEGRFSQFAQDFRARYF

>d1aj2_ c.1.21.1 (-) Dihydropteroate synthetase {*Escherichia coli*}

MKLFAQGTSLDLPHVMGILNVTDFSDGGTHNSLIDAVKHANLMINAGATHIDVGGESTRPGAA
EVSVEEELQRVIPVEAIAQRFEVWISVDTSKPEVIRESAKVGAAHIINDIRSLSEPGALEAAAETGLPVC
LMHMQGNPKTMQEAPKYDDVFAEVNRYFIEQIARCEQAGIAKEKLLLDPGFGFGKNSHNYSLAR
LAEFHFNPLLVGMSRKS MIGQLLNVGPSERLSGSLACAVIAAMQGAHIIRVHDVKETVEAMRVVE
ATLSAKENKRYE

>d1ad1a_ c.1.21.1 (A:) Dihydropteroate synthetase {*Staphylococcus aureus*}

TKTKIMGILNVTDFSDGGKFNNEVSAVTRVKAMMDEGADIIDVGGVSTRPGHEMITVEEELNRVL
PVVEAIVGFVVKISVDTFRSEVAEACLKLGVDIINDQWAGLYDHRMFQVVAKYDAEIVLMHNGNGNR
DEPVVEMLTSLLAQAHAQAKIAGIPSNKIWLDPGIGFAKTRNEEA EVMARLDELVATEYPVLLATSR

KRFTKEMMGYDTPVERDEVTAATTAYGIMKGVRAVRVHVELNAKLAKGIDFLKENENARHN

>d1eye_a_ c.1.21.1 (A:) Dihydropteroate synthetase {Mycobacterium tuberculosis}

PVQVMGVLNVTDDSFSDGGCYLDLDDAVKHGLAMAAAGAGIVDVGESSRPGATRVDPAVETSRI
PVVKELAAQGITVSIIDTMRADVARAALQNGAQMVNDVSGGRADPAMGPLLAEADVPWVLMHWRA
VSADTPHVPVRYGNVVAEVRADLLASVADAVAAGVDPARLVLDPGLGFAKTAQHNWAILHALPELVA
TGIPVLVGASRKRFLGALLAGPDGVMRPTDGRDTATAVISALAALHGAWGVRVHVDVRASVDAIKVVE
AWMGAE

>d1f6ya_ c.1.21.2 (A:) Methyltetrahydrofolate: corrinoid/iron-sulfur protein
methyltransferase MetR {Moorella thermoacetica}

MLIIGERINGMFGDIKRAIQERDPAPVQEWARRQEEGGARALDLNVGPAVQDKVSAMEWLVEVTQE
VSNLTCLDSTNIKAIEAGLKKCKNRAMINSTNAEREKVEKLFPLAVEHGAALIGLTMNKTGIPKDS
TRLAFAMELVAAADEFGLPMEDLYIDPLILPANVAQDHAPEVLKTLQIQIKMLADPAPKTVLGLSNVS
QNCQNRPLINRTFLAMAMACGLMSAIADACDEALIETAATAEILLNQTVYCDSEVFKMFKTR

>d1uroa_ c.1.22.1 (A:) Uroporphyrinogen decarboxylase, UROD {Human (Homo sapiens)}

GFPELKNDFLRAAWGEETDYTPVWCMRQAGRYLPEFRETRAAQDFSTCRSPEACCELTLQPLRR
FPLDAAIIFSDILVVPQALGMEVTMVPKGKPSFPEPLREEQDLERLRDPEVVASELGYVFQAITLRQR
LAGRVPLIGFAGAPWTLMTYMEVGGSSSTMAQAKRWLYQRPQASHQLLRILTALVPYLVGQVVAG
AQALQLFESHAGHLGPQLFNKFALPYIRDVAKQVKARLREAGLAPVPMIIFAKDGHFALEELAQAGY
EVLGLDWTVPKKARECVGKTVTLQGNLDPALYASEEEIGQLVKQMLDDFGPHRYIANLGHGLYP
DMDPEHVGAFVDAVHKHSRLLRQ

>d1j93a_ c.1.22.1 (A:) Uroporphyrinogen decarboxylase, UROD {Tobacco (Nicotiana
tabacum), UROD-III}

TQPLLLDAVRGKEVERPPVWLMRQAGRYMKSQQLCEKYPLFRDRSENVDLVVEISLQPWKVFVRPD
GVILFSDILTPLSGMNIPFDIHKGKGPVIFDPLRTAADVEKREFIPEKSVPYVGEALTILRKEVNNQAA
VLGFVVGAPFTLASVVEGGSSKNFTKIKRLAFAEPKVLHALLQKFATSMAYIRYQADSGAQAVQIFD
SWATELSPVDFEESLPLKQIVDSVKLTHPNLPLILYASGSGLLERLPLTGVDVSLDWTVDMDAG
RRRLGPNVAIQGNVDPGVLFSGKEFITNRINDTVKKAGKKGKHLNLGHGKIKVGTPEENFAHFFEIAK
LRY

>d1b5ta_ c.1.23.1 (A:) Methylene tetrahydrofolate reductase {Escherichia coli}

GQINVSFEFFPRTSEMEQTLWNSIDRLSSLKPKFVSVTYGANSGERDRTHSIKGIKDRGTGLEAAPHL
TCIDATPDELRTIARDYWNNGIRHIVALRGDLPPGSGKPEMYASDLVTLLEKADDFDISVAAYPEVHP
EAKSAQADLLNLKRKVDAGANRAITQFFDVESYLRFRDRCVSAGIDVEIIPGILPVSNFQAKKPAD
MTNVRIPAWMAQMFQDGLDDDAETRKLVGANIAMDVMKILSREGVKDFHFYTLNRAEMSYAICHTL
GVRPA

>d1heta2 c.2.1.1 (A:175-324) Alcohol dehydrogenase {Horse (Equus caballus)}

GFSTGYGSAVKVAVTQGSTCAVFLGGVGLSVIMGCKAAGAARIIGVDINKDKFAKAKEVGATECVN
PQDYKKPIQEVLTMSNGGVDFSEVIGRLDMVTALSCCQEAYGVSIVGVPPDSQNLMSNPMLL
SGRTWKGAIFGGFKS

>d1d1ta2 c.2.1.1 (A:175-324) Alcohol dehydrogenase {Human (Homo sapiens), different
isozymes}

GFSTGYGAAVKTGKVKPGSTCVVFLGGVGLSVIMGCKSAGASRIIGIDLNKDFEKAMAVGATECISP
KDSTKPISEVLSEMTGNVGYTFEVIHLETMIDALASCHMNYGTSVVGVPPSAKMLTYDPMMLFT
GRTWKGCVFGLLKS

>d1ht0a2 c.2.1.1 (A:175-324) Alcohol dehydrogenase {Human (Homo sapiens), different

isozymes}

GFSTGYGSAVKVAVTPGSTCAVFLGGVGLSVVMGCKAAGAARIIVDINKDKFAKAKELGATECIN
PQDYKKPIQEVLEMTDGGVDFSEFVIGQLDTMMASLLCCHEACGTSVIVGVPPDSQNLINPMLLL
TGRTWKGAIFGGFKS

>d1teha2 c.2.1.1 (A:175-324) Alcohol dehydrogenase {Human (Homo sapiens), different
isozymes}

GISTGYGAAVNTAKLEPGSVCAVFLGGVGLAVIMGCKVAGASRIIGVDINKDKFARAKEFGATECINP
QDFSKPIQEVLIEMTDGGVDYSFECIGNVKVMRAALEACHKGGVSVVVGVAAASGEEIATRPFLVT
GRTWKGTAFGGWKS

>d1e3ia2 c.2.1.1 (A:175-324) Alcohol dehydrogenase {Mouse (Mus musculus), class II}

LIGCGFSSGYGAAINTAKVTPGSTCAVFLGCVGLSAIIGCKIAGASRIIAIDINGEKFPKAKALGATDCL
NPRELDKPVQDVITELTAGGVDYSLDCAGTAQTLKAAVDCTVLGWSCTVVGAKVDEMTIPTVDVIL
GRSINGTFFGGW

>d1cdoa2 c.2.1.1 (A:176-324) Alcohol dehydrogenase {Cod (Gadus callarias)}

GVSTGFGAAVNTAKVEPGSTCAVFLGAVGLAAVMGCHSAGAKRIIVDLNPKFEKAKVFGATDFV
NPNDHSEPIQVLSKMTNGGVDFSLCEVGNVGMRNALESCLKGGVSVLVGWTDLHDVATRPIQL
IAGRTWKGSFMGGFKG

>d1keva2 c.2.1.1 (A:151-314) Bacterial secondary alcohol dehydrogenase {Clostridium
beijerinckii}

MMTTGFHGAELADIQMGSSVVVIGIGAVGLMGIAGAKLRGAGRIIGVSRPICVEAAKFYATDILNY
KNGHIVDQVMKLTNGKGVDRVIMAGGGSETLSQAVSMVKPGGIISNINYHSGDALLIPRVEWCGM
AHKTIKGGGLCPGGRLRAEMLRDMVVYNRV

>d1ykfa2 c.2.1.1 (A:151-314) Bacterial secondary alcohol dehydrogenase
{Thermoanaerobacter brockii}

MMTTGFHGAELADIELGATVAVLGGVGLMAVAGAKLRGAGRIIIVSRPVCVDAAKYATDIVNY
KDGPIESQIMNLTEGKGVDAIIAGGNADIMATAVKIVKPGGTIANVNYFGEVLPVPRLEWCGM
AHKTIKGGGLCPGGRLRMERLIDLVFYKRV

>d1e3ja2 c.2.1.1 (A:151-313) Ketose reductase (sorbitol dehydrogenase) {Silverleaf whitefly
(Bemisia argentifolii)}

LEPLSVGVHACRRAGVQLGTTVLVIGAGPIGLVSVLAAKAYGAFVVCTARSPRRLEVAKNCGADVTLV
VDPAKEEESSIIERIRSAIGDLPNVTIDCSGNEKCITIGINITRTGGTLMVGMGSQMVTVPLVNACARE
IDIKSVFRYCNDYPIALEMVASGRC

>d1qora2 c.2.1.1 (A:136-265) Quinone oxidoreductase {Escherichia coli}

YEIKPDEQFLFHAAAGGVLIACQWAKALGAKLIGTVGTAQKAQSALKAGAWQVINYREEDLVERLK
EITGGKKVRVVYDSVGRDWTWERSLDCLQRRGLMVSFGNSSGAVTGVNLGILNQKGSlyVTRPS

>d1udc_ c.2.1.2 (-) Uridine diphosphogalactose-4-epimerase (UDP-galactose 4-epimerase)
{Escherichia coli}

MRVLVTGGSGYIGSHTCVQLLQNGHDVHLDNLCNSKRSVLPVIERLGGKHPTFVEGDIRNEALMTEI
LHDHAIDTVIHFAGLKAVGESVQKPLEYYDNNVNGTLRLISAMRAANVKNFIFSSSATVYGDQPKIPY
VESFPTGTPQSPYGKSKLMVEQILTDLQKAQPDWSIALLRYPVGAHPSGDMGEDPQGIPNNLMP
YIAQVAVGRRDSLAIFGNDYPTEDGTGVRDYIHVMDLADGHVAMEKLANKPGVHIYNLGGVNS
VLDVVNAFSKACGKPVNYHFAPRREGDLPAYWADASKADRELNWRVTRTLDEMAQDTWHWQSR
HPQGYPD

>d1ek6a_ c.2.1.2 (A:) Uridine diphosphogalactose-4-epimerase (UDP-galactose 4-epimerase)

{Human (Homo sapiens)}

MAEKVLVTGGAGYIGSHTVLELLEAGYLPVVIDNFHNAFRGGGSLPESLRRVQELTGRSVEFEEMDIL
DQGalQRLFKKYSFMAVIHFAGLKAVGESVQKPLDYRVNLTGTIQLLEIMKAHGKLVFSSSATVY
GNPQYLPLDEAHPTGGCTNPYGKSKFFIEEMIRDLQCQADKTWNAVLLRYFNPTGAHASGCIGEDPQ
GIPNNLMPYVSQVAIGRREALNVFGNDYDTEdGTGVRDYIHVVDLAKGHIAALRKLKEQCgcRIYNL
GTGTGYSVLQMVQAMEKASGKKIPYKVVARREGDVAACYANPSLAQEELGWTAALGLDRMCEDLW
RWQKQNPSGFGT

>d1bxka_c.2.1.2 (A:) dTDP-glucose 4,6-dehydratase (RmlB) {Escherichia coli}

MRKILITGGAGFIGSALVRYIINETSDAVVVVDKLTyAGNLMslAPVAQSERFAFEKVDICDRAELARV
FTEHQpDCVMHLAAESHVDRSIDGPAAFIETNIVGTyTLLAARAYWNALTEdKKSaFRFHHISTDE
VYGDlhSTDDFFtETTPYAPSSPySASKASSDHLVRAWLRTYGLPTLITNCSNnyGPYHFPEKLIPLM
ILNALAGKSLPVYGNQqIRDWLYVEDHARALYCVATTGKVGETYnIGGHNERKNLDVVETICELLE
ELAPNKPHGVahYRDLITFVADRPghDLRYAIDASKIARELGCVPQETfESGMrKTVQWYLANESW
WKQVQDGSYQGER

>d1kepa_c.2.1.2 (A:) dTDP-glucose 4,6-dehydratase (RmlB) {Streptococcus suis, serotype 2}

QFKNIIVTGGAGFIGSNFVHYVYNNHPDVHVTVLdKLTyAGNkanLEAILGDRVELVVGDIADAELVD
KLAAKADaIVHYAAESHNDNSLNDPSFIHTNFIGTyTLLAARKYDIRFHHVSTDEVYGDLPRED
LPGHGEGPGEKfTAETNYNPSSPySSTKAASDLIVKAWVRSFGVKATISNCSNnyGPYQHIEKFIPRQI
TNILAGIKPKLYGEGKNVRDWIHTNDHSTGVWAILTKGRMGETyLIGADGEKNNKEVLELILEKMG
QPKDAYDHVTDRAGHDLRYAIDASKLRDELGWTPQFTDFSEGLEETIQWYTDNqDWWKAEKEAV
EANYAKTQEVik

>d1kewa_c.2.1.2 (A:) dTDP-glucose 4,6-dehydratase (RmlB) {Streptococcus suis, serotype 2}

MKILITGGAGFIGSAVVRHIIKNTQDTVVNIDKLTyAGNLESLSDISESNRYNFEHADICDSAEITRIFE
QYQPDaVMHLAAESHVDRSITGPAAFIETNIVGTyALLEVARKYWSALGEDKKNnFRFHHISTDEVY
GDLPHpDEVENSVTLPLFTETTAYAPSSPySASKASSDHLVRAWRRTYGLPTIVTNCNnyGPYHFPE
KLIPLVILNALEGKPLPIYGKGDQIRDWLYVEDHARALHMVVTEGKAGETyNIGGHNEKKNLDVVFT
ICDLLDEIVPKATSYREQITYVADRPghDRRYAIDAGKISRELGWKPLETFESGIRKtVewYLANtQ
WVNNVKSGAYQSWIEQNYEGRQ

>d1e6ua_c.2.1.2 (A:) GDP-4-keto-6-deoxy-d-mannose epimerase/reductase (GDP-fucose synthetase) {Escherichia coli}

AKQRVFIAGHRGMVGSaIRRQLEQRGDVELVLRTRDELNLLDSRAVHDFfASERIDQVYLAAAKVGG
IVANNTYPADFIYQNMmIESNIIHAAHQNDVNKLLFLGSSCIYPKLAKQPMaESELLQGTLEPTNEPY
AIAKIAGIKLcESYNRQYGRDYRSVMPTNLYGPHDNFhPSNSHVIPALLRRFHEATAQKAPDvvvWG
SGTPMREFLHVDDMAAASIHVMELaHEVWLENTQPMLSHINVTGVDCTIRELaQTIaKVVGyKGR
VVFDAKPDGTPRKLldVTRLHQLGWYHEISLEAGLAsTYQWfLENQ

>d1db3a_c.2.1.2 (A:) GDP-mannose 4,6-dehydratase {Escherichia coli}

SKVALITGVTGQDGSYLAeFLLEKGYEVHGikRRASSFNTERVDHIYQDPHTCNPKFHLHYGDLSDTS
NLTRILREVQPDEVYnLGAMSHVAVSFESPEYtADVDAMGTLRLLLeAIRFLGLEKKTRfYQASTSELY
GLVQeIPQKETTfPYPRSPYAVAKLYAYWITVNYRESYGMACNGILFNHESPRRGETfVTRKITRAIA
NIAQGLESLYLGnMDSLrdWGHAKDYVKMQWMLLQEQEPEDFVIATGVQYSVRQfVEMAAAQL
GIKlRFEGTGVeeKIVSVTGHdAPGVKPGDVIIAVDPRYFRPAEVETLLGDPTKaHEKLGWkPEIT
LREMVSEMvANDLEAAKkHS

>d1eq2a_c.2.1.2 (A:) ADP-L-glycero-D-mannoheptose 6-epimerase {Escherichia coli}

MIIVTGGAGFIGSNIVKALNDKGITDILVVDNLKDGTKFVNlVLDLNIADYMDKEDFLIQIMAGEEFGD

VEAIFHEGACSSSTTEWDGKYMMDNNYQYSKELLHYCLEREIPFLYASSAATYGGRTSDFIESREYEKP
LNVYGYSKFLFDEYVRQILPEANSQIVGFYFNVYGPREGHKGSMASVAFHLNTQLNNGESPCLFEFS
ENFKRDFVYVGDVADVNLWFLENGVSGIFNLGTGRAESFQAVADATLAYHKKGQIEYIPFPDKLKGR
YQAFQTQADLTNLRAAGYDKPFKTVAEGVTEYMAWLN

>d1qrra_ c.2.1.2 (A:) Sulfolipid biosynthesis protein SQD1 {Thale cress (*Arabidopsis thaliana*)}

KRVMVIGGDGYCGWATALHLSKKNYEVCIVDNLVRRFLFDHQLGLESPTIASIHDRISRWKALTGKSI
ELYVGDICDFEFLAESFKSFEPSVVFHGEQRSAPYSMIDRSRAVYQHNHNVIGTLNVLFAIKEFGEEC
HLVKLGTMGEGYTPNIDIEEGYITITHNGRTDTPYPKQASSFYHLSKVHDSHNIAFTCKAWGIRATD
LNQGVVYGVKTDTEMHEELRNRLDYDAVFGTALNRFVQAAVGHPLTVYGGGQTRGYLDIRDTV
QCVEIAIANPAKAGEFRVFNQFTEQFSVNELASLVTKAGSKLGLDVKKMTVPNPRVEAEHYYNAK
HTKLMELGLEPHYLSDSLSDLLNFAVQFKDRVDTKQIMPVSVWKKIGVKTKS

>d1k6xa_ c.2.1.2 (A:) Negative transcriptional regulator NmrA {*Aspergillus nidulans*}

QQKKTIAVNVNATGRQAASLRVAAAAGHHVRAQVHSLKGLIAEELQAIPNVTLFQGPLLNNVPLMDT
LFEGAHLAFINTTSQAGDEIAIGKDLADAAKRAGTIQHYIYSSMPDHSLYGPWPAVPMWAPKFTVEN
YVRQLGLPSTFVYAGIYNNFTSLPYPLFQMEMLMPDGTFEWHAPFDPDIPLPWLD AEHDVGPALLQ
IFKDGPKWNGHRIALTFETLSPVQVCAAFSRALNRRVTVYVQVPKVEIKVNIPVGYREQLEAIEVVFG
EHKAPYFPLPEFSRPAAGSPKGLGPANGKAGAGMMQGGPQVSRVTD EARKLWSGWRDMEEYA
REVFPIEEEANGLDWML

>d1cyda_ c.2.1.2 (A:) Carbonyl reductase {Mouse (*Mus musculus*)}

LNFSGLRALVTGAGKIGRDTV KALHASGAKVVAVTRTNSDLVSLAKECPGIEPVCVDLGDWDATEK
ALGGIGPVDLLVNNAAALVIMQPFLEVTKEAFDRSFSVNLRSVFQVSQMVARDMINRGVPGSIVNVSS
MVAHVTFPNLITYSSTKGAMTMLTKAMAMELGPHKIRVNSVNPTVVLTDMGKKVSADPEFARKLK
ERHPLRKFAEVEDVNSILFLLSDRSASTSGGGILVDAGYLAS

>d1oaa_ c.2.1.2 (-) Sepiapterin reductase {Mouse (*Mus musculus*)}

ADGLGCAVCVLTGASRGFRALAPQLARLLSPGSVMLVSARSESMLRQLKEELGAQQPDLKVVAAAA
DLGTEAGVQRLLSAVRELPRPEGLQRLLLINNAATLGDVSKGFLNVNDLAEVNNYWALNLTSMCLT
SGTLNAFQDSPGLSKTVVNISSCALQPYKGWGLYCAGKAARDMLYQVLAEEPSVRVLSYAPGPLD
NDMQQLARETSKDPELRSKLQKLKSDGALVDCGTSQAQKLLGLLQKDTFQSGAHVDFYD

>d1hdr_ c.2.1.2 (-) Dihydropteridin reductase (pteridine reductase) {Human (*Homo sapiens*)}

EARRVLVYGGRGALGSRVQAFRARNWWVASVDVVENEEASASIIVKMTDSFTEQADQVTAEVGKL
LGEEKVDAILCVAGGWAGGNAKSKSLFKNCDLMWKQSIWTSTISSHLATKHLKEGGLLTLGAKAA
LDGTPGMIGYGMAGAVHQLCQSLAGKNSGMPPGAAAIAVLPVTLDTPMNRKSMPEADFSWTP
EFLVETFDHWITGKNRPSSGSLIQVVTTEGRTELPAYF

>d1e7wa_ c.2.1.2 (A:) Dihydropteridin reductase (pteridine reductase) {*Leishmania major*}

TVPVALVTGAAKRLGRSIAEGLHAEGYAVCLHYHRSAAEANALSATLNARRPNSAITVQADLSNVATA
PVSGADGSAPVTLFTRCAELVAACYTHWGRCDVLVNNASSFYPTPLLRNDEDGHEPCVGDREAMET
ATADLFGSNAIAPYFLIKAFHRVAGTPAKHRGTNYSIINMVDAMTNQPLLGYTIYTMKGALEGLTR
SAALELAPLQIRVNGVGPGLSVLVDDMPPAVWEGHRSKVPLYQRDSSAAEVSDVVIFLCCSSKAKYITG
TCVKVDGGYSLTRA

>d1fds_ c.2.1.2 (-) Human estrogenic 17beta-hydroxysteroid dehydrogenase {Human (*Homo sapiens*)}

ARTVVLTGCSGIGLHLAVRLASDPSQSFKVYATLRDLKTQGRLEWAARALACPPGSLETQLDVRD

SKSVAAARERVTEGRVDVLCNAGLGLLPLEALGEDAVASVLDVNVVGTVRMLQAFLPDMKRRGS
GRVLVTGSVGLMGLPFNDVYCASKFALEGLCESLAVLLLPGVHLSLIECGPVHTAFMEKVLGSPEE
VLDRTDIHTFHRFYQYLAHASKQVFREAAQNPEEVAEVFLTALRAPKPTLRYFTTTERFLPLLRMLDD
PSGSNYVTAMHREVFVDV

>d1fmca_ c.2.1.2 (A:) 7-alpha-hydroxysteroid dehydrogenase {Escherichia coli}
MFNSDNLRLDGKCAITGAGAGIGKEIAITFATAGASVVSDINADAANHVVEIQQLGGQAFACRCDI
TSEQELSALADFAISKLKVDILVNNAGGGGPKPFDMPMADFRRAYELNVFSFFHLSQLVAPEMEKN
GGGVILTITSMAAENKNINMTSYASSKAAASHLVRNMAFDLGEKNIRVNGIAPGAILTDALKSVITPEI
EQKMLQHTPIRRLGQPQDIANAALFLCSPAASWVSGQILTVSGGGVQELN

>d1hdca_ c.2.1.2 (A:) 3-alpha,20-beta-hydroxysteroid dehydrogenase {Streptomyces
hydrogenans}

NDLSGKTVIIITGGARGLGAEAAARQAVAAGARVVLADVLDEEGAATARELGDAARYQHLDVTIEEDW
QRVVAYAREEFGSVDGLVNNAGISTGMFLETESVERFRKVVVEINLTGVFIGMKTVIPAMKADAGGSIV
NISSAAGLMGLALTSSYGASKWGVRLSKLA AVELGTDRIRVNSVHPGMTYTPMTAETGIRQEGENY
PNTPMGRVGEPEIAGAVVKLLSDTSSYVTGAELAVDGGWTTGPTVKYVMGQ

>d1fjha_ c.2.1.2 (A:) 3-alpha-hydroxysteroid dehydrogenase {Comamonas testosteroni}
MSIIVISGCATGIGAATRQVLEAAGHQIVGIDIRDAEVIADLSTAEGRKQAIADVLAKCSKGM DGLVLC
GLGPQTKVLGNVSVNYFGATELMDAFLPALKKQHQA AVVISVSAHLAFDKNPLALALEEGEEA
KARAIVEHAGEQGGNLAYAGSKNALTVAVRKRAAAWGEAGVRLNTIAPGATETPLLQAGLQDPRYG
ESIAKFVPPMGRRAEPSEMASVIAFLMSPAASYVHGAQIVIDGGIDAVMRPTQF

>d1bdb_ c.2.1.2 (-) Cis-biphenyl-2,3-dihydrodiol-2,3-dehydrogenase {Pseudomonas sp.,
lb400}

MKLKGEAVLITGGASGLGRALVDRFVAEGAKVAVL DKSAERLAELETDHGDNLV GIVGDVRSLEDQK
QAASRCVARFGKIDTLIPNAGIWDYDALVDLPEESLDAAFDEVFHINVKGYIHAVKACLPALVASRGN
VIFTISNAGFYPPNGGPLYTAAKHAI VGLVRELAFELAPYVRVNGV GSGGINSDLRGPSSLGMGSKAIS
TVPLADMLKSVLPIGRMPEVEEYTGAYVFFATRGDAAPATGALLNYDGG LGVRGFFSAGGNDLLEQ
LNIH

>d1b16a_ c.2.1.2 (A:) Drosophila alcohol dehydrogenase {Fruit fly (Drosophila
lebanonensis)}

MDLTNKNVIFVAALGGIGLDT SRELVKRNLKNFVILDRVENPTALAE LKAINPKVNITFHTYDVTVPV
AESKLLKKIFDQLKTV DILINGAGILDDHQIERTIAINFTGLVNTTTAILDFWDKRKGGPGGIIANICS
VTGFNAIHQVPVYSASKAAVVSFTNSLAKLAPITGVTAYSINPGITRTPLVHTFNSWLDVEPRVAELL
SHPTQTSEQCGQNFVKAIEANKNGAIWKLDLGTLEAIEWTKHWDSHI

>d1gcoa_ c.2.1.2 (A:) Glucose dehydrogenase {Bacillus megaterium}

MYKDLEGKVVVITGSSTGLGKSM AIRFATEKAKVVVNYRSKEDEANSVLEEIKKVGGEAIAVKGDVT
VESDVINLVQSAIKEFGKLDV MINNAGLENPVSSHMSLSDWNKVIDTNLTGAFLGSREAIKYFVEN
DIKGTVINMSSVHEKIPWPLFVHYAASKGGMKLM TETLALEYAPKGIRVNNIGPGAINTPINA EK FAD
PEQRADVESMIPMGYIGEP EEEIAAVAAWLASSEASYVTGITL FADGGMTQYPSFQAGRG

>d1gega_ c.2.1.2 (A:) meso-2,3-butanediol dehydrogenase {Klebsiella pneumoniae}

KKVALVTGAGQGIGKAIALRLVKDGF AVAIADYNDATAKAVASEINQAGGHAVAVKVDVSDRDQVFAA
VEQARKTLGGFDVIVN NAGVAPSTPIESITPEIVDKVYNINVKGVWGIQA AVEAFKKEGHGGKIINAC
SQAGHVGNPELAVYSSSKFAVRGLTQTAARDLAPLGITVNGYCPGIVKTPMWAEIDRQVSEAAGKPLG
YGTAFAK RITLGRLEPEDVAACVSYL ASPDSYMTGQSLIDGGMVFN

>d1h5qa_ c.2.1.2 (A:) Mannitol dehydrogenase {Mushroom (Agaricus bisporus)}

PGFTISFVNKTIIVTGGNRGIGLAFTRAVAAAGANVAVIYRSAADAVEVTEKVGKEFGVTKAYQCDVS
NTDIVTKTIQQIDADLGPISGLIANAGVSVVKPATELTHEDFAFVYDVNVFGVFNTCRAVAKLWLQKQ
QKGSIVVTSSMSSQIINQSSLNGSLTQVFYNSSKAACSNLVKGLAAEWASAGIRVNALSPGYVNTDQTA
HMDKKIRDHQASNIPLNRFAQPEEMTGQAILLLSDHATYMTGGGEYFIDGGQLIW

>d1edoa_ c.2.1.2 (A:) beta-keto acyl carrier protein reductase {Oil seed rape (Brassica napus)}

SPVVVVVTGASRGIGKAIASLKGAGCKVLVNYARSAKAAEEVSKQIEAYGGQAITFGGDVSKEADVEA
MMKTAIDAWGTIDVVVNNAGITRDTLLIRMKKSQWDEVIDLNLTVFLCTQAATKIMMKRKRGRRII
NIASVVLIGNIGQANYAAAKAGVIGFSKTAAREGASRNINNVVCPGFASDMTAKLGEDMEKKILG
TIPLGRTGQPENAVGLVEFLALSPAASYITGQAFITIDGGIAI

>d1i01a_ c.2.1.2 (A:) beta-keto acyl carrier protein reductase {Escherichia coli}

MNFEGKIALVTGASRGIGRAIAETLAARGAKVIGTATSENGAQAI SDYLGANGKGLMLNVTDPASIES
VLEKIRAEFGEVDILVNNAGITRDNLLMRMKDEEWNIIETNLSSVFRLSKAVMRAMMKRHRGRII
TIGSVVGTMGNGGQANYAAAKAGLIGFSKSLAREVASRGITVNVVAPGFIETDMTRALSDDQRAGILA
QVPAGRLGGAQEIANAVAFLASDEAAAYITGETLHVNGGM

>d1eno_ c.2.1.2 (-) Enoyl-ACP reductase {Oil seed rape (Brassica napus)}

LPIDLGRKRAFIAGIADDNGYGWAVAKSLAAAGAEILVGTWVPALNIFETSLRRGKFDQSRVLPDGSL
MEIKKVYPLDAVFDNPEDVPEDVKANKRYAGSSNWTVQEAECVRQDFGSIDILVHSLANGPEVSKP
LLET SRKGYLAAISASSYSFVSLLSHFLPIMNPGGASISLTYIASERIIPGYGGMSSAKAALES DTRVLA
FEAGRKQNI RVNTISAGPLGSRAAKAIGFIDTMIEYSYNNAPIQKTLTADEVGNA AFLVSPLASAITG
ATIYVDNGLNSMGVALDSPVFK

>d1eny_ c.2.1.2 (-) Enoyl-ACP reductase {Mycobacterium tuberculosis, TB, gene InhA}

AGLLDGKRILVSGIITDSSIAFHARVAQEQAQLVLTGFDRRLRIQRITDRLPAKAPLLELDVQNEEHL
ASLAGRVTEAIGAGNKLDGVVHSIGFMPQTMGINPFFDAPYADVSKGIHISAYSASYMAKALLPIMN
PGGSIVGMDFDPSRAMPAYNWMTVAKSALESVNRFVAREAGKYGVRNLVAAGPIRTLAMSAIVGGA
LGEEAGAQLLEEGWDQRAPIGWNMKDATPVAKTVCALLSDWLPATTGDIIYADGGAHTQLL

>d1qg6a_ c.2.1.2 (A:) Enoyl-ACP reductase {Escherichia coli}

GFLSGKRILVTGVASKLSIAYGIAQAMHREGAELAFYQNDKLGKRVEEFAAQLGSDIVLQCDVAEDAS
IDTMFAELGKVWPKFDG FVHSIGFAPGDQLDGDYVNAV TREGFKIAHDISSYSFVAMAKACRSMLNP
GSALLTSLYLGAERAIPNYNVMGLAKASLEANVRYMANAMGPEGVRVNAISAGPIRTLAASGIKDFR
KMLAHCEAVTPIRRTVTIEDVGNSAAFLCSDLSAGISGEVVHVDGGFSIAAMNE

>d1ae1a_ c.2.1.2 (A:) Tropinone reductase {Jimsonweed (Datura stramonium), I}

RWSLKGTTALVTGGSKGIGYAIVEELAGLGARVYTC SRNEKELDECLI WREKGLNVEGSVCDLLSRT
ERDKLMQTVAHVFDGKLNILVNNAGVVIHKEAKDFTEKDYNIMGTNFEEAYHLSQIAYPLLKASQN
GNVIFLSSIAGFSALPSVSLYSASKGAINQMTKSLACEWAKDNIRVNSVAPGVILTPLVETAIKKNPHQK
EEIDNFIVKTPMGRAGKPQEV SALIAFLCFPAASYITGQIIWADGGFTANGGF

>d2ae2a_ c.2.1.2 (A:) Tropinone reductase {Jimsonweed (Datura stramonium), II}

AGRWNLEGCTALVTGGSRGIGY GIVEELASLGASVYTC SRNQKELNDCLTQWR SKGFKVEASVCDLSS
RSERQELMNTVANHFHGKLNILVNNAGIVYIYKEAKDYTVEDYSLIMSINFEEAYHLSVLAHPFLKASE
RGNVVFISVSGALAVPYEAVYGATKGAMDQLTRCLAFEWAKDNIRVNGVGPVIATSLVEMTIQDPE
QKENLNKLIDRCALRRMGEPKELAA MVAFLCFPAASYVTGQIIYVDGGLMANCGF

>d1g0oa_ c.2.1.2 (A:) 1,3,8-trihydroxynaphthalene reductase (THNR, naphthol reductase) {Rice blast fungus (Magnaporthe grisea)}

KYDAIPGPLGPQSASLEGKVALVTGAGRGIGREMAMELGRRGCKVIVNYANSTESAEEVVAIAIKKNGS

DAACVKANVGVEDIVRMFEEAVKIFGKLDIVCSNSGVVSGHVKDVTPEEFDRVFTINTRGQFFVA
REAYKHLEIGGRLILMGSITGQAKAVPKHAVYSGSKGAIETFARCMAIDMADKKITVNVVAPGGIKTD
MYHAVCREYIPNGENLSNEEVDEYAAVQWSPLRRVGLPIDIARVVCFLASNDGGWVTGKVIIGDGA
CM

>d1ja9a_ c.2.1.2 (A:) 1,3,6,8-tetrahydroxynaphthalene reductase {Rice blast fungus
(Magnaporthe grisea)}

SKPLAGKVALTTGAGRGIGRGIAIELGRRGASVVVNYGSSSKAAEEVVAELKKLGAQGVAIQADISKPS
EVVALFDKAVSHFGGLDFVMSNSGMEVWCDELEVTQELFDKVFNLNTRGQFFVAQQGLKHCRRGG
RIILTSSIAAVMTGIPNHALYAGSKAAVEGFCRAFAVDCGAKGVTVNCIAPGGVKTDMFDENSWHYAP
GGYKGMPEKIDEGLANMNP LKRIGYPADIGRAVSALCQESEWINGQVIKLTGGGI

>d1hdoa_ c.2.1.2 (A:) Biliverdin IX beta reductase {Human (Homo sapiens)}

MAVKKIAIFGATGQTGLTTLAQAVQAGYEVTVLVRDSSRLPSEGPRPAHVVDVLAADVDKTVAG
QDAVIVLLGTRNDLSPPTVMSEGARNIVAAMKAHGVDKVVACTSAFLLDPTKVPVRLQAVTDDHI
RMHKVLRRESGLKYVAVMPPHIGDQPLTGAYTVTLDRGPRSRVSKHDLGHFMLRCLTTDEYDGHST
YPSHQY

>d1e6wa_ c.2.1.2 (A:) 3-hydroxyacyl-CoA dehydrogenase {Rat (Rattus norvegicus)}

SVKGLVAVITGGASGLGLSTAKRLVGQGATAVLLDVPNSEGETEAKKLGNCIFAPANVTSEKEVQAAL
TLAKEKFRIDVAVNCAGIAVAIKTYHEKKNQVHTLEDFQRVINVNLIGTFNVIRLVAGVMGQNEPD
QGGQRGVIINTASVAAFEGQVGAAYSASKGGIVGMTLPIARDLAPIGIRVVTIAPGLFATPLLTLPDK
VRNFLASQVPPSRLGDPAEYAHLVQMVIENPFLNGEVIRLDGAIRMQP

>d1hu4a_ c.2.1.2 (A:) Carbonyl reductase/20beta-hydroxysteroid dehydrogenase {Pig (Sus
scrofa)}

SSNTRVALVTGANKGIGFAIVRDLCRQFAGDVVLTARDVARGQAAVKQLQAEGLSRPFHQLDIIDLQSI
RALCDFLRKEYGGLDVLVNNAAIAFQLDNPTPFHQIQAELTMKTNFMGTRNVCTELLPLIKPQGRVVN
VSSTEGVRALNECSPELQQKFKSETITEEELVGLMKNKFVEDTKNGVHRKEGWSYSTYGVTKIGVSVL
SRIYARKLREQRAGDKILLNACCPGWVRTDMGGPKAPKSPEVGAETPVYLLALLPSDAEGPHGQFVT
DKKVVEWGVPPESYPWVNA

>d1gado1 c.2.1.3 (O:0-148,O:313-330) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
{Escherichia coli}

TIKVINGFGRIGRIVFRAAQKRSIDIEIVAINDLLDADY MAYMLKYDSTHGRFDGTVEVKDGHVING
KKIRVTAERDPANLKWDEVGVDVVAEATGLFLTDE TARKHITAGAKKVVMTGPSKDNTPMFVKGA
NFDKYAGQDIVSNASXNETGYSNKVLDLIAHISK

>d1gd1o1 c.2.1.3 (O:0-148,O:313-333) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
{Bacillus stearothermophilus, nca 1503}

AVKVGINGFGRIGRNVFRAALKNPDI EVVAVNDLTDANTLAHLLKYDSVHGRLDAEVS VNGNNLV
NGKEIIVKAERDPENLAWGEIGVDIVVESTGRFTKREDAAKHLEAGAKKVIISAPAKNEDITIVMGVN
QDKYDPKAHHVISNASXNETGYSHRVVLAAYIASKGL

>d1cero1 c.2.1.3 (O:1-148,O:313-333) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
{Thermus aquaticus}

MKVGINGFGRIGRQVFRILHSRGVEVALINDLTDNKT LAHLLKYDSIYHRFPGEVAYDDQYLYVDGKA
IRATAVKDPKEIPWAEAGVGVVIESTGVFTDADKAKAHLEGGAKKVIITAPAKGEDITIVMGVNHEAY
DPSRHHIISNASXNEWGYANRVADLVELVLRKGV

>d1hdgo1 c.2.1.3 (O:1-148,O:313-331) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
{Thermotoga maritima}

ARVAINGFRIGRLVYRIIYERKNPDIEVVAINDLTDTKTLAHLKLYDSVHKKFPGKVEYTENSLIVDG
KEIKVFAEPDPSKLPWKDLGVDFVIESTGVFRNREKAELHLQAGAKKVIITAPAKGEDITVVIGCNED
QLKPEHTIISCASXNEYGYSNRVVDLELLKLM

>d1b7go1 c.2.1.3 (O:1-138,O:301-340) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
{Archaeon *Sulfolobus solfataricus*}

MVNVAVNGYGTIGKRVADAIKQPDMKLVGVAKTSPNYEAFIAHRRGIRIYVPQQSIKKFEESGIPVAG
TVEDLIKTSDIVDTPNGVGAQYKPIYLQLQRNAIFQGGEKAEVADISFSALCNYNEALGKKYIRVVS
XESIVPENIDAIRASMKLMSAEDSMRITNESLGILKGYLI

>d1cf2o1 c.2.1.3 (O:1-138,O:304-336) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
{Archaeon *Methanothermus fervidus*}

MKAVAINGYGTIGKRVADAIQDDMKVIGVSKTRPDFEARMALKKGYDLYVAIPERVKLFKAGIE
VAGTVDDMLDEADIVIDCTPEGIGAKNLKMYKEKGKAIKAIQGGGEKHEDIGLSFNLSNYEESYGKDYT
RVVXIVPENVDVRAILEMEEDKYKSINKTNKAMNIL

>d1ggaa1 c.2.1.3 (A:1-164,A:334-358) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
{*Trypanosoma brucei brucei*, glycosome}

TIKVINGFGRIGRMVFQALCDDGLLNEIDVVAVVDMNTDARYFAYQMKYDSVHGKFKHSVSTTKS
KPSVAKDDTLVVNGHRILCVKAQRNPADLPWGKLGVEYVIESTGLFTVKSAEGLRGGARKVVISA
PASGGAKTFVMGVNHNHNNYNPREQHVSNASXNEWGYSHRVVDLVRHMAARDRAAKL

>d1i32a1 c.2.1.3 (A:1-165,A:335-358) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
{*Leishmania mexicana*}

APIKVGINGFGRIGRMVFQAIQDQGLIGTEIDVVAVVDMSTNAEYFAYQMKHDTVHGRPKYTVEAVK
SSPSVETADVLVVNGHRIKCVKAQRNPADLPWGKLGVDYVIESTGLFTDKLKAEGHIKGGAKKVVISA
PASGGAKTIVMGVNQHEYSPASHHVSNASXNEWAYSHRVVDLVRMAAKDAASS

>d1dssg1 c.2.1.3 (G:1-148,G:313-334) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
{Lobster (*Palinurus versicolor*)}

SKIGINGFGRIGRLVLRRAALEMGAQVVAVNDPFIALEYMVYMFKYDSTHGMFKGEVKAEDGALVVDG
KKITVFNEMKPENIPWSKAGAIEYIVESTGVFTTIEKASAHFKGGAKKVIISAPSADAPMFVCGVNLEK
YSKDMKVVSNASXNEFGYSQRVIDLIKHMQKVDSA

>d3gpdg1 c.2.1.3 (G:1-150,G:315-334) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
{Human (*Homo sapiens*)}

GKVKVGVDGFRIGRLVTRAAFNSGKVDIVAINDPFIDLHYMVYMFQYDSTHGKFGHTVKAEDGKL
VIDGKAITIFQERDPENIKWGDAGTAYVVESTGVFTTMEKAGAHKGGAKRIVISAPSADAPMFVVG
VNHFKYANSLKIISNASXNEFGYSERVVDLMAHMASKE

>d1jn0a1 c.2.1.3 (A:0-148,A:313-333) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
{Spinach (*Spinacia oleracea*)}

KLKVAINGFGRIGRNFLRCWHGKDSPLDVVVINDTGGVKQASHLLKYDSILGTFDADVKTAGDSAISV
GKVIKVVSDRNPVNLPWGDMDLVIETGVFVDRDGAGKHLQAGAKKVLITAPGKGDIPYVVGVN
EEGYTHADTIISNASXNEWGYSQRVVDLADIVANKWQ

>d1gl3a1 c.2.1.3 (A:1-133,A:355-367) Aspartate beta-semialdehyde dehydrogenase
{*Escherichia coli*}

MKNVGFIVWRGMVGSVLMQRMVEERDFDAIRPVFFSTSQLGQAAPSGGTTGTLQDAFDLEALKAL
DIIVTCQGGDYTNEIYPKLRESGWQGYWIDAASSLRMKDDAIILDPVNQDVITDGLNNGIRTFVGGX
AAEPLRRMLRQLA

>d1ebfa1 c.2.1.3 (A:2-150,A:341-359) Homoserine dehydrogenase {Baker's yeast}

{*Saccharomyces cerevisiae*}

STKVVNVAVIGAGVVGSFAFLDQLLAMKSTITYNLVLLAEAERSLISKDFSPLNVGSDWKAALAASTTK
TLPLDDLIAHLKTSPKPVILVDNTSSAYIAGFYTKFVENGISIATPNKKAFSSDLATWKALFSNKPTNG
FVYHEATVGAGLXAAVTAAGVLGDVIKIAQRL

>d1e5qa1 c.2.1.3 (A:2-124,A:392-450) Saccharopine reductase {Rice blast fungus
{*Magnaporthe grisea*}

ATKSVLMLGSGFVTRPTLDVLTDSGIKVTVACRTLESAKKLSAGVQHSTPISLDVNDDAALDAEVAKH
DLVISLIPYTFHATVIKSAIRQKKHVVTTSYVSPAMMELDQAAKDAGITVMNEIGXYSAMAKLVGVPC
AVAVKFLDGTISDRGVLAPMNSKINDPLMKELKEKYGIECKEKVVA

>d1f06a1 c.2.1.3 (A:1-118,A:269-320) Diaminopimelic acid dehydrogenase (DAPDH)
{*Corynebacterium glutamicum*}

MTNIRVAIVGYGNLGRSVEKLIKQPMDLVGIFSRRLDTKTPVFDVADVVDKHADDVDVFLFCMG
SATDIPEQAPKFAQFACTVDTYDNHRDIPRHRQVMNEAATAAGNVALVSTGXRNPFTASSQIAFGR
AAHRMKQQGQSGAFTVLEVAPYLLSPENLDDLIARDV

>d1dih_1 c.2.1.3 (2-130,241-273) Dihydrodipicolinate reductase {*Escherichia coli*}

HDANIRVAIAGAGGRMGRQLIQAALALEGVQLGAALEREGSSLLGSDAGELAGAGKTGVTVQSSDA
VKDDFDVDFTRPEGTNLHLAFCRQHGKGMVIGTTGFDEAGKQAIRDAAADIAIVFAANFSXMTFA
NGAVRSALWLSGKESGLFDMRDVLDLNNL

>d1k5ha2 c.2.1.3 (A:1-125,A:275-300) 1-deoxy-D-xylulose-5-phosphate reductoisomerase
{*Escherichia coli*}

MKQLTILGSTGSIGCSTLDVVRHNPEHFRVVALVAGKNVTRMVEQCLEFSPRYAVMDDEASAKLLKT
MLQQQGSRTTEVLGQQAACDMAALEDVDQVMAAIVGAAGLLPTLAAIRAGKTILLANKXDMRTPIA
HTMAWPNRVNSGVKPLDFC

>d1gcua1 c.2.1.3 (A:1-128,A:247-292) Biliverdin reductase {Rat (*Rattus norvegicus*)}

MDAEPKRKFGVVVVGVGRAGSVRLRDLKDPRSAAFNLIGFVSRRELGLSLEDEVQISLEDALRSQEID
VAYICSESSSHEDYIRQFLQAGKHVLEYPMTLSFAAAQELWELAAQKGRVLHEEHVELLXKNIFLKD
QDIFVQKLLDQVSAEDLAAEKKRIMHCLGLASDIQKLCH

>d1evja1 c.2.1.3 (A:30-160,A:323-381) Glucose-fructose oxidoreductase, N-terminal domain
{*Zymomonas mobilis*}

RRFGYAIVGLGKYALNQILPGFAGCQHSRIEALVDGNAEKAKIVAAEYGVDPKRIYDYSNFDKIAKDPK
IDAVYIILPNSLHAEFAIRAFKAGKHVMCEKPMATSVADCQRMIDAAKAANKKLMIGYRCHYXNQFS
AQLDHLAEAVINNKPVRSPEEGMQDVRLIQAIYEAAARTGRPVENTDWGYVRQGGY

>d1h6da1 c.2.1.3 (A:51-212,A:375-433) Glucose-fructose oxidoreductase, N-terminal
domain {*Zymomonas mobilis*}

QAATLPAGASQVPTTPAGRPMPYAIRPMPEDRRFGYAIVGLGKYALNQILPGFAGCQHSRIEALVSGN
AEKAKIVAAEYGVDPKRIYDYSNFDKIAKDPKIDAVYIILPNSLHAEFAIRAFKAGKHVMCEKPMAT
VADCQRMIDAAKAANKKLMIGYRCHYXNQFSAQLDHLAEAVINNKPVRSPEEGMQDVRLIQAIYE
AARTGRPVENTDWGYVRQGGY

>d1dpga1 c.2.1.3 (A:1-181,A:413-426) Glucose 6-phosphate dehydrogenase, N-terminal
domain {*Leuconostoc mesenteroides*}

VSEIKTLVTFGGTGD LAKRKLPSVFNLKKGYLQKHFAIVGTARQALNDDDEFKQLVRDCIKDFTDD
QAQAEAFIEHFSYRAHDVTDAAASYAVLKEAIEEAADKFDIDGNRIFYMSVAPRFFGTIAKYLKSEGLL
ADTGYNRLMIEKPFGTSYDTAAELQNDLENAFDDNQLFRIDHYLGXEPYERMIHDTMNGD

>d1qkia1 c.2.1.3 (A:12-199,A:435-449) Glucose 6-phosphate dehydrogenase, N-terminal

domain {Human (Homo sapiens)}

VCGILREELFQGD AFHQSDTHIFIIMGASGDLAKKKIYPTIWWLFRDGLLPENTFIVGYARSRLTVADI
RKQSEPFKATPEEKLKLEDFFARN SYVAGQYDDAASYQRLNSHMNALHLGSQANRLFYLALPPTVY
EAVTKNIHESCMSQIGWNRIIVEKPFGRDLQSSDRLSNHISSLFREDQIYRIXDAYERLILDVFCGSQ

>d2naca1 c.2.1.4 (A:148-335) Formate dehydrogenase {Pseudomonas sp., strain 101}

ISVAEHVMMILSLVRNYLPSHEWARKGGWNIADCVSHAYDLEAMHVGTVAAGRIGLAVLRRRLAPF
DVHLHYTDRHRLPESVEKELNLTWHATREDMYPVCDVVTLNCPHPETEHEMINDETCLKFKRGAY
IVNTARGKLCDRDAVARALESGLAGYAGDVWFPQPAPKDHPWRTMPYNGMTPHISG

>d1qp8a1 c.2.1.4 (A:83-263) Putative formate dehydrogenase {Archaeon Pyrobaculum
aerophilum}

ADAVAEFALALLLAPYKRRIQYGEKMKRGDYGRDVEIPLIQGEKVAVLGLGEIGTRVGKILAALGAQVR
GFSRTPKEGPWRFTNSLEEALREARAAVCALPLNKHTRGLVKYQHLALMAEDAVFVNVGRAEVL
RDGVLRLKERPFIFASDVWWRNDFAKDAEFFSLPNVVATPWVAG

>d1dxy_1 c.2.1.4 (101-299) D-2-hydroxyisocaproate dehydrogenase {Lactobacillus casei}

SPAAIAEFALDTLYLLRNMGKVQAQLQAGDYEKAGTFIGKELGQQTGVGMGTGHIGQVAIKLFGKFG
AKVIAYDPPMKGDHPDFDYVSLEDLFKQSDVIDLHVPGLIEQNTHIINEAAFNLMPGAI VINTARPN
LIDTQAMLSNLKSGKLAGVGIDTYEYETEDLLNLAKHGSFKDPLWDEL LGMPNVVLSPHIAYY

>d1gdha1 c.2.1.4 (A:101-291) D-glycerate dehydrogenase {Hyphomicrobium
methylovorum}

VTVATAEIAMLLLLGSARRAGEGKEMIRTRSWPGWEPELELVGEKLDNKTLGIYGFSGIQALAKRAQ
GFDMDIDYFDTHRASSSDEASYQATFHDSLDSLSVSQFFSLNAPSTPETRYFFNKATIKSLPQGAIVV
NTARGDLVDNELVVALEAGRLAYAGFDVFAGEPNINEGYDLPNTFLFPHIGSA

>d1psda1 c.2.1.4 (A:108-295) Phosphoglycerate dehydrogenase {Escherichia coli}

NTRSVAEVIGELLLLLRGVPEANAKAHRGVWNKLAAGSFEARGKKGIIYGYGHIGTQLGILAESLGM
YVYFYDIENKLPNGATQVQHLSDLLNMSDVVSLHVPENPSTKNMMGAKEISLMKPGSLLINASRG
VVDIPALCDALASKHLGAAIDVFPTEPATNSDPFTSPLCEFDNVLLTPHIGG

>d2dl da1 c.2.1.4 (A:104-300) D-lactate dehydrogenase {Lactobacillus helveticus}

PNAIAEHAAIQAARVLRQDKRMDEKMAKRDLRWAPTIGREVRDQVGVVGTGHIGQVFM RIMEGF
GAKVIAYDIFKNPELEKKGYYVDSLDDLYKQADVLSLHVPDPANVHMINDKSIAEMKDG VVIVNCSR
GRLVDTDAVIRGLDSGKIFGFVMDTYEDEVG VFNKD WEGKEFPDKRLADLIDRPNVLT PHTAF

>d1pjca1 c.2.1.4 (A:136-303) L-alanine dehydrogenase {Phormidium lapideum}

AGRLSVQFGARFLERQQGGRGVLLGGVPGVKPGKVVILGGGVGT EAAKMAVGLGAQVQIFDINVER
LSYLETLFGRVELLYSNSAEIETAVAEADLLIGAVLVPGRRAPILVPASLVEQMRTG SVIVDVAVDQGG
CVETLHPTSHTQPTYEVFGVVHYGVPNMPGA

>d1f8ga1 c.2.1.4 (A:144-326) Nicotinamide nucleotide transhydrogenase dI component
{Rhodospirillum rubrum}

AGYRAVIDGAYEFARAFPMMMTAAGTVPPARVLVFGVGVAGLQAIATAKRLGAVVMATD VRAATKE
QVESLGGKFITVDDEAMKTAETAGGYAKEMGEEFRKKQAEAVLKELVKT DIAIT TALIPGKPAPVLIT
EEMVTKMKPGSVIIDLAVEAGNCPLSEPGKIVVKHGVKIVGHTNVPSR

>d1b3ra1 c.2.1.4 (A:190-352) S-adenosylhomocystein hydrolase {Rat (Rattus norvegicus)}

NLYGCRESLIDGIKRATDVMIAGKVAVVAGYGDVKGCAQALRGFGARVIITEIDPINALQAAMEGYEV
TTMDEACKEGNIFVTTTGCVDIILGRHF EQMKDDAIVCNIGHFDVEIDVKWLNENAVEKVNIPQV
DRYLLKNGHRIILLAEGRVLNLGCAMGH

>d1gpja2 c.2.1.10 (A:144-302) Glutamyl tRNA-reductase middle domain {Archaeon

Methanopyrus kandleri}

SEGAVSIGSAAVELAERELGSLHDKTVLVVGGAGEMGKTVAKSLVDRGVRAVLVANRTYERAVELARD
LGGEAVRFDELVDHLARSDVVVSATAAPHPVIHVDDVREALRKRDRRSPILIIDIANPRDVEEGVENI
EDVEVRTIDDLRVIARENLERRRK

>d1mlda1 c.2.1.5 (A:1-144) Malate dehydrogenase {Pig (Sus scrofa)}

AKVAVLGASGGIGQPLSLLKNSPLVSRLTLYDIAHTPGVAADLSHIETRATVKGYLGPQLPDCLKGC
DVVVIPAGVPRKPGMTRDDLNTNATIVATLTAACAQHCPDAMICIISNPVNSTIPITAEVFKKHGVY
NPNKIFG

>d5mdha1 c.2.1.5 (A:1-154) Malate dehydrogenase {Pig (Sus scrofa)}

SEPIRVLTGAAGQIAYSLYSIGNGSVFGKDQPIHLVLLDITPMMGVLDGVLMEQLDCALPLLKDVIAI
DKEEIAFKDLVDVAILVGSMPRRDGMERKDLLKANVKIFKCQGAALDKYAKKSVKIVVGNPANTNCL
TASKSAPSIPKENFSC

>d7mdha1 c.2.1.5 (A:23-197) Malate dehydrogenase {Sorghum (Sorghum vulgare),
chloroplast}

DCFGVFCTTYDLKAEDKTKSWKKLVNIAVSGAAGMISNHLFLKASGEVFGQDQPIALKLLGSERSF
QALEGVAMELEDSLYPLLREVSIGIDPYEVFEDVDWALLIGAKPRGPGMERAALLDINGQIFADQGKA
LNAVASKNVKVLVGNPCNTNALICLKNAPDIPAKNFHAL

>d1civa1 c.2.1.5 (A:12-193) Malate dehydrogenase {Flaveria bidentis, chloroplast}

LPAKQKPECFGVFCLTYDLKAEETKSWKKIINVAVSGAAGMISNHLFLKASGEVFGPDQPISLKL
GSERSFAALEGVAMELEDSLYPLLQVSIGIDPYEIFQDAEWALLIGAKPRGPGMERADLLDINGQIFA
EQGKALNAVASPNVKVMVGNPCNTNALICLKNAPNIPPKNFHAL

>d2cmd_1 c.2.1.5 (1-145) Malate dehydrogenase {Escherichia coli}

MKVAVLGAAGGIGQALALLKTQLPSGSELSLYDIAPVTPGVAVDLSHIPTAVKIKGFSGEDATPALEG
ADVVLISAGVRRKPGMDRSDLFNVNAGIVKNLVQQVAKTCPKACIGIITNPVNTTVAIAAEVLKKAGV
YDKNKLF

>d1bdma1 c.2.1.5 (A:0-154) Malate dehydrogenase {Thermus flavus}

MKAPVRVAVTGAAGQIGYSLFRIAAGEMLGKDQPVILQLEIPQAMKALEGVVMELEDCAFPLLAG
LEATDDPDVAFKDADYALLVGAAPRKAGMERRDLLQVNGKIFTEQGRALAEVAKKDVKVLVGNPA
NTNALIAYKNAPGLNPRNFTAM

>d2hpa1 c.2.1.5 (A:22-162) Malate dehydrogenase {Archaeon Haloarcula marismortui}

TKVSVVGAAGTVGAAAGYNIALRDIADVVVDIPDKEDDTVGQAADTNHGIAYDSNTRVRQGGYE
DTAGSDVVVITAGIPRQPGQTRIDLADGNAPIMEDIQSSLDEHNDYISLTTSNPVDLLNRHLYEAGD
RSREQVIG

>d1b8pa1 c.2.1.5 (A:3-158) Malate dehydrogenase {Aquaspirillum arcticum}

KTPMRVAVTGAAGQICYSLLFRIANGDMLGKDQPVILQLEIPNEKAQKALQGVMMMEIDDCAFPLLA
GMTAHADPMTAFKDADVALLVGARPRGPGMERKDLLEANAQIFTVQKKAIDAVASRNKVLVGNP
ANTNAYIAMKSAPSLPAKNFTAM

>d1guya1 c.2.1.5 (A:1-143) Malate dehydrogenase {Chloroflexus aurantiacus}

MRKKISHIGAGFVGS'TTAHWLAAKELGDIVLLDIVEGVPQGKALDLYEASPIEGFDVVRTGTNNYADT
ANSDIVVVTSGAPRPGMSREDLIKVNADITRACISQAAPLSPNAVIIMVNNPLDAMTYLAAEVSGFP
KERVIGQ

>d1gv0a1 c.2.1.5 (A:1-142) Malate dehydrogenase {Chlorobium tepidum}

MKITVIGAGNVGATTAFRLAEKQLARELVLLDVEGIPQKALDMYESGPVGLFDTKVTGSNDYADT
ANSDIVVITAGLPRKPGMTREDLLSMNAGIVREVTGRIMEHSKNPIIVVSNPLDIMTHVAWQKSL

PKERVIGM

>d1guza1 c.2.1.5 (A:1-142) Malate dehydrogenase {Chlorobium vibrioforme}
MKITVIGAGNVGATTAFLAEKQLARELVLLDVEGIPQGGKALDMYESGPVGLFDTKVTSNDYADT
ANSDIVITAGLPRKPGMTRELLMKNAGIVKEVTDNIMKHSKNPIIIVVSNPLDIMTHVAWVRSGLP
KERVIGM

>d1hya1 c.2.1.5 (A:21-166) L-2-hydroxyisocaproate dehydrogenase, L-HICDH
{Lactobacillus confusus}
ARKIGIILGNVGA AVAHGLIAQGVADDYVFIDANEAKVKADQIDFQDAMANLEAHGNIVINDWAAL
ADADVISTLGNIKLQQDNPTGDRFAELKFTSSMVQSVGTNLKESGFHGVLVVISNPVDVITALFQHV
TGFPAAHKVIGT

>d5ldh_1 c.2.1.5 (1-162) Lactate dehydrogenase {Pig (Sus scrofa)}
ATLKEKLIAPVAQQETTIPDNKITVVGQVGMACAISILGKSLTDELALVDVLEDKCLKGEMMDLQH
GSLFLQTPKIVANKDYSVTANSKIVVVTAGVRQQEGESRLNLVQRNVNVFKFIIPQIVKYSPNCIIIVVS
NPVDILTYVAWKLSGLPKHRVIG

>d9lta1 c.2.1.5 (A:1-162) Lactate dehydrogenase {Pig (Sus scrofa)}
ATLKDQLIHNLKKEEHVPHNKITVVGAVGMACAISILMKELADEIALVDVMEKCLKGEMMDLQH
GSLFLRTPKIVSGKDYNVTANSRLVVITAGARQQEGESRLNLVQRNVNIFKFIIPNIVKYSPNCKLLVVS
NPVDILTYVAWKISGFPKNRVIG

>d1i0za1 c.2.1.5 (A:1-160) Lactate dehydrogenase {Human (Homo sapiens), heart isoform
(H chain)}
ATLKEKLIAPVAEEEEATVPNNKITVVGQVGMACAISILGKSLADELALVDVLEDKCLKGEMMDLQH
GSLFLQTPKIVADKDYSVTANSKIVVVTAGVRQQEGESRLNLVQRNVNVFKFIIPQIVKYSPDCIIIVVS
NPVDILTYVTWKLSGLPKHRVIG

>d1i10a1 c.2.1.5 (A:1-159) Lactate dehydrogenase {Human (Homo sapiens), muscle isoform
(M chain)}
ATLKDQLIYNLLKKEEQTPQNKITVVGAVGMACAISILMKDLADELALVDVIEDKCLKGEMMDLQHG
SLFLRTPKIVSGKDYNVTANSKLVIIITAGARQQEGESRLNLVQRNVNIFKFIIPNVVVKYSPNCKLLIVSN
PVDILTYVAWKISGFPKNRVIG

>d2ldx_1 c.2.1.5 (1-159) Lactate dehydrogenase {Mouse (Mus musculus)}
STVKEQLIQNLVPEDKLSRCKITVVGVDVGMACAISILLKGLADELALVDADTDKLRGEALDLQHGS
LFLSTPKIVFGKDYNVSANSKLVIIITAGARMVSGQTRLDLLQRNVAIMKAIVPGVIQNSPDCKIIVVTN
PVDILTYVVWKISGFVGRVIG

>d1ldm_1 c.2.1.5 (1-160) Lactate dehydrogenase {Dogfish (Squalus acanthias)}
ATLKDKLIGHLATSQEPRSYNKITVVGAVGMACAISILMKDLADEVALVDVMEKCLKGEMMDLQ
HGSLFLHTAKIVSGKDYSVSAGSKLVVITAGARQQEGESRLNLVQRNVNIFKFIIPNIVKHSPDCIILVVS
NPVDVLTYYVAWKLSGLPMHRIIG

>d1ceqa1 c.2.1.5 (A:19-163) Lactate dehydrogenase {Malaria parasite (Plasmodium
falciparum)}
PKAKIVLVGSGMIGGVMATLIVQKNLGDVFLDIVKNMPHGKALDTSHTNVMAYSNCKVSGSNTYD
DLAGSDVVIVTAGFTKAPGKSDKEWNRDPLNKNIMIEIGGHIKKNCPNAFIIVVTNPVDVMVQL
LHQHSGVPKNKIIGL

>d1ldna1 c.2.1.5 (A:15-162) Lactate dehydrogenase {Bacillus stearothermophilus}
MKNNGGARVVVIGAGFVGASYVFALMNQGIADIEIVLIDANESKAIGDAMDFNHGKVFAPKPVDIWH
GDYDDCRDADLVVICAGANQKPGETRLDLVDKNIAIFRSIVESVMASGFQGLFLVATNPVDILTYATW

KFSGLPHERVIGSG

>d1llc_1 c.2.1.5 (13-164) Lactate dehydrogenase {*Lactobacillus casei*}

ASITDKDHQKVLVGDGAVGSSYAFAMVLQGIHQEIGIVDIFKDKTKGDAIDLNALPFTSPKKIYSAEY
SDAKDADLVVITAGAPKQPGETRLDLVNKNLKILKSIVDPVDSGFNLIFLVAANPVDILTYATWKLSG
FPKNRVVGS

>d1ez4a1 c.2.1.5 (A:16-162) Lactate dehydrogenase {*Lactobacillus pentosus*}

SMPNHQKVVVLVGDGAVGSSYAFAMAQQGIAEEFVIVDVVKDRTKGDALDLEDAQAFTAPKKIYSGEY
SDCKDADLVVITAGAPKQPGESRLDLVNKNLNILSSIVKPVVDSGFDGIFLVAANPVDILTYATWKFSG
FPKERVIGSG

>d1llda1 c.2.1.5 (A:7-149) Lactate dehydrogenase {*Bifidobacterium longum*, strain am101-2}

PTKLAVIGAGAVGSTLAFAAAQRGIAREIVLEDIAKERVEAEVLDMQHGSFYPTVSIIDGSDDPEICRD
ADMVVITAGPRQKPGQSRLELVGATVNILKAIMPNLVKVPNAIYMLITNPVDIATHVAQKLTGLPEN
QIFGSG

>d1a5z_1 c.2.1.5 (22-163) Lactate dehydrogenase {*Thermotoga maritima*}

MKIGIVGLGRVGSSTAFALLMKGFAREMLIDVDKKRAEGDALDLIHGTPFTRRANIYAGDYADLKGS
DVVIVAAGVPQKPGETRLQLLGRNARVMKEIARNVSKYAPDSIVIVVTNPVDVLTYYFFLKESGMDPR
KVFGS

>d1hyea1 c.2.1.5 (A:1-145) MJ0490, lactate/malate dehydrogenase {*Archaeon Methanococcus jannaschii*}

MKVTHIGASGRVGSATALLAKEPFMKDLVLIGREHSINKLEGLREDIYDALAGTRSDANIYVESDENL
RIIDESDVVIITSGVPRKEGMSRMDLAKTNAKIVGKYAKKIAEICDTKIFVITNPVDVMTYKALVDSKF
ERNQVFG

>d1qnga2 c.2.1.6 (A:82-307) Acetohydroxy acid isomeroeductase, ketoacid reductoisomerase (KARI) {*Spinach (Spinacia oleracea)*}

SATTFDFDSSVFKKEKVTLSGHDEYIVRGGRNLFPLLPDAFKGIKQIGVIGWGSQAPAQAQNLKDSL
EAKSDVVVIGLRKGSNSFAEARAAGFSEENGLGDMWETISGSDLVLLLISDSAQADNYEKVFSHM
KPNLILGSLHGLLQSLGQDFPKNISVIAVCPKMGPSVRRRLVQKQKEVNGAGINSSFAVHQDVD
GRATDVALGWSIALGSPFTFATT

>d2pgd_2 c.2.1.6 (1-176) 6-phosphogluconate dehydrogenase {*Sheep (Ovis orientalis aries)*}

AQADIALIGLAVMGQNLILNMNDHGFVVCFAFNRTVSKVDDFLANEAKGTVLGAHSLEEMVSKLKK
PRRIILLVKAGQAVDNFIEKLVPLLDIGDIIIDGGNSEYRDTMRRRCRDLKDKGILFVGSVSGGEDGAR
YGPLMPPGNGKEAWPHIKAIFQGIAAKVGTGPECCDWVGDD

>d1pgja2 c.2.1.6 (A:1-178) 6-phosphogluconate dehydrogenase {*Trypanosoma brucei*}

SMDVGVVGLGVMGANLALNIAEKGFVAVFNRTYSKSEEFMKANASAPFAGNLKAFETMEFAAASL
KKPRKALILVQAGAATDSTIEQLKKVFEKGDILVDTGNAHFQDQGRRAQQLAAGLRFGLGMGISGGE
EGARKGPAFFPGTSLVWEEIRPIVEAAAAKADDGRPCVTMNGSG

>d1f0ya2 c.2.1.6 (A:12-203) Short chain L-3-hydroxyacyl CoA dehydrogenase {*Human (Homo sapiens)*}

KIIVKHVTVIGGGLMGAGIAQVAAATGHTTVVLVDQTEDILAKSKKIEESLRKVAKKKFAENPKAGDE
FVEKTLSTIATSTDAASVHSTDLVVEAIVENLKVKNELFKRLDKFAAEHTIFASNTSSLQITSIANAT
TRQDRFAGLHFFNPVPMKLVKVEIKTPMSTQKTFESLVDFSKALGKHPVSKDTP

>d1dlja2 c.2.1.6 (A:1-196) UDP-glucose dehydrogenase (UDPGDH) {*Streptococcus pyogenes*}

MKIAVAGSGYVGLSLGVLLSLQNEVTIVDILPSKVDKINGLSPIQDEYIEYYLKSQLSIKATLDSKAA

YKEAELVIIATPTNYNSRINYFDTQHVETVIKEVLSVNSHATLIKSTIPIGFITEMRQKFQTDRIIFSPE
FLRESKALYDNLPSRIIVSCEENDSPKVKADAIEKFAALLKSAKKNNVPVLIMG
>d1bg6_2 c.2.1.6 (4-187) N-(1-D-carboxylethyl)-L-norvaline dehydrogenase {Arthrobacter,
strain 1c}
SKTYAVLGLGNGGHAFAYLALKGQSVLAWDIDAQRKEIQDRGAIIEGPGLAGTAHPDLLTSDIGLA
VKDADVILIVVPAIHHASIAANIASYISEGQLIILNPGATGGALEFRKILRENGAPEVTIGETSSMLFTCR
SERPGQVTVNAIKGAMDFACLPAKAGWALEQIGSVLPQYVAVE
>d1evya2 c.2.1.6 (A:9-188) Glycerol-3- phosphate dehydrogenase {Trypanosome
(Leishmania mexicana)}
KDELLYLKAVVFGSGAFGTALAMVLSKKCREVCVWHMNEEEVRLVNEKRENVLFLKGVQLASNIT
FTSDVEKAYNGAEIILFVIPTQFLRGFFEKSGGNLIAYAKEKQVPVLVCTKGIERSTLKFP AEIIGEF LPS
PLLSVLGAPSFAIEVATGVFTCVSIASADINVARRLQRIMSTG
>d1ks9a2 c.2.1.6 (A:1-167) Ketopantoate reductase PanE {Escherichia coli}
MKITVLGCGALGQLWLTALCKQGHEVQGWLRVPQPYCSVNLVETDGSIFNESLTANDPDLATSDLL
LVTLKAWQVSDAVKSLASTLPVTTPIILLHNGMGTIEELQNIQQPLLMGTTTHAARRDGNVIVHVN
GITHIGPARQQDGDYSYLADILQTVLPDVAWHN
>d1jaya_ c.2.1.6 (A:) Coenzyme F420H2:NADP+ oxidoreductase (FNO) {Archaeon
Archaeoglobus fulgidus}
MRVALGGTGNLKGGLALRLATLGHEIVVGSRRREEKAEAKAAEYRRIAGDASITGMKNEDAAEACDI
AVLTIPWEHAIDTARDLKNILREKIVVSPVSRGAKGFTYSSERSAAEIVAEVLESEKVVSAHTIPA
ARFANLDEKFDWDVPCGDDDESKKVVMSLISEIDGLRPLDAGPLSNSRLVESLTPLILNIMRFNGM
GELGIKFL
>d1bgva1 c.2.1.7 (A:195-449) Glutamate dehydrogenase {Clostridium symbiosum}
KARSFGGSLVRPEATGYGSVYYVEAVMKHENDTLVGKTVLAGFGNVAVGAAKLAELGAKAVTLS
GPDGYIIDPEGITTEEKINYMLEMRASGRNKVQDYADKFGVQFFPGEKPGWQKVDIIMPCATQNDV
DLEQAKKIVANNVYYYIEVANMPTTNEALRFLMQPNMVAAPSKAVNAGGVLVSGFEMSQNSERLS
WTAEVDSKHLQVMTDIHDGSAAAAERYGLGYNLVAGANIVGFQKIADAMMAQGI AW
>d1gtma1 c.2.1.7 (A:181-419) Glutamate dehydrogenase {Archaeon Pyrococcus furiosus}
GGSLGRIEATARGASYTIREAAKVLGWDTLKGTIAIQGYGNAGYYLAKIMSEDFGMKVAVS DSKGG
IYNPDGLNADEV LKWKNEHGSVKDFPGATNITNEELLELEVDVLAPAAIEEVITKKNADNIKAKIVA
EVANGPVTPEADEILFEKGILQIPDFLCNAGGVTVSYFEWVQ NITGYYWTIEEVRERLDKKMTKAFY
DVYNI AKEKNIHMRDAAYVVAVQRVYQAMLD RGVVKK
>d1euza1 c.2.1.7 (A:181-419) Glutamate dehydrogenase {Archaeon Thermococcus
profundus}
IGGSLGRGTATAQGAIFTIREAAKALGIDLKGGKIAVQGYGNAGYYTAKLAKEQLGMTVVAVS DSRGGI
YNPDGLDPDEVLKWKREHGSVKDFPGATNITNEELLELEVDVLAPAAIEEVITEKNADNIKAKIVAE
VANGPVTPEADDILREKILQIPDFLCNAGGVTVSYFEWVQNINGYYWTEEEVREKLDKKMTKAFW
EVYNT HKDKNIHMRDAAYVVAVSRVYQAMKDRGVVKK
>d1bvua1 c.2.1.7 (A:181-418) Glutamate dehydrogenase {Archaeon Thermococcus litoralis}
GGIVARMDATARGASYTVREAAKALGMDLKGKTI AIQGYGNAGYYMAKIMSEYGMKVAVS DTKG
GIYNPDGLNADEV LAWKKKTGSVKDFPGATNITNEELLELEVDVLAPSAIEEVITKKNADNIKAKIVA
ELANGPTTPEADEILYEKGIIPDFLCNAGGVTVSYFEWVQ NITGDYWTVEETRAKLDKKMTKAFW
DVYNT HKEKNINMRDAAYVVAVSRVYQAMKDRGVVKK
>d1b26a1 c.2.1.7 (A:179-412) Glutamate dehydrogenase {Thermotoga maritima}

GGSKGREETGRGVKVCAGLAMVDLGDIPKATVAVQGFNGVQFAALLISQELGSKVAVSDSRGGI
YNPEGFDVEELIRYKKEHGTVVVTPKGERITNEELLELDVDILVPAALEGAIHAGNAERIKAKAVVEG
ANGPTTPEADEILSRRGILVVPDILANAGGVTVSYFEWVQDLQSFWDLDQVRNALEKMMKGAFND
VMKVKEKYNVDMRTAAYILAIRVAYATKKRG

>d1hwx1 c.2.1.7 (A:209-501) Glutamate dehydrogenase {Cow (Bos taurus)}

HGRISATGRGVFHGIENFIENASYMSILGMTPGFGDKTFAVQGFNGVGLHSMRYLHRFGAKCVAVGES
DGSIWNPDGIDPKELEDFKLQHGHTILGFPKAKIYEGSILEVDCDILIPAASEKQLTKSNAPRVKAKIAE
GANGPTTPQADKIFLERNIMVIPDLYLNAGGVTVSYFQILKNLNHVSYGRLTFKYERDSNYHLLMSV
QESLERKFGKHGGTIPIVPTAEFQDRISGASEKDIVHSGLAYTMERSARQIMRTAMKYNLGLDLRTAA
YVNAIEKVFRVYNEAGVTFT

>d1leha1 c.2.1.7 (A:135-364) Leucine dehydrogenase {Bacillus sphaericus}

GISPAFGSSGNPSPVTAYGVYRGMKAAAKEAFGSDSLEGLAVSVQGLGNVAKALCKKLNTEGAKLVVT
DVNKA AVSAVAEEGADAVAPNAIYGVTCDIFAPCALGAVLNDF TIPQLKAKVIAGSADNQLKDPRH
GKYLHELGVYAPDYVINAGGVINVADELYGYNRTRAMKRVDGIYDSIEKIFAISKRDGVP SYVAADRM
AEERIAKVAKARSQFLQDQRNINLGR

>d1c1da1 c.2.1.7 (A:149-349) Phenylalanine dehydrogenase {Rhodococcus sp., M4}

SAFTTAVGVFEAMKATVAHRGLGSLDGLTVLVQGLGAVGGSLASLAAEAGAQLLVADTDTERVAHAV
ALGHTA VALEDVLPDVFAPCAMGGVITTEVARTLDCSVVAGAANNVIADEAASDILHARGILYAP
DFVANAGGAIHLVGREVLGWSESVHERAVAIGDTLNQVFEISDNDGVT PDEAARTLAGRRAREAS

>d1a4ia1 c.2.1.7 (A:127-296) Methylenetetrahydrofolate dehydrogenase/cyclohydrolase
{Human (Homo sapiens)}

LTSINAGRLARGDLNDCFIPCTPKGCLELIKETGVPIAGRHAVVVGRSKIVGAPMHDL LLWNNATVTT
CHSKTAHLDEEVNKG DILVVATGQPEMVKG EWIKPGAIVIDCGINYPDDKKPNGRKVVGDVAYDEA
KERASFITPVPGGVGPMTVAMLMQSTVESAKRFLE

>d1b0aa1 c.2.1.7 (A:123-288) Methylenetetrahydrofolate dehydrogenase/cyclohydrolase
{Escherichia coli}

FHPYNVGRLCQRAPRLRPCTPRGIVTLLERYNIDTFGLNAV VIGASNIVGRPMSMELLLAGCTTTVTH
RFTKNLRHHVENADLLIVAVGKPGFIPGDWIKGAIVIDVGINRLENGKVVGDVVFEDAAKRASYITP
VPGGVGPMTVATLIENTLQACVEYHDPQDE

>d1edza1 c.2.1.7 (A:149-319) Methylenetetrahydrofolate dehydrogenase/cyclohydrolase
{Baker's yeast (Saccharomyces cerevisiae)}

PCTPLAIVKILEFLKIYNNLLPEGNRLYGKKCIVINRSEIVGRPLAALLANDGATVYSVDVNNIQKFTR
GESLKL NKHHVEDLGEYSEDLLKKCSLSDV VITGVPSENYKFPTEYIKEGAVCINFACTKNFSDDVK
EKASLYVPMTGKVTIAMLLRNMLRLVRNVELSKE

>d1do8a1 c.2.1.7 (A:280-573) Mitochondrial NAD(P)-dependent malic enzyme {Human
(Homo sapiens)}

IQGTAVALAGLLAAQKVISKPISEHKILFLGAGEAALGIANLIVMSMVENGLSEQAQKKIWMFDKY
GLLVKGRKAKIDSYQEPFTHSAPESIPDTFEDAVNILKPSTIIGVAGAGRLFTP DVIRAMASINERPVIF
ALSNP TAAECTAE EAYTLTEGRCLFASGSPFGPVKLT DGRVFTPGQGNVYIFPGVALAVILCNTRHI
SDSVFLEAAKALTSQLTDEELA QGRLYPPLANIQEV SINIAIKVTEYLYANKMAFRYPEPEDKAKYVKE
RTWRSEYDSLLPDVYEW P

>d1id1a_ c.2.1.9 (A:) Rck domain from putative potassium channel Kch {Escherichia coli}

HRKDHFIVCGHSILAIN TILQLNQRGQNVTVISNLPEDDIKQLEQLGDNADVIPGDSNDSSVLKKAG
IDRCRAILALSNDADNAFVVL SAKDMSSDVKTVLAVSDSKNLNKIKMVHPDIILSPQLFGSEILARV

LNGEINNDMLVSMLLN

>d1jka1 c.2.1.8 (A:1-121) Succinyl-CoA synthetase, alpha-chain, N-terminal (CoA-binding) domain {Escherichia coli}

SILIDKNTKVICQGFTGSQGFHSEQAIAYGTKMVGVTTPGKGGTTHLGLPVFNTVREAVAATGATAS
VIYVPAPFCKDSILEAIDAGIKLIITITEGIPTLDMLTVKVKLDEAGVRMIGP

>d1euca1 c.2.1.8 (A:1-130) Succinyl-CoA synthetase, alpha-chain, N-terminal (CoA-binding) domain {Pig (Sus scrofa)}

CSYTASRKHLYVDKNTKVICQGFTGKQGFHSSQQALEYGTNLVGGTTPGKGGKTHLGLPVFNTVKEA
KEQTGATASVIYVPPFAAAINEAIDAEVPLVVCITEGIPQQDMVRVKHRLLRQKTRLIGP

>d1djna2 c.3.1.1 (A:490-645) Trimethylamine dehydrogenase, C-terminal domain {Methylophilus methylotrophus, w3a1}

RWNTDGTNCLTHDPIPGADASLPDQLTPEQVMDGKKKIGKRVVILNADTYFMAPSLAEKLATAGHE
VTIVSGVHLANYMHFTLEYPNMMRRLHELHVEELGDHFCRSRIEPRMEIYNIWGDGSKRTYRGPV
SPRDANTSHRWIEFDSLVLVTGRH

>d1cja1 c.3.1.1 (A:107-331) Adrenodoxin reductase of mitochondrial p450 systems {Cow (Bos taurus)}

HQALDIPGEELPGVFSARAFVWYNGLPENRELAPDLSCDTAVILGQGNVALDVARILLTPPDHLEKT
DITEAALGALRQSRVKTWVWVGRGRLQVAFTIKELREMIQLPGTRPMLDPADFLGLQDRIKEAARP
RKRLMELLRTATEKPGVEEAARRASASRAWGLRFFRSPQQVLPSPDGRRAAGIRLAVTRLEGIGEA
TRAVPTGDVEDLPCGLVLSSIGY

>d1h7wa3 c.3.1.1 (A:288-440) Dihydropyrimidine dehydrogenase, domain 3 {Pig (Sus scrofa)}

PKTDDIFQGLTQDQGFYTSKDFLPLVAKSSKAGMCACHSPLPSIRGAVIVLGAGDTAFDCATSALRCG
ARRVFLVFRKGFVNIRAVPEEVELAKEEKCEFLPFLSPRKVIVKGGRIVAVQFVRTEQDETGWNEDE
DQIVHLKADVVISAFGS

>d1coy_1 c.3.1.2 (4-318,451-506) Cholesterol oxidase {Brevibacterium sterolicum}

RTLADGDRVPALVIGSGYGGAVAALRLTQAGIPTQIVEMGRSWDTPGSDGKIFCGMLNPDKRSMWL
ADKTDQVSNFMGFGINKSIDRYVGVLDSEFSGIKVYQGRGVGGGSLVNGGMAVTPKRNYFEEILPS
VDSNEMYNKYFPRANTGLGVNNIDQAWFESTEWEYKFARTGRKTAQRSGFTTAFVNPVYDFEYMKK
EAAGQVTKSGLGGEVIYGNAGKSLDKTYLAQAATGKLTITTLHRVTKVAPATGSGYSVTMEQIDE
QGNVVATKVVTADRFFAAGSVGTSKLLVSMKAQGHLPNLSSQVGEGWXGVLLNKATDNFGRLEPY
PGLYVVDGSLVPGNVGNPFVTITALAERNMDKIISDI

>d1ijha1 c.3.1.2 (A:9-318,A:451-506) Cholesterol oxidase {Streptomyces sp.}

GYVPAVVIGTGYGAAVSALRLGEAGVQTLMLEMQLWNQPGPDGNIFCGMLNPDKRSSWFKNRTE
APLGSFLWLDVVRNIDPYAGVLDRVNYDQMSVYVGRGVGGGSLVNGGMAVEPKRSYFEEILPRVDS
SEMYDRYFPRANSMLRVNHIDTKWFEDTEWYKFARVSREQAGKAGLGTVPVNYDFGYMQREA
AGEVPKSALATEVIYGNHKGQSLDKTYLAAALGTGKVTIQTTLHQVKTIRQTKDGGYALTVEQKDTD
GKLLATKEISCRYLFLGAGSLGSTELLVRARDTGTLPNLSEVGAGWXGCVLGKATDDYGRVAGYKNL
YVTDGSLIPGSVGLPFVTITALAERNVERIIKQDV

>d1k0ia1 c.3.1.2 (A:1-173,A:276-394) p-Hydroxybenzoate hydroxylase, PHBH {Pseudomonas aeruginosa}

MKTQVAIIGAGPSGLLLGQLLHKAGIDNVILERQTPDYVLGRIRAGVLEQGMVDLLREAGVDRRMAR
DGLVHEGVEIAFAGQRRRIDLKRLSGGKTVTVYQGTEVTRDLMEAREACGATTVYQAAEVRLHDLQ
GERPYVTFERDGERLRLLDCDYIAGCDGFHGISRQSIPAERXMQHGRFLFLAGDAAHIVPPTGAKGLNL

AASDVSTLYRLLLKAYREGRGELLERYSAICLRRRIWKAERFSWWMTSVLHRFPD TDAFSQRIQQTEL
EYYLGSEAGLATIAENYVGLPYEEIE

>d1el8a1 c.3.1.2 (A:1-217,A:322-385) Sarcosine oxidase {*Bacillus* sp., strain b0618}
STHFDVIVVVGAGSMGMAAGYQLAKQGKTLVDAFDPPHTNGSHHGDTRIIRHAYGEGREYVPLAL
RSQELWYELEKETHHKIFTKTGVLVFGPKGESAFVAETMEAAKEHSLTVDLLEGDEINKRWPGITVP
ENYNAIFEPNSGVLFSENCIRAYRELAEARGAKVLTHTRVEDFDISPDSVKIETANGSYTADKLIVSMG
AWNSKLLSKLNDIPXDEHFIIDLHPEHSNVVIAAGFSGHGFKFSSGVGEVLSQLALTGKTEHDISIFSI
NRPALKESLQ

>d1foha5 c.3.1.2 (A:1-240,A:342-461) Phenol hydroxylase {Soil-living yeast (*Trichosporon
cutaneum*)}

TKYSESYCDVLIVGAGPAGLMAARVLSEYVRQKPD LKVRIIDKRSTKVYNGQADGLQCRTLES LKNLG
LADKILSEANDMSTIALYNPDENHIRRTDRIPDTLPGISRYHQVVLHQGRIERHILDSIAEISDTRIKV
ERPLIPEKMEIDSSKAEDPEAYPVTMTLRYMSDHESTPLQFGHKTENSLFHSNLQTQEEEDANYRLP
EGKEAGEIETVHCKYVIGCDGGHSWVRRTLGFEMIXVTEKFSKDERVFIAGDACHTHSPKAGQGMN
TSMMDTYNLGWKLGVLVTGRAKRDLKTYEEERHAFQAALIDFDHQFSRFLSFRPAKDVADEMGVS
MDVFKEAFVKNEFASGTAINYDE

>d1cf3a1 c.3.1.2 (A:3-324,A:521-583) Glucose oxidase {*Aspergillus niger*}

GIEASLLTDPKDVSGRTVDYIIAGGGTLGTLTAARLTENPNISVLVIESGSYESDRGPIIEDLNAYGDIFGS
SVDHAYETVELATNNQTALIRSGNGLGGSTLVNGGTWTRPHKAQVDSWETVFGNEGWNWDNVAA
YSLQAERARAPNAKQIAAGHYFNASCHGVNGTVHAGPRDTGDDYSPIVKALMSAVEDRGVPTKKDF
GCGDPHGVSMPNLTLEDQVRSDAAREWLLPNYQRPNLQVLTGQYVGVKVLSSQNGTTPRAVGVEF
GTHKGNTHNVYAKHEVLLAAGSAVSPTILEYSGIGMKSILEPLGIDTVVDLPVGLXCSMMPKEMGGV
VDNAARVYGVQGLRVIDGSIPPTQMSSHVMTVFYAMALKISDAILEDYASMQ

>d1gpea1 c.3.1.2 (A:1-328,A:525-587) Glucose oxidase {*Penicillium amagasakiense*}

YLPAQQIDVQSSLLSDPSKVAGKTYDYIIAGGGTLGTLVAAKLTENPKIKVLVIEKGFYESNDGAIIEDPN
AYGQIFGTTVDQNYLTVPLINNRTNNIKAGKGLGGSTLINGDSWTRPKVQIDSWEKVFGEWGN
WDNMFYEMKKAEEAARTPTAAQLAAGHSFNATCHGTNGTVQSGARDNGQPWSPIMKALMNTVSA
LGVPVQQDFLCGHPRGVSMIMNLDENQVRVDAARAWLLPNYQRSNLEILTGQMVGVKLVFKQTAS
GPQAVGVNFGTNKAVNFDVFAKHEVLLAAGSAISPLILEYSGIGLKSVDQANVTQLLDLPVGIXCSM
MSRELGGVVDATAKVYGTQGLRVIDGSIPPTQVSSHVMTIFYGMALKVADAILDDYAKSA

>d1b5qa1 c.3.1.2 (A:5-293,A:406-463) Polyamine oxidase {Maize (*Zea mays*)}

PRVIVVAGMSGISAAKRLSEAGITDLLILEATDHIGGRMHKTNFAGINVELGANWVEGVNGGKMNP
IWPIVNSTLKLNRNFRSDFDYLAQNVIKEDGGVYDEYVQKRIELADSVEEMGEKLSATLHASGRDD
MSILAMQRLNEHQPNPATPVDMMVVDYKFDYEFAPPRVTSLQNTVPLATFSDFGDDVYFVADQR
GYEAVVYLAGQYLKTDKSGKIVDPRLQLNKVVREIKYSPGGVTVKTEDNSVYSADYVMVSASLGV
LQSDLIQFKPKLPTWKVRAIQFXWPVGNRYEYDQLRAPVGRVYFTGEHTSEHYNGYVHGAYLSGI
DSAEILINCAQKKMC

>d1f8ra1 c.3.1.2 (A:4-319,A:433-486) L-amino acid oxidase {Malayan pit viper (*Calloselasma
rhodostoma*)}

RNPLAEFCQENDYEEFLEIARNGLKATSNPKHVIVGAGMAGLSAAYVLAGAGHQVTVLEASERPGG
RVRTYRNEEAGWYANLGPMLPEKHRIVREYIRKFDLRLNEFSQENDNAWYFIKNIKKVGEVKKD
PGLLKYPVKPSEAGKSAGQLYEESLGKVVVEELKRTNCSYILNKYD TYSTKEYLIKEGDLSPGAVDMIG
DLLNEDSGYVVSFIESLKHDDIFAYEKRFDEIVDGMKLP TAMYRDIQDKVHFNAQVIKIQNDQKV
TVVYETLSKETPSVTADYVIVCTTSRAVRLIKFNPPLPKKAHALRSVXFPTYQFQHFSDPLTASQGRI

YFAGEYTAQAHGWIDSTIKSGLRAARDVNLASEN

>d1gosa1 c.3.1.2 (A:4-289,A:402-500) Monoamine oxidase B {Human (Homo sapiens)}

KCDVVVVGGSISGMAAAKLLHDSGLNVVLEARDRVGGRTYTLRNQKVKYVDLGGSYVGPQTQRIL
RLAKELGLETYKNEVERLIHHVKGKSYFGRGPFPPVWNPITYLDHNNFWRTMDDMGREIPSDAP
WKAPLAEEDNMTMKELLDKLCWTESAKQLATLFFVNLCVTAETHEVSALWFLWYVKQCGGTTRI
ISTTNGGQERKFVGGSGQVSERIMDLLGDRVKLERPVIYIDQTRENVLVETLNHEMYEAKYVISAIPP
TLGMKIHFNPLPMMRNQMITRVXFPPGILTQYGRVLRQPVDRIYFAGTETATHWSGYMEGAVEAG
ERAAREILHAMGKIPEDIWQSEPVSDVPAQPITTTFLERHLPSVPGLLRLIGLTT

>d1d5ta1 c.3.1.3 (A:-2-291,A:389-431) Guanine nucleotide dissociation inhibitor, GDI {Cow (Bos taurus)}

HHMDEEYDVIVLGTGLTECILSGIMSVNGKVLHMDRNPYYGGESSITPLEELYKRFQLEGGPETM
GRGRDWNVDLIPKFLMANGQLVKMLLYTEVTRYLDFKVVESFVYKGGKIYKVPSTETEALASNL
GMFEKRRFRKFLVFVANFDENDPKTFEGVDPQNTSMRDVYRKFDLGQDVIDFTGHALALYRTDDYL
DQPCLETINRIKLYSESLARYGKSPYLYPLYGLGELPQGFARLSAIYGGTYMLNKPVDDIIMENGGV
VKSEGEVARCKQLICDPSYVPDRVXPIDDGSESQVFCSCSYDATTHFETTCNDIKDIYKRMAGSAFDF

>d1chua2 c.3.1.4 (A:2-237,A:354-422) L-aspartate oxidase {Escherichia coli}

NTPLEHSCDVLIGSGAAGLSLALRLADQHQVIVLSKGPVTEGSTFYAQGGIAAVFDETDSDSHVEDT
LIAGAGICDRHAVEFVASNARSCVQWLIDQGVLFDTIQPNGEESYHLTREGGSHRRILHAADATG
REVETTLVSKALNHPNIRVLERNAVDLIVSDKIGLPGTRRVVGAWVWNRNKETVETCHAKAVVLA
TGGASKVYQYTTNPDISSGDGIAMAWRAGCRVANXCGVMVDDHGRTDVEGLYAIGEVSYTGLHGA
NRMASNSLLECLVYGWSAAEDITRRMPYAHDISTLPPW

>d1fuma2 c.3.1.4 (A:1-225,A:358-442) Fumarate reductase flavoprotein subunit {Escherichia coli}

QTFQADLAIVGAGGAGLRAAIAAAQANPNKIALISKVYPMRSHTVAAEGGSAAVAQDHDSFEYHFH
DTVAGGDWLCEQDVVDYFVHHCPTEMTQLELWGPCWSRRPDGSVNVRRFGGMKIERTWFAADKT
GFHMLHTLFTSLQFPQIRFDEHFVLDILVDDGHVRGLVAMNMMEGTLVQIRANAVVMATGGAG
RVYRYNTNGGIVTGDGMGMALSHGVPLRDXMGGIETDQNCETRIKGLFAVGECSVGLHGANRLGS
NSLAELVVFGRLAGAQATERAATAGNGNEAAIEAQAAGVEQRLKDLVNQ

>d1qlaa2 c.3.1.4 (A:1-250,A:372-457) Fumarate reductase flavoprotein subunit {Wolinella succinogenes}

MKVQYCDSLVIGGGLAGLRAAVATQQKGLSTIVLSLIPVKRSHSAAAQGGMQASLGNSKMSDGDND
LHFMDTVKGSWGDQKVARMFVNTAPKAIRELAAWGPWPWTRIHKGDRMAIINAQKTTITEEDFR
HGLIHSRDFGGTKKWRCTADATGHTMLFAVANECLKLGVSIQDRKEAIALIHQDGKCYGAVVRDL
VTGDIIAYVAKGTLIATGGYGRYKNTTNAVVEGTGTAIALETGIAQLGNXMGGIRTDYRGEAKLKGL
FSAGEAACWDMHGFNRLGGNSVSEAVVAGMIVGEYFAEHCANTQVDLETKTLEKFFVKGQEAYMKSL
VES

>d1e39a2 c.3.1.4 (A:103-359,A:506-568) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella frigidimarina}

PTIAELAKDKSERQAALASAPHDTVDDVVVVGSGGAGFSAAISATDSGAKVILIEKEPVIGGNAKLAAG
GMNAAWTDQKAKKITDPELMFEDTMKGGQNINDPALVKVLSHSHKSDSVDWMTAMGADLTDVG
MMGGASVNRAHRPTGGAGVGAHVQVLYDNAVKRNIDLRMNRGIEVLKDDKGTVKGILVKGMKY
GYYWVKADAVILATGGFAKNNERVAKLDPSLKGFIETNQPAGVGDGLDVAENAGGALKDMXTMGGV
MIDTKAEVMNAKQVPIPLYGAGEVTGGVHGANRLGGNAISDIITFGRLAGEEAAKYS

>d1qo8a2 c.3.1.4 (A:103-359,A:506-565) Flavocytochrome c3 (respiratory fumarate

reductase) {Shewanella frigidimarina}

DGWDQDKIQKAI AAGPSETTQVLVVGAGSAGFNASLAACKAGANVILVDKAPFSGGNSMISAGGMN
AVGTKQQT AHGVEDKVEWFI EDAMKGGRRQNDIKLV TILAEQSADGVQWLES LGANLDDLKRS GG
ARVDRTHRPHGGKSSGPEIIDTLRKA AKEQGIDTRLNSRVV KLVVND DHSVVGAVVHGKHTGYMI
GAKSVV L ATGGYGMNKEMIA YRPTMKDM TSSNNITATGDGV LMAKEIGASMTDIDWVQAXAINTT
ASVLDLQSKPIDGLFAAGEVTGGVHGYNRLGGNAIADTVVFGRIAGDNAAKHALD

>d1d4ca2 c.3.1.4 (A:103-359,A:506-570) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella putrefaciens}

KFVVPV DADKAAQDKAIAAGVKETTDVVIIGSGGAGLAAAVSARDAGAKVILLEKEPIPGGNTKLAAG
GMNAAETK PQAKLGIEDKKQIMIDDTMKGGRNINDPELVKVLANNSSDSIDWL TSMGADMTDVGR
MGGASVNRSHRPTGGAGVGAHV AQVLWDNAVKRGTDIRLNSRVVRILEDASGKVTGVLVKG EYTG Y
YVIKADAVVIAAGGFAKNNERSKYDPKLGFKATNHPGATGDGLDVALQAGAATRDLEXMGGLVID
TKAEVKSEKTGKPITGLYAAGEVTGGVHGANRLGGNAISDIVTYGRIAGASAAKFAKD

>d1jnra2 c.3.1.4 (A:2-256,A:402-502) Adenylylsulfate reductase A subunit {Archaeon Archaeoglobus fulgidus}

VYYPKKYELYKADEVPTVEVETDILIIGGGFSGCGAAYEAAWAKLGG LKVTLEKAAVERSGAVAQG
LSAIN TYIDLTGRSERQNTLEDYVRYV TLDMMGLAREDLVADYARHVDGTVHLFEKWGLPIWKTPD
GKYVREGQWQIMIHGESYKPIIAEAAKMAVGEENIYERVFIFELLKDNNDPNAVAGAVGFSVREP KFY
VFKAKAVILATGGATLLFRPRSTGEAAGRTWY AIFDTGSGYYMGLKAGAMLTQXAGFWVCGPEDLM
PEEYAKLFLPKYNRMTTVKGLFAIGDCAGANPHK FSSGSFTEGRIAAKAAVRFIL EQPNPEIDDAV V
EELKKKAYAPMERFMQYKDLS

>d3grs_1 c.3.1.5 (18-165,291-363) Glutathione reductase {Human (Homo sapiens)}

VASYDYLVI GGGSGGLASARRAAELGARA AVVESHKLG GTCVNVGCVPKKVMWNTAVHSEFMH DH
ADYGFP SCEGKFNWRVIKEKRDAYVSRLN AIYQNNLTKSHIEIIRGHAAFTSDPKPTIEVSGK KYTAP
HILIATGGMPSTPHEXRVPNTKDL SLNKLGIQTDDKGHIIVDEFQNTNVKGIYAVGDVCGKALLTPVAI
AAGRKLAHRLF EYKEDSKLD

>d3grs_2 c.3.1.5 (166-290) Glutathione reductase {Human (Homo sapiens)}

SQIPGASLGITSDGFFQLEELPGRSVIVGAGYI AVEMAGILSALGSKTSLMIRHDKVLR SFDSMISTNCT
EEL ENAGVEVLKFSQVKEVKK TSLGLEVSMVTAVPGRLPVMTMIPDV DCLLWAIG

>d1gera2 c.3.1.5 (A:147-262) Glutathione reductase {Escherichia coli}

DIPGVEY GIDSDGFFALPALPERVAVVGAGYI AVELAGVINGLGAKTHL FVRKHAPLRSFDP MISETLV
EVMNAEGPQLHTNAIPKAVVKN TDGSLTLELEDGRSETVDCLIWAIG

>d1gesa1 c.3.1.5 (A:3-146,A:263-335) Glutathione reductase {Escherichia coli}

KHYDYIAIGGGSGGIASINRAAMYGQK CALIEAKELGGTCVNVGCVPKKVMWHAAQIREAIHMYGPD
YGFDTTINKFNWETLIASRTAYIDRIHTSYENVLGKNNVDVIKGFARFVDAKTLEVNGETITADHILIA
TGGRPSHPXREPANDNINLEAAGVKTNEKGYIVVDKYQNTNIEGIYAVGDNTGAVELTPVAVAAGRRL
SERLFNKNPDEHLD

>d1gesa2 c.3.1.5 (A:147-262) Glutathione reductase {Escherichia coli}

DIPGVEY GIDSDGFFALPALPERVAVVGAGYI GVELGGVINGLGAKTHL FEMFDAPLPSFDP MISETLV
EVMNAEGPQLHTNAIPKAVVKN TDGSLTLELEDGRSETVDCLIWAIG

>d1feca1 c.3.1.5 (A:1-169,A:287-357) Trypanothione reductase {Crithidia fasciculata}

SRAYDLV VIGAGSGGLEAGWNAASLHKKRVAVIDLQKHHGPPHYAALGGTCVNVGCVPKKLMVTGA
NYMDTIRESAGFGWELDRESVRPNWKALIAAKNKAVSGINDSYEGMFADTEGLTFHQGF GALQDN
HTVLVRESADPNSAVLETLDTEYILLATG SWPQHLGIEXVPRSQT LQLEKAGVEVAKNGAIKVDAYS K

TNVDNIYAIGDVTDRVMLTPVAINEGAAFVDTVFANKPRATD

>d1feca2 c.3.1.5 (A:170-286) Trypanothione reductase {Crithidia fasciculata}
GDDLCSNEAFYLDEAPKRALCVGGYISIEFAGIFNAYKARGGQVDLAYRGDMILRGFDSELRKQLT
EQLRANGINVRTHENPAKVTKNADGTRHVVVFESGAEADYDVVMLAIGR

>d1aoga1 c.3.1.5 (A:3-169,A:287-357) Trypanothione reductase {Trypanosoma cruzi}
SKIFDLVVIGAGSGGLEAAWNAATLYKKRVAVIDVQMVHGPPFFSALGGTCVNVGCVPKKLMVTGAQ
YMEHLRESAGFGWEFDRITTLRAEWKNLIAVKDEAVLNINKSYDEMFRDTEGLEFFLGWGSLESKN
VVNVRESADPASAVKERLETEHILLASGSWPHMPNXGRSPRTKDLQLQNAGVMIKNGGVQVDEYSR
TNVSNIAIGDVTNRVMLTPVAINEAAAALVDTVFGTTPRKT

>d1aoga2 c.3.1.5 (A:170-286) Trypanothione reductase {Trypanosoma cruzi}
IPGIEHCISSNEAFYLPEPPRRVLTVGGGFISVEFAGIFNAYKPKDGQVTLCYRGEMILRGFDHTLREEL
TKQLTANGIQILTKENPAKVELNADGSKSVTFESGKKMDFDLVMMAI

>d1h6va1 c.3.1.5 (A:10-170,A:293-366) Mammalian thioredoxin reductase {Rat (Rattus norvegicus)}
SYDFDLIIIGGGSGGLAAAKEAAKFDKKVMVLDVFTPTPLGTNWGLGGTCVNVGCVPKKLMHQAALL
GQALKDSRNYGWKLEDTVKHDWEKMTESVQNHIGSLNWGYRVALREKKVVYENAYGKFIGPHKIM
ATNNKGKEKVYSAERFLIATGERPRYLGIKXRDSTRITIGLETGVKINEKTGKIPVTDEEQTNVPYIYA
IGDILEGKLELTPVAIQAGRLLAQRLYGGSTVKCD

>d1h6va2 c.3.1.5 (A:171-292) Mammalian thioredoxin reductase {Rat (Rattus norvegicus)}
PGDKEYCISDDLFSPLPYCPGKTLVVGASYVALECAGFLAGIGLDVTVMVRSILLRGFDQDMANKIGE
HMEEHGKIFIRQFVPTKIEQIEAGTPGRLKVTAKSTNSEETIEDEFNTVLLAVG

>d1trb_1 c.3.1.5 (1-118,245-316) Thioredoxin reductase {Escherichia coli}
GTTKHSKLLILGSGPAGYTAAVYAARANLQPVLTGMEKGGQLTTTTEVENWPGDPNDLTGPLLMER
MHEHATKFETEIIFDHINKVDLQNRPFRLNGDNGEYTCDALIATGASARYXHPNTAIFEGQLELEN
GYIKVQSGIHGNATQTSIPGVFAAGDVM DHIYRQAITSAGTGCMAALDAERYLDGL

>d1trb_2 c.3.1.5 (119-244) Thioredoxin reductase {Escherichia coli}
LGLPSEEAFFKGRGVSACATSDGFFYRNQKVAVIGGGNTAVEEALYLSNIASEVHLIHRRDGFRAEKILI
KRLMDKVENGNILHTNRTLEEVTGDQMGVTGVRLRDTQNSDNIESLDVAGLFVAIG

>d1vdc_1 c.3.1.5 (1-117,244-316) Thioredoxin reductase {Mouse-ear cress (Arabidopsis thaliana)}
LETHNTRLCIVGSGPAAHTAAIYAARAELKPLLFEGWMANDIAPGGQLTTTTDVENFPGFPEGILGV
ELTDKFRKQSERFGTTIFTETVTKVDFSSKPFKLF TDSKAILADAVILAIGAVAKXGHEPATKFLDGGV
ELSDSDGYVVTKPGTTQTSVPGVFAAGDVQDKKYRQAITAAGTGCMAALDAEHYLQEI

>d1vdc_2 c.3.1.5 (118-243) Thioredoxin reductase {Mouse-ear cress (Arabidopsis thaliana)}
RLSFVGSGEVLGGFWNRGISACAVCDGAAPIFRNKPLAVIGGGDSAMEEANFLT KYGSKVYIIHRRDA
FRASKIMQQRALSNPKIDVIWNSSVVEAYGDGERDVLGGLKVKNVVTGDVSDLKVSGLFFAI

>d1hyua1 c.3.1.5 (A:199-325,A:452-521) Alkyl hydroperoxide reductase subunit F (AhpF),
C-terminal domains {Salmonella typhimurium}
AEKRAAEALNKRDAYDVLIVGSGPAGAAA AVYSARKGIRTGLMGERFGGQVLDTVDIENYISVPKTE
GQKLAGALKAHVSDYDVIDS QSASKLVPAATEGGLHQIETASGAVLKARSIIIATGAKXLPNTHWL
EGALERNRMGEIIDA KCETS VKGVFAAGDCTTVPYKQIIIATGEGAKASLSAFDYLRITKIA

>d1fl2a1 c.3.1.5 (A:212-325,A:452-521) Alkyl hydroperoxide reductase subunit F (AhpF),
C-terminal domains {Escherichia coli}
AYDVLIVGSGPAGAAA IYSARKGIRTGLMGERFGGQILD TVDIENYISVPKTEGQKLAGALKVHVDE

YDVDVIDSQSASKLIPAAVEGGLHQIETASGAVLKARSIIIVATGAKXLPNTNWLEGAVERNRMGEIHD
AKCETNVKGVFAAGDCTTVPYKQIIATGEGAKASLSAFDYLRITKTA
>d1fl2a2 c.3.1.5 (A:326-451) Alkyl hydroperoxide reductase subunit F (AhpF), C-terminal
domains {Escherichia coli}
WRNMNVPGEDQYRTKGVTYCPHCDGPLFKGKRVAVIGGGNSGVEAAIDLAGIVEHVTLLLEFAPEMK
ADQVLQDKLRSLKNVDIILNAQTTEVKGDGSKVVGLEYRDRVSGDIHNIELAGIFVQIGL
>d1nhp_1 c.3.1.5 (1-119,243-321) NADH peroxidase {Enterococcus faecalis}
MKVIVLGSSHGGYEAVEELLNLHPDAEIQWYKGDVFISFLSAGMQLYLEGKVKDVNSVRYMTGEKM
ESRGNVFSNTEITAIQPKHQVTVKDLVSGEERVENYDKLIISPGAVPFELDXGVRPNTAWLKGTLE
LHPNGLIKTDEYMRTPSEPDVFAVGDATLIKYNPADTEVNIALATNARKQGRFAVKNLEEPVKPFP
>d1nhp_2 c.3.1.5 (120-242) NADH peroxidase {Enterococcus faecalis}
IPGKDLDNIIYLMRGRQWAIKQKQTVDPVNNVVVIGSGYIGIEAAEFAKAGKKVTVIDILDRPLGV
YLDKEFTDVLTEEMEANNITATGETVERYEGDGRVQKVVTDKNAYDADLVVVAV
>d1d7ya1 c.3.1.5 (A:5-115,A:237-308) NADH-dependent ferredoxin reductase, BphA4
{Pseudomonas sp., KKS102}
ALKAPVVVLGAGLASVSFVAELRQAGYQGLITVVGDEAERPYPDRPPLSKDFMAHGDAEKIRLDCKRA
PEVEWLLGVTAQSFDPQAHTVALSDGRTLPGYTLVLATGAAPRAXVLANDALARAAGLACDDGIFVD
AYGRITCPDVYALGDVTRQRNPLSGRFERIETWSNAQNQGIAVARHLVDP
>d1d7ya2 c.3.1.5 (A:116-236) NADH-dependent ferredoxin reductase, BphA4 {Pseudomonas
sp., KKS102}
LPTLQGATMPVHTLRTLEDARRIQAGLRPQRSLLIVGGGVIGLELAATARTAGVHVSIVETQPRLMR
AAPATLADVFVARYHAAQGVDLRFERSVTGSVDGVVLLDDGTRIAADMVVVIG
>d1lv_1 c.3.1.5 (1-150,266-335) Dihydrolipoamide dehydrogenase {Pseudomonas putida}
QQTIQTLLIIGGGPGGYVAAIRAGQLGIPTVLVEGQALGGTCLNIGCIPSKALIHVAEQFHQASRFTEP
SPLGISVASPRLDIGQSVAWKDGIVDRLTTGVAALLKKHGVKVVHGWAKVLDGKQVEVDGQRIQCEH
LLLATGSSSVLPXRRPRTKGFNLECLDLKMNGAAIAIDERCQTSMHNVWAIGDVAGEPMLAHRAM
AQGEMVAEIIAGKARRFE
>d1lv_2 c.3.1.5 (151-265) Dihydrolipoamide dehydrogenase {Pseudomonas putida}
MLPLGGPVISSTEALAPKALPQHLLVVGGGYIGLELGIAYRKLGAQVSVVEARERILPTYDSELTAPVA
ESLKKLGIALLHLSVEGYENGCLLANDGKGGQLRLEADRVLVAVG
>d1lpfa1 c.3.1.5 (A:1-158,A:278-348) Dihydrolipoamide dehydrogenase {Pseudomonas
fluorescens}
SQKFDVVVIGAGPGGYVAAIRAAQLGLKTACIEKYIGKEGKVALGGTCLNVGCIPSKALLDSSYKYHEA
KEAFKVHGIEAKGVITIDVPAMVARKANIVKNLTGGIATLFGKANGVTSFEGHGKLLANKQVEVTGLDG
KTQVLEAENVIIASGSRPVEIPXRRPVTTDLAADSGVTLDERGFIYVDDHCKTSVPGVFAIGDVVRG
AMLAHKASEEGVMVAERIAGHKAQMN
>d1lpfa2 c.3.1.5 (A:159-277) Dihydrolipoamide dehydrogenase {Pseudomonas fluorescens}
PAPLSDDIIVDSTGALEFQAVPKKLVIGAGVIGLELGSVWARLGAEVTVLEALDKFLPAADEQIAKEA
LKVLTQQLNIRLGARVTASEVKKKQVTVTFTDANGEQKETFDKLIVAVG
>d3lada1 c.3.1.5 (A:1-158,A:278-348) Dihydrolipoamide dehydrogenase {Azotobacter
vinelandii}
SQKFDVIVIGAGPGGYVAAIKSAQLGLKTALIEKYKKEGKTALGGTCLNVGCIPSKALLDSSYKFHEA
HESFKLHGISTGEVAIDVPTMIARKDQIVRNLTGGVASLIKANGVTLFEGHGKLLAGKKVEVTAADGS
SQVLDTENVILASGSKPVEIPXRRPVTTDLAADSGVTLDERGFIYVDDYCATSVPGVYAIGDVVRGA

MLAHKASEEGVVVAERIAAGHKAQMN

>d3lada2 c.3.1.5 (A:159-277) Dihydrolipoamide dehydrogenase {Azotobacter vinelandii}
PAPVDQDVIDDSTGALDFQNVPGKLGIVIGLELGSVWARLGAEVTVLEAMDKFLPAVDEQVAK
EAQKILTKQGLKILLGARVTGTEVKNKQVTVKVFVDAEAGEKSQAFDKLIVAVG

>d1ebda1 c.3.1.5 (A:7-154,A:272-346) Dihydrolipoamide dehydrogenase {Bacillus
stearothermophilus}

AIETETLVVAGPGGYVAAIRAAQLGQKVITVEKGNLGGVCLNVGCIPSKALISASHRYEQAKHSEEM
GIKAENVTIDFAKVQEWKASVVKKLTGGVEGLLKGNKVEIVKGEAYFVDANTVRVVNGDSAQTYTFK
NAIIATGSRPIELXVGRRPNTDELGLEQIGIKMTNRGLIEVDQQRCSVNPINIFAIGDIVPGPALAHKASY
EGKVAAEAIAGHPSAVDYV

>d1ebda2 c.3.1.5 (A:155-271) Dihydrolipoamide dehydrogenase {Bacillus
stearothermophilus}

PNFKFSNRILDSTGALNLGEVPSLVVIGGGYIGIELGTAYANFGTKVTILEGAGEILSGFEKQMAAIK
KRLKKKGVEVVTNALAKGAEEREDGVTVTYEANGETKTIDADYVLT

>d1ojt_1 c.3.1.5 (117-275,401-470) Dihydrolipoamide dehydrogenase {Neisseria
meningitidis}

GSADAEDVVLGGGPGGYSAFAAADEGLKVAIVERYKTLGGVCLNVGCIPSKALLHNAAVIDEVRH
LAANGIKYPEPELDDMLRAYKDGVSRLTGGLAGMAKSARKVDVIQGDGQFLDPHHEVSLTAGDAY
EQAAPTGEKKIVAFKNCIIAAGSRXAPNGKLISAEEKAGVAVTDRGFIEVDKQMRTNVPPIYAIGDIVGQ
PMLAHKAVHEGHVAAENCAGHKAYFD

>d1ojt_2 c.3.1.5 (276-400) Dihydrolipoamide dehydrogenase {Neisseria meningitidis}

VTKLPFIPEDPRIIDSSGALALKEVPGKLLIIGGGIIGLEMGTVYSTLGSRLDVVEMMDGLMQGADRDL
VKVWQKQNEYRFDNIMVNTKTVAVEPKEDGVYVTFEGANAPKEPQRYDAVLVAAGR

>d1jeha1 c.3.1.5 (A:1-160,A:283-355) Dihydrolipoamide dehydrogenase {Baker's yeast
{Saccharomyces cerevisiae}}

TINKSHDVVIIGGGPAGYVAAIKAAQLGFNTACVEKRGKLGGTCLNVGCIPSKALLNNSHLFHQMHT
AQKRGIDVNGDIKINVANFQKAKDDAVKQLTGGIPELLFKKNKVTYYKNGSFEDETKIRVTPVDGLE
GTVKEDHILDVKNIIATGSEVTPFXVGRRPYIAGLGAEKIGLEVDKRGRLVIDDQFNSKFPPIKVVGD
VTFGPMLAHKAE EEGIAAVEMMLKTGHGHVN

>d1jeha2 c.3.1.5 (A:161-282) Dihydrolipoamide dehydrogenase {Baker's yeast
{Saccharomyces cerevisiae}}

PGIEIDEEKIVSSTGALSLEIPKRLTIIGGGIIGLEMGSVYRSLGSKVTVVEFQPQIGASMDGEVAKATQ
KFLKKQGLDFKLSKVISAKRNDKNNVEIVVEDTKTNKQENLEAEVLLVA

>d1dxla1 c.3.1.5 (A:4-152,A:276-347) Dihydrolipoamide dehydrogenase {Garden pea (Pisum
sativum)}

SDENDVVIIGGGPAGYVAAIKAAQLGFKTTICIEKRGALGGTCLNVGCIPSKALLHSSHMYHEAKHSFA
NHGVKVSNEIDLAAAMMGQKDKAVSNLTRGIEGLFKKNKVTYVKGYGKVFVSPSEISVDTIEGENTVV
KKGHIIATGSDVKXGRTPFTSGLNLDKIGVETDKLGRILVNERFSTNVSGVYAIGDIVPGPMLAHKAE
EDGVACVEYLAGKVGHVD

>d1dxla2 c.3.1.5 (A:153-275) Dihydrolipoamide dehydrogenase {Garden pea (Pisum
sativum)}

SLPGVTIDEKKIVSSTGALALSEIPKKLVVIGAGYIGLEMGSVWGRIGSEVTVVEFASEIVPTMDAEIRK
QFQRSLEKQGMKFKLTKVVGVDTSKGVKLTVEPSAGGEQTIIEADVLLVSA

>d1fca1 c.3.1.5 (A:1-114,A:256-327) Flavocytochrome c sulfide dehydrogenase, FCSD,

flavin-binding subunit {Purple phototrophic bacterium (Chromatium vinosum)}
AGRKVVVVGGGTGGATAAKYIKLADPSIEVTLIEPNTDYYTCYLSNEVIGGDRKLESIKHGYDGLRAH
GIQVVHDSATGIDPDKKLVKTAGGAIEFGYDRCVVAPGIELIYDKIEXQRAGKIAQIAGLTNDAGWCPV
DIKTFESSIHKGIVIGDASIANPMPKSGYSANSQKVA AAAVVLLK GEE
>d1fca2 c.3.1.5 (A:115-255) Flavocytochrome c sulfide dehydrogenase, FCSD, flavin-binding
subunit {Purple phototrophic bacterium (Chromatium vinosum)}
GYSEEAALKPHAWKAGEQTAILRKQLEDMADGGTVVIAPPAAPFRCPPGYPYERASQVAYYLKAHK
PMSKVIILDSSQTFKQSQFSKQWERLYGFGTENAMIEWHPGPDSAVVKVDGGEMMVETAFGDEFK
ADVINLIPP
>d1djna3 c.4.1.1 (A:341-489,A:646-729) Trimethylamine dehydrogenase, middle domain
{Methylophilus methylotrophus, w3a1}
DIRVCIGCNVCISRWEIGGPPMICTQNATAGEEYRRGWHPKFRQTKNKDSVLIVGAGPSGSEAARVL
MESGYTVHLTDTAEKIGGHLNQVAALPGLGEWSYHRDYRETQITKLLKKNKESQLALGQKPMTADD
VLQYGADKVIATGAXSECTLWNLKARESEWAENDIKGIYLIGDAEAPRLIADATFTGHRVAREIEEA
NPQIAIPYKRETIAWGTPHMPGGNFKIEYKV
>d1cja2 c.4.1.1 (A:6-106,A:332-460) Adrenodoxin reductase of mitochondrial p450 systems
{Cow (Bos taurus)}
TPQICVVGSGPAGFYTAQHLLKHHSRAHVDIYEKQLVFPGLVRFVAPDHPEVKNVINTFTQTARSDR
CAFYGNVEVGRDVTVQELQDAYHAVVLSYGAEDXKSRPIDPSVFPDPKLGVPVPMMEGRVVDVPGLYC
SGWVVRGPTGVITTTMTDSFLTQILLQDLKAGHLPSGPRPGSAFIKALLDSRGVWPVFSFDWEKLD
AEEVSRGQASGKPREKLLDPQEMLRLLGH
>d1h7wa4 c.4.1.1 (A:184-287,A:441-532) Dihydropyrimidine dehydrogenase, domain 2 {Pig
(Sus scrofa)}
EAYSAKIALLGAGPASISCASFLARLGYSDITIFEKQEYVGGSTSEIPQFRLPYDVVNFEIELMKDLGV
KIICGKSLSENEITLNTLKEEGYKAAFIGIGLPEXVLRDPKVKEALSPIKFNRWDLPEVDPETMQTSEP
WVFAGGDIVGMANTTVESVNDGKQASWYIHKYIQAQYGASVSAKPELPLFYTPVDLVD
>d1an9a1 c.4.1.2 (A:1-194,A:288-340) D-amino acid oxidase, N-terminal domain {Pig (Sus
scrofa)}
MRVVVIGAGVIGLSTALCIHERYHSVLQPLDVKVYADRFTPFPTTDDVAAGLWQPYTSEPSNPQEANW
NQQTFFNYLLSHIGSPNAANMGLTPVSGYNLFREAVPDPYWKDMVLGFRKLTPRELDMFPDYRYGW
FNTSLILEGRKYLQWLTERLTERGVKFFLRKVESFEEVARGGADVINCTGVWAGVLQPDPLXQVRLE
REQLRFGSSNTEVIHNYGHGGYGLTIHWGCALEVAKLFGKVLEERNLL
>d1c0pa1 c.4.1.2 (A:999-1193,A:1289-1361) D-amino acid oxidase, N-terminal domain
{Yeast (Rhodotorula gracilis)}
LMMHSQKRVVVLGSGVIGLSSALILARKGYSVHILARDLPEDVSSQTFASPWAGANWTFPMTLTDGP
RQAKWEESTFKKWVELVPTGHAMWLKGTTRRFAQNEDGLLGHWYKDITPNYRPLPSSECPPGAIGV
TYDTLVHAPKYCQYLARELQKLGATFERRTVTSLEQAFDGLVNVNATGLGAKSIAGIDDQAXRGG
PRVEAERIVLPLDRTKSPLSLGRGSARAAKEKEVTLVHAYGFSSAGYQQSWGAAEDVAQLVDEAFQR
YHG
>d1i8ta1 c.4.1.3 (A:1-244,A:314-367) UDP-galactopyranose mutase, N-terminal domain
{Escherichia coli}
MYDYIIVGSGLFGAVCANELKKNKVLVIEKRNHIGGNAYTEDCEGIQIHKYGAHIFHTNDKYIWDY
VNDLVEFNFRFTNSPLAIYKDKLFNLPFNMTFHQMVGKDPQEAQNIINAQKKKYGDKVPENLEE
QAISLVGEDLYQALIKGYTEKQWGRSAKELPAFIIKRIPVRFVFDNNTYFSDRYQGIPVGGYTKLIEKML

EGVDVKLGIDFLKDKDSLASKAHRIIYTGPIDQYFDYRFGALXNDNKNMELFKKYRELASREDKVIFG
GRLAEYKYYDMHQVISAALYQVKNIMSTD

>d2uaga1_c.5.1.1 (A:1-93) UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase MurD,
N-terminal domain {Escherichia coli}

ADYQGKNVVIIGLGLTGLSCVDFFLARGVTPRVMDTRMTPPGLDKLPEAVERHTGSLNDEWLMAAD
LIVASPGIALAHPSLSAAADAGIEIVG

>d1tml__c.6.1.1 (-) Cellulase E2 {Thermomonospora fusca, strain yx}

NDSPFYVNPNMSSAEWVRNNPNDPRTVPVIRDRIASVPQGTWFAHHNPGQITGQVDALMSAAQAAG
KIPILVVYNAPGRDCGNHSSGGAPSHSAYRSWIDEFAAGLKNRPAYIIVEPDLISLMSSCMQHVVQEV
LETMAYAGKALKAGSSQARIYFDAGHSAWHSPAQMASWLQQADISNSAHGIATNTSNYRWTADEVA
YAKAVLSAIGNPSLRAVIDTSRNGNGPAGNEWCDPSGRAIGTPSTTNTGDPMIDAFWLKLPGEADG
CIAGAGQFVPPQAAAYEMAIAA

>d1qjwa_c.6.1.1 (A:) Cellobiohydrolase II (Cel6) {Trichoderma reesei, Cel6a}

ATYSGNPFVGVTPWANAYYASEVSSLAIPSLTGAMATAAAAVAKVPSFMWLDTLDKTPLMEQTLADI
RTANKNGGNYAGQFVVFDPDRDCAALASNGEYSIADGGVAKYKNYIDTIRQIVVEYSDIRTLLVIEP
DSLNLVTLNLGTPKCANAQSAYLECIYAVTQLNLPNVAMYLDAGHAGWLGWPANQDPAAQLFAN
VYKNASSPRALRGLATNVANYNGWNITSPPSYTQGNNAVYNEKLYIHAIGPLLANHGWSNAFFITDQG
RSGKQPTGQQWGDWCNVIGTGFGIRPSANTGDSLLDSFVWVKPGGEDGTSDSSAPRFDSDHCALP
DALQPAPQAGAWFQAYFVQLLTNANPSFL

>d2bvwa_c.6.1.1 (A:) Cellobiohydrolase II (Cel6) {Humicola insolens, Cel6a}

NGNPFEGVQLWANNYYRSEVHTLAIPQITDPALRAASAVAEVPSFQWLDRNVTVDTLVQTLSEIR
EANQAGANPQYAAQIVVYDLPDRDCAAAASNGEWAIANNGVNNYKAYINRIREILISFSDVRTILVIE
PDSLANMVTNMNPKCSGAASYRELTIALKQLDLPHVAMYMDAGHAGWLGWPANIQPAALFA
KIYEDAGKPRAVRGLATNVANYNAWSVSSPPPYTSPNPNYDEKHIEAFRPLLEARGFPAQFIVDQG
RSGKQPTGQKEWGHWCNAIGTGFGMRPTANTGHQYVDAFVWVKPGGEDGTSDTTAARYDYHCG
LEDALKPAPEAGQWFNEYFIQLLRNANPPF

>d1dysa_c.6.1.1 (A:) Cellobiohydrolase II (Cel6) {Humicola insolens, Cel6b}

GNPFSGRLLVNSDYSSKLDQTRQAFLSRGDQTNAAKVKYVQEKVGTIFYWISNIFLLRDIDVAIQNAR
AAKARGENPIVGLVLYNLPDRDCSAGESSELKLSQNGLNRYKNEYVNPFAQKLKAASDVQFAVILEP
DAIGNMVTGTSAFCRNARGPQQEAIGYAIQLQASHIHLVLDVANGGWLGWADKLEPTAQEVATILQ
KAGNNAKIRGFSSNVSNYPYSTSNPPPYTSGSPSPDESRYATNIANAMRQRGLPTQFIIDQSRVALSG
ARSEWGQWCNVNPAGFGQPFTTNTNPNVDAIVWVKPGGESDGQCGMGGAPAAGMWFDAYAQM
LTQNAHDEIA

>d1cm5a_c.7.1.1 (A:) Pyruvate formate-lyase, PFL {Escherichia coli}

SELNEKLATAWEGFTKGDWQNEVNVDRDFIQKNYTPYEGDESFLAGATEATTTLWVKMEGVKLEN
RTHAPVDFDTAVASTITSHDAGYINKQLEKIVGLQTEAPLKRALIPFGGIKMIEGSCKAYNRELDPMIK
KIFTEYRKTHTNQGVFDVYTPDILRCRKSGLTGLPDAYGRGRIIGDYRRVALYGIDYLMKDKLAQFTSL
QADLENGVNLEQTIRLREEIAEQHRALGQMKEMAAKYGYDISGPATNAQEAIQWTFYGLAAVKSQ
NGAAMSFGRSTSTFLDVYIERDLKAGKITEQEAQEMVDHLMKLRMVRFLRTPEYDELFSGDPIWAT
ESIGGMGLDGRTLVTKNSFRFLNTLYTMGPSPEPNMTILWSEKLPLNFKKFAAKVSIDTSSLQYEND
DLMRPDFNNDYIAIAAVSPMIVGKQMQFFGARANLAKTMLYAINGGVDEKLMQVGPKSEPIKGD
VLNYDEVMERMDHFMDWLAKQYITALNIIHYMHDKYSYEASLMALHDRDVIRTMACGIAGLSVAA
DSLSAIKYAKVKPIRDEDGLAIDFEIEGEYPQFGNNDPRVDDLAVDLVERFMKKIQKLHTYRDAIPTQ
SVLTITSNVYVYKKTGNTPDGRRAGAPFGPGANPMHGRDQKGAVALTSVAKLPFAYAKDGISYTFSI

VPNALGKDDEVRKTNLAGLMDGYFHHEASIEGGQHLNVNVMNREMLLDAMENPEKYPQLTIRVSG
YAVRFNSLTKEQQQDVITRTFTQSM

>d1qhma_ c.7.1.1 (A:) Pyruvate formate-lyase, PFL {Escherichia coli}

NEKLATAWEGFTKGDWQNEVNVRDFIQKNYTPYEGDESFLAGATEATTTLWDKVMEGVKLENRT
HAPVDFDTAVASTITSHDAGYINKQLEKIVGLQTEAPLKRALIPFGGIKMEGSKAYNRELDPMIKKI
FTEYRKTHNQGVFDVYTPDILRCRKSGVLTGLPDAYGRGRIIGDYRRVALYGIDYLMKDKLAQFTSLQ
ADLENGVNLEQTIRLREEIAEQHRALGQMKEMAACYGYDISGPATNAQEAIQWTFYGYLAAVKSQN
GAAMSFGRSTFLDVYIERDLKAGKITEQEAQEMVDHLVMKLRMVRFLRTPEYDELFSGDPIWATE
SIGGMGLDGRTLVTKNSFRFLNTLYTMGPSPEPNMTILWSEKLPLNFKKFAAKVSIDTSSLQYENDD
LMRPFDFNDDYAIACCVSPMIVGKQMFFGARANLAKTMLYAINGGVDEKLMQVGPKEPIKGDV
LNYDEVMERMDHFMDWLAKQYITALNIIHYMHDKYSYASLMALHHRDVIRTMACGIAGLSVAAD
SLSAIKYAKVKPIRDEDGLAIDFEIEGEYPPQFGNNDPRVDDLAVDLVERFMKKIQKLHTYRDAIPTQS
VLTITSNVYGGK

>d1rlr_2 c.7.1.2 (222-748) R1 subunit of ribonucleotide reductase, C-terminal domain
{Escherichia coli}

FSSCVLIECGDSLDSINATSSAIVKYVSQRAGIGINAGRIRALGSPIRGGEAFHTGCIPFYKHFQTAVKSC
SQGGVVRGGAATLFYPMWHLEVESLLVLKNNRGEVGNRVRHMDYGVQINKLMYTRLLKGEDITLFS
SDVPGLYDAFFADQEEFERLYTKYEKDDSIKQKRVKAVELFSLMMQERASTGRIYIQNVHDHCNTHSP
FDPAIAPVRQSNLCLEIALPTKPLNDVNDENGEIALCTLSAFNLGAINNDELDELAILAVRALDALL
DYQDYPIPAAKRGAMGRRTLIGVINFAAYLAKHGKRYSDGSANNLTHKTFEAIQYLLKASNELAKE
QGACPWFNETTYAKGILPIDTYKKDLDTIANEPLHYDWEALRESIKTHGLRNSTLSALMPSETSSQIS
NATNGIEPPRGYVSIKASKDGILRQVVPDYEHLHDAYELLWEMPGNDGYLQLVGIMQKFIDQISANT
NYDPSRFPSPGKVPMQQLKDLLTAYKFGVKTLYYQNTREDDIDDLNDFQL

>d1b8ba_ c.7.1.3 (A:) Class III anaerobic ribonucleotide triphosphate reductase NRDD
subunit {Bacteriophage T4}

SRVFPTQRDLMAGIVSKHIAKNMVPSFIMKAHESGIIHVHDIDYSPALPFTNCCLVDLKGMLENGFKL
GNAQIETPKSIGVATAIMAQITAQVASHQYGGTTFANVDKVLSPYVKRTYAKHIEDAEKWQIADALNY
AQSKTEKDVFYDAFQAYEYEVNTLFSSNGQTPFVTLTFTGTDWTERMIQKAILKNRIKGLGRDGITPI
FPKLVMFVEEGVNLKDDPNYDIKQLALECASKRMYPDIISAKNNKAITGSSVPVSPMGCERSFLSVW
KDSTGNEILDGRNNLGVVTLNLPRIALDSYIGTQFNEQKFVELFNERMDLCFEALMCRISLKGKVA
TVAPILYQEGAFGVRLKPDDDIIELFKNGRSSVSLGYIGIHELNILVGRDIGREILTKMNAHLKQWTER
TGFAFSLYSTPAENLCYRFCKLDTEKYGSVKDVTDKGWYTNFSFHVSVVEENITPFKISREAPYHFIAT
GGHISYVELPDMKNNLKGLEAVWDYAAQHLDYFGVNPVDKCFTCGSTHEMTPTENGFCVCSICGET
DPKKMNTIRRTCAYLGNPNERG

>d1kbla2 c.8.1.1 (A:377-509) Pyruvate phosphate dikinase, central domain {Clostridium
symbiosum}

LHPTFNPAALKAGEVIGSALPASPGAAAGKVYFTADEAKAAHEKGERVILVRLETSPEDIEGMHAAE
GILTVRGGMTSHAAVARGMGTCVSGCGEIKINEEAKTFELGGHTFAEGDYISLDGSTGKIYKGD

>d1zma2 c.8.1.2 (A:3-21,A:145-249) N-terminal domain of enzyme I of the PEP:sugar
phosphotransferase system {Escherichia coli}

SGILASPGIAFGKALLKEXKIIDLSAIQDEVILVAADLTPSETAQLNLKKVLGFITDAGGRTSHTSIMAR
SLELPAIVGTGSVTSQVKNDDYLILDVANNQVYVNPTEVIDKMRAVQEQVASE

>d1aco_1 c.8.2.1 (529-754) Aconitase, C-terminal domain {Cow (Bos taurus)}

VDVSPTSQRLQLLEPFDKWDGKDLEDLQILIKVKGKCTTDHISAAGPWLKFRGHLDNISNLLIGAI

NSENRKANSVRNAVQTQEFGPVPTARYYKQHGIRWVWIGDENYEGSSREHSALEPRFLGGRAIITK
SFARIHETNLKKQGLPLTFADPADYNKIHPVDKLTIQGLKDFAPGKPLTCIIKHPNGTQETILLNHTF
NETQIEWFRAGSALNRMKELQQK
>d1a9xb1 c.8.3.1 (B:1502-1652) Carbamoyl phosphate synthetase, small subunit N-terminal
domain {Escherichia coli}
IKSALLVLEDGTQFHGRAIGATGSAVGEVFNSTMTGYQEILTDPYSRQIVTLTYPHIGNVGTNDADE
ESSQVHAQGLVIRDLPLIASNFRNTEDLSSYLKRHNIVAIADIDTRKLRLLREKGAQNGCIIAGDNP
AALALEKARAFPG
>d1de4c2 c.8.4.1 (C:190-382) Transferrin receptor ectodomain, apical domain {Human
(Homo sapiens)}
IQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKKDFEDLYTPVNGSIVIV
RAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHHLGTGDPYTPGFPSFNHTQFP
SSGLPNIPVQTSIRAAAEKLFGNMEGDCPSDWKTDSTCRMVTSSEKSNVCLTVSNVVK
>d1dk7a_ c.8.5.1 (A:) GroEL {Escherichia coli}
EGMQFDRGYLSPYFINKPETGAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLIIAEDVEGEAL
ATLVVNTMRGIVKVA AVKAPGFGDRRKAMLQDIATLTGGTVISEEIGMELEKATLEDLGQAKRVV
KDTTTHIDGV
>d1kid_ c.8.5.1 (-) GroEL {Escherichia coli}
GLVPRGSEGMQFDRGYLSPYFINKPETGAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLIIAE
DVEGEALATLVVNTMRGIVKVA AVKAPGFGDRRKAMLQDIATLTGGTVISEEIGMELEKATLEDLGQ
AKRVVINKDTTTHIDGVGEEAAIQGRVAQIRQQIEEATSDYDREKLQERVAKLAGGV
>d1oela2 c.8.5.1 (A:191-366) GroEL {Escherichia coli}
EGMQFDRGYLSPYFINKPETGAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLIIAEDVEGEAL
ATAVVNTIRGIVKVA AVKAPGFGDRRKAMLQDIATLTGGTVISEEIGMELEKATLEDLGQAKRVV
INKDTTTHIDGVGEEAAIQGRVAQIRQQIEEATSDYDREKLQ
>d1ioka2 c.8.5.1 (A:191-366) GroEL {Paracoccus denitrificans}
EGMQFDRGYLSPYFVTNADKMIAELEDAYILLHEKKLSSLQPMVPLLESVIQSQKPLIIAEDVEGEA
LATLVVNLKRGGLKIAAVKAPGFGDRRKAMLQDIAILTGGQVISED LGMKLENTIDMLGRAKKVSI
NKDNTTIVDGAGEKAEI EARVSQIRQQIEETSDYDREKLQ
>d1srva_ c.8.5.1 (A:) GroEL {Thermus thermophilus}
GYQFDKGYISPYFVTNPETMEAVLEDAFILIVEKKVSNVRELLPILEQVAQTGKPLIIAEDVEGEALA
TLVVNKLRTLSVA AVKAPGFGDRRKEMLKDIAAVTGGTVISEELGFKLENATLSMLGRAERVITK
DETTIVGGK
>d1a6db2 c.8.5.2 (B:216-367) Thermosome {Archaeon Thermoplasma acidophilum}
GIIVDKEKVHMPGMPDVVKDAKIALLDAPLEIKKPEFDTNLRIEDPSMIQKFLAQEENMLREMVDKIK
SVGANVVITQKIGIDMAQHLYSRAGIYAVRRVKKSDMDKLAKATGASIVSTIDEISSDLGTAERVEQV
KVGEDYMTFVTGCKNP
>d1ass_ c.8.5.2 (-) Thermosome {Archaeon Thermoplasma acidophilum}
MSGIVIDKEKVHSMKMPDVVKNAKIALIDSALEIKKTEIEAKVQISDPSKIQDFLNQETNTFKQMVEKI
KKGANVVLCKQKIGIDVAQHLYLAKEGIYAVRRVKKSDMEKLAATGAKIVTDLDDLTSPVLGAEETV
EERKIGDDRMTFVMGCK
>d1ay7b_ c.9.1.1 (B:) Barstar (barnase inhibitor) {Bacillus amyloliquefaciens}
KKAVINGEQIRSISDLHQTLKKELALPEYYGENLDALWDCLTGWVEYPLVLEWRQFEQSKQLTENGA
ESVLQVFREAKAEGCDITHLS

>d1jj2x_c.9.2.1 (X:) Ribosomal protein L32e {Archaeon Haloarcula marismortui}
TELQARGLTEKTPDLSDEDARLLTQRHRVKGKPFNRQDHHKKRVSTSWRKPRGQLSKQRRGIKKG
GDTVEAGFRSPTAVRGKHPSGFEEVRVHNVDDLEGVDGDTEAVRIASKVKGARKRERIEEEAEDAGIR
VLNPTYVEV

>d1e8ca1_c.98.1.1 (A:3-87) UDP-N-acetylmuramyl tripeptide synthetase MurE {Escherichia coli}
RNLRDLLAPWVPDAPSRALREMTLDSRVAAAGDLFVAVVGHQADGRRYIPQAIAGVAAIIAEAKDE
ATDGEIREMHGVPVIYLS

>d1gg4a3_c.98.1.1 (A:1-81) UDP-murNac-tripeptide D-alanyl-D-alanine-adding enzyme MurF {Escherichia coli}
MISVTLSQLTDILNGELQGADITLDAVTTDTRKLTGCLFVALKGERFDAHDFADQAKAGGAGALLVS
RPLDIDLPLQIVK

>d2bnh_c.10.1.1 (-) Ribonuclease inhibitor {Pig (Sus scrofa)}
MNLDIHCEQLSDARWTELLPLLQYEVVRLDDCGLTEEHCCKDIGSALRANPSLTELCLRTNELGDAG
VHLVLQGLQSPCKIQKLSLQNCSTEAGCGVLPSTLRSLPTLRELHLSNPLGDAGLRLCEGLLDP
QCHLEKLQLEYCRITAASCEPLASVLRATRALKELTVSNNDIGEAGARVLGQGLADSACQLETLRLEN
CGLTPANCKDLGIVASQASLRELDLGSNGLGDAGIAELCPGLLSPASRLKTLWLWECEDITASGCRDLC
RVLQAKETLKELSLAGNKLGDGEGARLLCESLLQPGCQLESWVKSCSLTAACQHVSLMLTQNKHLL
ELQLSSNKLGDGSIQELCQALSQPGTTLRVLCLGDCEVTNSGCSLALLANRSLRELDLSNNCVGD
PGVLQLLGSLEQPGCALEQLVLYDTYWTEEVEDRLQALEGSKPGLRVIS

>d1a4ya_c.10.1.1 (A:) Ribonuclease inhibitor {Human (Homo sapiens)}
SLDIQSLDIQCEELSDARWAELLPLLQCCQVVRLLDDCGLTEARCKDISSALRVNPAELNLSNELG
DVGVHCVLQGLQTPSCKIQKLSLQNCCLTGAGCGVLSSTLRTLPTLQELHLSNLLGDAGLQLLCEGL
LDPQCRLEKLQLEYCSLSAASCEPLASVLRKPDFKELTVSNNDINEAGVRVLCQGLKDSQCQLEALK
LESCGVTSDNCRDLCGIVASKASLRELALGSNKLGDVGMALCPGLLHPSSRLRTLWIWECGITAKGC
GDLCRVLRAKESLKELSLAGNELGDEGARLLCETLLEPGCQLESWVKSCSFTAACCSHFSSVLAQNR
FLELQISNNRLEDAGVRELCQGLGQPGSVLRVWLADCDVSDSSCSLAATLLANHSLRELDLSNNC
LGDAGILQLVESVRQPGCLLEQLVLYDIYWSEEMEDRLQALEKDKPSLRVIS

>d1yrqa_c.10.1.2 (A:) Rna1p (RanGAP1), N-terminal domain {Fission yeast (Schizosaccharomyces pombe)}
ARFSIEGKSLKLDAITTEDEKSVFAVLEDDSVKEIVLSGNTIGTEAARWLSENIASKKDLEIAEFSDF
TGRVKDEIPEALRLLLQALLKCPKLHTVRLSDNAFGPTAQEPLIDFLSKHTPLEHLYLHNNGLGPQAG
AKIARALQELAVNKKAKNAPPLRSIICGRNRENGSMKEWAKTFQSHRLLHTVKMVQNGIRPEGIE
HLLLEGLAYCQELKVLDLQDNTFTHLGSSALAIKSWPNLRELGLNDCLLSARGAAVVDAFSKLE
NIGLQTLRLQYNEIELDAVRTLKTVIDEKMPDLLFLELNGNRFSEEDDVVDEIREVFSTRGRGELDEL
DDME

>d1fqva2_c.10.1.3 (A:146-431) Cyclin A/CDK2-associated p19, Skp2 {Human (Homo sapiens)}
ESLWQTLDLTGKNLHPDVTGRLLSQGVIAFRCPRSFMDQPLAEHFSPFRVQHMDLSNSVIEVSTLHG
ILSQCSKLQNLSEGLRSLDPIVNTLAKNSNLVRLNLSGCSGFSEFALQTLSSCSRLDELNLSWCFDF
TEKHVQVAHVSETITQLNLSGYRKNLQKSDLSTLVRRCPNLVHLDLSDSVMLKNDCFQEFFQLNY
LQHLSLRICYDIIPETLLELGEIPTLKTQVFGIVPDGTLQLLKEALPHLQINCSHFTTIARPTIGNKKN
QEIWGIKCRLLTQ

>d1fs2a2_c.10.1.3 (A:146-401) Cyclin A/CDK2-associated p19, Skp2 {Human (Homo sapiens)}

sapiens}}

ESLWQTLDEFVRVQHMDLSNSVIEVSTLHGILSQCSKLQNLSSLEGLRLSDPIVNTLAKNSNLVRLNLSG
CSGFSEFALQTLSSCSRLEDELNLSWCFDFTEKHVQVAVAHVSETITQLNLSGYRKNLQKSDLSTLVR
RCPNLVHLDLSDSVMLKNDQCFQEFFQLNYLQHLSLSRCYDIIPETLLELGEIPTLKTQLVFGIVPDGTL
QLLKEALPHLQIN

>d1h6ta2 c.10.2.1 (A:31-240) Internalin B {*Listeria monocytogenes*}

GPLGSETITVPTPIKQIFSDDAFAETIKDNLKKKSVTDAVTQNELNSIDQIANNNSDIKSVQGIQYLPNV
TKLFLNGNKLTDIKPLANLKNLWFLDENKVKDLSSLKDLKSLKSLSEHNGISDINGLVHLPQLE
SLYLGNNKITDITVLSRLTKLDTLSLEDNQISDIVPLAGLTKLQNLKLYLKNHISDLRALAGLKNLDVLEL
FSQ

>d1h6ua2 c.10.2.1 (A:36-262) Internalin H {*Listeria monocytogenes*}

GSITQPTAINVIFPDPALANAIAAGKSNVTDVTVQADLDGITTLTSAFGTGVTTIEGVQYLNLLIGLEL
KDNQITDLAPLKNLTKITELELSGNPLKNVSAIAGLQSIKTLDTSTQITDVTPLAGLSNLQVLYLDLN
QITNISPLAGLTLQYLSIGNAQVSDLTPLANLSKLTTLKADDNKISDISPLASLPNLIHVHLKNNQISD
VSPLANTSNLFIIVTLTNQ

>d1j15a_ c.10.2.6 (A:) Leucine rich effector protein YopM {*Yersinia pestis*}

KSKTEYYNAWSEWERNAPPGNGEQREMAVSRLRDCLDRQAHELELNNLGLSSLPELPPHLESLVAS
CNSLTELPELPQSLKSLVDNNNLKALSDDLPLEYLGVSNQLEKLPQLQSSFLKIIDVDNNSLKKL
PDLPPSLEFIAAGNNQLEELPELQNLPLTAIYADNNSLKKLPDLPLSLESIVAGNNILEELPELQNLPL
LTTIYADNLLKTLPLDLPPSLEALNVRDNYLTDLPELPQSLTFLDVSSENFSGLSELPPNLYLNASSN
EIRSLCDLPPSLEELNVSNNKLIELPALPPRLERLIASFNHLAEVPELPQNLKQLHVEYNPLREFPDIP
ESVEDLRMNS

>d1dcea3 c.10.2.2 (A:444-567) Rab geranylgeranyltransferase alpha-subunit, C-terminal domain {*Rat (Rattus norvegicus)*}

RVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRALPPALAALRCLEVLQASDNALENVDGVANLPRL
QELLLCNRLQQAIAIPLVSCPRLVLLNLQGNSLCQEEGIERLAEMLPVSSILT

>d1koha1 c.10.2.3 (A:201-362) mRNA export factor tap {*Human (Homo sapiens)*}

LNELKPEQVEQLKLIMSKRYDGSQQALDLKGLRSDPLVAQNIDVVLNRRSSMAATLRIIEENIPELL
SLNLSNNRLYRLDDMSSIVQKAPNLKILNLSGNELKSERELDKIKGLKLEELWLDGNSLSDTFRDQST
YISAIRERFPKLLRLDGHELPPPIAF

>d1a9na_ c.10.2.4 (A:) Splicesomal U2A' protein {*Human (Homo sapiens)*}

VKLTAELIEQAAQYTNVAVRDRELDLRYKIPVIENLGATLDQFDAIDFSNEIRKLDGFPLLRRLKTL
VNNNRICRIGEGLDQALPDLTELILTNNLVELGDLPLASLKSLEYLCILRNVPVTKKHRYLYVIYKV
PQVRVLDVQKVKLKERQEAEMFK

>d1igra1 c.10.2.5 (A:1-149) L1 and L2 domains of the type 1 insulin-like growth factor receptor {*Human (Homo sapiens)*}

EICGPGIDIRNDYQQLKRLNCTVIEGYLHILLISKAEDYRSYRFPKLTVITEYLLLFRVAGLESLGDLFP
NLTVIRGWKLFYNYALVIFEMTNLKDIGLYNLRNITRGAIRIEKNADLCYLSTVDWLSLILDAVSNNYIV
GNKPPKECG

>d1igra2 c.10.2.5 (A:300-478) L1 and L2 domains of the type 1 insulin-like growth factor receptor {*Human (Homo sapiens)*}

KVCEEEKKTIDSVTSAQMLQGCTIFKGNLLINIRRGNNIASELENFMGLIEVVTGYVKIRHSHALVS
LSFLKNLRLILGEEQLEGNYSFYVLDNQNQLQVLDWDHNRNLTIKAGKMYFAFNPKLCVSEIYRMEE
VTGTKGRQSKGDINTRNNGERASCESDVDDDDKEQKLISEEDLN

>d1ds9a_ c.11.1.1 (A:) Outer arm dynein light chain 1 {Green algae (Chlamydomonas reinhardtii)}

MAKATTIKDAIRIFEERKSVVATEAEKVELHGMIPPIEKMDATLSTLKACKHLALSTNNIEKISSLSGM
ENLRILSLGRNLIKKIENLDAVADTLEELWISYNQIASLSGIEKLVNLRVLYMSNNKITNWGEIDKLAA
LDKLEDLLLAGNPLYNDYKENNATSEYRIEVVKRLPNLKKLDGMPVDVDEREQANVARGG

>d1jj2k_ c.12.1.1 (K:) Ribosomal protein L15 (L15p) {Archaeon Haloarcula marismortui}

TSKKKRQGRSRTTHGGGSHKNRRGAGHRGGRGDAGRDKHEFHNEPLGKSGFKRPQKVQEEAATID
VREIDENVTLAADDVAEVEDGGFRVDVRDVVEEADDADYVKVLGAGQVRHELTLIADDFSEGARE
KVEGAGGSVELTDLGEERQ

>d1jj2n_ c.12.1.1 (N:) Ribosomal protein L18e {Archaeon Haloarcula marismortui}

SKTNPRLSSLIADLKSAAARSSGAVWGDVAERLEKPRRTHAEVNLGRIERYAQEDETUVVPGKVLGS
GVLQKDVTVAAVDFSGTAETKIDQVGEAVSLEQAIENNPEGSHVRVIR

>d1aua_2 c.13.1.1 (97-299) C-terminal domain of phosphatidylinositol transfer protein
sec14p {Baker's yeast (Saccharomyces cerevisiae)}

YDEKPLIAKFYPQYYHKTDKDGPRVYFEELGAVNLHEMNKVTSEERMLKNLVWEYESVVQYRLPAC
SRAAGHLVETSCTIMDLKGISISSAYSVMYSVREASYISQNYPERMGKFYIINAPFGFSTAFRLFKPFL
DPVTVSKIFILGSSYQKELLKQIPAENLPVKFGGKSEVDESKGGLYLSDIGPWRDPKYIGPEGEAPE

>d1h4xa_ c.13.2.1 (A:) Anti-sigma factor antagonist SpoIIaa {Bacillus sphaericus}

AFQLEMVTRETVVIRLFGELDHHAVEQIRAKISTAIFQGAVTTIWNFERLSFMDSSGVGLVLRMRE
LEAVAGRTILLNPSPTMRKVFQFSGLGPWMMDATEEEEAIDRVR

>d1auz_ c.13.2.1 (-) Anti-sigma factor antagonist SpoIIaa {Bacillus subtilis}

SLGIDMNVKESVLCIRLTGELDHHTAETLKQKVTQSLEKDDIRHIVLNLEDLSFMDSSGLGVILGRYK
QIKQIGGEMVVCAISPAVKRLFDMSGFLFKIIRFEQSEQQALLTLGVAS

>d1tyfa_ c.14.1.1 (A:) Clp protease, ClpP subunit {Escherichia coli}

SRGERSFDIYSRLLKERVIFLTGQVEDHMANLIVAQMLFLEAENPEKDIYLYINSPGGVITAGMSIYDT
MQFIKPDVSTICMGQAASMGAFLLTAGAKGKRFCLPNSRVMIHQPLGGYQGQATDIEIHAREILKVKG
RMNELMALHTGQSLEQIERDTERDRFLSAPEAVEYGLVDSILTHRN

>d1fc6a4 c.14.1.2 (A:78-156,A:249-463) Photosystem II D1 C-terminal processing protease
{Algae (Scenedesmus obliquus)}

VTSEQLLFLEAWRAVDRAVDKSFNGQSWFKLRETYLKKEPMDRRAQTYDAIRKMLAVLDDPFTR
FLEPSRLAALRRGTXXKVTINPVTFTTCSNVAALPPGAAKQQLGYVRLATFNSNTTAAQQAFTL
SKQGVAGLVLDIRNNGGLFPAGVNVARMLVDRGDLVLIADSQGIRDIYSADGNSIDSATPLVVLVNRG
TASASEVLGALKDSKRGLIAGERTFGKGLIQTVVVLDSDGSGVAVTVARYQTPAGVDINKIGVSPDVQL
DPEVLPTDLEGVCRVLGSDAAPRLF

>d1k32a4 c.14.1.2 (A:680-762,A:854-1061) Tricorn protease {Archaeon Thermoplasma
acidophilum}

SSIHEEFLQMYDEAWKLARDNYWNEAVAKEISERIYEKYRNLVPLCKTRYDLSNVIVEMQGEYRTSH
SYEMGGTFTDKDPPFRSXDDRFIRYRSWVEANRRYVHERSKGTIGYIHIPDMGMMGLNEFYRLFINES
SYQGLIVDVRFNNGGFVSQLIIEKLMNKRIGYDNPRRGTLSPYPTNSVRGKIIAITNEYAGSDGDIFSFS
FKKLGLGKLIGTRTWGGVVGITPKRRLIDGTVLTQPEFAFWFRDAGFGVENVYGVDPDVEIEYAPHDY
LSGKDPQIDYALIEELRN

>d1j7xa_ c.14.1.2 (A:) Interphotoreceptor retinoid-binding protein IRBP {African clawed frog
(Xenopus laevis)}

DPSVTHVLHQLCDILANNYAFSERIPTLLQHLPNLDYSTVISEEDIAAKLNYELQSLTEDPRLVLKSKT

DTLVMPGDSIQAENIPEDEAMLQALVNTVFKVSILPGNIGYLRFDQFADVSVIAKLAPFIVNTVWEPI
TITENLIIDLRYNVGGSSTAVPLLLSYFLDPETKIHFLTLHNRQQNSTDEVYSHPKVLGKPYGSKKGVY
VLTSHQTATAAEFAYLMQSLSRATHIIGEITSGNLMHSHKVFPGDTQLSVTVPIINFIDSNQDYWLGGG
VVPDAIVLADEALDKAKEIIAFHPPLA

>d1nzya_ c.14.1.3 (A:) 4-Chlorobenzoyl-CoA dehalogenase {Pseudomonas sp., strain CBS-3}
MYEAIGHRVEDGVAEITIKLPRHRNALSVMKAMQEVTDALNRAEEDDSVGAVMITGAEDAFCAAGFYL
REIPLDKGVAGVRDHFRIAALWWHQMIHKIIRVSRVLAALINGVAAGGGLGISLASDMAICADSAKF
VCAWHTIGIGNDTATSYSLARIVGMRRAMELMLNRTLYPEEAKDWGLVSRVYPKDEFREVAWKVA
RELAAAPTHLQVMAKERFHAGWMQPVEECTEFEIQNVIASVTHPHFMPCLTRFLDGHRAADRPQVE
LPAGV

>d1ey3a_ c.14.1.3 (A:) Enoyl-CoA hydratase (crotonase) {Rat (Rattus norvegicus)}
FQYIITEKKGKNSVGLIQLNRPKALNALCNGLIEELNQALETFEEDPAVGAIVLTGGEKAFAAGADIK
EMQNRFTQDCYSGKFLSHWDHITRIKPVIAAVNGYALGGGCELAMMCDIYAGEKAQFGQPEILLG
TIPGAGGTQRLTRAVGKSLAMEMVLTGDRISAQDAKQAGLVSKIFPVETLVEEAIQCAEKIANNKIIIV
AMAKESVNAAFEMTLTEGNKLEKLFYSTFATDDRREGMSAFVEKRKANFKDH

>d1dcia_ c.14.1.3 (A:) Dienoyl-CoA isomerase (delta3-delta2-enoyl-CoA isomerase) {Rat
(Rattus norvegicus)}
AYESIQVTSAQKHVHLHVQLNRPEKRNAMNRAFWRELVECFQKISKSDCRAVVVSGAGKMFTSGID
LMDMASDILQPPGDDVARIAWYLRDLISRYQKFTFTVIEKCPKPVIAAIHGGCIGGGVDLISACDIRYCT
QDAFFQVKEVDVGLAADVGTQRLPKVIGNRSLVNELTFTARKMMADEALDSGLVSRVFPDKDVML
NAAFALAADISSKSPVAVQGSKINLIYSRDHSVDESLDYMATWNMSMLQTQDIKSVQAAMEKKDSK
SITFSKL

>d1hnua_ c.14.1.3 (A:) Dienoyl-CoA isomerase (delta3-delta2-enoyl-CoA isomerase) {Baker's
yeast (Saccharomyces cerevisiae)}
NEKISYRIEGPFFIIHLINPDNLNALEGEDYIYLGELELADRNRDVYFTIIQSSGRFFSSGADFKGIAKA
QGDDTNKYPSETSKWVSNFVARNVYVTDAFIKHSHKVLICCLNGPAIGLSAALVALCDIVYSINDKVYLL
YPFANLGLITEGGTTVSLPLKFGTNTTYECLMFNKPFKYDIMCENGFISKNFNMPSNAEAFNAKVL
EELREKVKGLYLPSCGLMKLLKSNHIDAFNKANSVEVNESLKYWVDGEPLKRFRQ

>d1hzda_ c.14.1.3 (A:) AUH protein {Human (Homo sapiens)}
EDELVRVHLEENRGIVVLGINRAYGKNSLSKNLIKMLSKAVDALKSDKKVRTIIRSEVPGIFCAGAD
LKERAKMSSEVGPVSKIRAVINDIANLPVPTIAAIDGLALGGGLELALACDIRVAASSAKMGLVETK
LAIIPGGGGTQRLPRAIGMSLAKELIFSARVLDGKEAKAVGLISHVLEQNQEGDAAYRKALDLAREFL
PQGPVAMRVAKLAINQGMVLDLVTGLAIEEACYAQTIPKDRLEGLLAFKEKRPPRYKGE

>d1ef8a_ c.14.1.3 (A:) Methylmalonyl CoA decarboxylase {Escherichia coli}
MSYQYVNVVTINKVAVIEFNYGRKLNLSKVFIDDLMQALSDLNRPDIRCIIIRAPSGSKVFSAGHDIH
ELPSGGRDPLSYDDPLRQITRMIQKFPKPIISMVEGSVWGGAFEMIMSSDLIIAASTSTFSMTPVNLG
VPYNLVGIHNLTRDAGFHIVKELIFTASPITAQRALAVGILNHVVEVEELEDFTLQMAHHISEKAPLAI
AVIKEELRVLGEAHTMNSDEFERIQGMRAVYDSEDYQEGMNAFLEKRKPNFVGH

>d1jnxx1 c.15.1.3 (X:1649-1757) Breast cancer associated protein, BRCA1 {Human (Homo
sapiens)}
RMSMVVSGLTPEEFMLVYKFARKHHITLTNLITEETTHVVMKTDAEFVCERTLKYFLGIAGGKVVVS
YFWVTQSIKERKMLNEHDFEVRGDVVNGRNHQGPKRARESQD

>d1jnxx2 c.15.1.3 (X:1758-1859) Breast cancer associated protein, BRCA1 {Human (Homo
sapiens)}

RKIFRGLICCYGPFTNMPTDQLEWMVQLCGASVVKELSSFTLGTGVHPIVVVQPDAWTEDNGFHAI
GQMCEAPVVTREWVLDVALYQCQELDTYLIPQIP
>d1cdza_c.15.1.1 (A:) DNA-repair protein XRCC1 {Human (Homo sapiens)}
ELPDFQGGKHFLLYGEFPGDERRKLIRYVTAFNGELEDYMSDRVQFVITAQEWDPSEALMDNPSL
AFVVRPRWIYSCNEKQKLLPHQLYGVVPPQA
>d1in1a_c.15.1.2 (A:) DNA ligase III alpha {Human (Homo sapiens)}
GSADETLQCQTKVLLDIFTGVRLYLPPSTPDFSRLRRYFVAFDGLVQEFDMTSATHVLGSRDKNPAA
QQVSPewiwacirkrrlvapc
>d1dgtb3_c.15.1.2 (B:2582-2660) NAD+-dependent DNA ligase, domain 4 {Thermus
filiformis}
EEVSDLLSGLTFVLTGELSRPREEVKALLGRLGAKVTDSVSRKTSYLVVGENPGSKLEKARALGVAULT
EEEFWRFLKE
>d1rvv1_c.16.1.1 (1:) Lumazine synthase {Bacillus subtilis}
MNIHQGNLVGTGLKIGIVVGRFNDFITSKLLSGAEDALLRHGVDTNDIDVAWVPGAFEIPFAAKKMAE
TKKYDAIITLGTVIRGATTHYDYVCNEAAKGIAQAANTTGVPVIFGIVTTENIEQAIERAGTKAGNKGV
DCAVSAIEMANLNRSE
>d1di0a_c.16.1.1 (A:) Lumazine synthase {Brucella abortus}
TSFKIAFIQARWHADIVDEARKSFVAELAAKTGGVSEVEIFDVPAYEIPLHAKTLARTGRYAAIVGAA
FVIDGGIYDHFVATAVINGMMQVQLETEVPVLSVVLTPHHFHESKEHHDFHAFKVKGVAAHA
ALQIVSERSIAA
>d1hqka_c.16.1.1 (A:) Lumazine synthase {Aquifex aeolicus}
MQIYEGKLTAEGLRFGIVASRFNHALVDRLVEGAIDCIVRHGGREEDITLVRVPGSWEIPVAAGELARK
EDIDAVIAIGVLIRGATPHFDYIASEVSKGLANLSLELRKIPITFGVITADTLEQAIERAGTKHGNKGWE
AALSAIEMANLFKSLR
>d1c41a_c.16.1.1 (A:) Lumazine synthase {Rice blast fungus (Magnaporthe grisea)}
GPTPQQHDGSALRIGIVHARWNETIIEPLLAGTKAKLLACGVKESNIVVQSVPGSWELPIAVQRLYSA
SQLQTPSSGPSLSAGDLLGSSTDLTALPTTTASSTGPFDALIAIGVLIKGETMHFEYIADSVSHGLMRV
QLDTGVPVIFGVLTVLTDDQAKARAGVIEGSHNHGEDWGLAAVEMGVRRRDWAAGKT
>d1c2ya_c.16.1.1 (A:) Lumazine synthase {Spinach (Spinacia oleracea)}
MNELEGYVTKAQSFRAIVVARFNEFVTRRLMEGALDTFKKYSVNEDIDVVVWVPGAYELGVTAQAL
GKSGKYHAIIVCLGAVVKGDTSHYDAVVNSASSGVLSAGLNSGVPCVFGVLTCDNMDQAINRAGGKAG
NKGAESALTAIEMASLFEHHLK
>d1ejba_c.16.1.1 (A:) Lumazine synthase {Baker's yeast (Saccharomyces cerevisiae)}
AVKGLGKPDQVYDGSKIRVGIHARWNRVIIDALVKGAIERMASLGVENNIIIETVPGSYELPWGTRK
FVDRQAKLKGKPLDVVIPIGVLIKGSTMHFEYISDSTTHALMNLQEKVDMPIVIFGLLTCMTEEQALAR
AGIDEAHSMHNHGEDWGAAVEMAVKFGKNAF
>d1cp3a_c.17.1.1 (A:) Apopain (caspase-3, cpp32) {Human (Homo sapiens)}
NSYKMDYPEMGLCIIINKNFHKSTGMTSRSGTDVDAANLRETFRNLYEVNRKNDLTREEIVELM
RDVSKEDHRSRSSFVCLLSHGEEIIFGTNGPVDLKKITNFFRGDRCSLTGKPKLFIQACRGTELD
CGIETDSGVDDDMACHKIPVDADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHIL
TRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH
>g1ibc.1_c.17.1.1 (A,B:) Interleukin-1beta converting enzyme (a cysteine protease) {Human
(Homo sapiens)}
GNVKLCSLEEAQRIWKQKSAEIYPIMDKSSRTRLALIICNEEFDSIPRRTGAEVDITGMTMLLQNLGY

SVDVKKNLASDMTTELEAFAHRPEHKTS DSTFLVFM SHGIREGICGKKHSEQVPDILQLNAIFNML
NTKNCPSLKD KPKVIIIQACRGD SPGVVWFKDXAIKKAHIEKDFIAFCSSTPDNVSWRHPTMGSVFIG
RLIEHMQEYACSCDV EEIFRKVRF SFEQPAGRAQMPTTERTVTLTRCFYLFPGH

>d1f1ja_ c.17.1.1 (A:) Caspase-7 {Human (Homo sapiens)}

YQYNMNF EKL GKCIINNKNF DKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYND CSCAKMQDLL
KKASEEDHTNAACFACILLSHGEENV IYGKDGVTPIKDLTAHFRGDRSKTLL EKPKLFFIQACRGTEL
DDGIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRG SWFVQALCSILEEHGKDLEIM
QILTRVND RVARHFESQSDDPHFHEKKQIPCVVSMLTKELYFS

>g1qtn.1 c.17.1.1 (A;B:) Caspase-8 {Human (Homo sapiens)}

DKVYQMK SKPRGYCLIINNHNFAKAREKVPKLHSIRDRNGTHLDAGALTTT FEELHFEIKPHDDCTV
EQIYEILKIYQLMDHSNMDCFICCILSHGDKGIYGTGDGQEAPIYELTSQFTGLKCP SLAGKPKVFFIQA
CQGDNYQKGIPVETDXTRYIPDEADFL LGMATVNNCVSYRNPAEGTWYIQLCQSLRERCPRGDDIL
TILTEVNYEVS NKDDKKNMGKQMPQPTFTLRKKLVF PSD

>d1jxqa_ c.17.1.1 (A:) Caspase-9 {Human (Homo sapiens)}

MGALES LRGNADLAYILSMEPCGHCLIINN VNF CRESGLRTRTGSNIDCEKLR RRFSSLFHFMVEVKGD
LTAKKMVLALLELARQDHGALDCCV VVILSHGCQASHLQFPGAVYGT DGCPVSVEKIVNIFNGTSCPS
LGGKPKLFFIQACGGEQKDHGF EFASTSPEDESPGSNPEP DATPFQEGLRTFDQLDAISSLPTPSDIFV
SYSTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFN FLRKK
LFFKTS

>d1cvra2 c.17.1.2 (A:1-350) Gingipain R (RgpB), N-terminal domain {Porphyromonas
gingivalis}

YTPVEEK ENGRMIVIVAKKYEGDIKDFVDWKNQRGLRTEVKVAEDIASPV TANAIQQFVKQEYEKEG
NDLTYVLLVGDHKDIPAKITPGIKSDQVYQGIVGN DHYNEVFGRFSCESKEDLKTQIDRTIHYERNIT
TEDKWL GQALCIASAEGGPSADNGESDIQHENVIANLLTQYGYTKIIKCYDPGVTPKNIIDAFNGGISL
VNYTGHGSETAWGTSHFGTTHVKQLTNSNQLPFIFDVACVNGDFLFSMPCFAEALMRAQKDGKPTG
TVAI IASTIDQYWAPPMRGQDEMNEILCEKHPNNIKRTFGGVTMNGMFAMVEKYKKDGENMLDT
WTVFGDPSLLVRTLV

>d1akz_ c.18.1.1 (-) Uracil-DNA glycosylase {Human (Homo sapiens)}

MEFFGESWKKHLSGEFGKPYFIKLMGFVAEERKH YTVYPPPHQVFTWTQMCDIKDVKVVILGQDP
YHGPNQAHGLCF SVQRVPPPPSLENIYKELSTDIEDFVHPGHGDL SGWAKQGVLLNNAVLTVRAHQ
ANSHKERGWEQFTDAVSWLNQNSNGLV FLLWGSYAQKKGSAIDRKRHHVLQTAHPSPLSVYRGFF
GCRHFSKTNELLQKSGKKPIDWKEL

>d1laue_ c.18.1.1 (E:) Uracil-DNA glycosylase {Herpes simplex virus type 1}

LDWTTFR RVFLIDDAWRPLMEPELANPLTAHLLAEYNRRCQTEEVLP PREDVFSWTRYCTPDEVR
VVIIGQDPYHHPGQAHGLAFSVRANVPPPSLRNVLA AVKNCYPEARMSGHGCKLEKWARDGVLLLN
TTLTVKRGAAASHRIGWDRFVGGVIRRLAARRPGLV FMLWGTHAQNAIRPDPRVHCVLKFSHPSP
LSKV PFGTCQHFLVANRYLETRSISPIDWSV

>d3euga_ c.18.1.1 (A:) Uracil-DNA glycosylase {Escherichia coli}

LTWHDVLAEEKQPHFLNLTQTVASERQSGVTIYPPQK DVFNAFRFTELGDVKVVILGQDPYHGP
QAHGLAFSVRPGIAIPPSLLNMYKELENTIPGFTRPNHGYLESWARQGVLLNNTVLTVRAGQAHSHA
SLGWETFTDKVISLINQHREGVV FLLWGSHAQKKGAIIDKQRHHVLKAPHSPLSAHRGFFGCNHFV
LANQWLEQHGETPIDWMPVLP AESE

>d1muga_ c.18.1.2 (A:) G:T/U mismatch-specific DNA glycosylase {Escherichia coli}

MVEDILAPGLRVVFCGINPGLSSAGTGFPFAHPANRFWKVIYQAGFTDRQLKPQEAQHLLDYRCGVT

KLVD RPTVQANEVSKQELHAGGRKLIKIEDYQPQALAILGKQAYEQGFSQRGAQWGKQTLTIGSTQI
WVLPNPSGLSRVSLEKLVEAYRELDQALVV
>d1mla_1 c.19.1.1 (3-127,198-307) Catalytic domain of malonyl-CoA ACP transacylase
{*Escherichia coli*}
QFAFVFPQGSQTVGMLADMAASYPIVEETFAEASAALGYDLWALTQQGPAEELNKTWQTQPALLT
ASVALYRVWQQQGGKAPAMMAGHSLGEYSALVCAGVIDFADAVRLVEMRGKFMQEAVPEXVPSHCA
LMKPAADKLAVELAKITFNAPTVPVNNVDVKCETNGDAIRDALVRQLYNPVQWTKSVEYMAAQQ
VEHLYEVGPGKVLTLTKRIVDTLTASALNEPSAMAAAL
>d1g7sa3 c.20.1.1 (A:329-459) Initiation factor IF2/eIF5b, domain 3 {Archaeon
Methanobacterium thermoautotrophicum}
DPEKVREELSEIEDIKIDTDEAGVVVKADTLGSLVAVVKILRDMYVPIKVADIGDVSRRDVVNAGIAL
QEDRVYGAIIAFNVKVIPSAQELKNSDIKLFQGNVIYRLMEEYEEWVRGIEEEKKKKWMEEA
>d1jj2i_ c.21.1.1 (I:) Ribosomal protein L13 {Archaeon *Haloarcula marismortui*}
AEFDADVVDARDCIMGRVASQVAEQALDGETVAVVNAERAVITGREEQIVEKEYEKRVDIGNDNGYF
YPKRPDGIFKRTIRGMLPHKKQRGREAFESVRVYLGPNPYDEDGEVLDGTSLDRLSNIKFVTLGEISET
LGANKTW
>d1dmga_ c.22.1.1 (A:) Ribosomal protein L4 {*Thermotoga maritima*}
AQVDLLNVKGEKVGTLAISDFVFNIDPNYDVMWRYVDMQLSNRRAGTASTKTRGEVSGGGRKPWP
QKHTGRARHGSIRSPIWRHGGVVHGPKPRDWSKKNKKMKKLALRSALSVKYRENKLLVDDLK
ERPKTSLKEILQNLQLSDKTLIVLPWKEEGYMNVLKSGRNLDPVKVIIADNPNNSKNGEKAVRID
GLNVFDMLKYDYLVLRDMVSKIEEVLG
>d1jj2c_ c.22.1.1 (C:) Ribosomal protein L4 {Archaeon *Haloarcula marismortui*}
MQATIYDLGNTDGEVDLPDVFETPVRSDLIGKAVRAAQANRQDYGSDEYAGLRTPAESFGSGRGQ
AHVPKLDGRARRVPQAVKGRSAHPPKTEKDRSLDLNDRKERQLAVRSALAATADADLVADRGEFDR
DEVVVVSDDFEDLVKTQEVVSLLEALDVHADIDRADETKIKAGQGSARGRKYRRPASILFVTSDEPS
TAARNLAGADVATASEVNTEDLAPGGAPGRLTVFTESALAEVAER
>d1hey_ c.23.1.1 (-) CheY protein {*Escherichia coli*}
DKELKFLVVGNGGTGKSTVRNLLKELGFNNVEDAEDGVDALNKLQAGGYGFVISDWNMPNMDGLE
LLKTIRADGAMSALPVLMTAEAKKENIIAAAQAGASGYVVKPFTAATLEEKLNKIFEKLG
>d1jbea_ c.23.1.1 (A:) CheY protein {*Escherichia coli*}
ADKELKFLVDDFSTMRIRVRLNLLKELGFNNVEEAEDGVDALNKLQAGGYGFVISDWNMPNMDGL
ELLKTIRADGAMSALPVLMTAEAKKENIIAAAQAGASGYVVKPFTAATLEEKLNKIFEKLG
>d1tmy_ c.23.1.1 (-) CheY protein {*Thermotoga maritima*}
GKRVLIVDDAAFMRMMLKDIITKAGYEVAGEATNGREAVEKYKELKPDIVTMDITMPENMGIDA
EIMKIDPNAKIIVCSAMGQQAMVIEAIKAGAKDFIVKPFQPSRVVEALNKVS
>d1a04a2 c.23.1.1 (A:5-142) Nitrate/nitrite response regulator (NARL), receiver domain
{*Escherichia coli*}
EPATILLIDDHPMLRTGVKQLISMAPDITVVGEASNGEQGIELAESLDPDLILLDLNMPGMNGLETLD
KLREKSLSGRIVVFSVSNHEEDVVTALKRGADGYLLKDMEPEDLLKALHQAAGEMVLSEALTPVLA
ASL
>d1ntr_ c.23.1.1 (-) NTRC receiver domain {*Salmonella typhimurium*}
MQRGIVVVVDDSSIRWVLERALAGAGLTCTTFENGNEVLAALASKTPDVLLSDIRMPGMDGLALL
KQIKQRHPMLPVIIMTAHSDLDAAVSAYQQGAFDYLKPKFDIDEAVALVERAISHYQE
>d1dbwa_ c.23.1.1 (A:) Transcriptional regulatory protein FixJ, receiver domain {*Rhizobium*

meliloti}

MQDYTVHIVDDEEPPVRKSLAFMLTMNGFAVKMHQSAAFLAFAPDVRNGVLVTDLRMPDMSGVEL
LRNLGDLKINIPISIVITGHGDVPMAVEAMKAGAVDFIEKPFEDTVIIEAIERASEHLV

>d1qkka_ c.23.1.1 (A:) Transcriptional regulatory protein DctD, receiver domain
{Sinorhizobium meliloti}

PSVFLIDDDRDRLRKAMQQTLELAGFTVSSFASATEALAGLSADFAGIVISDIRMPGMDGLALFRKILA
LDPDLPMILVTGHGDIPMAVQAIQDGAYDFIAKPFAADRLVQSARRAEKRRRLVMENRSLRRAAEAA
SEGL

>d1dz3a_ c.23.1.1 (A:) Sporulation response regulator Spo0A {Bacillus stearothermophilus}
SIKVCIAADDNRELVSLLDEYISSQPDMEVIGTAYNGQDCLQMLEEKRPDILLDDIIMPHLDGLAVLERI
RAGFEHQPNVIMLTAFGQEDVTKKAVELGASYFILKPFDMENLAHHIRQVYGKT

>d1nat_ c.23.1.1 (-) Sporulation response regulator Spo0F {Bacillus subtilis}

NEKILIVDDQYGIRILLNEVFNKEGYQTFQAANGLQALDIVTKERPDLVLLDMKIPGMDGIEILKRMK
VIDENIRVIIMTAYGELDMIQESKELGALTHFAKPFIDEIRDAVKKYLPL

>d1a2oa1 c.23.1.1 (A:1-140) Methylsterase CheB, N-terminal domain {Salmonella
typhimurium}

MSKIRVLSVDDALMRQIMTEIINSHSDMEMVATAPDPLVARDLIKKFNPVLTLDVEMPRMDGLD
FLEKLMRLRPMPVVMVSSLTGKGSEVTLRALELGAIDFVTKPQLGIREGMLAYSEMIAEKVRTAARA
RIAAHKP

>d1kgsa2 c.23.1.1 (A:2-123) PhoB receiver domain {Thermotoga maritima}

NVRVLVVEDERDLADLITEALKKEMFTVDVCYDGEEGMYMALNEPFDVVILDIMLPVHDGWEILKS
MRESGVNTPVLMALTALSDVEYRVKGLNMGADDYLPKPFDLRELIARVRALIRRKSE

>d1b00a_ c.23.1.1 (A:) PhoB receiver domain {Escherichia coli}

ARRILVVEDEAPIREMVCVLEQNGFQPVAEEDYDSAVNQLNEPWPDLILLDWMLPGGSGIQFIKHL
KRESMTRDIPVVMLTARGEEDRVRGLETGADDYITKPFSPKELVARIKAVMRR

>d1dcfa_ c.23.1.2 (A:) Receiver domain of the ethylene receptor {Thale cress (Arabidopsis
thaliana)}

HMSNFTGLKVLVMDENGVSVMVTKGLLVHLGCEVTTVSSNEECLRVVSHEHKVVFMDVCMGPVEN
YQIALRIHEKFTKQRHQRPLLVALSGNTDKSTKEKCMSFGLDGVLLKPVSLDNIRDVLSDLLEPRVLY
E

>d1qo0d_ c.23.1.3 (D:) Negative regulator of the amidase operon AmiR {Pseudomonas
aeruginosa}

SANSLGSLRELQVLVLNPPGEVSDALVLQLIRIGCSVRQCWPPPEAFDVPVDVVFTSIFQNRHHDEI
AALLAAGTPRTTLVALVEYESPAVLSQIIELECHGVITQPLDAHRVLPVLSARRISEEMAKLKQKTEQ
LQDRIAGQARINQAKVLLMQRHGWDEREAHQHLSREAMKRREPILKIAQELL

>d1fyva_ c.23.2.1 (A:) Toll-like receptor 1, TLR1 {Human (Homo sapiens)}

NIPLEELQRNLQFHAFISYSGHDSFWVKNELLPNLEKEGMQICLHERNFVPGKSIVENIITCIEKSYKS
IFVLSPNFVQSEWCHYELYFAHNNLFHEGSNSLILILLEPIQPYSIPSSYHKLKSLMARRTYLEWPKEK
SKRGLFWANLRAAINIKLTEQAK

>d1fywa_ c.23.2.1 (A:) Toll-like receptor 2, TLR2 {Human (Homo sapiens)}

SRNICYDAFVSYSERDAYWVENLMVQELFNPNPFKLCLHKRDFIPGKWIIDNIIDSIEKSHKTVFVL
SENFVKSEWCKYELDFSHFRLF DENNDAAI LILLEPIEKKAIPQRFCCLRKIMNTKTYLEWPMDEAQ
REGFWVNLRAAIKS

>d1eiwa_ c.23.3.1 (A:) Hypothetical protein MTH538 {Archaeon Methanobacterium

thermoautotrophicum}

VTAEIRLYITEGEVEDYRVFLERLEQSGLEWRPATPEDADAVIVLAGLWGTRRDEILGAVDLARKSSK
PIITVRPYGLENVPPELEAVSSEVVGWNPHCIRDALEDALDVI

>d1kja2 c.23.4.1 (A:122-287) Succinyl-CoA synthetase, alpha-chain, C-terminal domain
{*Escherichia coli*}

NCPGVITPGECKIGIQPGHIHKPGKVGIVSRSGTLTYEAVKQTTDYGFGQSTCVGIGGDPIPGSNFIDILE
MFEKDPQTEAIVMIGEIGGSAEEEEAAAYIKEHVTKPVVGYIAGVTAPKPKRMGHAGAIAGGKGTADE
KFAALEAAGVKTVRSLADIGEALKTVL

>d1euca2 c.23.4.1 (A:131-306) Succinyl-CoA synthetase, alpha-chain, C-terminal domain
{*Pig (Sus scrofa)*}

NCPGVINPGECKIGIMPQHIHKKGRIGIVSRSGTLTYEAVHQTQVGLGQSLCVGIGGDPFNGTDFDTC
LEIFLNDPATEGIILIGEIGGNAEENAAEFLKQHNSGPKSKPVVSVFIAGLTAPPGRRMGHAGAIAGGKG
GAKEKITALQSAGVVVSMSPAQLGTTIYKEFEKRKML

>d1kjb1 c.23.4.1 (B:239-388) Succinyl-CoA synthetase, beta-chain, C-terminal domain
{*Escherichia coli*}

DPREAQAAQWELNYVALDGNIGCMVNGAGLAMGTMDIVKLHGGEPANFLDVGGGATKERVTEAFK
IILSDDKVKAVLVNIFGGIVRCDLIADGIIGAVAEVGVNVPVVRLEGNNAELGAKKLADSGLNIIAAKG
LTDAAQQVVAAVEGK

>d1eucb1 c.23.4.1 (B:246-393) Succinyl-CoA synthetase, beta-chain, C-terminal domain {*Pig (Sus scrofa)*}

EPIENEAAKYDLKYIGLDGNIACFVNGAGLAMATCDIIFLNGGKPANFLDLGGGVKESQVYQAFKLLT
ADPKVEAILVNIFGGIVNCAIANGITKACRELELKVPLVVRLEGTNVHEAQNILNSGLPITSAVDLED
AAKAVASVT

>d2fcr_ c.23.5.1 (-) Flavodoxin {*Chondrus crispus*}

KIGIFFSTSTGNTTEVADFIGKTLGAKADAPIDVDDVTPDQALKDYDLLFLGAPTWNTGADTERSGT
SWDEFLYDKLPEVDMKDLPVAIFGLGDAEGYPDNFCDAIEEIHDCFAKQGAKPVGFSNPDDYDYEES
KSVRDGKFLGLPLDMVNDQIPMEKRVAGWVEAVVSETGV

>d1f4pa_ c.23.5.1 (A:) Flavodoxin {*Desulfovibrio vulgaris*}

PKALIVYGSTTGNTTEYTAETIARELADAGYEVDSRDAASVEAGGLFEGFDLVLLGCSTWGDDSIELQD
DFIPLFDSLEETGAQGRKVACFCGDSSEWYFCGAVDAIEEKLKNLGAEIVQDGLRIDGPRAARDDI
VGWAHDVRGAI

>d1rcf_ c.23.5.1 (-) Flavodoxin {*Anabaena*, pcc 7119 and 7120}

SKKIGLFYGTQTGKTESVAEIRDEFNDVVTLDHVSQAEVTDLNDYQYLIIGCPTWNIGELQSDWEG
LYSELDDVDFNGKLVAYFGTGDQIGYADNFQDAIGILEEKISQRGGKTVGYWSTDGYDFNDSKALRNG
KFVGLALDEDNQSDLTDDRIKSWVAQLKSEFGL

>d1ag9a_ c.23.5.1 (A:) Flavodoxin {*Escherichia coli*}

AITGIFFGSDTGNTENIAKMIQKQLGKDVADVHDIKSSKEDLEAYDILLGIPTWYYGEAQCDWDD
FFPTLEEIDFNGKLVALFGCGDQEDYAEYFCDALGTIRDIIEPRGATIVGHWPAGYHFEASKGLADD
DHFVGLAIDEDRQPELTAERVEKWVKQISEELHLDEILNA

>d1czna_ c.23.5.1 (A:) Flavodoxin {*Anacystis nidulans* and *Synechococcus*, pcc 7942}

AKIGLFYGTQTGVTQTIAESIQEFGGESIVDLNDIANADASDLNAYDYLIIGCPTWNVGELQSDWEGI
YDDLDSVNFQGKKVAYFGAGDQVGYSDNFQDAMGILEEKISLSQTVGYWPIEGYDFNESKAVRNN
QFVGLAIDEDNQPDLTKNRIKTWVSQLKSEFGL

>d5nul_ c.23.5.1 (-) Flavodoxin {*Clostridium beijerinckii*}

MKIVYWSGTGNTTEKMAELIAKGIHESGKDVNTINVSDVNIDELLNEDILILGCSAMTDEVLEESEFEP
FIEEISTKISGKKVALFGSYGWGDGKWMRDFEERMNGYGCVVVETPLIVQNEPDEAEQDCIEFGKKI
ANI

>d1fuea_ c.23.5.1 (A:) Flavodoxin {Helicobacter pylori}

GKIGIFFGTDSGNAEIAEKISKAIGNAEVVDVAKASKEQFNGFTKVILVAPTAGAGDLQTDWEDFLG
TLEASDFANKTIGLVGLGDQDTYSETFAEGIFHIYEKAKAGKVVGQTSTDGYHFAASKAVEGGKVFVGL
VIDEDNQDDLDERIAKWVEQVRGSFA

>d1bvyf_ c.23.5.1 (F:) FMN-binding domain of the cytochrome P450bm-3 {Bacillus
megaterium}

NTPLLVLVYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNGHPPDNAK
QFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADRGEADASDDFEG
TYEEWREHMWSDVAAYFNL

>d1e5da1 c.23.5.1 (A:251-402) Rubredoxin oxygen:oxidoreductase (ROO), C-terminal
domain {Desulfovibrio gigas}

PTNKVVIFYDSMWHSTEKMARVLAESFRDEGCTVKLMWCKACHHSQIMSEISDAGAVIVGSPTHN
NGILPYVAGTLQYIKLRPQNKIGGAFGSFGWSGESTKVLAEWLTGMGFDMPATPVKVKNPVTHAD
YEQLKTMQTIARALKAKLAA

>d1ja1a2 c.23.5.2 (A:63-239) NADPH-cytochrome p450 reductase, N-terminal domain {Rat
(Rattus norvegicus)}

PVKESSFVEKMKKTGRNIIVFYGSQTGTAEFANRLSKDAHRYGMRGMSADPEEYDLADLSSLPEID
KSLVVFVCMATYGECDPTDNAQDFYDWLQETDVDLTVGKFAVFGVGLGNKTYEHFNAMGKYVDQRLEQ
LGAQRIFELGLGDDDDGNLEEDFITWREQFWPAVCEFFGVEATGEE

>d1b1ca_ c.23.5.2 (A:) NADPH-cytochrome p450 reductase, N-terminal domain {Human
(Homo sapiens)}

SSFVEKMKKTGRNIIVFYGSQTGTAEFANRLSKDAHRYGMRGMSADPEEYDLADLSSLPEIDNALV
VFCMATYGECDPTDNAQDFYDWLQETDVDLTVGKFAVFGVGLGNKTYEHFNAMGKYVDKRLEQLGA
QRIFELGLGDDDDGNLEEDFITWREQFWPAVCEHFGV

>d1dxqa_ c.23.5.3 (A:) NAD(P)H:quinone reductase {Mouse (Mus musculus)}

AARRALIVLAHSEKTSFNAMKEAAVEALKKRGWEVLESPLYAMNPNPIISRNDITGELKDSKNFQY
PSESSLAYKEGRLSPDIVAEHKKLEAADLVIFQFPLQWFGVPAILKGWFERVLVAGFAYTYAAMYDNG
PFQNKKTLLSITTTGGSGSMYSLQGVHGD MNVILWPIQSGILRFCGFQVLEPQLVYSIGHTPPDARMQI
LEGWKKRLETVWEETPLYFAPSSFLDLNFQAGFLLMKEVQEEQKKNKFGLSVGHHLGKSIPADNQI
KARK

>d1qrda_ c.23.5.3 (A:) NAD(P)H:quinone reductase {Rat (Rattus rattus)}

AVRRALIVLAHAERTSFNAMKEAAVEALKKKGWEVLESPLYAMNPNPLISRNDITGEPKDSNFQY
PVESLAYKEGRLSPDIVAEQKKLEAADLVIFQFPLYWFGVPAILKGWFERVLVAGFAYTYATMYDKG
PFQNKKTLLSITTTGGSGSMYSLQGVHGD MNVILWPIQSGILRFCGFQVLEPQLVYSIGHTPPDARVQV
LEGWKKRLETVWEESPLYFAPSSFLDLNFQAGFLLKKEVQEEQKKNKFGLSVGHHLGKSIPADNQI
ARK

>d1d4aa_ c.23.5.3 (A:) NAD(P)H:quinone reductase {Human (Homo sapiens)}

VGRRALIVLAHSERTSFNAMKEAAAAALKKKGWEVLESPLYAMNPNPIISRNDITGKLDKDPANFQY
PAESVLAYKEGHLSPDIVAEQKKLEAADLVIFQFPLQWFGVPAILKGWFERVFIGEFAYTYAAMYDKG
PFRSKKAVLSITTTGGSGSMYSLQGIHGD MNVILWPIQSGILHFCGFQVLEPQLVYSIGHTPADARIQILE
GWKKRLENIWDEETPLYFAPSSFLDLNFQAGFLMKKEVQDEEKNKKFGLSVGHHLGKSIPADNQIKA

RK

>d1qr2a_c.23.5.3 (A:) Quinone reductase type 2 (menadione reductase) {Human (Homo sapiens)}

AGKKVLIVYAHQEPKSFNGSLKNVAVDELSRQGCTVTVSDLYAMNFEPRATDKDITGTLSNPEVFNY
GVETHEAYKQRSLASDITDEQKKVREADLVIFQFPLYWFSVPAILKGWMDRVLCQGFADIPGFYDSG
LLQGKLALLSVTTGGTAEMYTKTGVNDSRYFLWPLQHGTLHFCGFKVLAPQISFAPEIASEEERKG
MVAAWSQRLQTIWKEEPIPCTAHWHFGQ

>d1bmta2_c.23.6.1 (A:741-896) Methionine synthase, C-terminal domain {Escherichia coli}
EQGKTNGKMVIATVKGDVHDIGKNIVGVVLQCNNYEIVDLGVMVPAEKILRTAKEVNADLIGLSGLIT
PSLDEMNVNAKEMERQGFITPLLIGGATTSKAHTAVKIEQNYSGPTVYVQNASRTVGVVAALLSDTQ
RDDFVARTRKEYETVRIQHGR

>d1fmfa_c.23.6.1 (A:) Glutamate mutase, small subunit {Clostridium tetanomorphum}
MEKKTIVLGVIGSDCHAVGNKILDHSFTNAGFNVVNIGVLSSQEDFINAAIETKADLICVSSLYGQGEI
DCKGLREKCD EAGLKGIKL FVGGNIVVGKQNWPDVEQRFKAMGFDRVYPPGTSPETTIADMKEVLG
VE

>d1ccwa_c.23.6.1 (A:) Glutamate mutase, small subunit {Clostridium cochlearium}
MEKKTIVLGVIGSDCHAVGNKILDHAFNAGFNVVNIGVLSPQELFIKAAIETKADAILVSSLYGQGEI
DCKGLRQKCD EAGLEGILLYVGGNIVVGKQHWPDVEKRFKDMGYDRVYAPGTPPEVGIADLKKDLNI
E

>d7reqa2_c.23.6.1 (A:561-728) Methylmalonyl-CoA mutase C-terminal domains of alpha and
beta subunits {Propionibacterium freudenreichii, subsp. shermanii}
AQIRTISGVYSKEVKNTPEVEEARELVEEFQAEGRPRILLAKMGQDGHDRGQKVIATAYADLGFV
DVGPLFQTPETARQAVEADVHVVGVSLLAGGHLTLVPALRKELDKLGRPDILITVGGVIPEQDFDEL
RKDGAVEIYTPGTVIPESAISLVKKLRASLDA

>d7reqb2_c.23.6.1 (B:476-638) Methylmalonyl-CoA mutase C-terminal domains of alpha and
beta subunits {Propionibacterium freudenreichii, subsp. shermanii}
TKPFPAAPARKGLAWHRDSEVFEQLMDRSTSVSERPKVFLACLGTTRRDFGGREGFSSPVWHIAGID
TPQVEGGTTAEIVEAFKKSQAQVADLCSAKVYAQQGLEVAKALKAAAGAKALYLSGAFKEFGDDAAE
AEKLIDGRLFMGMDVVDTLSSSTLDILGVAK

>d1c4ka1_c.23.7.1 (A:1-107) Ornithine decarboxylase N-terminal "wing" domain
{Lactobacillus sp., strain 30a}
SSSLKIASTQEARQYFDTDRVVVDVAVGSDFTDVGAVIAMDYETDVIDAADATKFGIPVFAVTKDAQAI
SADELKKIFHIIDLENKFDATVNAREIETAVNNYEDSIL

>d1qcza_c.23.8.1 (A:) N5-carboxyaminoimidazole ribonucleotide (N5-CAIR) mutase PurE
{Escherichia coli}
PARVAIVMGSKSDWATMQFAAEIFEILNVP HHVEVVS AHRTPKLFSFAESAEEENGYQVIIAGAGGAA
HLPGMIAAKTLVPVLGVPVQSAALSGVDSLVSIVQMPRGIPVGT LAIGKAGAANAALLAAQILATHDK
ELHQRLNDWRKAQTDEVLENPDPRGAA

>d1cex_c.23.9.1 (-) Cutinase {Fungus (Fusarium solani), subsp. pisi}
RTTRDDLINGNSASCADVIFIYARGSTETGNLGLTGPSIASNLES AFGKDG VVIQVGGAYRATLGDN
ALPRGTSSAAIREMLGLFQQANTKCPDATLIAGGYSQGAALAAASIEDLDSAIRDKIAGTVLFGYTKN
LQNRGRIPNYPADRTKVCNTGDLVCTGSLIVAAPHLAYGPDARGPAPEFLIEKVRVAVRGS

>d1g66a_c.23.9.1 (A:) Acetylxy lan esterase {Penicillium purpurogenum}
SCP AIHVFGARETTASPGYSSSTV VNGVLSAYPGSTAEAINYPACGGQSSCGGASYS SVAQGIAAVAS

AVNSFNSQCPSTKIVLVGYSQGGIMDVALCGGGDPNQYNTNTAVQLSSSAVNMVKA AIFMGDPMFR
AGLSYEVGTCAAGGFDQRPAGFSCPSAAKIKSYCDASDPYCCNGSNAATHQGYGSEYGSQALAFVKSK
LG

>d1qoza_ c.23.9.1 (A:) Acetylxyylan esterase {Trichoderma reesei}

ECPAIHVFGARETTVSQGYGSSATVVNLVIQAHPGTTSEAIVYPACGGQASC GGISYANSVVNGTNA AAA
AAINNFHNSCPDTQLVLVGYSGAQIFDNALCGGGDPGEGITNTAVPLTAGAVSAVKAAIFMGDPRNI
HGLPYNVGTCTTQGF DARPAGFVCP SASKIKSYCDAADPYCCTGNDPNVHQGYGQEQYQQALAFINS
QLS

>d1esc_ c.23.10.1 (-) Esterase {Streptomyces scabies}

DPVPTVFFGDSY TANFGIAPVTN QDSERGWCFQAKENYPAVATRSLADKGITLDVQADVSCGGALIH
HFWEKQELPFGAGELPPQQDALKQDTQLTVGSLGGNTLGFNRILKQCSDELKPSLLPGDPVDGDEP
AAKCGEFFGTGDGKQWLDDQFERVGAEELELLDRIGYFAPDAKRVLVGYPRLPEDTTKCLTAAPGQ
TQLPFADIPQDALPVL DQIQKRLNDAMKKAADGGADFVDLYAGTGANTACDGADRIGIGLLEDSQ
LELLGTKIPWY AHPNDKGRDIQAKQVADKIEEILN

>d1flca2 c.23.10.2 (A:1-150,A:307-427) Esterase domain of haemagglutinin-esterase-fusion
glycoprotein HEF1 {Influenza C virus}

EKIKICLQKQVNSSFSLHNGFGGNLYATEEKRMFELVKPKAGASVLNQSTWIGFGDSRTDKSNSAFPR
SADVSAKTADKFRFLSGGSLM LSMFGPPGKVDYLYQCGGKHKVFYEGVNWSPHAAINCYRKNWTDI
KLN FQKN IYELASQSHXEKGPVTAVQSIWGGKRESYAVDQACLSTPGCMLIQKQKPYIGEADDHHG
DQEMRELLSGLDYEARCISQSGWVNETSPFTEKYLLPPKFGRCPLAAKEESIPKIPDGLLIPTSGTDT
TVT

>d1es9a_ c.23.10.3 (A:) Platelet-activating factor acetylhydrolase {Cow (Bos taurus)}

ENPASKPTPVQDVQGDGKWM SLHHRFVADSKDKEPEVVF IGDSLVLQMLHQCEIWRELF SPLHALN
FGIGGDSTQHVLWRL ENGELEHIRPKIVVVVWGTNNHGH TAEQVTGGIKAIVQLVNERQPQARVVV
LGLLPRGQHPNPLREKNRRVNE LVRAALAGHPRAHFLDADPGFVHSDGTISHHDMYDYLHLSRLGY
TPVCRALHSLLLRLL

>d1fxwf_ c.23.10.3 (F:) Platelet-activating factor acetylhydrolase {Cow (Bos taurus)}

SNPAAIPHAAEDIQGD RRWMSQHNRFLVDCKDKEPDVLFVGD SMVQLMQQEIWRELF SPLHALN
FGIGGD TTRHVLWRLKNGELENIPKIVVVVWGTNNHENTAEVAGGIEAIVQLINTRQPQAKIIVLG
LLPRGEKPNPLRQKNAKV NQLLKVSLPKLANVQLLDTDGGFVHSDGAISCHDMFDFLHLTGGGYAKI
CKPLHELIMQLL

>d1k7ca_ c.23.10.4 (A:) Rhamnogalacturonan acylesterase {Fungus (Aspergillus
aculeatus)}

TTVYLAGDSTMAKNGGGSGTNGWGEY LASYLSATVVND AVAGRSARSY TREGRFENIADVVTAGDY
VIVEFGHNDGGSLSTDN GRTDCSGTGA EVCYSVYDGVNETILT FPAYLENAAKLFTAKGAKVILSSQTP
NNPWETGT FVNSPTRFVEYAE LAE VAGVEYVDHWSYVDSIYETLGNATVNSYFPIDHTHTSPAGA
EVVAEAF LKAVVCTG TSLKSVLTTTSFEGTCL

>d1iexa2 c.23.11.1 (A:389-603) Beta-D-glucan exohydrolase, C-terminal domain {Barley
(Hordeum vulgare)}

LVLKNGKTSTDA PLLPKKAPKILVAGSHADNLGYQCGGW TIEWQGD TGRTTVGT TILEAVKAAV
DPSTVVVFAENPDAEFVKSGGFSYAIVAVGEHPYTETKGDNLNLTIPEPGLSTVQAVCGGVRCATVLIS
GRPVVVQPLLAASDALVAAWLP GSEGQGVTDALFGDFGFTGRLPRTWFKSVDQLPMNVGDAHYDP
LFRLGYGLTTNATK

>d2naca2 c.23.12.1 (A:1-147,A:336-374) Formate dehydrogenase {Pseudomonas sp., strain

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AKVLCVLYDDPVDGYPKTYARDDLPKIDHYPGGQTLPTPKAIDFTPGQLLGSVSGELGLRKYLESNG
HTLVVTSKDGDPDSVFERELVDADVVISQPFWPAYLTPERIAKAKNLKALTAGIGSDHVDLQSAIDR
NVTVAEVTYCNSXTTLTAQARYAAGTREILECFEGRPIRDEYLIVQGGALA

>d1qp8a2 c.23.12.1 (A:1-82,A:264-302) Putative formate dehydrogenase {Archaeon
Pyrobaculum aerophilum}

MELYVNFELPPEAEEELRKYFKIVRGGDLGNVEAALVSRITAEELAKMPRLKFIQVVVTAGLDHLPWE
SIPPHVTVAGNAGSNXGYGNERVWRQMVMEAVRNLTITYATGGRPRNIAKREDYIG

>d1dxy_2 c.23.12.1 (1-100,300-330) D-2-hydroxyisocaproate dehydrogenase {Lactobacillus
casei}

MKIIAYGARVDEIQYFKQWAKDTGNTLEYHTEFLDENTVEWAKGFDGINSLQTTTPYAAGVFEKMHA
YGKFLTIRNVGTDNIDMTAMKQYGIRLSNPAYXTETAVHNMVYFSLQHLVDFLTKEGETSTEVTG

>d1gdha2 c.23.12.1 (A:2-100,A:292-321) D-glycerate dehydrogenase {Hyphomicrobium
methylovorum}

KKKILITWPLPEAAMARARESYDVIAHGDDPKITIDEMIETAKSVDALLITLNEKCRKEVIDRIPENIK
CISTYSIGFDHIDLDAKARGIKVGNAPHGXATQAREDMAHQANDLIDALFGGADMSYALA

>d1psda2 c.23.12.1 (A:7-107,A:296-326) Phosphoglycerate dehydrogenase {Escherichia
coli}

EKD KIKFLLVEGVHQKALESLRAAGYTNIEFHKGALDDEQLKESIRDHAFIGLRSRTHLTEDVINAAE
KLVAIGCFICIGNQVDLDAAKRGIPVFNAPFSXSTQEAQENIGLEVAGKLIKYSNMGSTLSAVN

>d2dlda2 c.23.12.1 (A:1-103,A:301-337) D-lactate dehydrogenase {Lactobacillus helveticus}

MTKVFAYAIRKDEEPFLNEWKEAHKDIDVDYTDKLLTPETAKLAKGADGVVVYQQLDYTADTLQAL
ADAGVTKMSLRNVGVDNIDMDKAKELGFQITNVPVYSXYTTHAVRNMVVKAFNNNLKLINGEKPD
SPVALNKNKF

>d1pjca2 c.23.12.2 (A:1-135,A:304-361) L-alanine dehydrogenase {Phormidium lapideum}

MEIGVPKEIKNQEFRVGLSPSSVRTLVEAGHTVFIETQAGIGAGFADQDYVQAGAQQVPSAKDAWSRE
MVVKVKEPLPAEYDLMQKQQLLFTYLHLAAARELTEQLMRVGLTAIAYETVELPNRSLPLLTTPMSIIX
VPWTATQALNNSTLPYVVKLANQGLKALETDDALAKGLNVQAHRLVHPAVQQVFPDLA

>d1f8ga2 c.23.12.2 (A:1-143,A:327-384) Nicotinamide nucleotide transhydrogenase dI
component {Rhodospirillum rubrum}

MKIAIPKERRPGEEDRVAISPEVVKKLVGLGFVIVEQGAGVGASITDDALTAAGATIASTAAQALSQAD
VVWVKVQRPMTAEEGTDEVALIKEGAVLMCHLGALTNRPVVEALTKRKITAYAMELMPRISRAQSM
ILSSQSNLXVAADASPLFAKNLLNFLTTPHVDKDTKTLVMKLEDET VSGTCVTRDGAIVHPALTGQGA

>d1a7aa2 c.23.12.3 (A:2-189,A:353-432) S-adenosylhomocystein hydrolase {Human (Homo
sapiens)}

SDKLPYKVADIGLAAWGRKALDIAENEMPGLMRMRERYSASKPLKGARIAGCLHMTVETAVLIETLV
TLGAEVQWSSCNIFSTQNHA AAAIAKAGIPVYAWKGETDEEYLWCIEQTLYFKDGPLNMILDDGGDL
TNLIHTKYPQLLPGIRGISEETTTGVHNLKMMANGILKVPAINVNSVTKSKFXHPSFVMSNSFTN
QVMAQIELWTHPKYPVGVHFLPKKLEAVAE AHLGKLVKLT KLTEKQAQYLGMSCDGPFKPDH
YRY

>d1b3ra2 c.23.12.3 (A:4-189,A:353-431) S-adenosylhomocystein hydrolase {Rat (Rattus
norvegicus)}

LPYKVADIGLAAWGRKALDIAENEMPGLMRMREMYASASKPLKGARIAGCLHMTVETAVLIETLVAL
GAEVRWSSCNIFSTQDHA AAAIAKAGIPVFAWKGETDEEYLWCIEQTLHFKDGPLNMILDDGGDLT

NLIHTKHPQLLSGIRGISEETTTGVHNLKMMANGILKVPAINVNDVTKSKFDXPSFVMSNSFTNQ
VMAQIELWTHPKYPVGVHFLPKKLDEAVAEHLGKLVKLTCLTEKQAQYLGMPINGPFKPDHYR
Y

>d2dhqa_ c.23.13.1 (A:) Type II 3-dehydroquinatase {Mycobacterium tuberculosis}

LIVNVINGPNLGRRLGRREPAVYGGTTHDELVALIEREAAELGLKAVVRQSDSEAQLLDWIHQADAA
EPVILNAGGLTHTSVALRDACAELSAPLIEVHISNVHAREEFRRHSYLSPIATGVIVGLGIQGYLLALRY
LAEH

>d1d0ia_ c.23.13.1 (A:) Type II 3-dehydroquinatase {Streptomyces coelicolor}

PRSLANAPIMILNGPNLNLGQRQPEIYGSDDLADVEALCVKAAAAHGGTVDFRQSNHEGELVDWI
HEARLNHCIVINPAAYSHTSVAILDALNTCDGLPVVEVHISNIHQREPFRHHSYVSQRADGVVAGCG
VQGYVFGVERIAALAG

>d1f8ya_ c.23.14.1 (A:) Nucleoside 2-deoxyribosyltransferase {Lactobacillus leichmannii}

PKKTIYFAGWFTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYKIRVDEHPEYLHDKVWATA
TYNNDLNGIKTNDIMLVYIPDEEDVGLGMELGYALSQGKYVLLVIPDEEDYGKPINLMSWGVSDNVI
KMSQLKDFNFNKPRFDFYEGAVY

>d1fjgb_ c.23.15.1 (B:) Ribosomal protein S2 {Thermus thermophilus}

VKELLEAGVHFGHERKRWNPKFARYIYAERNGIHIIDLQKTMEELETRFRFIEDLAMRGGTILFVGTK
KQAQDIVRMEAERAGMPYVNRWLGGMLTNFKTISRVRLEELEALFASPEIEERPKKEQVRLKH
ELERLQKYLSGFRLLKRLPDAIFVVDPTKEAIAVREARKLFIPVIALADTSDPDLDVYIIPGNDDAIRS
IQLILSRAVDLIIQARGGVVEPSYALVQEAE

>d1f2va_ c.23.17.1 (A:) Precorrin-8x methylmutase {Pseudomonas denitrificans}

PEYDYIRDGNAIYERSFAIIRAEADLSRFSEEEADLAVRMVHACGSVEATRQFVFSDFVSSARAALK
AGAPILCDAEMVAHGVTRARLPAGNEVICTLRDPRTPALAAEIGNTRSAAALKLWSERLAGSVVAIG
NAPTALFFLLEMLRDGAPKPAAILGMPVGFVGAESKDALAENSYGVPFAIVRGRLLGGSAMTAAALN
SLARPGL

>d1gpma2 c.23.16.1 (A:3-207) GMP synthetase {Escherichia coli}

ENIHKHRILILDFGSQYTLVARRVRELGVYCELWAWDVTEAQIRDFNPSGIILSGGPESTTEENSRA
PQYVFEAGVPVFGVCYGMQTMAMQLGGHVEASNEREFGYAQVEVVNDSALVRGIEDALTADGKPLL
DVWMSHGDKVTAIPSDFITVASTESCPFAIMANEEKRFYGVQFHPEVTHTRQGMRLERFVRDICQ
CEAL

>d1a9xb2 c.23.16.1 (B:1653-1880) Carbamoyl phosphate synthetase, small subunit C-terminal domain {Escherichia coli}

LNGMDLAKEVTTAEAYSWTQGSWTLTGGLPQAKKEDELPHVAVYDFGAKRNILRMLVDRGCRLTI
VPAQTSIEDVLMNPDGIFLSNGPDAPCDYAITAIQKFLETIPVFGICLGHQLLALASGAKTVKM
KFGHHGGNHPVKDVEKNVVMITAQNHGFVDEATLPANLRVTHKSLFDGTLQGIHRTDKPAFSFQG
NPEASPGPHDAAPLFDHFIELIEQYRKT

>d1qdlb_ c.23.16.1 (B:) Anthranilate synthase GAT subunit, TrpG {Archaeon Sulfolobus solfataricus}

MDLTLIIDNYDSFVYNIQIVGELGYPVIRNDEISIKGIERIDPDRLIISPGPGTPEKREDIGVSLDVIK
YLGKRTPIILGVCLGHQAIGYAFGAKIRRRARKVFHKGISNIILVNNSPSLYYGIAKEFKATRYHSLVDE
VHRPLIVDAISAEDNEIMAIHHEEYPIYGVQFHPEVGTSLGYKILYNFLNRV

>d1i1qb_ c.23.16.1 (B:) Anthranilate synthase GAT subunit, TrpG {Salmonella typhimurium}

ADILLLDNIDSFTWNLADQLRTNGHNVVIYRNHIPAQTLIDRLATMKNPVLMLSPGPGVPSEAGCM

PELLTRLRGKLPPIIGICLGHQAIVEAYGGYVQGAGEILHGKATSIEHDGQAMFAGLANPLPVARYHSLV
GSNVPAGLTINAHFNMGVMAVRHDADRVCQFQHPESILTTQGARLLEQTLAWAQK
>d1i7qb_c.23.16.1 (B:) Anthranilate synthase GAT subunit, TrpG {*Serratia marcescens*}
ADILLDNVDSFTYNLVDQLRASGHQVVIYRNQIGAEVIERLQHMEQPVLMLSPGPGTPSEAGCMP
ELLQRLRGQLPIIGICLGHQAIVEAYGGVQVQAGEILHGKASIAIHDGEGMFAGMANPLPVARYHSLV
GSNIPADLTVNARFGEMVMAVRDDRRRVCQFQHPESILTTTHGARLLEQTLAWALAK
>d1k9vf_c.23.16.1 (F:) GAT subunit (or domain) of imidazoleglycerolphosphate synthase
HisF {*Thermotoga maritima*}
MRIGIISVGPGNIMNLYRGVKRASENFEDVSIELVESPRNDLYDLLFIPGVGHFEGEMRRLRENDLIDF
VRKHVEDERYVGVCLGMQLLFESEEEAPGVKGLSLIEGNVVKLRSRRLPHMGWNEVIFKDTFPNG
YYYYFVHTYRAVCEEEHVLGTTEYDGEIFPSAVRKGRILGFQFHPEKSSKIGRKLLEKVICLSLR
>d1jvna2_c.23.16.1 (A:-3-229) GAT subunit (or domain) of imidazoleglycerolphosphate
synthase HisF {*Baker's yeast (Saccharomyces cerevisiae)*, His7}
GSHMPVVHVIDVESGNLQSLTNAIEHLGYEVQLVKSPKDFNISGTSRLILPGVGNYGHFVDNLFNRGF
EKPIREYIESGKPIMGICVGLQALFAGSVESPKSTGLNYIDFKLSRFDDSEKPVPEIGWNSCIPSENLF
GLDPYKRYFVHSAAILNSEKKKLENDGWKIAKAKYGSSEFIAAVNKNNIFATQFHPEKSGKAGL
NVIENTLQKQSPPIPNSAEEKELLMN
>d1g2ia_c.23.16.2 (A:) Intracellular protease {*Archaeon Pyrococcus horikoshii*}
MKVFLTANEFEDVELIYPYHRLKEEGHEVYIASFERGTITGKHGYSVKVDLTFDKVNPEEFDALVLP
GGRAPERVRLNEKAVSIARKMFSEGKPVASICHGPQILISAGVLRGRKGTSPYGIKDDMINAGVEWVD
AEVVVDGNWVSSRVPADLYAWMREFVKLLK
>d1cf9a1_c.23.16.3 (A:598-753) Catalase, C-terminal domain {*Escherichia coli*, HPII}
VKGRVVAILLNDEVRADLLAILKALKAKGVHAKLLYSRMGEVTADDGTVLPIAATFAGAPSLTVDVAV
IVPCGNIADIADNGDANYLMEAYKHLKPIALAGDARKFKATIKIADQGEEGIVEADSADGSFMDELL
TLMAAHRVWSRIPKIDKIPA
>d1fyea_c.23.16.4 (A:) Aspartyl dipeptidase PepE {*Salmonella typhimurium*}
MELLLLNSSTLPGKAWLEHALPLIANQLNGRRSAVFIPFAGVTQTWDEYTDKTAEVLAPLGVNVTGI
HRVADPLAAIEKAEIIVGGGNTFQLLKESRERGLLAPMADRVRKRGALYIGWSAGANLACPTIRTTND
MPIVDPNGFDALDLFPLQINPHFTNALPEGHKGETREQRIRELLVVAPELTVIGLPEGNWIQVSNQQA
VLGGPNTTWVFKAGEEVALEAGHRF
>d1a9xa2_c.24.1.1 (A:936-1073) Carbamoyl phosphate synthetase, large subunit allosteric,
C-terminal domain {*Escherichia coli*}
NSTMKKHGRALLSVREGDKERVVDLAAKLLKQGFELDATHGTAIVLGEAGINPRLVNKVHEGRPHI
QDRIKNGEYTYIINTTSGRRAIEDSRVIRRSALQYKVHYDRTLNGGFATAMALNADATEKVISVQEMH
AQIK
>d1b93a_c.24.1.2 (A:) Methylglyoxal synthase, MgsA {*Escherichia coli*}
MELTTRTLTPARKHIALVAHDHCKQMLMSWVERHQPLLEQHVLVYATGTTGNLISRATGMNVNAML
GPMGGDQVQVQALISEGKIDVLIFFWDPLNAVPHDPDVKALLRLATVWNIPVATNVATADFIQSPHF
NDAVDILIPDYQRYLA
>d1g8ma1_c.24.1.3 (A:4-200) IMP cyclohydrolase domain of bifunctional purine biosynthesis
enzyme ATIC {*Chicken (Gallus gallus)*}
RQQLALLSVSEKAGLVEFARSLNALGLGLIASGGTATALRDAGLPVRDVS DLTGFPEMLGGRVKTLP
AVHAGILARNIPEDNADMNKQDFSLVRVVV CNLYPFVKTVSSPGVTVPEAVEKIDIGGVALLRAAAKN
HARVTVCDPADYSSVAKEMAASKDKDTSVETRRHLALKAFTHTAQYDAAISDYFRKEYSK

>d1fnc_2 c.25.1.1 (155-314) Ferredoxin reductase (flavodoxin reductase) {Spinach (*Spinacia oleracea*)}

MLMPKDPNATIIMLGTGTGIAPFRSFLWKMFPEKHDDYKFNGLAWLFLGVPTSSSLLYKEEFKMK
EKAPDNFRLDFAVSREQTNEKGEKMYIQTRMAQYAVELWEMLKKDNTYVYMCGLKGMKGGIDDIM
VSLAAAEGLDWIEYKRQLKKAQWVVEVY

>d1qfza2 c.25.1.1 (A:154-308) Ferredoxin reductase (flavodoxin reductase) {Garden pea (*Pisum sativum*)}

DPNATVIMLGTGTGIAPFRSFLWKMFPEKHEDYQFNGLAWLFLGVPTSSSLLYKEEFKMKKEKAP
NFRLDFAVSREQVNDKGEKMYIQTRMAQYAEELWELLKKDNTFVYMCGLKGMKGGIDDIMVSLAA
KDGIDWIEYKRTLKKAQWVVEVS

>d1fb3a2 c.25.1.1 (A:208-362) Ferredoxin reductase (flavodoxin reductase) {Paprika (*Capsicum annuum*)}

DPNATVIMLGTGTGIAPFRSFLWKMFPEKHDDYKFNGLAWLFLGVPTSSSLLYKEEFKMKKEKAP
NFRLDFAVSREQTNEKGEKMYIQTRMAQYAEELWTLKKDNTFVYMCGLKGMKGGIDDIMSSLAA
KEGIDWADYKQKQLKKAQWVVEVY

>d1gawa2 c.25.1.1 (A:157-314) Ferredoxin reductase (flavodoxin reductase) {Maize (*Zea mays*), leaf isoform}

MPKDPNATIIMLATGTGIAPFRSFLWKMFPEKHDDYKFNGLAWLFLGVPTSSSLLYKEEFGKMKER
APENFRVDYAVSREQTNAAGERMYIQTRMAEYKEELWELLKKDNTYVYMCGLKGMKGGIDDIMVS
LAEKDGIDWFDYKQKQLKRGDQWVVEVY

>d1jb9a2 c.25.1.1 (A:163-316) Ferredoxin reductase (flavodoxin reductase) {Maize (*Zea mays*), root isoform}

DPNATHIMIATGTGVAPFRGYLRRMFMEDVPNYRFGGLAWLFLGVANSDSLIDEEFTSYLKQYPD
NFRYDKALSREQNRSQKMYVQDKIEEYSDEIFKLLDGGAHYFCGLKGMMPGIQDTLKKVAERRG
ESWDQKLAQLKKNKQWHVEVY

>d1que_2 c.25.1.1 (142-303) Ferredoxin reductase (flavodoxin reductase) {Cyanobacterium (*Anabaena* sp.), pcc 7119}

LPDDPEANVIMLATGTGIAPMRTYLWRMFKDAERAANPEYQFKGFSWLVFVPTTPNILYKEELEEI
QQKYPDNFRLTYAISREQNPKQGGRMYYQDRVAEHADQLWQLIKNQKTHYICGLRGMEEGIDAAL
SAAAAGEGVTWSDYQKDLKAGRWVHVEY

>d1fdr_2 c.25.1.1 (101-248) Ferredoxin reductase (flavodoxin reductase) {*Escherichia coli*}

DEVPHCETLWMLATGTAIGPYLSILRLGKDLDRFKNLVLVHAARYAADLSYLPMLQELEKRYEGKLR
IQTVVSRETAAGSLTGRIPALIESGELESTIGLPMNKETSHVMLCGNPQMVRDTQQLKQTRQMTKH
LRRRPGHMTAEHYW

>d1a8p_2 c.25.1.1 (101-258) Ferredoxin reductase (flavodoxin reductase) {*Azotobacter vinelandii*}

TSDLLPGKHLMLSTGTGLAPFMSLIQDPEVYERFEKVVLIHGVRQVNELAYQQFITEHLPQSEYFGE
AVKEKLIYYPTVTRESFHNQGRITDLMRSGKLFEDIGLPPINPQDDRAMICGSPSMLDESCEVLDGF
GLKISPRMGEPGDYLIERAFVEK

>d1qfja2 c.25.1.1 (A:98-232) NAD(P)H:flavin oxidoreductase {*Escherichia coli*}

RDDEERPMILIAGGTGFSYARSILLTALARNPNRDITYYWGGREEQHLYDLCELEALSLEKHPGLQVVP
VVEQPEAGWRGRTGTVLTAVLQDHGTLAEHDIYIAGRFEMAKIARDLFCSEARNAREDRFLGDFAFI

>d2cnd_2 c.25.1.1 (125-270) Nitrate reductase {Corn (*Zea mays*)}

GSFVINGKQRNARRLAMICGGSGITPMYQIIQAVLRDQPEDHTEMHLVYANRTEDDILLRDELDRWA

AEYDRLKVVYVIDQVKRPEEGWKYSVGFVTEAVLREHVPEGGDDTLALACGPPPMIQFAISPNE
KMKYDMANSFVVF

>d1ndh_2 c.25.1.1 (126-272) cytochrome b5 reductase {Pig (Sus scrofa), liver}
GKFAIRPDKSSPVIKTVKSVGMIAGGTGITPMLQVIRAIMKDPDDHTVCHLLFANQTEKDILLRPEL
EELRNEHSARFKLWYTVDRAPAWDYSQGFVNEEMIRDHLPPPEEEPLVLMCGPPPMIQYACLPNL
ERVGHPKERCFAF

>d1i7pa2 c.25.1.1 (A:154-300) cytochrome b5 reductase {Rat (Rattus norvegicus)}
GKFAIRADKKNPVRTVKSVMGIAGGTGITPMLQVIRAVLKDPNDHTVCYLLFANQSEKDILLRPEL
EELRNEHSSRFKLWYTVDKAPDAWDYSQGFVNEEMIRDHLPPPGEETLILMCGPPPMIQYACLPNL
ERVGHPKERCFTF

>d2pia_2 c.25.1.2 (104-223) Phthalate dioxygenase reductase {Pseudomonas cepacia, db01}
EFPLDKRAKSFILVAGGIGITPMLSMARQLRAEGLRSFRLLYLTRDPEGTAFFDELTSDEWRSVDKIH
HDHGDPTKAFDFWSVFEKSKPAQHVVYCCGPQALMDTVRDMTGHWPSTVHFE

>d1ep3b2 c.25.1.3 (B:103-262) Dihydroorotate dehydrogenase B, PyrK subunit {Lactococcus
lactis, isozyme B}
PVAEVTSTDKILIIGGGIGVPPLYELAKQLEKTGCQMTILLGFASENVKILENEFSNLKNVTLKIATDDG
SYGTKGHVGMMLNEIDFEVDALYTCGAPAMLKAVAKKYDQLERLYISMESRMACGIGACYACVEHDK
EDESALKVCEDGPVFLGKQLSL

>d1ja1a3 c.25.1.4 (A:519-678) NADPH-cytochrome p450 reductase {Rat (Rattus
norvegicus)}
RLPFKSTTPVIMVGPGTGIAPFMGFIQERAWLREQKEVGETLLYYGCRRSEDEDYLYREELARFHKD
GALTQLNVAFSREQAHKVYVQHLLKRDRHLWKLIEGGAHYVAGDARNMAKDQNTFYDIVAEF
GPMEHTQAVDYVKKLMTKGRYSLNVWS

>d1ddga2 c.25.1.4 (A:447-599) Sulfite reductase flavoprotein {Escherichia coli}
LPANPETPVIMIGPGTGIAPFRAFMMQRAADEAPGKNWLVFFGNPHFTEDFLYQVEWQRYVKEGVLT
RIDLAWSRDQKEKVYVQDKLREQGAELWRWINDGAHIYVCGDANRMAKDVEQALLEVIAEFGGM
DTEAADEFLSELRVERRYQRDVY

>d1f20a2 c.25.1.4 (A:1233-1397) Neuronal nitric-oxide synthase FAD/NADP+ domain {Rat
(Rattus norvegicus)}
SFHLPRNPQVPCILVGPGTGIAPFRSFWQQRQFDIQHKGMNCPMVLVFGCRQSKIDHIYREETLQA
KNKGVFRELYTAYSREPDRPKKYVQDVLQEQLAESVYRALKEQGGHIYVCGDVTMAADVLKAIQRIM
TQQGKLSEEDAGVFISRLRDDNRYHEDIFGV

>d1cqxa3 c.25.1.5 (A:262-403) Flavohemoglobin, C-terminal domain {Alcaligenes
eutrophus}
DVDAKTPIVLISGGVGLTPMVSMKVALQAPPRQVVFVHGARNSAVHAMRDLREAAKTYENLDF
VFYDQPLPEDVQGRDYDYPGLVDVKQIEKSILLPDADYYICGPIPFMRMQHDALKNLGIHEARIHYEV
FGPDLFAE

>d4ts1a_ c.26.1.1 (A:) Tyrosyl-tRNA synthetase (TyrRS) {Bacillus stearothermophilus, nca
1503}
MDLLAELQWRGLVNQTTDEDGLRKLLENEERVTLYCGFDPTADSLHIGHLATILTMRRFQQAGHRPI
ALVGGATGLIGDPSGKKSERTLNAKETVEAWSARIKEQLGRFLDFEADGNPAKIKNNYDWIGPLDVI
TFLRDVGKHFVSNYMMAKESVQSRIETGISFTEFSYMLLQAYDFLRLYETEGCRLQIGGSDQWGNIT
AGLELIRKTKGEARAFGLTIPLVTKADGTFKFGKTESGTIWLKKEKTSPEYFYQFWINTDDRDVIRYLK
YFTFLSKEEIEALEQELREAPEKRAAQKTLAEVTKLVHGEEALRQAIRYA

>d1jila_c.26.1.1 (A:) Tyrosyl-tRNA synthetase (TyrRS) {Staphylococcus aureus}
 TNVLIEDLKWRGLIYQQTDEQGIEDLLNKEQVTLYCGADPTADSLHIGHLLPFLTLLRRFQEHGHRPIV
 LIGGGTGMIGDPSGKSEERVLQTEEQVDKNIEGISKQMHNIFEFGTDHGAVLVNNRDWLGQISLISFL
 RDYGKHVGVNYMLGKDSIQSRLEHGISYTEFTYITLQAIDFGHLNRELNCKIQVGGSDQWGNITSGIE
 LMRRMYGQTDAYGLTIPLVTKSDGKKFKGKSESGAVWLDAEKTSPYEFYQFWINQSDDEVIKFLKYFT
 FLGKEEIDRLEQSKNEAPHLREAQKTLAAEVTKFIHGEDALNDAIRISQALF

>d1i6la_c.26.1.1 (A:) Tryptophanyl-tRNA synthetase (TrpRS) {Bacillus stearothermophilus}
 MKTIFSGIQPSGVITIGNYIGALRQFVELQHEYNCFIVDQHAIWVWQDPHELQRNIRRLAALYLAV
 GIDPTQATLFIQSEVPAHAQAAMWLQCIVYIGELERMTQFKEKSAGKEAVSAGLLTYPPLMAADILLY
 NTDIVPVGEDQKQHIELTRDLAERFNKRYGELFTIPEARIPKVGARIMSLVDPTKKMKSDDPNPKAYI
 TLLDDAKTIEKKIKSAVTDSEGTIRYDKEAKPGISNLLNIYSTLSGQSIEELERQYEGKGYGVFKADLAQ
 VVIETLRPIQERYHHWMESEELDRVLDEGAEKANRVAEMVRKMEQAMGLGR

>d1gtra2_c.26.1.1 (A:8-338) Glutamyl-tRNA synthetase (GlnRS) {Escherichia coli}
 TNFIRQIIDEEDLASGKHTTVHTRFPPEPNGYLHIGHAKSICLNFGIAQDYKGCNLRFDNTPVKEDI
 EYVESIKNDVEWLGFWHSGNVRYSSDYFDQLHAYAIELINKGLAYVDELTPEQIREYRGTLTQPGKNS
 PYRDRSVEENLALFEKMRAGGFEEGKACLRAKIDMASPFIVMRDPVLYRIKFAEHHQTGNKWCIIYP
 MYDFTHCISDALEGITHSLCTLEFQDNRRLYDWVLDNITIPVHPRQYEF SRLNLEYTVMSKRKLNLL
 VTDKHVEGWDDPRMPTISGLRRRGYTAASIREFCKRIGVTKQDNTIEMASLESCIREDLNEN

>d1gln_2_c.26.1.1 (1-305) Glutamyl-tRNA synthetase (GluRS) {Thermus thermophilus}
 MVVTRIASPTGDPHVGTAYIALFNIAWARRNNGRFIVRIEDTDRARYVPGAEEERILAALKWLGLSY
 DEGPDVAAPTGPYRQSERLPLYQKYAEELLKRGWAYRAFETPEELEQIRKEKGGYDGRARNIPPEEA
 EERARRGEPHVIRLKVPRPGTTEVKDELRGVVVDNQEIPDVVLLKSDGYPTYHLANVDDHLMGV
 TDVIRAEWLVSTPIHVLLYRAFGEAPRFYHMLLRNPDKTKISKRSHTSLDWYKAEGFLPEAL
 RNYLCMGSMPDGREIFTLEEFIQFTWERVSLGGPVF

>d1a8h_2_c.26.1.1 (1-348) Methionyl-tRNA synthetase (MetRS) {Thermus thermophilus}
 MEKVFFYVTTPIYYVNAEPHLGHAYTTVVADFLARWHRLDGYRTFFLTGTDEHGETVYRAAQAGE
 DPKAFVDRVSGRFKRAWDLLGIAYDDFIRTTEERHKKVQVLKVKVEAGDIYYGEYGLYCVSCERF
 YTEKELVEGLCPIHGRPVERRKEGNYFFRMEKYRPWLQEYIQENPDLIRPEGYRNEVLAMLAEPIGD
 LSISRPKSRVPWGIPLWDENHVTVVWFDALLNYVSALDYPEGEAYRTFWPHAWHLIGDILKPHA
 VFWPTMLKAAGIPMYRHLNVGGFLLGPDGRKMSKTLGNVVDPFALLEKYGRDALRYLLREIPYQG
 DTPVSEELRTRYEAD

>d1f4la2_c.26.1.1 (A:4-140,A:176-388) Methionyl-tRNA synthetase (MetRS) {Escherichia coli}
 AKKILVTCALPYANGSIHLGHMLEHIQADVWVRYQRMRGHEVNFICADDAHGTPIMLKAQQLGITP
 EQMIGEMSQEHTDFAGFNISYDNYHSTHSEENRQLSELIYSRLKENGFIKNRTISQLYDPEKGMFLP
 DRFXVVSAGATPVMRDSEHFFFDLPSFSEMLQAWTRSGALQEQVANKMQEWFESGLQQWDISRDA
 YFGFEIPNAPGKYFYVWLDAPIGYMGSKNLCDKRGDSVSFDEYWKKDSTAELYHFIGKDVIYFHSL
 FWPAMLEGSNFRKPSNLFVHGYYTVNGAKMSKSRGTFIKASTWLNHFDADSLRYYYTAKLSSRIDDI
 DLNLEDFVQRVNADIVNK

>d1ile_3_c.26.1.1 (1-197,387-641) Isoleucyl-tRNA synthetase (IleRS) {Thermus thermophilus}
 MFKEVGEPNFPKLEEEVLAFWKREKIFQKSVENRKGGRPYTVYEGPPTANGLPHVGHQAQARSYKDL
 FPRYKTMRGYAPRRAGWDTHGLPVELEVEKKLGLKSKREIEAYGIERFNQACRESVFTYEKEWEA
 FTERIAYWVDLEDAYATLEPTYIESIWWSLKNLFDGRGLLYRDHKVVPYCPRCGTPLSSHEVALGYXPH

CWRCSTPLMYATESWFIKNTLFKDELIRNNQEIHWVPPHIKEGRYGEWLKNLVDWALSRNRYWG
TPLPIWVCQACGKEEAIGSFQELKARATKPLPEPFDPHRPYVDQVELACACGGTMRRVPYVIDVWY
DSGAMPFASLHYPFEHEEVFRESFPADFAEGIDQTRGWFNSLHQLGVMLFGSIAFKNVICHGLILDE
KGQKMSKSKGNVDPWDIIRKFGADALRWYIYVSAPPEADRRFGPNLVRETVRD

>d1ffya3 c.26.1.1 (A:1-200,A:395-644) Isoleucyl-tRNA synthetase (IleRS) {Staphylococcus aureus}

MDYEKTLMPKTDFFMRGGLPNKEPQIQEKWDAEDQYHKALEKNKGNETFILHDGPPYANGNLH
MGHALNKILKDFIVRYKTMQGFYAPYVPGWDTHGLPIEQALTKKGVDRKKMSTAEFREKCKEFALE
QIELQKKDFRRLGVRGDFNDPYITLKPEYEEAAQIRIFGEMADKGLIYKGGKPVYWSSESSESLAEAEI
EYXPHDWRTKKPVIFRATPQWFASISKVRQDILDAIENTNFKVNWGKTRIYNMVRDRGEWVISRQR
VWGVPLPVFYAENGEIIMTKETVNHVADLFAEHGSNIWFEREAKDLLPEGFTHPGSPNGTFTKETDI
MDVWFDSGSSHRGVLETRPELSFPADMYLEGSDQYRGWFNSSITTSVATRGVSPYKFLLSHGFMVMD
GEGKMSKSLGNVIVPDQVVKQKGADIARLWVSSTDYLDVLRISDEILKQTSDD

>d1gaxa3 c.26.1.1 (A:1-189,A:343-578) Valyl-tRNA synthetase (ValRS) {Thermus thermophilus}

MDLPKAYDPKSVEPKWAEKWAKNPFVANPKSGKPPFVIFMPPPNVTGSLHMGHALDNSLQDALIR
YKRMRGFEAVWLPGTDHAGIATQVVVERLLLKEGKTRHDLGREKFLERVWQWKEESGGTILKQLK
RLGASADWSREAFTMDEKRSRAVRYAFSRYHEGLAYRAPRLVNWCPRCETTLSDELEVEXTCSRCG
TPIEYAIFFQWWLRMRPLAEVLKGLRRGDIAFVPERWKKVNDWLENVKDWNISRQLWWGHQI
PAWYCEDCQAVNVPRPERYLEDPTSCEACGSPRLKRDEDVFDTWFSALWPLSTLGWPEETEDLKA
FYPGDVLVTGYDILFLWVSRMEVSGYHFMGERPFKTVLLHGLVLDEKGQKMSKSGNVIDPLEMVE
RYGADALRFALIYLATGGQDIRLDRWLEMARNF

>d1f7ua2 c.26.1.1 (A:136-483) Arginyl-tRNA synthetase (ArgRS) {Baker's yeast (Saccharomyces cerevisiae)}

SCKLVENKKVIIIFSSPNIAKPFHAGHLRSTIIGGFLANLYEKLGWVIRMNYLGDWKGQFGLLAVGF
ERYGNEEALVKDPIHHLFDVYVRINKDIEEEGDSIPLEQSTNGKAREYFKRMEDGDDEALKIWKFRFR
EFSIEKYIDTYARLNKYDVYSGESQVSKESMLKAIDLFEKGLTHEDKGAVLIDLTKFNKKGKAIQV
KSDGTTLYLTRDVGAAVDRYEKYHFDKMIYVIASQQDLHAAQFFEILKQMGFEWAKDLQHVNFQM
VQGMSTRKGTVVFLDNILEETKEKMHEVMKKENKYAQIEHPPEEVADLVGISAVMIQDMQGRINN
YEFKWERMLSFE

>d1iq0a2 c.26.1.1 (A:97-466) Arginyl-tRNA synthetase (ArgRS) {Thermus thermophilus}

PFPRRPGVVLVEHTSVNPNKELHVGHRLNIALGDAIARILAYAGREVLVNLNYIDDTGRQAAETLFALR
HYGLTWDGKEKYDHFAGRAYVRLHQDPEYERLQPAIEEVLHALERGEREEVNRILLAQMATHAL
NARYDLLVWESDIVRAGLLQKALALLEQSPHVFRPREGKYAGALVMDASPVIPGLEDPFFVLLRSNG
TATYYAKDIAFQFWKMGILEGLRFRPYENPYYPGLRTSAPEGEAYTPKAEETINVDVRQSHQPALV
RAALALAGYPALAEKAHHLAYETVLLRGRQMSGRKGLAVSVDEVLEEATRARRARAIVEEKNPDHPDK
EEAARMVALGAIRFSMVKTEPKKQIDFRYQEALSFE

>d1coza_ c.26.1.2 (A:) CTP:glycerol-3-phosphate cytidyltransferase {Bacillus subtilis}

MKKVITYGTFDLLHWGHKLLERAKQLGDYLVVAISTDEFNLQKQKKAYHSYHRKLILETIRYVDEV
IPEKNWEQKKQDIIDHNIDVFMGDDWEGKFDLKDQCEVVYLPRTREGISTTKIKEEI

>d1qja_ c.26.1.3 (A:) Phosphopantetheine adenyltransferase {Escherichia coli}

KRAIYPGTDPITNGHIDIVTRATQMFHDVILAIASPSKKPMFTLEERVALAQQATAHLGNVEVVG
SDLMANFARNQHATVLRGLRAVADFEYEMQLAHMNRHLMPELESVFLMPSKEWSFISSSLVKEVA
RHQGDVTHFLPENVHQALMAKLA

>d1f9aa_ c.26.1.3 (A:) Nicotinamide mononucleotide (NMN) adenylyltransferase {Archaeon *Methanococcus jannaschii*}

LRGFIIGRFQPFFHKGHLEVIKIAEEVDEIIIGISAQKSHTLENPFTAGERILMITQSLKDYDLTYPIPI
KDIEFNISIVSVESLTPPFDIVYSGNPLVRVLFEEERGYEVKRPEMFNRKEYSGTEIRRRMLNGEKW
EHLVPKAVVDVIKEIKGVERLRKLA

>d1ej2a_ c.26.1.3 (A:) Nicotinamide mononucleotide (NMN) adenylyltransferase {Archaeon *Methanobacterium thermoautotrophicum*}

MRGLLVGRMQPFHRGHLQVIKSILEEVDLIIICIGSAQLSHSIRDPPFTAGERVMMLTKALSENGIPASR
YYIIPVQDIECNALWVGHIKMLTTPPFDRVYSGNPLVQRLFSEGDGYEVTAPPLFYRDRYSGTEVRRRML
DDGDWRSLLPESVVEVIDEINGVERIKHLA

>d1iho_ c.26.1.4 (A:) Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC) {*Escherichia coli*}

MLIETLPLLRQQIRRLMEGKRVALVPTMGNLHDGHMMLVDEAKARADVVSIFVNPQMDFDRPE
DLARYPRTLQEDCEKLNKRKVDLVFAPSVEKIYPNGTETHTYVDVPGLSTMLEGASRPGHFRGVSTI
VSKLFNLVQPDIAFCGEKDFQQLALIRKMOVADMGFDIEIVGVPIIMRAKDGALSSRNGYLTAEQRKIA
PGLYKVLSSIADKLQAGERDLDEIITAGQELNEKGRADDIQIRDADTLLEVSETSKRAVILVAAWLG
DARLIDNKMVEL

>d1g8fa2 c.26.1.5 (A:169-389) ATP sulfurylase central domain {Baker's yeast (*Saccharomyces cerevisiae*)}

YPGLRKTPAQLRLEFQSRQWDRVVAFQTRNPMHRAHRELTVRAAREANAKVLIHPVVGLTKPGDID
HHTRVRVYQEIIKRYPNGIAFLSLLPLAMRMSGDREAVWHAIIRKNYGASHFIVGRDHAGPGKNSKG
VDFYGPYDAQELVESYKHELDIEVVPFRMVTYLPDEDRYAPIDQIDTTKTRTLNISGTELRRRLRVGG
EIPWFSYPEVVKILRESNP

>d1i2da2 c.26.1.5 (A:171-390) ATP sulfurylase central domain {Fungus (*Penicillium chrysogenum*)}

YVALRYTPAELRVHFDKLGWSRVVAFQTRNPMHRAHRELTVRAARSQANVLIHPVVGLTKPGDID
HFTRVRAYQALLPRYPNGMAVLGLLGLAMRMGGPREAIWHAIIRKNHGATHFIVGRDHAGPGSNSK
GEDFYGPYDAQHAVEKYKDELGIEVVEFQMVTYLPDTEYRPVDQVPAGVKTLNISGTELRRRLRSG
AHIPEWFSYPEVVKILRESNP

>d1jhda2 c.26.1.5 (A:174-396) ATP sulfurylase central domain {unnamed symbiont of *Riftia pachytila*}

PDTFRTAVEIRNEIKEHGWSKVVAFQTRNPMHRAHEELCRMAMESLDADGVVHMLLGLKLLKGGDI
PAPVRDAIRTMAEVYFPNTVMVTGYGFDMLYAGPREAVLHAYFRQNMGATHFIIGRDHAGVGDY
YGAFDAQTIFDDEVPEGAMEIEIFRADHTAYSKKLNKIVMMRDVPDHTKEDFVLLSGTKVREMLGQ
GIAPPEFSRPEVAKILMDYYQSINS

>d1gpma1 c.26.2.1 (A:208-404) GMP synthetase, central domain {*Escherichia coli*}

WTPAKIIDDAVARIREQVGDDKVLGLSGGVDSVTAMLLHRAIGKNLTCVFDNGLLRNLNEAEQVL
DMFGDHFLNIVHVPADRFSLALAGENDPEAKRKIIIGRVFVEVFDEEALKLEDVKWLAQGTIYDPD
IESAASATGKAHVIKSHHNVGGLPKEMKMGLVEPLKELFKDEVRKIGLELGLPYDMLYRHPFP

>d1ih8a_ c.26.2.1 (A:) NH₃-dependent NAD⁺-synthetase {*Bacillus subtilis*}

SMQEIMRELHVKPSIDPKQEIEDRVNFLKQYVKKTGAKGFVLGISGGQDSTLAGRLAQLAVESIREE
GGDAQFIAVRPHGTQQDEDDAQLALKFIKPKDPSWKFDIKSTVSAFSDQYQYQETGDQLTDFNKG
KARTRMIAQYAIQQEGLLVLTGDHAAEAVTGFFTKYGDGGADLLPLTGLTKRQGRLLKELGAPERL
YLKEPTADLLDEKPPQSDTELGISYDEIDDYLEGKEVSAKVSEALEKRYSMTEHKRQVPASMFDD

WWK

>d1ct9a1 c.26.2.1 (A:193-516) Asparagine synthetase B, C-terminal domain {*Escherichia coli*}

RDWFDYDAVKDNVTDKNELRQALEDSVKSHLMSDVPYGVLLSGGLDSSIISAITKKYAARRVEDQER
SEAWWPQLHSFAVGLPGSPDLKAAQEVANHLGTVHHEIHFTVQEGLDAIRDVIYHIETYDVTTIRAS
TPMYLMSRKIKAMGIKMVLSGEGSDEVFGGYLYFHKAPNAKELHEETVRKLLALHMYDCARANKA
MSAWGVEARVPFLDKKFLDVAMRINPQDKMCGNGKMEKHILRECFEAYLPASVAWRQKEQFSDGV
GYSWIDTLKEVAAQVSDQQLETARFRFPYNTPTSKEAYLYREIFEELFPLPSAAECVPG

>d1jga1 c.26.2.1 (A:210-508) beta-Lactam synthetase {*Streptomyces clavuligerus*}

PGLSRRILPEGEAAVAARAALKAVAQRVTPGDTPLVVLSSGGIDSSGVAACAHRAAGELDTVSMGTD
SNEFREARAVVDHLRTRHREITIPTELLAQLPYAVWASESVDPIIEYLLPLTALYRALDGPERRILT
GYGADIPLGGMHREDRLPALDVTVAHDMATFDGLNEMSPVLSTLAGHWTTHPYWDREVLDLLVSL
EAGLKRRHGRDKWVLRAAMADALPAETVNRPKLGVHEGSGTSSFSRLLLDHGVAEDRVHEAKRQ
VVRELFDLTVGGGRHPSEVDTDDVVRSVADRT

>d1k92a1 c.26.2.1 (A:1-188) Argininosuccinate synthetase, N-terminal domain {*Escherichia coli*}

TTILKHLVPGQRIGIAFSGGLDTSALLWMRQKGAVPYAYTANLGQPDEEDYDAIPRRAMEYGAENA
RLIDCRKQLVAEGIAAIQCGAFHNTTGGLTYFNTTPLGRAVTGTMLVAAMKEDGVNIWGDGSTYKGN
DIERFYRYGLLTNAELQIYKPWLDTDFIDELGGRHEMSEFMIAACGFYKMSVEK

>d1sur_ c.26.2.2 (-) Phosphoadenylyl sulphate (PAPS) reductase {*Escherichia coli*}

SKLDLNLALNELPKVDRLALAEETNAELEKLDAGEGRVAVALDNLPGEYVLSSTFGIQAASLHLVNQIR
PDIPVILDTGYLFPETYRFIDELTDKLLNLKVYRATESAAWQEARYGKLWEQGVIEKYNDINKV
EPMNRALKELNAQTWFAGLRREQSGSRANLPVLAIQRGVFKVLP IIDWDNRITYQYLQKHGLKYHP
LWDEGYLSVGDTH

>d1dlja3 c.26.3.1 (A:295-402) UDP-glucose dehydrogenase (UDPGDH), C-terminal (UDP-binding) domain {*Streptococcus pyogenes*}

AKQIINVLKEQESPVKVVGVYRLIMKSNNSDNFRESAIKDVIDILKSKDIKIIYEPMLNKLESEDQSVLV
NDLENFKKQANIIVTNRYDNELQDVKNKVYSRDIFGRD

>d2tpt_2 c.27.1.1 (71-335) Thymidine phosphorylase {*Escherichia coli*}

DWKSLLHNGPIVDKHXSTGGVDVTSMLLGMVAACGGYIPMISGRGLGHTGGTLDKLESIPGFDIFP
DDNRFREIHKDVGVAIIGQTSSLAPADKRFYATRDITATVDSIPLITASILAKKLAEGLDALVMDVKVGS
GAFMPTYELSEALAEIIVGVANGAGVRTTALLTDMNQVLASSAGNAVEVREAVQFLTGEYRNPRLFD
VTMALCVELISGKLAKDDAEARAKLQAVLDNGKAAEVFGRMVAAQKGP TDFVENYAKYLP

>d1brwa2 c.27.1.1 (A:71-330) Pyrimidine nucleoside phosphorylase {*Bacillus stearothermophilus*}

LSSIRGVKVDKHXSTGGVDVTSMLLGMVAACGGYIPMISGRGLGHTGGTLDKLESVPGFHVEISKDE
FIRLVNENGLIIGQTGDLTPADKLYALRDVTATVNSIPLIASSIMSKKIAAGADAIVLDVKTGAGAFM
KKLDEARRLARVMVDIGKRVGRRTMAVISDMSQPLGYAVGNALEVKEAIETLKGNGPHDLTELCLTL
GSHMVYLAEKAPSLDEARRLLEEAIRSGAAIAAFKTFLLAAQGGDASVDDLDKLP

>d1dnpa2 c.28.1.1 (A:1-200) N-terminal domain of DNA photolyase {*Escherichia coli*}

TTHLVWFRQDLRLHDNLALAAACRNSSARVLALYIATPRQWATHNMSPRQAEELINAQLNGLQIALA
EKGIPLLFREVDDFVASVEIVKQVCAENSVTHLFYNYQYEVNERARDVEVERALRNVVCEGFDDSVIL
PPGAVMTGNHEMYKVFTPFKNAWLKRLREGMPECVAAPKVRSSGSIEPSITLNYPRQSFDTAHF

>d1iqra2 c.28.1.1 (A:2-171) N-terminal domain of DNA photolyase {*Thermus thermophilus*}

GPLLVWHRGDLRLHDPALLEALARGPVVGLVVLDPNNLKTTPRRRAWFLENVRALREAYRARGG
ALWVLEGLPWEKVPEAARRLKAKAVYALTSHTPYGRYRDGRVREALPVPLHLLPAPHLLPPDLRA
YRVYTPFSRLYRGAAPPLPPPEALPKGPEEGEIPREDPG

>d1qnf_2 c.28.1.1 (1-204) N-terminal domain of DNA photolyase {*Anacystis nidulans*}
MAAPILFWHRRDLRLSDNIGLAAARAQSAQLIGLFLCLDPQILQSADMAPARVAYLQGCLQELQQRYYQ
QAGSRLLLLQGGDPQHLPQLAQQQLQAEAVYWNQDIEPYGRDRDGGVAAALKTAGIRAVQLWDQLLH
SPDQILSGSGNPYSVYGPFWKNWQAQPKPTPVATPTELVDLSPEQLTAIAPLLLSELPTLKQLGFDW
DGGF

>d1efva1 c.29.1.1 (A:20-207) Electron transfer flavoprotein, EFTP {Human (*Homo sapiens*)}
QSTLVIAEHANDSLAPITLNTITAATRLGGEVSLVAGTKCDKVAQDLCKVAGIAKVLVAQHADVYKGLL
PEELTPLILATQKQFNHYTHICAGASAFGKNLLPRVAAKLEVAPISDIIAIKSPDTFVRTIYAGNALCTVK
CDEKVKVFSVRGTSFDAAATSGGSASSEKASSTSPVEISEWLDQKLTKS

>d1efvb1 c.29.1.1 (B:) Electron transfer flavoprotein, EFTP {Human (*Homo sapiens*)}
LRVLVAVKRVIDYAVKIRVKPDRTGVVTDGVKHSMPFCEIAVEEAVRLKEKLLVEKVIASVCGPAQC
QETIRTALAMGADRGHVEVPPAEERLGPLQVARVLAKLAEKEKVDLVLLGKQAIDDDCNQTGQM
TAGFLDWPQGTAFASQVTLLEGDKLVEREIDGGLETLRLKLPVVTADLRLNEPRYATLPNIMKAKKK
KIEVIKPGDLGVDLTSKLSVISVEDPPQRTAGVKVETTEDLVAKLKEIGRI

>d1efpa1 c.29.1.1 (A:2-184) Electron transfer flavoprotein, EFTP {*Paracoccus denitrificans*}
AVLLLGEVTNGALNRDATAKAVAAVKALGDVTVLCAGASAKAAAEAAKIAGVAKVLVAEDALYGHR
LAEPTAALIVGLAGDYSHIAAPATDDAKNVMPRVAALLDVMVLSVSDVSAILDADTFERPIYAGNAIQVV
KSKDAKKVFTIRTASFDAAGEGTAAPVTETAAAADPGLSSWVADEVAE

>d1efpb1 c.29.1.1 (B:) Electron transfer flavoprotein, EFTP {*Paracoccus denitrificans*}
MKVLVPVKRLIDYVVKARVKS DSGVDLANVKMSMPFDEIAVEEAIKRLKEKQAEEIIAVSIGVKQA
AETLRTALAMGADRILVVAADDVQQDIEPLAVAKILAAVARAEGTELIAGKQAIDNDMNATGQML
AAILGWAQATFASKVEIEGAKAKVTRVDGGLQTIASLPAVVTADLRLNEPRYASLPNIMKAKKKPL
DEKTAADYGVDPVAPRLEVVSREPEGRKAGIKVGSVDELVGKL

>d1mjha_ c.29.1.2 (A:) "Hypothetical" protein MJ0577 {*Archaeon Methanococcus jannaschii*}
VMYKKILYPTDFSETAEIALKHVKAFKTLKAEVILLHVIDEREIKKRDI FSLLLGVAGLNKSVEEFEN
ELKNKLTEEAKNKMENIKKELEDVGFVKDIIVVGIPHEEIVKIAEDEGVDIIMGSHGKTNLKEILLG
SVTENVIKKSNKPVLVVKRKN

>d1jmva_ c.29.1.2 (A:) Universal stress protein A, UspA {*Haemophilus influenzae*}
MYKHILVAVDLSEESPILLKAVGIAKRHDAKLSIIHVDVNFSDLYTGLIDVNMSSMQDRISTETQKAL
LDLAESVDYPISEKLSGSGDLGQVLSDAIEQYDVDLLVTGHHQDFWSKLMSTRQVMNTIKIDMLVV
PLRD

>d1dv1a2 c.30.1.1 (A:1-114) Biotin carboxylase (BC) subunit of acetyl-CoA carboxylase
{*Escherichia coli*}
MLDKIVIANRGEIALRILRACKELGIKTVAVHSSADRDLKHVLLADETVICIGPAPSVKSYLNIPAIISAA
EITGAVAIHPGYGFLSENANFAEQVERSGFIFIGPKAETIRLMG

>d1gsoa2 c.30.1.1 (A:-2-103) Glycinamide ribonucleotide synthetase (GAR-syn).
{*Escherichia coli*}
EFMKVLVINGGREHALAWKAAQSPLVETVVFVAPGNAGTALEPALQNVAIGVTDIPALLDFAQNEKI
DLTIVGPEAPLVKGVVDTFRAAGLKIFGPTAGAAQLEG

>d1b6ra2 c.30.1.1 (A:1-78) N5-carboxyaminoimidazole ribonucleotide synthetase, AIRC,
PurK {*Escherichia coli*}

MKQVCVLGNGQLGRMLRQAGEPLGIAVWPVGLDAEPAAVPFQQSVITAEIERWPETALTRQLARHP
AFVNRDVFPIIA
>d1eyza2 c.30.1.1 (A:2-112) Glycinamide ribonucleotide transformylase PurT {Escherichia coli}
TLLGTALRPAATRVMMLLGSSELGKEVAIECQRLGVEVIAVDYADAPAMHVAHRSHVINMLDGDALR
RVVELEKPHYIVPEIEAIATDMLIQLEEEGLNVVPCARATKLTM
>d1a9xa3 c.30.1.1 (A:1-127) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia coli}
MPKRTDIKSILGAGPIVIGQACEFDYSGAQACKALREEGYRVINVNSNPATIMTDPEMADATYIEPI
HWEVVRKIEKERPDAVLPTMGGQTALNCALELERQGVLEEFVMTIGATADAIDKAE
>d1a9xa4 c.30.1.1 (A:556-676) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia coli}
STDREKIMVLGGGPNRIGQIEFDYCCVHASLALREDGYETIMVNCNPETVSTDYDTSRDLRFEPVTL
EDVLEIVRIEKPKGVIVQYGGQTPLKLARALEAAGVPVIGTSPDAIDRAEDRE
>d1iow_1 c.30.1.2 (1-96) D-Ala-D-Ala ligase {Escherichia coli, gene ddlB}
MTDKIAVLLGGTSAEREVSLNSGAAVLAGLREGGIDAYPVDPKVEVDVTQLKSMGFQKVFIALHGRGG
EDGTLQGMLELMGLPYTGSGVMASALSMD
>d1ehia1 c.30.1.2 (A:3-134) D-alanine:D-lactate ligase, VanA {Leuconostoc mesenteroides, Ddl2}
KKRVALIFGGNSSEHDVSKRSAQNFYNAIEATGKYEIIVFAIAQNGFFLDTESSKILALEDEQPIVDAF
MKTVDASDPLARIHALKSAGDFDIFFPVVHGNLGEDGTLQGLFKLLDKPYVGAPLRGHAVSF
>d1e4ea1 c.30.1.2 (A:2-131) D-alanine:D-lactate ligase, VanA {Enterococcus faecium}
NRKIVAILFGGCSEEHVSVKSAIEIAANINKEKYEPLYIGITKSGVWKMCEKPCAEWENENCYSAVLS
PDKKMHGLLVKKNHEYEINHVDVAFSALHGKSGEDGSIQGLFELSGIPFVGCIDIQSSAICM
>d1gsa_1 c.30.1.3 (1-122) Prokaryotic glutathione synthetase, N-terminal domain {Escherichia coli}
MIKLGIVMDPIANINIKDSSFAMLLAQRRGYELHYMEMGDLYLINGEARAHTRTLNVKQNYEEW
FSFVGEQDLPLADLDVILMRKDPDFDTEFIYATYILERAEEKGLTIVNKPQSLRDC
>d2hgsa1 c.30.1.4 (A:202-303) Eukaryotic glutathione synthetase {Human (Homo sapiens)}
PNALVLLIAQEKERNIFDQRAIENELLARNIHVIRRTFEDISEKGLDQDRRLFVDGQEIAVVYFRDGY
MPRQYSLQNWEARLLERSHAAKCPDIATQLAG
>d1auva1 c.30.1.5 (A:112-213) Synapsin Ia domain {Cow (Bos taurus)}
AARVLLVIDEPHTDWAKYFKGKKIHGEIDIKVEQAEFSDLNLVAHANGGFSVDMEVLRNGVKVVRSL
KPDFVLIRQHAFSMARNGDYRSLVIGLQYAGIPSI
>d1dhs_ c.31.1.1 (-) Deoxyhypusine synthase, DHS {Human (Homo sapiens)}
APAGALAAVLKHSSTLPPESTQVRGYDFNRGVNYRALLEAFGTTGFQATNFGRAVQQVNAMIEKKLE
PLTSTIFLGYTNSLISSGIRETIRYLVQHNMVLDVLTAGGVEEDLIKCLAPTYLGEFSLRGKELRENG
INRIGNLLVPNENYCKFEDWLMPILDQMVMEQNTGKWTSPSKMIARLGKEINNPESVYVYWAQKN
HIPVFPALTDGSLGDMIFFHSYKNPGLVLDIVEDLRLINTQAIFAKCTGMILGGGVVKKHHIANANLM
RNGADYAVYINTAQEFDGSDSGARPDEAVSWGKIRVDAQPVKVYADASLVFPLLAETFAQKMDAFM
HEKNED
>d1efva2 c.31.1.2 (A:208-331) C-terminal domain of the electron transfer flavoprotein alpha subunit {Human (Homo sapiens)}
DRPELTGAKVVVSGGRGLKSGENFKLLYDLADQLHAAVGASRAAVDAGFVPNDMQVGQTGKIVAPEL

YIavgisGAIqHLAGMKDSKTIVAINKDPEAPIFQVADYgIVADLfkVvPEMTEILK
>d1efpa2 c.31.1.2 (A:185-308) C-terminal domain of the electron transfer flavoprotein alpha subunit {Paracoccus denitrificans}
SDRPElTSARRVvSGRGLGSkesFAIIEELADKLGAavGASRAAVDSGyAPNDWQVGqTGKVVAPeL
YVavgisGAIqHLAGMKDSKVIVAINKDEEAPIFQIADYGLVgDLFSVvPELTGKL
>d1poxa1 c.31.1.3 (A:183-365) Pyruvate oxidase {Lactobacillus plantarum}
YASANNyQTPLlPEPDVQAVTRlTQTLLAAERPLIyYGIGARKAGKELEQLSKTLKIPLMSTYPAKGIV
ADRYPAYLGSANRVAQKPANEALAQADVVLfVGNnYPFAEVSKAFKNTRYfLQIDIDPAKLGKRHKt
DIAVLADAQKTLAAILAQVSERESTPWWQANLANVKNWRAYLASLED
>d1pvda1 c.31.1.3 (A:182-360) Pyruvate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}
QTPIDMSLkPNDAESEKEVIDTILALVKDAKNPvILADACCSRHdVKAETKklIDLTQFPafVTPMGK
GSISeqHPryGGVYVgTLskPEVKEAVESADLILSVGALLSDKTKNIVeFHSDHMKIRNATfPGVQMK
FVLQKLLTNIADAAGYKPVAVPARTPANAaVP
>d1qpba1 c.31.1.3 (A:182-360) Pyruvate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}
QTPIDMSLkPNDAESEKEVIDTILVLIKDAKNPvILADACCSRHdVKAETKklIDLTQFPafVTPMGK
GSIDEqHPryGGVYVgTLskPEVKEAVESADLILSVGALLSDFNTGSFSYSYKTKNIVeFHSDHMKIRN
ATfPGVQMKFVLQKLLTAIADAAGYKPVAVPARTPANAaVP
>d1zpd1 c.31.1.3 (A:188-362) Pyruvate decarboxylase {Zymomonas mobilis}
EASDEASLNAaVDETLKFIANRDkVAVLVGSKLRAAGAEeAAVKFTDALGGAVATMAAAKsFFPEEN
ALYIGTSWGEVSYPGVEKTMKEADAVIALAPVFNDYSTTGWTDIPDPKklVLAePRSVVvNGIRfPS
VHLKDYlTRLAQKVSkkTGSldFFKSLNAGELKKAAPADPS
>d1bfd_1 c.31.1.3 (182-341) Benzoylformate decarboxylase {Pseudomonas putida}
SVRLNDQDLdILVKALNSASNPaiVLGPdVDAANANADCVMLAERLkAPVvWVAPSAPRCpFPTRHP
CFRGLMPAGIAAISQLLEGHDVVLVIGAPVFRYHQYDPGQYLKPGTRLISVTCDPLEAAARAPMGDAIV
ADIGAMASALANLVEESSRQLPTAAP
>d1jsca1 c.31.1.3 (A:280-460) Acetohydroxyacid synthase catalytic subunit {Baker's yeast (Saccharomyces cerevisiae)}
AQDEFVMQsINKAADLINLAKKPVLYVGAGILNHADGPRllKELSDRAQIPVTTTLQGLGSFDQEDP
KSLDMLGMHGcATANLAVQNADLIiAVGARFDDRVTGNISKFAPEARRAAAEGRGGIIHFEVSPKNIN
KVVQTQIAVEGDATtNLGKMMSKIFPVKERSEWFAQINKWKKEYPY
>d1d4oa_ c.31.1.4 (A:) Transhydrogenase domain III (dIII) {Cow (Bos taurus)}
GTHTEINLDNAIDMIREANSIIITPGYGLCAAKAQYPIADLVKMLSEQGKKVRFGIHPVAGRMPGQLN
VLLAEAGVPYDIVLEMDEINHDFPDTDLVLVIGANDTVNSAAQEDPNSIIAGMPVLEVWKSQVIVM
KRSLGVGYAAVDNPIFYKPNtAMLLGDakKTCDALQAKVRES
>d1hzzc_ c.31.1.4 (C:) Transhydrogenase domain III (dIII) {Rhodospirillum rubrum}
SVKAGSAEDAAfIMKNASKViiVPGYGMaVAQAQHALREMAVlKKEGVEVSyAIHPVAGRMPGHM
NVLLAEANVPYDEVFELEEINSSfQTADVAFVIGANDVTNPAAKTDpSSPIYGMPILDVEKAGTVLFI
KRSMASGYAGVENELFFRNNTMMLFGDAKKMTEQIVQAMN
>d1icia_ c.31.1.5 (A:) AF1676 sir2 homolog {Archaeon Archaeoglobus fulgidus}
GSHHHHHHGSHMDEKLLKTIAESKYLVALTGAGVSAESGIPTFRGKDGLWNRYRPEELANPQAFak
DPEKVWKWYAWRMekVFNAPNKAHQAFaelERLGLVKCLITQNVDDLHERAGSRNVIHLHGSL
RVVrCTSCNNSFEVESAPKIPPLPKCDKCGSLLRPGVVWFGEMLPPDVLDRAMREVERADVIIVAGT

SAVVQPAASLPLIVKQRGGAIIEINPDETPLTPIADYSLRGKAGEVMDELVRHVRKALS
>d1j8fa_c.31.1.5 (A:) Sirt2 histone deacetylase {Human (Homo sapiens)}
GEADMDFLRNLSQTLSSQKERLLDELTLLEGVARYMQSERCRRVICLVGAGISTSAGIPDFRSPSTG
LYDNLEKYHLPYPEAIFEISYFKKHPEPFFALAKELYPGQFKPTICHYFMRLKDKGLLRRCYTQNIDT
LERIAGLEQEDLVEAHGTFYTSHCVSASCRHEYPLSWMKEKIFSEVTPKCEDCQSLVKPDIVFFGESL
PARFFSCMQSDFLKVLLLLVMGTSLQVQPFASLISKAPLSTPRLINKEKAGQSDPFLGMIMGLGGGM
DFDSKKAYRDVAWLGECDQGCLALAEELGWKKELEDLVRREHASIDAQS
>d1fsz_1 c.32.1.1 (23-231) Cell-division protein FtsZ {Archaeon Methanococcus jannaschii}
SPEDKELLEYLQQTAKKITVVGCGGAGNNTITRLKMEGIEGAKTVAINQDAQLIRTKADKKILIGKK
LTRGLGAGGNPKIGEEAAKESAEIKAQSDSMVFITCGLGGGTGTGSAPVVAEISKKIGALTVAVVT
LPFVMEGKVRMKNAMEGLERLQHTDTLVVIPNEKLFVPMPLKLAFKVADEVLINAVKGLVELI
TKDGL
>d1tuba1 c.32.1.1 (A:1-245) Tubulin alpha-subunit {Pig (Sus scrofa)}
MRECISIHVQAGVQIGNACWELYCLEHGIQPDGQMPSPDKTIGGGDDSFNTFFSETGAGKHVPRAVF
VDLEPTVIDEVRTGTYRQLFHPEQLITGKEDAANNYARGHYTIGKEIDLVLDRIRKLADQCTGLQGF
SVFHSFGGGTSGSFTSLLMERLSVDYGGKSKLEFSIYPAPQVSTAVVEPYNSILTHTTLEHSDCAFV
DNEAIYDICRRNLDIERPTYTNLNLRLIGQIVSSITASLRFD
>d1tubb1 c.32.1.1 (B:1-245) Tubulin beta-subunit {Pig (Sus scrofa)}
MREIVHIQAGQCGNQIGAKFWEVISDEHGIDPTGSYHGSDQLERINVYYNEAAGNKYVPRAILVD
LEPGTMDSVRSRPFQIFRPDNFVFGQSGAGNNWAKGHYTEGAELVDSVLDVVRKESESCDCLQGF
QLTHSLGGGTSGMGMTLLISKIREEYPDRIMNTFSVVPSPKVSDDTVVEPYNATLSVHQLVENTDETYC
IDNEALYDICFRTLKLTPTTYGDLNHLVSATMSGVTTCLRFP
>d1nbaa_c.33.1.1 (A:) N-carbamoylsarcosine amidohydrolase {Arthrobacter sp.}
TFNDIEARLAAVLEEAFAEAGTSIYNERGFKRRIGYGNRPAVIHIDLANAWTQPGHPFSCPGMETIIPN
VQRINEAARAKGVPVFYTTNVYRNRDASSGTNDMGLWYSKIPTETLPADSYWAQIDDRIAPADGEV
VIEKNRASAFPQNTLELFLTSNRIDTLIVTGATAAGCVRHTVEDAIAKGFRIIPRETIGDRVPGVVQW
NLYDIDNKFQDVESTDSVVQYLDALPQFEDTVPKTLSDPQPEVEAPADPV
>d1im5a_c.33.1.2 (A:) Pyrazinamidase/nicotinamidase {Archaeon Pyrococcus horikoshii}
PEEALIVVDMQRDFMPPGALPVPEGDKIIPKVNEYIRKFEKKGALIVATRDWHPENHISFRERGGPW
PRHCVQNTPGAEFVVDLPEDAVIISKATEPDKEAYSGFEGTDLAKILRGNGVKRVYICGVATEYCVRA
TALDALKHGFVYLLRDAVKGIKPEDEERALEEMKSRGIKIVQF
>d1yaca_c.33.1.2 (A:) YcaC {Escherichia coli}
TKPYVRLDKNDAAVLLVDHQAGLLSLVRDIEPDKFKNNVLALGDLAKYFNLPTILTSTAETGPNGPL
VPELKAQFPDAPYIARPGNINAWDNEDFVKAVKATGKKQLIAGVVTEVCVAFPALSAIEEGFDVFFV
TDASGTFNEITRHSWDRMSQAGAQLMTWFGVACELHRDWRNDIAGLATLFSNHIPDYRNLMTSY
DTLT
>d1hi9a_c.99.1.1 (A:) Zn-dependent D-aminopeptidase DppA {Bacillus subtilis}
MKLYMSVDMEGISGLPDDTFVDSGKRNYERGLIMTTEANYSIAEAFNSGCTEVLVNDSSHSMNNL
MVEKLHPEADLISGDVKPFSMVEGLDDTFRGALFLGYHARASTPGVMSHSMIFGVRHFYINDRPVG
ELGLNAYVAGYYDVPVLMVAGDDRAAKEAEELIPNVTTAAVKQTISRSVAVKCLSPAKRGRLLTEKTAF
ALQNKDKVKPLTPPDRPVLSIEFANYQAEWANLMPGTEIKTGTTVQFQAKMLEAYQAMLVMT
ELAMRTSFC
>d1e20a_c.34.1.1 (A:) Halotolerance protein Hal3 {Mouse-ear cress (Arabidopsis thaliana)}
RKPRVLLAASGSVAAIKFGNLCHCFTEWAEVRAVVTKSSLHFLDKLSLPQEVTLTYTDEDEWSSWNKI

GDPVLHIELRRWADV LVIAPLSANTLGKIAGGLCDNLLTCIIRAWDYTKPLFVAPAMNTLMWNNPFT
ERHLLSLDELGITLIPPIKKRLACGDYNGGAMAEP SLIYSTVRLFWESQAH
>d1g5qa_c.34.1.1 (A:) Epidermin modifying enzyme (peptidyl-cysteine decarboxylase) EpiD
{Staphylococcus epidermidis}
MYGKLLICATASINVININHYIVELKQHFDEVNLFSPSSKNFINTDVLKLFCDNLYDEIKDPLLNNINI
VENHEYILVLPASANTINKIANGICDNLLTTVCLTGYQKLFIFPNMNMIRMWGNPFLQKNIDLLKNNNDV
KVYSPDMNKSFEISSGRYKNNITMPNIENVLNFVLN
>d1k1ea_c.108.1.5 (A:) Probable phosphatase YrbI {Haemophilus influenzae, HI1679}
KLENIKFVITDVDGVLTDGQLHYDANGEAIKSFHVRDGLGIKMLMDADIQVAVLSGRDSPILRRRIAD
LGIKLFFLGKLEKETACFDLMKQAGVTAEQTAYIGDDSVLPAFAACGTSFAVADAPIYVKNVAVDHVL
STHGGKGA FREMSDMLQAQGKSSVFDTAQGFLKSVKSMGQ
>d1zrn_c.108.1.1 (-) L-2-Haloacid dehalogenase, HAD {Pseudomonas sp., strain YL}
YIKGIAFDLYGTLFDVHSVVGRCDEAFPGRGREISALWRQKQLEYTWLRSLMNRVYVNFQQATEDALR
FTCRHLGLDL DARTRSTLCDAYLRLAPFSEVPDSLRELKRRGLKLAILSNGSPQSIDAVVSHAGLRDG
FDHLLSVDPVQVYKPDNRVYELAEQALGLDRSAILFVASNAWDATGARYFGFPTCWINRTGNVFEE
MGQTPDWEVTS LRAVVELF
>d1qq5a_c.108.1.1 (A:) L-2-Haloacid dehalogenase, HAD {Xanthobacter autotrophicus}
MIKAVVFDAYGTLFDVQSVADATERAYPGRGEYITQVWRQKQLEYSWLRALMGRYADFW SVTREAL
AYTLGTLGLEPDESFLADMAQAYNRLTPYPDAAQCLAELAPLKRAILSNGAPDMLQALVANAGLTDS
FDAVISVDAKR VFKPHPDSYALVEEVLGVT PAEVLVSSNGFDVGGAKNFGFSVARVARLSQEALARE
LVSGTIAPLTMFKALRMREETYAEAPDFVVPALGDL PRLVRGMA
>d1ek1a1_c.108.1.2 (A:4-225) Epoxide hydrolase, N-terminal domain {Mouse (Mus
musculus)}
RVAAFDLGVLALPSIAGAFRRSEEALALPRDFLLGAYQTEFPEGPTQLMKGKITFSQWVPLMDES
YRKSSKACGANLPENFISISQIFSQAMAARSINR PMLQAAIALKKGFTTCIVTNNWLDDGDKRDSL A
QMMCELSQHFDLIESCQVGMKPEPQIYNFLDLTKAKPNEVFLDDFGSNLKPARDMGMVTVILV
HNTASALRELEKVTGTQFPEAP
>d1feza_c.108.1.3 (A:) Phosphonoacetaldehyde hydrolase {Bacillus cereus}
KIEAVIFDWAGTTVDYGCFAPLEVFMEIFHKRGVAITAE EARKPMGLLKIDHVRALTEMPRIASEWN
RVFRQLPTEADIQEMYEEFEEILFAILPRYASPINAVKEVIASLRERGIKIGSTTG YTREMMDIVAKEAA
LQGYKPDFLVPDDVPAGRPYPWMCYKNAMELGVYPMNHMIKVGDTVSDMKEGRNAGMWTVGV
ILGSSELGLTEEEVENMDSVELREKIEVVRNRNFV ENGAHFTIETMQELESVMEHIE
>d1j97a_c.108.1.4 (A:) Phosphoserine phosphatase {Archaeon Methanococcus jannaschii}
EKKKKLILFDSTLVNNETIDEIAREAGVEEEVKKITKEAMEGKLNFEQSLRKRVSLLKDLPIEKVE
KAIKRITPEGAEETIKELKNRGYVVAVVSGGF DIAVNKIKEKLGLDYAFANRLIVKDGKLTGDVEGEV
LKENAKGEILEKIAKIEGINLEDTVAVGDGANDISMFKKAGLKIAFCAK PILKEKADICIEKRDLREILK
YIK
>d1fs5a_c.35.1.1 (A:) Glucosamine 6-phosphate deaminase/isomerase {Escherichia coli}
MRLIPLTTAEQVGKWAARHIVNRINAFKPTADRPFVLGLPTGGTPM TTYKALVEMHKAGQVSFKHV
VTFNMDEYVGLPKEHPESYYSFMHRNFFDHVDIPAENINLLNGNAPDIDAECRQYEEKIRSYGKIHL
FMGGVGN DGHIAFNEPASSLASRTRIKTLTHDTRVANSRFFDNDVNQVPKYALT VGVGTL LLDAAEVM
ILVLSQKALALQAAVEGCVNHMWTISCLQLHPKAIMVCDEPSTMELKVKTLRYFNELEAENIKGL
>d1d9ta_c.35.1.1 (A:) Glucosamine 6-phosphate deaminase/isomerase {Human (Homo
sapiens)}

MKLIILEHYSQASEWAAKYIRNRHQFNPQPEKYFTLGLPTGSTPLGKYKLIIEYYKNGDLSFKYVKTF
NMDEYVGLPRDHPESYHSFMWNNFFKHIDHPENTHILDGNAVDLQAECDAFEKIKAAAGGIELFV
GGIGPDGHIAFNEPGSSLSRTRVKTAMDTILANARFFDGETLKVPTMALTGVGTVMADAREVMILI
TGAHKAFALYKAIEEGVNHMWTVSAFQQHPRTVFCDEDATLELKVKTVMKYFKGLMLVHNKLVDP
YSIKEKETEKSQ

>d1ig3a2 c.100.1.1 (A:10-178) Thiamin pyrophosphokinase, catalytic domain {Mouse (Mus musculus)}

HSSGLVPRGSHMEHAFTPLELLPTGNLKYCLVVLNQPLDARFRHLWKKALLRACADGGANHLYDL
TEGERESFLPEFVSGDFDSIRPEVKEYYTKKGCGLISTPDQDHTDFTKCLQVLQRKIEEKELQVDVIV
TLGGLGGRFDQIMASVNTLFQATHITPVPIIIQK

>d1ig0a2 c.100.1.1 (A:3-223) Thiamin pyrophosphokinase, catalytic domain {Baker's yeast (Saccharomyces cerevisiae)}

EECIENPERIKIGTDLINIRNKMNLKELIHPNEDENSTLLILNQKIDIPRPLFYKIWKLHDLKVCADGA
ANRLDYLDDETLRIKYLPNYIIGDLDSLSEKVKYKYYRKNKVTIHKQTTQYSTDFTKCVNLISLHFNS
PEFRSLISNKDNLQSNHGIELEKGIHTLYNTMTESLVFSKVTPISELLALGGIGGRFDQTVHSITQLYTSL
ENASYFKLCYMTF

>d1f75a_ c.101.1.1 (A:) Undecaprenyl diphosphate synthase {Micrococcus luteus}

NINAAQPKHIAIIMDGNGRWAKQKKMPRIKGYEGMQTVRKITRYASDLGVKYLTYAFSTENWSR
PKDEVNYLMKLPDGLNFTFLPELIEKNVKVETIGFIDDLPDHTKKAVLEAKEKTKHNTGLTLVFALN
YGGRKEIISAVQLAERYKSGEISLDEISETHFNEYLFANMPDPELLIRTSGEERLSNFLIWQCSYSEF
VFIDEFWPDFNEESLAQCISIQNR

>d1jp3a_ c.101.1.1 (A:) Undecaprenyl diphosphate synthase {Escherichia coli}

LPAHGCRHVAIIMDGNGRWAKQKIRAFGHKAGAKSVRRRAVSFAANNGIEALTYAFSSSENWNRPA
QEVSALEMELFVWALDSEVKSLSHRHNVRLRIIGDTSRFSRLQERIRKSEALTAGNTGLTLNIAANYGG
RWDIVQGVRLAEKVQQGNLQPDQIDEEMLNQHVCMHLELAPVDLVIRTGGEHRISNFWLWQIAYAE
LYFTDVLWPDFDEQDFEGALNAFANRE

>d1pvda2 c.36.1.1 (A:2-181) Pyruvate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}

SEITLKGKYLFERLKQVNVNTVFGLPGDFNLSLLDKIYEVEGMRWAGNANELNAAAYAADGYARIKMS
CIITTFVGVGELSALNGIAGSYAEHVGLHVGVGPSISHTLGNDFTVFHRMSANISETTAMITDIATA
PAEIDRCIRTTYVTQRPVYGLPANLVDLNVPKLL

>d1pvda3 c.36.1.1 (A:361-556) Pyruvate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}

ASTPLKQEWMMWNQLGNFLQEGDVVIAETGTSAFGINQTTFPNNTYGISQVLWGSIGFTTGATLGAAF
AAEIDPKKRVLFIGDGSLLQTVQEISTMIRWGLKPYLFLVNLNDGYTIEKLIHGPKAQYNEIQGWDH
LSLLPTFGAKDYETHRVATTGEWDKLTQDKSFNDNSKIRMIEIMLPVFDAPQNLVKQAKLT

>d1zpd2 c.36.1.1 (A:2-187) Pyruvate decarboxylase {Zymomonas mobilis}

SYTVGTYLAERLVQIGLKHFFAVAGDYNLVLNLLLNKNMEQVYCCNELNCGFSAEGYARAKGAAA
AVVTYSVGALSFAIDAIGGAYAENLPVILISGAPNNNDHAAGHVLHHALGKTDYHYQLEMAKNITAAA
EAIYTPPEAPAKIDHVIKTALREKPPVYLEIACNIASMPCAAPGPASALFND

>d1zpd3 c.36.1.1 (A:363-566) Pyruvate decarboxylase {Zymomonas mobilis}

APLVNAEIRQVEALLTPNTTVAIETGDSWFNAQRMKLPNGARVEYEMQWGHIGWSVPAAFGYAV
GAPERRNILMVGDSFQLTAQEVAQMVRLLPVIIFLINNYGYTIEVMIHDGPYNNIKNWDYAGLME
VFNGNGGYDSGAAGLAKKTGGELAEAIKVALANTDGPTLIECFIGREDCTEELVKWGWKRVAAANSR

KPVNK

>d1poxa2 c.36.1.1 (A:9-182) Pyruvate oxidase {Lactobacillus plantarum}
TNILAGAAVIKVLLEAWGVDHLYGIPGGSINSIMDALSAERDRIHYIQVRHEEVGAMAAAADAKLTGKI
GVCFGSAGPGGTHLMNGLYDAREDHVPVLALIGQFGTTGMNMDTFQEMNENPIYADVADYNVTAV
NAATLPHVIDEARRAYAHQGVAVVQIPVDLPWQQISAEDW

>d1poxa3 c.36.1.1 (A:366-593) Pyruvate oxidase {Lactobacillus plantarum}
KQEGPLQAYQVLRVANKIAEPDAIYSIDVGDINLNANRHLKLTPSNRHITSNLFATMGVGPAGIAAKL
NYPERQVFNLAGDGGASMTMQDLVTQVQYHLPVINVVFTNCQYGFYKDEQEDTNQNDFIGVEFNDI
DFSKIADGVHMQAFRVNKIEQLPDVFEQAKAIAQHEPVLIDAVITGDRPLPAEKLRLLDSAMSSAADIE
AFKQRYEAQDLQPLSTYLKQFGLDD

>d1bfd_2 c.36.1.1 (2-181) Benzoylformate decarboxylase {Pseudomonas putida}
ASVHGTTYELLRRQGITVFGNPGSNELPFLKDFPEDFRYILALQEACVVGIADGYAQRKPAFINL
HSAAGTGNAMGALSNAWNSHPLIVTAGQQTRAMIGVEALLTNVDAANLPRPLVKWSYEPASAAEV
PHAMSRAIHMASMAPQGPVYLSVPYDDWDKADPQSHHLFDRHVSS

>d1bfd_3 c.36.1.1 (342-524) Benzoylformate decarboxylase {Pseudomonas putida}
EPAKVDQDAGRLHPETVFDLNDMAPENAIYLNSTSTTAQMWRQLNMRNPGSYFFCAAGGLGFA
LPAAIGVQLAEPERQVIAVIGDGSANYSISALWTAQYNIPTIFVIMNNGTYGALRWFAGVLEAENVP
GLDVPGIDFRALAKGYGVQALKADNLEQLKGSLEALSAGKPVLEIVSTV

>d1jsca2 c.36.1.1 (A:83-270) Acetohydroxyacid synthase catalytic subunit {Baker's yeast
(Saccharomyces cerevisiae)}
PDMDTSFVGLTGGQIFNEMMSRQNVDTVFGYPGGAILPVYDAIHNSDKFNFVLPKHEQGAGHMAE
GYARASGKPGVVLVTSVSGPNTNVVTPMADAFADGIPMVVFTGQVPTSAIGTDAFQEADVVGISRSCT
KWNVMVKSVEELPLRINEAFEIATSGRPGPVLVDLPKDVTAAILRNPIPTKTTLPS

>d1jsca3 c.36.1.1 (A:461-648) Acetohydroxyacid synthase catalytic subunit {Baker's yeast
(Saccharomyces cerevisiae)}
AYMEETPGSKIKPQTVIKKLSKVANDTGRHVIVTTGVGQHQMWAAQHWTWRNPHTFITSGGLGTM
GYGLPAAIGAQVAKPESLVIDIDGDASFNMTLTELSSAVQAGTPVKILILNNEEQGMVTQWQSLFYEH
RYSHTHQLNPDFIKLAEAMGLKGLRVKKQEELDAKLEFVSTKGPVLEVEVDKK

>d1gpua1 c.36.1.2 (A:3-337) Transketolase, TK {Baker's yeast (Saccharomyces cerevisiae)}
QFTDIDKLAIVSTIRILAVDTVSKANSHPGAPLGMAPAHHVLSQMRMNPNTPDWINRDRFVLSN
GHAVALLYSMLHLTGYDLSIEDLKQFRQLGSRTPGHPEFELPGVEVTTGPLGQGISNAVGMAMAQAN
LAATYNKPGFTLSDNITYVFLGDGCLQEGISSEASSLAGHLKLGNIYDDNKITIDGATSISFDEDV
AKRYEAYGWEVLYVENGNEDLAGIAKAIQAQKLSKDKPTLIKMTTITIGYSLHAGSHSVHGAPLKAD
DVKQLKSKFGFNPDKSFVVPQEVYDHYQKTLKPGVEANNKWNKLFSEYQKKFPELGAELARRLSG
Q

>d1gpua2 c.36.1.2 (A:338-534) Transketolase, TK {Baker's yeast (Saccharomyces
cerevisiae)}
LPANWESKLPTYTAKDSAVATRKLSETVLEDVYNQLPELIGGSADLTPSNLTRWKEALDFQPPSSGS
GNYSGRYIRYGIREHAMGAIMNGISAFGANYPYGGTFLNFVSYAAGAVRLSALSHPVIVVATHDSI
GVGEDGPTHQPIETLAHFRSLPNIQVWRPADGNEVSAAYKNSLESKHTPSIIALSQRNLPLQ

>d1dtwa1 c.36.1.3 (A:) Branched-chain alpha-keto acid dehydrogenase {Human (Homo
sapiens)}
PQFPGASAEFIDKLEFIQPNVISGPIYRVMDRQGGIINPSEDPHLPKEKVLKLYKSMILLNTMDRILY
ESQRQGRISFYMTNYGEEGTHVGSAAALDNTDLVFGQYREAGVLMYRDYPLELFMAQCYGNISDLG

KGRQMPVHYGCKERHFVTTISSPLATQIPQAVGAAYAAKRANANRVVICYFGEGAASEGDAHAGFNFA
ATLECPHFFCRNNGYAISTPTSEQYRGDIAARGPGYGIMSIRVDGNDVFAVYNATKEARRRAVAENQ
PFLIEAMTYRIGHHSTSDSSAYSRSVDEVNYWDKQDHPISRLRHYLSSQGWWDDEEQEKAWRKQSR
RKVMEAFEQAERKPKPNPNULLFSDVYQEMPAQLRKQQESLARHLQTYGEHYPLDHFDFK

>d1dtwb1 c.36.1.3 (B:17-204) Branched-chain alpha-keto acid dehydrogenase {Human
(Homo sapiens)}

QTQKMNLFSVTSALDNSLAKDPTAVIFGEDVAFGGVFRCTVGLRDKYKDRVFNTPLCEQGIVGFG
IGIAVTGATAIAEIQFADYIFPAFDQIVNEAAKYRYSRGLFNCGSLTIRSPWGCVGHGALYHSQSPEAF
FAHCPGIKVVIPRSPFQAKGLLLSCIEDKNPCIFFEPKILYRAAAEEVPIE

>d1qs0a1 c.36.1.3 (A:) 2-oxoisovalerate dehydrogenase, E1B {Pseudomonas putida}

NEYAPRLRHVPEPTGRPGCQTDfsYLRRLNDAGQARKPPVDVDAADTADLSYLVRVLDEQGDAQGP
WAEDIDPQILRQGMRAMLKTRIFDSRMVVAQRQKMSFYMQSLGEEAIGSGQALALNRTDMCFPT
YRQQSILMARDVSLVEMICQLLSNERDPLKGRQLPIMYSVREAGFFTISGNLATQFVQAVGWAMASAI
KGDTKIASAWIGDGATAESDFHTALTFAHVYRAPVILNVVNNQWAISTFQAIAGGESTTFAGRGVGGC
IASLRVDGNDVAVYAASRWAAERARRGLGPSLIEWVTYRAGPHSTSDPSKYRPADDWSHFPLGD
PIARLKQHLIKIGHWSEEEHQATTAEFEEAVIAAQKEAEQYGTLANGHIPSAAAMFEDVYKEMPDHL
RRQRQEL

>d1qs0b1 c.36.1.3 (B:2-205) 2-oxoisovalerate dehydrogenase, E1B {Pseudomonas putida}

ATTTMTMIQALRSAMDVMLERDDNVVYQDVGYFGGVFRCTEGLQTKYKSRVFDAPISESGIVGT
AVGMGAYGLRPVVEIQFADYFYPASDQIVSEMARLRYRSAGEFIAPLTLRMPCGGGIYGGQTHSQSPE
AMFTQVCGLRVTMPSNPYDAKGLLIASIECDPVIFFLEPKRLYNGPFDGHHDRPVTTPWSKHPHSAVP
DG

>d1ik6a1 c.36.1.3 (A:1-191) E1-beta subunit of pyruvate dehydrogenase {Archaeon
Pyrobaculum aerophilum}

VAGVVMANMAKAINMALHEEMERDERVVVLGEDVGGKGGVFLVTEGLYERFGPERVIDTPLNEG
GILGFAMGMAMAGLKPVAEIQFVDFIWLGADLLNHIKLRYSRGGNYKAPLVVTRTPVSGSTRGGGLY
HSNSPEAIFVHTPGLVVMPSTPYNAKGLLKAAIRGDDPVVFFLEPKILYRAPREEVPEG

>d1keka1 c.36.1.4 (A:2-258) Pyruvate-ferredoxin oxidoreductase, PFOR, domains I and VI
{Desulfovibrio africanus}

GKKMMTTDGNATATAHVAYAMSEVAAIYITPSSTMGEEADDWAAQGRKNIFGQTLTIREMQSEAGA
AGAVHGALAAGALTTTFTASQGLLLMIPNMYKISGELLPGVFHVVTARAIAAHALSIFGDHQDIYAARQ
TGFAMLASSSVQEAHDMALVAHLAAIESNVPFMHFFDGFRTSHEIQKIEVLDYADMASLVNQKALAE
FRAKSMNPEHPHVRGTAQNPDYFQGREANPYLKVPGIVA EYMQKVASLTGRSY

>d1keka2 c.36.1.4 (A:786-1232) Pyruvate-ferredoxin oxidoreductase, PFOR, domains I and
VI {Desulfovibrio africanus}

VKSEVLPRDSLKGSQFQEPLMEFSGACSGCGETPYVRVITQLFGERMFIANATGCSSIWGASAPSMFY
KTNRLGQGPWAGNSLFEDAAEYFGMNMSMFARRTHLADLAAKALES DASGDVKEALQGWLAGK
NDPIKSKEYGDKLKKLLAGQKDGLLQIAAMSDLYTKKSVWIFGGDWAYDIGYGGDLHVLASGEDV
NVFVMDTEVYSNTGGQSSKATPTGAVAKFAAAGKRTGKKDLARMVMTYGYVYVATVSMGYSKQQF
LKVLEKAESFPGPSLVIAATCINQGLRKGMGKSQDVMNTAVKSGYWPLFRYDPRLAAQGNPFQLD
SKAPDGSVEEFMAQNRFAVLDRSPEDAKRLRAQVAHELDVRFKELEHMAATNIFESFAPAGGKA
DGSVDFGEGAEFCTRDDTPMMARPDSGEACDQNRAGTSEQQDLSKRTRK

>d1gky_ c.37.1.1 (-) Guanylate kinase {Baker's yeast (Saccharomyces cerevisiae)}

SRPVISGPGSGTGKSTLLKKLFAEYPPDSFGFSVSTTRTPRAGEVNGKDYNFVSVDEFKSMIKNNEFIE

WAQFSGNYYGSTVASVKQVSKSGKTCILDIDMQGVKSVKAIPELNARFLFIAPPSVEDLKKRLEGRGT
ETESINKRLSAAQAELAYAETGAHDKVIVNDDLKAYKELKDFIFAEK
>d1kgda_ c.37.1.1 (A:) Guanylate kinase-like domain of Cask {Human (Homo sapiens)}
HMRKTLVLLGAHGVGRRHIKNTLITKHPDRFAYPIPHTRPPKKDEENGKNYYFVSHDQMMQDISN
NEYLEYGSHEDAMYGTKLETIRKIHEQGLIAILDVEPQALKVLRTAEFAPFVVFIAAPTITPGLNEDES
LQRLQKESDILQRTYAHYFDLTIINNEIDETIRHLEEAVELVC
>d1kja2_ c.37.1.1 (A:526-724) Guanylate kinase-like domain of Psd-95 {Rat (Rattus
norvegicus)}
VTQMEVHYARPIILGPTKDRANDLLSEFPDKFGSCVPHTTRPKREYEIDGRDYHFVSSREKMEKD
IQAHKFIEAGQYNHLYGTSVQSVREVAEQGKHCILDVSNANAVRRLQAAHLHPAIAFIRPRSLNVLEI
NKRITEEQARKAFDRATKLEQEFTECFSAIVEGDSFEEIYHKVKRVIEDLSGPYIWWPARERL
>d1ukz_ c.37.1.1 (-) Uridylate kinase {Baker's yeast (Saccharomyces cerevisiae)}
PAFSPDQVSVIFVLGGPGAGKGTQCEKLVKDYSFVHLSAGDLLRAEQGRAGSQYGELIKNCIKEGQIVP
QEITLALLRNAISDNVANKHKFLIDGFPRKMDQAISFERDIVESKFILFFDCPEDIMLERLLERKTS
GRSDDNIESIKKRFNTFKETSMPVIEYFETKSKVVRVRCDRSVEDVYKDVQDAIRDSL
>d1deka_ c.37.1.1 (A:) Deoxynucleoside monophosphate kinase {Bacteriophage T4}
MKLIFLSGVKRSKGDTTADFIMSNYSYAVKYQLAGPIKDALAYAWGVFAANTDYPCLTRKEFEGIDYDR
ETNLNLTKLEVITIMEQAFCYLNGKSPIKGVFVFDDEGKESVNFVAFNKITDVINNIEDQWSVRRML
QALGTDLIVNNFDRMYWVKLFALDYLDKFNSGYDYIVPDTRQDHEMDAARAMGATVIHVVRPGQ
KSNDRHITEAGLPIRDGDLVITNDGSLEELFSKIKNTLKV
>d1j90a_ c.37.1.1 (A:) Deoxyribonucleoside kinase {Fruit fly (Drosophila melanogaster)}
TQPFTVLIENIGSGKTTYLNHFKEYKNDICLLTEPVEKWRNVNGVNLLELMYKDPKKWAMPFQSY
VTTLMLQSHAPTNNKKLIMERSIFSARYCFVENMRRNGSLEQGMYNTELEWYKFIEESIHVQADLII
YLRTSPEVAYERIRQRARSEESCPLKYLQELHELHEDWLIHQRRPQCKVLVLDADLNLE
>d1jaga_ c.37.1.1 (A:) Deoxyguanosine kinase {Human (Homo sapiens)}
GPRRLSIEGNIYVAVGKSTFVKLLTKTYPEWHVATEPVATWQNIQAAGNQKACTAQLGNLLDMMYRE
PARWSYTFQTFSLRSLKLVQLEPFPEKLLQARKPVQIFERSVYSDRYIFAKNLFENGSLSDIEWHIYQD
WHSFLLWEFASRITLHGFYIYQASPQVCLKRLYQRAREEEKGIELAYLEQLHGQHEAWLIHKTTKLH
FEALMNPVVLVDVNDDFSEEVTKQEDLMREVNTFVKNL
>d1ckea_ c.37.1.1 (A:) CMP kinase {Escherichia coli}
AIAPVITIDGSPGAGKGTLCAMAALQWHLLEDGAIYRVLALAAALHHHVDVASEDALVPLASHLDV
RFVSTNGNLEVILEGEDVSGEIRTQEVANAASQVAAPRVREALLRRQRAFRELPLIADGRDMGTV
VFPDAPVKIFLDASSEERAHRRMLQLQVKGFSVNERLLAEIKERDDRDRNRVAVPLVPAADALVLD
STTLSIEQVIEKALQYARQKLALA
>d1qf9a_ c.37.1.1 (A:) UMP/CMP kinase {Dictyostelium discoideum}
MEKSKPNVVFVLGGPGSGKGTQCANIVRDFGWVHLSAGDLLRQEQQSGSKDGEMIATMIKNGEIVP
SIVTVKLLKNAIDANQGNFLVDGFPRNEENNNSWEENMKDFVDTKFVLFDCPEEVMQTRLLKR
GESSGRSDDNIESIKKRFNTFNVQTKLVIDHYNKFVKIIPANRDVNEVYNDVENLFSKSMGF
>d1e2ka_ c.37.1.1 (A:) Thymidine kinase {Herpes simplex virus type 1, different strains}
MPTLLRVYIDGPHGMGKTTTTQLLVALGSRDDIVYVPEPMTYWRVLGASETIANIYTTQHRLDQGEI
SAGDAAVVMTSAQITMGMPYAVTDAVLAPHIGGEAGSSHAPPALTLIFDRHPAALLCYPAARYLMG
SMTPQAVLAFVALIPPTLPGTNIVL GALPEDRHIDRLAKRQRPGERLDLAMLAAIRRVYGLLANTVR
YLQCGGSWREDWGQLSGTAVPPQGAEPQSNAGPRPHIGDTLFTLFRAPPELLAPNGDLYNVFAWALD
VLAKRLRSMHVFILDYDQSPAGCRDALLQLTSGMVQTHVTTPGSIPTICDLARTFAREMGE

>d3adk_ c.37.1.1 (-) Adenylate kinase {Pig (*Sus scrofa*)}
MEEKLKKSKIIFVVGPGSGKGTQCEKIVQKYGYTHLSTGDLLRAEVSSGSARGKMLSEIMEKGQLVP
LETVLDMLRDAMVAKVDTSKGFLLDGYPREVKQGEFERKIGQPTLLLYVDAGPETMTKRLKRG
TSGRVDDNEETIKKRLITYYKATEPVIAFYEKRGIVRKVNNAEGSVDDVFSQVCTHLDLTK

>d1nksa_ c.37.1.1 (A:) Adenylate kinase {Archaeon *Sulfolobus acidocaldarius*}
MKIGIVTGIPGVGKSTVLAKVKEILDNQGINNKIINYGDFMLATALKLGAKDRDEMRLKSVEKQKKL
QIDAAKGIAEEARAGGEGYLFIDTHAVIRTPSGYLPGLPSYVITEINPSVIFLLEADPKIILSRQKRDTR
NRNDYSDESIVLETINFARYAATASAVLAGSTVKVIVNVEGDPSIAANEIIRSMK

>d2ak3a1 c.37.1.1 (A:0-124,A:162-225) Adenylate kinase {Cow (*Bos taurus*), mitochondrial
izozyme-3}
GASARLLRAAIMGAPGSGKGTVSSRITKHFELKHLSSGDLLRDNMLRGTEIGVLAKTFIDQGKLPDD
VMTRLVLHELKNLTQYNWLLDGFPRTPQAEALDRAYQIDTVINLNPFEVIKQRLTXDRPETVVKR
LKAYEAQTEPVLEYRKKGVLETFSGTETNKIWPVHYAFLQTKLPQRSQETSVTP

>d1ak2_1 c.37.1.1 (14-146,177-233) Adenylate kinase {Cow (*Bos taurus*), mitochondrial
izozyme-2}
PKGVRVLLGPPGAGKGTQAPKLAKNFCVCHLATGDMLRAMVASGSELGKKLKATMDAGKLVSD
MVLELIEKNLETPPCKNGFLLDGFPRTPVQAEMLDLMEKRKEKLDVIEFSIPDSSLIRRITGRLIH
XSSDNKALKIRLEAYHTQTTPLVEYYSKRGHSAIDASQTPDVVFASILAASFKATS

>d1aky_1 c.37.1.1 (3-130,169-220) Adenylate kinase {Baker's yeast (*Saccharomyces
cerevisiae*)}
ESIRMVLIGPPGAGKGTQAPNLQERFHAHLATGDMLRSQIAKGTQLGLEAKKIMDQGGVSDDIMV
NMIKDELTTNPACKNGFILDGFPRTPQAEKLDQMLKEQGTPLEKAIELKVDELVARITXNADAL
KKRLAAYHAQTEPIVDFYKKTGIWAGVDASQPATVWADILNKLGN

>d1e4ya1 c.37.1.1 (A:1-121,A:157-214) Adenylate kinase {*Escherichia coli*}
MRIILLGALVAGKGTQAQFIMEKYGIPQISTGDMLRAAVKSGSELGKQAKDIMDAGKLVTDDELVIALVK
ERIAQEDCRNGFLLDGFPRTPQADAMKEAGINVDYVLEFDVPDELIVDRIVXKDDQEETVRKRLVE
YHQMTAPLIGYYSKEAEAGNTKYAKVDGTPVAEVRADLEKILG

>d1zaka1 c.37.1.1 (A:3-127,A:159-222) Adenylate kinase {Maize (*Zea mays*)}
ADPLKVMISGAPASGKGTQCELIKTKYQLAHISAGDLLRAEIAAGSENGKRAKEFMEKGQLVPDEIVV
NMVKERLRQPDAQENGWLLDGYPRYSQAMALETLEIRPDTFILLDVPDELLVERVVXFDDTEEKV
KLRLITYYQNISSLSTYENIIVKVQGDATVDAVFAKIDELLSILEKKNEMVSS

>d1zin_1 c.37.1.1 (1-125,161-217) Adenylate kinase {*Bacillus stearothermophilus*}
MNLVLMGLPGAGKGTQAEKIVAAYGIPHISTGDMFRAAMKEGTPLGLQAKQYMDRGDLVPDEVTIGI
VRERLSKDDCQNGFLLDGFPRTPVAQAEALETMLADIGRKLVDYVIHIDVRQDVLMERLTXADDNEAT
VANRLEVNMMKQMKPLVDFYEQKGYLRNINGEQDMEKVFADIRELLGGLAR

>d1tmka_ c.37.1.1 (A:) Thymidylate kinase {Baker's yeast (*Saccharomyces cerevisiae*)}
GRGKLILIEGLDRTGKTTQCNILYKQLPNCKLLKFPERSTRIGGLINEYLTDDSFQLSDQAIHLLFSAN
RWEIVDKIKKDLLEGKNIVMDRYVYSGVAYSAAKGTNGMDLDWCLQPDVGLLKPDLTLFLSTQDVD
NNAEKSGFGDERYETVKFQEKVKQTFMKLLDKEIRKGDSEITIVDVTNKGIQEVEALIWQIVPVLST
HIDHDKFSFF

>d1e9ea_ c.37.1.1 (A:) Thymidylate kinase {Human (*Homo sapiens*)}
ARRGALIVLEGVDRAGKSTQSRKLVEALCAAGHRAELLRFPERSTEIGKLLSSYLQKKSVDHSHVHL
LFSANRWEQVPLIKEKLSQGVTLVVDRYAFSGVAYTGAKENFSLDWCKQPDVGLPKPDLVFLQLQL
ADAAKRGAFGHERYENGAFQERALRCFHQLMKD'TTLNWKMVDAKSIEAVHEDIRVLSEDAIAATAT

EKPLKELWK

>d4tmka_c.37.1.1 (A:) Thymidylate kinase {*Escherichia coli*}

RSKYIVIEGLEGAGKTTARNVVVETLEQLGIRDMVFTREPGGTQLAEKLRSLLLDIKSVGDEVITDKA
EVLMFYAARVQLVETVIKPALANGTWVIGDRHDLSTQAYQGGGRGIDQHMLATLRDAVLGDFRPDL
TLYLDVTPEVGLKRARARGELDRIEQESFDFNRRARYLELAAQDKSIHTIDATQPLEAVMDAIRTT
VTHWVKEL

>d1g3ua_c.37.1.1 (A:) Thymidylate kinase {*Mycobacterium tuberculosis*}

MLIAIEGVDGAGKRTLVEKLSGAFRAAGRSVATLAFPRYGQSVAAADIAAEALHGEHGLASSVYAMAT
LFALDRAGAVHTIQGLCRGYDVVILDYVASNAAYSAARLHENAAGKAAAWVQRIEFARLGLPKPD
WQVLLAVSAELAGERSRGRAQRDPGRARDNYERDAELQRTGAVYAELAAQGWGGRWLWVGADV
DPGRLAATLA

>d1e6ca_c.37.1.2 (A:) Shikimate kinase {*Erwinia chrysanthemi*}

MTEPIFMVGARGCGMTTVGRELARALGYEFDVTDIFMQHTSGMTVADVAAEGWPGFRRRESEAL
QAVATPNRVVATGGGMVLEQNRQFMRAHGTVVYLFAPAEELALRLQASLQAHQRPTLTGRPIAEE
MEAVLREREALYQDVAHYVVDATQPPAAIVCELMQTMRL

>d1qha_c.37.1.3 (A:) Chloramphenicol phosphotransferase {*Streptomyces venezuelae*}

MTTRMILNNGSSAGKSGIVRCLQSVLPEPWLAFGVDSLIEAMPLKMQSAEGGIEFDADGGVSIGPEF
RALEGAWAEGVAMARAGARIHDDVFLGGAAAQERWRSFVGDLDVWVGVRCDGAVAEGRETARG
DRVAGMAAKQAYVVHEGVEYDVEVDTTHKESIECAWAIAAHVVP

>d1d6ja_c.37.1.4 (A:) Adenosine-5'phosphosulfate kinase (APS kinase) {*Penicillium chrysogenum*}

HASALTRSERTELNRQGLTIWLTGLSASGKSTLAVELEHQLVDRRRVHAYRLDGDNIRFGLNKDLG
FSEADRNIENIRIAEVAKLFAADNSIAITSFISPYRKDRDARQLHEVATPGEETGLPFVEVYVDPVE
VAEQRDPKGLYKKAREGVKEFTGISAPYEAPANPEVHVKNYELPVQDAVKQIIDYLDTKGYLPAKK

>d1g8fa3_c.37.1.15 (A:390-511) ATP sulfurylase C-terminal domain {*Baker's yeast (Saccharomyces cerevisiae)*}

PRPKQGSFIVLGNLSLTVSREQLSIALSTFLQFGGGRYKIFEHNNKTELLSLIQDFIGSGSLIIPDQW
EDDKDSVVGKQNVYLLDTSSSADIQLESADEPISHIVQKVVLFLLEDNGFFVF

>d1i2da3_c.37.1.15 (A:391-573) ATP sulfurylase C-terminal domain {*Fungus (Penicillium chrysogenum)*}

PRATQGFITFLTGYMNSGKDAIARALQVTLNQQGGRSVSLLLGDVTRHELSELGFTREDRHTNIQRI
AFVATELTRAGAAVIAAPIAPYEESRKFARDAVSQAGSFFLVHVATPLEHCEQSDKRGYAAARRGEIK
GFTGVDDPYETPEKADLVVDFSKQSVRSIVHEIILVLESQGFLERQ

>d1aqua_c.37.1.5 (A:) Estrogen sulfotransferase {*Mouse (Mus musculus)*}

EYYEVFGEFRGLMDKRFTKYWEDVEMFLARPDDLVIATYPKSGTTWISEVVYMIYKEGDVEKCKE
DAIFNRIPYLECRNEDLINGIKQLKEKESPRIVKTHLPPKLLPASFWKNCMIYLCRNAKDVAVSYY
YFLMITSYPNPKSFSEFVEKFMQGVQVPYGSWYDHVKAWWEKSKNSRVLFMFYEDMKEDIRREVV
KLIEFLERKPSAELVDRIHQHTSFQEMKNNPSTNYTMMPEEMMNQKVSPFMRKGIIGDWKNHFPE
ALRERFDEHYKQMKDCTVKFRME

>d1efha_c.37.1.5 (A:) Hydroxysteroid sulfotransferase {*Human (Homo sapiens)*}

DFLWFEGIAFPTMGFRSETLRKVRDEFVIRDEDVILTYPKSGTNWLAEILCLMHSKGDWIKVSVPI
WERSPWVESEIGYTALSETESPRLFSSHLPIQLFPKSFSSKAKVIYLMRNPRDVLVSGYFFWKNMKF
IKKPKSWEEYFEWFCQGTVLYGSWFDHIHGWMMPMREEKNFLLSYEELKQDTGRTIEKICQFLGKT
LEPEELNLILKNSSFQSMKENKMSNYSLSDVYVVDKAQLLRKGVSGDWKNHFTVAQAEDFDKLFQ

EKMADLPRKLAAALE

>d1cjma_ c.37.1.5 (A:) Aryl sulfotransferase sult1a3 {Human (Homo sapiens)}

SRPPLEYVKGVPLIKYFAEALGPLQSFQARPDDLINTYPKSGTTWVSQILDMIYQGGDLEKCNRAPI
YVRVPFLEVNDPGEPSGLETLKDTPPPRLIKSHLPLALLPQTLLDQKVKVYVARNPKDVAVSYYHF
HRMEKAHPEPGTWDSFLEKFMAGEVSYGSWYQHVQEWELSRTHPVLYLFYEDMKENPKREIQK
ILEFVGRSLPEETMDFMVQHTSFKEMKKNPMTNYTTVPQELMDHSISPFMRKGMAGDWKTTFTV
AQNERFDADYAEKMAGCSLSFRS

>d1nsta_ c.37.1.5 (A:) Heparan sulfate N-deacetylase/N-sulfotransferase domain {Human (Homo sapiens)}

DPLWQDPCEDKRHKDIWSKEKTCDRFPKLLIIGPQKTGTTALYLFLGMHPDLSSNYPSSSETFEEIQFF
NGHNYHKGIDWYMEFFPIPSNTTSDFYFEKSANYFDSEVAPRRAAALLPKAKVLTILINPADRAYSW
YQHQRHDDPVALKYTFHEVITAGSDASSKLRLQNRCLVPGWYATHIERWLSAYHANQILVLDGKL
LRTEPAKVMMDMVQKFLGVTNTIDYHKTLAFDPKKGFWCQLLEGGKTKCLGKSKGRKYPEMDLSR
AFLKDYRRDHNIELSKLLYKMGQTLPTWLREDLQ

>d1fmja_ c.37.1.5 (A:) Retinol dehydratase {Fall armyworm (Spodoptera frugiperda)}

PFPEYFRELNPEEDKLVKANLGAFTTYVKLGPKGYMVYRYPYLKDAANIYNMPLRPTDVFVASYQRS
GTTMTQELVWLIENDLNFEAAKTYMSLRYIYLDGFMIDPEKQEEYNDILPNPENLDMERYLGLLE
YSSRPGSSLLAAVPPTEKRFVKTHTLPLSLMPPNMLDVTVMVYLARDPRDVAVSSFHARLLYLLNKQ
SNFKDFWEMFHRGLYTLTPYFEHVKEAWAKRHDPNMLFLFYEDYLDLPGCIARIADFLGKKLSEE
QIQRLCEHLNFEKFKNNGAVNMEDYREIGILADGEHFIRKKGKAGCWRDYFDEEMTKQAEKWIKDN
LKDTDLRYPNM

>d1a7j_ c.37.1.6 (-) Phosphoribulokinase {Rhodobacter sphaeroides}

SKKHPIISVTGSSGAGTSTVKHTFDQIFRREGVKAVSIEGDAFHRFRNADMKAELDRRYAAGDATFSH
FSYEANELKELERVFREYGETGQGRTRTYVHDDAEAARTGVAPGNFTDWRDFSDSHLLFYEGLHG
AVVNSEVNIAGLADLKIGVVPVINLEWIQKIHRDRATRGTTEAVTDVILRRMHAYVHCIVPQFSQTD
INFQRVPVVDTSNPFARWIPTADESVVIRFRNPRGIDFPYLTSMIHGSWMSRANSIVVPGNKDLA
MQLILTPLIDRVVRESKV

>d1esma_ c.37.1.6 (A:) Pantothenate kinase PanK {Escherichia coli}

QTLMTPYLQFDRNQWAALRDSVPMTLSEDEIARLKGINEDLSLEEVAEYIPLSRLNLFYISSNLRRQ
AVLEQFLGTNGQRIPYIISIAGSVAVGKSTTARVLQALLSRWPEHRRVELITTDGFLHPNQVLKERGL
MKKKGFPESYDMHRLVKFVSDLKSGVPNVTAPVYSHLIYDVIPDGDKTVVQPDILILEGLNVLQSGM
DYPHDPHHVVFVSDVDFSIYVDAPEDLLQTWYINRFLKFREGAFTDPDSYFHNYAKLTKEEAIKTAM
TLWKEINWLNKQNILPTRERASLILTKSANHAVEEVRLRK

>d1bif_1 c.37.1.7 (37-249) 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, kinase domain {Rat (Rattus norvegicus)}

CPTLIVMVGLPARGKTYISKKLTRYLNFIGVPTREFNVGQYRRDMVKTYKSFEFFLPDNEEGLKIRKQ
CALAALNDVRKFLSEEGGHVAVFDATNTTRERRAMIFNFGEQNGYKTFVSESICVDPEVIAANIVQV
KLGSPDYVNRDSDEATEDFMRRIECYENSYESLDEEQDRDLSYIKIMDVGQSYVVNRVADHIQSRIVY
YLMNIHVTPR

>d1ctqa_ c.37.1.8 (A:) cH-p21 Ras protein {Human (Homo sapiens)}

MTEYKLVVVGAGVGKSAITQLIQNHVFDEYDPTIEDSYRKQVVIDGETCLLDILTADTAGQEEYSAMR
DQYMRTGEGFLCVFAINNTKSFEDIHQYREQIKRVKSDSDVPMVLVGNKCDLAARTVESRQAQDLA
RSYGIPYIETSAKTRQGVEDAFYTLVREIRQH

>d1ds6a_ c.37.1.8 (A:) Rac {Human (Homo sapiens)}

MQAIKCVVVDGAVGKTCLLISYTTNAFPGEYIPTVFDNYSANVMVDSKPVNLGLWDTAGQEDYDR
LRPLSYPQTDVFLICFSLVSPASYENVRKWFPEVRHHCPSTPIILVGTGLDLRDDKDTIEKLKEKKLA
PITYPQGLALAKEIDSVKYLECSALTQRGLKTVFDEAIRAVLCPQP

>d1mh1_ c.37.1.8 (-) Rac {Human (Homo sapiens)}

GSPQAIKCVVVDGAVGKTCLLISYTTNAFPGEYIPTVFDNYSANVMVDGKPVNLGLWDTAGQEDYD
RLRPLSYPQTDVSLICFSLVSPASFENVRKWFPEVRHHCPNTPPIILVGTGLDLRDDKDTIEKLKEKKL
TPITYPQGLAMAKEIGAVKYLECSALTQRGLKTVFDEAIRAVLCPPP

>d1c1ya_ c.37.1.8 (A:) Rap1A {Human (Homo sapiens)}

MREYKLVVLGSGVGGKSALTVQFVQGIFVEKYDPTIEDSYRKQVEVDCQQCMLEILD TAGTEQFTAM
RDLYMKNQGQFALVYSITAQSTFNDLQDLREQILRVKDTEDVPMILVGNKCDLEDERVVGKEQGQNL
ARQWCNCAFLESSAKSKINVNEIFYDLVRQINR

>d1kao_ c.37.1.8 (-) Rap2a {Human (Homo sapiens)}

MREYKVVVLGSGVGGKSALTVQFVTGT FIEKYDPTIEDFYRKEIEVDSSPSVLEILD TAGTEQFASMRD
LYIKNGQGFI LVS LNQQSFQDIKPMRDQIIRVKRYEKVPVILVGNKVDLESEREVSSSEGRALAEW
GCPFMETSAKSKTMVDELFAEIVRQMNYA

>d3raba_ c.37.1.8 (A:) Rab3a {Rat (Rattus norvegicus)}

NFDYMFKILIIGNSSVGKTSFLFRYADDSFTPAFVSTVIGIDFKVKT IYRNDKRIKLQIWD TAGQERYRTI
TTAYYRGAMGFILMYDITNEESFNAVQDWSTQIKTYSWDNAQVLLVGNKCDMEDERVVSSERGRQL
ADHLGFEFFEASAKDNINVKQTFERLVDVICEK

>d1huqa_ c.37.1.8 (A:) Rab5c {Mouse (Mus musculus)}

ICQFKLVLLGESAVGKSSLVLRVFKGQFHEYQESTIGAAFLTQTVCLDDTTVKFEIWD TAGQERYHSLA
PMYYRGAQAAIVVYDITNTDTFARAKNWWKELQRQASPNIVIALAGNKADLASKRAVEFQEAQAYA
DDNSLLFMETSAKTAMNVNEIFMAIAKKL

>d1d5ca_ c.37.1.8 (A:) Rab6 {Malaria parasite (Plasmodium falciparum)}

KYKLVFLGEQAVGKTSIITRFMYDTFDNNYQSTIGIDFLSKTLYLDEGPVRLQLWDTAGQERFRSLIPS
YIRDSAAIVVYDITNRQSFENTTKWIQDILNERGKDVIIALVGNKTDLGDLRKVTYEEGMKAQEQY
NTMFHETSAKAGHNIKVLFKK TASKL

>d1g16a_ c.37.1.8 (A:) Rab-related protein Sec4 {Baker's yeast (Saccharomyces cerevisiae)}

SIMKILLIGDSGVGKSCLLVRFVEDKFNPSFIT TIGIDFKIKTV DINGKKV KLQIWD TAGQERFRTITTA
YYRGAMGIILVYDITDERTFTNIKQWFKTVNEHANDEAQLLLVGNKSDMETRVVTADQGEALAKEL
GIPFISSAKNDDNVNEIFFTLAKLIQEKI

>d1byua_ c.37.1.8 (A:) Ran {Dog (Canis familiaris)}

EPQVQFKLVLVGDGGTGKTT FV KRHLTGEFEK KYVPTLGV E VHPLV FHTNRGPIKFNVWD TAGQE K
FGGLRDGYYIQAQCAIIMFDVTSRVTYKNVPNWHRDLVRVCENIPIVLCGNKVDIKDRKVKAKSIVFH
RKNLQYYDISAKSNYNFEKPFLWLARKLIGDPNLEFVAMPALAPPEVMDPALAAQYEHDLVAQ
TT

>d1i2ma_ c.37.1.8 (A:) Ran {Human (Homo sapiens)}

QVQFKLVLVGDGGTGKTT FV KRHLTGEFEK KYVATLGV E VHPLV FHTNRGPIKFNVWD TAGQE KFG
GLRDGYYIQAQCAIIMFDVTSRVTYKNVPNWHRDLVRVCENIPIVLCGNKVDIKDRKVKAKSIVFHR
KKNLQYYDISAKSNYNFEKPFLWLARKLIGDPNLEFV

>d1tx4b_ c.37.1.8 (B:) RhoA {Human (Homo sapiens)}

AIRKKLVIVGDGACGKTCLLIVNSKDQFPEVYVPTVFENYVADIEVDGAQVELALWDTAGQEDYDRL
RPLSYPD TDVILMCFSIDSPD SLENIPEKWTPEVKHF CPNVPIILVGNKKDLRND EHTRRELAKMKQ
EPVKPEEGRDMANRIGAFGYMECSAKTKDGVREVFEMATRAAL

>d1hura_c.37.1.8 (A:) ADP-ribosylation factor {Human (Homo sapiens), ARF1}
GNIFANLFKGLFGKKEMRILMVGLDAAGKTTILYKLLKGEIVTTIPTIGFNVETVEYKNISFTVWDVG
GQDKIRPLWRHYFQNTQGLIFVVDSDNRERVNEAREELMRMLAEDELRDVLLVFANKQDLPNAM
NAAEITDKLGLHSLRHRNWYIQATCATSGDGLYEGLDWLSNQLRNQK

>d1e0sa_c.37.1.8 (A:) ADP-ribosylation factor {Human (Homo sapiens), ARF6}
GKVLISKIFGNKEMRILMLGLDAAGKTTILYKLLKQSVTTIPTVGFNVETVTKNVKFNVDVGGQ
DKIRPLWRHYTGTQGLIFVVDCAADRDRIDEARQELHRIINDREMRDAILIFANKQDLPDAMKPHE
IQEKLGLTRIRDRNWYVQPSCATSGDGLYEGLTWLTSNYK

>d1fzqa_c.37.1.8 (A:) ADP-ribosylation factor {Mouse (Mus musculus), ARL3}
GLLSILRKLKSPDQEVRIILLGLDNAGKTTLLKQLASEDISHITPTQGFNIKSVQSQGFKLNVDIGG
QRKIRPYWRSYFENTDILYVIDSADRKRFEETGQELTELEEEELKSCVPVLIFANKQDLLTAAPASEIA
EGLNLHTIRDRVWQIQSCSALTGEGVQDGMNWVCKNV

>d1f6ba_c.37.1.8 (A:) SAR1 {Chinese hamster (Cricetulus griseus)}
SSVLQFLGLYKKTGKLVFLGLDNAGKTTLLHMLKDDRLGQHVPTLHPTSEELTIAGMTFTTDFDLGGH
IQARRVWKNYLPAINGIVFLVDCADHERLLESKEELDSLMTDETIANVPILILGNKIDRPEAISEERLR
EMFGLYGQTTGKGSVSLKELNARPLEVFMCSVLKRQGYGEGFRWMAQYID

>d2ngra_c.37.1.8 (A:) CDC42 {Human (Homo sapiens)}
MQTIKCVVVDGAVGKTCLLISYTTNFKPSEYVPTVFDNYAVTMIGGEPYTLGLFDTAGQEDYDRL
RPLSYPQTDVFLVCFVSPSSFENVKEKWVPEITHHCPKTPFLLVGTQIDLRDDPSTIEKLAKNKQK
PITPETAEKLARDLKAVKYVECSALTQKGLKNVFDEAILAALEPPEPKSRRCVLL

>d1ek0a_c.37.1.8 (A:) Ypt51 {Baker's yeast (Saccharomyces cerevisiae)}
VTSIKLVLLGEEAVGKSSIVLRFVSNDFEAENKEPTIGAAFLTQRVTINEHTVKFEIWDTAGQERFASLA
PMYYRNAQAALVVYDVTKPQSFIKARHWVKELHEQASKDIIIALVGNKIDMLQEGGERKVAREEGEK
LAEKGLLFFETSAKTGENVNDVFLGIGEKIPLK

>d1h65a_c.37.1.8 (A:) Chloroplast protein translocon GPase Toc34 {Garden pea (Pisum sativum)}
VREWSGINTFAPATQTKLLELLGNLQEDVNSLTILVMGKGGVGSSTVNSIIGERVVSISPFQSEGPR
PVMVSRSRAGFTLNIIDTPGLIEGGYINDMALNIIKSFLDKTIDVLLYVDRLDAYRVDNLDKLVAKAI
TDSFGKGIWNKAIVALTHAQFSPDGLPYDEFFSKRSEALLQVVRSGASLKKDAQASDIPVLIENSG
RCNKNDSDEKVLPNGIAWIPHLVQTITEVALNKSESIFVDKNLIDKLAAD

>d1azsc2 c.37.1.8 (C:36-66,C:202-393) Transducin (alpha subunit) {Cow (Bos taurus)}
VYRATHRLLLLGAGESGKSTIVKQMRILHVNXVLTSGIFETKFQVDKVNFMFDVGGQRDERRKWI
QCFNDVTAIIFVASSSYNMVIREDNQTNRLQEALNLFKSIWNNRWLRTISVILFLNKQDLLAEKVL
GKSKIEDYFPEFARYTTPEDATPEPGEDPRVTRAKYFIRDEFRLISTASGDGRHYCYPHFTCAVDTENI
RRVFNDCRDIIQRMHLRQYEL

>d1tada2 c.37.1.8 (A:27-56,A:178-342) Transducin (alpha subunit) {Cow (Bos taurus)}
ARTVKLLLLGAGESGKSTIVKQMKIIHQDGTGIIETQFSFKDLNFRMFDVGGQRSERKKWIHCFEGV
TCIIFIAALSAYDMVLVEDDEVNRMHESLHLFNSICNHRYFATTSIVLFLNKKDVFSEKIKKAHLSICF
PDYNGPNTYEDAGNYIKVQFLELNMRRDVKEIYSHMTCATDTQNVKFVFDVAVTDIIIKE

>d1bof_2 c.37.1.8 (10-60,182-354) Transducin (alpha subunit) {Rat (Rattus norvegicus)}
KAAVERSKMIDRNLRDGEKAAREVKLLLLGAGESGKSTIVKQMKIIHEAGXTGIVETHFTFKDLHF
KMFVGGQRSERKKWIHCFEGVTAIIFCVALS DYDLVLAEDEEMNRMHESMKLFDSICNNKWFTDT
SIILFLNKKDLFEKIKKSPLTICYPEYAGSNTYEEAAAYIQCFEDLNKRKDTKEIYTHFTCATDTKN
VQFVFDVAVTDVIIKNNLKDGLF

>d1cipa2 c.37.1.8 (A:32-60,A:182-347) Transducin (alpha subunit) {Rat (Rattus norvegicus)}

REVKLLLLGAGESGKSTIVKQMKIIHEAGXTGIVETHFTFKDLHFKMFDVGGQRSERKKWIHCFEV
TAIFCVALSVDYDLVLAEDEEMNRMHESMKLFDSICNNKWFTDTSIILFLNKKDLFEEKIKKSPLTICY
PEYAGSNTYEEAAAYIQCFEDLNKRKDTKEIYTHFTCATDTKNVQVFDAVTDVVIKNN

>d1fja2 c.37.1.8 (A:28-60,A:182-344) Transducin (alpha subunit) {Rat (Rattus norvegicus)}

RTVKLLLLGAGESGKSTIVKQMKIIHQDGYSELEXETQFSFKDLNFRMFDVGGQRSERKKWIHCFEV
TAIFCVALSVDYDLVLAEDEEMNRMHESMKLFDSICNNKWFTDTSIILFLNKKDLFEEKIKKSPLTICY
PEYAGSNTYEEAGNYIKVQFLELNMRRDVKEIYSHMTCATDTQNVKVFDAVTDIIIKENL

>d1gota2 c.37.1.8 (A:6-60,A:182-343) Transducin (alpha subunit) {Rat (Rattus norvegicus)}

SAEEKHSRELEKCLKEDAEDARTVKLLLLGAGESGKSTIVKQMKIIHQDGYSELEXETQFSFKDLNFR
MFDVGGQRSERKKWIHCFEVTAIFCVALSVDYDLVLAEDEEMNRMHESMKLFDSICNNKWFTDTS
IILFLNKKDLFEEKIKKSPLTICYPEYAGSNTYEEAGNYIKVQFLELNMRRDVKEIYSHMTCATDTQNV
KFVDAVTDIIIKEN

>d1efca3 c.37.1.8 (A:8-204) Elongation factor Tu (EF-Tu), N-terminal (G) domain {Escherichia coli}

TKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGAARAFDQIDNAPEEKARGITINTSHVEYDTPTR
HYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTRHILLGRQVGPYIIVFLNKCDMV
DDEELLELVEMEVRELLSQYDFPGDDTPIVIRGSALKALEGDAEWEAKILELAGFLDSYIPEPER

>d1efm_1 c.37.1.8 (12-190) Elongation factor Tu (EF-Tu), N-terminal (G) domain {Escherichia coli}

VNVGTIGHVDHGKTTLTAAITTVLAKTYGGAARXXXXXXXXXXXXXXXXXGITINTSHVEYDTPTRHYAHV
DCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTRHILLGRQVGPYIIVFLNKCDMVDDEEL
LELVEMEVRELLSQYDFPGDDTPIVIRGSALKALEGDAEWEAKILE

>d1etu_1 c.37.1.8 (5-200) Elongation factor Tu (EF-Tu), N-terminal (G) domain {Escherichia coli}

FERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGAAXXXXXXXXXXXXXXXXXXGITINTSHVEYDTP
TRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTRHILLGRQVGPYIIVFLNKCD
MVDDEELLELVEMEVRELLSQYDFPGDDTPIVIRGSALKALEGDAEWEAKILELAGFLDSYIP

>d1exma3 c.37.1.8 (A:3-212) Elongation factor Tu (EF-Tu), N-terminal (G) domain {Thermus thermophilus}

GEFIRTKPHVNVGTIGHVDHGKTTLTAAITFVTAENPNVEVKDYGDIDKAPEERARGITINTAHVEY
ETAKRHYSHVDCPGHADYIKNMITGAAQMDGAILVVAADGMPMPQTRHILLARQVGPYIIVFMN
KVDMDVDDPELLDLVEMEVRLDLLNQYEFPGDEVPVIRGSALLALEQMHRNPKTRRGENEVVDKIW
ELLDAAIDEYIPT

>d1d2ea3 c.37.1.8 (A:55-250) Elongation factor Tu (EF-Tu), N-terminal (G) domain {Cow (Bos taurus), mitochondrial}

KPHVNVGTIGHVDHGKTTLTAAITKILAEGGAKFKKYEIDNAPEERARGITINAHVEYSTAARHY
AHTDCPGHADYVKNMITGTAPLDGCILVVAANDGMPMPQTRHILLARQIGVEHVVVVYVVKADAVQ
DSEMVELVELEIRELLTEFGYKGEETPIIVGSALCALEQRDPELGLKSVQKLLDAVDTYIPVP

>d1f60a3 c.37.1.8 (A:2-240) Elongation factor eEF-1alpha, N-terminal (G) domain {Baker's yeast (Saccharomyces cerevisiae)}

GKEKSHINVVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAAELGKGSFKYAWVLDKKAERER
GITIDIALWKFETPKYQVTVIDAPGHRDFIKNMITGTSQADCAILIIAGGVGEFEAGISKDGTREHAL

LAFTLGVRQLIVAVNKMDSVKWDESRFQEIVKETS NFIIKKVGYNPKTVPFVPIGWNGDNMIEATT
NAPWYKWEKETKAGVVKGKTLLEAIDAIEQPSRPT
>d1jnya3 c.37.1.8 (A:4-227) Elongation factor eEF-1alpha, N-terminal (G) domain {Archaeon
Sulfolobus solfataricus}
KPHLN LIVIGHVDHGKSTLVGRLLMDRGFIDEKTVKEAEEAAKKGKESKFAFLLDRLKEERERGV
TINLTFMRFETKKYFFTIIDAPGHRDFVKNMITGASQADAAILVVS AKKGEYEAGMSVEGQ TREHIL
AKTMGLDQLIVAVNKMDLTEPPYDEKRYKEIVDQVSKFMRSYGFNTN KVRVFPVVPVAPSGDNITHKS
ENMKWYNGPTLEEYLDQLELPPK
>d1dar_2 c.37.1.8 (1-282) Elongation factor G (EF-G), N-terminal (G) domain {Thermus
thermophilus}
MAVKVEYDLKRLRNIGIAAHIDAGKTTTTTERILYYTGRIHKIGEVHEGAATMDFMEQERERGITITAA
VTTCFWKDHRINIIDTPGHVDFTIEVERSMRVLDGAIVVFDSSQGVPEQSETVWRQA EKYKVPRIAF
ANKMDKTGADLWLVRTMQERLGARPVVMQLPIGREDTFSGIIDVLRMKAYTYGNDLGT DIREIPI
EEYLDQAREYHEKLVEVAADF DENIMLKYLEGEEPT EELVAAIRKGTIDLKITPVFLGSALKNKGVQ
LLLDVVDYLP
>d1g7sa4 c.37.1.8 (A:1-227) Initiation factor IF2/eIF5b, N-terminal (G) domain {Archaeon
Methanobacterium thermoautotrophicum}
MKIRSPIVSLGHVDHGKTTLLDHIRGS AVASREAGGITQHIGATEIPMDVIEGICGDFLKKFSIRETLP
GLFFIDTPGHEAFTTLRKRGGALADLAILVDINEGFKPQTQEALNILRMYRTPFVVAANKIDRIHW
RVHEGRPFMETFSKQDIQVQKLDTKVYELVGKLHEEGFESERFDRVTFASQVSIIPISAITGEGIPE
LLTMLMGLAQYLREQLKIE
>d1egaa1 c.37.1.8 (A:4-182) GTPase Era, N-terminal domain {Escherichia coli}
DKSYCGFIAIVGRPNVGKSTLLNKL LGQKISITSRKAQTTRHRIVGIHTEGAYQAIYVDT PGLHMEEKR
AINRLMNKAASSSIGDVELVIFVVEGTRWTPDDEMVLNKLREGKAPVILAVNKVDNVQEKADLLPH
LQFLASQMNFLDIVPISAETGLNVDTIAAIVRKHLPEATHHFPE
>d1f5na2 c.37.1.8 (A:7-283) Interferon-induced guanylate-binding protein 1 (GBP1),
N-terminal domain {Human (Homo sapiens)}
MTGPMCLIENTNGR LMANPEALKILSAITQPMVVVAIVGLYRTGKSYLMNKL AGKKKGFSLGSTVQS
HTKGIWMWCVPHPKPGHILVLLDTEGLGDVEKGDNQNSWIFALAVLLSSTFVYNSIGTINQQAM
DQLYYVTELT HRIRSKSSPDENENEVEDSAD FVSFFPDFVWTLRDFSLDLEADGQPLTPDEYL TYSLK
LKKGTSQKDETFNLPRLCIRKFFPKKCFVDRPVHRRKLAQLEKLQDEELDPEFVQVADFC SYIFS
NSKTKTLS
>d1jwyb_ c.37.1.8 (B:) Dynammin G domain {Slime mold (Dictyostelium discoideum)}
DQLIPVINKLQDVFN TLGSDPLDLPQIVVVGSSGKSSVLENIVGRDFLPRGSGIVTRRPLILQLTHLP
IADDGSQTQE WGEFLHKPN DMFYDFSEIREEIIRD TDRMTGKNKGISAQPINLKIYSPHVNLTLVDL
PGITKVPVGDQPTDIEQQIRRMVMAYIKKQNAIIVAVTPANTDLANS DALQLAKEVDPEGKRTIGVIT
KLDLMDKGT DAMEVLTGRVIPLTLGFIGVINRSQEDI IAKKSIRESLKSEILYFKNHPIYKSIANRSGTAY
LSKTLNKL LMFHIRDTLPDLKVKVSKMLS
>d1br2a2 c.37.1.9 (A:80-789) Myosin S1, motor domain {Chicken (Gallus gallus), pectoral
muscle}
PPKFSKVEDMAELTCLNEASVLHNL RERYFSGLIYTYSGLFCV VINPYKQLPIYSEKIIDMYKGKKRHE
MPPHIYAIADTAYRSM LQDREDQSILCTGESGAGKTENTKKVIQYLAVVASSHKGKKDTSITQGPSFSY
GELEKQLLQANPILEAFGNAKT VKN DNSSRFGK FIRINFDVTGYIVGANIETYLLEKSR AIRQAKDERT
FHIFYLIAGASEQMRNDL LLEGFNNTFLSN GHVPIPAQQDDEM FQETLEAMTIMGFTEEEQTSIL

RVVSSVLQLGNIVFKKERNTDQASMPDNTAAQKVCHLMGINVTDFTRSILTPIKVGDRDVVQKAQTK
EQADFAIEALAKAKFERLFRWILTRVNKALDKTKRQGASFLGILDIAGFEIFEINSFEQLCINYTNEKL
QQLFNHTMFILEQEEYQREGIEWNFIDFGLDLQPCIELIERPTNPPGVLALLDEECWFPKATDTSFV
EKLIQEQGNHAKFQKSKQLKDKTEFCILHYAGKVTYNASAWLTKNMDPLNDNVTSLLNQSSDKFVA
DLWKDVDRIVGLDQMAKMTESLPSASKTKKGMFRTVVGQLYKEQLTKLMTTLRNTNPNFVRCIIPN
HEKRAGKLD AHLVLEQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILANAIPKGFMDGKQACILM
IKALELDPNLYRIGQSKIFFRTGVL AHLEEERD

>d2mysa2 c.37.1.9 (A:4-33,A:80-843) Myosin S1, motor domain {Chicken (*Gallus gallus*),
pectoral muscle}

DAEMAAFGEAAPYLKSEKERIEAQNKPFDXMNPPKYDKIEDMAMMTHLHEPAVLYNLKERYAAW
MIYTYSGLCVTVNPKVWLPVYNPKVVLAYRGKKRQEAPPHIFSISDNAYQFMLTDRENQSILITGES
GAGKTVNTRVIQYFATIAASGEKKKEEQSGKMQGTLEDQIISANPLLEAFGNAKTVRNDNSSRFGK
FIRIHFGATGKLASADIETYLLKSRVTFQLPAERSYHIFYQIMSNNKPELIDMLLITNPNYDYHYVSEG
EITVPSIDDQEELMATDS AIDILGFSADKTAIYKLTGAVMHYGNLKFQKQREEQAEPDGTVEADKA
AYLMGLNSAELLKALCYPRVGVGNEAVTKGETVSEVHNSVGALAKAVYEKMF LWMVIRINQQLDTK
QPRQYFIGVLDIAGFEIFDFNSFEQLCINF TNEKLQFFNHMFVLEQEEYKKEGIEWEFIDFGMDL
AACIELIEKPMGIFSILEEECMFPKATDTSFKNKLYDEHLGKSNNFQKPKPAKGKAEAHFSLVHYAGT
VDYNISGWLEKNKDPLNETVIGLYQSSVKTLALLFATYGGEAEGGGGKGGKGGKSSSFQTVSALFRE
NLNKL MANLRSTHPHFVRCIIPNETKTPGAMEHELVLHQLRCNGVLEGIRICRKGFP SRVLYADFKQ
RYRVLNASAIPEGQFMDSKKASEKLLGGGDVDHTQYAFGHTKVFFKAGLLG LLEEMRDDKLA EIITA
TQARCRGFLMRVEYRAMVERRESIFCIQYNVRSFMNVKHWPWMK LFFKIKPLLK

>d1b7ta4 c.37.1.9 (A:5-28,A:77-835) Myosin S1, motor domain {Bay scallop (*Aequipecten
irradians*)}

FSDPDFQYLAVDRKKLMKEQTAAFXMNPPKFEKLEDMANM TYLNEASVLYNLSRYTSGLIYTYSG
LFCIAVNPYRRLPIYTDSVIAKYRGKRKTEIPPHLFSVADNAYQNMVTDRENQSCLITGESGAGKTEN
TKKVIMYLAKVACAVKKKDEEASDKKEGSLEDQIIQANPVLEAYGNAK TTRNNNSSRFGKFIRIHFGP
TGKIAGADIETYLLKSRVTYQQAERNYHIFYQICSNAIPELNDVMLVTPDSGLYSFINQGCLTVDNI
DDVEEFKLCDEAFDILGFTKEEKQSMFKCTASILHMGEMKFKQRPREEQAESDGTAEAEKVAFLCGI
NAGDLLKALLPKVKVGTGEMVTKGQNMNQVNSVGALAKSLYDRMFNWLVRVKNKTLDTKAKRN
YYIGVLDIAGFEIFDFNSFEQLCINYTNERLQFFNHMFVLEQEEYKKEGIAWEFIDFGMDLQMCID
LIEKPMGILSILEEECMFPKADDSFQDKLYQNHMGKNRMFTKPGKPTRPNQGP AHFELHHYAGNV
PYSITGWLEKNKDPINENVVALLGASKEPLVAELFKAPEEPAGGGKGGKGGKSSAFQTISAVHRESLNK
LMKNLYSTHPHFVRCIIPNELKQPLVDAELVLHQLCNGVLEGIRICRKGFP SRRLIYSEFKQRY SILAP
NAIPQGFVDGKTVSEKILAGLQMDPAEYRLGTTKVFFKAGVLGNLEEMRDERLSKIISM FQAHIRGYL
IRKAYKKLQDQRIGLSVIQRNIRKWLVLRNWQWWKLYSKVKP

>d1lvk_2 c.37.1.9 (2-33,80-759) Myosin S1, motor domain {Slime mold (*Dictyostelium
discoideum*)}

NPIHDRTSDYHKYLKVKQGDSDLFKLTVSDKRXRNPIKFDGVEDMSELSYLNPAVFHNLRVRYNQ
DLIYTYSGFLVAVNPFKRIPIYTQEMVDIFKGRRRNEVAPHIFAISDVAYRSMLDDRQNQSLLITGESG
AGKTENTKKVIQYLASVAGRNQANGSGVLEQQILQANPILEAFGNAK TTRNNNSSRFGKFIEIQFNN
AGFISGASISYLLKSRVVFQSTSERNYHIFYQLLAGATAEKKALHLAGPESFN YLNQSGCVDIKGV
SDEDEFKITRQAMDIVGFSQEEQMSIFKIIAGILHLGNIKFEKGAGEGAVLKDKTALNAASTVFGVNPS
VLEKALMEPRILAGRDLVAQHLNVEKSSSRDALVKALYGRFLWLVLKINNVLCSERKAYFIGVLDIS
GFEIFKVNSFEQLCINYTNEKLQFFNHMFVLEQEEYKKEGIAWEFIDFGMDLQMCID

GILALLDEQSVFPNATDNTLITKLHSHFSKKNAYEPRFSKTEFGVTHYAGQVMYEIQDWLEKNK
DPLQQDLELCFKDSSDNVVTKLFNDPNIASRAKKGANFLTVAAYKEQLASLMATLETTNPHFVRCI
IPNNKQLPAKLEDKVVDQLRCNGVLEGRITRKGFNRIIYADFVKRYDLAPNVPRDAEDSQKATD
AVLKHLNIDPEQFRFGITKIFFRAGQLARIEEARE

>d1mnd_2 c.37.1.9 (2-33,80-690) Myosin S1, motor domain {Slime mold (Dictyostelium discoideum)}

NPIHDRTSDYHKYLKVKQGSDSLFKLTVSDKRXRNPIKFDGVEDMSELSYLNPAVFNHNLRVRYNQ
DLIYTYSGFLVAVNPFKRIPIYTQEMVDIFKGRRRNEVAPHIFAISDVAYRSMDDRRQNQSLLITGESG
AGKTENTKKVIQYLASVAGRNQANGSGVLEQQILQANPILEAFGNAKTTRNNNSSRFGKFIQFNN
AGFISGASIQSYLLEKSRVVFQSETERNYHIFYQLLAGATAEKKALHLAGPESFNLYNQSGCVDIKGV
SDEDEFKITRQAMDIVGFSQEEQMSIFKIIAGILHLGNIKFEKGAGGAVLKDKTALNAASTVFGVNPS
VLEKALMEPRILAGRDLVAQHLNVEKSSSRDALVKALYGRLFLWLKINNVLCSERAAAYFIGVLDIS
GFEIFKVNSEQLCINYTNEKLQQFFNHMFKVEQEEYLKEKINWTFIDFGLDSQATIDLIDGRQPPG
ILALLDEQSVFPNATDNTLITKLHSHFSKKNAYEPRFSKTEFGVTHYAGQVMYEIQDWLEKNKD
PLQQDLELCFKDSSDNVVTKLFNDPNIASRAKKGANFITVAAYKEQLASLMATLETTNPHFVRCIIP
NNKQLPAKLEDKVVDQLRCNGVLEGRITRK

>d1bg2_ c.37.1.9 (-) Kinesin {Human (Homo sapiens)}

DLAECNIKVMCRFRPLNESEVNRGDKYIAKFQGEDTVVIASKPYAFDRVFSSTSQEQQVYNDCAKKI
VKDVLEGYNGTIFAYGQTSSGKTHMTEGKLHDPEGMGIIPRIVQDIFNYIYSMDENLEFHIKVSYFEIY
LDKIRDLLDVSKTNLSVHEDKNRVPYVKGCTERFVCSPEVMDTIDEGKSNRHVAVTNMNEHSSRS
HSIFLINVKQENTQTEQKLSGKLYLVDLAGSEKVSKTGAEGAVLDEAKNINKSLSALGNVISALAEGST
YVPYRDSKMTRILQDSLGGNCRTTIVICCSPPSYNESETKSTLLFGQRAKTI

>g2kin.1 c.37.1.9 (A,B:) Kinesin {Rat (Rattus norvegicus)}

ADPAECSIKVMCRFRPLNEAEILRGDKFIPKFKGEETVVIGQGKPYVFDRLVPPNTTQEQQVYNACAK
QIVKDVLEGYNGTIFAYGQTSSGKTHMTEGKLHDPQLMGIIPRIAHDFDHIYSMDENLEFHIKVSYF
EIYLDKIRDLLDVSKTNLAVHEDKNRVPYVKGCTERFVSSPEEVMVIDEGKANRHVAVTNMNEHS
SRSHSIFLINIKQENVETEKKLSGKLYLVDLAGSEKVSXAKNINKSLSALGNVISALAEGTKTHVPYRDS
KMTRILQDSLGNCRRTTIVICCSPPSVFNEAETKSTLMFGQRAKTIKNTVSVNLELTAEEWKKKYEKE
KE

>d1i6ia_ c.37.1.9 (A:) Kinesin {Mouse (Mus musculus), kif1a}

GASVKVAVRVRPFNSREMSRDSKCIQMSGSTTTIVNPKQPKETPKSFSFDYSYWSHTSPEDINYASQ
KQVYRDIGEEMLQHAPEGYNVCIFAYGQTGAGKSYTMMGKQEKDQGGIIPQLCEDLFSRINDTTNDN
MSYSVEVSYMEIYCERVRDLLNPKNKGNLRVREHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKAR
TVAATNMNETSSRSHAVFNIFTQKRHDAETNITTEKVSISLVDLAGSERADSTGAKGTRLKEGANI
NKSLTTLGKVISALAEEMDSGPNKKNKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINY
DETLSTLRYADRAKQIRNTVSVNHHHHH

>d1ii6a_ c.37.1.9 (A:) Kinesin {Human (Homo sapiens), mitotic kinesin eg5}

GKNIQVVVRCRPFNLAERKASAHSIVECDPVRKEVSVRTGGLADKSSRKYTFDMVFGASTKQIDVY
RSVVCPILEDEVIMGYNCTIFAYGQTGTGKTFTMEGERSPNEEYTWEEEDPLAGIIPRTLHQIFEKLTDN
GTEFSVKVLSLEIYNEELFDLLNPSDVDSERLQMFDDPRNKRGVVIKGLEEITVHNKDEVYQILEKGA
AKRTTAATLMNAYSSRSVSVTIHMKETTIDGEEVLKIGKLNLDLAGSENIGRSGAVDKRAREAG
NINQSLTLGRVITALVERTPHVPYRESKLRILQDSLGGRTSIIATISPASLNLEETLSTLEYAHRAK
NILNKPEV

>d1goja_ c.37.1.9 (A:) Kinesin {Neurospora crassa}

SSSANSIKVVARFRPQNRVEIESGGQPIVTFQGPDTCTVDSKEAQGSFTFDRVDFMCKQSDIFDFSIK
PTVDDILNGYNGTVFAYGQTGAGKSYTMMGTSIDDPDGRGVIPRIVEQIFTSILSSAANIEYTVRVSYM
EIYMERIRDLLAPQNDNLPVHEEKNRGVYVKGLLEIYVSSVQEVYEMRRGGNARAVAATNMNQES
SRSHSIFVITITQKNVETGSAKSGQLFLVDLAGSEKVGKTGASGQTL EEAKKINKSLSALGMVINALTD
GKSSHVPYRDSKLTRILQESLGGNSRTT LIINCSPSSYNDAETLSTLRFGMRAKSIKNAKVN AELSPA
ELKQMLAKAKTQ

>d2ncda_ c.37.1.9 (A:) Kinesin motor Ncd (non-claret disjunctional) {Fruit fly (*Drosophila melanogaster*)}

LRQRTEELLRCNEQAAAELETCKEQLFQSNMERKELHNTVMDLRGNIRVFCRIRPPLESEENRMCC
TWTYHDESTVELQSIDAQAKSKMGQQIFSFQVVFHPLSSQSDIFEMVSPLIQSALDGYNICIFAYGQTG
SGKTYTMDGVPESVGVIPRTVDLLFDSIRGYRNLGWEYEIKATFLEIYNEVLYDLLSNEQKDMEIRM
AKNNKNDIYVSNITEETVLDPNHLRHLMHTAKMNRATASTAGNERSRSHAVTKLELIGRHA EKQE
ISVGSINLVDLAGSESPKTSTRMTETKNINRSLSELTNVILALLQKQDHIPYRNSKLTHLLMPSLGGNS
KTLMFINVSPFQDCFQESVKSLRFAASVNSC

>d1f9va_ c.37.1.9 (A:) Kinesin motor Ncd (non-claret disjunctional) {Baker's yeast (*Saccharomyces cerevisiae*), Kar}

GNIRVYCRIRPALKNLENSDTSLINVNEFDDNSGVQSMEVTKIQNTAQVHEFKFDKIFDQDQDTNVDV
FKEVGQLVQSSLDGYNVCIFAYGQTGSGKFTMLNPGDGIIPSTISHIFNWINKLKTGWWDYKVNCEF
IEIYNENIVDLLRSDNNNKEDTSIGLKHEIRHDQETKTTTTITNVTSCLESEEMVEIILKKANKLRSTA
STASNEHSSASHSIFIIHLSGNAKTGAHSYGLNLVLDLAGSERINVSQVVGDRLETQNKLSLCLG
DVIHALGQPDSTKRHIPFRNSKLTLYLLQYSLTGDSKTLMFVNISPSSSHINETLNSLRFASKVNSTRLV

>d1byi_ c.37.1.10 (-) Dethiobiotin synthetase {*Escherichia coli*}

SKRYFVTGTDTEVGKTVASCALLQAAKAAGYRTAGYKPVASGSEKTPEGLRNSDALALQRNSSLQLD
YATVNPYTFAEPTSPHIISAQEGRPISLVM SAGLRALEQQADWVLVEGAGGWFTPLSDTFTFADWV
TQEQLPVILVVGKLGKINHAMLTAQVIQHAGLTLAGWVANDVTPPGKRHA EYMTTLTRMIPAPLLG
EIPWLAENPEN AATGKYINLALL

>d1qf5a_ c.37.1.10 (A:) Adenylosuccinate synthetase, PurA {*Escherichia coli*}

GNNVVVLGTQWGDEGKGVLDLLTERAKYVVRYQGGHNAGHTLVINGEKTVLHHLIPSGILRENVT SII
GNGVVLSPALMKEMKELEDRGIPVRERLLLSEACPLILDYHVALDNAREKARGAKAIGTTGRGIGPA
YEDKVARGLRVGDLDFKETFAEKLEKMEYHNFQLVNYKAEAVDYQKVLDDTMAVADILTS MVV
DVSDLLDQARQRGDFVMFEQAQGTLLDIDHGTYPYVTSSNTTAGGVATGSGLGP RYVDYVLGILKAY
STRVGAGPFPTLFDLDETFEFLCKQGNFEGATTGRRRRRTGWLDTVAVRRRAVQLNSLSGFCLTKLDVLD
GLKEVKLCVAYRMPDGREVTTTTPLAADDWKGVEPIYETMPGWSESTFGVKDRSGLPQAALNYIKRI
EELTGVPIDIISTGPDRTE TMILRDPFDA

>d1dj2a_ c.37.1.10 (A:) Adenylosuccinate synthetase, PurA {Mouse-ear cress (*Arabidopsis thaliana*)}

IGSLSQVSGVLGCQWGDEGKGLVDILAQHFDIVARCQGGANAGHTIYNSEGKFKFALHLVPSGILNED
TTCVINGV VVHLPGLFKEIDGLESNGV SCKGRILVSDRAHLLDFDFHQEVDGLRESELA KSFIGTTKR
GIGPAYSSK VIRNGIRVGD LRHMDTLPQKLDLLS DAAARFQGFKYTPEMLREEVEAYKRYADRLEP
YITDTVHFINDSISQKKKVLVEGGQATMLDIDFGTYPFVTSSSPSAGGICTGLGIAPSVVGD LIGVVKAY
TTRVSGPFPTENLGTGGDLLRLAGQEFGTTTGRPRRCGWLDIVALKFSCQINGFASLNLT KLDVLS
LNEIQLGVAYKRS DGTVPKSFPGDLRLLEELHVEYEVLPGWKSDISSVRNYS DLPKAAQYVERIEEL
VGVPIHYIGIPGRDALIYK

>d1dj3a_ c.37.1.10 (A:) Adenylosuccinate synthetase, PurA {Bread wheat (*Triticum*

aestivum)}}}

ADRVSSLSNVSGVLGSQWGDEGKGLVDLAPRFDIVARCQGGANAGHTIYNSEGKKFALHLVPSGIL
HEGTLCVVGNGAVIHVPGFFGEIDGLQSNVSCDGRILVSDRAHLLFDLHQTVDGLREAELANSFIGT
TKRIGGPCYSSKVTRNGLRVCDLRHMDTFGDKLDVLFEDAAARFEGFKYSKGMGLKEEVERYKKFAE
RLEPFIADTVHVLNESIRQKKKILVEGGQATMLDIDFGTYPFVTSSSPSAGGICTGLGIAPRVIGDLIGV
VKAYTTRVSGSPFPTELLGEEGDVLRKAGMEFGTTTGRPRRCGWLDIVALKYCCDINGFSSLNLTKL
DVL SGLPEIKLGVSYNQMDGEKLSFPGLDLEQVQVNYEVLPGWDS DISSVRSYSELQAARRYV
ERIEELAGVPVHYIGVGPGRDALIYK

>d1j4ba_ c.37.1.10 (A:) Adenylosuccinate synthetase, PurA {Mouse (Mus musculus)}

AAATGSRVTVVLGAQWDEGKGVVLDLATDADIVSRCQGGNAGHTVVVDGKEYDFHLLPSGIIN
TKAVSFIGNGVVIHLPLGFEEAEKNEKGLKDWKRLIISDRAHLVDFDHQAVDGLQEVQRQAQEGK
NIGTTKKGIGPTYSSKAARTGLRICDLLSDFDEFSARFKNLAHQHSMFPTLEIDVEGQLKRLKGF
RIRPMVRDGVYFMYEALHGPPKVLVEGANAAALLDIDFGTYPFVTSSNCTVGGVCTGLGIPPQ
NIGD VYGVV KAYTTRVIGAFPTQINEIGDLLQNRGHEWGVTTGRKRRCGWLDLMILRYAHMVNGFTAL
ALTCLDILDVLEIKVGISYKLNKRIPIYFPANQEILQKVEVEYETLPGWKADTTGARKWEDLPPQA
QSYVRFVENHMGVAVKVVGVGKSRESMIQLF

>d1eg7a_ c.37.1.10 (A:) Formyltetrahydrofolate synthetase {Moorella thermoacetica}

DIEIAQAAMKPMELARGLGIQEDEVELYGYKAKISLDVYRRLKDKPDGKLILVTAITPTPAGEGK
TTTTSVGLTDALARLGKRVMLCLREPSLGPSPFGIKGGAAGGGYAQVVPMEDINLHFTGDIHAVTYAHN
LLAAMVDNHLQQGNVLNIDPRTITWRRVIDLNERALRNIVIGLGGKANGVPRETFDISVASEVMAC
LCLASDLMDLKERFSRKVVGYTYDGKPVTAGDLEAQGSMALLMKDAIKPNLVQTLNTPAFIHGGPF
ANIAHGCNSIATKTALKLADYVVTEAGFGADLGAEKFYDVKCRYAGFKPDATVIVATVRALKMHGG
VPKSDLATENLEALREGFANLEKHIEINIGKFGVPAVVAINAFPTDTEAELNLLYELCAKAGAEVALSW
AKGGEGGLELARKVLQTLERSPSNFHVLYNLDLSIKDKIAKIAIEIYGADGVNYTAEADKAIQRYESLG
YGNLPVMAKTQYSFSDDMTKLGRPRNFTITVREVRLSAGGRLIVPITGAIMTMPGLPKRPAACNIDI
DADGVITG

>d1fp6a_ c.37.1.10 (A:) Nitrogenase iron protein {Azotobacter vinelandii}

AMRQCAIYGKGGIGKSTTTQNLVAALAEMGKKVMIVGCDPKADSTRLLHLSKAQNTIMEMAAEAGT
VEDLELEDVLKAGYGGVKCVESGGPEPGVGCAGRGVITAINFLEEEGAYEDDLDFVYFDVLDVCGG
FAMPIRENKAQEIIYVCSGEMMAMYAANNISKGIVKYANSGSVRLGGLICNSRNTDREDELIALANK
LGTQMIHFVPRDNVQRAEIRRMTVIEYDPKAKQADEYRALARKVVDNKLIPNPITMDELEELL
MEFGIMEVEDESIVGKTAEEV

>d1cp2a_ c.37.1.10 (A:) Nitrogenase iron protein {Clostridium pasteurianum}

MRQVAIYGKGGIGKSTTTQNLTSGLHAMGKTIMVVGCDPKADSTRLLLGLLAQKSVLDTLREEGEDV
ELDSILKEGYGGIRCVESSGGPEPGVGCAGRGIITSINMLEQLGAYTDDLDFYFDVLDVCGGFAMPI
REGKAQEIIYVCSGEMMALYAANNISKGIQKYAKSGGVRLLGGIICNSRKVANNEYELLDFAKELGSQLI
HFVPRSPMVTKAEINKQTVIEYDPTCEQAEYRELARKVDANELFVIPKPMPTQERLEEILMQYG

>d1hyqa_ c.37.1.10 (A:) Cell division regulator MinD {Archaeon Archaeoglobus fulgidus}

VRTITVASGKGGTGKTTITANLGVLAQLGHDVTIVDADITMANLELILGMEGLPVTLQNVLAGEARI
DEAIYVPGGVKVVPAVGSLEGLRKANPEKLEDVLTQIMESTDILLDAPAGLERSAVIAIAAAQELLL
VVNPEISSITDGLKTKIVAERLGTKVLGVVNRITTLGIEMAKNEIEAILEAKVIGLIPEDPEVRRAAAY
GKPVVLRSPNSPAARAIVELANYIA

>d1g3qa_ c.37.1.10 (A:) Cell division regulator MinD {Archaeon Pyrococcus furiosus}

MGRHISIVSGKGGTGKTTVTANLSVALGDRGRKVLAVDGLTMANLSVLGVDDPDVTLHDVLAGEA

NVEDAIYMTQFDNVYVLPGAVDWEHV LKADPRKLPEVIKSLKDKFDFILIDCPAGLQLDAMSAMLS
GEEALLVTNPEISCLTDTMKVGIVLKKAGLAILGFVLNRYGRSDRDIPPEAAEDVMEVPLLAVIPEDPA
IREGTLEGIPAVKYKPEKGAQAFV KLAEEIEKLA

>d1iona_ c.37.1.10 (A:) Cell division regulator MinD {Archaeon Pyrococcus horikoshii}
MTRIISIVSGKGGTGT TTVTANLSVALGEMGRKVLAVDGLTMANLSLVLGVDDVNITLHDVLAGDA
KLEDAIYMTQFENVYILPGA VDWEHVIKADPRKLPEVIKSLKDKYDFILIDCPAGLQLRAMSAMLSGE
EAILVTNPEISCLTDTMKVGMVLKKAGLAILGFILNRYGRSERDIPPEAAQDVM DVPLLAVIPEDPVIR
EGTLEGIPAVKYKPEKGAQAFIKLAEV DKLAKIKAKI

>d1jpna2 c.37.1.10 (A:89-296) GTPase domain of the signal sequence recognition protein
Ffh {Thermus aquaticus}
EARLPVLKDRNLWFLVGLQGSGKTTTAAKLALYKGGKRRPLLVAADTQRPAAREQLRLLGEKVGVP
VLEVMDGESPE SIRRVEEKARLEARDLILVDTAGRLQIDEPLMGELARLKEVLGPDEVLLVDAMT
GQEALSVARAFDEKVGVTGLVLT KLDGDARGGALSARHVTGKPIYFAGVSEKPEGLEPFYPERLAGR
ILMGMD

>d1j8mf2 c.37.1.10 (F:87-297) GTPase domain of the signal sequence recognition protein
Ffh {Archaeon Acidianus ambivalens}
DKEPKVIPDKIPYVIMLVGVQGTGKTTTAGKLAYFYKKGFKVGLVGADVYRPAALEQLQQLGQQIGV
PVYGEPEKDVVGI AKRGVEKFLSEKMEIIIVDTAGRHYGEEAALLEEMKNIYEAIKPDEVTLVIDAS
IGQKAYDLASKFNQASKIGTIIITKMDGTAKGGALS AVAATGATIKFIGTG EKIDELEVFNPRRFVARL
HHHH

>d1fts_2 c.37.1.10 (285-495) GTPase domain of the signal recognition particle receptor FtsY
{Escherichia coli}
PLNVEGKAPFVILMVG VNGVGKTTTIGKLARQFEQQGKSVMLAAGDTFRAAAVEQLQVWGQRNNI
PVIAQHTGADSASVIFDAIQAAKARNIDVLIADTAGRLQNKSHLMEELKKIVRVMKKLDVEAPHEVM
LTIDASTGQNAVSQAKLFHEAVGLTGITLTKLDGTAKGGVIFSVADQFGIPIRYIGVGERIEDLRPFKAD
DFIEALFAR

>d1ihua1 c.37.1.10 (A:1-296) Arsenite-translocating ATPase ArsA {Escherichia coli}
MQFLQNIPPYLFFTGKGGV GKTSISCATAIRLAEQGKRVLVSTDPASN VGQVFSQTIGNTIQAIASVPG
LSALEIDPQAAAQYRARI VDPKIGVLPDDVVSINEQLSGACTTEIAAFDEFTGLLTDASLLTRFDHII
FDTAPTGH TIRLLQLPGAWSSFIDSNPEGASCLGPMAGLEKQREQYAYAVEALSDPKRTRLVVARLQ
KSTLQEVARTHLELA AIGLKNQYLVINGVLPKTEAANDTLAAAIWEREQEALANLPADLAGLPTDTL
FLQPVMVGV SALSRLSTQP

>d1ihua2 c.37.1.10 (A:308-586) Arsenite-translocating ATPase ArsA {Escherichia coli}
QRPDIPSLSALVDDIARNEHGLIMLMGKGGV GKT TMAAAIAVRLADMGFVHLT TSDPAAHLSMTL
NGSLNNLQVSRIDPHEETERYRQH VLETGK KELDEAGKRLLEEDLRSPCTEEIAV FQAFSRVIREAGK
RFVVM DTA PTGHTLLLL DATGAYHREIAKKMGEKGHFTTPMMLLQDPERTKVLLVTL PETTPVLEA
ANLQADLERAGIHPWGW IINNSLSIADTRSPLL RMRAQQELPQIESVKRQH ASRVALVPVLASEPTGI
DKLKQLAGHHH

>d2reb_1 c.37.1.11 (3-268) RecA protein, ATPase-domain {Escherichia coli}
DENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGRIVEIYGPESG
KTTLT LQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPDTGEQALEICDALARSGAVD
VIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNP
ETTTGGNALKFYASVRLDIRRIGAVKEGENVVGSETRVKVVKNKIAAPFKQAEFQILYGEGI

>d1g19a1 c.37.1.11 (A:1-269) RecA protein, ATPase-domain {Mycobacterium tuberculosis}

MTQTPDREKALELAVAQIEKSYGKGSVMRLGDEARQPISVIPTGSIALDVALGIGGLPRGRVIEIYGPES
SGKTTVALHAVANAQAAGGVAAFIDAHEHALDPDYAKKLGVDTDSSLVSQPDTGEQALEIADMLIRSG
ALDIVVIDSVAALVPRAELEGEEMGDSHVGLQARLMSQALRKMTGALNNSGTTAIFINQLRDKIGVMF
GSPETTTGGKALKFYASVRMDVRRVETLKDGTNAVGNRTRVKVVKNKCLAPFKQAEFDILYGGKI
>d1cr1a_ c.37.1.11 (A:) Gene 4 protein (g4p, DNA primase), helicase domain {Bacteriophage
T7}

MRERIREHLSSEESVGLLFSGCTGINDKTLGARGGEVIMVTSGSGMGKSTFVRQQALQWGTAMGKK
VGLAMLEESVEETAEDLIGLHNRVRLRQSDSLKREIENGKFDQWFDELFGNDTFHLYDSFAEAETD
RLAKLAYMRSGLGCDVIILDHISIVVSASGESDERKMIDNLMTKLKGFAKSTGVVLVICHKLPDK
GKAHEEGRPVISITDLRSGALRQLSDTIALERNQQGDMPNLVLRILKCRFTGDTGIAGYMEYNKET
GWLEPSSY

>d1g8ya_ c.37.1.11 (A:) Hexameric replicative helicase repA {Escherichia coli, plasmid
rsf1010}

ATHKPINILEFAAAAPPPLDYVLPNMVAGTVGALVSPGGAGKSMLALQLAAQIAGGPDLLVEGELPTG
PVIYLP AEDPPTAIHRLHALGAHLSAEERQAVADGLLIQPLIGSLPNIMAPEWFDGLKRAAEGRRL
MVLDTLRRFHIEENASGPMAQVIGRMEIAAADTGCIVFLHHASKGAAMMGAGDQQQASRGSSVL
VDNIRWQSYLSSMTSAEAEWGVDDDDQRRFFVRFVSKANYGAPFADRWFRRHDGGVLPKA

>d1e9ra_ c.37.1.11 (A:) Bacterial conjugative coupling protein TrwB {Escherichia coli}

VGQGEFGGAPFKRFLRGRTRIVSGGKLKRMTRKAKQVTVAGVPMRDAEPRHLLVNGATGTGKSVL
LRELAYTGLLRGDRMVIVDPNGDMLSKFGRDKDIILNPYDQRTKGWSFFNEIRNDYDWQRYALS
PRGKTDEAEWASYGRLLLRETAKKLALIGTPSMRELFHWTTIATFDDLGRFLEGTLAESLFAGSNE
ASKALTSARFVLSDKLPEHVTMPDGFDSIRSWLEDPNGGNLFIWREDMGPALRPLISAWVDVVCT
SILSLPEEPKRRLLWLFIDELASLEKLASLADALTKGRKAGLRVVAGLQSTSQLDDVYGVKEAQT
FRSLVVLGGSRTPKTNEDMSLSLGEHEVERDRYSKNTGKHHSTGRALERVRERVMMPAEIANLPDL
TAYVGFAGNRPIAKVPLEIKQFANRQPAFVEGT

>d1e79a3 c.37.1.11 (A:95-379) Central domain of alpha and beta subunits of F1 ATP
synthase {Cow (Bos taurus)}

VDVPVGEELLGRVVDALGNAIDGKGPISKARRRVLKAPGIIPRISVREPMQTGKAVDSLVPPIGRGQ
RELIIGDRQTGKTSIAIDTIINQKRFNDGTDEKKKLYCIYVAIGQKRSTVAQLVKRLTDADAMKYTIVVS
ATASDAAPLQYLAPYSGCSMGEYFRDNGKHALIYDDLSKQAVAYRQMSLLLRPPGREAYPGDVLYL
HSRLLERAAMNDAFGGSLTALPVIETQAGDVSAYIPTNVISITDGGQIFLETIFYKIRPAINVGLSV
SRVGSAAQ

>d1e79d3 c.37.1.11 (D:82-357) Central domain of alpha and beta subunits of F1 ATP
synthase {Cow (Bos taurus)}

IRIPVGPETLGRIMNVIGEPIDERGPIKTKQFAAIHAEAPEFVEMSVEQEILVTGIKVVDLLAPYAKGGK
IGLFGGAGVGKTVLIMELINNVAKAHGGYSVFAGVGERTREGNDLYHEMIESGVINLKDATSKVALVY
GQMNEPPGARARVALTGLTVAEYFRDQEGQDVLFDINIFRFTQAGSEVSALLGRIPSAVGYQPTLAT
DMGMTMERITTTKKSITSVQAIYVPADDLTDPAATTF AHLDATTVLSRAIAELGIYPAVDPLDSTSR
I

>d1skyb3 c.37.1.11 (B:96-371) Central domain of alpha and beta subunits of F1 ATP
synthase {Bacillus sp., strain ps3}

EVPVGETLIGRVVNPLGQPVDGLGPVETTETRPIESRAPGVMDRRSVHEPLQTGKIDALVPIGRGQ
RELIIGDRQTGKTSVAIDTIINQKDNMICIYVAIGQKESTVATVVETLAKHGAPDYTIVVTASASQPAP
LLFLAPYAGVAMGEYFIMMGKHLVVIDDLSKQAAAYRQLSLLLRPPGREAYPGDIFYLHSRLLERA

AKLSDAKGGGSLTALPFVETQAGDISAYIPTNVISITDGGQIFLQSDLFFSGVRPAINAGLSVSRVGGAAQ
>d1skye3 c.37.1.11 (E:83-356) Central domain of alpha and beta subunits of F1 ATP
synthase {Bacillus sp., strain ps3}

ISVPVQGVTLGRVFNVLGEPIDLEGDIPADARRDPIHRPAPKFEELATEVEILETGIKVVDLLAPYIKGG
KIGLFGGAGVGKTVLIQELIHNIAQEHGGISVFAGVGERTREGNDLYHEMKDSGVISKTAMVFGQMN
EPPGARMRVALTGLTMAEYFRDEQGDGLLFIDNIFRFTQAGSEVSALLGRMPAIGYQPTLATEMG
QLQERITSTAKGSITSIQAIYVPADDYTD PAPATTFSHLDATTNLERKLAEMGIYPAVDPLVSTSRALA
P

>d1fx0a3 c.37.1.11 (A:97-372) Central domain of alpha and beta subunits of F1 ATP
synthase {Spinach (Spinacia oleracea), chloroplast}

QIPVSEAYLGRVINALAKPIDGRGEITASESRLIESPAPGIMSRRSVYEPLQTGLIAIDAMIPVGRGQREL
IIGDRQTGKTAVATDTILNQQGQNVICVYVAIGQKASSVAQVVTNFQERGAMEYTTIVVAETADSPATLQ
YLAPYTGAAAEYFMYRERHTLIYDDLKQAQAYRQMSLLLRRPPGREAYPGDVFLHSRLLERAA
KLSSLLGEGSMTALPIVETQAGDVSAYIPTNVISITDGGQIFLSADLFNAGIRPAINVIGISVSRVGSAAQ

>d1fx0b3 c.37.1.11 (B:98-377) Central domain of alpha and beta subunits of F1 ATP
synthase {Spinach (Spinacia oleracea), chloroplast}

LSVPVGGPTLGRIFNVLGEPVDNLRPVDTRTTSPIHRSAPAFQDLTKLSIFETGIKVVNLLAPYRRGG
KIGLFGGAGVGKTVLIMELINNIKAHGGVSVFVGGEREGRNDLYMEMKESGVINEQNIAESKVAL
VYGQMNPPGARMRVGLTALTMAEYFRDVNEQDVLLFIDNIFRFVQAGSEVSALLGRMPSAVGYQPT
LSTEMGSLQERITSTKEGSITSIQAVYVPADDLTD PAPATTF AHLDATTVLSRGLAAKGIYPAVDPLDS
TSTMLQP

>d1cbua_ c.37.1.11 (A:) Adenosylcobinamide kinase/adenosylcobinamide phosphate
guanylyltransferase CobU {Salmonella typhimurium}

MILVTGGARSGKSRHAEALIGDAPQVLYIATSQILDDEMAARIQHKKDGRPAHWRTAECWRHLDTLI
TADLAPDDAILLECITTMVTNLLFALGGENDPEQWDYAAMERAIDDEIQILIAACQRCPAKVVLVTN
EVMGIVPENRLARHFRDIAGRNVNQLAAADEVVLVSGIGVKIK

>d1g5ta_ c.37.1.11 (A:) ATP:corrinoid adenosyltransferase CobA {Salmonella typhimurium}
ERGIIVFTGNGKGTAAFGTAARAVGHGKNVGVVQFIKGTWPNGERNLLEPHGVEFQVMATGFT
WETQNREADTAACMAVWQH GKRLADPLLDMMVVLDELTYMVAYDYLPLEEVISALNARPGHQTV
IITGRGCHRDILDLADTVSELRPVKHA

>d1g64b_ c.37.1.11 (B:) ATP:corrinoid adenosyltransferase CobA {Salmonella typhimurium}
QQRQKVKDRVDARVAQAQEERGIIVFTGNGKGTAAFGTAARAVGHGKNVGVVQFIKGTWPNG
ERNLLEPHGVEFQVMATGFTWETQNREADTAACMAVWQH GKRLADPLLDMMVVLDELTYMVAY
DYLPLEEVISALNARPGHQTVIITGRGCHRDILDLADTVSELRPVKHAFDAGVKAQMGIDY

>d1b0ua_ c.37.1.12 (A:) ATP-binding subunit of the histidine permease {Salmonella
typhimurium}

NKLHVIDLHKRYGGHEVLKGVSLQARAGDVISIIGSSGSGKSTFLRCINFLEKPSGAIIVNGQNINLVR
DKDGQLKVADKNQLRLLRRLTMVFQHFNLWSHMTVLENVMEAPIQVLGLSKHDARERALKYLAK
VGIDERAQKYPVHLSGGQQQRVSIARALAMEPDVLLFDEPTSALDPELVGEVLRIMQQLAEEGKT
MVVVTHEMGFARHVSSHVIFLHQKIEEEDPEQVFGNPQSPRLQQFLKGSLLKLEH

>d1g6ha_ c.37.1.12 (A:) MJ1267 {Archaeon Methanococcus jannaschii}

TMEILRTENIVKYFGEFKALDGVSVSNKGDVTLIIGPNGSGKSTLINVITGFLKADEGRVYFENKIDIT
NKEPAELYHYGIVRTFQTPQPLKEMTVLENLLIGEICPGESPLNSLFYKKWIPKEEEMVEKAFKILEF
LKLSHLYDRKAGELSGGQMKLVEIGRALMTNPKMIVMDEPIAGVAPGLAHDIFNHVLELKAAGITFLI

IEHRLDIVLNYIDHLYVMFNGQIIAEGRGEIEIKNVLSDPKVVEIYIGE
>d1f3oa_ c.37.1.12 (A:) MJ0796 {Archaeon Methanococcus jannaschii}
MIKLNVTKTYKMGEEIYALKNVNLNIKEGEFVSIMGPSGSKSTMLNIIGCLDKPTEGEVYIDNIKT
NDLDDDELTKIRRDKIGFVFQQFNLIPLLTALENVLPLIFKYRGAMSGEERRKRALECLKMAELEER
FANHKNQLSGGQQQRVAIARALANNPPIILADEPTGALDSKTGEKIMQLLKKLNEEDGKTVVVVV
HDINVARFGERIYLLKDGEVEREEKLRGF
>d1jj7a_ c.37.1.12 (A:) Peptide transporter Tap1, C-terminal ABC domain {Human (Homo sapiens)}
GLLTPLHLEGLVQFDVFSFAYPNRPDVLVLQGLTFTLRPGEVTALVGPNGSGKSTVAALLQONLYQPTG
GQLLLDGKPLPQYEHRYLHRQVAAVGQEPQVFGSRSLQENIAYGLTQKPTMEEITAAAVKSGAHSFISG
LPQGYDTEVDEAGSQLSGGQRQAVALARALIRKPCVLILDDATSALDANSQLQVEQLLYESPERYSRS
VLLITQHLSLVEQADHILFLEGGAIREGGTHQQLMEKKGCYWAMVQA
>d1g2912 c.37.1.12 (1:1-240) Maltose transport protein MalK, N-terminal domain {Archaeon Thermococcus litoralis}
MAGVRLVDVWVKVFEVTAVREMSLEVKDGEFMILLGPSGCGKTTTLRMIAGLEEPSRGQIYIGDKLV
ADPEKGIFVPPKDRDIAMVVFQSYALYPHMTVYDNIAFPLKLRKVPRQEIDQRVREVAELLGTELLNR
KPRELSSGQRQVALGRAIVRKPQVFLMDEPLSNLDAKLVRMRAELKKLQRQLGVTTIYVTHDQV
EAMTMGDRIAVMNRGVLQQVQVSPDEVYDKPANTFVAGFI
>g1f2t.1 c.37.1.12 (A,B:) Rad50 {Archaeon Pyrococcus furiosus}
MKLERVTVKNFRSHSDTVVEFKEGINLIIGQNGSGKSSLLDAILVGLYWPLRIKDIKKDEFKVGARD
TYIDLIFEKDGTKYRITRRFLKGYSSGEIHAMKRLVGNEWKHVTEPSSKAISAFMEKLIPYNIFLNAIY
IRQQIDAILESXAREAALSIGELASEIFAETFEGKYSEVVRAEENKVRLFVWEGKERPLTFLSGG
ERIALGLAFRLAMSLYLAGEISLLILDEPTYLDEERRRKLITIMERYLKKIPQVILVSHDEELKDAADH
VIRISLENGSSKVEVVS
>g1ii8.1 c.37.1.12 (A,B:) Rad50 {Archaeon Pyrococcus furiosus}
MKLERVTVKNFRSHSDTVVEFKEGINLIIGQNGSGKSSLLDAILVGLYWPLRIKDIKKDEFKVGARD
TYIDLIFEKDGTKYRITRRFLKGYSSGEIHAMKRLVGNEWKHVTEPSSKAISAFMEKLIPYNIFLNAIY
IRQQIDAILESDEAREKVVREVLNLDKFETAYKLSLKTINNRIKEYRDILARTEXRERVKKEIKD
LEKAKDFTEELIEKVKKYKALAREAALSIGELASEIFAETFEGKYSEVVRAEENKVRLFVWEGK
ERPLTFLSGGERIALGLAFRLAMSLYLAGEISLLILDEPTYLDEERRRKLITIMERYLKKIPQVILVSH
DEELKDAADHVIRISLENGSSKVEVVS
>d1e69a_ c.37.1.12 (A:) Smc head domain {Thermotoga maritima}
MRLKKLYLKGFKSFGPRLIGFSDRVTAIVGPNNGSGKSNIIDAIKWVVFGEQSKKELRASEKFDMIFAGS
ENLPPAGSAYVELVFEENGEITVARELKRTGENTYYLNGSPVRLKDIRDRFAGTGLGVDFYSIVGQG
QIDRIVNASPEELRLESSKHPTSLVPRGSYQRVNESFNRFISLLFFGGEGRLNIVSEAKSILDAGFEISIR
KPGRRDQKLSLLSGGEKALVGLALLFALMEIKPSPFYVLEVDSPDDYNAERFKRLLKENSHTQFI
VITHNKIVMEAADLLHGVTMVNGVSAIVPVEV
>d1qhla_ c.37.1.12 (A:) Cell division protein MukB {Escherichia coli}
RGKFRSLTLINWNGFFARTFDLDELVTTLSSGNGAGKSTTMAAFVTALIPDLTLLHFRNTTEAGATS
GSRDKGLHGKLGKAGVCYSMLDTINSRHRQVVVGVRLQVQVAGRDRKVDIKPFAIQGLPMSVQPTQLVT
ETLNERQARVLPNELKDKLEAMEGVQFKQFNSITDYHSLMFDLGIARRLRSASDRSKFYRLIEASL
YGGISSAITRSLRDYLLPEN
>d1ewqa2 c.37.1.12 (A:542-765) DNA repair protein MutS, the C-terminal domain {Thermus aquaticus}

YVPRPFGDRLQIRAGRHPVVERRTEFVPNDLEMAHELVLITGPNMAGKSTFLRQTALIALLAQVGSF
VPAEEAHLPLFDGIYTRIGASDDLGGKSTFMVEMEEVALILKEATENSLVLLDEVGRGTSSLDGVAIA
TAVAEALHERRAYTLFATHYFELTALGLPRLKNLHVAAREEAGGLVIFYHQVLPGPASKSYGVEVAAM
AGLPKEVVARARALLQAMAAR

>d1e3ma2 c.37.1.12 (A:567-800) DNA repair protein MutS, the C-terminal domain
{*Escherichia coli*}

YTCPTFIDKPGIRITEGRHPVVEQVLNEPFIANPLNLSPPRRMLIITGPNMGGKSTYMRQTALIALMA
YIGSYVPAQKVEIGPIDRIFTRVGAADDLASGRSTFMVEMTETANILHNATEYSVLMDIEGRGTSTY
DGLSLAWACAENLANKIKALTLFATHYFELTQLPEKMEGVANVHLDALHGDITAFMHSVQDGAAS
KSYGLAVAALAGVPKEVIKRRARQKLRELESI

>d1pjr_1 c.37.1.13 (1-318) DEXX box DNA helicase {*Bacillus stearothermophilus*, PcrA}

MNFLSEQLLAHLNKEQQEAVRTTEGPLLIMAGAGSGKTRVLTHRIAYLMAEKHVAPWNILAITFTN
KAAREMRERVQSLGAAEDVWISTFHSMCVRILRRDIDRIGINRNFSLDPTDQLSVMKTILKEKNI
DPKKFEPRTILGTISAAKNELLPPEQFAKRASTYYEKVSDVYQEYQQRLLRNHSLDFDDLIMTTIQL
FDRVPDLVHYYQYKFQYIHIDEYQDTNRAQYTLVKKLAERFQNICAVGDADQSIYRWRGADIQNILSF
ERDYPNAKVILLEQNYRSTKRILQAANEVIEHNVNRKPKRIWTENPEG

>d1pjr_2 c.37.1.13 (319-651) DEXX box DNA helicase {*Bacillus stearothermophilus*, PcrA}

KPILYEAMNEADEAQFVAGRIEAVERGERRYRDFAVLYRTNAQSRVMEEMLLKANIPYQIVGGLK
FYDRKEIKDILAYLRVIANPDDDLSSLRIINVPKRGIGASTIDKLVRYAADHELSEALGELEMIGLGA
KAAGALAAFRSQLEQWTQLQEYVSVTELVVEVLDSKGYREMLKAERTIEAQSRLNLDLFLSVTKHF
ENVSDDKSLIAFLTDLALISDLDELDTGTEQAAEGDAVMLMTLHAAKGLEFPVFLIGMEEGIFPHNR
SLEDDDEMEEERLAYVGITRAEEELVLTSAQMRTLFGNIQMDPPSRFLNEIPAHLETASR

>g1qhh.1 c.37.1.13 (A;B;C;D) DEXX box DNA helicase {*Bacillus stearothermophilus*, PcrA}

MNFLSEQLLAHLNKEQQEAVRTTEGPLLIMAGAGSGKTRVLTHRIAYLMAEKHVAPWNILAITFTN
KAAREMRERVQSLGAAEDVWISTFHSMCVRILRRDIDRIGINRNFSLDPTDQLSVMKTILKEKNI
DPKKFEPRTILGTISAAKNELLPPEQFAKRXYYEKVSDVYQEYQQRLLRNHSLDFDDLIMTTIQLFD
RVPDLVHYYQYKFQYIHIDEYQDTNRAQYTLVKKLAERFQNICAVGDADQSIYRWRGADIQNILSF
ERDYPNAKVILLEQNYRSTKRILQAANEVIEHNVNRKPKRIWTENPEGKPILYEAMNEADEAQFVAGR
IREAVERGERRYRDFAVLYRTNAQSRVMEEMLLKANIPYQIVGGLKFYDRKEIKDILAYLRVIANPDD
DLSSLRIINVPKRGIGASTIDXLFEALGELEMIGLGAAGALAAFRSQLEQWTQLQEYVSVTELVVEE
LDKSGYREMLKAERTIEAQSRLNLDLFLSVTKHFENVSDDKSLIAFLTDLALISXGDAVMLMTLHA
AKGLEFPVFLIGMEEGIFPHNRSLEDDDEMEEERLAYVGITRAEEELVLTSAQMRTLFGNIQMDP
PSRFLNEIPAHLETASR

>d1uaaa1 c.37.1.13 (A:2-307) DEXX box DNA helicase {*Escherichia coli*, RepD}

RLNPGQQQAVEFVTGPCLVLGAGSGKTRVITNKIAHLIRGCGYQARHIAAVTFTNKAAREMKERVG
QTLGRKEARGLMISTFHTLGLDIKREYAALGMKANFSLFDDTDQLALLKELTEGLIEDDKVLLQQLI
STISNWKNDLKTPSQAAASAIGERDRIFAHCYGLYDAHLKACNVLDFDDLILLPTLLLQANEVVRKR
WQNKIRYLLVDEYQDTNTSQYELVKLLVGSRRARFTVVGDDDDQSIYSWRGARPQNLVLLSQDFPALKV
IKLEQNYRSSGRILKAANILIANPHVFEKRLFSELG

>d1uaaa2 c.37.1.13 (A:308-640) DEXX box DNA helicase {*Escherichia coli*, RepD}

YGAELKVL SANNEHEAERTV GELIAH HFVNKTQYKDYAILYRGNHQSRVFEKFLMQNRIPYKISGG
TSFFSRPEIKDLLAYLRVLTNPDDDSAFLRIVNTPKREIGPATLKKLGEWAMTRNKSMTASFDMGL
SQTLSSGRGYEALTRFTHWLAEIQRLAEREPIAAVRDLIHGMDYESWLYETSPSPKAAEMRMKNVNQ
LFSWMTLEGLSELDEPMTLTQVVTRFTLRDMMERGESEEEELDQVQLMTLHASKGLEFPYVYMV

GMEEGFLPHQSSIDEDNIDEERRLAYVGITRAQKELTFTLCKERRQYGELVRPEPSRFLELQPDDLI
W

>d1hv8a1 c.37.1.13 (A:3-210) Putative DEAD box RNA helicase {Archaeon Methanococcus
jannaschii}

VEYMNFNELNLSNINLNAIRNKGFEKPTDIQMKVIPLFLNDEYNIVAQARTGSGKTASFAIPLIELVNE
NNGIEAIIPTRELAIQVADEIESLKGKLNKIAKIYGGKAIYPQIKALKNANIVVGTGPRILDHINRGT
LNLKNVKYFILDEADEMLNMGFIKDVKILNACNKDKRILLFSATMPREILNLAKKYMGDYSFIKAKI

>d1hv8a2 c.37.1.13 (A:211-365) Putative DEAD box RNA helicase {Archaeon Methanococcus
jannaschii}

NANIEQSYVEVNENERFEALCRLLNKEFYGLVFCKTKRDTKELASMLRDIGFKAGAIHGDLSQSQR
EKVIRLFKQKKIRILIATDVMSRGIDVNDLNCVINYHLPQNPESYMHRIGRTGRAGKKGKAISIINRRE
YKKLRYIERAMKLIKIKLK

>d1gm5a3 c.37.1.13 (A:286-549) RecG helicase domain {Thermotoga maritima}

ETLPERILEKRKLLGVKDAYYGMHFPKTFYHLEKARERLAYEELFVLQLAFQKIRKEREKHGGIPKKI
EGKLAEEFIKSLPFKLTNAQKRAHQEIRNDMISEKPMNRLQGDVGSKTVVAQLAILDNYEAGFQT
AFMVPPTSILAIQHYRRTVESFSKFNHVALLIGATTPSEKEKIKSGLRNGQIDVVIGTHALIQEDVHFK
NLGLVIIDEQHRFGVKQREALMNKGMVDTLMSATPIPRSMALAFYGDLDVTVIDEMPP

>d1gm5a4 c.37.1.13 (A:550-755) RecG helicase domain {Thermotoga maritima}

GRKEVQTMLVPMDRVNEVYEFVVRQEVMRGGQAFIVYPLIEESDKLVKSAVEMYEYLSKEVFPEFK
LGLMHGRLSQEEKDRVMLEFAEGRYDILVSTTVIEVGIDVPRANVMVIENPERFGLAQLHQLRGRVG
RGGQEAYCFLVVDVGEEMERLRFFTLNTDGFKIAEYDLKTRGPGEFFGVKQHGLSGFKVADLYRD
LKLEEW

>d1fuka_ c.37.1.13 (A:) Initiation factor 4a {Baker's yeast (Saccharomyces cerevisiae)}

IKQFYVNVEEEYKYECLTDLYDSISVTQAVIFCNTRRKVEELTKLRNDKFTVSAIYSDLPQQRDTI
MKEFRSGSSRILISTDLLARGIDVQVSLVINYLDPANKENYIHRIGRGGFRGKGVAINFVTNEDVGA
MRELEKFYSTQIEELPSDIATLLN

>d1qdea_ c.37.1.13 (A:) Initiation factor 4a {Baker's yeast (Saccharomyces cerevisiae)}

IQTNYDKVVYKFDDMELDENLLRGVFGYGFEEPSAIQQRAIMPIIEGHDVLAQAQSGTGKTGTFISAA
LQRIDTSVKAPQALMLAPTRELALQIQKVMALAFHMDIKVHACIGGTSFVEDAEGLRDAQIVVGTG
GRVFDNIQRRRFRTDKIKMFILDEADEMLSSGFKEQIYQIFTLPPPTQVLLSATMPNDVLEVTTKF
MRNPVRILV

>d1c4oa1 c.37.1.13 (A:2-409) Nucleotide excision repair enzyme UvrB {Thermus
thermophilus}

TFRYRGPSPKGDQPKAIALVEALRDGERFVTLGATGTGKTVTMAKVIEALGRPALVLPNKILAAQ
LAAEFRELPENAVEYFISYYDYQPEAYVPGKDLIEKDASINPEIERLRHSTTRSLLTRRDVIVVASV
SAIYGLGDPREYRARNLVVERGKPYPREVLLERLLELGYQRNDIDLSPGRFRAKGEVLEIFPAYETEP
RVELFGDEVERISQVHPVTGERLRELPGFVLPATHYLSPEGLEEILKEIEKELWERYVFEERGEVLY
AQRLKERTLYDLEMLRVMGTCPGVENYARYFTGKAPGEPYTLDDYFPEDFLVFLDESHVTVPQLQG
MYRGDYARKKTLVDYGFRLPSALDNRPLRFEEFLERSQVVFVSATPGPFELAHSGRVVEQIIRP

>d1c4oa2 c.37.1.13 (A:410-583) Nucleotide excision repair enzyme UvrB {Thermus
thermophilus}

TGLLDPLVRVKPTENQILDLMEGIRERAARGERTLVTVLTVRMAEELTSFLVEHGIRARYLHHELD
KRQALIRDLRLGHYDCLVGINLLREGLDIPEVSLVAILDADKEGFLRSERSLIQTIGRAARNARGEVWL
YADRVSEAMQRAIIEETNRRRALQEAYNLEHGITPETV

>d1d9xa1 c.37.1.13 (A:2-414) Nucleotide excision repair enzyme UvrB {Bacillus caldotenax}
EGRFQLVAPYEPQGDQPQAIKLVLDGLRRGVKHQTLGATGTGKTFTISNVIAQVNKPTLVIAHNKTL
AGQLYSELKEFFPHNAVEYFVSYDYQPEAYVPQTDYIEKDAKINDEIDKLRHSATSALFERRDVII
VASVSCIYGLGSPEEYRELVVSLRVGMEIERNALLRRLVDIQYDRNDIDFRGTFRVRGDVVEIFPASRD
EHCIRVEFFGDEIERIRAEVDALTKVVGEREHVAIFPASHFVTREEKMRLAIQNIQELEERLAEELRA
QGKLLAQRLERTRYDLEMMREMGFCSGIENYSRHLALRPPGSTPYTLDDYFPDDFLIIVDESHVT
LPQLRGMVNGDRARKQVLVDHGFRLPSALDNRPLTFEEFEQKINQIIVSATPGPYELEHSPGVVEQI
IRP

>d1d9xa2 c.37.1.13 (A:415-595) Nucleotide excision repair enzyme UvrB {Bacillus caldotenax}

TGLLDPTIDVRPTKGQIDDLIGEIRERVERNERTLVTTTLTKKMAEDLTDYLKEAGIKVAYLHSEIKTLE
RIEIRDLRLGKYDVLVGINLLREGLDIPEVSLVAILDADKEGFLRSERSLIQTIGRAARNANGHVIMYA
DTITKSMEIAIQETKRRRAIQEEYNRKHGIVPRTVKKEIRDV

>d1jr3a2 c.37.1.13 (A:3-242) gamma subunit of DNA polymerase III, N-domain {Escherichia coli}

YQVLARKWRPQTFADVVGQEHVLTALANGLSLGRIHHAYLFSGTRGVGKTSIARLLAKGLNCETGITA
TPCGVCDNCREIEQGRFVDLIEIDAASRTKVEDTRDLLDNVQYAPARGRFKVYLIDEVHMLSRHSFN
ALLKTLEEPPEHVKFLLATTPQKLPVTILSRCLQFHLKALDVEQIRHQLEHILNEEHIAHEPRALQL
LARAAEGSLRDALSLTDQAIASGDGQVSTQAVSAMLG

>d1a5t_2 c.37.1.13 (1-207) delta prime subunit of DNA polymerase III, N-domain {Escherichia coli}

MRWYPWLRPDEFKLVASYQAGRGHHALLIQALPGMGDDALIYALSRYLCCQPQGHKSCGHCRGCQ
LMQAGTHPDYITLAPEKGNKNTLGVDAREVTEKLNHARLGGAKVVWVTDAAALLTDAANALLKT
LEEPPAETWFFLATREPERLLATLRSRCLHYLAPPPEQYAVTWLSREVTMSQDALLAALRLSAGSP
GAALALFQG

>d1jq1b_ c.37.1.13 (B:) delta subunit of DNA polymerase III, N-domain {Escherichia coli}

MIRLYPEQLRAQLNEGLRAAYLLLGNLPLLLQESQDAVRQVAAAQGFEEHHTFSIDPNTDWNAINFSL
CQAMSLFASRQTLNLLLPENGPNAINEQLLTLTGLLHDDLLLVIRGNKLSKAQENAAWFTALANRS
VQVTCQ

>d1jr3d2 c.37.1.13 (D:1-211) delta subunit of DNA polymerase III, N-domain {Escherichia coli}

MIRLYPEQLRAQLNEGLRAAYLLLGNLPLLLQESQDAVRQVAAAQGFEEHHTFSIDPNTDWNAINFSL
CQAMSLFASRQTLNLLLPENGPNAINEQLLTLTGLLHDDLLLVIRGNKLSKAQENAAWFTALANRS
VQVTCQTPEQAQLPRWVAARAKQLNLELDDAANQVLCYCYEGNLLALAQUALERLSLLWPDGKLTLP
RVEQAVNDAAH

>d1iqpa2 c.37.1.13 (A:2-232) Replication factor C {Archaeon Pyrococcus furiosus}

SEEIREVKVLEKPPWVEKYRPQLDDIVGQEHIVKRLKHVYKTSMPHLLFAGPPGVGKTAAALALAR
ELFGENWRHNFLELNASDERGINVIREKVKEFARTKPIGGASFKIIFLDEADALTQDAQALRRTME
MFSSNVRFILSCNYSSKIIEPIQSRCAIFRFRPLRDEDIAKRLRYIAENEGLELTEEGLQAILYIAEGDMR
RAINILQAAAALDKKITDENVMVAS

>d1hqca2 c.37.1.13 (A:5-242) Holliday junction helicase RuvB {Thermus thermophilus}

ALRPKTLDEYIGQERLKQKLRVYLEAAKARKEPLEHLLFGPPGLGKTTLAHVIAHELGVNLRVTSG
PAIEKPGDLAAILANSLEEGDILFIDEIHRLSRQAEHLYPAMEDFVMDIVIGQGAARTIRLELPRFTL
IGATTRPGLITAPLLSRFGIVEHLEYTPEELAQGVMRDARLLGVRITEEAALEIGRRSRGTMRAKRL

FRRVRDFAQVAGEEVITRERALEALAALGLDE

>d1in4a2 c.37.1.13 (A:17-254) Holliday junction helicase RuvB {*Thermotoga maritima*}
QFLRPKSLDEFIQENVKKLSLALAAKMRGEVLDHVLLAGPPGLGKTTLAHIIASELQTNIHVTSG
PVLVKQGDMAAILTSLERGDVLFIDEIHRLNKAVEELLYSAIEDFQIDIMIGKGPSAKSIRIDIQPFTLVG
ATTRSGLSSPLRSRFGIILELDFYTVKELKEIKRAASLMDVEIEDAAAEMIAKRSRGTPIAIRLTKR
VRDMLTVVKADRINTDIVLKTMEVLNIDD

>d1fna2 c.37.1.13 (A:1-276) CDC6, N-domain {Archaeon *Pyrobaculum aerophilum*}
AIVVDDSVFSPSYVPKRLPHREQQLQQLDILLGNWLRNPGHHYPRATLLGRPGTGKTVTLRKLWEL
YKDKTTARFVYINGFIYRNFTAIIGEIARSLNIPFRRGLSRDEFLLALLVEHLRERDLYMFLVLDLAFN
LAPDILSTFIRLGQEADKLGAFRIALVIVGHNDVAVLNNLDPSTRGIMGKYVIRFSPYTKDQIFDILLDR
AKAGLAEGSYSEDILQMIADITGAQTPLDTNRGDARLAIDILYRSAYAAQQNGRKHIAPEDVRKSSKE
VLFQ

>d1d2na_ c.37.1.13 (A:) Hexamerization domain of N-ethylmaleimide-sensitive fusion (NSF)
protein {Chinese hamster (*Cricetulus griseus*)}
EDYASYIMNGIHKWGDVTRVLDDGELLVQQTKNSDRTPLVSVLLEGPPHSGKTALAAKIAEESNFPF
IKICSPDKMIGFSETAKCQAMKKIFDDAYKSQLSCVVDDIERLLDYVPIGPRFSNLVLQALLVLLKKA
PPQGRKLLIIGTTSRKDVLQEMEMLNAFSTTIHVPNIAATGEQLLEALELLGNFKDKERTTIAQQVKGK
KVWIGIKKLLMLIEMSLQMDPEYRVRKFLALLREEGASPLD

>d1e32a2 c.37.1.13 (A:201-458) Membrane fusion atpase p97, D1 domain {Mouse (*Mus musculus*)}
VGYDDVGGCRKQLAQIKEMVELPLRHPALFKAIGVKPPRGILLYGPPGTGKTLIARAVANETGAFFFLI
NGPEIMSKLAGESESNLKAFEEAEKNAPAIIFIDELDAIAPKREKTHGEVERRIVSQLLTLMDGLKQ
RAHVIVMAATNRPNISIDPALRRFGRFDREVDIGIPDATGRLEILQIHTKNMKLADDVDLEQVANETH
GHVGADLAALCSEAAALQAIKKMDLIDLEDETIDAEMNSLAVTMDDFRWALSQ

>d1g6oa_ c.37.1.13 (A:) Hexameric traffic ATPase, HP0525 {*Helicobacter pylori*}
LSAEDKKFLEVERALKEAALNPLRHATEELFGDFLKMENITEICYNGNKVVWVLKNNGEWQPFQV
RDRKAFSLSRMLMHFARCCASFKKKTIDNYENPILSSNLANGERVQIVLSPVTVNDETISISIRIPSKTTY
PHSFFEEQGFYNLLDNKEQAISAIKDGAIGKNVIVCGGTGSGKTTYIKSIMEFIPKEERIISIEDTEEIV
FKHHKNYTLFFGGNITSADCLKSCLMRPDRILGELRSSEAYDFYNVLCSGHKGTTLTLHAGSSEE
AFIRLANMSSNSAARNIKFESLIEGFKDLIDMIVHINHKKQCDEFYIK

>d1ht1e_ c.37.1.13 (E:) HslU {*Escherichia coli*}
HSEMPREIVSELDKHIIGQDNAKRVAIALRNRWRRMQLNEELRHEVTPKNILMIGPTGVGKTEIAR
RRLAKLANAPFIKVEATKFTEVGYVGKEVDSIIRDLTDAAVKMVRVQAIEKNRYRAEELAEERILDVL
IPPAKNNWGQTEQQQEPSAARQAFRKKLREGQLDDKEIEIDLAAAPMGVEIMAPPGMEEMTSQLQ
SMFQNLGGQKQKARKLKIKDAMKLLIEEEAAKLVNPEELKQDAIDAVEQHGVIFIDEIDKICKRGESS
GPDVSREGVQRDLLPLVEGCTVSTKHGMVKT DHILFIASGAFQIAKPSDLIPELQGRPIRVELQALTT
SDFERILTEPNASITVQYKALMATEGVNIEFTDSGIKRIEAAWQVNESTENIGARRLHTVLERLMEE
ISYDASDLSGNITIDADYVSKHLDALVADEDLSRFIL

>d1g41a_ c.37.1.13 (A:) HslU {*Haemophilus influenzae*}
SEMPREIVSELDQHIIGQADAKRAVAIALRNRWRRMQLQEPLRHEVTPKNILMIGPTGVGKTEIAR
RLAKLANAPFIKVEATKFTEVGYVGKEVDSIIRDLTDSAMKLVQRQEIAKNRARAEDVAEERILDALL
PPAKNQWGEVENHDSHSSTRQAFRKKLREGQLDDKEIEIDVSAGVSMGVEIMAPPGMEEMTNQLQ
SLFQNLGSDKTKRKMKIKDALKALIDDEAAKLNPEELKQKAIIDAVEQNGVIFIDEIDKICKKGEYSG
ADVSRREGVQRDLLPLVEGSTVSTKHGMVKT DHILFIASGAFQVARPSDLIPELQGRPIRVELTALSAA

DFERILTEPHASLTEQYKALMATEGVNIAFTTDAVKKIAEAAFRVNEKTENIGARRLHTVMERLMDK
ISFSASDMNGQTVNIDAAYVADALGEVVENEDLSRFIL

>d1g8pa_ c.37.1.13 (A:) ATPase subunit of magnesium chelatase, Bchl {Rhodobacter
capsulatus}

RPVFPFSAIVGQEDMKLALLLTAVDPGIGGVLVFGDRGTGKSTAVRALAALLPEIEAVEGCPVSSPNVE
MIPDWATVLTSTNVIRKPTPVVDLPLGVSEDRVVGALDIERAISKGEKAFEPGLLARANGYLYIDECN
LLEDHIVDLLLLDVAQSGENVVERDGLSIRHPARFVLVSGSNPEEGDLRPQLLDRFGLSVEVLSRPDVE
TRVEVIRRRDITYDADPKAFLEEWPRKMDIRNQILEARERLPKVEAPNTALYDCAALCIALGSDGLR
GELTLLRSARALAALEGATAVGRDHLKRVATMALSHRLRRDPLDEAGSTARVARTVEETLP

>d1a1va1 c.37.1.14 (A:190-325) HCV helicase domain {Human hepatitis C virus (HCV),
different isolates}

PPAVPQSFQVAHLHAPTGSKGSTKVPAAYAAQGYKVLVLPNSVAATLGFAYMSKAHGVDPNIRTGV
RTITTTGSPITYSTYKFLADGGCSGGAYDIICDECHSTDATSILGIGTVLDQAETAGARLVLATATP

>d1a1va2 c.37.1.14 (A:326-624) HCV helicase domain {Human hepatitis C virus (HCV),
different isolates}

PGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIKGRHLIFCHSKKKCDELAACKLVALGINAVAYYRGL
DVSVIPTSGDVVVVATDALMTGFTGDFDSDVICNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRG
RTGRGKPGIYRFVAPGERPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLE
FWEGVFTGLTHIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPT
PLLYRLGAVQNEVTLTHPITKYIMTCMS

>d1cu1a3 c.37.1.14 (A:326-631) HCV helicase domain {Human hepatitis C virus (HCV),
different isolates}

PGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEAIRGGRHLIFCHSKKKCDELAACKLSGLGINAVAYYRGL
DVSVIPTIGDVVVVATDALMTGYTGDFDSDVICNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRG
RTGRGRRGIYRFVTPGERPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPGLPVCQDHLE
FWESVFTGLTHIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPT
PLLYRLGAVQNEVTLTHPITKYIMACMSADLEVVT

>d1gkub1 c.37.1.16 (B:1-250) Helicase-like "domain" of reverse gyrase {Archaeon
Archaeoglobus fulgidus}

AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAASLCLFPEDFLLKEFVEFFRKCVCGEPRAIQKMWA
KRILRKESFAATAPTGVGKTSFGLAMSLFLALKGKRCYVIFPTSLLVIQAAETIRKYAEKAGVGTENLIG
YYHGRIPKREKENFMQNLRFKIVITTTQFLSKHYRELGHFDFIFVDDVDAILKASKNVDKLLHLLG
FHYDLKTKSWVGEARGCLMVSTATAKKGKKAELFRQLLNFDIGSSRIT

>d1gkub2 c.37.1.16 (B:251-498) Helicase-like "domain" of reverse gyrase {Archaeon
Archaeoglobus fulgidus}

VRNVEDVAVNDESISTLSSILEKLTGGIYARTGEEAEEIYESLKNKFRIGIVTATKKG DYEFVEGEID
HLIGTAHYGGTLVRGLDLPERIRFAVFGCPSFRVTIEDIDSLSPQMVKLLAYLRNVDEIERLLPAVER
HIDEVREILKKVMGKERPQAKDVVREGEVIFPDLRTYIQGSGRTSRLFAGGLTKGASFLLEDDSELL
SAFIERAKLYDIEFKSIDEVDFEKL SRELDES RDRYRRR

>d1gl9b1 c.37.1.16 (B:2-250) Helicase-like "domain" of reverse gyrase {Archaeon
Archaeoglobus fulgidus}

IPVVYSNLCPVCGGDLESKEIEKHVCFRKKRSLCLFPEDFLLKEFVEFFRKCVCGEPRAIQKMWAKRIL
RKESFAATAPTGVGKTSFGLAMSLFLALKGKRCYVIFPTSLLVIQAAETIRKYAEKAGVGTENLIGYYH
GRIPKREKENFMQNLRFKIVITTTQFLSKHYRELGHFDFIFVDDVDAILKASKNVDKLLHLLGFHY

DLKTKSWVGEARGCLMVSTATAKKGKKAELFRQLLNFDIGSSRIT

>d1ble_ c.38.1.1 (-) Fructose permease, subunit IIb {*Bacillus subtilis*}

MNIVLARIDDRFIHGQILTRWIKVHAADRIIVVSDDIAQDEMRTLILSVAPSNVKASAVSVSKMAKA
FHSPRYEGVTAMLLFENPSDIVSLIEAGVPIKTVNVGGMRFENHRRQITKSVSVTEQDIKAFETLSDK
GVKLELRQLPSDASEDFVQILRNVT

>d1d0va_ c.39.1.1 (A:) Nicotinate mononucleotide:5,6-dimethylbenzimidazole
phosphoribosyltransferase (CobT) {*Salmonella typhimurium*}

LHALLRDIPAPDAEAMARTQQHIDGLLKPPGSLGRLETLAVQLAGMPGLNGTPQVGEKAVLVMCAD
HGVWDEGVAVSPKIVTAIQAANMTRGTTGVCVLAQAQAKVHVIDVGIDAEPVGVVNMVRVARGCG
NIAVGPAMSRLQAEALLLEVSRYACDLAQRGVTFLGVLGELGMANTTPAAAMVSVFTGSDAKEVVGIG
ANLPPSRIDNKVDVRRRAIAINQPNPRDGIDVLSKVGDFDLVGMTGVMLGAARCGLPVLLDGFLSYS
AALAACQIAPAVRPYLIPSHFSAEKGARIAHLAHLMEPYLHMAMRLGEGSAAALAMPIVEAACAMFH
NMGELAASNIVLP

>d1chd_ c.40.1.1 (-) Methyltransferase CheB, C-terminal domain {*Salmonella typhimurium*}

LLSSEKLIAGASTGGTEAIRHVLQPLPLSSPAVIITQHMPGPFTRSFARLNKLCQISVKEAEDGERVL
PGHAYIAPGDKHMEARSGANYQIKIHDGPPVNRHRPSVDVLFHSAKHAGRNAVGIVLTGMGNDG
AAGMLAMYQAGAWTIAQNEASCVVFGMPREAINMGGVSEVVVDSQVSQQMLAKISAGQAIRI

>d1csee_ c.41.1.1 (E:) Subtilisin {*Bacillus subtilis*, carlsberg}

AQTVPYGIPLIKADKQVQAQGFKGANVKVAVLDTGIQASHPDLNVVGGASFVAGEAYNTDGNHGHGTHV
AGTVAALDNTTGVLGVAPSVSLYAVKVLNSSGSGSYSGIVSGIEWATTNGMDVINMSLGGASGSTMAMK
QAVDNAYARGVVVAAAGNSGNSGSTNTIGYPAKYDSVIAVAVDSNSNRASFSSVGAELVMPGA
GVYSTYPTNTYATLNGTSMASPHVAGAAALILSKHPNLSASQVRNRLSSTATYLGSSFYGKGLINVEA
AAQ

>d1bh6a_ c.41.1.1 (A:) Subtilisin {*Bacillus licheniformis*}

AQTVPYGIPLIKADKQVQAQGYKGANVKVGIIDTGIASSHTDLKVVGGASFVSGESYNTDGNHGHGTHVA
GTVAALDNTTGVLGVAPNVSLYAIKVLNSSGSGSYSAIVSGIEWATQNGLDVINMSLGGPSGSTALLKQA
VDKAYASGIVVVAAGNSGNSGSQNTIGYPAKYDSVIAVAVDSNKNRASFSVSGSELEVMAPGVSVY
STYPSNTYTSLNGTSMASPHVAGAAALILSKYPTLSASQVRNRLSSTATNLGDSFYGKGLINVEAAA
Q

>d1gci_ c.41.1.1 (-) Subtilisin {*Bacillus lentus*}

AQSVPWGISRVQAPAAHNRGLTGSGVKVAVLDTGISTHPDLNIRGGASFVPGEPSTQDGNHGHGTHVA
GTIAALNNSIGVLGVAPSAELYAVKVLGASGSGSVSSIAQGLEWAGNNGMHVANLSLGSPPSATLEQA
VNSATSRGVLVVAASGNSGAGSISYPARYANAMAVGATDQNNNRASFQYAGLDIVAPGVNVQSTYP
GSTYASLNGTSMATPHVAGAAALVKQKNPSWSNVQIRNHLKNTATSLGSTNLYGSLVNAEAATR

>d1s01_ c.41.1.1 (-) Subtilisin {*Bacillus amyloliquefaciens*, Novo/BPN'}

AQSVPYGVSQIKAPALHSQGYTGSNVKVAVIDSGIDSSHPDLKVVAGGASFVPGEPSTQDGNHGHGTHV
AGTVAALDNTSIGVLGVAPSSALYAVKVLGDAGSGQYSWIINGIEWAIANNMDVINMSLGGPSGSAALK
AAVDKAVASGVVVVAAAGNEGSTGSSSTVGYPGKYPSVIAVAVDASNQRASFSSVGPPELDVMPGVSVY
ICSTLPGNKYGAKSGTSMASPHVAGAAALILSKHPNWTNTQVRSSLQNTTTKLGDSFYGKGLINVQ
AAAQ

>d1sue_ c.41.1.1 (-) Subtilisin {*Bacillus amyloliquefaciens*, Novo/BPN'}

AKCVSYGVSQIKAPALHSQGYTGSNVKVAVIDSGIDSSHPDLNVAGGASFVPGEPSTQDGNHGHGTHV
AGTVLAVAPSASLYAVKVLGDAGSGQYSWIINGIEWAIANNMDVINMSLGGPSGSAALKAAVDKAVAS
GVVVVAAAGNEGSTGSSSTVGYPGKYPSVIAVAVDSSNQRASFSSVGPPELDVMPGVSVICSTLPGNK

YGAKSGTSMASPHVAGAAALILSKHPNWTNTQVRSSLENTTTKLGDSFYYGKGLINVEAAAQ
>d1sup_ c.41.1.1 (-) Subtilisin {*Bacillus amyloliquefaciens*, Novo/BPN'}
AQSVPYGVSIKAPALHSQGYTGSNVKVAVIDSGIDSSHPDLKVVAGGASMPSETNPFQDNNSHGTH
VAGTVAALNNSIGVLGVAPSASLYAVKVLGADGSGQYSWIINGIEWAIANNMDVINMSLGGPSGSAAL
KAAVDKAVASGVVVVAAAGNEGTSGSSTVGYPGKYPSVIAVGAVDSSNQRAFSSVGPPELDVMAPGV
SIQSTLPGNKYGAYNGTSMASPHVAGAAALILSKHPNWTNTQVRSSLENTTTKLGDSFYYGKGLIN
QAAAQ
>d1meea_ c.41.1.1 (A:) Mesentericopeptidase {*Bacillus mesentericus*}
AQSVPYGISQIKAPALHSQGYTGSNVKVAVIDSGIDSSHPDLNVRGGASFPSETNPYQDGSSHGTHVA
GTIAALNNSIGVLGVAPSASLYAVKVLGADGSGQYSWIINGIEWAISNNMDVINMSLGGPTGSTALLKTV
VDKAVSSGIVVAAAAGNEGSSGSTSTVGYPAKYPSTIAVGAVNSANQRAFSSAGSELDVMAPGVSIQS
TLPGGTYGAYNGTSMATPHVAGAAALILSKHPTWTNAQVRDRLESTATYLGSSFYYGKGLINVQAAA
Q
>d1dbia_ c.41.1.1 (A:) Thermostable serine protease {*Bacillus* sp., AK.1}
WTPNDTYQYQYQYGPQNTYTDYAWDVTKGSSGQEIIVDTGVQSNHPDLGKVKIKGYDFVDNDYDYP
MDLNNHGTHVAGIAAAETNNATGIAGMAPNTRILAVRALDRNGSGTLSADIADAIYAADSGAEVINLS
LGCDCHTTTTLENVAVNYAWNKGSVVVAAAGNNGSSTTFEPASYENVIAVGAVDQYDRLASFSNYGTW
VDVVPAGVDIVSTITGNRYAYMSGTSMASPHVAGLAALLASQGRNNEIRQAIEQTADKISGTGTYFKY
GRINSYNAVTY
>d1thm_ c.41.1.1 (-) Thermitase {*Thermoactinomyces vulgaris*}
YTPNDPYFSSRQYGPQKIAPQAWDIAEGSGAKIAIVDTGVQSNHPDLGKVVGGWDFVDNDSTPQ
NGNGHGHGTHCAGIAAAVTNNSTGIAGTAPKASILAVRVLNDSGSGTWTAVANGITYAADQGAKVISLSL
GGTVGNSGLQAVNYAWNKGSVVVAAAGNAGNTAPNYPAYYSNAIAVASTDQNDNKSSFSTYGSVW
DVAAPGSSISTYPTSTYASLSGTSMATPHVAGVAGLLASQGRSASNIRAAIENTADKISGTGTYWAKG
RVNAYKAVQY
>d1ic6a_ c.41.1.1 (A:) Proteinase K {Fungus (*Tritirachium album*), strain limber}
AAQTNPWGLARISSTSPGTSTYYYDESAGQGSCVYVIDTGIEASHPEFEGRAQMVKTYYYSSRDGN
GHGTHCAGTVGSRTYGVAKKTQLFGVKVLDDNGSGQYSTIIAGMDFVASDKNNRNCPKGVVASLSL
GGYSSSVNSAAARLQSSGVMVAAGNNNADARNYSPASEPSVCTVGASDRYDRRSSFSNYGSVLDIF
GPGTDILSTWIGGSTRSISGTSMATPHVAGLAAYLMTLGKTTAASACRYIADTANKGDLNIPFGTVN
LLAYNNYQA
>d1ga6a_ c.41.1.2 (A:) Serine-carboxyl proteinase PSCP {*Pseudomonas* sp.}
AGTAKGHNPTEFPTIYDASSAPTAANTTVGIITIGGVSQTLQDLQQTTSANGLASVNTQTIQTGSSNG
DYSDDQQGGGEWDLDSQSIVGSAGGAVQQLLFYMADQSASGNTGLTQAFNQAVSDNVAKVINVSLG
WCEADANADGTLQAEDRIFATAAAQGQTFSVSSGDEGVYECNNRGYPDGSTYSVSWPASSPNVIAVG
GTTLYTTSAGAYSNETVWNEGLDSNGKLWATGGGYSVYESKPSWQSVVSGTPGRLLPDISFDDAAQG
TGALIYNYGQLQQIGGTSLASPIFVGLWARLQSANSNSLGFPAASFYSAISSTPSLVHDVKSNGNGYGG
YGYNAGTGWDYPTGWGSLDIKLSAYIRSNGF
>d1d3va_ c.42.1.1 (A:) Arginase {Rat (*Rattus norvegicus*)}
KPIEIIIGAPFSKQPRGGVEKGAALRKAGLVEKLEKETEYNVRDHGDLAFVDVPNDSPFQIVKNPRSV
GKANEQLAAVVAETQKNGTISVVLGGDHSMAGSISGHARVHPDLCVIWVDAHTDINTPLTTSSGNL
HGQPVAFLKELKGFDPVPGFSWVTPCISAKDIVYIGLRDVPGEHYIIKTLGIKYFSMTEVDKLGIG
KVMEETFSYLLGRKKRPIHLSFDVDGLDPVFTPATGTPVVGGLSYREGLYITEEIIYKTGLLSGLDIMEV
NPTLGKTPPEVTRTVNTAVALTLSCFGTKREGNHK

>d2ceva_c.42.1.1 (A:) Arginase {*Bacillus caldovelox*}
KPISIIGVPMDLGQTRRGVDMGPSAMRYAGVIERLERLHYDIEDLGDIPIGKAERLHEQGDSRLRNLK
AVAEANEKLAAAVDQVVQRGRFPLVLGGDHSIAIGTLAGVAKHYERLGVVIWYDAHGDVNTAETSPSG
NIHGMPLAASLGFHPALTQIGGYSPKIKPEHVVLIGVRSLEGEKFFIREKGIKIYTMHEVDRLGMT
RVMEETIAYLKERTDGVHLSLDLDGLDPSDAPGVGTPVIGGLTYRESHLAMEMLAEAQIITSAEFVEV
NPILDERNKTASVAVALMGSLFGEKLM

>d1c3pa_c.42.1.2 (A:) HDAC homologue {*Aquifex aeolicus*}
KKVKLIGTLDYGYRYPKNHPLKIPRVSLLLRFKIDAMNLIIDEKELIKSRPATKEELLFHTEDYINTL
MEAERCQCVPKGAREKYNIGGYENPVSYAMFTGSSLATGSTVQAIEEFLKGNVAFNPAGGMHHAFKS
RANGFCYINNPVAVGIEYLRKKGFKRILYIDLDAHHCDDGVQEAIFYDTDQVFVLSLHQSPEYAFPFKEGF
LEEIGEGKGGYNLNIPLPKGLNDNEFLFALEKSLEIVKEVFEPEVYLLQLGTDPLLEDYLSKFNLSNV
AFLKAFNIVREVFGEVYLGGGYHPYALARAWTLIWCELSGREVPEKLNKAKELLKSIDFEEDD
EVDRSYMLETLKDPWRGGEVRKEVKDTLEKAKA

>d1hf2a2_c.102.1.1 (A:1-99) Cell-division inhibitor MinC, N-terminal domain {*Thermotoga
maritima*}
MVDFKMTKEGLVLLIKDYQNL EEVLNAISARITQMGGFFAKGDRISLMIENHNKHSQDIPRIVSHLR
NLGLEVSQILVGSTVEGKENDLKVQSRTTVES

>d1jkea_c.110.1.1 (A:) D-Tyr tRNA^{tyr} deacylase {*Escherichia coli*}
MIALIQRVTRASVTVEGEVTGEIGAGLLVLLGVEKDDDEQKANRLCERVLGYRIFSDAEGKMNLNVQ
QAGGSVLVVSQFTLAADTERGMRPSFSKASPDRAEALYDYFVERCRQQEMNTQTGRFAADMQVSL
VNDGPVTFWLQV

>d1nocb_c.43.1.1 (B:) Chloramphenicol acetyltransferase {*Escherichia coli*}
ITGYTTVDISQWHRKEHFQSV AQCTYNQTVQLDITAFKTVKKNKHKFYPAFIHILARLMNAHP
EFRMAMKDGELVIWDSVHPCYTVFHEQTETFSLSWSEYHDDFRQFLHIYSQDVACYGENLAYFPKG
FIENMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYTQGDKVLMLAIQVHHAVCDGFHVG
RMLNELQYCYCDEWQG

>d3cla_c.43.1.1 (-) Chloramphenicol acetyltransferase {*Escherichia coli*}
MNYTKFDVKNWVRREHFYRHLPCGFSLSKIDITLKKSLDSDAYKFYPVMIYLIAQAVNQFDE
LRMAIKDDELIVWDSVDPQFTVFHQETETFSALSCPYSDDIDQFMVNYLSVMERYKSDTKLFPQGV
PENHLNISALPWVNFDSFNLNVANFTDYFAPITMAKYQQEGDRLLLPLSVQVHHAVCDGFHVARFI
NRLQELCNSKLLK

>d1eaf_c.43.1.1 (-) Dihydrolipoamide acetyltransferase {*Azotobacter vinelandii*}
IPPIPPVDFAKYGEIEEVP MTRLMQIGATNLHRSWLVNPHVTQFESADITELEAFRVAQKAVAKKAG
VKLTVLPLLLKACAYLLKELPDFNSSLAPSGQALIRKKYVHIGFAVDTPDGLLVPIRVNDQKSLQLA
AEAAELA EKARSKKLGADAMQGACFTISSLGHIGGTAFTPIVNAPEVAILGVSKASMQPVWDGKAFQ
PRLMLPLSLSYDHRVINGAAAARFTKRLGDLADIRAILL

>d1b5sa_c.43.1.1 (A:) Dihydrolipoamide acetyltransferase {*Bacillus stearothermophilus*}
AAAKPATTEGEFPETREKMSGIRRAIAKAMVHSHKHTAPHVTLMDEADVTKLVAHRKKFKAIAAEK
IKLTFLPYVVKALVSALREYPV LNTSIDDETEEIIQKHYYNIGIAADTDRGLLVPIKHADRKPIFALAQ
EINELA EKARDGKLT PGEMKGASCTITNIGSAGGQWFTPVINHPEVAILGIGRIAEKPIVRDGEIVAAP
MLALSLSFDHRMIDGATAQKALNHIKRLSDPELLLM

>d1e2o_c.43.1.1 (-) Dihydrolipoamide succinyltransferase {*Escherichia coli*}
ARSEKRVPMTRLRKRVAERLLEAKNSTAMLTTFNEVNMKPIMDLRKQYGEAFEKRHGIRLGFMSFY
VKAVVEALKRYPEVNASIDGDDVVYHNYFDVSMVSTPRGLVTPVLRDVDTLGMADIEKKIKELAVK

GRDGKLTVEDLTGGNFTITNGGVFGSLMSTPIINPPQSAILGMHAIKDRPMAVNGQVEILPMMYLAL
SYDHRLLIDGRESVGLVTIKELLEDPTRLLLLDV
>d1phr_ c.44.1.1 (-) Tyrosine phosphatase {Cow (Bos taurus)}
VTKSVLFLVCLGNICRSPIAEAVFRKLVTDQNI SDNWVIDSGAVSDWNVGRSPDPRAVSLRNHGINTA
HKARQVTKEDFVTFDYILCMDES NLRDLNRKSNQVKNCRAKIELLGSYDPQKQLIIEDPYYGNDADF
ETVYQQCVRCCRAFLEKVR
>d5pnt_ c.44.1.1 (-) Tyrosine phosphatase {Human (Homo sapiens)}
AEQATKSVLFLVCLGNICRSPIAEAVFRKLVTDQNI SENWRVDSAATSGYEIGNPPDYRGQSCMKRHGI
PMSHVARQITKEDFATFDYILCMDES NLRDLNRKSNQVKTCKAKIELLGSYDPQKQLIIEDPYYGNDS
DFETVYQQCVRCCRAFLEKAH
>d1d1qa_ c.44.1.1 (A:) Tyrosine phosphatase {Baker's yeast (Saccharomyces cerevisiae)}
IEKPKISVAFIALGNFCRSPMAE AIFKHEVEKANLENRFNKIDSFGT SNYHVGESPDHRTVSICKQHG
VKINHKGKQIKTKHFDEYDYIIGMDES NINLKKIQPEGSKAKVCLFGDWNTNDGTVQTHIEDPWYG
DIQDFEYNFKQITYFSKQFLKKEK
>d1jf8a_ c.44.1.1 (A:) Arsenate reductase ArsC {Staphylococcus aureus}
DKKTIYFISTGNSARSQMAEGWGKEILGEGWNVYSAGIETHGVNPKAIEAMKEVDIDISNHTSDLID
NDILKQSDLVVTLCSADANNCPILPPNVKKEHWGFDDPAGKEWSEFQVRVDEIKLAI EKFKLR
>d1jl3a_ c.44.1.1 (A:) Arsenate reductase ArsC {Bacillus subtilis}
NKIIYFLCTGNSCRSQMAEGWAKQYL GDEWKVYSAGIEAHGLNPNAV KAMKEV GIDISNQTSDIIDS
DILNNADLVVTL CGDAADKCPMTPPHVKREHWGFDDPARAQGT EEEKWAFFQVRVDEIGNRLKEF
AETGK
>d1iiba_ c.44.2.1 (A:) Enzyme IIB-cellobiose {Escherichia coli}
KKHIYLFSSAGMSTSLLVSKMRAQA EKYEVPIIEAFPETLAGEKGNADVVLLGPQIAYMLPEIQRL
LPNKPVEVIDSLLYGKVDGLGVLKAAVA AIKAAA
>d1vhra_ c.45.1.1 (A:) VH1-related dual-specificity phosphatase, VHR {Human (Homo sapiens)}
SVQDLNDLLSDGSGCYLSPQCNEVTPRIYVGNASVAQDIPKLQKLGITHVLNAAEGRSFMHVNTN
ANFYKDSGITYLGIKANDTQEFNLSAYFERAADFIDQALAQKNGRVLVHCREGYSRSP TLVIAYLMMR
QKMDVKSALSIVRQNREIGPNDGFLAQLCQLNDRLAKEGKLP
>d1mkp_ c.45.1.1 (-) Mapk phosphatase Pyst1 (mkp3) {Human (Homo sapiens)}
ASFPVEILPFLYLGC AKDSTNLDVLEEFGIKYLNVTPNL PNLFENAGEFKYKQIPISDHWSQNLSQFF
PEAISFIDEARGKNC GVLVHSLAGISRSVTVTVAYLMQKLNLSMNDAYDIVKMKKSNISPNFNFMGQL
LDFERTL
>d1d5ra2 c.45.1.1 (A:14-187) Phosphoinositide phosphatase Pten (Pten tumor suppressor),
N-terminal domain {Human (Homo sapiens)}
RRYQEDGFDDLTYIYPNIIAMGFPAERLEGVYRNID DVVRF LDSKHKNHYKIYNLCAERHYDTAK
FNCRVAQYPFEDHNPPQLELIKPFCELDQWLSEDDNHVAAIHCKAGKGR TGVMICAYLLHRGKFL
KAQEALDFYGEVTRDKKGV TIPSQRRYVYYSYLLKNHLD
>d1i9sa_ c.45.1.1 (A:) mRNA capping enzyme, triphosphatase domain {Mouse (Mus musculus)}
KIPRWLNCPRRQPVAGRFLPLK TMLGPRYDSQVAEENRFHPSMLS NYLKSLKVKMSLLVDLTNT
SRFYDRNDIEKEGIKYLQCKGHGECPTTENTET FIRLCERFNERSPPELIGVHCTHGFNRTGFLICA
FLVEKMDWSIEAAVATFAQARPPGIYKGDY LKELFRRYGDIEEAPPPVLPDWC FEDED
>d1fpza_ c.45.1.1 (A:) Kinase associated phosphatase (kap) {Human (Homo sapiens)}

TPIHISWLSLRVNCSQLGLCALPGCKFKDVRNRVQKDTEELKSCGIQDIFVFCTRGELSKYRVPNLL
DLYQQCGIITHHHPIADGGTPDIASCCEIMEELTTCLKNYRKTLIHSYGGGLGRSCLVAACLLLYLSDTISP
EQAIDSLRDLRGSGAIQTIKQYNYLHEFRDKLAAHL

>d1eeoa_ c.45.1.2 (A:) Tyrosine phosphatase {Human (Homo sapiens), 1B}

EMEKEFEQIDKSGSWAAIYQDIRHEASDFPCRVAKLKPKNKNRNRVDPFDSRIKLHQEDNDYIN
ASLIKMEEAQRSYILTQGPLNNTCGHFWEMVWEQKSRGVVMLNRVMEKGLKCAQYWPQKEEKE
MIFEDTNLKLTLISEDIKSYTVRQLELENLTTQETREILHFHYTTWPDFGVPESPASFLNFLFKVRES
GSLSPEHGPPVVHSSAGIGRSGTFCLADTCLLLMDKRKDPSSVDIKKVLLEMRKFRMGLIQTADQLR
FSYLAVIEGAKFIMGDSSVQDQWKELSHED

>d1rpma_ c.45.1.2 (A:) Tyrosine phosphatase {Human (Homo sapiens), mu}

AIRVADLLQHITQMKCAEGYGFKEEYESFFEGQSAPWDSAKKDENRMKNRYGNIIAYDHSRVRLQTI
EGDTNSDYINGNYIDGYHRPNHYIATQGPMQETIYDFWRMVWHENTASIIMVTNLVEVGRVKCKKY
WPDDTEIYKDIKVTLIETELLAEYVIRTFAVEKRGVHEIREIRQFHFTGWPDHGVPYHATGLLGFVRQ
VKSKSPSAGPLVVHCSAGAGRTGCFIVIDIMLMAEREGVVDIYNCVRELSRRVNMVQTEEQYVFI
HDAILEACL

>d1yfoa_ c.45.1.2 (A:) Tyrosine phosphatase {Mouse (Mus musculus)}

KYPPLPVDKLEEEINRRMADDNKLFREEFNALPACPIQATCEAASKEENKEKNRYVNILPYDHSRVH
LTPVEGVPDSYINASFINGYQEKKNFIAAQGPKEETVNDFWRMIWEQNTATIVMVTNLKERKECK
CAQYWPDQGCWYGNVRSVEDVTVLVDYTVRKFCIQVGDVTNRKPQRLITQFHFTSWPDFGVP
FTPIGMLKFLKKVKACNPQYAGAIVVHCSAGVGRGTGFVIDAMLDMMSERKVDVYGFVSRIRAQ
RCQMVQTDMMQYVFIYQALLEHYLY

>d2shpa1 c.45.1.2 (A:219-525) Tyrosine phosphatase {Human (Homo sapiens), shp-2}

TRINAAEIESRVRELSKLAETTDKVKQGFWEFETLQQQECKLLYSRKEGQRQENKNKNRYKNILPF
DHTRVVLHDGDPNEPVS DYINANIIMPEFETKCNNSKPKSYIATQGCLQNTVNDFWRMVQENSR
VIVMTTKEVERGKSKCVKYWPDEYALKEYGVMRVRNVKESAAHDYTLRELKLSKVGQNTERTVW
QYHFRTWPDHGVPSDPGGVLD FLEEVHHKQESIMDAGPVVVHCSAGIGRTGTFIVIDILIDIIREKGV
DCDIDVPKTIQMVRSGRSGMVQTEAQYRSIYMAVQHYIETL

>d1fpra_ c.45.1.2 (A:) Tyrosine phosphatase {Human (Homo sapiens), shp-1}

GFWEFESLQKQEVKNLHQRLEGQRPENKGNRYKNILPFDHSRVILQGRDSNIPGSDYINANYIKN
QLLGPDENAKTYIASQGCLEATVNDFWQMAWQENSRVIVMTTREVVEKGRNKCVPYWPVEGVMQRA
YGPYSVTNCGEHD TTEYKLR TLQVSPLDNGDLIREIWHYQYLSWPDHGVPSPPGGVLSFLDQINQRQ
ESLPHAGPIVHSSAGIGRTGTIIVIDMLMENISTKGLDCDIDIQKTIQMVRAQRSGMVQTEAQYKFIYV
AIAQFIETTKKKLEVL

>d1jlina_ c.45.1.2 (A:) Tyrosine phosphatase {Mouse (Mus musculus), ptp-sl/br7}

GSPREKVAMEYLQSASRVLTRSQRD VVASSHLLQSEFMEIPMNFVDPKEIDIPRHGTKNRYKTILPN
PLSRVCLRPKNITDSLSTYINANYIRGYSGKEKAFIATQGP MINTVNDFWQMVWQEDSPVIVMITKL
KEKNEKCVLYWPEKRGYKVEVLVTGVTECDNYTIRNLVLKQGSHTQHVKHYWYTSWPDHKTPD
SAQPLLQLMLDVEEDRLASEGRPVVVHCSAGIGRTGCFIATSIGCQQLKEEGVVDALSIVCQLRVDR
GGMVQTSEQYEFVHHALCLFESRLSPETV

>d1ypta_ c.45.1.2 (A:) Tyrosine phosphatase {Yersinia enterocolitica}

PEARAE LSSRLTTLRNTLAPATNDPRYLQACGGEKLNFRDIQCRRTAVRADLNANYIQVGNTRTI
ACQYPLQSQLESHFRMLAENRTPVLAVLASSSEIANQRFGMPDYFRQSGTYGSITVESKMTQQVGLG
DGIMADMYTLTIREAGQKTISVPVVHVGNWPDQTAVSSEVTKALASLVDQTAETKRNMYESKSSAV
ADDSKLRPVIHCRAVGRTAQLIGAMCMNDSRNSQLSVEDMVSQMRVQRNGIMVQKDEQLDVLIK

LAEGQGRPLLNS

>d1g4us2 c.45.1.2 (S:297-539) SptP tyrosine phosphatase, catalytic domain {Salmonella typhimurium}

PQTMSGPTLGLARFAVSSIPINQQTQVKLSDGMPVVPVNTLTFDGGKPVVALAGSYPKNTPDALAEAHMK
MLLEKECSCLVVLTSQDQMAKQLPPYFRGSYTFGEVHTNSQKVSSASQGEAIDQYNMQLSCGKRY
TIPVLHVKNWPDHQPLPSTDQLEYLADRKNSNQNGAPGRSSDKHLPMIHLGGVGRGTMAAAA
LVLKDNPHSNLEQVRADFRDSRNNRMLLEDASQFVQLKAMQAQLLM

>d1lara1 c.45.1.2 (A:1307-1623) RPTP Lar {Human (Homo sapiens)}

MITDLADNIERLKNANDGLKFSQEYESIDPGQQFTWENSNLEVNKPKNRYANVIAYDHSRVILTSIDGV
PGSDYINANYIDGYRKQNAYIATQGPLPETMGDFWRMVWEQRTATVMMTRLEEKSRVKCDQYW
PARGTETCGLIQVTLTDTVELATYTVRTFALHKSQSSEKRELRFQFMAWPDHGVPEYPTPILAFRLR
RVKACNPLDAGPMVVHCSAGVGRGTGCFIVIDAMLERMKHEKTVDIYGHVTCMRSQRNYMVQTEDQ
YVFIHEALLEAATCGHTEVPARNLYAHIQKLGQVPPGESVTAMELEFKLLASS

>d1lara2 c.45.1.2 (A:1628-1876) RPTP Lar {Human (Homo sapiens)}

SRFISANLPCNKFKNRLVNIMPYELTRVCLQPIRGVEGSDYINASFLDGYRQQKAYIATQGPLAESTED
FWRMLWEHNSTIIVMLTKLREMGREKCHQYWPAERSARYQYFVVDPMAYNMPQYILREFKVTD
ARDGQSRTIRQFQFTDWPEQGVPKTGEGFIDFIGVHKTKEQFGQDGPITVHCSAGVGRGTGVFITLSI
VLERMRYEGVDMFQTVKTLRTQRPAMVQTEDQYQLCYRAALEYLGFS

>d1larb1 c.45.1.2 (B:1340-1623) RPTP Lar {Human (Homo sapiens)}

TWENSNLEVNKPKNRYANVIAYDHSRVILTSIDGVPGSDYINANYIDGYRKQNAYIATQGPLPETMGD
FWRMVWEQRTATVMMTRLEEKSRVKCDQYWPARGTETCGLIQVTLTDTVELATYTVRTFALHKS
GSSEKRELRFQFMAWPDHGVPEYPTPILAFRLRRVACNPLDAGPMVVHCSAGVGRGTGCFIVIDAM
LERMKHEKTVDIYGHVTCMRSQRNYMVQTEDQYVFIHEALLEAATCGHTEVPARNLYAHIQKLGQV
PPGESVTAMELEFKLLASS

>d1c25_ c.46.1.1 (-) CDC25a {Human (Homo sapiens)}

MLIGDFSKGYLFHTVAGKHQDLKYISPEIMASVLNGKFANLIKEFVIIDCRYPYEEYEGGHIKAVNLH
MEEVEEDFLLKPKIVPTDGRVIVVFHCFSSERGPVMCRVYRERDRDLGNEYPKLHYPELYVLKGGY
KEFFMCKQSYCEPPSYRPMHHEDFKE

>d1qb0a_ c.46.1.1 (A:) CDC25b {Human (Homo sapiens)}

DHRELIGDYSKAFLLQTVDGKHQDLKYISPETMVALLTGKFSNIVDKFVIVDCRYPYEEYEGGHIKTAV
NLPLERDAESFLLKSPIAPCSLDKRVILIFHCFSSERGPVMCRFIRERDRAVNDYPSLYPEMYILKG
GYKEFFPQHPNFCEPQDYRPMNHEAFKDELKTFRLKTRSWA

>d1hzma_ c.46.1.1 (A:) Erk2 binding domain of Mapk phosphatase mkp-3 {Human (Homo sapiens)}

MIDTLRPVPPFASEMAISKTVAWLNEQLELGNRLLLLMDCRPQELYESSHIESAINVAIPGIMLRRLQK
GNLPVRALFTRGEDRDRFTRRCGTDTVVLYDESSDWNENTGGESLLGLLLKLLKDEGCRAFYLEG
GFSKFQAEFSLHCETNLDGS

>d1gmxa_ c.46.1.3 (A:) Sulfurtransferase GlpE {Escherichia coli}

MDQFECINVADAHQKLQEKAVLVDIRDPQSFAMGHAVQAFHLTNDTLGAFMRDNDFDTPVMVM
CYHGNSSKGAQYLLQQGYDVVYSIDGGFEAWQRQFPAEVAYGA

>d1rhs_1 c.46.1.2 (1-149) Rhodanese {Cow (Bos taurus)}

VHQVLYRALVSTKWLAEVSRAGKVGPLRVLDASWYSPGTREARKEYLERHVPASFFDIEECRDK
ASPYEVMPLPSEAGFADYVGSGLISNDTHVVYDGGDLGSFYAPRVWWMFRVFGHRTVSVLNGGFRN
WLKEGHPVTSEPSRPEP

>d1rhs_2 c.46.1.2 (150-293) Rhodanese {Cow (Bos taurus)}
AIFKATLNRSLLKTYEQVLENLESKRFLVDSRAQGRYLGTQPEPDAVGLDSGHIRGSVNMPFMNFL
TEDGFESPEELRAMFEAKKVDLTKPLIATCRKGV TACHIALAAYLCGKPDVAIYDGSWFEFWHRAP
PETWVSQGGK

>d1e0ca1 c.46.1.2 (A:1-135) Sulfurtransferase {Azotobacter vinelandii}
MDDFASLPLVIEPADLQARLSAPELILVDLTSARYAEGHIPGARFVDPKRTQLGQPPAPGLQPPREQL
ESLFGELGHRPEAVYVVYDDEGGGWAGRFIWL LDVIGQQRYHYLNGGLTAWLAEDRPLSREL PAPA

>d1e0ca2 c.46.1.2 (A:136-271) Sulfurtransferase {Azotobacter vinelandii}
GGPVALSLHDEPTASRDYLLGRLGAADLAIWDARSPQEYRGEKVLAAKGGHIPGAVNFEWTAAMDP
SRALRIRTDIAGRLEELGITPDKEIVTHCQTHRSGLTYLIAKALGYPRVKGYAGSWGEGWGNHPDTP
VEL

>d2trxa_ c.47.1.1 (A:) Thioredoxin {Escherichia coli}
SDKIHLTDDSFDTDVLKADGAILVDFWAEWCGPCKMIAPILDEIADEYQGKLTVAKLNIDQNPGTAP
KYGIRGIPTLLLFKNGEVAATKVGALSKGQLKEFLDANLA

>d1thx_ c.47.1.1 (-) Thioredoxin {Anabaena sp., pcc 7120}
SKGVITITDAEFESEVLKAEQPVLVYFWASWCGPCQLMSPLINLAANTYSDR LKVVKLEIDPNPTTV
KKYKVEGVPALRLVKGEQILDSTEGVISKDKLLSFLDTHLN

>d1dbya_ c.47.1.1 (A:) Thioredoxin {Chlamydomonas reinhardtii}
MEAGAVNDDTFKNVLESSVPLVDFWAPWCGPCR IAPVVDEIAGEYKDKLKCVKLNTDESPNVA
SEYGIRSIPTIMVFKGGKKCETIIGAVPKATIVQTVEKYL N

>d1ep7a_ c.47.1.1 (A:) Thioredoxin {Chlamydomonas reinhardtii}
GGSVIVIDSKAAWDAQLAKGKEEHKPIVVDFTATWCGPCKMIAPL FETLSNDYAGKVIFLKV D VDAV
AAVAEAAGITAMPTFHVYKDGVKADDLVGASQDKL KALVAKHAAA

>d1quwa_ c.47.1.1 (A:) Thioredoxin {Bacillus acidocaldarius}
ATMTLTDANFQQAIQGDKPVLVDFWAAWCGPCRMMAPVLEEF AEAHADKVTVAKLNV DENPETT
SQFGIMS IPTLLLFKGGRPVKQLIGYQPKEQLEAQLADVLQ

>d1f9ma_ c.47.1.1 (A:) Thioredoxin {Spinach (Spinacia oleracea), thioredoxin F}
MEAIVGK VTEVNKDTFWPIVKAAGDKPVVLD MFTQWCGPCKAMAPKYEKLAEEYLDVIFLKLDCN
QENKTLAKELGIRVVPTFKILKENS VVGEVTGAKYDKLLEAIQAARS

>d1fb6a_ c.47.1.1 (A:) Thioredoxin {Spinach (Spinacia oleracea), thioredoxin M}
VQDVNDSSWKEFVLESEVPVMVDFWAPWCGPCKLIAPVIDELAKEYSGKIAVYKLN TDEAPGIATQ
YNIRSIPTV LFFKNGERKESIIGAVPKSTLTDSIEKYL

>d1erv_ c.47.1.1 (-) Thioredoxin {Human (Homo sapiens)}
MVKQIESKTAFQEALDAAGDKLVVDF SATWCGPCKMIKPFHSLSEKYSNVIFLEVDVDDCQDVAS
ECEVKSMPTFQFFKKGQKVG EFGANKEKLEATINELV

>d1aba_ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Bacteriophage T4}
MFKVYGYDSNIHKCGPCD NAKRLLTVKKQPF EFINIMPEKGVDFDDEKIAELLTKLGRDTQIGL TMPQV
FAPDGS HIGGFDQLREYFK

>d1qfna_ c.47.1.1 (A:) Glutaredoxin (Thioltransferase) {Escherichia coli}
MQTVIFGRSGCPYSVRAKDLAEKLSNERDDFQYQYVDIRAEGITKEDLQQKAGKPVETVPQIFVDQQ
HIGGYTDFAAWVKENLDA

>d3grx_ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Escherichia coli, GRX3}
ANVEIYTKETCPYSHRAKALLSSKGVSFQELPIDGNAAKREEMIKRSGRTTVPQIFIDAQHIGGYDDL Y
ALDARGGLDPLLK

>d1kte_ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Pig (Sus scrofa)}
 AQAFVNSKIQPGKVVVFIKPTCPFCRKTQELLSQLPFKEGLLEFVDITATSDTNEIQDYLQQLTGARTV
 PRVFIGKECIGGCTDLESMHMRGELLTRLQVGVAVK

>d1jhb_ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Human (Homo sapiens)}
 AQEFVNCKIQPGKVVVFIKPTCPYCRRAQEILSQLPIKQGLLEFVDITATNHTNEIQDYLQQLTGARTV
 PRVFIGKDCIGGCSLVSLQQSGELLTRLKQIGALQ

>d1h75a_ c.47.1.1 (A:) Glutaredoxin-like NRDH-redoxin {Escherichia coli}
 MRITIYTRNDVCVQCHATKRAMENRGDFEMINVDRVPEAAEALRAQGFRQLPVVIAGDLSWSGFRP
 DMINRLHPAP

>d1fo5a_ c.47.1.1 (A:) MJ0307, thioredoxin/glutaredoxin-like protein {Archaeon
 Methanococcus jannaschii}
 MSKVKIELFTSPMCPHCPAAKRVEEVANEMPDAVEVEYINVMENPQKAMEYGIMAVPTIVINGDV
 EFIGAPTKEALVEAIKKRL

>d1iloa_ c.47.1.1 (A:) MTH985, a thioredoxin {Archaeon Methanobacterium
 thermoautotrophicum}
 MMKIQIYGTGCANCQMLEKNAREAVKELGIDAEFEKIKEMDQILEAGLTALPGLAVDGELKIMGRVA
 SKKEIKKILS

>d1gh2a_ c.47.1.1 (A:) Thioredoxin-like protein, N-terminal domain {Human (Homo
 sapiens)}
 VGVKVPVGSDFQPELSGAGSRLAVVKFTMRGCGPCLRIAPAFSSMSNKYPQAVFLEVDVHQCQGT
 ATNNISATPTFQFFRNKVRIDQYQGADAVGLEEKIKQHLE

>d1bjx_ c.47.1.2 (-) Protein disulfide isomerase, PDI {Human (Homo sapiens)}
 AATTLPGAAAESLVESSEVAVIGFFKDVESDSAKQFLQAAEAIDDIPFGITSNSDVFVSKYQLDKDGVV
 LFKKFDEGRNNFEGETKENLLDFIKHNQLPLVIEFTEQTA

>d1mek_ c.47.1.2 (-) Protein disulfide isomerase, PDI {Human (Homo sapiens)}
 DAPEEEDHVLVLRKSNFAEALAAHKYLLVEFYAPWCGHCKALAPEYAKAAGKKAEGSEIRLAKVDA
 TEESDLAQQYGVRYPTIKFFRNGDTASPKEYTAGREADDIVNWLKRTGPAA

>d1a8l_1 c.47.1.2 (1-119) Protein disulfide isomerase, PDI {Archaeon Pyrococcus
 furiosus}
 MGLISDADKKVIKEEFFSKMVNPVKLIVFVRKDHQYCDQLKQLVQELSELTDKLSYEIVDFDTPEGK
 ELAKRYRIDRAPATTITQDGKDFGVRYFGLPAGHEFAAFLEDIVDVSREET

>d1a8l_2 c.47.1.2 (120-226) Protein disulfide isomerase, PDI {Archaeon Pyrococcus
 furiosus}
 NLMDETKQAIRNIDQDVRILVFVTPTCPYCPLAVRMAHKFAIENTKAGKKGKILGDMVEAIEYPEWAD
 QYNVMAVPKIVIQVNGEDRVEFEGAYPEKMFLEKLLSALS

>d1hyua3 c.47.1.2 (A:1-102) Alkyl hydroperoxide reductase subunit F (AhpF), N-terminal
 domain {Salmonella typhimurium}
 MLDTNMKTQLRAYLEKLTTPVELIATLDDSAKSAEIKELLAEIAELSDKVTFKEDNTLPVRKPSFLIT
 NPGSQQGPRFAGSPLGHEFTSLVLALLWTGGHPS

>d1hyua4 c.47.1.2 (A:103-198) Alkyl hydroperoxide reductase subunit F (AhpF), N-terminal
 domain {Salmonella typhimurium}
 KEAQSLEQIRDIDGDFEFETYYSLSCHNCPDVVQALNLMAVLNPRIKHTAIDGGTFQNEITERNVM
 GVPAVFNKGKEFGQGRMTLTEIVAKVDTG

>d1a8y_1 c.47.1.3 (3-126) Calsequestrin {Rabbit (Oryctolagus cuniculus)}
 GLDFPEYDGVDRVINVNAKNYKNVFKKYEVLALLYHEPPEDDKASQRQFEMEELILELAAQVLEDK

GVGFGLV DSEKDA AVAKKLGLTEEDSIYVFKEDVIEYDGEFSADTLVEFLLDVLEDP
>d1a8y_2 c.47.1.3 (127-228) Calsequestrin {Rabbit (*Oryctolagus cuniculus*)}
VELIEGERELQAFENIEDEIKLIGYFKNKDSEHYKAFKEAAEEFHPYIPFFATFDSKVAKKLT LKLN EI
DFYEAFMEEPVTIPDKPNSEEEIVNFVEEHRRS
>d1a8y_3 c.47.1.3 (229-347) Calsequestrin {Rabbit (*Oryctolagus cuniculus*)}
TLRKLKPESMYETWEDDMDGIHIVAF AEEADPDGYEFLEILKSVAQDNTDNP DLSIIWIDPDDFPLL
VPYWEKTFDIDLSAPQIGVVNVT DADSVWMEMDDEEDLPSAELEDWLEDVL
>d1fvka2 c.47.1.4 (A:1-64,A:129-188) Disulphide-bond formation facilitator (DSBA)
{*Escherichia coli*}
AQYEDGKQYTTLEKPVAGAPQVLEFFSFFCPHCYQFEEVLHISDNVKKKLP EGVKMTKYHVNFMXF
VVKSLVAQQEKAAADVQLRGVPAMFVNGKYQLNPQGM DTSNMDV FVQYADTVKYLSEK
>d1bed_2 c.47.1.4 (1-62,127-181) Disulphide-bond formation facilitator (DSBA) {*Vibrio*
cholerae}
AQFKEGEHYQVLKTPASSPVVSEFFSFYCPHCNTFEPHIAQLKQQLPEGAKFQKNHVSFMGXFAVDS
MVRRFDKQFQDSGLTGVP AVVVNNRYLVQGQSVKSLDEYFDLVNYLLTLK
>d1aqwa2 c.47.1.5 (A:1-76) Glutathione S-transferase {Human (*Homo sapiens*), class pi}
PPYTVVYFPVRGRCAALRMLLADQGQSWKEEVTVETWQEGSLKASCLYGQLPKFQDGDLTLYQSN
TILRH LGRTL
>d2gsra2 c.47.1.5 (A:1-76) Glutathione S-transferase {Pig (*Sus scrofa*), class pi}
PPYTITYFPVRGRCEAMRMLLADQDQSWKEEVVTMETWPPLKPSCLFRQLPKFQDGDLTLYQSNAI
LRHLGRSFG L
>d1glqa2 c.47.1.5 (A:1-78) Glutathione S-transferase {Mouse (*Mus musculus*), class pi}
PPYTIVYFPVRGRCEAMRMLLADQGQSWKEEVVTIDTWMQGLLKPTCLYGQLPKFEDGDLTLYQSN
AILRH LGRSGL
>d1gtua2 c.47.1.5 (A:1-84) Glutathione S-transferase {Human (*Homo sapiens*), class mu}
PMILGYWDIRGLAHAIRL LLEYTDSSYEEKKYTMGDAPDYDRSQWLNEKFKLGLDFPNLPYLIDGA
HKITQSNAILCYIARKHN
>d1hna_2 c.47.1.5 (1-84) Glutathione S-transferase {Human (*Homo sapiens*), class mu}
PMTLGYWNIRGLAHSIRL LLEYTDSSYEEKKYTMGDAPDYDRSQWLNEKFKLGLDFPNLPYLIDGT
HKITQSNAILRYIARKHN
>d3gtub2 c.47.1.5 (B:1-84) Glutathione S-transferase {Human (*Homo sapiens*), class mu}
SCESSMVLGYWDIRGLAHAIRL LLEFTDTSYEEKRYTCGEAPDYDRSQWLDVKFKLGLDFPNLPYLL
DGKNKITQSNAILRYIA
>d2gsta2 c.47.1.5 (A:1-84) Glutathione S-transferase {Rat (*Rattus norvegicus*), class mu}
PMILGYWNV RGLTHPIRLLLEYTDSSYEEKRYAMGDAPDYDRSQWLNEKFKLGLDFPNLPYLIDGSR
KITQSNAIMRYLARKHH
>d1gsua2 c.47.1.5 (A:1-84) Glutathione S-transferase {Chicken (*Gallus gallus*), class mu}
VVTLGYWDIRGLAHAIRL LLEYTETPYQERRYKAGPAPDFDPSDWTNEKEK LGLDFPNLPYLIDGDV
KLTQSNAILRYIARKHN
>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}}

RPKLHYPNGRGRMESVRWVLAAGVEFDEEFLETKEQLYKLQDGNHLLFQQVPMVEIDGMKLVQT
RSILHYIADKHN

>d1f3aa2 c.47.1.5 (A:1-79) Glutathione S-transferase {Mouse (Mus musculus), class alpha
{a1-1}}

AGKPVLFHYFNARGRMECIRWLLAAAGVEFEEKFIQSPEDLEKLLKKGDNLMFDQVPMVEIDGMKLA
QTRAILNYIATKYD

>d1b48a2 c.47.1.5 (A:2-79) Glutathione S-transferase {Mouse (Mus musculus), class alpha
{a1-4}}

AAKPKLYYFNNGRGRMESIRWLLAAAGVEFEEEFLETREQYKMQKDGHLLFGQVPLVEIDGMMLTQ
TRAILSYLAAY

>d1ljra2 c.47.1.5 (A:1-79) Glutathione S-transferase {Human (Homo sapiens), class theta}

MGLEFLDLVSPRAVYIFAKKNGIPELRTVDLVKQGHKSKEFLQINSLGKPLTKDGDGFILTESSAI
LIYLSCKYQ

>d1pd212 c.47.1.5 (1:1-75) Glutathione S-transferase {Rat (Rattus norvegicus), class sigma}

MPNYKLLYFNMRGRAEIIRYIFAYLDIKYEDHRIEQADWPKIKPTLPGKIPVLEVEGLTLHQSLAIAR
YLTNT

>d2gsq_2 c.47.1.5 (1-75) Glutathione S-transferase {Squid (Ommastrephes sloani pacificus),
class sigma}

PKYTLHYFPLMGRAELCRFVLAAGHEEFTDRVEMADWPNLKATMYSNAMPVLDIDGTMKMSQSM
CIARHLAREFG

>d1eema2 c.47.1.5 (A:5-102) Glutathione S-transferase {Human (Homo sapiens), class
omega}

SARSLGKGSAPPGPVPEGSIRIYSMRFCPFAERTRVLKAKGIRHEVININLKNKPEWFFKKNPFGLVP
VLENSQGQLIYESAITCEYLDEAYPGKKL

>d1fw1a2 c.47.1.5 (A:5-87) Glutathione S-transferase {Human (Homo sapiens), class zeta}

KPILYSYFRSSCSWRVRIALALKGIDYKTPVINLIKDGQQFSKDFQALNPMKQVPTLKIDGITIHQSL
AIIEYLEETRPTPR

>d1duga2 c.47.1.5 (A:1-80) Glutathione S-transferase {Schistosoma japonicum}

SPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKTQS
MAIRYIADKHNM

>d1fhe_2 c.47.1.5 (1-80) Glutathione S-transferase {Fasciola hepatica}

PAKLGWKLRLGLAQPVRLLFLEYLGEYEEHLYGRDDREKWMSEKFNMGDLPLNLPYYIDDKCKLTQ
SVAIMRYIADKHGM

>d2fhea2 c.47.1.5 (A:1-80) Glutathione S-transferase {Fasciola hepatica}

PAKLGWKIRGLQPVRLLEYLEYGEKYEEQIYERDDGEKWFSKKFELGLDLPLNLPYYIDDKCKLTQS
LAILRYIADKHGM

>d1gnwa2 c.47.1.5 (A:2-85) Glutathione S-transferase {Mouse-ear cress (Arabidopsis
thaliana)}

GIKVFGHPASIATRRVLIALHEKNLDFELVHVELKDGEHKKEPFLSRNPFQVPAFEDGDLKLFESRA
ITQYIAHRYENQGTNL

>d1axda2 c.47.1.5 (A:1-80) Glutathione S-transferase {Maize (Zea mays), type I}

APMKLYGAVMSWNLTRCATALEEAGSDYEIVPINFATAEHKSPEHLVRNPFQVPAQDGLDLYLFESR
AICKYAARKNKP

>d1aw9_2 c.47.1.5 (2-82) Glutathione S-transferase {Maize (*Zea mays*), type III}
APLKLYGMPLSPNVVRVATVLNEKGLDFEIVPVDLTTGAHKQPDFLALNPFQIPALVDGDEVLFESR
AINRYIASKYASE

>d1e6ba2 c.47.1.5 (A:8-87) Glutathione S-transferase {Mouse-ear cress (*Arabidopsis thaliana*), class zeta}
KLKLYSYWRSSCAHRVRIALALKGLDYEYIPVNLKGDQFDSDFKINPMGTVPALVDGDVVINDSFA
IIMYLDEKYPEP

>d1a0fa2 c.47.1.5 (A:1-80) Glutathione S-transferase {*Escherichia coli*}
MKLFYKPGACSLASHITLRESGKDFTLVSVDLMKKRLENGDDYFAVNPKGQVPALLLDDGTLLEGEV
AIMQYLADSVPR

>d1pmt_2 c.47.1.5 (1-80) Glutathione S-transferase {*Proteus mirabilis*}
MKLYYTPGSCSLSPHIVLRETGLDFSIERIDLRTKKTESGKDFLAINPKGQVPVLQLDNGDILTEGVAIV
QYLADLKPDR

>d1f2ea2 c.47.1.5 (A:1-80) Glutathione S-transferase {*Sphingomonas paucimobilis*}
MKLFISPGACSLAPHIALRETGADFEAVKVDLAVRKTEAGEDFLTVNPSGKVPALTLDSGETLTENPA
ILLYIADQNPAS

>d1g7oa2 c.47.1.5 (A:1-75) Glutaredoxin 2 {*Escherichia coli*}
MKLYIYDHCPCYCLKARMIFGLKNIPVELHVLLNDDAETPTRMVGQKQVPILQKDDSRYPESMDIV
HYVDKLDGK

>d1k0da2 c.47.1.5 (A:109-200) Yeast prion protein ure2p, nitrogen regulation fragment
{*Baker's yeast (Saccharomyces cerevisiae)*}
QPLEGYTLFHSRSAPNGFKVAIVLSELGFHYNTIFLDFNLGEHRAPEFVSVNPNARVPALIDHGMDN
LSIWESGAILLHLVNKYYKETGNPL

>d1k0dd2 c.47.1.5 (D:99-200) Yeast prion protein ure2p, nitrogen regulation fragment
{*Baker's yeast (Saccharomyces cerevisiae)*}
YSRITKFFQEQLPEGYTLFHSRSAPNGFKVAIVLSELGFHYNTIFLDFNLGEHRAPEFVSVNPNARVP
ALIDHGMDNLSIWESGAILLHLVNKYYKETGNPL

>d1k0ma2 c.47.1.5 (A:6-91) Chloride intracellular channel 1 (clic1) {Human (*Homo sapiens*)}
PQVELFVKAGSDGAKIGNCPFSQRLFMVLWLKGVTFNVTVDTKRRTETVQKLCPPGELPFLLYGTE
VHTDTNKIEEFLEAVLCP

>d2trcp_ c.47.1.6 (P:) Phosducin {Rat (*Rattus norvegicus*)}
EGQATHTGPKGVINDWRKFKLESEDGDSIPPSKKEILRQMSSPQSRDDKDSKERMSRKMSIQEYELI
HQDKEDEGCLRKYRRQCMQDMHQKLSFGPRYGFVYELETGEQFLETIEKEQKVTIVVNIYEDGVR
GCDALNSSLECLAAEYPMVKFCKIRASNTGAGDRFSSDVLPTLLVYKGGELISNFISVAEQFAEDFFAA
DVESFLNEYGLLPER

>d1a0rp_ c.47.1.6 (P:) Phosducin {Cow (*Bos taurus*)}
FEGQASHTGPKGVINDWRKFKLESDSDVAHSKKEILRQMSSPQSRDDKDSKERFSRKMSVQEYE
LIHKDKEDENCLRKYRRQCMQDMHQKLSFGPRYGFVYELESGEQFLETIEKEQKITTIVVHIYEDGIK
GCDALNSSLICLAAEYPMVKFCKIKASNTGAGDRFSSDVLPTLLVYKGGELLSNFISVTEQLAEFFFTG
DVESFLNEYGLLPEK

>d1g7ea_ c.47.1.7 (A:) Endoplasmic reticulum protein ERP29, N-domain {Rat (*Rattus norvegicus*)}
LHTKGALPLDVTFTFYKVIPKSKFVLVKFDTQYPYGEKQDEFKRLAENSASSDDLVAEVLGSDYGDKL

NMELSEKYKLDKESYPVFYLFDRDGFENPVPYSGAVKVGAIQRWLKGGVYVYVLM
>d1qgva_ c.47.1.8 (A:) spliceosomal protein U5-15Kd {Human (Homo sapiens)}
SYMLPHLHNGWQVDQAILSEEDRVVVIRFGHDWDPTCMKMDEVLYSIAEKVKNFAVIYLVLDITEVP
DFNKMYELYDPCTVMFFFRNKHIMIDLGTGNNNKINWAMEDKQEMVDIIEVYRGARKGRGLVVS
PKDYST
>d1eeja1_ c.47.1.9 (A:61-216) Disulfide bond isomerase, DsbC, C-terminal domain
{Escherichia coli}
NVTNKMLLKQLNALEKEMIVYKAPQEKHVITVFTDITCGYCHKLHEQMADYNALGITVRYLAFPRQ
GLSDSAEKEMKAIWCAKDKNKAFFDDVMAGKSVAPASCDVDIADHYALGVQLGVSGTPAVVLSNGTL
VPGYQPPKEMKEFLDEHQKMTSGK
>d1gp1a_ c.47.1.10 (A:) Glutathione peroxidase {Cow (Bos taurus)}
RTVYAFSARPLAGGEPFNLSSLRQKVLLENVASLXGTTVRDYTMNDLQRRLGPRGLVVLGFPCNQ
FGHQENAKNEEILNCLKYVRPGGGFEPNFMFLFEKCEVNGEKAPLFAFLREVLPTPSDDATALMTD
PKFITWSPVCRNDVSWNFELVGPDPGVPVRRYSRRFLTIDIEPDIETLLSQ
>d1qk8a_ c.47.1.10 (A:) Tryparedoxin I {Crithidia fasciculata}
GLDKYLPGLIEKLRGGEVEVKSLAGKLVFFYFSASWCPPCRGFTPQLIEFYDKFHESKNFEVVFCT
WDEEEDGFAGYFAKMPWLAVPFAQSEAVQKLSKHFNVESIPTLIGVDADSGDVVTTTRARATLVKDP
EGEQFPWKDA
>d1i5ga_ c.47.1.10 (A:) Tryparedoxin II {Crithidia fasciculata}
SGLKFFPYSTNVLKGAADIALPSLAGKTVFFYFSASWCPPSRAFTPQLIDFYKAHAEKKNFEVMLI
SWDESAEDFKDYAKMPWLALPFEDRKGMEFLTTFGFDVKSIPITLVGVEADSGNIITTTQARTMVVKD
PEAKDFPWPVN
>d1e2ya_ c.47.1.10 (A:) Tryparedoxin peroxidase (thioredoxin peroxidase homologue)
{Crithidia fasciculata}
GAAKLNHPAPEFDDMALMPNGTFKKVSLSSYKGYVVLFFYPMDFTFVCPTEIIFSDDAKRFAEIN
TEVISCSCDSEYSHLQWTSVDRKKGGLGPMIPLADKTKAIARAYGVLEDESGVAYRGVFIIDPNKG
LRQIIINDMPIGRNVEEVIRLVEALQFVEEHG
>d1qq2a_ c.47.1.10 (A:) Thioredoxin peroxidase 2 (thioredoxin peroxidase B, 2-cys
peroxiredoxin) {Norway rat (Rattus norvegicus)}
SGNAKIGHPAPSFKATAVMPDGQFKDISLSDYKGYVVLFFYPLDFTFVCPTEIIFSDRAEEFKKLNK
QVIGASVDSHSHLAWINTPKKQGGGLPMNIPLVSDPKRTIAQDYGVLEKADGEGISFRGLFIIDDKGILR
QITINDLPVGRSVDEILRLVQAFQFTDKHGEVCPA
>d1qmva_ c.47.1.10 (A:) Thioredoxin peroxidase 2 (thioredoxin peroxidase B, 2-cys
peroxiredoxin) {Human (Homo sapiens)}
SGNARIGKPAPDFKATAVVDGAFKEVKLSDYKGYVVLFFYPLDFTFVAPTEIIFSNRAEDFRKLGK
EVLGVSVDSDQFTHLAWINTPRKEGGLGPLNIPLADVTRRLSEYGVLEKADGEGISFRGLFIIDDKGILR
RQITVNDLPVGRSVDEALRLVQAFQYTDHGEVCPAGWKPGSDTIKPNVDDKEYFSKH
>d1hd2a_ c.47.1.10 (A:) Peroxiredoxin 5 {Human (Homo sapiens)}
APIKVGDAIPAVEVFEGEPGNKVNLAELFKGKGVLFVPGAFTPGCSKTHLPGFVEQAEALKAKGV
QVVAHSVNDFAVFTGEWGRAHKAEGKVRLLADPTGAFGKETDLLLLDSDLSVIFGNRRLLKRFMSMVVQ
DGIVKALNVEPDGTGLTCSLAPNIISQL
>d1prxa_ c.47.1.10 (A:) HorF6 peroxidase {Human (Homo sapiens)}
LLLGDVAPNFEANTTVGRIRFHDFLGDSWGILFSHPDRFTPVCTTELGRAAKLAPEFAKRNVKLI
SIDSVEDHLAWSKDINAYNSEEPTEKLPFIIDDRNRELAILLGMLDPAEKDEKMPVTARVVFVFGP

DKKLKLSILYPATTGRNFDEILRVVISLQLTAEKRVATPVDWKDGDSVMVLPTIPEEEAKKLFPGKGVF
TKELPSGKKYLRYTPQP

>d1kyga_c.47.1.10 (A:) Alkyl hydroperoxide reductase AhpC {*Salmonella typhimurium*}
SLINTKIKPFKNQAFKNGEFIEVTEKDTEGRWSVFFFYPADFTFVCPTELGDVADHYEELQKLGVDV
YSVSTDTHFTHKAWHSSSETIAKIKYAMIGDPTGALTRNFDNMREDEGLADRATFVVDPPQGIIQAIE
VTAEGIGRDASDLLRKIKAAQYVAAHPGEVCP

>d1jfua_c.47.1.10 (A:) Membrane-anchored thioredoxin-like protein TlpA, soluble domain
{*Bradyrhizobium japonicum*}
TGDPACRAAVATAQKIAPLAHGEVAALTMASAPLKLPLDAFEDADGKPKKLSDFRGTLLVNLWAT
WCVPCRKEMPALDELQKLSGPNFEVVAINIDTRDPEKPKTFLKEANLTRLGYFNDQKAKVFQDLK
AIGRALGMPTSVLVDPPQGCEIATIAGPAEWASEDALKLIRAATG

>d1foha3_c.47.1.10 (A:462-662) Phenol hydroxylase, C-terminal domain {Soil-living yeast
(*Trichosporon cutaneum*)}
NLVTDKKSSKQELAKNCVVGTRFKSQPVVRHSEGLWMHFGDRLVTDGRFRIIVFAGKATDATQMSR
IKKFSAYLDSSENSVISLYTPKVSDRNSRIDVITIHSCHRDDIEMHDFPAPALHPKWQYDFIYADCDSW
HHPHPKSYQAWGVDETKGAVVVVRPDGYTSLVTDLEGTAIEDRYFSGILVEPKEKSGAQTEADWTKS

>d1f37a_c.47.1.11 (A:) Thioredoxin-like 2Fe-2S ferredoxin {*Aquifex aeolicus*}
AEFKHVFCVQDRPPGHPQGSQAQRGSREVFQAFMEKIQTDPQLFMTTIVITPTGCMNACMMGPVV
VVYPDGVWYGQVKPEDVDEIVEKHLKGGEPVERLVISKGKPPGM

>d1j9ba_c.47.1.12 (A:) Arsenate reductase ArsC {*Escherichia coli*}
NITIIYHNACGTSRNTLEMIRNSGTEPTIILYLENPPSRDELVKLIADMGISVRALLRKNVEPYEQLGL
AEDKFTDDQLIDFMLQHPILINRPIVVTPGLTRLCRPSEVVDILQDAQKGAFTKEDGKVVDEAGK
RL

>d1qmha1_c.47.2.1 (A:185-279) RNA 3'-terminal phosphate cyclase, RPTC, insert domain
{*Escherichia coli*}
ERGNIVQMRGEVLLAGVPRHVAEREIATLAGSFSLEHQNIHNLPRDQPGNTVSLEVESENITERFFV
VGEKRVSAEVVAAQLVKEVKRYLASTA

>d1gpua3_c.48.1.1 (A:535-680) Transketolase {*Baker's yeast (Saccharomyces cerevisiae)*}
EGSSIESASKGGYVLQDVANPDIIIVATGSEVSLSVEAAKTAAKNIKARVVSPLDFFTFDKQPLEYRLS
VLPDNPIMSVEVLATTCWGKYAHQSFIDRFGASGKAPEVFKFFGFTPEGVAERAQKTIAFYKGDK
LISPLKCAF

>d1dtwb2_c.48.1.2 (B:205-342) Branched-chain alpha-keto acid dehydrogenase {*Human
(Homo sapiens)*}
PYNIPLSQAEVIQEGSDVTLVAVGTQVHVIREVASMKEKLGVSCEVIDLRTHIIPWDVDTICKSVIKTG
RLISHEAPLTGGFASEISSTVQEECFNLLEAPISRVCYDTPFPHIFEPFYIPDKWKCYDALRKMINY

>d1qs0b2_c.48.1.2 (B:206-339) 2-oxoisovalerate dehydrogenase E1b {*Pseudomonas putida*}
YYTVPLDKAAITRPGNDVSVLTYGTTVYVAQVAEESGVDAEVIDLRSLWPLDLDTIVESVKKTGRCV
VVHEATRTCGFGAELVSLVQEHCFFHLEAPIERTVGTWDTYPHPAQEWAYFPGPSRVGAALKKVMV

>d1ik6a2_c.48.1.2 (A:192-326) E1-beta subunit of pyruvate dehydrogenase {*Archaeon
Pyrobaculum aerophilum*}
DYVVEIGKARVAREGDDVTLVYGAHVHKALEAAERVKASVEVVDLQTLNPLDFDTVLKSVSKTGRL
IIAHDSPKTGGLGAEVRALVAEKALDRLTAPVIRLAGPDVPQSPIAADAAYAPTVERIIKAIYVMRY

>d1keka3_c.48.1.3 (A:259-415) Pyruvate-ferredoxin oxidoreductase, PFOR, domain II
{*Desulfovibrio africanus*}

KLFDYVVGAPDAERVIVSMGSSCETIEEVINHLAAKGEKIGLIKVRLYRPFVSEAFFAALPASAKVITVLD
RTKEPGAPGDPLYLDVCSAFVERGEAMPKILAGRYGLGSKEFSPAMVKSVDNMSGAKKNHFTVGIE
DDVTGTSPLVDNAFADTPK
>d1a49a3 c.49.1.1 (A:396-530) Pyruvate kinase, C-terminal domain {Rabbit (*Oryctolagus cuniculus*)}
ELARSSSHSTDLMEAMAMGSVEASYKCLAAALIVLTESGRSAHQVARYRPRAPIIAVTRNHQTARQA
HLYRGIFPVVCKDPVQEAWAEDVDLRVNLAMNVGKARGFFKKGDVVIVLTGWRPFGSGFTNTMRVV
PVP
>d1pkla3 c.49.1.1 (A:358-498) Pyruvate kinase, C-terminal domain {*Leishmania mexicana*}
NEYVFFNSIKKLQHIPMSADEAVCSSAVNSVYETKAKAMVVLSTGRSARLVAKYRPNCPIVCVTTRL
QTCRQLNITQGVESVFFDADKLGHDGEGKEHRVAAGVEFAKSKGYVQTGDYCVVIHADHKVKGYANQ
TRILLVE
>d1a3wa3 c.49.1.1 (A:367-500) Pyruvate kinase, C-terminal domain {*Baker's yeast (Saccharomyces cerevisiae)*}
DMRNCTPKPTSTTETVAASAVAAVFEQKAKAIIVLSTSGTTPRLVSKYRPNCPILVTRCPRAARFSLH
YRGVFPFVFEKEPVSDDTDDVEARINFGIEKAKEFGILKKGDYVSIQGFKAGAGHSNTLQVSTV
>d1e0ta3 c.49.1.1 (A:354-470) Pyruvate kinase, C-terminal domain {*Escherichia coli*}
ITEAVCRGAVETAEKLDAPLIVVATQGGKSARAVRKYFPDATILALTNEKTAHQVLVLSKGVVPQLVKE
ITSTDDFYRLGKELALQSGLAHKGDVVVMVSGALVPSGTTNTASVHVL
>d1e79g_ c.49.2.1 (G:) ATP syntase (F1-ATPase), gamma subunit {*Cow (Bos taurus)*}
ATLKDITRRLKSIKNIQKITKSMKMVAAAKYARAERELKPARVYGVGSLALYEKADIKTPEDKKKHLII
GVSSDRGLCGAIHSSVAKQMKSEANLAAAGKEVKIIGVGDKIRSILHRTHSDQFLVTFKEVGRRPPT
FGDASVIALELLNSGYEFDEGSIIFNRFRSVISYKTEEKPIFSLDTISSAESMSIYDDIDADVLQNYQEYS
LANIIYSLKESTTSEQSARMTAMDNASKNASEMIDKLTFTNRTRQAVITKELIEIISGAAAL
>d1mabg_ c.49.2.1 (G:) ATP syntase (F1-ATPase), gamma subunit {*Rat (Rattus norvegicus)*}
RDITRRLKSIKNIQKITKSMKMVAAAKYARAERELKPARVYGTGSLALYEKAEIKGPEDKKKHLIIGVS
SDRGLCGAIHSSVAKQMKNDMAALTAAGKEVMIVGIGEKIKSILYRTHSDQFLVSKVDVGRKPPPTFGD
ASVIALELLNSGYEFDEGSIIFNQFKSVISYKTEEKPIFSFSTVVAENMSIYDDIDADVLQNYQEYNLA
NIIYSLKESTTSEQSARMTAMDNASKNASDMIDKLTFTNRTRQAVITKELIEIISGAAALD
>d1fs0g_ c.49.2.1 (G:) ATP syntase (F1-ATPase), gamma subunit {*Escherichia coli*}
KITKAMEMVAASKMRKSQDRMAASRPYAEIMRKVIGHLAHGNLEYKHPYLEDRDVKRVGYLVVST
DRGLCGGLNINLFFKLLAEMKTWTDKGVQCDLAMIGSKGVSFFNSVGGNVVAQVTGMGDNPSLSEL
IGPVKVMLQAYDEGRDLKLYIVSNKFINTMSQVPTISQLPLPASDDDDLLKHKSWDYLYEPDPKALL
DTLLRRYVESQVYQGVVENLASEQAARMVAMK
>d1lam_1 c.50.1.1 (1-159) Leucine aminopeptidase, N-terminal domain {*Cow (Bos taurus)*}
TKGLVLGIYSKEKEEDEPQFTSAGENFNKLVSGKLREILNISGPPLKAGKTRTFYGLHEDFPSVVVGL
GKKTAGIDEQENWHEGKENIRAABAAGCRQIQDLEIPSVEVDPCGDAQAAAEGAVLGLYEYDDLKQK
RKVVVSAKLHGSEDQEAQWQRGVL
>d1kmma1 c.51.1.1 (A:326-424) Histidyl-tRNA synthetase (HisRS), C-terminal domain
{*Escherichia coli*}
DPVVDIYLVASGADTQSAAMALAERLRDELPGVKLMTNHGGGNFKKQFARADKWGARVAVVLGES
EVANGTAVVKDLRSGEQTAVAQDSVAHLRLLG
>d1qe0a1 c.51.1.1 (A:326-420) Histidyl-tRNA synthetase (HisRS), C-terminal domain
{*Staphylococcus aureus*}

IEENLDFIVTMGDQADRYAVKLLNHLRHNGIKADKDYLRKIKGQMKQADRLGAKFTIVIGDQELE
NNKIDVKNMTTGESETIELDALVEYFKK
>d1h4vb1 c.51.1.1 (B:326-421) Histidyl-tRNA synthetase (HisRS), C-terminal domain
{*Thermus thermophilus*}
EKGPDLYLIPLTEEAVAEAFYLAEALRPRLRAEYALAPRKPAKGLLEEALKRGAAGFAGFLGEDEL RAGE
VTLKRLATGEQVRLSREEVPGYLLQALG
>d1atia1 c.51.1.1 (A:395-505) Glycyl-tRNA synthetase (GlyRS), C-terminal domain {*Thermus
thermophilus*}
QLAPIKVAVIPLVKNRPEITEYAKRLKARLLALGLGRVLYEDTGNIGKAYRRHDEVTGTPFAVTVDYDTI
GQSKDGTTRLKDTVTVRDRDTMEQIRLHVDELEGFLRERLRW
>d1qf6a1 c.51.1.1 (A:533-642) Threonyl-tRNA synthetase (ThrRS), C-terminal domain
{*Escherichia coli*}
FPTWLAPVQVVMNITDSQSEYVNELTQKLSNAGIRVKADLRNEKIGFKIREHTLRRVPYMLVCGDK
EVESGKVAVRTRRGKDLGSM DVNEVIEKLQQEIRSRSLKQLEE
>d1hc7a1 c.51.1.1 (A:277-403) C-terminal domain of ProRS {*Thermus thermophilus*}
RGLVLPRLAPIQVVIVPIYKDESRERVLEAAQGLRQALLAQGLRVHLDDRDQHTPGYKFHEWELKG
VPPRVELGPKDLEGGQAVLASRLGGKETLPLAALPEALPGKLD AFHEELYRRALAFREDH
>d1g5ha1 c.51.1.1 (A:343-469) The aaRS-like accessory subunit of mitochondrial
polymerase gamma, C-terminal domain {*Mouse (Mus musculus)*}
RKVLKLPCLAPIKVALDVGKGPTVELRQVCQGLLNELLENGISVWPGYSETVHSSLEQLH SKYDEM
SVLFSVLVTETTLENGLIQLRSRDTTMKEMMHISKLRDFLVKYLASASNVAALDHHHHH
>d1crza2 c.51.2.1 (A:7-140) TolB, N-terminal domain {*Escherichia coli*}
DSGVDSGRPIGVVFPQWAGPGAAPEDIGGIVAADLRNSGKFNPLDRARLPQQPGSAQEVQPAAWSA
LGIDAVVVGQVTPNPDGSYNVAYQLVDTGGAPGTVLAQNSYKVNKQWLR YAGHTASDEVFEKLTGIK
G
>d1eexb_ c.51.3.1 (B:) Diol dehydratase, beta subunit {*Klebsiella oxytoca*}
GFLTEVGEARQGTQQDEVIIAVGPAFGLAQTVNIVGIPHKSILREVIAGIEEEGIKARVIRCFKSSDVAFV
AVEGNRLSGSGISIGIQSKGTTVIHQQLPPLSNLELFPQAPLLTLETYRQIGKNAARYAKRESPQVP
TLNDQMARP KYQAKSAILHIKETKYVVVTGKNPQELRVA
>d1b78a_ c.51.4.1 (A:) XTP pyrophosphatase {*Archaeon Methanococcus jannaschii*}
KIYFATGNPNKIKEANIILKDLKDVEIEQIKISYPEIQGTLEEVAEFGAKWVYNILKKPVIVEDSGFFVE
ALNGFPGTYSKFVQETIGNEGILKLLLEGKDNRNAYFKTVIGYCDENG VRLFKGIVKGRVSEEIRSKGYG
FAYDSIFIP EEEERTFAEMTTEEK SQISHRKKAFEEFKKFLLDRI
>d1ex2a_ c.51.4.2 (A:) Maf protein {*Bacillus subtilis*}
MTKPLILASQSPRRKELLDLLQLPYSIIVSEVEEKLNRNFSPEENVQWLAKQKAKAVADLHPHAIVIG
ADTMVCLDGECLGKPDQEEAASMLRRLSGRSHSVITAVSIQAENHSETFYDKTEVAFWSLSEEEIW
TYIETKEPMDKAGAYGIQGRGALFVKKIDGDYYSVMGLPISKTMRALRHF
>d1ihna_ c.103.1.1 (A:) Hypothetical protein MT938 (MTH938) {*Archaeon
Methanobacterium thermoautotrophicum*}
SHMFSDCRFGSVTYRGREYRSDIVVHVDG SVTPRRKEISRKYGTSHVMAEEEELEELLEEKPEIIIIGS
GVHGALETGFRSDATVLP TCEAIKRYNEERSAGRRVAIIHVTC
>d1ckqa_ c.52.1.1 (A:) Restriction endonuclease EcoRI {*Escherichia coli*}
SQGVIGIFGDYAKAHD LAVGEVSKLVKKALSNEY PQLSFRYRDSIKKTEINEALKKIDPDLGGTLFVSN
SSIKPDGGIVEVKDDYGEWRVVLVAEAKHQGKDIINIRNGLLVGKRGDQDLMAAGNAIERSHKNISEI

ANFMLESEHFPPYVLFLEGSNFLTENISITRPDGRVVNLEYNSGILNRLDRLTAANYGMPINSNLCINKF
VNHKDKSIMLQAASIYTQGDGREWDSKIMFEIMFDISTTSLRVLGRDLFEQLTSK

>d1az3a_c.52.1.2 (A:) Restriction endonuclease EcoRV {Escherichia coli}
SLRSDLINALYDENQKYDVCGIISAEGKIYPLGSDTKVLSTIFELFSRPIINKIAEKHGYIVEEPKQQNH
PDFTLYKPSEPNNKIAIDIKTTYTNKENEKIKFTLGGYTSFIRNNTKNIVYFPDQYIAHWIIGVYTRV
ATRKSSLKTYNINELNEIPKPYKGVKVFQDKWVIAGDLAGSGNTTNIGSIHAHYKDFVEGKGFIDSE
DEFLDYWR

>d1eona_c.52.1.2 (A:) Restriction endonuclease EcoRV {Escherichia coli}
SLRSDLINALYDENQKYDVCGIISAEGKIYPLGSDTKVLSTIFELFSRPIINKIAEKHGYIVEEPKQQNH
PDFTLYKPSEPNNKIAIDIKTTYTNKENEKIKFTLGGYTSFIRNNTKNIVYFPDQYIAHWIIGVYTRV
ATRKSSLKTYNINELNEIPKPYKGVKVFQDKWVIAGDLAGSGNTTNIGSIHAHYKDFVEGKGFIDSE
DEFLDYWRNYERTSQLRNDKYNNISEYRNWIYRGRK

>d1bam_c.52.1.3 (-) Restriction endonuclease BamHI {Bacillus amyloliquefaciens}
MEVEKEFITDEAKELLSKDKLIQQAYNEVKTSICSPIWPATSKTFTINTEKNCNGVVPKELCYTLL
DTYNWYREKPLDILKLEKKKGGPIDVYKEFIENSELKRVMFETGNISSAHRSMNKKLLGLKHGEI
DLAAILMPIKQLAYYLTDRVTNFEELPYFELTEGQPFIFIGFNAEAYNSNVPLIPKGS DGM SKRSIKK
WKDKVENK

>d1dmua_c.52.1.4 (A:) Restriction endonuclease BglI {Bacillus subtilis}
MYNLHREKIFMSYNQNKQYLEDNPEIQEKIELYGLNLLNEVISDNEEEIRADYNEANFLHPFWMNY
PPLDRGKMPKGDQIPWIEVGEKAVGSKLTRLVVSQREDITVREIGLPTGPDERYLLTSPITYSLTNGFTD
SIMMFVDIKSVGPRSDYDLVLSNPQVSGNGDWAQLEGGIQNNQQTIQGPRSSQIFLPTIPPLYILSDG
TIAPVVHLFIKPIYAMRSLTKGDTGQSLYKIKLASVPNGLGLFCNPGYAFDSAYKFLFRPGKDDRTKSL
LQKRVRVDLRVLDKIGPRVMTIDMDK

>d1dfma_c.52.1.5 (A:) Restriction endonuclease BglII {Bacillus subtilis}
MKIDITDYNHADEILNPQLWKEIEETLLKMPLHVKASDQASKVGLIFDPVGTNQYIKDELVPKHWK
NNIPIPKRFDFLGTDIDFGKRDTLVEVQFSNYPFLNNTVRSSELFHKSNDIDEEGMKVAIIITKGHM
FPASNSSLYEQAQNQLNSLAEYNVFDVPIRLVGLIEDFETDIDIVSTTYADKRYRTITKRDTVKGKVI
DTNTPNTRRRKRGITIVY

>d3pvia_c.52.1.6 (A:) Restriction endonuclease PvuII {Proteus vulgaris}
SHPDLNKLLELWPHIQEYQDLALKHGINDIFQGGGKLLQVLLITGLTVLPGREGNDAVDNAGQEYE
LKSINIDLTKGFSTHHMNPVIIAKYRQVPWIFAIYRGIAIEAIYRLEPKDLEFYDYDKWERKWYSDGH
KDINNPPIPVKYVMEHGTKIY

>d1cfr_c.52.1.7 (-) Restriction endonuclease Cfr10I {Citrobacter freundii}
MDIISKSGEGNKYTINSAIAFVAYASHIDINTTEFSKVLGLRDFINDEAIRLGGKISDGSFNKCGDWY
EWLIGIRAIEFFLESETNFIVVKMPNATSFVMSIYKSCLEFIYDLRSKLSLNNVNLITSNPDFSIIDIR
GRREELKSMKDISFSNISLSTISEIDNLYKNFIDYAELEHIKSFLSVKTTFRPDRRLQLAHEGSLMKAL
YTHLQTRTWTINPTGIRYAAATSIGNADVIGLKT VATHSITDVKSLPQSAVDEIFKINSVLDVDSCLS
HIL

>d1knva_c.52.1.7 (A:) Restriction endonuclease Bse634I {Bacillus stearothermophilus}
NLTNSNCVEEYKENGKTKIRIKPFNALIELYHHQTPTGSIKENLDKLENYVKDVKAKGLAIPTS GAF
SNTRGTWFEVMIAIQSWNYRVKRELNDYLIKMPNVKTFDFRKIFDNETREKLHQLKSLTHKQQ
VRLITSNPDLLIIRQKDLIKSEYNLPINKLTHENIDVALTLFKDIEGKCKWDSLVAGVGLKTSLRPDRRL
QLVHEGNILKSLFAHLKMRYWNPKAEFKYGASSEPVSKADDDALQTAATHIVNVNSTPERAVDDI
FSLTSFEDIDKMLDQIIKK

>d1d02a_ c.52.1.8 (A:) Restriction endonuclease MunI {Eubacteria (Mycoplasma unidentified)}

LSGRLNWQALAGLKASGAEQNLYNVFNAVFEGETKYVLYEKPKHLKNLYAQVVL PDDVIKEIFNPLIDL
STTQWGVSPAFAIENTETHKILFGEIKRQDGWVEGKDP SAGRGN AHERSCKLFTPGLLKAYRTIGGIN
DEEILPFWVVFEGDITRDPKRVREITFWYDHYQDNYFMWRPNESGEKLVQHFNEK LKKYLD

>d1ev7a_ c.52.1.9 (A:) Restriction endonuclease NaeI {Nocardia aerocolonigenes}

EPDDDLERV RATLYSLDPDGDRTAGVLRDTLDQLYD GQRTGRWNFDQLHKTEKTHMGTLVEINLH
REFQFGDGFETDYEIAGVQVDCKFMSQGAWMLPPESIGHICLVIWASDQQCAW TAGLVKVIPQFLG
TANRDLKRRLTPEGRAQVVKLWPDHGK LQENLLLHIPGDVRDQIFSAKSSRGNQH GQARVNELFRR
VHGRLIGRAVIATVAQQDDFMKRV RSGGARSILRPEGIILGHQDNDPKVANDLGLPVP RKGQVVAA
RVVPADEGDQRQTAEIQRRWAVAVPGDPIVEAPVV

>d1fiua_ c.52.1.10 (A:) Restriction endonuclease NgoIV {Neisseria gonorrhoeae}

MQPLFTQERRIFHKLLDGNILATNNRGVVSNADGSNTRSFNIAKGIADLLHSETV SERLPGQTSGN
AFEAICSEFVQSAFEKLQHIRPGDWNV KQVGSRNRL EARIYQQY AHLTALAKAAEENPELAAALGSD
YTITPDIIVTRNLIADAEINRNEFLVDENIATYASLRAGNGNMPLLHASISCKW TIRSDRAQNARSEGL
NLVRNRKGR LPHIVVTA EPTPSRISSIALGTGEIDCVYHFALYELEQILQSLNYEDALDLFYIMVNGK
RLKDISDLPLDLAV

>d1dc1a_ c.52.1.11 (A:) Restriction endonuclease BsoBI {Bacillus stearothermophilus}

KPFENHLKSVDDLKTTYEEYRAGFIAFALEKNKRSTPYIERARALKVAASVAKTPKDLLYLEDIQDAL
LYASGISDKAKKFLTEDDKKESINNL IENFLEPAGEEFIDELIFRYLLFQGD SLGGTMRNIAGALAQK L
TRAIISALDIANIPYKWLDSRD KKYTNWMDKPEDDY ELETFAKGISW TINGKHR TLMYNITVSLVKK
NVDICLFNCEPEIYTPQKVHQQPEKYLLL GELKGGIDPAGADEHWKTANTALTRIRNK FSEKGLSPKT
IFIGAAIEHSM AEEIWDQLQSGSLTNSANLTKTEQVGS LCRWIINI

>d1kc6a_ c.52.1.19 (A:) Restriction endonuclease HincII {Haemophilus influenzae}

SFIKPIYQDINSILIGQKVKRPKSGT LSGHAAGEPF EKLVYKFLKENLSDLTFKQYEYLN DLFMKNPAII
GHEARYKLFNSPTLLFLLSRGKAATENWSIENLFEEKQNDTADILLVKDQFYELLDVKTRNISKSAQA
PNIISAYKLAQTCAK MIDNKEFDLFDINYLEVDWELNGEDLVCVSTSF AELFKSEPSELYINWAAAMQ
IQFHVRDL DQGFNGTREEWAKSYLKH FVTQAEQRAISMIDKFVKPFK KYIL

>d2foka4_ c.52.1.12 (A:387-579) Restriction endonuclease FokI, C-terminal (catalytic domain) {Flavobacterium okeanoicoites}

KSELEEKSELRHKLKYVPHEYIELIEIARNSTQDRILEMKVMEFFMKVYGYRGKHLGGSRKPDGAIY
TVGSPIDYGVIVDTKAYSGGYNLPIGQADEMQRV EENQTRNKHINPNEW WKVYPSSVTEFKFLFVS
GHFKGNYKAQLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLTLEEVRRKFNNGEINF

>d1avqa_ c.52.1.13 (A:) lambda exonuclease {Bacteriophage lambda}

SHMTPDIILQRTGIDVRAVEQGD DAWHKLRLGVITASEVHNVI AKPRSGKKWPD MKMSYFHTLLAE
VCTGV APEVNAKALAWGKQYENDARTLFEFTSGVNVTESPIIYRDESMRTACSPDGLCSDGNGL ELK
CPFTSRDFMKFRLGGFEAIKSAYMAQVQYS MWVTRKN AWYFANYDPRMKREGLHYV VIERDEKY
MASFDEIVPEFIEKMDEALAEIGFVFGEQWR

>d1azo_ c.52.1.14 (-) DNA mismatch repair protein MutH from {Escherichia coli}

PRLLSPPETEEQLLAQAQQLSGYTLGEL AALVGLVTPENLKRDKGWIGV LLEIWL GASAGSKPEQDF
AALGVELKTIPVDSLGRPLETTFVCVAPLTGNSGVTWETSHVRHKLKRVLWIPVEGEASIP LAQRRV
GSPLLWSPNEEEDRQLREDWEELMDMIVLGQVERITARHGEYLQIRPKAANAKALTEAIGARGERIL
TLPRGFYLLKKNFTSALLARHFLIQ

>d1cw0a_ c.52.1.15 (A:) Very short patch repair (VSR) endonuclease {Escherichia coli}

ADVHDKATRSKNMRAIATRDTAIEKRLASLLTGQGLAFRVQDASLPGRPDFVVEYRCVIFTHGCFW
HHHHCYLFKVPATRTEFWLEKIGKNVERDRRDISRLQELGWRVLIWECALRGREKLTDEALTERL
EEWICGEGASAQIDTQGIHLLA

>d1vsra_ c.52.1.15 (A:) Very short patch repair (VSR) endonuclease {Escherichia coli}
AIEKRLASLLTGQGLAFRVQDASLPGRPDFVVEYRCVIFTHGCFWHHHHCYLFKVPATRTEFWLEK
IGKNVERDRRDISRLQELGWRVLIWECALRGREKLTDEALTERLEEWICGEGASAQIDTQGIHLLA

>d1f1za2 c.52.1.16 (A:8-168) TnsA endonuclease, N-terminal domain {Escherichia coli}
FSEVQIARRIKEGRGQGHGKDYIPWLTVQEVPSGRSHRIYSHKTGRVHHLLSDLELAVFLSLEWESS
VLDIREQFLLPSDTRQIAIDSGIKHPVIRGVDQVMSTDFLVDCKDGPFEQFAIQVKPAAALQDERTL
EKLELERRYWQQKQIPWFIFTDKEI

>d1fzra_ c.52.1.17 (A:) Endonuclease I (Holliday junction resolvase) {Bacteriophage T7}
SGLEDKVSKQLESKGIKFEYEEWKVPYVIPASNHTYTPDFLLPNGIFVKTGLWESDDRKKHLLIRE
QHPELDIRIVFSSRRTKLYKGSPTSYPGEFCEKHGKIFADKLIPAEWIKEPKKEVPFDRLKRR

>d1gefa_ c.52.1.18 (A:) Archaeal Holliday junction resolvase Hjc {Archaeon Pyrococcus
furius}
MYRKAQAERELIKLLEKHGFVRSAGSKKVDLVAGNGKKYLCIEVKVTKKDHLVVGKRDGMRLIE
FSRRFGGIPVLAVKFLNVGWRFIEVSPKIEKFVFTPSSGVSLEVLLGIQKTLE

>d1hh1a_ c.52.1.18 (A:) Archaeal Holliday junction resolvase Hjc {Archaeon Sulfolobus
solfataricus}

SAVERNIVSRLRDKGFVVRAPASGSKRKDPIPDIALKNGVILIEMKSRKDIEGKIYVRREQAEGIIIEF
ARKSGSLFLGKPKPGVLKFIPEKLRRTETGNYVADSEIEGLDLEDLVRLVEAKISRTLD

>d1a79a1 c.52.2.1 (A:83-179) tRNA splicing endonuclease, C-terminal domain {Archaeon
Methanococcus jannaschii}
ERLCLKYLVIKDLRTRGYIVKTGLKYGADFRLYERGANIDKEHSVYLVKVPEDSSFLLSELTGFVRVA
HSVRKLLIAIVDADGDIVYYNMTYVKP

>d1dzfa1 c.52.3.1 (A:5-143) Eukaryotic RPB5 N-terminal domain {Baker's yeast
(Saccharomyces cerevisiae)}
NERNISRLWRAFRTVKEMVKDRGYFITQEEVELPLEDFKAKYCDMSGRPQRKMMSFQANPTEESIS
KFPDMGSLWVEFCDEPSVGVTMKTFFVIHQEKNFQTGIFVYQNNITPSAMKLVSPATIETFNEA
ALVVN

>d1gdta2 c.53.1.1 (A:1-140) gamma,delta resolvase, catalytic domain {Escherichia coli}
MRLFGYARVSTSQQSLDIQVRALKDAGVKANRIFTDKASGSSDRKGLDLLRMKVEEGDVILVKKLD
RLGRDTADMIQLIKEFDAQGVSIKFIDGISTDGEMGKVVTTILSAVAQAERQRILERTNEGRQEAM
AKGVVF

>d1hx7a_ c.53.1.1 (A:) gamma,delta resolvase, catalytic domain {Escherichia coli}
MRLFGYARVSTSQQSLDIQVRALKDAGVKANRIFTDKASGSSDRKGLDLLRMKVEEGDVILVKKLD
RLGRDTADMIQLIKEFDAQGVSIKFIDGISTDGEMGK

>d2rsla_ c.53.1.1 (A:) gamma,delta resolvase, catalytic domain {Escherichia coli}
MRLFGYARVSTSQQSLDIQVRALKDAGVKANRIFTDKASGSSDRKGLDLLRMKVEEGDVILVKKLD
RLGRDTADMIQLIKEFDAQGVSIKFIDGISTDGEMGKVVTTILSAVAQAERQRI

>d1tfr_2 c.53.1.2 (12-180) T4 RNase H {Bacteriophage T4}
KEGICLIDFSQIALSTALVNFDPKEKINLSMVRHLILNSIKFNVKKAKTLGYTKIVLCIDNAKSGYWRR
DFAYYYKKNRGKAREESTWDWEGYFESSHKVIDELKAYMPYIVMDIDKYEADDHIAVLVKKFSLEG
HKILIISSDGDFTQLHKYPNVKQWSPMHKKWVKI

>d1bgxt2 c.53.1.2 (T:1-173) 5' to 3' exonuclease domain of DNA polymerase <i>Taq</i>
{*Thermus aquaticus*}

MRGMLPLFEPKGRVLLVDGHHLAYRTFHALKGLTTSRGPVQAVYGFASLLKALKEDGDAVIVVFD
AKAPSRHEAYGGYKAGRPTPEDFPRQLALIKELVDLLGLARLEVPGYEADDVLASLAKKAEKEGY
EVRILTADKDLQLLSDRIHVLHPEGYLITPAWLWEKYG

>d1xo1a2 c.53.1.2 (A:19-185) T5 5'-exonuclease {Bacteriophage T5}

RRNLMIVDGTNLGFRFKHNSKPPFASSYVSTIQSLAKSYSARTTIVLGDGKGSVFRLEHLPEYAGNR
DEKYAQRTEEEKALDEQFFEYLKDAFELCKTTFTFTIRGVEADDMAYIVKLIGHLYDHVWLST
GDWDTLLTDKVSRSFTTRREYHLRDMYEHNN

>d1a77_2 c.53.1.2 (2-208) Flap endonuclease-1 {Archaeon *Methanococcus jannaschii*}

GVQFGDFIPKNIISFEDLKGKKVAIDGMNALYQFLTSIRLQDGSPLRNRKGEITSAYNGVFYKTIHLL
DITPIWVFDGEPKLEKTRKVRREMKEKAELKMKEAIKKEDFEEAAKYAKRVSYLTPKMVENCKY
LLSLMGIPYVEAPSEGEAQASYMAKKGDVWAVVSQDYDALLYGAPRVVRNLTTTKEMPELIELNEVL
EDLR

>d1b43a2 c.53.1.2 (A:1-219) Fen-1 nuclease {Archaeon *Pyrococcus furiosus*}

GVPIGEIIPRKEIELENYGKKIAIDALNAIQFLSTIRQKDGTPLMDSKGRITSHLSGLFYRTINLMEAG
IKPVYVFDGEPPEFKKLEKRREAREEAEKWKREALEKGEIEEARKYAQRATRVNEMLIEDAKLL
ELMGIPVQAPSEGEAQAYMAAKGSVYASASQDYDLSLFGAPRLVRNLTTGKRKLPKKNVYVEIKP
ELIILEEVLKELK

>d1ekja_ c.53.2.1 (A:) beta-carbonic anhydrase {Pea (*Pisum sativum*)}

EASERIKTGFLHFKEKYDKNPALYGELAKGQSPPFMVAFACSDSRVCPSHVLDVDFQPGAEFVVRNVAN
LVPPYDQAKYAGTGAAIEYAVLHLKVSNIIVVIGHSACGGIKGLLSFPFDGTYSTDFIEEWVKIGLPAKA
KVKAQHGDAPFAELCTHCEKEAVNASLGNLLTYPFVREGLVNKTLALKGGYDFVKGSEFELWGLEFG
LSSTFSV

>d1g5ca_ c.53.2.1 (A:) beta-carbonic anhydrase {Archaeon *Methanobacterium thermoautotrophicum*}

IIKDILRENQDFRFRDLSDLKHSPKLCIITCMLSRLIDLLERALGIGRDAKVIKNAGNIVDDGVIRSA
VAIYALGDNEIIVGHTDCGMARLDEDLIVSRMRELGVVEEVIENFSIDVLPVGDDEENVIIEGVKRLK
SSPLIPESIGVHGLIIDINTGRLKPLYLDE

>d1i6pa_ c.53.2.1 (A:) beta-carbonic anhydrase {*Escherichia coli*}

KDIDTLISNNALWSKMLVEEDPGFFEKLAQAQKPRFLWIGCSDSRVPAERLTGLEPGELFVHRNVAN
LVIHTDLNCLSVVQYAVDVLEVEHIIICGHYCGGVQA AVENPELGLINNWLLHIRDIWFKHSSLLGE
MPQERRDLTCELNVMEQVYNLGHSTIMQSAWKRQKVTIHGWAYGIHDGLLRDLDTATNRETL
EQRYRHGISNLKLLK

>d1ddza1 c.53.2.1 (A:84-325) beta-carbonic anhydrase {Red alga (*Porphyridium purpureum*)}

VMSDLEKKFIELEAKLVAQPAGQAMPKSNIFANNEAWRQEMLKQDPEFFNRLANGQSPEYLWIGC
ADSRVPANQLLDLPAGEV FVHRNIANQCIHSDISFLSVLQYAVQYLKVKHILVCGHYCGGAKAALGD
SRLGLIDNWL RHIRDVRRMNAKYLDKCKDGEELNRLIELNVLEQVHNVCATSIVQDAWDAGQELT
VQGVVYGVGDGKLRDLGVVVNSDDISKFYRTKSDSGALKAG

>d1ddza2 c.53.2.1 (A:326-564) beta-carbonic anhydrase {Red alga (*Porphyridium purpureum*)}

NPNAPLVQVTKGGESELDSTMEKLTAEVQQTGPKLKEGANRVFVNNENWRQKMLKQDPQFFSNL
AHTQTPEILWIGCADSRVPANQIINLPAGEV FVHRNIANQCIHSDMSFLSVLQYAVQYLKVKRVVVCG

HYACGGCAAALGDSRLGLIDNWLRRHVDVRRHNQAELSRITDPKDSLNRLEINVLEQMHNVCATSI
VQDAWDAGQELEVQGVVYGVGDGKLRDMGVVAKANDDIG
>d1pdo_ c.54.1.1 (-) IIA domain of mannose transporter, IIA-Man {Escherichia coli}
TIAIVIGTHGWAAEQLLKTAEMLLGEQENVGWIDFVPGENAETLIEKYNAQLAKLDTTKGVLFLVDT
WGGSPFNAASRIVVDKEHYEVIAGVNIPMLVETLMARDDDDPSFDELVALAVETGREGVKALK
>d1bupa1 c.55.1.1 (A:4-188) Heat shock protein 70kDa, ATPase fragment {Cow (Bos
taurus)}
GPAVGIDLGSTYSCVGVFQHGKVEIANDQGNRTTPSYVAFTDTERLIGDAAKNQVAMNPTNTVFDA
KRLIGRRFDDAVVQSDMKHWPFMVVNDAGRPKVQVEYKGETKSFYPEEVSSMVLTKMKEIAEAYL
GKTVTNAVVTVPAYFNDSQRQATKDAGTIAGLNVLRIINEPTAAAIAYGLDKK
>d1bupa2 c.55.1.1 (A:189-381) Heat shock protein 70kDa, ATPase fragment {Cow (Bos
taurus)}
VGAERNVLIFFDLGGGTFDVSILTIEDGIFEVKSTAGDTHLGGEDFDNRMVNHFAIEFKRKHKKDISEN
KRAVRRRLRTACERAKRTLSSSTQASIEIDSLYEGIDFYTSITRARFEELNADLFRGTLDPVEKALRDAK
LDKSQIHDIVLVGGSTRIPKIQKLLQDFFNGKELNKSINPDEAVAYGAAVQAAILS
>d1hjoa1 c.55.1.1 (A:3-188) Heat shock protein 70kDa, ATPase fragment {Human (Homo
sapiens)}
KAAAIGIDLGTTYSCVGVFQHGKVEIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPQNTVFD
AKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEISSMVLTKMKEIAEAYL
GYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGLDRT
>d1hjoa2 c.55.1.1 (A:189-382) Heat shock protein 70kDa, ATPase fragment {Human (Homo
sapiens)}
GKGERNVLIFFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNHVVEEFKRKHKKDISQN
KRAVRRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRARFEELCSDLFRSTLEPVEKALRDAK
LDKAQIHDIVLVGGSTRIPKVQKLLQDFFNGRDLNKSINPDEAVAYGAAVQAAILMG
>d1dkgd1 c.55.1.1 (D:3-185) Heat shock protein 70kDa, ATPase fragment {Escherichia coli,
gene dnaK}
KIIGIDLGTTNSCVAIMDGTTPRVLENAEGDRTPPSIIAYTQDGETLVGQPAKRQAVTNPQNTLFAIKR
LIGRRFQDEEVQRDVSIMPFKIIAADNGDAWVEVKGQKMAPPQISAEVLKMKKTAEDYLGEVTE
AVITVPAYFNDAQRQATKDAGRIAGLEVKRIINEPTAAALAYGLDKGT
>d1dkgd2 c.55.1.1 (D:186-383) Heat shock protein 70kDa, ATPase fragment {Escherichia
coli, gene dnaK}
GNRTIAVYDLGGGTFDISIIEIDEVDGEKTFEVLATNGDTHLGGEDFDSRLINYLVEEFKKDQGIDLRN
DPLAMQRLKEAAEKAKIELSSAQQTVDVNLPIYITADATGPKHMNIKVTRAKLESVLVDLVNRSIELLKV
ALQDAGLSVSDIDDVILVGGQTRMPMVQKKVAEFFGKEPRKDVNPDEAVAIGAAGVQGGVLT
>d1j6za1 c.55.1.1 (A:4-146) Actin {Rabbit (Oryctolagus cuniculus)}
ETTALVCDNGSGLVKAGFAGDDAPRAVFPISVGRPRHQGVVMGMGQKDSYVGDEAQSKRGILTLYP
IEHGIIITNWDDMEKIWHHTFYNELRVAPPEEHPTLLTEAPLNPKANREKMTQIMFETFNVPAMYVAI
QAVLSLYASG
>d1j6za2 c.55.1.1 (A:147-372) Actin {Rabbit (Oryctolagus cuniculus)}
RTTGIVLDSGDGVTHNVPIYEGYALPHAIMRLDLAGRDLTDYLMKILTERGYSFVTTAEREIVRDIKE
KLCYVALDFENEMATAASSSSLEKSYELPDGQVITIGNERFRCPETLFQPSFIGMESAGIHETTYNSIM
KCDIDIRKDLYANNVMSGGTTMYPGIADRMQKEITALAPSTMKIKIIPPERKYSVWIGGSILASLSTF
QQMWITKQEYDEAGPSIVHR

>d1d4xa1 c.55.1.1 (A:4-146) Actin {Nematode (Caenorhabditis elegans)}
EVAALVVDNGSGMCKAGFAGDDAPRAVFP SIVGRPRHQGVMVGMGQKDSYVGDEA QSKRGILT LKY
PIEHGIVTNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAPLNPKANREKMTQIMFETFNTPAMYV
AIQAVLSLYASG

>d1d4xa2 c.55.1.1 (A:147-375) Actin {Nematode (Caenorhabditis elegans)}
RTTG VVLDSDGDGVTHTVPIYEGYALPHAILRLDLAGRDLTDYLMKILTERGYSFTTTAEREIVRDIKEK
LCYVALDFEQEMATAASSSLEKSYELPDGQVITVGNFRFCPEAMFQPSFLGMESAGIHETSYSIM
KCDIDIRKDL YANTVLSGGTTMYPGIADRMQKEITALAPSTMKIKI IAPPERKYSVWIGGSILASLSTF
QQMWISKQEYDESGPSIVHRKCF

>d1c0fa1 c.55.1.1 (A:1-146) Actin {Slime mold (Dictyostelium discoideum)}
DGEDVQALVIDNGSGMCKAGFAGDDAPRAVFP SIVGRPRHTGKDSYVGDEA QSKRGILT LKYPIEHGI
VTNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAPLNPKANREKMTQIMFETFNTPAMYVAIQAVL
SLYASG

>d1dga2 c.55.1.1 (A:147-375) Actin {Slime mold (Dictyostelium discoideum)}
RTTGIVMDSGDGVSH TVPIYEGYALPHAILRLDLAGRDLTDYMMKILTERGYSFTTTAEREIVRDIKE
KLAYVALDFEQEMATAASSSALEKSYELPDGQVITIGNERFRCPEALFQPSFLGMESAGIHETTYNSI
MKCDVDIRKDL YGNVVLGGTTMFPGIADRMNKELTALAPSTMKIKI IAPPERKYSVWIGGSILASLS
TFQQMWISKEEYDESGPSIVHRKCF

>d1yaga1 c.55.1.1 (A:4-146) Actin {Baker's yeast (Saccharomyces cerevisiae)}
EVAALVIDNGSGMCKAGFAGDDAPRAVFP SIVGRPRHQGIMVGMGQKDSYVGDEA QSKRGILT RYPI
EHGIVTNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAPMNPKNREKMTQIMFETFNVP AFYVSI
QAVLSLYSSG

>d1yaga2 c.55.1.1 (A:147-375) Actin {Baker's yeast (Saccharomyces cerevisiae)}
RTTGIVLDSGDGVTHV VPIYAGFSLPHAILRIDLAGRDLTDYLMKILSERGYSFSTTAEREIVRDIKEKL
CYVALDFEQEMQTAAQSSSIEKSYELPDGQVITIGNERFRAPEALFHPSVLGLESAGIDQTTYSIMKC
DVDVRKELYGNIVMSGTTMFPGIAERMQKEITALAPSSMKVKI IAPPERKYSVWIGGSILASLTTFQ
QMWISKQEYDESGPSIVHHKCF

>d1jcfa1 c.55.1.1 (A:1-140) Prokaryotic actin homolog MreB {Thermotoga maritima}
MLRKDIGIDLGTANTLVFLRGKIVVNEPSVIAIDSTTGEILKVGLEAKNMIGKTPATIKAIRP MRDGV I
ADYTVALVMLRYFINKAKGGMNLFKPRVVIGVPIGITDVERRAILDAGLEAGASKVFLIEEPMAAAIGS
N

>d1jcfa2 c.55.1.1 (A:141-336) Prokaryotic actin homolog MreB {Thermotoga maritima}
LNVEEPSGNMVVDIGGGTTEVAVISLGSIVTWESIRIAGDEMDEAIVQYVRETYRVAIGERTAERVKIE
IGNVFPSKENDELETTVSGIDLSTGLPRKLT LKGGEVREALRSVVVAIVESVRTTLEKTPPELVSDIIE R
GIFLTGGGSLRGLD TLLQKETGISVIRSEEPLTAVAKGAGMVL DKVNILKKLQGAG

>d1k8ka1 c.55.1.1 (A:3-160) Actin-related protein 3, Arp3 {Cow (Bos taurus)}
GRLPACVVDCGTGYTKLGYAGNTEPQFIIPSCIAIKESAKVGDQAQRVMKGVDDLDFFIGDEAIEKPT
YATKWPIRHGIVEDWDLMERFMEQVIFKYLRAEPEDHYFLLTEPPLNTPENREYTAEIMFESFNVP
GLYIAVQAVLALAASWTSRQVGE

>d1k8ka2 c.55.1.1 (A:161-418) Actin-related protein 3, Arp3 {Cow (Bos taurus)}
RTLGTVIDSGDGVTHVIPVAEGYVIGSCIKHIPIAGR DITYFIQQLLRDREVGIPPEQSLETAKAVKERY
SYVCPDLVKEFNKYD TDGSKWIKQYTGINAISKKEFSIDVGYERFLGPEIFFHPEFANPDF TQPISEVV
DEVIQNCPIDVRRPLYKNIVLSGGSTMFRDFGRRLQRDLKRTVDARLKLSEELSGGRLKPKPIDVQVI
THHMQR YAVWFGGSM LASTPEFYQVCHTKKDYEEIGPSICRHNPVFGVMS

>d1k8kb1 c.55.1.1 (B:154-343) Actin-related protein 2, Arp2 {Cow (Bos taurus)}
GVVVDSGDGVTHICPVYEGFSLPHLTRRLDIAGRDITRYLIKLLLLRGYAFNHSADFETVRMIKEKLCY
VGYNIEQEQKLALETTVLVESYTLPDGRIIKVGGGERFEAPEALFQPHLINVEGVGVAELLFNTIQAADI
DTRSEFYKHIVLSGGSTMYPGPLPSRLERELKQLYLERVLKGDVEKLSKFKIR

>d1e4ft1 c.55.1.1 (T:7-199) Cell division protein FtsA {Thermotoga maritima}
TVFYTSIDIGSRYIKGLVLGKRQDEWEALAFSSVKSRLDEGEIKDAIAFKESVNTLLKELEEQLQKSL
RSDFFVISFSSVSFEREDTVIERDFGEEKRSITLDILSEMQSEALEKLEKENGKTPHIFSKRYLLDDERIV
FNPLDMKASKIAIEYTSIVVPLKVYEMFYNFLQDTVKSPFQLKSSLVSTAEGVL

>d1e4ft2 c.55.1.1 (T:200-390) Cell division protein FtsA {Thermotoga maritima}
TTPEKDRGVVVVNLGYNFTGLIAYKNGVPIKISYVVPVGMKHVIKDVSAVLDTSEESERLIITHGNNAVY
NDLKEEEIQYRGLDGNITIKTTTAKKLSVIIHARLREIMSKSKKFFREVEAKIVEEGEIGIPGGVVLTTGG
GAKIPRINELATEVFKSPVRTGCYANSRPSIINADEVANDPSFAAAFGNVFA

>d1huxa_ c.55.1.5 (A:) Hydroxyglutaryl-CoA dehydratase component A {Acidaminococcus fermentans}
SIYTLGIDVGSTASKCIILKDGKEIVAKSLVAVGTGTSGPARSISEVLENAHMKKEDMAFTLATGYGRNS
LEGIADKQMSELSCHAMGASFIWPNVHTVIDIGGQDVKVIHVENGTMNFMNDKCAAGTGRFLD
VMANILEVKVSDLAELGAKSTKRVAISSTCTVFAESEVISQLSKGTDKIDIIAGIHRSVASRVIGLANRVG
IVKDVVMTGGVAQNYGVRGALEELGVEIKTSPLAQYNGALGAALYAYKKA

>d1g99a1 c.55.1.2 (A:1-156) Acetate kinase {Archaeon Methanosarcina thermophila}
MKVLVINAGSSSLKYQLIDMTNESALAVGLCERIGIDNSIITQKKFDGKKLEKLTDLPTHKDALEEVVK
ALTDDEFVGIKDMGEINAVGHRVHVHGGEKFTTSALYDEGVEKAIKDCFELAPLHNPMMGISACAE
IMPGTPMVIVFDTAHFHTMP

>d1g99a2 c.55.1.2 (A:157-398) Acetate kinase {Archaeon Methanosarcina thermophila}
PYAYMYALPYDLYEKHGVRKYGFHGTSHKYVAERAALMLGKPAEETKIITCHLNGSSITAVEGGKSV
ETSMGFPTLEGLAMGTRCGSIDPAIVPFLMEKEGLTTREIDTLMNKKSGVLGVSGLSNDFRDLDEAA
SKGNRKAELALEIFAYKVKKFIGEYSAVLNGADAVVFTAGIGENSASIRKRILTGLDGIGIKIDDEKNI
RGQEIDISTPDAKVRVFIPTNEELAIARETKEIVET

>d1ig8a1 c.55.1.3 (A:18-224) Hexokinase {Baker's yeast (Saccharomyces cerevisiae), pII}
DVPKELMQQIENFEKIFTVPTETLQAVTKHFISELEKGLSKKGGNIPMIPGWVMDFPTGKESGDFLAI
DLGGTNLRVVLVVLKGGDRFTDTTQSKYRLPDAMRTTQNPDELWEFIADSLKAFIDEQFPQGISEPIP
LGFTFSFPASQNKINEGILQRWTKGFDIPNIENHDVVPMLQKQITKRNIPIEVVALINDTTGTLVASYY
TDP

>d1ig8a2 c.55.1.3 (A:225-486) Hexokinase {Baker's yeast (Saccharomyces cerevisiae), pII}
ETKMGVIFGTGVNGAYYDVCSIDIEKLQGLSDDIPPSAPMAINCEYGSFDNEHVLPRTKYDITIDEE
SPRPGQQTFEKMSSGYLGEILRLALMDMYKQGFIFKNQDLSKFDKPFVMDTSYPARIEEDPFENLE
DTDDLQNEFGINTTVQERKLIRRLSELIGARAARLSVCGIAAICQKRGYKTGHIAADGGSVYNYRYPGF
KEKAANALKDIYGTWQTSLDDYPIKIVPAEDGSGAGAAVIAALAQAQKRIAEGKSVGIIGA

>d1bdg_1 c.55.1.3 (13-222) Hexokinase {Blood fluke (Schistosoma mansoni)}
FSDQQLFEKVVEILKPFDLVVDYEEICDRMGESMRLGLQKSTNEKSSIKMFPSYVTKTPNGTETGN
FLALDLGGTNYRVLSVTLEGKGSQPRIQERTYCIPEAKMSGSGTELFKYIAETLADFLENNGMKDKKF
DLGFTFSFPCVQKGLTHATLVRWTKGFSADGVEGHNAELLQTELDKRELVKCVAVVNDTVGTLAS
CALEDP

>d1bdg_2 c.55.1.3 (223-460) Hexokinase {Blood fluke (Schistosoma mansoni)}
KCAVGLIVGTGTNVAYIEDSSKVELMDGVKEPEVVINTEWGFGEKGEKELDCWRTQFDKSMIDSLHP

GKQLYEKMVSGMYLGELVRHIIVYLVEQKILFRGDLPERLKVRNSLLTRYLTDVERDPAHLLYNTHYM
LTDDLHVPVVEPIDNRIVRYACEMVVKRAAYLAGAGIACILRRINRSEVTVGVDGSLYKFHPKFCERM
TDMVDKLPKNTFRCLRLSEDSGSGKAAAIAASC

>d1czan1 c.55.1.3 (N:16-222) Mammalian type I hexokinase {Human (Homo sapiens)}
DDQVKKIDKYLYAMRLSDETLIDIMTRFRKEMKNGLSRDFNPTATVKMLPTFVRSIPDGSEKGFIA
LDLGGSSFRILRVQVNHEKNQNVHMESEVYDTPENIVHGSGSQLFDHVAECLGDFMEKRKIKDKKL
PVGFTFSFPCQQSKIDEAILITWTKRFKASGVEGADVVKLLNKAIKKRGDYDANIVAVVNDTVGTMM
TCGYDDQ

>d1czan2 c.55.1.3 (N:223-465) Mammalian type I hexokinase {Human (Homo sapiens)}
HCEVGLIIGTGTNACYMEELRHIDLVEGDEGRMCINTEWGAFGDDGSLEDIRTEFDRAIDAYS LNPG
KQLFEKMVSGMYLGELVRLILVKMAKEGLLFEGRITPELLTRGKFNTSDVSAIEKNKEGLHNAKEILT
RLGVEPSDDDCVSVQHVTIVSFRSANLVAATLGAILNRLRDNKGTPRLRRTTVGVDGSLYKTHPQYSR
RFHKTLRRLVPDSDVRFLSESGSGKGAAMVTAVAYRLAE

>d1czan3 c.55.1.3 (N:466-670) Mammalian type I hexokinase {Human (Homo sapiens)}
QHRQIEETLAHFHLTKDMLLEVKKRMRAEMELGLRKQTHNNAVVKMLPSFVRRTPDGTENGDFL
ALDLGGTNFRVLLVKIRSGKKRTVEMHNKIYAIPLEIMQGTGEELFDHIVSCISDFLDYMGIKGPRMPL
GFTFSFPCQQTSLDAGILITWTKGFKATDCVGHVVTLLRDAIKRREEFDLDVVAVVNDTVGTMMT
CAYEEP

>d1czan4 c.55.1.3 (N:671-913) Mammalian type I hexokinase {Human (Homo sapiens)}
TCEVGLIVGTGSNACYMEEMKNVEMVEGDQGMCMINMEWGAFDNGCLDDIRTHYDRLVDEYSLN
AGKQRYEKMISGMYLGEIVRNILIDFTKKGFLFRGQISETLKTGRGIFETKFLSQIESDR LALLQVRAILQ
QLGLNSTCDD SILVKTVCVVSRRAAQLCGAGMAAVVDKIRENRGLDRLNVTGVDGTYLKLHPHFS
RIMHQT VKELSPKCNVSFLLEDSGSGKGAALITAVGVRLRT

>d1bg3a1 c.55.1.3 (A:1-222) Mammalian type I hexokinase {Rat (Rattus norvegicus)}
MIAAQLLAYYFTELKDDQVKKIDKYLYAMRLSDEILIDILTRFKKEMKNGLSRDYNPTASVKMLPTFV
RSIPDGSEKGFIALDLGGSSFRILRVQVNHEKNQNVSMSEIYDTPENIVHGSGTQLFDHVADCLGD
FMEKKKIKDKKL PVGFTFSFPCRQSKIDEAVLITWTKRFKASGVEGADVVKLLNKAIKKRGDYDANI
VAVVNDTVGTMMTCGYDDQ

>d1bg3a2 c.55.1.3 (A:223-465) Mammalian type I hexokinase {Rat (Rattus norvegicus)}
QCEVGLIIGTGTNACYMEELRHIDLVEGDEGRMCINTEWGAFGDDGSLEDIRTEFDRELD RGS LNPG
KQLFEKMVSGMYMGEVRLILVKMAKEGLLFEGRITPELLTRGKFNTSDVSAIEKDKEGIQNAKEILT
RLGVEPSDVDCVSVQHICTIVSFRSANLVAATLGAILNRLRDNKGTPRLRRTTVGVDGSLYKMHPQYSR
RFHKTLRRLVPDSDVRFLSESGTGKGAAMVTAVAYRLAE

>d1bg3a3 c.55.1.3 (A:466-670) Mammalian type I hexokinase {Rat (Rattus norvegicus)}
QHIRQIEETLAHFRLSKQTLMEVKKRLRTEMEMGLRKETNSKATVKMLPSFVRSIPDGTEHGDFLA
LDLGGTNFRVLLVKIRSGKKRTVEMHNKIYSIPLEIMQGTGDELFDHIVSCISDFLDYMGIKGPRMPL
GFTFSFPCHQTNLDCGILISWTKGFKATDCEGHVAVSLLRDAVKRREEFDLDVVAVVNDTVGTMMT
CAYEEP

>d1bg3a4 c.55.1.3 (A:671-911) Mammalian type I hexokinase {Rat (Rattus norvegicus)}
TCEIGLIVGTGTNACYMEEMKNVEMVEGNQGMCMINMEWGAFDNGCLDDIRTD FDKV VDEYSLN
SGKQRF EK MISGMYLGEIVRNILIDFTKKGFLFRGQISEPLKTRGIFETKFLSQIESDR LALLQVRAILQ
QLGLNSTCDD SILVKTVCVVSKRAAQLCGAGMAAVVEKIRENRGLDHLNVTGVDGTYLKLHPHFS
RIMHQT VKELSPKCTVSFLLEDSGSGKGAALITAVGVRL

>d1bu6o1 c.55.1.4 (O:3-253) Glycerol kinase {Escherichia coli}

KKYIVALDQGTSSRAVVMHDANIISVSQREFEQIYPKPGWVEHDPMEIWATQSSTLVEVLTKADIS
SDQIAAIGITNQRETTIVWEKETGKPIYNAIVWQCRRTAEICEHLKRDGLEDYIRSNTGLVIDPYFSGT
KVKWILDHVEGSRERARRGELLFGTVDTWLIWKMTQGRVHVTDYTNASRTMLFNIHTLDWDDK
MLEVLDPREMLPEVRSSEVYQTNIGGKGGTRIPISGIAGDQQAALFGQ
>d1bu6o2 c.55.1.4 (O:254-499) Glycerol kinase {Escherichia coli}
LCVKEGMAKNYGTGCFMLMNTGEKAVKSENGLLTTIACGPTGEVNYALEGAVFMAGASIQWLRDE
MKLINDAYDSEYFATKVQNTNGVYVPAFTGLGAPYWDYPYARGAIFGLTRGVNANHIIRATLESIAEQ
TRDVLEAMQADSGIRLHALRVDGGAVANNFLMQFQSDILGTRVERPEVREVTALGAAYLAGLAVGF
WQNLDELQEKAVIEREFRPGIETTERNYRYAGWKKAVKRAMAWEEH
>d1chma1 c.55.2.1 (A:2-156) Creatinase {Pseudomonas putida}
QMPKTLRIRNGDKVRSTFSAQEYANRQARLRAHLAAENIDAAIFTSYHNINYYSDFLYCSFGRPYALV
VTEDDVISISANIDGGQPWRRVTGTDNIVYTDWQRDNYFAAIQALPKARRIGIEHDHLNLQNRDK
LAARYPDAELVDVAAACMRMR
>d1az9_1 c.55.2.1 (1-176) Aminopeptidase P {Escherichia coli}
SEISRQEFQRRRQALVEQMMPGSAALIFAPEVTRSADSEYPYRQNSDFWYFTGFNEPEAVLVLIKSD
DTHNHSVLFNRVRDLTAEIWFGRRLGQDAAPEKLGVDRALAFSEINQQLYQLLNGLDVVYHAQGEY
AYADVIVNSALEKLRKGSRQNLTPATMIDWRPVVHEMRLFK
>d1jl1a_ c.55.3.1 (A:) RNase H (RNase HI) {Escherichia coli}
KQVEIFTAGSALGNPGGYGAILRYRGREKTFSAGYTRTTNRMELMAAIVALEALKEHAEVILSTD
SQYVVRQGITQWIHNWKKRGWKTADKKPVKNVDLWQRLDAALGQHQIKWEWVKGHAGHPENER
ADELARAAAAMNPTLEDTGQVE
>d1ril_ c.55.3.1 (-) RNase H (RNase HI) {Thermus thermophilus}
RKRVALFTDGAACLNPGPGGWAALLRFHAHEKLLSGGEACTTNNRMELKAAIEGLKALKEPCEVDL
YTDShYLKKAFTEGWLEGWRKRGWRTAEGKPVKNRDLWEALLAMAPHRVRFHFVKGHTGHPE
NERVDREARRQAQSQAQT
>d1jl2a_ c.55.3.1 (A:) RNase H (RNase HI) {Chimeric (Escherichia coli/Thermus
thermophilus)}
KQVEIFTDGSALGNPGGYGAILRYRGREKTFSAGYTRTTNRMELKAAIEGLKALKEPAEVDLYT
DSHYLKKAFTEGWLEGWRKRGWRTAEGKPVKNRDLWEALLAMAPHRVRFHFVKGHAGHPENE
RADELARAAAAMNPTLEDTGQ
>d1ekea_ c.55.3.1 (A:) Class II ribonuclease H (RNase HII) {Archaeon Methanococcus
jannaschii}
MIIGIDEAGRGPVLGPMVVCFAFAIEKEREELKKGKDSKELTKNKRAYLKKLLENLGYVEKRILEA
EEINQLMNSINLNDIEINAFSKVAKNLIKLNIRDDEIEIYIDACSTNTKKFEDSFKDKIEDIIKERNLNI
KIAEHKADAKYPVVSAAIIAKAERDEIIDYYKKIYGDIGSGYPSDPKTIKFLDYFKKHKKLPDIART
HWKTCKRILDKSKQT
>d1i39a_ c.55.3.1 (A:) Class II ribonuclease H (RNase HII) {Archaeon Archaeoglobus
fulgidus}
MKAGIDEAGKGCVIGPLVVAGVACSDEDRLRKLGVKDSKLSQGRREELAEIIRKICRTEVLKVSPEN
LDERMAAKTINEILKECYAEIILRLKPEIAYVSPDVIPERLSRELEEITGLRVVAEHKADEKYPLVAAA
SIIAKVEREREIERLKEKFGDFGSGYASDPRTREVLKEWIASGRIPSCVRMRWKTVSNLRQK
>d1io2a_ c.55.3.1 (A:) Class II ribonuclease H (RNase HII) {Archaeon Thermococcus
kodakaraensis}
MKIAGIDEAGRGPVIGPMVIAAVVVDENSLPKLEELKVRDSKKLTPKRREKLFNEILGVLDYVILEL

PPDVIGSREGTLNEFEVENFAKALNSLKVKPDVIYADAADVDEERFARELGERLNFEAEVVAHKHAD
DIFPVVSAASILAKVTRDRAVEKLKEEYGEIGSGYPSDPRTAFLENYYREHGEPPIVRKGWKTLKK
IAEKVESEKK

>d1c9ra1 c.55.3.1 (A:430-558) HIV RNase H (Domain of reverse transcriptase) {Human immunodeficiency virus type 1}

EKEPIVGAETFYVDGAANAATKLGKAGYVTNKGRQKVPLTNTTNQKTELQAIYLALQDSGLEVNIV
TDSQYALGIIQAQPKSESELVNQIIEALIKKEAVYLAWVPAHAGIGGNAAVDALVSAGIAA

>d1hrha1 c.55.3.1 (A:432-556) HIV RNase H (Domain of reverse transcriptase) {Human immunodeficiency virus type 1}

EPIVGAETFYVDGAANRETKLGKAGYVTNKGRQKVPLTNTTNQKTELQAIYLALQDSGLEVNIVTD
SQYALGIIQAQPKSESELVNQIIEQLIKKEKVYLAWVPAHKGIGGNEQVDKLVSAGI

>d1jlaa1 c.55.3.1 (A:430-553) HIV RNase H (Domain of reverse transcriptase) {Human immunodeficiency virus type 1}

EKEPIVGAETFYVDGAANRETKLGKAGYVTNRGRQKVPLTNTTNQKTELQAIYLALQDSGLEVNIV
TDSQYALGIIQAQPKSESELVNQIIEQLIKKEKVYLAWVPAHKGIGGNEQVDKLVS

>d1vrta1 c.55.3.1 (A:430-539) HIV RNase H (Domain of reverse transcriptase) {Human immunodeficiency virus type 1}

EKEPIVGAETFYVDGAANRETKLGKAGYVTNRGRQKVPLTNTTNQKTELQAIYLALQDSGLEVNIV
TDSQYALGIIQAQPKSESELVNQIIEQLIKKEKVYLAWVPAH

>d1asu_ c.55.3.2 (-) Retroviral integrase, catalytic domain {Rous sarcoma virus (RSV, avian sarcoma virus)}

PLREPRGLGPLQIWQTDFTLEPRMAPRSWLAVTVDTASSAIVVTQHGRVTSVAAQHHWATAIAVLG
RPAIKTDNGSCFTSKSTREWLLARWGIAHTTGIPGNSQGQAMVERANRLKDKIRVLAEGDGFMK
RIPTSKQGELLAKAMYALNHFERGENTKTNL

>d1c0ma2 c.55.3.2 (A:49-216) Retroviral integrase, catalytic domain {Rous sarcoma virus (RSV, avian sarcoma virus)}

GVNPRGLGPLQIWQTDFTLEPRMAPRSWLAVTVDTASSAIVVTQHGRVTSVAVQHHWATAIAVLGR
PKAIKTDNGSCFTSKSTREWLLARWGIAHTTGIPGNSQGQAMVERANRLKDRIRVLAEGDGFMKRI
PTSKQGELLAKAMYALNHKERGENTKTPIQKHWRPT

>d1cxqa_ c.55.3.2 (A:) Retroviral integrase, catalytic domain {Rous sarcoma virus (RSV, avian sarcoma virus)}

GRGLGPLQIWQTDFTLEPRMAPRSWLAVTVDTASSAIVVTQHGRVTSVAAQHHWATAIAVLGRPKA
IKTDNGSCFTSKSTREWLLARWGIAHTTGIPGNSQGQAMVERANRLKDKIRVLAEGDGFMKRIPTS
KQGELLAKAMYALNH

>d1exqa_ c.55.3.2 (A:) Retroviral integrase, catalytic domain {Human immunodeficiency virus type 1}

SSPGIWQLDCTHLEGKVLVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKTIHTDNGSNFTG
ATVRAACDWAGIKQEDGIPYNPQSQGVVSMNKELKKIIGQVRDQAEHLKTAVQMAVFIHNKKRKG
GIGGYSAGERIVDIIATDIQ

>d1hya_ c.55.3.2 (A:) Retroviral integrase, catalytic domain {Human immunodeficiency virus type 1}

SPGIWQLDCTHLEGKVLVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKTVHTDNGSNFTST
TVKAACWWAGIKQEFIPYNPQSQGVIESMKNELKKIIGQVRDQAEHLKTAVQMAVFIHNKKRKGGI
GGYSAGERIVDIIATDIQT

>d1c6va_ c.55.3.2 (A:) Retroviral integrase, catalytic domain {Simian immunodeficiency virus}

NSDLGTWQMDCTHLEGKIVIVAVHVASGFIEAEVIPQETGRQTALFLLKLAGRWPITHLHTDNGANF
ASQEVKMAVWAGIEHTFGVPYNPQSQGVVEAMNHHLKNQIDRIREQANSVETIVLMAVHCMNH
KRRGGIGDMTPAERLINMITTEQEIQFQ

>d1bco_2 c.55.3.3 (258-480) mu transposase, core domain {Bacteriophage mu}

EHLDAMQWINGDGYLHNVFVRWFNGDVIRPKTWFWQDVKTRKILGWRCDSVENSIRSLSFMDV
VTRYGIPEDFHITIDNTRGAANKWLTGGAPNRYRFKVKEDDPKGLFLLMGAKMHWTSVAVAGKGGW
QAKPVERAFVGGLEEVVDKHPALAGAYTGPNPQAKPDNYGDRAVDAELFLKTLAEGVAMFNART
GRETEMCGGKLSFDDVFEREYARTIVRKP

>d1b7ea_ c.55.3.4 (A:) Transposase inhibitor (Tn5 transposase) {Escherichia coli}

SAEAIKAGAMQTVKLAQEFPELLAIEDTTSLSYRHQVAEELGKLSIQDKSRGWVHVSLLLEATT
FRTVGLLHQEWWMRPDDPADADEKESGKWLAAAATSRLRMGSMMSNVIAVCDREADIHAYLQDK
LAHNERFVVRSKHPRKDVESGLYLYDHLKNQPELGGYQISIPQKGVVDKRGKRKNRPARKASLSLRS
GRITLKQGNITLNAVLAEIINPPKGETPLKWLLLTSEPVESLAQALRVIDIYTHRWRIEEFHKAWKTG
AGAERQRMEEPDNLERMVSILSFVAVRLLQLRESFTLPQALRAQGLLKEAEHVESQAETVLTDEC
QLLGYLDKGRKRKEKAGSLQWAYMAIARLGGFMDSKRTGIASWGALWEGWEALQSKLDGFLAAKD
LMAQ

>d1f3ia_ c.55.3.4 (A:) Transposase inhibitor (Tn5 transposase) {Escherichia coli}

ALHRAADWAKSVFSSAALGDPRTARLVNVAQLAKYSGKSITISSEGSKAAQEGAYRFINPNVSAE
AIRKAGAMQTVKLAQEFPELLAIEDTTSLSYRHQVAEELGKLSIQDKSRGWVHVSLLLEATTFR
VGLLHQEWWMRPDDPADADEKESGKWLAAAATSRLRMGSMMSNVIAVCDREADIHAYLQDKLA
HNERFVVRSKHPRKDVESGLYLYDHLKNQPELGGYQISIPQKGVVDKRGKRKNRPARKASLSLRS
GRITLKQGNITLNAVLAEIINPPKGETPLKWLLLTSEPVESLAQALRVIDIYTHRWRIEEFHKAWKTG
AGAERQRMEEPDNLERMVSILSFVAVRLLQLRESFTLPQALRAQGLLKEAEHVESQAETVLTDEC
QLLGYLDKGRKRKEKAGSLQWAYMAIARLGGFMDSKRTGIASWGALWEGWEALQSKLDGFLAAKDL
MAQGIKIG

>d1kfsa1 c.55.3.5 (A:324-518) Exonuclease domain of prokaryotic DNA polymerase
{Escherichia coli}

MISYDNYVTILDEETLKAWIAKLEKAPVFAFDTETDSDLNISANLVGLSFAIEPGVAAAYIPVAHDYLD
PDQISRERALELLKPLLEDEKALKVGNLKYDRGILANYGIELRGIAFDTMLESYILNSVAGRHDMS
LAERWLKHKTTITFEEIAGKGNQLTFNQIALEEAGRYAAEDADVTLQLHLKMWPDLQK

>d1qtma1 c.55.3.5 (A:293-422) Exonuclease domain of prokaryotic DNA polymerase
{Thermus aquaticus}

ALEEAPWPPPEGAFFVGLSRKEPMWADLLALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLS
VLALREGLGLPPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEEAGERAAALSERLFANLWGRLEG

>d1xwl_1 c.55.3.5 (297-468) Exonuclease domain of prokaryotic DNA polymerase {Bacillus
stearothermophilus, newly identified strain as yet unnamed}

AKMAFTLADRVTEEMLADKAALVVEVVEENYHDAPIVGIAVVNEHGRFFLRPETALADPQFVAWL
DETKKSMFDSKRAAVALKWKGIELCGVSFDLLAAYLLDPAQGVDDVAAAAKMKQYEAVRPDEAV
YGKGAKRAVPDEPVLAEHLVRKAAAIWELERPFDELRRN

>d1t7pa1 c.55.3.5 (A:1-210) Exonuclease domain of T7 DNA polymerase {Bacteriophage T7}

MIVSDIEANALLESVTKFHCGVIYDYSTAIEYVSYRPSDFGAYLDALEAEVARGGLIVFHNGHKYDVPAL
TKLAKLQLNREFHLPRENCIDTLVLSRLIHSNLKDTDMGLLRSGKLPGALEAWGYRLGEMKGEYKD

DFKRMLEEQGEYVDGMEWWNFNEMMDYINVQDVVVTKALLEKLLSDKHYFPPEIDFTDVGYYT
FWSES

>d1noya_ c.55.3.5 (A:) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Bacteriophage T4}

DEFYISIE TVGNNIVERYIDEN GKERTREVEYLPTMFRHCKEESKYKDIYGKNCAPQKFPSMKDARD
WMKRMEDIGLEALGMNDFKLAYISDTYGSEIVYDRKFVRVANCDIEVTGDKFPDPMKAEYEIDAIT
HYDSIDDRFYVFDLLNSMYGSVSKWDAKLA AKLDCEGGDEVPQEILDRVIYMPFDNERDMLMEYIN
LWEQKRPAIFTGWNIEGFDVPYIMNRVKMILGERSMKRFSPIGRVKSKLLQNMYGSKEIYSIDGVSIL
DYLDLYKKFAFTNLPFSLESVAQHETKKGKLPYDGPINKLRETNHQRYISYNIIDVESVQAIDKIRGFI
DLVLSMSYYAKMPFSGVMSPIKTWD AIIFNSLKE

>d1ih7a1 c.55.3.5 (A:1-375) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Bacteriophage RB69}

MKEFYLTVEQIGDSIFERYIDSN GRERTREVEYKPSLFAHCPE SQATKYFDIYGKPCTRKLFANMRDA
SQWIKRMEDIGLEALGMDDFKLAYS DTYNYEIKYDHTKIRVANFDIEVTSPDGFPEPSQAKHPIDAI
THYDSIDDRFYVFDLLNSPYGNVEEWSIEIAAKLQE QGGDEVPSEIIDKIIYMPFDNEKELLMEYLN
WQKQTPVILTGWNVESFDIPYVYNRIKNIFGESTAKRLSPHRKTRVKVIENMYGSREIITLFGISVLDY
IDLYKKFSFTNQPSYSLDYISEFELNVGKLYDGPISKLR ESNHQRYISYNIIDVYRVLQIDAKRQFINLS
LDMGYAKIQISVFSPIKTWD AIIFNSLKE

>d1tgoa1 c.55.3.5 (A:1-347) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Archaeon Thermococcus gorgonarius}

MILDTDYITEDGKPVIRIFK KENGEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTVRVRAE
KVKKKFLGRPIEVWKLYFTHPQD VPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKM
LAFDIETLYHEGEEFAEGPILMISYADEEGARVITWKNIDL PYVDVSTEKEMIKRFLKVVKEKDPDV
LITYNGDNDFAYLKKRSEKLGVKFILGREGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYT
LEAVYE AIFGQPKKVVYAE EIAQAWETGEGLERVARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSL
WDVSRS

>d1qhta1 c.55.3.5 (A:1-347) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Archaeon Thermococcus sp., 9on-7}

MILDTDYITENGKPVIRVFK KENGEFKIEYDRTFEPYFYALLKDDSAIEDVKKVTAKRHGTTVVKVRA
EKVQKKFLGRPIEVWKLYFNHPQD VPAIRDRIRAHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELT
MLAFAIATLYHEGEEFGTGPI LMISYADGSEARVITWKKIDLPYVDVSTEKEMIKRFLRVVREKDPD
VLITYNGDNDFAYLKKRCEELGIKFTLGRDGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTY
TLEAVYEAVFGPKKVVYAE EIAQAWESGEGLERVARYSMEDAKVTYELGREFFPMEAQLSRLIGQS
LWDVSRS

>d1d5aa1 c.55.3.5 (A:1-347) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Archaeon Desulfurococcus tok}

MILDADYITEDGKPVIRVFK KEGEFKIDYDRDFEPYIYALLKDDSAIEDIKKITAERHGTTVRVTRAE
RVKKKFLGRPVEVWKLYFTHPQD VPAIRDKIREHPAVVDIYEYDIPFAKRYLIDRGLIPMEGDEELRM
LAFDIETLAHAGAAAGAGPILMISYADEEGARVITWKNIDL PYVESVSTEKEMIKRFLKVIQEKDPDV
LITYNGDNDFAYLKKRSEMLG VKFILGRDGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTY
TLETVYEPVFGQPAEKVYAE EIAEAWASGEGLERVARYSMEDAKATYELGKEFFPMEAQLSRLVGQS
LWDVSRS

>d1gcxa1 c.55.3.5 (A:1-347) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Archaeon Pyrococcus kodakaraensis}

MILDTDYITEDGKPVIRIFKKENGEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVE
KVQKKFLGRPVEVWKLYFTHPQDVPKIREHPAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKM
LAFDIETLYHEGEEFAEGPILMISYADEEGARVITWKNVDLPYVDVSTEREMIKRFLRVVKEKDPDV
LITYNGDNDFAYLKKRCEKLGINFALGRDSEPKIQRMGDRFAVEVKGRIHFDLVPVIRRTINLPTYT
LEAVYEAVFGQPKEKVYAEIITAWETGENLERVARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSL
WDVSRS

>d1fxa_ c.55.3.5 (A:) Exonuclease I {Escherichia coli}

QSTFLFDYETFGTHPALDRPAQFAAIRTDSEFNVIAGEPEVYCKPADDYLPQPGAVLITGITPQEARA
KGENEAAFAARIHSLFTVPKTCILGYNNVRFDDDEVTRNIFYRNFYDPYAWSWQHDNSRWDLLDVM
RACYALRPEGINWPENDDGLPSFRLEHLTKANGIEHSNAHDAMADVATIAMAHLVTRQPRFLDY
LFTHRNKHKLMALIDVPQMPLVHVSGMFGAWRGNTSWVAPLAWHPENRNAVIMVDLAGDISPL
LELSDTLRERLYTAKTDLGDNAAVPVKLVHINKCPVLAQANTLRPEDADRLGINRQHCLDNLKILR
ENPQVREKVVAIFAEAEPTPSDNVDAQLYNGFFSDADRAAMKIVLETEPRNLPALDITFVDKRIEKL
LFNYRARNFPGLDYAEQQRWLEHRRQVFTPEFLQGYADELQMLVQYADDKEKVALLKALWQYA
DEIVEH

>d1hja_ c.55.3.6 (A:) RuvC resolvase {Escherichia coli}

AHLGIDPGSRVTGYGVIRQVGRQLSYLGSQCIRTKVDDLPSRLKLIYAGVTEIITQFQPDYFAIEQVFMA
KNADSALKLGQARGVAIVA AVNQELPVFEYAAARQVKQTVVVGIGSAEKSQVQH MVRTLLKLPANPQAD
AADALAIATHCHVSQNAMQ

>d1kca2 c.55.3.7 (A:39-256) Mitochondrial resolvase ydc2 catalytic domain {Fission yeast
{Schizosaccharomyces pombe}}

TSRVLGIDLGIKNFSYCFASQNEFSKVIHNWSVENLTEKNGLDIQWTEDFQPSSMADLSIQLFNTLH
EKFNPHVILMERQYRSGIATIPWTLRVNMLESMYALHYAEKRNSIEQKIYQPFLLSLSPKSTYSY
WASVLNTKASFSSKSRVQMVKELIDGQKILFENEALYKWNNGSRVEFKKDDMADSALIASGWM
RWQAQLKHYRNFCKQFL

>d1jj2m_ c.55.4.1 (M:) Ribosomal protein L18 (L18p) {Archaeon Haloarcula marismortui}

ATGPRYKVP MRRRREARTDYHQRLRLKSGKPRLVARKSNKHVRAQLVTLGPNGGDTLASAHSSDL
AEYGWAEPTGNMPSAYLTGLLAGLRAQEAGVEEAVLDIGLNSPTPGSKVFAIQEGAI DAGLDIPHND
DVLADWQRTRGAHIAEYDEQLEEPLYSGDFDAADLPEHFDELRETLDDGDIEL

>d1fjgk_ c.55.4.1 (K:) Ribosomal protein S11 {Thermus thermophilus}

KRQVASGRAYIHASYNNTIVTITDPDGNPITWSSGGVIGYKGSRKGTYPYAAQLAALDAKKAMAYGM
QSVDVIVRGTGAGREQAIRALQASGLQVKSIVDDTPVPHNGCRPKKKFRKAS

>d1dt9a1 c.55.4.2 (A:143-276) Middle domain of eukaryotic peptide chain release factor
subunit 1, ERF1 {Human (Homo sapiens)}

DSKFGFVIDGSGALFGTLQGNTREVLHKFTVDLPKKGHRGGQSALRFARLRMEKRHNHYVRKVAET
AVQLFISGDKVNVAGLVLAGSADFKTELSQSDMFDQRLQSKVLKLVDISYGGENGFNQAIELSTEVLS

>d1eo1a_ c.55.5.1 (A:) Hypothetical protein MTH1175 {Archaeon Methanobacterium
thermoautotrophicum}

MKIAIASSGTDLGSEVSRFFGRAPYFMIVEMKKGNI ESSEVIENPSASASGGAGIRTAQIIANNVKA
ASSPGPNAFEVLNELGIKIYRATGTSVEENLKLFTEGNLEEIRSPGSGRGRRRR

>d1ewqa3 c.55.6.1 (A:121-266) DNA repair protein MutS, domain II {Thermus aquaticus}

LLQESLLPREANYLAAIATGDGWGLAFLDVSTGEFKGTVLKSKSALYDELFRHRPAEVL LAPELLENG
AFLDEFKRFRPVMLEAPFEPEGEGPLALRRARGALLAYAQR TQGGALS LQPFRFYDPGAFMRLPEA
TLRALEVF EPL

>d1e3ma3 c.55.6.1 (A:117-269) DNA repair protein MutS, domain II {Escherichia coli}
GTISDEALLQERQDNLLAAIWQDSKGFYATLDISSGRFRLSEPADRETMAAELQRTNPAELLYAEDF
AEMSLIEGRRLRRRPLWEFEIDTARQQLNLQFGTRDLVGFVGNAPRGLCAAGCLLQYAKDTQRTT
LPHIRSITMEREQDSIIM

>d1sfe_2 c.55.7.1 (12-92) Ada DNA repair protein {Escherichia coli}
LAVRYALADCELGRCLVAESERGICAILLGDDDATLISELQQMFPAADNAPADLMFQQHVREVIASLN
QRDTPLTLPLDIR

>d1qnta2 c.55.7.1 (A:6-91) O6-alkylguanine-DNA alkyltransferase {Human (Homo sapiens)}
EMKRTTLDSPGKLELSGCEQGLHEIKLLGKGTSAADAVEVPAPAAVLGGPEPLMQCTAWLNAYFHQ
PEAIEEFPVPALHHPVFQQ

>d1mgta2 c.55.7.1 (A:1-88) O6-alkylguanine-DNA alkyltransferase {Archaeon Pyrococcus
kodakaraensis}
MLSVEKFRVGERVVWIGVIFSGRVQGIAFADRGTLMKRIHDLAEHLGKRGVSISLDVQPSDYPEKVF
KVLIGELDNASFLRELSFEG

>d1cfza_ c.56.1.1 (A:) Hydrogenase maturing endopeptidase HybD {Escherichia coli}
MRILVLGVGNILLTDEAIGVRIVEALEQRYILPDYVEILDGGTAGMELLGDMANRDHLIADAIIVSKKN
APGTMILRDEEVPALFTNKISPHQLGLADVLSALRFTGEFPPKLLTVGVIPESLEPHIGLTPTEAMI
EPALEQVLAALRESGVEAIPRSDS

>d1c8ba_ c.56.1.2 (A:) Germination protease {Bacillus megaterium}
MEKELDSQYSVRTDLAVEAKDIALENQPKPNNQSEIKGVIVKEKEEQGVKISMVEITEEGAEIGKK
KGRYVTLSEVGIREQDTEKQEEAMEEVFAKELNFFIKSLNIPDDASCLVVLGNLSVTPDALGPKAVD
NLLITRHLFELQPESVQDGFPRVSAIVPGVMGMTGIETSDIIFGVVKKVNPDFIIAIDALAARSIERVNA
TIQISDSGIHPGSGVGNKRKEISYETLGIPIVIAIGIPTVVDVAVSITSDTIDFILKHFGRMKEQGKPSKSL
LPSGMTFGEKKKLTEDDLNNEEQRTYLGMIPTLPDEEKRRLIHEVLAPLGHNLMTVPKEVDMFIE
DMANVVAGGLNAALHHEVDQENFGAYTH

>d1ulb_ c.56.2.1 (-) Purine nucleoside phosphorylase, PNP {Human (Homo sapiens)}
MENGTYTYEDYKNTAEWLLSHTKHRPQVAIICGSLGGLTDKLTQAQIFDYSEIPNFPRSTVPGHAGRL
VFGFLNGRACVMMQGRFHMIEGYPLWKVTFPVRVFLHLLGVDTLVVTNAAGGLNPNFEVGDIMLIR
DHINLPGFSGQNPLRGPNDERFGDRFPAMSDAYDRMTMRQALSTWKQMGEQRELEQEGTYVMVAG
PSFETVAECRVLQKLGADAVGMSTVPEVIVARHCGLRVFGFSLITNKVIMDYESLEKANHEEVLAAGK
QAAQKLEQFVSILMASIPLPKAS

>d1b8oa_ c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP {Cow (Bos taurus)}
NGTYTYEDYQDTAKWLLSHTEQRPQVAVICGSLGGLVNKLTQAQTFDYSEIPNFPESTVPGHAGRLV
GILNGRACVMMQGRFHMIEGYPFWKVTFPVRVFRLLGVETLVVTNAAGGLNPNFEVGDIMLIRDHI
NLPGFSGENPLRGPNEERFGVRFAMPAMSDAYDRDMRQKAHSTWKQMGEQRELEQEGTYVMLGGPNF
ETVAECRLLRNLGADAVGMSTVPEVIVARHCGLRVFGFSLITNKVIMDYESQGANHEEVLEAGKQA
AQKLEQFVSLLMASI

>d1k9sa_ c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP {Escherichia coli}
ATPHINAEMGDFADVLLMPGDPLRAKYIAETFLEDAREVNNVRGMLGFTGTYKGRKISVMGHGMGI
PSCSIYTKELITDFGVKKIIRVGSAGVLPVHVKLRDVGIMGACTDSKVNRIKFDHDFAAIADFDMV
RNAVDAAKALGIDARVGNLFSADLFYSPDGEMFDVMEKYGILGVEMEAAGIYGVAEFGAKALTICT
VSDHIRTHEQTAAERQTTFNMIKIALESVLLGDK

>d1qe5a_ c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP {Cellulomonas sp.}
PPLDDPATDPFLVARAAADHIAQATGVEGHDMALVLGSGWGGAELLGEVVAEVPVTHEIPGFSSVTR

SIRVERADGSVRHALVLGSRTHLYEGKGVRAVVHGVRTAAATGAETLILTNGCGGLNQEWWAGTPVL
LSDHINLTARSPLEGPTFVDLTDVYSPRLRELAHRVDPTLPEGVYAQFPGPHYETPAEVRMAGILGAD
LVGMSTTLEAIAARHCGLEVLGVSLVTNLAAGISPTPLSHAIEVIEAGQAAGPRISALLADIKR
>d1g2oa_ c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP {Mycobacterium tuberculosis}
DPDELARRAAQVIADRTGIGEHDVAVVLGSGWLPVAALGSPTTVLPQAELPGFVPPTAAGHAGELL
SVPIGAHRVVLVLAGRIHAYEGHDLRYVVHPVRAARAAGAQMVLTAAGGLRADLQVGPVLSIDL
NLTARSPLVGGFVDLTDAYSRLRELARQSDPQLAEGVYAGLPGPHYETPAEIRMLQTLGADLVGMS
TVHETIAARAAGAIEVLGVSLVTNLAAGITGEPLSHAIEVLAAGAASATRMGALLADVIARF
>d1k3fa_ c.56.2.1 (A:) Uridine phosphorylase {Escherichia coli}
MSKSDVFHLGLTKNDLQGATLAIVPGDPDRVEKIAALMDKPVKLAHREFTTWRAELDGPVIVCS
TGIGGPSTSIAVEELAQLGIRTFRLRIGTTGAIQPHINVDVLTASVRLDGASLHFAPLEFPVAVDFEC
TTALVEAAKSIGATTHVGVTTASSDTFYPGQERYDYSGRVVRHFKGSMEEWQAMGVMNYEMESATL
LTMCASQGLRAGMVAGVIVNRTQQEIPNAETMKQTESHAVKIVVEAARRLL
>d1cb0a_ c.56.2.1 (A:) 5'-deoxy-5'-methylthioadenosine phosphorylase {Human (Homo
sapiens)}
AVKIGIIGGTGLDDPEILEGRTEKYVDTPFGKPSDALILGKIKNVDCVLLARHGRQHTIMP SKVNYQA
NIWALKEEGCTHVIVTTACGSLREEIQPGDIVIIDQFIDRTTMRPQSFYDGS HSCARGVCHIPMAEPFC
PKTREVLIETAKKGLRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVVLAKEAGICY
ASIAMATDYDCWKEHEEAVSVDRLKTLKENANKAKSLLLTIPQIGSTEWSETLHNLKNMAQFSV
LLP
>d1je0a_ c.56.2.1 (A:) 5'-deoxy-5'-methylthioadenosine phosphorylase {Archaeon Sulfolobus
solfataricus}
PVHILAKKGEVAERVLVVGDPGRARLLSTLLQNPKLTNENRGFLVYTGKYNGETVSIATHGIGGPSIAI
VLEELAMLGANVFIRYGTGALVPYINLGEYIIVTGASYNQGLFYQYLRDNACVASTPDFELTNKLV
SFSKRNLKYYVGNVFSDDAFYAEDEEFVKKWSSRGNIAVEMECATLFTLSKVKGWKSATVLVSDNL
AKGGIWITKEELEKSVMDGAKAVLDTLTS
>d2pth_ c.56.3.1 (-) Peptidyl-tRNA hydrolase {Escherichia coli}
TIKLIVGLANPGAIEAATRHAGAWFVDLLAERLRAPLREEAKFFGYTSRVTLGGEDVRLLVPTTFM
NLSGKAVAAMASFFRINPDEILVAHDELDLPPGVAKFKLGGGHGGHNGLKDII SKLGNNPNFHRLRIG
IGHPGDKNKVVGFLVGLKPPVSEQLIDEAIDEAARCTEMWFTDGLTKATNRLHAFKAQ
>d1a2za_ c.56.4.1 (A:) Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
{Archaeon Thermococcus litoralis}
MKKVLITGFEPFGGDSKNPTEQIAKYFDRKQIGNAMVYGRVLPVSVKRATIELKRYLEEIKPEIVINLG
LAPTYSNITVERIAVNIIDARIPDNDGYQPIDEKIEEDAPLAYMATLPVRAITKTLRDNIPATISYSAG
TYLCNYVMFKTLHFSKIEGYPLKAGFIHVYPYTPDQVVNKFFLLGKNTPSMCLEAEIKAIELAVKVS
LDYLEKDRDDIKIPL
>d1auga_ c.56.4.1 (A:) Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
{Bacillus amyloliquefaciens}
MEKKVLLTGDFPFGGETVNP SWEAVKRLNGAAEGPASIVSEVPTVFYKSLAVLREAIKKHQPDIIIC
VGQAGGRMQITPERVAINLNEARIPDNEGNQPVGEDISQGGPAAWTGLPIKRIVEEIKKEGIPAAVSY
TAGTFVCNHLFYGLMDEISRHHPHIRGGFIHIPYIPEQTLQKSAPSLSLDHITKALKIAAVTA AVHEDD
IETG
>d1iofa_ c.56.4.1 (A:) Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
{Archaeon Pyrococcus furiosus}

MKVLVTGFEPFGGEKINPTERIAKDLDDGKIGDAQVFGRLPVVFGKAKEVLEKTLEEIKPDIAIHVGL
APGRSAISIERIAVNAIDARIPDNEGKKIEDEPIVPGAPTAYFSTLPIKKIMKKLHERGIPAYISNSAGLYL
CNYVMYLSLHHSATKGYPKMSGFIHVPYIPEQIIDKIGKQVPPSMCYEMELEAVKVAIEVALEELL
>d2ctc_ c.56.5.1 (-) Carboxypeptidase A {Cow (Bos taurus)}
ARSTNTFNYATYHTLDEIYDFMDLLVAEHPQLVSKLQIGRSYEGRPYVLFKSTGGSNRPAIWIDLGIH
SREWITQATGVWFAKKFTEDYGDPSFTAILDSMDIFLEIVTNPDGFAFTHSQNRLWRKTRSVTSSS
LCVGV DANRNWDAGFGKAGASSSPCSEYHGKYANSEVEVKSIVDFVKDHGNFKAFLSIHSYSQLLL
YPYGYTTQSIPDKTELNQVAKSAVEALKSLYGTSYKYGSIIITTIYQASGGSIDWSYNQGIKYSFTFELRD
TGRYGFLLPASQIIPTAQETWLGVLTIMEHTLNN
>d1pca_1 c.56.5.1 (1-308) Carboxypeptidase A {Pig (Sus scrofa)}
ARTTSTFNYATYHTLEEIYDFMDILVAEHPALVSKLQIGRSYEGRPYVLFKSTGGSNRPAIWIDSGIHS
REWITQASGVWFAKKITENYQNSSFTAILDSMDIFLEIVTNPNGFAFTHSDNRLWRKTRSKASGSL
CVGSDSNRNWDAGFGGAGASSSPCAETYHGKYPNSEVEVKSITDFVKNNGNIKAFISIHSYSQLLLYP
YGYKTQSPADKSELNQIAKSAVAALKSLYGTSYKYGSIIITVIYQASGGVIDWTYNQGIKYSFSFELRDTG
RRGFLLPASQIIPTAQETWLALLTIMEHTLNN
>d1dtda_ c.56.5.1 (A:) Carboxypeptidase A {Human (Homo sapiens)}
FNFAYHTLEEISQEMDNLVAEHPGLVSKVNISSFENRPMNVLFKSTGGDKPAIWL DAGIHAREWV
TQATALWTANKIVSDYKDKPSITSILDALDIFLLPVTNPDG YVFSQTKNRMWRKTRSKVSAGSLCVG
VDPNRNWDAGFGGPGASSNPCSDSYHGPSANSEVEVKSIVDFIKSHGKVKAFIILHSYSQLLMFPYGY
KCTKLDDFDELSEVAQKAAQSLRSLHGTYKVGPICSVIYQASGGSIDWSYDYGIKYSFAFELRDTGRY
GFLLPARQILPTAETWLGKKAIMEHVRDHPY
>d1nsa_1 c.56.5.1 (4-308) Carboxypeptidase B {Pig (Sus scrofa)}
TTGHSYKEYNNWETIEAWTEQVTSKNPDLISRSAIGTTFDGDNIYLLKVGKPGSNKPAIFMDCGFHA
REWISQAFQCQWFVRDAVRTYGYEAHMTEFLDNLDYVLPVLNIDGYIYTWTNRMWRKTRSTNA
GSSCTGTDPNRNFNAGWCTVGASVNPCNETYCGSAAESEKETKALADFIRNNLSSIKAYLTIHSYSQ
MILYPYSYDYKLPENDAELNSLAKGAVKELASLYGTSYSYGPSTTIYPAAGSDDWAYNQGIKYSFTF
ELRDKGRFGFVLPESQIQATCQETMLAVKYVTNYTLEHL
>d1cpb_ c.56.5.1 (-) Carboxypeptidase B {Cow (Bos taurus)}
TTGHSYKEYNNWETIEAWTEQVASENPDLISRSAIGTTF LGNTIYLLKVGKPGSNKPAVFMDCGFHA
REWISPAFCQWFVREXXXXXXXXX EIHMT EFLDKLDFYVLPVVIDGYIYTWTNRMWRKTRSTRAGS
SCTGTDLNRNFDAGWCSIGASNNPCSEYCGSAAESEKESKAVADFIRNHLSSIKAYLTIHSYSQMML
YPYSYDYKLPKNNVELNTLAKGAVKKLASLHGTTYSYGP GATTIYPASGGSDDWAYDQGIKYSFTFEL
RDKGRYGFVLPESQIQPTCEETMLAIKYVTSYVLEHL
>d1h8la2 c.56.5.1 (A:4-304) Carboxypeptidase D, catalytic domain {Crested duck
(Lophonetta specularioides)}
QAVQPVD FRHHHFS DMEIFLRRYANEYPSITR LYSVGSVELRELYVMEISDNPGIHEAGEPEFKYIGN
MHGNEVVGRELLLN LIEYLCKNFGTDPEVTDLVQSTRIHIMPSMNP DGYEKSQEGDRGGTVGRNNS
NNYDLNRNFPDQFFQVTDPPQPETLAVMSWLKTYPFVLSANLHGGLVVNYPFDDDEQIAIYSKS
PDDAVFQQLALSYSKENKKMYQGS PCKDLYPTEYFPHGITNGAQWYNVPGGMQDWNYLNTNCFE
VTIELGCVKYPKAEELPKYWEQNRRSLLQFIKQVHR
>d1obr_ c.56.5.2 (-) Carboxypeptidase T {Thermoactinomyces vulgaris}
DFPSYDSGYHNYNEMVNKINTVASNYPNIVKKFSIGKSYEGRELWAVKISDNVGT DENEPEVLYTAL
HHAREHLTVEMALYTLDFLTQNYNLD SRITNLVNNREIYIVFNINPDGGEYDISSGSYKSWRKNRQP
NSGSSYVGTDLNRNYGYKWGCCGSSGSPSSEYRGRSAFSA PETAAMRDFINSRVVGGKQIKTLIT

FHTYSELILYPYGYTYTDVPSDMTQDDFNVFKTMANTMAQTNGYTPQQASDLYITDGDMDTDWAYG
QHKIFAFTFEMYPTSYPNGFYPPDEVIGRETSRNKEAVLYVAEKADCPYSVIGKSC
>d1lam_2 c.56.5.3 (160-484) Leucine aminopeptidase, C-terminal domain {Cow (Bos
taurus)}

FASGQNLARRLMETPANEMTPTKFAEIVEENLKSASIKTDVVFIRPKSWIEEQEMGSFLSVAKGSEEP
VFLEIHYPKGNASEPPLVFGVKGITFDSGGISIKAAANMDLMRADMGGAAATCSAIVSAAKLDLPINI
VGLAPLCENMPGKANKPGDVVRARNGKTIQVDNTDAEGRLLADALCYAHTFNPKVIINAATLTGA
MDIALGSGATGVFTNSSWLWNKLFESIETGDRVWRMPLFEHYTRQVIDCQLADVNNIGKYRSAGA
CTAAAFLEKFEVTHPKWAHLDIAGVMTNKDEVPLYLRKGMAGRPTRTLIEFLFRFSQ
>d1amp_ c.56.5.4 (-) Aminopeptidase {Aeromonas proteolytica}

MPPITQQATVTAWLPQVDASQITGTISSLESFTNRFYTTTSGAQASDWIASEWQALSASLPNASVKQV
SHSGYNQKSVVMTITGSEAPDEWIVIGGHLSTIGSHTNEQSVAPGADDDASGIAAVTEVIRVLSENN
FQPKRSIAFMAYAAEEVGLRGSQDLANQYKSEGNVVSALQLDMTNYKGSAQDVVFITDYTDSNFT
QYLTQLMDEYLPSTLYGFDTCGYACSDHASWHNAGYPAAMPFESKFNDYNPRIHTTQDTLANSPT
GSHAKKFTQLGLAYAIEMGSATG
>d1qq9a_ c.56.5.4 (A:) Aminopeptidase {Streptomyces griseus}

APDIPLANVKAHLTQLSTIAANNGGNRAHGRPGYKASVDYVVKAKLDAAGYTTTLQFTSGGATGYN
LIANWPGGDPNKVLMAGAHLDVSSGAGINDNGSGSAAVLETALAVSRAGYQPKHLRFWWGAE
ELGLIGSKFYVNNLPSADRSKLAGYLNFDMIGSPNPGYFVYDDDPVIEKTFKNYFAGLNVPTETETEG
DGRSDHAPFKNVGVPVGGFTGAGYTKSAAQAQKWGGTAGQAFDRCYHSSCDLSLNINDTALDRNS
DAAAHAIWTLSS
>d1cg2a1 c.56.5.4 (A:26-213,A:327-414) Carboxypeptidase G2, catalytic domain
{Pseudomonas sp., strain rs-16}

QKRDNVLFQAATDEQPAVIKTLEKLVNIETGTGDAEGIAAAGNFLEAELKNLGFVTRSKSAGLVVGD
NIVGKIKGRGGKNNLLMSHMDTVYLKGLAKAPFRVEGDKAYGPGIADDKGGNAVILHTLKLKEYG
VRDYGTITVLFNTDEEKGSFGSRDLIQEEAKLADYVLSFEPTSAGDEKLSLGTXFNAGEGKKLVDKA
VAYYKEAGGTLGVEERTGGGTDAAYAALSGKPVIESLGLPGFGYHSDKAEYVDISAIPRRLYMAARLI
MDLGAG
>d1de4c3 c.56.5.5 (C:122-189,C:383-608) Transferrin receptor ectodomain, protease-like
domain {Human (Homo sapiens)}

LYWDDLKRKLSEKLDSTDFSTIKLLNENSYPREAGSQKDENLALYVENQFREFKLSKVWRDQHF
VKXEIKILNIFGVIKGFVEPDHYVVGAQRDAWGPGAAGKSGVGTALLLKLQMFSDMVLKDFQPSR
SIIFASWSAGDFGSGATEWLEGYLSSLHLKAFTYINLKDKAVLGTSNFKVSASPLLYTLIEKTMQNVK
HPVTGQFLYQDSNWASKVEKLTLDNAAFPFLAYSIGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPE
LNKVARAAAEEVAGQFVIKLTHDVELN
>d1boub_ c.56.6.1 (B:) LigB subunit of an aromatic-ring-opening dioxygenase LigAB
{Pseudomonas paucimobilis}

ARVTTGITSSHIPALGAAIQTGTSNDYWGVPVFKGYQPIRDWIKQPGNMPDVVILVYNDHASAFDMN
IIPFAIGCAETFKPADEGWGPRVVDVKGHPDLAWHIAQSLILDEFDMTIMNQMDVDHGCTVPLS
MIFGEPEEWPCVKVIPPVNVVYTPPPSGKRCFALGDSIRAAVESFPEDLNVHVWGTGGMSHQLQGP
RAGLINKEFDLNFIDKLISDPEELSKMPHIQYLRESGSEGVLMWLIMRGALPEKVRDLYTFYHIPA
SNTALGAMILQPEETAGTPLEPRKVMMSGHSL
>d1di6a_ c.57.1.1 (A:) MogA {Escherichia coli}

ATLRIGLVSISDRASSGVYQDKGIPALEEWLTSALTTPELETRLIPDEQAIEQTLCELVDEM SCHLVLT

TGGTGPARRDVTPDATLAVADREMPGFGEQMRQISLHFVPTAILSQRQVGVIRKQALILNLPGQPKSIK
ETLEGVKDAEGNVVVHGIFASVPYCIQLLEGPYVETAPEVVAAFRPKSARR
>d1jlja_ c.57.1.1 (A:) Gephyrin N-terminal domain {Human (Homo sapiens)}
HQIRVGVLTVSDSCFRNLAEDRSGINLKDVLVQDPSLLGGTISAYKIVPDEIEEIKETLIDWCDEKELNLI
LTTGGTGFAPRDVTPEATKEVIEREAPGMALAMLMGSLNVTPLGMLSRPVCGIRGKTLIINLPGSKKG
SQECFQFILPALPHAIDLLRDAIVKVKEVHD
>d1eava_ c.57.1.1 (A:) Plant CNX1 G domain {Mouse-ear cress (Arabidopsis thaliana)}
GPEYKVAILTVDSTVSAGAGPDRSGPRAVSVVDSSEKLGGAQVAVVAVPDEVERIKDILQKWSDVD
EMDLILTLGGTGFTRPDVTPEATKKVIERETPGLLFVMMQESLKITPFAMLSRSAAGIRGSTLIINMP
GNPNAVAECMEALLPALKHALKQI
>d1g8la3 c.57.1.2 (A:178-326) MoeA, central domain {Escherichia coli}
VRVALFSTGDELQLPGQPLGDGQIYDTNRLAVHLMLEQLGCEVINLGIIRDDPHALRAAFIEADSQAD
VVISSGGVSVGEADYTKTILEELGEIAFWKLAIKPGKPFAGFKLSNSWFCGLPGNPVSATLTFYQLVQP
LLAKLSGNTASG
>d1bgva2 c.58.1.1 (A:1-194) Glutamate dehydrogenase {Clostridium symbiosum}
SKYVDRVIAEVEKKYADEPEFVQTVEEVLSSLGPVVDHAPEYEEVALLERMVIPERVIEFRVPWEDD
NGKVHVNTGYRVQFNAGAIPYKGLRFAPSVNLSIMKFLGFQAFKDSLTLPLMGGAKGGSDFDPNG
KSDREVMRFCQAFMTELYRHIGPDIDVPAGDLGVGAREIGYMYGQYRKIVGGFYNGVLTG
>d1gtma2 c.58.1.1 (A:3-180) Glutamate dehydrogenase {Archaeon Pyrococcus furiosus}
ADPYEIVIKQLERAAQYMEISEEAEFLKRPQRIVEVTIPVEMDDGSVKVFTGFRVQHNWARGPTKG
GIRWHPEETLSTVKALAAWMTWKTAVMDLPYGGGKGGIIVDPKCLSREKERLARGYIRAIYDVISP
YEDIPAPDVYTNPQIMAWMMDEYETISRRKTPAFGIITGKPLSI
>d1euza2 c.58.1.1 (A:4-180) Glutamate dehydrogenase {Archaeon Thermococcus
profundus}
IDPFEMAVKQLERAAQYMDISEEAELEWLKPMRIVEVSVPIEMDDGSVKVFTGFRVQHNWARGPTK
GGIRWHPAETLSTVKALATWMTWKVAVVDLPYGGGKGGIIVNPKELSEREQERLARAYIRAVYDVIG
PWTDIPAPDVYTNPKIMGWMMDEYETIMRRKGPAPFGVITGKPLS
>d1bvua2 c.58.1.1 (A:3-180) Glutamate dehydrogenase {Archaeon Thermococcus litoralis}
QDPFEIAVKQLERAAQYMDISEEAEFLKRPQRIVEVSIPVEMDDGSVKVFTGFRVQYNWARGPTKG
GIRWHPEETLSTVKALAAWMTWKTAVMDLPYGGGKGGVICNPKEMSDREKERLARGYVRAIYDVI
SPYTDIPAPDVYTNPQIMAWMMDEYETISRRKDPSPFGVITGKPPSV
>d1b26a2 c.58.1.1 (A:4-178) Glutamate dehydrogenase {Thermotoga maritima}
SLYEMAVEQFNRAASLMDLESDLAEVLRPRKRVLIVEFPVRMDDGHVEVFTGYRVQHNVARGPAGK
GIRYHPDVTLDDEVKALAFWMTWKTAVMNLFPYGGGKGGVVRVDPKLSRNELERLSRRFFSEIQVIIGP
YNDIPAPDVNTNADVIAWYMDTYSMNVGHTVLGIVTGKPVEL
>d1hwx2 c.58.1.1 (A:1-208) Glutamate dehydrogenase {Cow (Bos taurus)}
ADREDDPNFFKMVEGFFDRGASIVEDKLVEDLKTQRTQEQKRNVRGILRIKPCNHVLSLSFPIRRD
DGSWEVIEGYRAQSHQRTPCGGIRYSTDVSDEVKALASLMTYKCAVVDVPFGGAKAGVKINPK
NYTDEDLEKITRRFTMELAKKGFIPGVDPAPNMSTGEREMSWIADTYASTIGHYDINAHACVTG
KPISQGGI
>d1leha2 c.58.1.1 (A:1-134) Leucine dehydrogenase {Bacillus sphaericus}
MEIFKYMEKYDYEQLVFCQDEASGLKAVIAIHDTTLGPALGGARMWTYNAEEEEAIEDALRLARGMT
YKNAAGLNLGGGKTVIIGDPFADKNEDMFRALGRFIQGLNGRYITAEDVGTTVDDMDLIHQETDY
VT

>d1c1da2 c.58.1.1 (A:1-148) Phenylalanine dehydrogenase {Rhodococcus sp., M4}
SIDSALNWDGEMTVTRFDAMTGAHFVIRLDSTQLGPAAGGTRAAQYSNLADALTDAGKLAGAMTL
KMAVSNLPMGGGKSVIALPAPRHSIDPSTWARILRIHAENIDKLSGNYWTGPDVNTNSADMDTLND
TTEFVFGRSLEGGAGS

>d1a4ia2 c.58.1.2 (A:2-126) Tetrahydrofolate dehydrogenase/cyclohydrolase {Human
(Homo sapiens)}
APAEILNGKEISAQIRARLKNQVTQLKEQVPGFTPRLAILQVGNRDDSPLYINVKLKAAEEIGIKATHI
KLPRTTTESEVMKYITSLNEDSTVHGFLVQLPLDSENSINTEEVINAIPEKDVDG

>d1b0aa2 c.58.1.2 (A:2-122) Tetrahydrofolate dehydrogenase/cyclohydrolase {Escherichia
coli}
AAKIIDGKTIAQQVRSEVAQKVQARIAAGLRAPGLAVVLVGSNPASQIYVASKRKACEEVGFVSRSYDL
PETTSEAELELIDTLNADNTIDGILVQLPLPAGIDNVKVLERIHDPDKVDG

>d1edza2 c.58.1.2 (A:3-148) Tetrahydrofolate dehydrogenase/cyclohydrolase {Baker's yeast
(Saccharomyces cerevisiae)}
KPGRTLASKVAETFNTEIINNVEEYKKTHTNGQGPLLVGFLANNDPAAKMYATWTQKTSSEMGFRY
DLRVIEDKDFLEEAIIQANGDDSVNGIMVYFPVFGNAQDQYLQQVVCKEKDVEGLNHVYYQNLVHN
VRYLDKENRLKSIL

>d1do8a2 c.58.1.3 (A:21-279) Mitochondrial NAD(P)-dependent malic enzyme {Human
(Homo sapiens)}
IKEKGKPLMLNPRNTKGMFTLQERQMLGLQGLLPPKIETQDIQALRFHRNLKMTSPLEKYIYIM
GIQERNEKLFYRILQDDIESLMPIVYTPTVGLACSQYGHIFRRPKGLFISISDRGHVRSIVDNWPENHV
KAVVVTDGERILGLGDLGVYGMGIPVGKLCCLYTACAGIRPDRCLPVCIDVGTDNIALLKDPFYMGLYQ
KRDRTQQYDDLIDEFMKAITDRYGRNTLIQFEDFGNHNFRFLRKYREKYCTFNDD

>d2uaga2 c.59.1.1 (A:298-437) UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase MurD
{Escherichia coli}
GLPHRFEVVLEHNGVRWINDSKATNVGSTEAAALNGLHVDGTLHLLLGGDGKSADFSPLARYLNGDN
VRLYCFGRDGAQLAALRPEVAEQTETMEQAMRLAPRVQPGDMVLLSPACASLDQFKNFEQRGNEF
ARLAKELG

>d1e8ca2 c.59.1.1 (A:338-497) UDP-N-acetylmuramyl tripeptide synthetase MurE
{Escherichia coli}
VCGRMEVFTAPGKPTVVVDYAHTPDALAKALQAARLHCAGKLWCVFGCGGDRDKGKRPLMGAI
AE
EFADVAVVTDDNPRTEEPRAIINDILAGMLDAGHAKVMEGRAEAVTCAVMQAKENDVVLVAGKGHE
DYQIVGNQRLDYSRVTVARLLGVIARSH

>d1gg4a1 c.59.1.1 (A:313-447) UDP-murNac-tripeptide D-alanyl-D-alanine-adding enzyme
MurF {Escherichia coli}
VPGRLFPIQLAENQLLLDDSYNANVGSMTAAVQVLAEMPGYRVLVVGDMAELGAESEACHVQVGEA
AKAAGIDRVLSVGKQSHAISTASGVGEHFADKTALITRLKLLIAEQVITILVKGRSAAMEEVVRLQ

>d1jbwa1 c.59.1.2 (A:297-425) Folyl polyglutamate synthetase, C-terminal domain
{Lactobacillus casei}
WPARLEKISDTPLIVIDGAHNP DGINGLITALKQLFSQPITVIAGILADKDYAAMADRLTAAFSTVYLV
PVPGTPRALPEAGYEALHEGRLKDSWQEALAAASLNDVPDQPIVITGSLYLASAVRQTLLG

>d1qhfa_ c.60.1.1 (A:) Phosphoglycerate mutase {Baker's yeast (Saccharomyces cerevisiae)}
PKLVLRHGQSEWNEKNLFTGWVDVKLSAKGQQAARAGELLKEKKVYPDVLYTSKLSRAIQTANI
ALEKADRLWIPVNRSWRLNERHYGDLQGKDKAETLKKFGEEKFNTRYRRSFDVPPPIDASSPFSQK

GDERYKYVDPNVL PETESLALVIDRLLPYWQDVIAKDLLSGKTMIAAHGNSLRGLVKHLEGISDADI
AKLNIPTGIPLVFELDENLKPSKPSYYLDPEAAAAGAAAV

>d3pgm_ c.60.1.1 (-) Phosphoglycerate mutase {Baker's yeast (*Saccharomyces cerevisiae*)}
PKLVLRHGQSEWNEKNLFTGWVDVKLSAKGQQAARAGELLKEKGVNVLVDYTSKLSRAIQTANI
ALEKADRLWIPVNRSWRLNERHYGDLQGKDKAQTLLKFGEEKFNTRYRRSFDVPPPIDASSPFSQK
GDERYKYVDPNVL PETESLALVIDRLLPYWQDVIAKLVGKTSMAAHGNSLRGLVKHLEGISDADI
LNIPPGTILVFELDENLKPSKPSYYLDPEA

>d1fzta_ c.60.1.1 (A:) Phosphoglycerate mutase {Yeast (*Schizosaccharomyces pombe*)}
MTTEAAPNLLVLRHGESEWNLNFTGWKDPALSETGIKEAKLGGERLKSRYKFDIAFTSALQR
AQKTCQIILEEVGEPNLETIKSEKLNERYGDLQGLNKDDARKKWGAEQVQIWRRSYDIAPPNGESL
KD TAERVLPYYKSTIVPHILKGEKVLIAAHGNSLRALIMDLEGLTGDQIVKRELATGVPIVYHLDKDG
KYVSKELIDN

>d1e58a_ c.60.1.1 (A:) Phosphoglycerate mutase {*Escherichia coli*}
AVTKLVLRHGESQWKNENRFTGWYDVLSEKGVSEAKAAGKLLKEEGYSFDFAYTSVLKRAIHTL
WNVLDELQAWLPVEKSWKLNERNHYGALQGLNKAETAKEYGDEQVKQWRRGFVTPPELTKDDE
RYPGHDPYAKLSEKELPLTESLALTIDRVIWNETILPRMKS GERVIAAHGNSLRALVKYLDNMS
EEEILENIPGTGPLVYEFDENFKPLKRYLGNAD EIAAKAAAVANQGK

>d1ebba_ c.60.1.1 (A:) Broad specificity phosphatase YhfR {*Bacillus stearothermophilus*}
ATTLYLRHGETKWNVERRMQGWQDSPLTEKGRQDAMRLGKRLEAVELAAIYTSTSGRALETAIEV
RGGRLPIYQDERLREIHLGDWEGKTHDEIRQMDPIAFDHFVWQAPHLYPQRGERFCDVQQRAL EA
VQSIVDRHEGETVLIVTHGVVLKTLMAAFKDTPLDHLWSPPYMYGTSVTIIEVDGGTFHVAVEGDVS
HIE

>d1rpa_ c.60.1.2 (-) Acid phosphatase {Rat (*Rattus norvegicus*)}
KELKFVTLVFRHGD RGP IETFPNDPIKESSWPQGFQGLTKWGMGQHYELGSYIRRRYGRFLNNSYK
HDQVYIRSTVDVRTLMSAMTNLAALFPPEGNSIWNPRLLWQPIPVHTVSLSEDRLLYLPFRDCPRF
QELKSETLKSEEFKRLQPYKSFIDTLPSLSGFEDQLDFEIWSRLYDPLYCESVHNFTLPTWATEDAM
TKLKELSELSLLSLYGIHKQKEKSRLQGGVLVNEILKNMKLATQPQKARKLIMYSAHDTTVSGLQMA
LDVYNGLLPPYASCHIMELYQDNGGHFVEMYRNETQNEPYPLTLPGCTHSCPLEKFAELLDPVIPQ
DWATECMG

>d2hpaa_ c.60.1.2 (A:) Acid phosphatase {Human (*Homo sapiens*)}
KELKFVTLVFRHGD RSPIDTFPTDPIKESSWPQGFQGLTQLGMEQHYELGEYIRKRYRFLNNSYKH
EQVYIRSTVDVRTLMSAMTNLAALFPPEGVSIWNPILLWQPIPVHTVPLSEDQLLYLPFRNCPRFQE
LESETLKSEEFKRLHYPYKDFIATLGKLSGLHGQDLFGIWSKVYDPLYCESVHNFTLPSWATEDTMT
KLRELSELSLLSLYGIHKQKEKSRLQGGVLVNEILNHNMRATQIPSYKKLIMYSAHDTTVSGLQMALD
VYNGLLPPYASCHLTEL YFEKGEYFVEMYRNETQHEPYPLMLPGCSPSCPLERFAELVGPVIPQDWS
TECMT

>d1ihp_ c.60.1.3 (-) Phytase (myo-inositol-hexakisphosphate-3-phosphohydrolase)
{*Aspergillus ficuum*}
SCDTV DQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARYPTDSKGGKYS A
LIEEIQQNATTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIA
SGKKFIEGFQSTKLKDPRAQPGQSSPKIDV VISEASSNNTLDPGTCTVFEDSELADTVEANFTATFVP
SIRQRENDLSGVTLDTEVTYLMDCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKYYG
HGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALG
LYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD

ALGRCTRDSFVRGLSFARSGGDWAECFA

>d1qfxa_ c.60.1.3 (A:) Phytase (myo-inositol-hexakisphosphate-3-phosphohydrolase)
{Aspergillus niger}

KQFSQEFRDGYSLKHYYGGNGPYSERVSYGIARDPPTSCEVDQVIMVKRHGERYPSPSAGKDIEEALA
KVYSINTTEYKGDLAFLNDWTYYVNECYNAETTSGPYAGLLDAYNHGNDYKARYGHLWNGETV
VPPFSSGYGRVIETARKFGEGFFGYNYSTNAALNIISESEVMGADSLTPTCDTDNDQTTCDNLTYQLP
QFKVAAAARLNSQNPGMNLASDVYNLMVMASFELNARPFNSWINAFTQDEWVVSFGYVEDLNYYC
AGPGDKNMAAVGAVYANASLTLNQGPKAEGSLFFNFAHDTNITPILAAALGVLIPNEDLPLDRVAFG
NPYSIGNIVPMGGHLTIERLSCQATALSDEGTYYVRLVLEAVLNFNDCTSGPGYSCPLANYSILNKNL
PDYTTTCNVASYPQYLSFWWNYNTTTELNYRSSPIACQEGDAMD

>d1dkla_ c.60.1.3 (A:) Phytase (myo-inositol-hexakisphosphate-3-phosphohydrolase)
{Escherichia coli}

SEPELKLESVVIVSRHGVRAPTKATQLMQDVTDPDAPWTPVVKLGWLTTPRGGELIAYLGHYQRQLV
ADGLLAKKGCPSQGVVAIADVDERTKRTGEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQ
LDNANVTDAILSRAGGSIADFTGHRQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSA
DNVSLTGAVSLASMLTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSA
TPLLDLIKTALTPHPQKQAYGVTLPSTVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVF
ERWRRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQIVN
EARIPACSL

>d1bif_2 c.60.1.4 (250-468) 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase,
phosphatase domain {Rat (Rattus norvegicus)}

SIYLCRHGESELNLKGRIGGDPGLSPRGREFSKHLAQFISDQNIKDLKVFTSQMKRTIQTAEALSVPYE
QFKVLNEIDAGVCEEMTYEEIQDHYPLEFALRDQDKYRYRYPKGESYEDLVQRLEPVIMELERQENV
LVICHQAVMRCLLAYFLDKAAEELPYLKPLHTVCLKTPVAYGCKVESIFLNVAAVNTHRDRPQNVDI
SRPSEEALVTVPAHQ

>d1fbta_ c.60.1.4 (A:) 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase
domain {Rat (Rattus norvegicus)}

RSIYLCRHGESELNLRGRIGGDSGLSARGKQYAYALANFIRSQGISSLKVWTSHEMKRTIQTAEALGVPI
EQWKALNEIDAGVCEEMTYEEIQEHYPPEFALRDQDKYRYRYPKGESYEDLVQRLEPVIMELERQE
NVLVICHQAVMRCLLAYFLDKSSDELPLYLKPLHTVCLKTPVAYGCRVESIYLVN

>d1nula_ c.61.1.1 (A:) Xantine-guanine PRTase (XPRase) {Escherichia coli}

EKYIVTWDMLQIHARKLASRLMPSEQWKGIIAVSRGGLVPGALLARELGIRHVDTVCISSYDHDNQR
ELKVLKRAEGDGEFIVIDDLVDTGGTAVAIEMYPKAHFVTIFAKPAGRPLVDDYVVDIPQDTWIEQ
PWDMGVVFPPIGR

>d1hgxa_ c.61.1.1 (A:) Hypoxantine-guanine-xanthine PRTase {Tritrichomonas foetus}

MDDLERVLYNQDDIQKRIELAAELTEFYEDKNPVMICVLTGAVFFYTDLLKHLDFQLEPDYIICSSYS
GTKSTGNLTISKDLKTNIEGRHVLVVEDIIDTGLTMYQLLNNLQMRKPASLKVCTLCDKDIGKKAYDV
PIDYCGFVENRYIIGYGFDFHNKYRNLPVIGILKE

>d1fsga_ c.61.1.1 (A:) Hypoxantine-guanine-xanthine PRTase {Toxoplasma gondii}

GSHMASKPIEDYGGKGRIEPMYIPDNTFYNADDFLVPPHCKPYIDKILLPGGLVKDRVEKLAYDIHR
TYFGEELHIICLKSRGFFNLLIDYLATIQKYGRESSVPPFFEHYVRLKSYQNDNSTGQLTVLSDDLISI
FRDKHVLIVEDIVDTGFTLTFGERLKAAGPKSMRIATLVEKRTDRSNSLKGDFVGFSDVWVWVGGC
YDFNEMFRDFDHVAVLSAARKKFEK

>d1gph11 c.61.1.1 (1:235-465) Glutamine PRPP amidotransferase, C-terminal domain

{*Bacillus subtilis*}

ICSMEYIYFSRPDSNIDGINVHSARKNLGKMLAQESAVEADVVTGVPDSSISAAIGYAEATGIPYELGLI
 KNRYVGRTFIQPSQALREQGVRMKLSAVRGVVEGKRVVMVDDSIVRGTTSRRIVTMLREAGATEVH
 VKISSPPIAHPCFYGIDTSTHEELIASSHSVDEIRQEIGADTSLFSLVEGLLKIGIRKYDDSNCGQCLACF
 TGKYPTEIYQDTVLPHVKEAVLTK

>d1ecfa1_c.61.1.1 (A:250-492) Glutamine PRPP amidotransferase, C-terminal domain
 {*Escherichia coli*}

NPCLFEYVYFARPDSFIDKISVYSARVNMGTGLGKIAREWEDLDIDVVIPIPETSCDIALEIARILGKP
 YRQGFVKNRYVGRTFIMPGQQLRRKSVRRKLNANRAEFRDKNVLLVDDSIVRGTTSEQIEMAREAG
 AKKVYLASAAPEIRFPNVYGIDMPSATELIAHGREVDEIRQIIGADGLIFQDLNDLIDAVRAENPDIQQ
 FECSVFNQVYVTKDQGYLDFLDTLRNDDAKAVQRQ

>d1dqna_c.61.1.1 (A:) Guanine PRTase {*Giardia lamblia*}

MICSVTGKPKVDLSTFFKDRNDVLESEVKKFHLLATFEECKALAADTARRMNEYKDVAPVTLVA
 LLTGAYLYASLLTVHLTFPYTLHFVKVSSYKGRQESVVFDEEDLKQLKEKREVVLIIDEYVDSGHTIFSI
 QEQIKHAKICSCFVKDQVDAIKKHSALADTKMFYGYTPMPKGSWLIGFGLDDNGLRRGWHLFDINL
 SESEVTEFRRLTEHIKGLNINGVNRY

>d1bzya_c.61.1.1 (A:) Hypoxantine-guanine PRTase (HGPRase) {*Human (Homo sapiens)*}

SPGVVISDDEPGYDLDFCIPNHYAEDLERVFIPHGLIMDRTERLARDVMKEMGGHHIVALCVLKGK
 YKFFADLLDYIKALNRNSDRSIPMTVDFIRLKSVCNDQSTGDIKVIIGDDLSTLTGKNVLIVEDIIDTG
 KTMQTLSSLVRQYNPKMVKVASLLVKRTPRSVGYKPDFVGFEPDKFVVGALDYNEYFRDLNHVCV
 ISETGKAKYKA

>d1cjba_c.61.1.1 (A:) Hypoxantine-guanine PRTase (HGPRase) {*Plasmodium falciparum*}

PIPNNPGAGENAFDPVFNDDDGVDLDSFMIPAHYKKYLTKVLPNGVIKNRIEKLAYDIKKVYNNE
 EFHILCCLKGSRGFFALLKHLRIHNYSAVETSKPLFGEHYVRVKSVCNDQSTGTLEIVSEDLSCCLKG
 KHVLIIVEDIIDTGKTLVKFCEYLKKEIKTVAIACLFIKRTPLWNGFKADFGVFSIPDHFVVGYSLDYN
 EIFRDLHDHCLVNDEGKKKYKAT

>d1tc1a_c.61.1.1 (A:) Hypoxanthine PRTase {*Trypanosoma cruzi*}

YEFAEKILFTEEEIRTRIKEVAKRIADDYKGGKGLRPYVNPLVLISVLKGSFMFTADLCRALCDFNVVPR
 MEFICVSSYGEGLTSSGQVRMLLDTRHSIEGHHVLIVEDIVDTALTLYLYHMYFTRRPASLKTVVLL
 DKREGRRVPFSADYVAVANIPNAFVIGYGLDYDDTYRELRLDIVVLRPE

>d1qb7a_c.61.1.1 (A:) Adenine PRTase {*Leishmania donovani*}

PFKEVSPNSFLDDSHALSQLLKKSYPVSPVSPRNVPFADVSSITESPETLKAIRDFLVQRYRAM
 SPATHILGFDARGFLFGPMIAVELEIPFVLMRKADKNAGLLIRSEPYEKEYKEAAPEVMTIRYGSIGK
 GSRVVLIDDVLATGGTALSGLQLVEASDAVVVEMVSILSIPFLKAAEKIHSTANSRYKDIKFISLLSDDA
 LTEENCGDSKNYTGPRVLSGCDVLAEHPH

>d1g2qa_c.61.1.1 (A:) Adenine PRTase {*Baker's yeast (Saccharomyces cerevisiae)*}

MPIASYAQELKLALHQYPNFPSEGILFEDFLPIFRNPGLFQKLIDAFKLHLEEFPEVKIDYIVGLESRG
 FLFGPTLALALGVGFVPRKAGKLPGEFCFATYEKEYGSDLFEIQKNAIPAGSNVHVDIIATGGSSAAA
 AGELVEQLEANLLEYNFVMEFLKGRSKLNAPVFTLL

>d1oroa_c.61.1.1 (A:) Orotate PRTase {*Escherichia coli*}

MKPYQRQFIEFALSQVLKFGFETLKSGRKSPYFFNAGLFNTGRDLALLGRFYAEALVDVSGIEFDLLF
 GPAYKGIPIATTTAVALAEHHDLDLPYCFNRKEAKDHGEGGNLVGSALQGRVMLVDDVITAGTAIRES
 MEHQANGATLAGVLISLDRQERGRGEISAIQEVEDYDYNCKVISIITLKDLIAYLEEKPEMAEHLAAVKA
 YREEFGV

>d1a3c_ c.61.1.1 (-) Uracil PRTase {Bacillus subtilis}
QKAVILDEQAIRRALTRIAHEMIERNKGMNNCILVGIKTRGIYLAKRLAERIEQIEGNPVTVEIDITLY
RDDLSKKTSNDEPLVKGADIPVDITDQKVILVDDVLYTGRTVRAGMDALVDVGRPSSIQLAVLVDRGH
RELPIRADYIGKNIPTSKSEKVMVQLDEVDQNDLVAIYEN

>d1bd3a_ c.61.1.1 (A:) Uracil PRTase {Toxoplasma gondii}
QEESILQDIITRFPNVVLMKQTAQLRAMMTIIRDKETPKKEEFVIFYADRLIRLLIEEALNELPFQKKEV
TTPLDVSYHGVSFYKICGVSIVRAGESMESGLRAVCRGVRIGKILIQRDETTAEPKLIYEKLPADIRER
WVMLLDPMCATAGSVCKAIEVLLRLGVKEERIIFVNILAAPQGIERVFKEYPKVIRMVTAAVDICLNSR
YYIVPGIGDFGDRYFGTM

>d1dkra1 c.61.1.2 (A:8-166) Phosphoribosylpyrophosphate synthetase {Bacillus subtilis}
NLKIFSLNSNPELAKEIADIVGVQLGKCSVTRFSDGEVQINIEESIRGCDCYIIQSTSDPVNEHIMELLI
MVDALKRASAKTINIVIPYYGYARQDRKARSREPITAKLFANLLETAGATRVIALDLHAPQIQGFFDIPI
DHLMGVPILGGEYFEGKNLE

>d1dkra2 c.61.1.2 (A:167-316) Phosphoribosylpyrophosphate synthetase {Bacillus subtilis}
DIVIVSPDHGGVTRARKLADRLKAPIAIDKRRPRPNVAEVMNIVGNIEGKTAILIDDIIDTAGTITLAA
NALVENGAKEVYACCTHPVLSGPAVERINNSTIKELVVVNSIKLPEEKKIERFKQLSVGPLLAEAIRVH
EQQSVSYLFS

>d1lfaa_ c.62.1.1 (A:) Integrin CD11a/CD18 (Leukocyte function associated antigen-1, LFA-1)
{Human (Homo sapiens)}
GNVDLVFLFDGSMQLPDEFQKILDFMKDVMKKLSNTSYQFAAVQFSTSYKTEFDSDYVKKRDPD
ALLKHVKHMLLLTNTFGAINVATEVVFREELGARPDATKVLIIITDGEATDSGNIDAAKDIIRYIIGIGK
HFQTKESQETLHKFASKPASEFVKILDTFEKLKDLFTLQKKIYVIE

>d1atza_ c.62.1.1 (A:) von Willebrand factor A3 domain {Human (Homo sapiens)}
QPLDVILLLDGSSFPASYFDEMKSFAKAFISKANIGPRLTQVSVLQYGSITTIDVPWNVVEKAHLLSL
VDVMQREGGSPQIGDALGFAVRYLTSEMHGARGPASKAVVILVTDVSVDSVDAADAARSNRVTVFP
IGIGDRYDAAQLRILAGPAGDSNVVVKLQRIEDLPTMVTLGNSFLHKL

>d1fnsa_ c.62.1.1 (A:) von Willebrand factor A1 domain {Human (Homo sapiens)}
MYCSRLLDLVFLLDGSSRLSEAEFEVLKAFVVDMMERLRVSKWVRVAVVEYHDGSHAYIGLKDRK
RPSELRRIASQVKYAGSQVASTSEVLKYTLFQIFSKIDRPEASRIALLMASQEPQRMSRNFVRYVQGL
KKKKVIVIPVGIGPHANLKQIRLIEKQAPENKAFVLSSVDELEQRDEIVSYLCDLAPEAP

>d1ido_ c.62.1.1 (-) Integrin CR3 (CD11b/CD18, Mac-1), alpha subunit {Human (Homo
sapiens)}
DSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSCTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLV
KPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYV
IGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNQLREK

>d1qc5a_ c.62.1.1 (A:) Integrin alpha1-beta1 {Human (Homo sapiens)}
STQLDIVIVLDGNSIYPWDSVTAFLNDLLERMDIGPKQTQVGIVQYGENVTHEFNLNKYSSTEEVLV
AAKIVQRGGRQTMALGTDARKEAFTEARGARRGVKKVMVIVTDGESHDNHRLKKVIQDCEDE
NIQRFSIAILGSYNRGNLSTEFVVEIKSIASEPTEKHFFNVSDIEALVTIVKTLGERI

>d1ck4a_ c.62.1.1 (A:) Integrin alpha1-beta1 {Rat (Rattus norvegicus)}
TQLDIVIVLDGNSIYPWESVIAFLNDLLKRMDIGPKQTQVGIVQYGENVTHEFNLNKYSSTEEVLVA
ANKIGRQGGQLTMTALGIDTARKEAFTEARGARRGVKKVMVIVTDGESHDNYRLKQVIQDCEDENI
QRFSIAILGHYNRGNLSTEFVVEIKSIASEPTEKHFFNVSDIEALVTIVKALGERIFA

>d1aoxa_ c.62.1.1 (A:) Integrin alpha2-beta1 {Human (Homo sapiens)}

SCPSLIDVVVVCDESNSIYPWDAVKNFLEKQVGLDIGPQTKTQVGLIQYANNPRVFNLTNTYKTKKEE
MIVATSQTSQYGGDLTNTFGAIQYARKYAYSAASGGRRSATKVMVVVTDGESHGDSMLKAVIDQCNH
DNILRFGIAVLGYLNRNALDTKNLIKEIKAIASIPTEYFFNVSDAALLEKAGTLGGEQIFSIEGGT
>d1jv2b2 c.62.1.1 (B:107-354) Integrin beta A domain {Human (Homo sapiens)}
VEDYPVDIYYLMDLSYSMKDDLWSIQNLGTLATQMRKLTNSLRIGFGAFVDKPVSPYMYISPPEAL
ENPCYDMKTTCLPMFYGKHLVLTLDQVTRFNVEEVKKQSVSRNRDAPEGGFDAIMQATVCDKIGW
RNDASHLLVFTTDAKTHIALDGRLAGIVQPNQGCHVGSNDHYSASTTMDYPSLGLMTEKLSQKNI
NLIFAVTENVVNLQNYSELIPGTTVGVLSDSSNVLQVLIVDAYGKIRSK
>d1poia_ c.63.1.1 (A:) Glutaconate-CoA transferase alpha {Acidaminococcus fermentans}
SKVMTLKDIAIKYVHSGDHIALGGFTTDRKPYAAVFEILRQGITDLTGLGGAAGGDWMLIGNRVRK
AYINCYTANSVGTNSRRFRKWFEEAGKLTMEDYSQDVIYMMWHAALGLPFLPVTLMQSGSLTDE
WGISKEVRKTLDKVPDDKFKYIDNPFKPGKVVAVPVPQVDVAIIHAQQASPDGTVRIWGGKFQDV
DIAEAAKYTIVTCEEIISDEEIRRDPKNDIPGMCVDAVVLAPYGAHPSQCYGLYDYNPFLKVYDKV
SKTQEDFADFCKEWWFDLKDHDDEYLNKLGATRLINLKVVPGLGYHIDMTKE
>d1poib_ c.63.1.1 (B:) Glutaconate-CoA transferase beta {Acidaminococcus fermentans}
DYTNYTNKEMQAVTIAKQIKNGQVTVGTGLPLIGASVAKRVYAPDCHIIVESGLMDCSPVEVPRSVG
DLRFMAHCGCIWPNVRFVGFENEYLHKANRLIAFIGGAQIDPYGNVNSTSIGDYHHPKTRFTGSGG
ANGIATYSNTIIMMQHEKRRFMNKIDYVTSFGWIDGPGGRERLGLPGDVGPPQLVVTDKGILKFDEKT
KRMYLEAAYPTSSPEDVLENTGFDLVDKAVELEAPDPAVIKLIREEIDPGQAFIQVP
>d1keka4 c.64.1.1 (A:416-668) Pyruvate-ferredoxin oxidoreductase, PFOR, domain III
{Desulfovibrio africanus}
GTIQCQFWGLGADGTGANKQAIKIGDNTDLFAQGYFSYDSKKS GGITISHLRFGEKPIQSTYLVNRA
DYVACHNPAYVGIYDILEGIDGGTFVLNSPWSSELEDMDKHLPSGIKRTIANKKLFYNI DAVKIATD
VGLGGRINMIMQTAFFKLAGVLPFEKAVDLLKKSIIHKAYGKKGEKIVKMNTDAVDQAVTSLQEFKYP
DSWKDAPAETKAEPMTNEFFKNVVKPILTQQGDKLPVSAFEADGRFPLG
>d1jkxa_ c.65.1.1 (A:) Glycinamide ribonucleotide transformylase, GART {Escherichia coli}
MNIVVLISGNGSNLQAIIDACKTNKIKGTVRVFSNKADAFGLERARQAGIATHTLIASAFDSREAYDR
ELIHEIDMYAPDVVVLVLAGFMRI LSPAFVSHYAGRLNIHPSLLPKYPGLHTHRQALENGDEEHGTSVH
FVTDEL DGGPVILQAKVPVFAGDSEDDITARVQTQEHA IYPLVISWFADGRLKMHENA AAWLDGQRL
PPQGYA
>d1fnta2 c.65.1.1 (A:1-206) Methionyl-tRNA^{fmet} formyltransferase {Escherichia coli}
SESLRIIFAGTPDFAARHL DALLSSGHNVVGVFTQPDRPAGRGKLMPSPVKVLAEKGLPVFQPVSL
RPQENQQLVAELQADVMVVVAYGLILPKAVLEMPRLGCINVHGSLLPRWRGA APIQRSLWAGDAET
GVTIMQMDVGLDTGDMLYKLSCPITAEDTSGTLYDKLAELGPQGLITTLKQLADGTAKPEVQDET LV
TYAEK
>d1vid_ c.66.1.1 (-) Catechol O-methyltransferase, COMT {Rat (Rattus norvegicus)}
TKEQRILRYVQQNAKPGDPQSVLEAIDTYCTQKEWAMNVGDAKGQIMDAVIREYSPSLVLELGAYCG
YSAVRMARLLQPGARLLTMEMNPDYAAITQQMLNFAGLQDKVTILNGASQDLIPQLKKKYD VDTLD
MVFLDHWKDRYLPDTLLLEKCGLLRKT VLLADNVIVPGTPDFLAYVRGSSSECTHYSSYLEYMKV
VDGLEKAIYQGPS
>d1fp1d2 c.66.1.12 (D:129-372) Chalcone O-methyltransferase {Alfalfa (Medicago sativa)}
RGYLASFTTFLCYPALLQVWMNFKEAVVDEDIDLKFNHGVTKYEFMGKDKKMNQIFNKSMVDVC
ATEMKRMLEIYTGFE GISTLV DVGGGSGRNLELIISKYPLIKGINFDLPQVIENAPPLSGIEHVGGDMFA
SVPQGDAMILKAVCHNWSDEKCI EFLSNCHKALSPNGKVIIVEFILPEEPNTSEESKLVSTLDNLMFIT

VGGRETEREKQYEKLSKLSGFSKFQVACRAFNSLGVMEFYK
>d1fp2a2_c.66.1.12 (A:109-352) Isoflavone O-methyltransferase {Alfalfa (Medicago sativa)}
LCLAPMVECVLDPTLSGSYHELKKWIYEEDLTLFGVTLGSGFWDFLDKNPEYNTSFNDAMASDSKLI
NLALRDCDFVFDGLSIVDVGGGTGTTAKIICETFPKLCIVFDRPQVVENLSGSNNLTYVGGDMFTSI
PNADAVLLKYILHNWTDKDCLRILKKCKEAVTNDGKRGKVTIIDMVIDKKKDENQVTQIKLLMDVN
MACLNGKERNEEEWKKLFIEAGFQHYKISPLTGFLSLIEIYP
>d1ej0a_c.66.1.2 (A:) RNA methyltransferase FtsJ {Escherichia coli}
GLRSRAWFKLDEIQQSDKLFKPGMTVVLDGAAPGGWSQYVVVTQIGGKGRIIACDLLPMDPIVGVDFL
QGDFRDELVMKALLERVGDSKVQVMSDMAPNMSGTPAVDIPRAMYLVELALEMCRDVLAPGGSF
VVKVFQGEFDEYLREIRSLFTKVKVRKPDSSRARSREYIVATGRKP
>d1fbna_c.66.1.3 (A:) Fibrillar homologue {Archaeon Methanococcus jannaschii}
MEDIKIKEIFENIYEVLDGLKRIATKSIVKGGKVVYDEKIIKIGDEEYRIWNPNSKLAIAIHKGLKV
MPIKRDSKILYLGASAGTTPSHVADIADKGVYAIYAPRIMRELLDACAERENIIPILGDANKPQEYAN
IVEKVDVIYEDVAQPNQAEILIKNAKWFLKGGYGMIAIKARSIDVTKDPKEIFKEQKEILEAGGFKIV
DEVDIPEFEKDHVMFVGIWEGK
>d1dusa_c.66.1.4 (A:) Hypothetical protein MJ0882 {Archaeon Methanococcus jannaschii}
FSEKPTTKSDVKIVEDILRGKCLKFKTDSGVFSYGVKVDKGTIKILVENVVVDKDDDLDLGCGYGVIGIA
LADEVKSTTMADINRRAIKLAKENIKLNNLDNYDIRVVHSDLYENVKDRKYNKIITNPPIRAGKEVL
HRIIEEGKELLKDNGEIVWVIQTKQGAKSLAKYMKDVFNGVETVTIKGGYRVLKSKKL
>d1im8a_c.66.1.14 (A:) Hypothetical protein HI0319 (YecO) {Haemophilus influenzae}
FIFDENVAEVPDPMIQRVPGYSNIITAIGMLAERFVTADSNVYDLGCSRGAATLSARRNINQPNVKII
GIDNSQPMVERCRQHIAAYHSEIPVEILCNDIRHVEIKNASMVILNFTLQFLPPEDRIALLTKIYEGLN
PNGVLVLSEKFRFEDTKINHLIDLHHQFKRANGYSELEVSQKRTALENVMRTDSIETHKVRLKNVG
FSQVELWFQCFNFGSMIAVK
>d1d2ha_c.66.1.5 (A:) Glycine <i>N</i>-methyltransferase {Rat (Rattus norvegicus)}
TAEYKAWLLGLLRQHGHCHRVLVACGTGVDSIMLVEEGFSVTSVDASDKMLKYALKERWNRKPEPA
FDKWVIEEANWLTLDKDVDPAGDGFDAVICLGNFAHLPSKGDQSEHRLALKNIASMVRPGLLVID
HKNYDYILSTGCAPPKNIYYKSDLTKDITTSVLTVNNAHMVTLDYTVQVPGAGRDGAPGFSKFR
SYPHCLASFTELVQEAFGGRCQHSLVLDGDFKPYRPGQAYVPCYFIHVLKKTG
>d1xvaa_c.66.1.5 (A:) Glycine <i>N</i>-methyltransferase {Rat (Rattus norvegicus)}
VDSVYRTRSLGVAEEGIPDQYADGEAARVWQLYIGDTRSRTAEYKAWLLGLLRQHGHCHRVLVACGT
GVDSIMLVEEGFSVTSVDASDKMLKYALKERWNRKPEPAFDKWVIEEANWLTLDKDVDPAGDGFDA
VICLGNFAHLPSKGDQSEHRLALKNIASMVRPGLLVIDHRNYDYILSTGCAPPKNIYYKSDLTK
DITTSVLTVNNAHMVTLDYTVQVPGAGRDGAPGFSKFRSYPHCLASFTELVQEAFGGRCQHSLV
GDFKPYRPGQAYVPCYFIHVLKKTG
>d1hnna_c.66.1.15 (A:) Phenylethanolamine N-methyltransferase, PNMTase {Human (Homo sapiens)}
AVASAYQRFEPRAYLRNNYAPPRGDLCPNGVGPWKLRLCLAQTFATGEVSGRTLIDIGSGPTVYQLLS
ACSHFEDITMTDFLEVNRQELGRWLQEEPGFNWSMYSQHAACLIIEGKGEWQDKERQLRARVKRV
LPIDVHQPPQLGAGSPAPLPADALVSAFCLEAVSPDLASFQRALDHITTLRPGGHHLLIGALEESWYL
AGEARLTVVPVSEEEVREALVRSYKVRDLRTYIMPAHLQTVGDDVKGVFFAWAQKVL
>d1khha_c.66.1.16 (A:) Guanidinoacetate methyltransferase {Rat (Rattus norvegicus)}
RWETPYMHSLAAAAASRGGRVLEVGFMAIAASRVQQAPIKEHWIIECNDGVFQRLQNWALKQPH
KVVPLKGLWEEVAPTLDPGHFDGILYDTPLESETWHTHQFNFIKTHAFRLKPGGILTYCNLTSWG

ELMKSQYTDITAMFEETQVPALLEAGFQRENICTEVMALVPPADCRYAFAFPQMITPLVTKH
>d1g6q1_ c.66.1.6 (1:) Arginine methyltransferase, HMT1 {Baker's yeast (*Saccharomyces cerevisiae*)}

DYYFDSYDHYGIHEEMLQDVTVRTLSYRNAIIQNKDLFKDKIVLDVGGGTGILSMFAAKHGAKHVIGV
DMSSIIEMAKELVELNGFSDKITLLRGKLEDVHLPFPKVDIIISEWMGYFLLYESMMDTVLYARDHYL
VEGGLIFPDKCSIHLAGLEDSQYKDEKLNWQDVYGFYDYSFVPLVLHEPIVDTVERNVNTTSDKLI
EFDLNTVKISDLAFKSNFKLTAKRQDMINGIVTWFDIVFPAPKGRPVFSTGPHAPYTHWKQTIFY
FPDDLDAETGDTIEGELVCSPNEKNNRDLNIKISYKFESNGIDGNSRSRKNEGSYLMH

>d1f3la_ c.66.1.6 (A:) Arginine methyltransferase, HMT1 {Rat (*Rattus norvegicus*)}

DLQEDEDGVYFSSYGHYGIHEEMLKDKVRTESYRDFIYQNPFIKDKVLDVGGGTGILSMFAAKAG
AKKVIAVDQSEILYQAMDIIRLNKLEDTIVLIKIGKIEEVSPLVEKVDVIISEWMGYFLFESMLDSVLYA
KSKYLAKGGSVYPDICTISLVAVSDVSKHADRIAFWDDVYGFNMSCMKKAVIPEAVVEVDHKTLLISD
PCDIKHIDCHTTISIDLEFSSDFLTRTTKTAMCTAVAGYFDIYFEKNCHNRVVFSTGPGQSTKTHWKQT
IFLLEKPPFPKAGEALKGKITVHKNKKDPRSLIVTLTLNSSTQTYSLQ

>d1dl5a1 c.66.1.7 (A:1-213) Protein-L-isoaspartyl O-methyltransferase {*Thermotoga maritima*}

MREKLFWILKKYGVSDHIAKAFLEIPREEFLTKSYPLSYVYEDIVLVSYDDGEEYSTSSQPSLMALFME
WVGLDKGMRVLEIGGGTYNAAVMSRVVGEKGLVVSVEYSRKICEIAKRNVERLGIENVFVCGDGY
GVPEFSPYDVIVTVGVDEVPETWFTQLKEGGRVIVPINLKLRRQPAFLFKKKDPYLVGNYKLETRF
ITAGGNLG

>d1jg1a_ c.66.1.7 (A:) Protein-L-isoaspartyl O-methyltransferase {Archaeon *Pyrococcus furiosus*}

EKELYEKWMRTVEMLKAEGIIRSKEVERAFLKYPRYLSVEDKYKKYAHIDEPLPIAGQTVSAPHMV
AIMLEIANLKPGMNILEVGTGSGWNAALISEIVKTDVYTIERIPELVEFAKRNLERAGVKNVHVILGD
GSKGFPKAPYDVIIVTAGAPKIPEPLIEQLKIGGKLIIPVGSYHLWQELLEVRKTKDGIKIKNHGGVAF
VPLIGEYGWK

>d1kr5a_ c.66.1.7 (A:) Protein-L-isoaspartyl O-methyltransferase {Human (*Homo sapiens*)}

ASHSELIHNLKNGIITDKVFEVMLATDRSHYAKCNPYMDSPQSIGFQATISAPMHAYALELLFDQ
LHEGAKALDVGSGSILTACFARMVGCTGKVIKIDHIKELVDDSVNVRKDDPTLLSSGRVQLVVGDG
RMGYAEEAPYDAIHVGAAAPVVPQALIDQLKPGGRLLIPVGPAGGNQMLEQYDKLQDGSIKMKPLM
GVIYVPLTDKEKQWSR

>d1i9ga_ c.66.1.13 (A:) Probable methyltransferase Rv2118c {*Mycobacterium tuberculosis*}

TGPFSIGERVQLTDAKGRRYTMSLTPGAEFHTHRGSIAHDAVIGLEQGSVVKSSNGALFLVLRPLLVDY
VMSMPRGPQVIYPKDAAQIVHEGDIFPGARVLEAGAGSGALTLSLLRAVGPAGQVISYEQRADHAEH
ARRNVSGCYGPPDNWRLVVSDDLADSELDPGSDRAVLDMAPWEVLDAVSRLLVAGGVLMMVYVA
TVTQLSRIVEALRAKQCWTEPRAWETLQRGWNVVGAVRPPQHSMRGHTAFLVATRRLAPGAVA

>d1af7_2 c.66.1.8 (92-284) Chemotaxis receptor methyltransferase CheR, C-terminal domain {*Salmonella typhimurium*}

NLTAFFREAHHPILAEHARRRHGEYRVWSAAASTGEEPYSIAITLADALGMAPGRWKVFASDIDTE
VLEKARSGIYRLSELKTLSPQQLQRYFMRGTGPHEGLVRVRQELANYVEFSSVNLEKQYNVPGPFD
AIFCRNVMIFYDKTTQEDILRRFVPLLKPDGLLFAGHSENFSLNLRVREFSLRGQTVYALS

>d3mag_ c.66.1.9 (-) Polymerase regulatory subunit VP39 {*Vaccinia virus*}

MDVVSLLDKPFMYFEEIDNELDYEPESANEVAKKLPYQGQLKLLLGELFFLSKLRHGILDGATVVYIG
SAPGTHIRYLRDHFYNLGVIIKWMLIDGRHHPILNGLRDVTLVTRFVDEEYLRSIKKQLHPSKIILIS

DVRSPKRGNESTADLLSNYALQNMISILNPVASSLKWRCPPDQWIKDFYIPHGKMLQPFAPSY
SAEMRLLSIYTGEMRLTRVTKSDAVNYEKKMYLNLKIVRNKVVVNFDPNQEYDYFHMYFMLRT
VYCNTFPPTKAKVFLQQSIFRFLNIP

>d1yub_ c.66.1.9 (-) rRNA methyltransferase {Streptococcus pneumoniae, Ermam}
MNKNIKYSQNFLTSEKVLNQIQLNLKETDTVYEIGTGKGLTTKLAKISKQVTSIELDSHLFNLSS
KLKLNTRVTLHQDILQFQFPNKQRYKIVGNIPYHLSTQIIKKVVFESRASDIYLIVEEGFYKRTLDIHR
TLGLLLHTQVSIQQLLKLPAECFHPKPKVNSVLIKLTRHTTDVPDKYWKLTYFVSKWVNREYRQLF
TKNQFHQAMKHAKVNNLSTITYEQVLSIFNSYLLFNGRK

>d1qama_ c.66.1.9 (A:) rRNA methyltransferase {Bacillus subtilis, Ermc'}
QNFIKSKHNIDKIMTNIIRLNEHDNIFEIGSGKGFHTLELVQRCNFVTAIEIDHKLCKTTENKLVLDHDN
FQVLNKDILQFKFPKNQSYKIFGNIPYNISTDIIRKIVFDSIADEIYLIVEYGFARLLNTRKSLALFLMA
EVDISILSMVPREYFHPKPKVNSLIRLNRKKSRIKDKQKYNFYVMKWVNKEYKKIFTKNQFNNS
LKHAGIDDLNNSIFEQFLSLFNSYKLFNK

>d1i4wa_ c.66.1.9 (A:) Transcription factor sc-mtTFB {Baker's yeast (Saccharomyces cerevisiae)}

PIPIKDISKLKFFYGFYKYLWNPTVYNKIFDKLDLTKTYKHPEELKVLDLYPGVGIGSAIFYNKYCPRQ
YSLLEKRSSLYKFLNAKFEQSPLQILKRDPYDWSTYSNLIDEERIFVPEVQSSDHINDKFLTANVTGE
GSEGLIMQWLSICIGNKNWLYRFGKVKMLLWMPSTTARKLLARPGMHSRSKCSVVREAFTDTKLIAI
SDANELKGFDSQCIEEWDPIFSAAEIWPTKGKPIALVEMDPIDFDVDNWDYVTRHLMILKRTPL
NTVMDSLGHGGQQYFNSRITDKDLLKCPIDLTNDEFIYLTKLFMWPFKP

>d6mhta_ c.66.1.10 (A:) DNA methylase HhaI, coenzyme-binding domain {Haemophilus haemolyticus}

MIEIKDKQLTGLRFIDLFAGLGGFRLADESCGAECVYSNEWDKYAQEVYEMNFGEKPEGDITQVNEK
TIPDHDILCAGFPCQAFSISGKQKGFEDSRGTLFFDIARIVREKKPKVFMENVKNFASHDNGNTLEV
VKNTMNELDYSFHAKVLNLDYGIQPKRERIYMICFRNDLNIQNFQFPKPFELNTFVKDLLLPDSEV
EHLVIDRKLDMVTNQEIEQTTPKTVRLGIVGKGGQGERIYSTRGIAITLSAYGGGIFAKTGGYLVNGKT
RKLHPRECARVMGYPDSYKVHPSTSQAYKQFGNSVIVNLQYIAYNIGSSLNFKPY

>d1g38a_ c.66.1.10 (A:) DNA methylase TaqI, coenzyme-binding domain {Thermus aquaticus}

VETPPEVDFMVSLEAPRGGRVLEPACAHGPFLRAFREAHTGYRFVGVVEIDPKALDLPWAEGIL
ADFLLEWEPGEAFDLILGNPPYGVGEASKYPIHVFKAVKDLYKAFSTWKGKYNLYGAFLEKAVRLLK
PGGVLVFPVATWLVLEDFALLREFLAREGKTSVYYLGEVFPQKKVSAVVIRFQKSGKGLSLWDTQES
ESGFTPIWAEYPHWEGEIIRFETEERKLEISGMPLGDLFHIRFAARSPEFKKHPAVRKEPGPLVP
VLTGRNLKPGWVDYKHNHSLWMPKERAKELRDFYATPHLVVAHTKGTRVVAAWDERAYPWREE
FHLLPKEGVRLDPSSLVQWLNSEAMQKHVRTLYRDFVPHLTLRMLERLPVREYGFHT

>d1dcta_ c.66.1.10 (A:) DNA methylase HaeIII, coenzyme-binding domain {Haemophilus aegyptius}

MNLISLFSGAGGLDLGFQKAGFRIICANEYDKSIWKTYESNHSKLIKGDISKISSDEFKCDGIIGPP
CQSWSEGGSLRGIDDPKGLFYEYIRILKQKPIFFLAENVKGMMAQRHNKAVQEFIQEFDNAGYDV
HIILLNANDYGVAQDRKRQVYIGFRKELNINYLPPPHLIKPTFKDVIWDLKDNIPALDKNKTNGNK
CIYPNHEYFIGSYSTIFMSRNRVRQWNEPAFTVQASGRQCQLHPQAPVMLKVSKNLNKFVEGKEHLY
RRLTVRECARVQGFDDFIFHYESLNDGYKMIGNAVPVNLAIEIAKTIKSAL

>d2dpma_ c.66.1.10 (A:) DpnM DNA adenine methyltransferase {Streptococcus pneumoniae}
TLQPFTKWTGGKRQLLPVIRELIPKTYNRYFEPFVGGGALFFDLAPKDAVINDFNAELINCYQQIKDN

PQELIEILKVHQEYNSKEYYLDLRSADRDERIDMMSEVQRAARILYMLRVNFNGLYRVNSKNQFNVP
YGRYKNPKIVDEELISAI SVYINNNQLEIKVGD FEKAIVDVRTGDFVYFDPPYIPLSETSAFTSYTHEGF
SFADQVRLRDAFKRLSDTGAYVMLSNSSSALVEELYKDFNIHYVEATRNGAKSSSRGKISEIIVTNYE
K

>d1g55a_ c.66.1.10 (A:) DNMT2 {Human (Homo sapiens)}

EPLRVLELYSGVGMHHALRESCIPAQVVAIDVNTVANEVYKYNFPHTQLLAKTIEGITLEEFDRLS
FDMILMSPPCQPFRIGRQGDMDTSRTNSFLHILDILPRLQKLPKYILLENVKGFEVSSTRDLLIQTIE
NCGFYQYEFLLSPTSLGIPNSRLRYFLIAKLQSEPLPFQAPGQVLMFEPKIEIHRKNQQSDLSVKML
KDFLEDDTDVNQYLLPPKSLLRYALLLDIVQPTCRRSVCFTKGYGSYIEGTGSVLQTAEDVQVENIYKS
LTNLSQEEQITKLLILKLRYPKEIANLLGFPEFGFPEKITVKQRYRLLGNSLNVHVAKLIKILYE

>d1booa_ c.66.1.11 (A:) m.PvuII N4 cytosine-specific DNA methyltransferase {Proteus
vulgaris}

NFGKKPAYTTSNGSMYIGDSLELLESFPEESISLVMTSPPFALQRKKEYGNLEQHEYVDWFLSFAKV
NKKLKP DG SFVDFGGAYMKGVPARSYINFRVLIRMIDEVGF LAEDFYWFNPSKLPSPIEWVNKRK
IRVKDAVNTVWWFSKTEWPKSDITKVLAPYSDRMKKLIEDPKFYTPKTRPSGHDIGKSFSKDNNG
SIPPNLLQISNESNGQYLANCKLMGIKAHPARFPAKLPEFFIRMLTEPDDLVDIFGGSNTTGLVAER
ESRKWISFEMKPEYVAASAFRFLDNNISEEKITDIYNRILNGESLDLNSI

>d1eg2a_ c.66.1.11 (A:) m.RsrI N6 adenosine-specific DNA methyltransferase {Rhodobacter
sphaeroides}

GTTRHVYDVCDCDLTLAKLPDDSVQLIICPPYNIMLADWDDHMDYIGWAKRWLAEAERVLSP
SIAIFGGLQYQGEAGSGDLISIISHMRQNSKMLLANLIHWNYPNGMSAQRFFANRHEEIAWFAKTKKY
FFDLDAVREPYDEETKAAYMKDKRLNPESVEKGRNPTNVWRMSRLNGNSLERVGHPTQKPAAVIE
RLVRALSHPGSTVLDFFAGSGVTARVAIQEGRNSICTDAAPVFKEYYQKQLTFLQDDGLIDKARSYEV
EGAANFGAALQR

>d1inla_ c.66.1.17 (A:) Spermidine synthase {Thermotoga maritima}

RTLKELERELQPRQHLWYFEYYTGNNVGLFMKMNRVIYSGQSDIQRIDIFENPDLGVVFALDGITMT
TEKDEFMYHEMLAHVPMFLHPNPKKVLIIIGGGDGGTLREVLKHDSVEKAILCEVDGLVIEAARKYL
KQTS CGFDDPRAEIVIANGAEYVRKFKNEFDVIIIDSTDP TAGQGGHLFTEEFYQACYDALKEDGVFS
AETEDPFYDIGWFKLAYRRISKVFPITRVYLGFM TTYPSGMWSYTFASKGIDPIKDFDPEKVRKFNK
ELKYYNEEVHVASFALPNFVKKELGLM

>d1kpga_ c.66.1.18 (A:) Mycolic acid cyclopropane synthase CmaA1 {Mycobacterium
tuberculosis}

DELKPHFANVQAHYDLSDDFFRLFLDPTQTYSCAYFERDDMTLQEAQIAKIDLALGKLG LQPGMTLL
DVGCGWGATMMRAVEKYDVNVVGLTSLKNQANHVQQLVANSENLRSKRVLLAGWEQFDEPVDRIV
SIGAFEHFGHERYDAFFSLAHRLLPADGVMLLHTITGLHPKEIHERGLPMSFTFARFLKFIVTEIFPGG
RLPSIPMVQECASANGFTVTRVQSLQPHYAKTLDLWSAALQANKGQAIALQSEEVYERYMKYLTGCA
EMFRIGYIDVNQFTCQK

>d1kpia_ c.66.1.18 (A:) Mycolic acid cyclopropane synthase CmaA1 {Mycobacterium
tuberculosis}

QLKPPVEAVRSHYDKSNEFFKLWLDPSMTYSCAYFERPDMTLEEAQYAKRKLALDKLNLEPGMTLL
DIGCGWGSTMRAVAEYDVNVIGLTLSENQYAHDKAMFDEVDSPRRKEVRIQGWEEFDEPVDRIVS
LGAFEHFADGAGDAGFERYDTFFKKFYNLTPDDGRMLLHTITIPDKEEAQELGLTSPMSLLRFIKFIL
TEIFPGGRLPRISQVDYSSNAGWKVERYHRIGANYVPTLNAWADALQAHKDEAIALKGQETCDIYM
HYLRGCSDLFRDKYTDVCQFTLVK

>d7aata_ c.67.1.1 (A:) Aspartate aminotransferase, AAT {Chicken (Gallus gallus), mitochondria}

SSWWSHVEMGPPDPILGVTEAFKRDTNSKKMNLGVBAYRDDNGKPYVLNCVRKAEAMIAAKKMD
KEYLPIAGLADFTRASAELALGENSEAFKSGRYVTVQGISGTGSLRVGANFLQRFFKFSRDVYLPKPS
WGNHTPIFRDAGLQLQAYRYYPKTCSLDFTGAMEDISKIPEKSILLHACAHNPTGVDPRQEQWKE
LASVVKRNLLAYFDMAYQGFASGDINRDAWALRHFIEQGIDVVLSQSYAKNMGLYGERAGAFVVIC
RDAEEAKRVESQLKILIRPMYSNPPMNGARIASLILNTPELRKEWLVEVKGMADRIISMRTQLVSNL
KKEGSSHNWQHITDQIGMFCFTGLKPEQVERLTKEFSIYMTKDGRISVAGVASSNVGYLAHAIHQVT
K

>d2csta_ c.67.1.1 (A:) Aspartate aminotransferase, AAT {Chicken (Gallus gallus), cytosolic form}

AASIFAAPRAPPVAVFKLTADFREDGDSRKVNLVGAYRTDEGQPWVLPVVRKVEQLIAGDGSLNH
EYLPILGLPEFRANASRIALGDDSPAIAQKRVGVSQGLGGTGALRIGAEFLRRWYNGNNNTATPVYVS
SPTWENHNSVFM DAGFKDIRTYRYWDAAKRGLDLQGLLDDMEKAPEFSIFILHACAHNPTGTDPT
PDEWKQIAAVMKRRCLFPFFDSAYQGFASGSLDKDAWAVRYFVSEGFELFCAQSFKNFGLYNERVG
NLSVVGKDEDNVQRVLSQMEKIVRTTWSNPPSQGARIVATTLTSPQLFAEWKDNVKT MADRVLLM
RSELRSRLESLGTPGTWNHITDQIGMFSFTGLNPKQVEYMIKEKHIYLMASGRINMCGLTTKNLDYV
AKSIHEAVTKIQ

>d1ajsa_ c.67.1.1 (A:) Aspartate aminotransferase, AAT {Pig (Sus scrofa), cytosolic form}

APPSVFAEVPQAQPVLVFKLIADFREDPDPRKVNLVGAYRTDDCQPWVLPVVRKVEQRIANSSSL
NHEYLPILGLAEFRTCASRLALGDDSPALQEKRVGGVQSLGGTGALRIGAEFLARWYNGTNNKDTPV
YVSSPTWENHNGVFTTAGFKDIRSYRYWDTEKRGLDLQGFSLDLENAPEFSIFVLHACAHNPTGTD
PTPEQWKQIASVMKRRFLFPFFDSAYQGFASGNLEKDAWAIYFVSEGFELFCAQSFKNFGLYNERV
GNLTVVAKEPDSILRVLSQM KIVRV TWSNPPAQGARIVARTLSDPELFHEWTGNVKT MADRILSM
RSELRARLEALKTPGTWNHITDQIGMFSFTGLNPKQVEYLINQKHIYLLPSGRINMCGLTTKNLDYV
ATSIHEAVTKIQ

>d1yaaa_ c.67.1.1 (A:) Aspartate aminotransferase, AAT {Baker's yeast (Saccharomyces cerevisiae), cytosolic form}

SATLFNNIPELLPPDALFGIKQRYGQDQRATKVDLIGAYRDDNGKPWVLPVSVKAAEKLIHNDSSYNH
EYLGITGLPSLTSNAAKIIFGTQSDALQEDRVISVQSLSGTGALHISAKFFSKFFPKLVYLSKPTWANH
MAIFENQGLKTATYPYWANETKSLDLNGLNIAIQKAPEGSIFVLHSCAHNPTGLDPTSEQWVQIVD
AIASKNHIALFDTAYQGFATGDLKDAYAVRLGVEKLSTVSPVFCQSFKNAGMYGERVGCFLHALT
KQAQNKTIKPAVTSQLAKIIRSEVS NPPAYGAKIVAKLLETPEL TEQWHKDMVTMSSRITKMRHALR
DHLVKGTPGNWDHIVNQC GMFSFTGLTPQMVKRLEETHAVYLVASGRASIAGLNQGNVEYVAKAI
DEVVRFYA

>d1qisa_ c.67.1.1 (A:) Aspartate aminotransferase, AAT {Escherichia coli}

MFENITAAPADPILGLADLFRADERPGKINLGIVYKDETGKTPVLTSVKKAEQYLLNETTKNYLGI
DGPIEFGRCTQELLFGKGSALINDKRARTAQTPGGTGALRVAADFLAKNTSVKRVVWSNPSWPNHK
SVFNSAGLEVREYAYYDAENHTLDFDALINSLNEAQAGDVVLFHGFCHNPTGIDPTLEQWQTLAQLS
VEKGWLP LDFDFAYQGFARGLEEDA EGLRAFAAMHKELIVASSYSKNFGLYNERVGACTLVAADSETV
DRAFSQMKAIRANYSNPPAHGASVVATILSN DALRAIWEQELTDMRQRIQRM RQLFVNTLQEKGA
NRDFSFIKQNGMFSFSGLTKEQVLRRLREEFVYAVASGRVNVAGMTPDNMAPLCEAIVAVL

>d1bjwa_ c.67.1.1 (A:) Aspartate aminotransferase, AAT {Thermus thermophilus}

MRGLSRRVQAMKPSATVAVNAKALELRRQGVDLVALTAGEPDFDTPPEHVKEAARRALAQGKTKYAP

PAGIPELREALAEKFRRENGLSVTPEETIVTVGGKQALFNLFQAILDPGDEVIVLSPYWVSYPEMVRF
AGGVVVEVETLPEEGFVDPDPERVRRAITPRTKALVVNSPNNPTGAVYPKEVLEALARLAVEHDFYLV
SDEIYEHLLEYEGEHFSPGRVAPEHTLTVNGAAKAFAMTGWIRIGYACGPKVEIKAMASVSSQSTTSPDT
IAQWATLEALTNQEASRAFVEMAREAYRRRRDLLEGLTALGLKAVRPSGAFYVLMDSPIAPDEVR
AAERLLEAGVAVVPGTDFAAFGHVRLSYATSEENLRKALERFARVL

>d2ay1a_ c.67.1.1 (A:) Aromatic aminoacid aminotransferase, AroAT {Paracoccus denitrificans}

MLGNLKPQAPDKILALMGEFRADPRQGKIDLVGVYKDATGHTPIMRAVHAAEQRMLETETTKTY
AGLSGEPEFQKAMGELILGDGLKSETTATLATVGGTGALRQALELARMANPDLRVFVSDPTWPNHV
SIMNFMGLPVQTYRYFDAETRGVDFEGMKADLAAAKKGDMLLHGCCHNPTGANLTLQWAEIAS
ILEKTGALPLIDLAYQGFQDGLLEEDAAGTRLIASRIPEVLIAASCSKNFGIYRERTGCLLALCADAATRE
LAQGAMAFLNRQTYSPFPFHGAKIVSTVLTTPELRADWMAELEAVRSGMLRLREQLAGELRDLSGS
DRFGFVAEHRGMFSRLGATPEQVKRIKEEFGIYMGDSRINIAGLNDNTIPILARAIIEVGV

>d3tata_ c.67.1.1 (A:) Aromatic aminoacid aminotransferase, AroAT {Escherichia coli}

MFQKVDAYAGDPILTLMERFKEDPRSDKVNLSIGLYNEDGIIPQLQAVAEAEARLNAQPHGASLYLP
MEGLNCRYRHAIAPLLFGADHPVLKQQRVATIQTGGSGALKVGGADFLKRYFPESGVVWSDPTWENH
VAIFAGAGFEVSTYPWYDEATNGVRFNDLLATLTKLTPARSIVLLHPCCHNPTGADLTNDQWDAVIEI
LKARELIPFLDIAYQGFQAGMEEDAYAIRAIASAGLPALVNSFSKIFSLYGERVGGLSVMCEDAEAAGR
VLGQLKATVRRNYSSPPNFGAQVVAAVLNDEALKASWLAEEVEEMRTRILAMRQELVKVLSTEMPER
NFDYLLNQRGMFSYTGLSAAQVDRLREEFGVYLIASGRMCVAGLNTANVQRVAKAFAAVM

>d1gdea_ c.67.1.1 (A:) Aromatic aminoacid aminotransferase, AroAT {Archaeon Pyrococcus horikoshii}

ALSDRLELVSAEIRKLFDAIAGMKDVISLGIGEPDFDTPQHIKEYAKEALDKGLTHYGNIGLLELRE
AIAEKLKKQNGIEADPKTEIMVLLGANQAFMLGSLAFLKDGEEVLIPTPAFVSYAPAVILAGGKPVVEV
PTYEEDEFRLNVDELKKYVTDKTRALIINSPCNPTGAVLTKKDLLEIADFVVEHDLIVISDEVYEHFIY
DDARHYSIASLDGMFERTITVNGFSKTFAMTGWRLGFVAAPSWIIRMVVKFQMYNATCPVTFIQYAA
AKALKDERSWKAVEEMRKEYDRRRKLVWKRLEMLGPTVVKPKGAFYIFPRIRDGTLSKFKFSELM
LKEARVAVVPGSAFGKAGEGYVRISYATAYEKLEEAMDRMERVLKERKLV

>d1bw0a_ c.67.1.1 (A:) Tyrosine aminotransferase (TAT) {Trypanosoma cruzi}

WDVSMNSHAGLVFNPIRTVSDNAKPSPPKPIIKLSVGDPTLDKNLLTSAAQIKKLKEAIDSQECNGY
FPTVGSPEAREAVATWWRNSFVHKEELKSTIVKDNVVLCSGGSHGILMAITAICDAGDYALVPQPGF
HYETVCKAYGIGMHFYNCRPENDWEADLDEIRRLKDDKTLLIVTNPSNPGSNFSRKHVEDIVRL
AEELRLPLFSDEIYAGMVFKGKDPNATFTSVADFETTVPVILGGTAKNLVVPGWRLGWLLYVDPHG
NGPSFLEGLKRVGMLVCGPCTVVQAALGEALLNTPQEHLQIVAKIEESAMYLYNHIGECIGLAPTMP
RGAMYLMSRIDLEKYRDIKTDFEVEKLEEEENVQVLPGTIFHAPGFTRLTTRPVEVYREAVERIKA
FCQRHAA

>d1fg7a_ c.67.1.1 (A:) Histidinol-phosphate aminotransferase {Escherichia coli}

TVTITDLARENVRNLTPYQSARRLGGNGDVWLNANEYPTAVEFQLTQQLNRYPECQPKAVIENYA
QYAGVKPEQVLVSRGADEGIELLIRAFCEPGKDAILYCPPTYGMYSVSAETIGVECRVPTLDNWQLD
LQGISDKLDGVKVVYVCSPPNPTGQLINPQDFRTLLELTRGKAIVVADEAYIEFCQASLAGWLAEYP
HLAILRTLSKAFALAGLRGFTLANEEVINLLMKVIAPYPLSTPVADIAAQALSPQGIVAMRERVAQII
AEREYLIAALKEIPCVEQVDFDSETNYILARFKASSAVFKSLWDQGIILRDQNKQPSLSGCLRITVGTRE
ESQRVIDALRAEQV

>d1kusa_ c.67.1.1 (A:) L-threonine-0-3-phosphate decarboxylase CobD {Salmonella}

enterica}

HGGNIREPATVLGISPDQLLDFSANINPLGMPVSVKRALIDNLDCIERYPDADYFHLHQALARHHQVP
ASWILAGNETESIFTVASGLKPRRAMIVTPGFAEYGRALAQSGCEIRRWSLREADGWQLTDAILEAL
TPDLDCFLCTPNNPTGLLPERPLLQAIADRCKSLNINLILDEAFIDFIPHETGFIPALKDNPHIWWLR
SLTKFYAIPGLRLGYLVNSDDAAMARMRRQQMPWSVNALAAALAGEVALQDSAWQQATWHWLREE
GARFYQALCQLPLLTVYPGRANYLLRCEREDIDLQRRLTQRILIRSCANYPGLDSRYRVAIRSAAQ
NERLLAALRNVLGTIAP

>d1jg8a_c.67.1.1 (A:) Low-specificity threonine aldolase {*Thermatoga maritima*}

MIDLRSDTVTKPTEEMRKAMAQAEVGDVYGEDPTINELERLAAETFGKEAALFVPSGTMGNQVSI
MAHTQRGDEVILEADSHIFWYEVGAMAVLSGVMPHPVPGKNGAMDPDDVRKAIRPRNIHFRTSLI
AIENTHNRSGRVPLENIKEICTIAKEHGINVHIDGARIFNASIASGVPVKEYAGYADSVMFCLSKGL
CAPVGSVVVGDRDFIERARKARKMLGGGMRQAGVLAAGIHALTKMVDRLKEDHENARFLALKLKE
IGYSVNPEDVKTNMVILRTDNLKVNAGHFIEALRNSGVLANAVSDTEIRLVTHKDVSRNDIEEALNIF
EKLFKFS

>d1tpla_c.67.1.2 (A:) Tyrosine phenol-lyase {*Citrobacter intermedius*}

MNYPAEPRIKSVETVSMIPRDERLKKMQEAGYNTFLLNSKDIYIDLLTDSGTNAMSQWAGMM
MGDEAYAGSENFYHLERTVQELFGFKHIVPTHQGRGAENLLSQLAIKPGQYVAGNMYKNGAVFVDIV
RDEAHDAGLNIAFKGDIDLKQLKLIIDEKAENIAYICLAVTVNLAGGQPVSMANMRVRELTAAHG
IKVFDATRCVENAYFIKEQEQGFENKSIAEIVHEMFSYADGCTMSGKKDCLVNIGGFLCMNDEM
SSAKELVVVYEGMPSYGLAGRDMEAMAIGLREAMQYIEHRVKQVRYLGDKKAAGVPIVEPVG
GHAVFLDARRFCEHLTQDEFPAQSLAASIYVETGVRSMERGIKLETVRLTIPRRVYTYAHMDVVADGI
IKLYQHKEDIRGLKFIYFFTARFDYI

>d1ax4a_c.67.1.2 (A:) Tryptophan indol-lyase (tryptophanase) {*Proteus vulgaris*}

AKRIVEPFRIKMVEKIRVPSREEREALKEAGYNPFLPSSAVYIDLLTDSGTNAMSQWAAAMITG
DEAYAGSRNYDLKDKAKELFNVDYIIPAHQGRGAENILFPVLLKYKQKEGKAKNPVFISNFHFDTTA
AHVELNGCKAINIVTEKAFDSEYDDWKGDFDIKKKENIAQHGANIVAVSTVTCNSAGGQPVSM
SNLKEVYEIAKQHGFVVMDSARFCENAYFIKARDPKYKNATIKEVIFDAMYKYADALTMSAKKDLL
NIGGLVAIRDNEEIFTLARQRCVPMEGFVTYGGLAGRDMAAMVQGLEEGTEEEYLHYRIGQVKYLG
RLREAGIPIQYPTGGHAVFVDCCKLVPQIPGDQFPAQAVINALYLESGVRAVEIGSFLGRDPATGEQK
HADMEFMRLTIARRVYTNHMDYIADALIGLKEKFATLKGLEFEYEPVLRHFTARLKPI

>d1js3a_c.67.1.6 (A:) DOPA decarboxylase {*Pig (Sus scrofa)*}

MNASDFRRRGKEMVDYDADYLEGIEGRQVYDPVQPGYLRPLIPATAPQEPDTFEDILQDVEKIIMPG
VTHWHSPYFFAYFPTASSYPAMLADMLCGAIGCIGFSWAASPACTELETVMMDWLKMLQLPEAFL
AGEAGEGGGVIQGSASEATLVALLAARTKVVRRLQAASPLTQGAVLEKLVAYASDAQHSSVERAGLIG
GVKKAIPSDGKFAMRASALQEALERDKAAGLIPFFVATLGTSSCCSFDNLLEVGPICHEEDIWLHV
DAAYAGSAFICPEFRHLLNGVEFADSFNPNHKWLLVNFDCSAMWVKRRTDLTGAFKLDPVYLKHS
HQGSLITDYRHWQLPLGRRFRSLKMWFVFRMYGVKGLQAYIRKHVQLSHEFEAFVLQDPRFEVCA
EVTGLVCFRLKGSDDLNEALLERINSARKIHLVPCRLRGQFVLRFAICSRKVESGHVRLAWEHIRGL
AAELLA

>d1cl1a_c.67.1.3 (A:) Cystathionine beta-lyase, CBL {*Escherichia coli*}

KLDTQLVNAGRSKKYTLGAVNSVIQRASSLVFDSVEAKKHATRNRANGELFYGRRGTLTHFSLQQAM
CELEGGAGCVLFCGAAAVANSILAFIEQGDHVLMTNTAYEPSQDFCSKILSKLGVTTSWFDPLIGADI
VKHLQPNTKIVFLESPGSITMEVHDVPAIVAAVRSVVPDAIIMIDNTWAAGVLFKALDFGIDVSIQAAT
KYLVGHSAMIGTAVCNARCWEQLRENAYLMGMVDADTAYITSRGLRTLGVRLRQHHESSLKVAE

WLAEHPQVARVNHLPALPGSKGHEFWKRDFGTSSGLFSFVLKKKLNNEELANYLDNFSLSMAYSW
GGYESLILANQPEHIAAIRPQGEIDFSGLTIRLHIGLEDVDDLIADLDAGFARIV

>d1ibja_c.67.1.3 (A:) Cystathionine beta-lyase, CBL {Thale cress (*Arabidopsis thaliana*)}

ASVSTLLVNLNDNKFPDAMSTPLYQTATFKQPSAIENGPYDYTRSGNPTRDALESLLAKLDKADRA
FCFTSGMAALSAVTHLIKNGEIVAGDDVYGGSDRLSQQVPRSGVVVVRVNTTKLDEVAAAIGPQT
KLVWLESPTNPRQQISDIRKISEMAHAQ GALVLVDNSIMSPVLSRPLELGADIVMHSATKFIAGHSDV
MAGVLAVKGEKLAKEVYFLQNSEGSLAPFDCWLCLRGIKTMALRIEKQQENARKIAMYLSSHPRV
KKVYVYAGLPDHPGHHLHFSQAKGAGSVFSFITGSVALSKHLVETTKYFSIAVSVFGSVKSLISMPCFMSH
ASIPAEVREARGLTEDLVRISAGIEDVDDLISDLIAFKTFPL

>d1cs1a_c.67.1.3 (A:) Cystathionine gamma-synthase, CGS {*Escherichia coli*}

RKQATIAVRSLNDDEQYGCVPPIHLSSTYNFTGFNEPRAHDYSRRGNPTRDQVQALAELEGGAG
AVLTNTGMSAIHLVTTVFLKPGDLLVAPHDCYGGSYRFLDSLAKRGCYRVLFVDQGDQALRAALAE
KPKLVLVESPSNPLLRVVDIAKICHLAREVGAHSVVDNTFLSPALQNPALGADLVLSCTKYLNHGS
DQVAGVVIKDPDVTELAWWANNIGVTGGAFDSYLLRGLRRTLVPVPRMELAQRNAQAIVKYLQTP
LVKKLYHPSLPENQGHIEAARQQKGFAMLSFELDGDEQTLRRFLGGLSLFTLAESLGGVESLISHAA
TMTHAGMAPEARAAAGISETLLRISTGIEDGEDLIADLENGFRAANKG

>d1qgna_c.67.1.3 (A:) Cystathionine gamma-synthase, CGS {Common tobacco (*Nicotiana tabacum*)}

MKYASFLNSDGSVAIHAGERLGRGIVTDAITTPVVNTSAYFFNKTSELIDFKEKRRASFYGRYGNPT
TVVLEEKISALEGAESTLLMASGMCASVMLLALVPAGGHIVTTTDCYRKTRIFETILPKMGITATVI
DPADVGALELALNQQKVNLFTEPTNPFLRCVDIELVSKLCHEKGALVCIDGTFATPLNQKALALGA
DLVLHSATKFLGGHNDVLAGCISGPKLVSEIRNLHHILGGALNPAAAYLIIRGMKTLHLRVQQNST
ALRMAEILEAHPKVRHVYYPGLQSHPEHHIAKKQMTGFGGAVSFEVDGDLTTAKFVDALKIPYIAP
SFGGCESIVDQPAIMSYWDLSDRAKYGIMDNLVRFSGVEDFDDLKADILQALDSI

>d1e5ea_c.67.1.3 (A:) Methionine gamma-lyase, MGL {*Trichomonas vaginalis*}

ERMTPATACIHANPQKQFGAAIPPIYQTSTFVFDNCQQGGRFAGQESGYIYTRLGNPTVSNLEGKI
AFLEKTEACVATSSGMGAIAATVLTILKAGDHLISDECLYGCTHALFEHALTKFGIQVDFINTAIPGEVK
KHKMPNTKIVYFETPANPTLKIIDMERVCKDAHSQEGVLVIADNTFCSPMITNPVDFGVDVVVHSAT
KYINGHTDVVAGLICGKADLLQQIRMVGIKIDITGSVISPHDAWLITRGLSTLNIRMKAESNAMKVAE
YLSKSHPAVEKVVYPGFEDHEGHDIKKQMRMYGSMITFILKSGFEGAKKLLDNLKLTAVSLGGCES
LIQHPASMTHAVVPKEEREAAGITDGMIRLSVGIEDADELIADFKQGLDALLR

>d1d2fa_c.67.1.3 (A:) Modulator in mal gene expression, MalY {*Escherichia coli*}

LLPFTISDMDFATAPCIIEALNQRLMHGVFGYSRWKNDLFLAAIAHWFSTQHYTAIDSQTVVYGPSVI
YMVSELIRQWSETGEGVVIHTPAYDAFYKAIEGNQRTVMPVALEKQADGWFCMDMGKLEAVLAKPEC
KIMLLCSPQNPTGKVWTCDELEIMADLCERHGVRVISDEIHMDMVWGEQPHIPWSNVARGDWALL
TSGSKSFNIPALTGAYGHIENSSSRDAYLSALKGRDGLSSPSVLALTAHIAAYQQGAPWLDALRIYLKDN
LTYIADKMNAAPPELNWQIPQSTYLAWDLRPLNIDDNALQKALIEQEKVAIMPGYTYGEEGRGFVR
LNAGCPRSKLEKGVAGLINAIRAVR

>d1c7na_c.67.1.3 (A:) Cystalysin {*Treponema denticola*}

MIYDFTTKISRKNLGLSKWDLMYSQNPEVGNVPLSVADMEFKNPPELIEGLKKYLDETIVLGYTG
PTEEYKKTVKKWMKDRHQWDIQTDWIINTAGVVPVAVNAVREFTKPGDGVIIITPVYYPFFMAIKN
QERKIIECELLEKDGYYTIDFQKLEKLSKDKNNKALLFCSPHNPVGRVWKKDELQKIKDIVLKS
LWSDEIHFDLIMPGYEHTVFQSIDEQLADKTITFTAPSKTFNIAGMGMSNIIKNPDIRERFTKSRDAT
SGMPFTTLGYKACEICYKECGKWLDCIKVIDKNQRIVKDFFEVNHPEIKAPLIEGTYLQWIDFRALK

MDHKAMEEFMIHKAQIFFDEGYIFGDGGIGFERINLAAPSSVIQESLERLNKALKDLK

>d1eg5a_c.67.1.3 (A:) NifS-like protein/selenocysteine lyase {*Thermotoga maritima*}

MRVYFDNNAATTRVDDRLEEMIVFYREKYGNPNSAHGMGIEANLHMEKAREKVAKVLGVSPSEIFF
TSCATESINWILKTVAETFEKRKRTHITTTPIEHKAVLETMKYLSMKGFVKYVPVDSRQVVKLEELEK
LVDEDTFLVSIMAAANNEVGTIQPVEDVTRIVKKNKETLVHVDAVQTIGKIPFSLEKLEVDYASFAH
KFHGPKGVGITYIRKGVPIRPLIHGGGQERGLRSGTQNVPGIVGAARAMEIAVEELSEAAKHMEKLRS
KLVSGLMNLGAHIITPLEISLPNTLSVSFPNIRGSTLQNLSSGYGIYVSTSSACTSKDERLRHVLDAMG
VDRRIAQGAIRISLCKYNTSEEEVDYFLKKIEEILSFL

>d1jf9a_c.67.1.3 (A:) NifS-like protein/selenocysteine lyase {*Escherichia coli*}

IFSVDKVRADFPVLSREVNGLPLAYLDSAASAQKPSQVIDAEAEFYRHGYAAVHRGIHTLSAQATEKM
ENVRKRASLFINARSAEELVFVRGTTEGINLVANSWGNNSVRAGDNIIISQMEHHANIVPWQMLCAR
VGAELRVIPLNPDGTLQLETLPFLFDEKTRLLAITHVSNVLGTENPLAEMITLAHQHGAKVLVDGAQ
AVMHPVVDVQALDCDFYVFSGHKLYGPTGIGILYVKEALLQEMPPWEGGSMIATVSLSEGTTWTK
APWRFEAGTPNTGGIIGLGALEYVSALGLNNAIEYEQNLMHYALSQLESVPDLTYGPQNRLGVIAF
NLGKHHAYDVGSFLDNYGIAVRTGHHCAMPLMAYYVNPAMCRASLAMYNTHHEVDRLVTGLQRIH
RLLG

>d1elua_c.67.1.3 (A:) Cystine C-S lyase {*Synechocystis* sp.}

QFPGLANKTYFNFGGQILPTVALEAITAMYGLQENGPFSIAANQHIQQLIAQLRQALAETFNVDPN
TITITDNVTTGCDIVLWGLDWHQGDEILLTDCHEPGHIAIVQAIAARFGITYRFFPVAATLNQGDAAAV
LANHLGPKTRLVILSHLLWNTGQVPLAEIMAVCRRHQGNYPVRVLVDGAQSAGSLPLDFSRLEVDY
YAFTGHKWFAGPAGVGGLYIHGDCLGEINPTYVGWRSITYGAKGEPTGWAEGGKRFEVATSAYPQYA
GLLAALQLHQRQGTAEERYQAICQRSEFLWRGLNQLPHVHCLATSAPQAGLVSFTVDSPLGHRAIVQ
KLEEQRILRTIADPDCIRACCHYITDEEEINHLLARLADFGP

>d2dkb_c.67.1.4 (-) Dialkylglycine decarboxylase {*Pseudomonas cepacia*}

LNDDATFWRNARHHLVRYGGTFEPMIERAKGSFVYDADGRAILDFTSGQMSAVLGHCHPEIVSVIG
EYAGKLDHLFSEMLSRPVVDLATRLANITPPGLDRALLSTGAESNEAAIRMAKLVTKGYEIVGFAQS
WHGMTGAAASATYSAGRKGVGPAAVGSFAIPAPFTYRPRFERNGAYDYLAELDYAFDLIDRQSSGNL
AAFIAEPISSGGIIELPDGYMAALKRKCEARGMLLILDEAQTGVGRTGTMFACQRDGVTPDILTSLKT
LGAGLPLAAIVTSAAIEERAHELGYLFYTTTHVSDPLPAAVGLRVLDVVQRDGLVARANVMGDRLRRG
LLDLMERFDCIGDVRGRGLLLGVEIVKDRRTKEPADGLGAKITRECMNLGLSMNIVQLPGMGGVFRI
APPLTVSEDEIDLGLSLLGQAIERAL

>d2gsaa_c.67.1.4 (A:) Glutamate-1-semialdehyde aminomutase (aminotransferase)
{*Synechococcus* sp., strain GR6}

FKTIKSDEIFAAAQKLMPPGVSSPVRAFKSVGGQPIVFDKDAYAWDVGDNRYIDYVGTWGPACG
HAHPEVIEALKVAMEKGSFSGAPCALENVLAEMVNDVAVSIEMVRFVNSGTEACMAVLRMLRAYTG
RDKIIFEGCYHGHADMFLVKAGSGVATLGLPSSPGVPKTTANTLTTPYNDLEAVKALFAENPGEIA
GVILEPIVGNISGFIVPDAGFLEGLREITLEDALLVFDEVMTGFRIAYGGVQEKFGVTPDLTTLGKIIGG
GLPVGAYGGKREIMQLVAPAGPMYQAGTLNPLAMTAGIKTLELLRQPGTYEYLDQITKRSLDGLLA
IAQETGHAACGGQVSGMFGFFFTEGPVHNYEDAKKSDLQKFSRFHRGMLEQGIYLAQFEAGFTSL
AHTEEDIDATLAAARTVMSAL

>d2zoata_c.67.1.4 (A:) Ornithine aminotransferase {Human (*Homo sapiens*)}

GPPTSDDIFEREYKYGAHNYHPLPVALERGGKIYLWDVEGRKYFDLSSYSAVNQGHCHPKIVNALK
SQVDKLTLSRAFYNNVLGEYEEYITKLFNYHKVLPMTGVEAGETACKLARKWGYTVKGIQKYKA
KIVFAAGNFWGRTLSAISSSTDPTSVDGFGPFMPGFDIIPYNDLPALERALQDPNVAAFMVEPIQGEA

GVVVPDPGYLMGVRELCTRHQVLFIADEIQTGLARTGRWLAVDYENVRPDIVLLGKALSGLYPVSA
VLCDDDIMLTIKPGEHGSTYGGNPLGCRVAIAALEVLEENLAENADKLGILRNELMKLPDSDVVTAV
RGKGLLNAIVIKETKDWDAWKVCLRLRDNGLLAKPTHGDIIRFAPPLVIKEDELRESIEIINKTILSF
>d1gtxa_ c.67.1.4 (A:) 4-aminobutyrate aminotransferase, GABA-aminotransferase {Pig (Sus
scrofa)}

FDYDGPLMKTEVPGPRSRELMKQLNIIQNAEAVHFFCNYEESRGNLYVDVDGNRMLDLYSQISSIPIG
YSHPALVKLVQQPQNVSTFINRPALGILPPENFVEKLRRESLLSVAPKGMSQLITMACGSCSNENAFKTI
FMWYRSKERGQSAFSKEELETMINQAPGCPDYSILSFMGAFHGRTMGCLATTHSKAIHKIDIPSFD
WPIAPFPRLKYPLEEFVKENQQEEARCLEEVEDLIVKYRKKKKTVAGIIVEPIQSEGGDNHASDDFFR
KLRDISRKHGCAFLVDEVQTTGGGSTGKFWAHEHWGLDDAADVMTFSKMMTGFFHKEEFRPNA
PYRIFNTWLGDPKLNLLAEVINIIRKEDLLSNAAHAGKVLLTGLLDLQARYPPQFISRVGRGTFCFSFD
TPDESIRNKLISIARNKGVMLGGCGDKSIRFRPTLVFRDHHHLFLNIFSDILADFK

>d1bt4a_ c.67.1.4 (A:) Phosphoserine aminotransferase, PSAT {Bacillus circulans, subsp.
alkalophilus}

SERAYNFNAGPAALPLEVLERAQAEFVDYQHTGMSIMEMSHRGAVYEAVHNEAQARLLALLGNPTG
YKVLFIQGGASTQFAMIPMNFLEKQGTANYVMTGSWASKALKEAKLIGDTHVAASSEASNYMTLPK
LQEIQLQDNAAYLHLTSNETIEGAQFKAFPDTGSVPLIGDMSSDILSRPFDLNQFGLVYAGAQNLP
SGVTVVIVREDLVAESPKHLPTMLRYDITYVKNNSLYNTPPSFGIYMVNEVLKWIIEERGGLEGVQQAN
RKKASLIYDAIDQSGGFYRGCVDVDSRSDMNITFRLASEELEKEFVKASEQEGFVGLKGHRVGGGLRA
SIYNAVYESCEALVQFMEHFKRSRG

>d1bjna_ c.67.1.4 (A:) Phosphoserine aminotransferase, PSAT {Escherichia coli}

QIFNFSSGPAMPLPAEVLKQAQQLRDWNGLGTSVMEVSHRGKEFIQVAEEAEKDFRDLLNVPSNYK
VLFCHGGGRGQFAAVPLNILGDKTTADYVDAGYWAASAIKEAKKYCTPNVFDKAVTVDGLRAVKPM
REWQLSDNAAYMHYCPNETIDGIAIDETPDFGADVVAADFSSTILSRPIDVSRYGVYAGAQNIGPA
GLTIVIVREDLLGKANIACPSILDYSILNDNGSMFNTPTFAWYLSGLVFKWLKANGGVAEMDKINQ
QKAELLYGVIDNSDFYRNDVAKRNRSRMNVPFQLADSALDKLFLEESFAAGLHALKGHRVGGMRA
SIYNAMPLEGVKALTDPMVEFERRHG

>d1cj0a_ c.67.1.4 (A:) Serine hydroxymethyltransferase {Rabbit (Oryctolagus cuniculus)}

WSSHEQMLAQPLKSDAEVYDIKKESNRQRVGLELIASENFASRAVLEALGSLNNKYSEGYPGQR
YYGGTEHIDELETLQKRALQAYGLDPQCWGVNVQPYSGSPANFAVYTALVEPHGRIMGLDLPDGGH
LTHGFMTDKKISATSIFFESMAYKVNPDYIDYDRLEENARLFHPKLIAGTSCYSRNLDYGRLRKI
ADENGAYLMADMAHISGLVAGVVPSPFEHCHVVTTHKTLRGCRAGMIFYRRGVRSVDPKTGKE
ILYNLESLINSAVFPGLQGGPHNHAIGVAVALKQAMTPEFKEYQRQVVANCRALSAALVELGYKIVT
GGSDNHLILVLDLRSKGTGGRAEKVLEACSIACNKNTCPGDKSALRPSGLRLGTPALTSRGLLEKDFQ
KVAHFIHRGIELTVQIQDDTGPRATLKEFKEKLAGDEKHQRAVRALRQEVESFAALFPLPGLPGF

>d1ejia_ c.67.1.4 (A:) Serine hydroxymethyltransferase {Mouse (Mus musculus)}

MADRDATLWASHEKMLSQPLKSDAEVYSIIKKESNRQRVGLELIASENFASRAVLEALGSSLNNKYS
EGYPGQRYGGTEFIDELEMLCQKRALQAYHLDPCWGVNVQPYSGSPANFAVYTALVEPHGRIMGL
DLPDGGHLTHGFMTDKKISATSIFFESMPYKVPETGYINYDQLEENASLFHPKLIAGTSCYSRNL
DYARLRKIADDNGAYLMADMAHISGLVAAGVVPSPFEHCHVVTTHKTLRGCRAGMIFYRKGVRS
VDPKTGKETYYELESINSAVFPGLQGGPHNHAIGVAVALKQAMTTEFKIYQLQVLANCRALSDALT
ELGYKIVTGGSDNHLILMDLRSKGTGGRAEKVLEACSIACNKNTCPGDKSALRPSGLRLGTPALTSR
GLLEEDFQKVAHFIHRGIELTLQIQSHMATKATLKEFKEKLAGDEKIQSAVATLREEVENFASNFLPG
LPDF

>d1bj4a_c.67.1.4 (A:) Serine hydroxymethyltransferase {Human (Homo sapiens)}
DADLWSSHDAMLAQPLKSDVEVYNIKKESNRQRVGLELIASENFASRAVLEALGSLNNKYSEGY
PGQRYYGTEFIDELETLCQKRALQAYKLDPQCWGVNVQPYSQSPANFAVYTALVEPHGRIMGLDLP
DGGHLTHGFMTDKKKISATSIFFESMPYKVNPDGTGYINYDQLEENARLFHPKLIAGTSCYSRNLEYA
RLRKIADENGAYLMADMAHISGLVAAGVVPSPFEHCHVVT'TTTHKTLRGCRAGMIFYRKGKVSVDP
ATGKEILYNLESLINSAVFPGLQGGPHNHAIAGVAVALKQAMTLEFKVYQHQQVANCRALEALTELG
YKIVTGGSDNHLILVDLRSKGTGGRAEKVLEACSIACNKNTCPGDRSALRPSGLRLGTPALTSRGLLE
KDFQKVAHFHIRGIELTLQIQSDTGVAATLKEFKERLAGDKYQAAVQALREEVESFASLFPLPGL

>d1dfoa_c.67.1.4 (A:) Serine hydroxymethyltransferase {Escherichia coli}
LKREMNIADYDAELWQAMEQEKVREEHIELIASENYTSRVMQAQGSQLTNKYAEGYPGKRYGG
CEYVDIVEQLAIDRAKELFGADYANVQPHSGSQANFAVYTALLEPGD'TVLGMNLAHGHLTHGSPVN
FSGKLYNIVPYGIDATGHIDYADLEKQAKEHKPKMIIGGFSAYSGVVDWAKMREIADSIGAYLFVDM
HVAGLVAAGVYPNPVPHAHVVT'TTTHKTLAGPRGGLILAKGGSEELYKLN SAVFPGGQGGPLMHVI
AGKAVALKEAMEPEFKTYQQQVAKNAKAMVEVFLERGYKVVSGGTDNHLFLVDLVDKNLTGKEAD
AALGRANITVKNKNSVPNDPKSPFVTS'GIRVGT'PAITRRGFKEAEAKELAGWMCDVLD'SINDEAVIERI
KGKVL'DICARYPVYA

>d1b9ha_c.67.1.4 (A:) 3-amino-5-hydroxybenzoic acid synthase (AHBA synthase)
{Amycolatopsis mediterranei}
KAPEFFAWPQYDDAERNGLVRALEQQQWWRMGDEVNSFEREF'AAHHGAAHALAVTNGTHALE
LALQVMGVGPGTEVIVPAFTFISSQAAQRLGAVTVPVDVDAATYNLDPEAVAAAVTPR'TKVIMPVH
MAGLMADMDALAKISADTGVPLLQDAAHAGARWQ'GKRVGELDSIATFSFQNGKLMTAGEGGAVV
FPDGETEKYETAFLRHSCGRPRDDRRYFHKIAGSNMRLNEFSASV'LRQLARLDEQIAVRDERWTL
LSRLLGAIDGVVPQGGDVRADRNSHYMAMFRIPGLTE'ERNALVDRLVEAGLPAAFAAFRAIYRTDAF
WELGAPDESVD'AIARRCPNTDAISSDCVWLHHRVLLAGEPELHATAEIIADAVARA

>d1fc4a_c.67.1.4 (A:) 2-amino-3-ketobutyrate CoA ligase {Escherichia coli}
GSHMRGEFYQQLTNDLETARA'EGLFKEERIITSAQQADITVADGSHVINFCANNYLGLANHPDLIAA
AKAGMDSHGFGMASVRFICGTQDSHKELEQKLA'AF'GMEDAILYSSCFDANGGLFETLLGAEDAIISD
ALNHASIIDGVRLCKAKRYRYANNDMQE'EARLKEAREAGARHVLIATDGVFSMDGVIANLKGVC'DL
ADKYDALVMVDDSHAVGFVGENGRGSHEYCDVMGRV'DIITGTLGKALGGASGGYTAARKEVVEWLR
QRSR'PYLFSNSLAPAIVAASIKVLEMVEAGSELRDRLWANARQFREQMSAAGFTLAGADHAIIPV'ML
GD'AVVAQKFARELQKEGIYVTGFFYPVVPKGQARIRTQMSAAHTPEQITRAVEAFTRIGKQLGVIA

>d1bs0a_c.67.1.4 (A:) PLP-dependent acyl-CoA synthase (8-amino-7-oxonanoate synthase,
AONS) {Escherichia coli}
SWQEKINAALDARRAADALRRRY'PVAQAGRWLVADDRQYLN'FSSNDYLGLSHHPQIIRAWQQGA
EQFGIGSGGSGHVSGYSVVHQALEEELAEWL'GYSRALLFISGFAANQAVIAAMMAKEDRIAADRLSH
ASLLEAASLSPSQLRRFAHNDV'THLARLLASPCPGQ'QM'VTEGVFSMDGDSAPLAEIQVTTQQHNG
WLMVDDAHGTGVIGE'QGRGSCWLQKVKPELLV'VTFGKGFVSGAAVLCSS'TVADYLLQFARHLYST
SMPPAQALRASLAVIRSDEGDARREKLAALITRFRAGVQDL'PFTLADSCSAIQPLIVGDNSRALQL
AEKLRQQGCWVTAIRPPTVPAGTARLRLTLTAAHEM'QDIDRLL'EV'LVHGNG

>d1qj5a_c.67.1.4 (A:) Adenosylmethionine-8-amino-7-oxonanoate aminotransferase,
BioA {Escherichia coli}
MTDDDLAFDQRHILHPYTSMTSPLPVY'PVVSAEGCELILSDGRRLVDGMSSW'WAAIHGYNHPQLNA
AMKSQIDAMSHVMFGGITHAPAI'ELCRKLVAMTPQPLECVFLADSGSVAVEVAMKMALQYWQAKGE
ARQRFLTFRNGYHGDTFGAMSVCDP'DNSMHS'WKGYPENLFAPAPQSRMDGEWDERDMVGFAR

LMAAHRHEIAAVIIEPIVQGAGGMRMYHPEWLKRIRKICDREGILLIADEIATGFGRTGKLFACHEAEI
APDILCLGKALTGGTMTLSATLTTREVAETISNGEAGCFMHGPTFMGNPLACAAANASLAILESGDW
QQQVADIEVQLREQLAPARDAEMVADVRVLGAIGVVETTHPVNMAALQKFFVEQGVWIRPFGLIY
LMPPYIILPQQLQRLTAAVNRAVQDETFFCQ

>d1b8ga_ c.67.1.4 (A:) 1-aminocyclopropane-1-carboxylate synthase (ACC synthase) {Apple
(*Malus domestica*)}

MLSRNATFNSHGQDSSYFLGWQEYEKNPYHEVHNTNGIIMGLAENQLCFDLLESWLAKNPEAAA
FKKNGESIFAELALFQDYHGLPAFKKAMVDFMAEIRGNKVTFDPNHLVLTAGATSANETFFCLADP
GEAVLIPTPYYPGFDRDLKWRTGVEIVPIHCTSSNGFQITETALEEAYQEAERNLRVKGVLTNPSN
PLGTTMTRNELYLLLSFVEDKGIHLISDEIYSGTAFSSPSFISVMEVLKDRNCDENSEVWQRVHVVS
LSKDLGLPGFRVGAISNDDMVVAAATKMSSFGLVSSQTQHLLSAMLSDKKLTKNYIAENHKRLKQR
QKKLVSGLQKSGISCLNGNAGLFCWVDMRHLLRSNTFEAEMELWKKIVYEVHLNISPSSCHCTEPG
WFRVCFANLPERTLDLQRLKAFVG

>d1iaya_ c.67.1.4 (A:) 1-aminocyclopropane-1-carboxylate synthase (ACC synthase) {Tomato
(*Lycopersicon esculentum*)}

ILSKLATNEEHGENSPYFDGWKAYDSDPFHPLKNPNGVIQMGLAENQLCLDLIEDWIKRNPKGSICS
EGIKSFKAIANFQDYHGLPEFRKAIKFMKTRGGRVRFDPERVVMAGGATGANETIIFCLADPGDA
FLVPSPPYPAFNRLRWRTGVQLPIHCESSNFKITSKAVKEAYENAQKSNIKVKGLILTNPSPNPLGT
TLDKDTLKSIVLSFTNQHNHLVCDIYAATVFDTPQFVSI AEILDEQEMTYCNKDLVHIVYSLSKDMG
LPGFRVGIISFNDDVVNCARKMSSFGLVSTQTQYFLAAMLSDEKFDVDFLRESAMRLGKRHKHFT
NGLEVVGKCLKNAGLFCWMDLRPLLRESTFDSEMSLWRVIINDVKLVNVPSSFECEPQWFRV
CFANMDDGTVDIALARIRRFVGVK

>d1c4ka2 c.67.1.5 (A:108-569) Ornithine decarboxylase major domain {*Lactobacillus* sp.,
strain 30a}

PPFFKSLKEYVSRYLQFDCPGHQGGQYRKHYPAGREFYDFFGGETVFRADLCNADVALGDLLIHEGPA
VAAEKHAARVYNADKTYFVLGGSSNANTVTLSALVSNGLVLFDRNNHKSIVNSALAMAGGRPYYL
QTNRPYGFYGGIYDSDFFDEKKIRELAAKVDPERAKWKRPFRLAVIQLGTYDGTIYNAHEVVKRIGH
LCDYIEFDSAWVGYEQFIPMMRNSSPLLIDDLGPEDPGIIVVQSVHKQQAGFSQTSQIHKKDSHIKQG
LRYCDHKHFNSFNLMSTSPFYPMYAALDVNAAMQEGEAGRKLWHDLLITIEARKKLIKAGSMF
RPFVPPVNGKKWEDGTDTEDMANNIDYWRFEKGAKWHAYEGYDGNQYYVDPNKFMLTTPGINPE
TGDYEDFGVPATIVANYLRDHGIIPEKSDLSILFLMTPAETPAKMNNLITQLLQLRLIEED

>d1qg8a_ c.68.1.1 (A:) Spore coat polysaccharide biosynthesis protein SpsA {*Bacillus*
subtilis}

PKVSVIMTSYNKSDYVAKSISSILSQTFSDFELFIMDDNSNEETLNVIRPFLNDNRVRFYQSDISGVKE
RTEKTRYAALINQAIEMAEGEYITYATDDNIYMPDRLLKVMRELDTHPEKAVIYSASKTYHLNENRD
IVKETVRPAAQVTWNAPCAIDHCSVMHRYSVLEKVKKEKFGSYWDESPAFYRIGDARFFWRVNHFYF
FYPLDEELDLNYITDQSIHFQLFELEKNEFVRNLPQRNCRELRESLKKLGMG

>d1j8wb_ c.68.1.2 (B:) beta 1,4 galactosyltransferase (b4GalT1) {Cow (*Bos taurus*)}

TACPEESPLLGPMLIEFNIPVDLKLVEQQNPKVKGGRYTPMDCISPHKVAIIPFRNRQEHLYWLY
YLHPILQRQQLDYGIYVINQAGESMFRKLLNVGFKEALKDYDYNCFVFSVDVLIIPMNDHNTYRCF
SQPRHISVAMDKFGFSLPYVQYFGGVSALSQKQFLSINGFPNNYWGWWGGEDDIYNRLAFRGMSSV
RPNNAVIGKCRMIRHSRDKKNEPNPQRFDRIAHTKETMLSDGLNSLTYMVLEVQRYPLYTKITVDIGT
PS

>d1ezia_ c.68.1.3 (A:) CMP acylneuramate synthetase {*Neisseria meningitidis*}

MEKQNIIVILARQNSKGLPLKNLRKMNGLISLLGHTINAAISSKCFDRIIVSTDGGLIAEEAKNFGVEVV
LRPAELASDTASSISGVIHALETIGSNSTVTLTLLQPTSPLRTGAHIREAFSLFDEKIKGSVVSACPMEEH
PLKTLQINNGEYAPMRHLSLEQPRQLPQAFRPNNGAIYINDTASLIANNCFFIAPTPLYIMSHQDSI
DIDTELDLQQAENILN

>d1ga8a_ c.68.1.4 (A:) Galactosyltransferase LgtC {*Neisseria meningitidis*}

MDIVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLDAGISEANRAAVAANLRGGGNIRFIDVNPE
DFAGFPLNIRHISITTYARLKLGEYIADCDCVLYLDIDVLRDLSLTPLDWDTDLGDNWLGASIDLFVERQ
EGYKQKIGMADGEYFVFNAGVLLINLKKWRRHDIFKMSSEWVEQYKQVMDQYQDQDILNGLFKGGVC
YANSRNFNMPNTNYAFMANWFASRHTDPLYRDRNTVMPVAVSHYCGPAKPWHRDCTAWGAERFT
ELAGSLTTVPEEWGKL

>d1g93a_ c.68.1.9 (A:) alpha-1,3-galactosyltransferase catalytic domain {Cow (*Bos taurus*)}

KLKLSDFWNPFKRPEVVMTTKWKAPVVWEGTYNRAVLDNYYAKQKITVGLTVFAVGRYIEHYLEEF
LTSANKHFVGHVIFVIMVDDVSRMPLIELGPLRSFKVFKIKPEKRWQDISMMRMKTIGEHIHVAHI
QHEVDFLFCMDVDVQVQDKFGVETLGEVSAQLQAWWYKADPNDFTYERRKESAAAYIPFGEGDFYY
HAAIFGGTPTQVLNITQECFKILKDKKNDIEAQWHDESHLNKYFLLNKPTKILSPEYCWYDHIGLP
ADIKLVKMSWQT

>d1hv9a2 c.68.1.5 (A:4-251) N-acetylglucosamine 1-phosphate uridyltransferase GlmU,
N-terminal domain {*Escherichia coli*}

NAMSVVILAAGKGTRMYSIDLKVLHLAGKAMVQHVIDAANELGAAHVHLVYGHGGDLLKQALKD
DNLNWWLQAEQLGTGHAMQQAAPFFADDEDILMLYGDVPLISVETLQRLRDAKPPGGIGLLTVKLD
DPTGYGRITRENGKVTGIVEHKDATDEQRQIQEINTGILANGADMKRWLAKLTNNNAQGEYYITDII
ALAYQEGREIVAVHPQRLSEVEGVNRLQLSRLERVYQSEQAEEKLLLAG

>d1hm9a2 c.68.1.5 (A:2-251) N-acetylglucosamine 1-phosphate uridyltransferase GlmU,
N-terminal domain {*Streptococcus pneumoniae*}

SNFAIILAAGKGTRMKSDLPKVLHKVAGISMLEHVFRSVGAIQPEKTVTVVGHKAELVEEVLAGQTEF
VTQSEQLGTGHAVMMTEPILEGLSGHTLVIAGDTPLITGESLKNLIDFHINHKNVATILTAETDNPFY
GRIVRNDNAEVLRIVEQKDATDFEKQIKEINTGTYVFDNERLFEALKNINTNNAQGEYYITDVIGIFR
ETGEKVGAYTLKDFDESLGVNDRVALATAESVMRRRINHKHMVNG

>d1fxoa_ c.68.1.6 (A:) glucose-1-phosphate thymidyltransferase RmlA {*Pseudomonas*
aeruginosa}

KRKGIILAGSGTRLHPATLAISKQLLPVYDKPMIYYPLSTLMLAGIREILIIISTPQDTPRFQQLLDGS
NWGLDLQYAVQSPDGLAQAFIIGESFIGNDLSALVLDNLYYGHDFHELLGSASQRQTGASVFAYHV
LDPERYGVVEFDQGGKAISLEEKPLEPKSNIYAVTGLYFYDQVVDIARDLKPSRGELEITDVNRAYL
ERQLSVEIMGRGYAWLDTGTHDSLLEAGQFIATLENRQGLKVACPEEIAAYRQKWIDAAQLEKLAAP
LAKNGYGQYLKRLLETETVY

>d1iina_ c.68.1.6 (A:) glucose-1-phosphate thymidyltransferase RmlA {*Salmonella*
enterica}

MKTRKGIILAGSGTRLYPVTMAVSQQLLPYDKPMIYYPLSTLMLAGIRDILIIISTPQDTPRFQQLL
DGSQWGLNLQYKVQSPDGLAQAFIIGEEFIGHDDCALVLDNIFYGHDLPKLMEAAVNKESGATVF
AYHVNDPERYGVVEFDQKGTAVSLEEKPLQPKSNIYAVTGLYFYDNSVEMAKNLKPSARGELEITDI
NRIYMEQGRLSVAMMGRGYAWLDTGTHQSLIEASNFIATIEERQGLKVSCPEEIAFRKNFINAQQVIE
LAGPLSKNDYGKYLKLMV

>d1h5ra_ c.68.1.6 (A:) glucose-1-phosphate thymidyltransferase RmlA {*Escherichia coli*}

KMRKGIILAGSGTRLYPVTMAVSKQLLPYDKPMIYYPLSTLMLAGIRDILIIISTPQDTPRFQQLLD

GSQWGLNLQYKVQSPDGLAQAFIIGEEFIGGDDCALVLGDNIFYGHDLPKLMEAAVNKESGATVFA
YHVNDPERYGVVEFDKNGTAISLEEKPLEPKSNYAVTGLYFYDNDVVQMAKNLKPSSARGELEITDIN
RIYLEQGRLSVAMMGRGYAWLDTGTHQSLIEASNFIATIEERQGLKVSCEPIAFRKGFDVEQVRKLA
VPLIKNNYGQYLYKMTKD

>d1fgga_c.68.1.7 (A:) 1,3-Glucuronyltransferase I (glcAT-I) {Human (Homo sapiens)}
MTIYVVPTPYARLVQKAELVRLSQTLSLVPRLHWLLVEDAEGPTPLVSGLLAASGLLFTHLVVLTPKA
QRLREGEPGWVHPRGVEQRNKALDWLRGRGGAVGGEKPPPPGTQGVVYFADDDNTYSRELFE
MRWTRGVSVPVGLVGGVRFEGPQVQDGRVVGFTAWEPSRPFVDMAGFAVALPLLLDKPNAQF
DSTAPRGHLESSLLSHLVDPKDLEPRAANCTRVLVWHTRTEKPKMKQEEQLRQGRGSDPAIEV

>d1fo8a_c.68.1.10 (A:) N-acetylglucosaminyltransferase I {Rabbit (Oryctolagus cuniculus)}
LAVIPILVIACDRSTVRRCLDKLLHYRPSAELFPIIVSQDCGHEETAQVIASYSVAVTHIRQPDLSNIAVQ
PDHRKFQGYKIHRYRWALGQIFHNFNYPAAVVVEDDLEVAPDFFEYFQATYPLLKADPSLWCVS
AWNDNGKEQMVDSSKPELLYRTDFFPGLGWLLELWAELEPKWPKAFWDDWMRRPEQRKGRA
CVRPEISRTMTFGRKGVSHGQFFDQHLKFIKLNQQFVFPFTQLDLSYLQAEYDRDFLARVYGAPQLQ
VEKVRTNDRKELGEVRVQYTGRDSFKAFKALGVMDDLKSGVPRAGYRGIVTFLFRGRRVHLAPPQ
TWDGYDPSWT

>d1e5ka_c.68.1.8 (A:) Molybdenum cofactor biosynthesis protein MobA {Escherichia coli}
MTTITGVVLAGGKARRMGGVDKGLLELNGKPLWQHVDALMTQLSHVVVNANRHQEIYQASGLKV
IEDSLADYPGPLAGMLSMQEQEAGEWFLFCPCDTPYIPDLAARLNHQRKDAPVVVWHDGERDHP
TIALVNRAIEPLLEYLQAGERVMVFMRLAGGHAVDFSDHKDAFVNVNTPEELARWQ

>d1i52a_c.68.1.13 (A:) 4-diphosphocytidyl-2-c-methylerythritol (CDP-me) synthase (YgbP)
{Escherichia coli}
HLDVCAVPAAGFGRMQTECPKQYLSIGNQTILEHSVHALLAHPRVKRVVIAISPGDSRFAQLPLAN
HPQITVVDDGDERADSVLAGLKAAGDAQWVLVHDAARPCLHQDDLARLLALSETSRGGILAAPVR
DTMKRAEPGKNAIAHTVDRNGLWHALTPQFFPRELLHDCLTRALNEGATITDEASALEYCGFHPQL
VEGRADNIKVTRPEDLALAEFYLTR

>d1h7ea_c.68.1.13 (A:) CMP:2-keto-3-deoxy-manno-octonic acid (CMP-KDO)synthetase,
KdsB {Escherichia coli}
SKAVIVIPARYGSSRLPGKPLLDIVGKPMIQHVYERALQVAGVAEVVWATDDPRVEQAVQAFGGKAIM
TRNDHESGTDRLVEVMHKVEADIYINLQGDEPMIRPRDVETLLQGMRRDDPALPVATLCHAISAEA
AEPSTVKVVVNTQRDALYFSRSPYPRNAEKARYLKHVGIYARRDVLQNYSQLPESMPEQAESLEQ
LRLMNAGINIRTFEVAATGPGVDTPACLEKVRALMAQELAENA

>d1jyka_c.68.1.13 (A:) CTP:phosphocholine cytidyltransferase LicC {Streptococcus
pneumoniae}
EIRVKAILAAGLGTTRLRPLTENTPKALVQVNQKPLIEYQIEFLKEKGINDIIVGYLKEQFDYLKEKYG
VRLVFNDKYADYNNFYSLYLVKEELANSYVIDADNYLFKNMFRNDLTRSTYFSVYREDCTNEWFLVY
GDDYKVQDIIVDSKAGRILSGVSFWDAPTAEKIVSFIDKAYVSGEFVDLYWDNMVKDNIKELDVYVE
ELEGNSIYEIDSVQDYRKLEEILK

>d1jw9b_c.111.1.1 (B:) Molybdenum cofactor biosynthesis protein MoeB {Escherichia coli}
AELSDQEMLRYNRQIILRGFDGQEQALKDSRVLIVGLGGLGCAASQYLASAGVGNLTLDFDFTVSL
NLQRQTLHSDATVGQPKVESARDALTRINPHIAITPVNALLDDAELAALIAEHLVLDCTDNVAVRN
QLNAGCFAAKVPLVSGAAIRMEGQITVFTYQDGEPCYRCLSRFLGENALTCVEAGVMAPLIGVIGSLQ
AMEAIKMLAGYKGPASGKIVMYDAMTCQFREMMLMRNPGCEVCG

>d1ea5a_c.69.1.1 (A:) Acetylcholinesterase {Electric ray (Torpedo californica)}

SELLVNTKSGKVMGTRVPVLSHISAFGLGIPFAEPPVGNMRFRRPEPKPWVSGVWNASTYPNNCQQ
YVDEQFPGFSGSEMWNPNREMSDCLYLNWVPSRPKSTTVMVWIYGGGFYSGSSTLDVYNGKYL
AYTEEVVLVLSYRVGAFGLALHGSQEAPGNVGLLDQRMALQWVHDNIQFFGGDKPTVTIFGESAG
GASVGMHILSPGSRDLFRRAILQSGSPNCWASVSVAEGRRAVELGRNLNCLNSDEELIHLREK
KPQELIDVEWNVLPFDSIFRFSFVVIDGEFFPTSLESMLNSGNFKKTQILLGVNKDEGSFFLLYGAPG
FSKDESKISREDFMSGVKLSVPHANDLGLDAVTLQYTDWMDNNGIKNRDGLDDIVGDHNVICPL
MHFVNKYTKFGNGTYLYFFNHRASNLVPEWVGVIHGYEIEFVFGPLPLVKELNYTAEELSRIM
HYWATFAKTGNPNEPHSQESKWPLFTTKEQKFIDLNTEPMKVHQRLRVQMCVFWNQFLPKLLNA
T

>d1maaa_c.69.1.1 (A:) Acetylcholinesterase {Mouse (Mus musculus)}

EDPQLLVRVRRGGQLRGIRLKAPGGPVSAFLGIPFAEPPVGSRRFMPPEPKRPVSGVLDATTFQNVCY
QYVDTLYPGFEGTEMWNPNTNRELSCLYLNWVTPYPRPASPTPVLWIYGGGFYSGAASLDVYDGR
FLAQVEGAVLVSMNYRVGTFGFLALPGSREAPGNVGLLDQRLALQWVQENIAAFGGDPMSVTLFGE
SAGAASVGMHILSPSRSLFHRAVLQSGTPNGPWATVSAGEARRRATLLARLVGCPPGGAGGNDTEL
IACLRTRPAQDLVDHEWHVLPQESIFRFSFVVPVVDGDFLSDTPEALINTGDFQDLQVLVGVVVKDEGS
YFLVYGVPGFSKDNESLISRAQFLAGVRIGVPQASDLAAEAVVLHYTDWLHPEDPTHLRDAMSAVVG
DHNVCVPAQLAGRLAAQGARVYAYIFEHRASLTWPLWVGPHGYEIEFIFGLPLDPSLNYTTEER
IFAQRLMKYWTNFARTGDPNDPRDRKSPQWPPYTAAQYVSLNPKLEVRRGLRAQTCAFWNR
LPKLLSAT

>d1f8ua_c.69.1.1 (A:) Acetylcholinesterase {Human (Homo sapiens)}

DAELLVTVRRGRLRGIRLKTPGGPVSAFLGIPFAEPPMGPRRFLPPEPKQPWVSGVVDATTFQSVCYQY
VDTLYPGFEGTEMWNPNTNRELSCLYLNWVTPYPRPTSPTPVLVWIYGGGFYSGASSLDVYDGRFLV
QAERTVLVSMNYRVGAFGLALPGSREAPGNVGLLDQRLALQWVQENIAAFGGDPMSVTLFQGSAG
AASVGMHLLSPPSRGLFHRAVLQSGAPNGPWATVGMGEARRRATQLAHLVGCPPGGTGGNDTELVA
CLRTRPAQVLVNHEWHVLPQESVFRFSFVVPVVDGDFLSDTPEALINAGDFHGLQVLVGVVVKDEGSYF
LVYGAPGFSKDNESLISRAEFLAGVRVGVVQVSDLAAEAVVLHYTDWLHPEDPARLREALSDVVDGH
NVVCPVAQLAGRLAAQGARVYAYVFEHRASLTWPLWVGPHGYEIEFIFGIPLDPSRNYTAEKIFA
QRLMRYWANFARTGDPNEPRDPKAPQWPPYTAGAQQYVSLDLRPLEVRRGLRAQACAFWNRFLP
KLLSAT

>d1dx4a_c.69.1.1 (A:) Acetylcholinesterase {Fruit fly (Drosophila melanogaster)}

DRLVVQTSSGPVRRSVTVQGREVHVYTGIPYAKPPVEDLRFRKPVPAEPWHGVLDATGLSATCVQE
RYEYFPGFSGEEIWNPNNTNRELSCLYINWAPAKARLRHGRGANGGEHPNGKQADTDHLIHNGNP
QNTTNGLPILWIYGGGFMTGSATLDIYNADIMAAVGNVIVASFQYRVGAFGLHLAPEMPSEFAEEA
PGNVGLWDQALAIRWLKDNAHAFGGNPEWMTLFGESAGSSSVNAQLMSPVTRGLVKRGMMSQSGT
MNAPWSHMTSEKAVEIGKALINDCNCNASMLKTNPAHVMSCMRSVDAKTISVQQWNSYSGILSFPS
APTIDGAFLPADPMTLMKTADLKDYDILMGNVRDEGTFFLYDFIDYFDKDDATALPRDKYLEIMN
NIFGKATQAEREAIIFQYTSWEGNPGYQNNQQIGRAVDHFFTCPTNEYAQAALAEERGASVHYFFTH
RTSTSLWGEWVGVLHGDEIEYFFGQPLNNSLQYRPVERELGKRMLSAVIEFAKTGNPAQDGEW
NFSKEDPVYIFSTDDKIEKLARGPLAARCSFWNDYLPKVRWS

>d2bce_c.69.1.1 (-) Bile-salt activated lipase (cholesterol esterase) {Cow (Bos taurus)}

AKLGSVYTEGGFVEGVNKKLSLFGDSVDIFKGIPFAAAPKALEKPERHPGWQGTLLKAKSFKKRCLQA
TLTQDSTYGNEDCLYLNWVPPQGRKEVSHDLVPMIWIYGGAFMLGASQGANFLSNLYDGEIATR
NVIVVTFNYRVGLGFLSTGDSNLPGNYGLWDQHMAIAWVKNIEAFGGDPDNITLFGESAGGASVS
LQTLSPYKGLIKRAISQSGVGLCPWAIQDPLFWAKRIAELVGCVPVDDTSMAGCLKITDPRALTLA

YKPLPGSTEYPKLHYLSFVFPVIDGDFIPDDPVNLYANAADVYIAGTNDMDGHLFVGMVDPAINSNK
QDVTEEDFYKLVSGLTVTKGLRGANATYEVYTEPWAQDSSQETRKKTMVDLETDILFLIPTKIAVAQ
HKSHAKSANTYTYLFSQPSRMPYIPKWMGADHADDLQYVFGKPFATPLGYRAQDRTVSKAMIAYW
TNFARTGDPNTGHSTVPANWDPYTLLEDDNYLEINKQMDSNSMKLHLRTNYLQFWTQTYQALPTV
TSAGASLLPPEDNSQASVPPADNSGAPTEPSAGDSEVAQMPVVIGF

>d1f6wa_ c.69.1.1 (A:) Bile-salt activated lipase (cholesterol esterase) {Human (Homo sapiens)}

AKLGAVYTEGGFVEGVNKKLGLLGDSDIFKGIFFAAPTCALENPQPHPGWQGTLKAKNFKKRCLQ
ATITQDSTYGDDECLYLNIWVPQGRKQVSRDLPVMIWIYGGAFMLGSGHGANFLNNYLYDGEEIATR
GNVIVVTFNYRVGPLGFLSTGDANLPGNYGLRDQHMAIAWVKRNIAAFGGDPDNITLFGESAGGASV
SLQTLSPYNKGLIRRAISQSGVALSPWVIQKNPLFWAKKVAEKVGCVPVGDAAARMAQCLKVTDPRALT
LAYKVPLAGLEYPMLHYVGFVFPVIDGDFIPDDPINLYANAADIDYIAGTNNMDGHIFASIDMPAINKG
NKKVTEEDFYKLVSEFTITKGLRGAKTTFDVYTESWAQDPSQENKKKTVVDFETDVLFLVPTEIALA
QHRANAKSAKTYAYLFSHPSRMPVYPKVVWVADHADDIYVFGKPFATPTGYRPQDRTVSKAMIAY
WTNFAKTGDPNMGDSAVPTHWEPTYTTENSGYLEITKKMGSSSMKRSLRTNFLRYWTLTYLALPTV
T

>d1qe3a_ c.69.1.1 (A:) Thermophilic para-nitrobenzyl esterase (PNB esterase) {Bacillus subtilis}

THQIVTTQYGVKGTTENGVHKWKGIPYAKPPVQWRFKAPEPEVWEDVLDATAYGPICPQPSDL
LSLSYTELPRQSEDCLYVNVFAPDTPSQNLPMVWIHGGAFYLGAGSEPLYDGSKLAAQGEVIVVTL
NYRLGPFGLHLSSFDEAYSNDLGLLDQAAALKWVRENISAFGGDPDNVTVFGESAGGMSIAALLA
MPAAKGLFQKAIMESGASRTMTKEQAASTAAFLQVLGINESQLDRLHTVAAEDLLKAADQLRIA
ENIFQLFFQPALDPKTLPEEPEKSIAEGAASGIPLLIGTTRDEGYLFFTPDSVHVSQETLDAALEYLLG
KPLAEKAADLYPRSLESQIHMMTDLLFWRPVAVAYASAQSHYAPVWVWYRFDWHPEKPPYNKAFHAL
ELPFVFGNLDGLERMAKAEITDEVKQLSHTIQSAWITFAKTGNPSTEAVNWPAYHEETRETVILDSE
ITIENDPESEKRQKLF

>d1jkma_ c.69.1.2 (A:) Carboxylesterase {Bacillus subtilis, brefeldin A esterase}

PGRLGDESSGPRTPRFSFAMVEALATFGLDAVAAAAPPVSASDDLPTVLAAVGASHDGFQAVYDSIAL
DLPTDRDDVETSTETILGVDGNEITLHVFRPAGVEGVLPGLVYTHGGGMTILTNDNRVHRRWCTDL
AAAGSVVVMVDFRNAWTAEGHHPFSPGVEDCLA AVLWVDEHRESLGLSGVVVQGESGGGNLAIAT
TLAKRRGRDLAIDGVYASIPYISGGYAWDHERRTELPSLVENDGYFIENGGMALLVRAYDPTGEHA
EDPIAWPYFASEDELRLGPPFVAVNELDPLRDEGIAFARRLARAGVDVAARVNIGLVHGADVIFRH
WLPAALESTVRDVAGFAADRARLR

>d1evqa_ c.69.1.2 (A:) Carboxylesterase {Alicyclobacillus acidocaldarius}

LDPVIQVLDQLNRMPAPDYKHLSAQQFRSQSLFPPVKKEPVAEVREFDMDLPGRTLKVRMYRPE
GVEPPYPALVYYHGGGWVVGDLETHDPVCRVLAKDGRAVVFVSDYRLAPEHKFPAAVEDAYDALQ
WIAERAADFHLDPARIAVGGDSAGGNLAAVTSILAKERGGPALAFQLLIYPSTGYDPAHPPASIEENA
EGYLLTGGMMLWFRDQYLNLEELTHPWFSPVLYPDLGLPPAYIATAQYDPLRDVGLYAEALNKA
GVKVEIENFEDLIHGFAQFYSLSPGATKALVRIA EKLRDALA

>d1jjia_ c.69.1.2 (A:) Carboxylesterase {Archaeon Archaeoglobus fulgidus}

MLDMPIDPVVYQLAEYFDSLKFDQFSSAREYREAINRIYEERNRQLSQHERVERVEDRTIKGRNGD
IRVRVYQKQKPDSPVLVYYHGGGFVICSIESHDALCRRIARLSNSTVVSVDYRLAPEHKFPAAVYDCYDA
TKWVAENAEELRIDPSKIFVGGDSAGGNLAAAVSIMARDSGEDFIKHQILYIPVVNFVAPTPSLLEFG
EGLWILDQKIMSWFSEQYFSREEDKFNPLASVIFADLENLPPALIITA EYDPLRDEGEVFGQMLRRAG

VEASIVRYRGLVHGFINYYPVLKAARDAINQIAALLVFD

>d1jffa_ c.69.1.2 (A:) Feruloyl esterase domain of the cellulosomal xylanase z {Clostridium thermocellum}

SLPTMPPSGYDQVRNGVPRGQVVNISYFSTATNSTRPARVYLPPGYSKDKKYSVLYLLHGIGGSEND
WFEGGGRANVIADNLIAEGKIKPLIIVTPNTNAAGPGIADGYENFTKDLLNSLIPYIESNYSVYTDREH
RAIAGLSMGGGQSFNIGLTNLDKFAYIGPISAAPNTYPNERLFPDGGKAAREKLKLLFIACGTNDSLIG
FGQRVHEYCVANNINHVVYWLIQGGGHDFNVWKPGLWNFLQMADEAGLTRD

>d1gkla_ c.69.1.2 (A:) Feruloyl esterase domain of the cellulosomal xylanase y {Clostridium thermocellum}

SFKYESAVQYRPAPDSYLNPCPQAGRIVKETYTGINGTKSLNVYLPYGYDPNKKYNIFYLMHGGEN
ENTIFSNDVKLQNILDHAIMNGELEPLIVVTPTFNGGNCTAQNFYQEFRQNVIPFVESKYSTYAESTT
PQGIAASRMHRGFGGFAMGGLTTWYVMVNCLDYVAYFMPLSGDYWYGNPQDKANSIAEAINRSG
LSKREYFVFAATGSEDIAYANMNPQIEAMKALPHFDYTSDFSKGNFYFLVAPGATHWWGYVRHYIID
ALPYFFHELEHHHHHH

>d1f0na_ c.69.1.3 (A:) Antigen 85b {Mycobacterium tuberculosis}

SRPGLPVEYLQVPSMGRDIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYYQSGLSI
VMPVGGQSSFYSDWYSPACGKAGCQTYKWETFLTSELQWLSANRAVKPTGSAAGLSMAGSSAMI
LAAYHPQQFIYAGSLSALLDPSQGMGPSLIGLAMGDAGGYKAADMWGPSSDPAWERNDPTQQIPKL
VANNTLWVYCGNGTPNELGGANIPAEFLENFVRSSNLKFQDAYNAAGGHNAVFNFPPNGTHSWE
YWGAQLNAMKGDQLQSSLGAG

>d1dqza_ c.69.1.3 (A:) Antigen 85c {Mycobacterium tuberculosis}

RPGLPVEYLQVPSASMGRDIKVFQGGGPHAVYLLDGLRAQDDYNGWDINTPAFEEYYQSGLSVIM
PVGQSSFYTDWYQPSQSNQNYTYKWETFLTEMPAWLQANKGVSPTGNAAVGLSMSGGSALILA
AYYPQQFPYAASLSGFLNPSESWWPTLIGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLV
ANNTRIWVYCGNGTPSDLGGDNIPAKFLEGLTLRTNQTFRDTYAADGGRNGVFNFPNGTHSWPY
WNEQLVAMKADIQHVLNG

>d1ju3a2 c.69.1.21 (A:5-351) Bacterial cocaine esterase N-terminal domain {Rhodococcus sp. mb1}

NYSVASNVMVPMRDGVRDLAVDLYRPDADGPVPLLVRNPYDKFDVFAWSTQSTNWLEFVRDGYAV
VIQDTRGLFASEGEFVPHVDDEADAEDTLWILEQAWCDGNVGMFGVSYLGVTTQWQAAVSGVGGGL
KAIAPSMASADLYRAPWYGPAGALSVEALLGWSALIGTGLITSRSDARPEDAADFVQLAAILNDVAG
AASVTPLAEQPLLGRIPWVIDQVVDHPDNDESWSISLFERLGGLATPALITAGWYDGFVGESLRT
FVAVKDNADARLVVGPWSHNSLTGRNADRKFIAATYPIQEATTMHKAFFDRHLRGETDALAGVPK
VRLFVMGIDEWRDETDW

>d1qfma2 c.69.1.4 (A:431-710) Prolyl oligopeptidase, C-terminal domain {Pig (Sus scrofa)}

DASDYQTVQIFYPKDGTKIPMFIVHKKGIKLDGSHPAFLYGYGGFNISITPNYSVSRILIFVRHMGVLL
AVANIRGGGEYGETWHKGGILANKQNCDFDQCAAELYKEGYTSPKRLTINGGSSNGLLVATCANQ
RPDLFGCVIAQVGVMDMLKFHKYTIHAWTTDYGCSDSKQHFELIKYSPLHNKLVPEADDIQYPS
MLLLTADHDDRVPVPLHSLKFIATLQYIVGRSRKQNNPLLIHVDTKAGHGAGKPTAKVIEEVSDMFAFI
ARCLNIDWIP

>g1wht.1 c.69.1.5 (A:,B:) Serine carboxypeptidase II {Wheat (Triticum vulgaris)}

GHAADRIARLPQPAVDFDMYSGYITVDEGAGRSLFYLLQEAPEDAQPAPLVLWLNNGGPCSSVAYG
ASEELGAFRVKPRGAGLVLNEYRWKVANVFLDSPAAGVGFSTNTSSDIYTSNGDNRTAHDSYAFLA
KWFERFPHYKYRDFYIAGESYAGHYVPELSQLVHRSKNPVINLKGFMVGNGLIDDYHDYVGTFFFW

WNHGIVSDDTYRRLKEACLHDSFIHSPACDAATDVATAEQGNIDMYSLYTPVCNIXSYDPCTERYST
AYYNNRRDVQMALHANVTGAMNYTWATCSDTINTHWHDAAPRSMPLPIYRELIAAGLRIWVFSGD
TDAVVPLTATRYSIGALGLPTTTTSWYPWYDDQEVGGWSQVYKGLTLVSVRGAGHEVPLHRPRQALVLFQY
FLQGKPMPGQ

>d1cpy_ c.69.1.5 (-) Serine carboxypeptidase II {Baker's yeast (*Saccharomyces cerevisiae*)}
KIKDPKILGIDPNVTQYTGYL DVEDEDKHFFFWTFESRNDPAKDPVILWLN GGP GCSSTGLFFALGP
SSIGPDLKPIGNPYSWNSNATVIFLDQPVNVGFSYSGSSGVSNTVAAGKDVYNFLELFFDQFPEYVNK
GQDFHIAGASYAGHYIPVFASEILSHKDRNFNLTSVLIGNGLTDPLTQYNYEPMACGEGGEP
SVLPSE
ECSAMEDSLERCLGLIESCYDSQSVWSCPATIIYCNAQLAPYQRTGRNVYDIRKDCEGGNLCYPTLQ
DIDDYLNQDYVKEAVGA EVDHYESC NFDINRNFLFAGDWMKPYHTAVTDLLNQDLPILVYAGDKDF
ICNWLGNKAWTDVLPWKYDEEFASQKVRNWTASITDEVAGEVKSYKHFTYLRVFN GGHMVPFDV
PENALSMVNEWIHGGFSL

>d1ac5_ c.69.1.5 (-) Serine carboxypeptidase II {Baker's yeast (*Saccharomyces cerevisiae*),
kex1(delta)p}

LPSSEYKVAYELL PGLSEVPDPSNIPQMHAGHIPLRSEDAEQDSSDLEYFFWKFTNND SNGNVDR
PLIWLNGGP GCSMDGALVESGPF RVNSDGKLYLNEGSWISKGDLLFIDQPTGTGFSVEQNKDEGKI
DKNKFDLEDLVTKHFMDFLENYFKIFPEDLTRKIILSGESYAGQYIPFFANILNHNKFSKIDGTY
DLKALLIGNWIDPNTQSLSYLPFAMEKKLIDESNPNFKHLTNAHENCQNLINSASTDEAAHFSYQE
CENILNLLSYTRESSQGTADCLNMYNFNLKDSYPSGCMNWPKDISFVSKFFSTPGVIDSLHLDSD
KIDHWKECTNSVGTKLSNPISKPSIHLLPGLLESGIEIVLFNGDKDLICNNKGVLDTIDNLKWGGIKGF
SDDAVSFDWIHKSSTDDSEEFSGYVKYDRNLTFVSVYNASHMVPFDKSLVSRGIVDIYSNDVMIIDN
NGKNVMITT

>d1ivya_ c.69.1.5 (A:) Human 'protective protein', HPP {Human (*Homo sapiens*)}

APDQDEIQRLPGLAKQPSFRQYSGYLKSSGSKHLHYWFVESQKDPENSPVVLWLN GGP GCSLDGLL
TEHGPFVLVQPDGVTLEYNPYSWNLIANVLYLESPAGVGFYSDDKFYATNDTEVAQSNFEALQDFFR
LFPEYKNNKFLFTGESYAGIYIPTLAVLVMQDPSMNLQGLAVGNLSSYEQNDNSLVYFAYYHLLGN
RLWSSLQTHCCSQNKCNFYDNKDLECVTNLQEVARIVGNSGLNIYNLYAPCAGGVPSHFRYKEDTVV
VQDLGNIFTRLPLKRMWHQALLRSGDKVRMDPPCTNTTAASTYLNNPYVRKALNIPEQLPQWDM
CNFLVNLQYRRLYRSMNSQYLKLLSSQYQILLYNGDVMACNFMGDEWFVDSL NQKMEVQRRPW
LVKYGDSGEQIAGFVKEFSHIAFLTIKGAGHMVPTDKPLAAFTMFSRFLNKQPY

>d1hlga_ c.69.1.6 (A:) Gastric lipase {Human (*Homo sapiens*)}

SPEVTMNISQMITYWGYPNEEYEVVTE DGYILEVNRIPYGGKNSGNTGQRPVVFLQHGLLASATNWI
SNLPNNSLAFILADAGYDVWLGNSRGNTWARRNLYSPDSVEFWAFSFD EMAKYDLPATIDFIVKK
TGQKQLHYVGHSGQTTIGFIAFSTNP SLAKRIKTFYALAPVATVKYTKSLINKLRFVPQSLFKFIFGDKI
FYPHNFFDQFLATEVCSREMLNLLCSNALFIICGFDSKNFNTRSRLDVYLSHNPAGTSVQNMFWHTQA
VKSGKFQAYDWGSPVQNRMHYDQSQPPYYNVTAMNVPIAVWNGGKDLLADPQDVGLLLPKLPNLI
YHKEIPFYNHLDFIWAMDAPQEYVNDIVSMISEDKK

>d1azwa_ c.69.1.7 (A:) Proline iminopeptidase {*Xanthomonas campestris*, pv. citri}

MRTLYPEITPYQQGSLKVD RHTLYFEQCGNPHGKPVVMLHGGPGGGCNDKMRRFHDPAKYRIVLF
DQRGSGRSTPHADLVDNTTWDLVADIERLRTHLGVDRWQVFGGSWGSTLALAYAQTHPQVTELV
LRGIFLLRRFELEWFYQEGASRLFPDAWEHYLNAIPPERADLMSAFHRRLTS DDEATR LAAAKAW
SVWEGATSFLHVDEDFVTGHEDA HFALAFARIENHYFVNGGFFEVEDQLLRDAHRIADIPGVIVHGR
YDVVCPLQSAWDLHKAWPKAQLQISPASGHS AFEPENVDALVRATDGFA

>d1qtra_ c.69.1.7 (A:) Proline iminopeptidase {*Serratia marcescens*}

LRGLYPPLAAYDSGWLDGTGDGHRIYWELSGNPNGKPAVFIHGGPGGGISPHHRQLFDPERYKVLFLD
QRGCGRSRPHASLDNNTTWHLVADIERLREMAGVEQWLVFGGSWGSTLALAYAQTHPERVSEMVL
RGIFTLRKQRLHWYYQDGASRFFPEKWERVLSILSDDERKDVIAAYRQRLTSADPQVQLEAAKLWSV
WEGETVTLLPSRESASFGEDDFALAFARIENHYFTHLGFLESDDQLLRNVPLIRHIPAVIVHGRYDMA
CQVQNAWDLAKAWPEAELHIVEGAGHSYDEPGILHQLMIATDRFAGK

>d1b6g_ c.69.1.8 (-) Haloalkane dehalogenase {Xanthobacter autotrophicus}

MVNAIRTPDQRFSNLDQYFPSPNYLDDLPGYPGLRAHYLDEGNSDAEDVFLCLHGEP TWSYLYRKM
IPVFAESGARVIAPDFFGFGKSDKPVDEEDYTFEFHRN FLLALIERLDLRNITLVVQDWGGFLGLTLP
MADPSRFKRLIIMNACLMTDPVTQPAFSAFVTQPADGFTAWKYDLVTPSDLRLDQFMKRWAPT LTE
AEASAYAAPFPDTSYQAGVRKFKPMVAQRDQACIDISTE AISFWQNDWNGQTFMAIGMKDKLLGPD
VMYPMKALINGCPEPLEIADAGHFVQEFGEQVAREALKHFAETE

>d1bn7a_ c.69.1.8 (A:) Haloalkane dehalogenase {Rhodococcus sp.}

IGTGFPPDPHYVEVLGERMHYVDVGP RDGTPVFLHGNPTSSYLWRNIIPHVAPSHRCIAPDLIGMG
KSDKPDLDYFFDDHVRYLDAFIEALGLEEVVLIHDWGSALGFHWAKRNPERVKGIACMEFIRPIPT
WDEWPEFARETFQAFRTADVGRELIIDQNAFIEGVL PKCVVRPLTEVEMDHYREPFLKPV DREPLW
RFPNEIPIAGEPANIVALVEAYMNWLHQSPVPKLLFWGT PGVLIPPAEAARLAESLPNCKTVDIGPGL
HYLQEDNPDLIGSEIARWLPGLA

>d1cv2a_ c.69.1.8 (A:) Haloalkane dehalogenase {Sphingomonas paucimobilis, UT26, LinB}

GAKPFGEKKFIEIKGRRMAYIDEGTGDPI LFQHGNTSSYLWRNIMPHCAGLGRLIACDLIGMGDSK
LDPSGPERYAYAEHRDYLDALWEALDLGDRVVLVHDWGSALGFDWARRHRERVQGIAYMEAIAM
PIEWADFPEQDRDLFQAFRSQAGEELVLQDNV FVEQVLPGLILRPLSEAMAAYREPFLAAGEARRP
TLSWPRQIPIAGTPADVVAIARDYAGWLS ESPIPKLFINAEPGALTTGRMRDFCRTWPNQTEITVAGA
HFIQEDSPDEIGAAIAAFVRRLRPA

>d1din_ c.69.1.9 (-) Dienelactone hydrolase {Pseudomonas sp., B13}

MLTEGISIQSYDGHTFGALVGSPAKAPAPVIVIAQEIFGVNAFMRET VSWLVDQGYAAVCPDLYARQAP
GTALDPQDERQREQAYKLWQAFDMEAGVGDLEAAIRYARHQ PYSNGKVGLVGYALGGALAF LVAAK
GYVDRAVGYYGVGLEKQLNKVPEVKHPALFHMGGQDHFVPAPSRQLITEGFGANPLLQVHWYEEAG
HSFARTSSSGYVASAAALANERTLDFLAPLQS

>d1c4xa_ c.69.1.10 (A:) 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase (BPHD)
{Rhodococcus sp., strain rha1}

TVEIIEKRFPSGTLASHALVAGDPQSPAVVLLHGAGPGAHAASNWRPIIPDLAENFFV VAPDLIGFGQS
EYPETYPGHIMSWVGMRVEQILGLMNHFGIEKSHIVGNSMGGAVTLQLVVEAPERFDKVALMG SVG
APMNARPELARLLAFYADPRLTPYRELIHSFYD PENFPGMEEIVKSRFEVANDPEVRRIQEVMFE
SMKAGMESLVIPPATLGRLP HDVLFHGRQDRIVPLDTSLYLTKHLKHAELVVLDRCGHWAQLERW
DAMGPMLMEHFRA

>d1ek1a2 c.69.1.11 (A:226-544) Mammalian epoxide hydrolase, C-terminal domain {Mouse
{Mus musculus}}

LPVPCNPNDVSHGYVTVKPGIRLHFVEMGSGPALCLCHGFPESWFSWRYQIPALAQAGFRVLAIDMK
GYGDSSSPPEIEEYAMELLCKEMVTFDLKLGIPQAVFIGHDWAGVMVWNMALFYPERVRAVASLNT
PFMPPDPDVSPMKVIRSIPVFNYQLYFQEPGVAEAELEKNMSRTFKSFFRASDETGFIAVHKATEIGGI
LVNTPEDPNLSKITTEEEIEFYIQF KKTGFRGPLNWYRNTERNWKWSCGLGRKILVPALMVTAE
KDIVLRPEMSKNMEKWIPFLKRGHIEDCGHWTQIEKPTEVNQILIKWLQTE

>d1ehya_ c.69.1.11 (A:) Bacterial epoxide hydrolase {Agrobacterium radiobacter}

AIRRPEDFKHYEVQLPDVKIHYVREGAGPTLLLLHGWPGFWWEW SKVIGPLAEHYDVIVPDLRGFG

DSEKPDNLNLSKYSYLDKAADDQAALLDALGIEKAYVVGHDFAAIVLHKFIRKYSRVIKAAIFDPIQP
DFGPVYFGLGHVHESWYSQFHQLDMAVEVVGSSREVCKKYFKHFFDHWSYRDELLTEEELEVHVD
NCMKPDNIHGGFNYYRANIRPDAALWTDLDHTMSDLPVTMIWGLGDTCPYAPLIEFVPKYYSNY
TMETIEDCGHFLMVEKPEIAIDRIKTAFR

>d1qo7a_ c.69.1.11 (A:) Bacterial epoxide hydrolase {*Aspergillus niger*}

KAKAFKFPSSASISPNPFTVSIPDEQLDDLKTLVRLSKIAPPTYESLQADGRFGITSEWLTTMREKWLS
EFDWRPFPEARLNSFPQFTTEIEGLTIHFAALFSEREDAVPIALLHGWPGSFVEFYPIQLFREEYTPET
LPFHLLVPSPLPGYTFSSGPPLDKDFGLMDNARVVDQLMKDLGFGSGYIIQGGDIGSFVGRLLGVGFDA
CKAVHLNLCAMRAPPEGPSIESLSAAEKEGIARMEKFM TDGLAYAMEHSTRPSTIGHVLSSSPIALLA
WIGEKYLQWVDKPLPSETILEMVSPLYWLTFSPRAIHTYRETTPTASAPNGATMLQKELYIHKPFGF
SFFPKDLCPVPRSWIATTGNLVFFRDHAEGGHFAALERPRELKTDLTAFVEQVW

>d1brt_ c.69.1.12 (-) Bromoperoxidase A2 {*Streptomyces aureofaciens*}

PFITVQGQENSTSIDLYYEDHGTGQPVVLIHGFP LSGHSWERQSAALLDAGYRVITYDRRGFGQSSQPT
TGYDYDTFAADLNTVLETLDLQDAVLVGFSTGTGEVARYVSSYGTARIAKVAFLASLEPFLKTD DNP
DGAAPQEFDGIVA AVKADRYAFYTGFFNDFYNLDENLGTRISEEAVRNSWNTAASGGFFAAAAAPT
TWYTD FRADIPRIDVPALILHGTGDRTLPIENTARVFHKALPSAEYVEVEGAPHGLLWTHAEVNTA
LLAFLAK

>d1a8q_ c.69.1.12 (-) Bromoperoxidase A1 {*Streptomyces aureofaciens*}

PICTTRDGVEIFYKDWGQGRPVVFIHGWPLNGDAWQDQLKAVVDAGYRGIAHRRRGHGHSTPVW
DGYDFDTFADDLNDLLTDLDRDVTLVAHSMGGGELARYVGRHGTGRLRSVLLSAIPPVMIKSDKN
PDGVPDEVFDALKNGLTERSQFWKDTAEGFFSANRPGNKVTQGNKDAFWYMAMAQTIEGGVRC
VDAFGYDTFTEDLKKFDIPTLVVHGDDDQVVPIDATGRKSAQIIPNAELKVYEGSSHG IAMVPGDKE
KFNRLLEFLNK

>d1a88a_ c.69.1.12 (A:) Chloroperoxidase L {*Streptomyces lividans*}

GTVTTSDGTNIFYKDWGPRDGLPVVFFHGWPLSADDWDNQMLFFLSHG YRVIAHRRRGHGRSDQ
PSTGHDMDTYAADVAALTEALDLRGAVHIGHSTGGGEVARYVARAEPGRVAKAVLVS AVPPVMVKSD
TNPDGLPLEVFDEFRAALANRAQFYIDVPSGPFYGFNREGATVSQGLIDHWWLQGMMAANAHY
ECIAAFSETDFTDDLKRIDVPVLVAHGTD DQVVPYADAAPKSAELLANATLKS YEGLPHGMLSTHPE
VLNPDLLAFVKS

>d1a8s_ c.69.1.12 (-) Chloroperoxidase F {*Pseudomonas fluorescens*}

TTFTTRDGTQIYYKDWGSGQP VIFSHGWPLNADSWESQMIFLAAQGYRVIAHRRRGHGRSSQPWS
GNDMDTYADDLAQLIEHLDLRDAVLFGFSTGGGEVARYIGRHGTARVAKAGLISAVPPLMLKTEANP
GGLPMEVFDGIRQASLADRSQLYKDLASGPF GFNQP GAKSSAGMVDWFWLQGMAAGHKNA YDCI
KAFSETDFTEDLKKIDVPTLVVHG DADQVVP IASG IASAALVKGSTLKIYSGAPHGLTDTHK DQLNA
DLLAFIKG

>d1thta_ c.69.1.13 (A:) Myristoyl-ACP-specific thioesterase {*Vibrio harveyi*}

QCKTIAHVLRVNNQELHVWETPPKENVPFKNNTILIASGFARRMDHFAGLAEYLSTNGFHVFRYD
SLHHVGLSSGSIDEFTMTTGKNSLCTVYHWLQTKGTQNI GLIAASLSARVAYEVISDLELSFLITAVGV
VNLRTLEKALGFDYLSLPIDELPNDLDFEGHKL GSEVFVRDCFEHHWDTLDSTLDKVANTS VPLIA
FTANNDWVKQEEVYDMLAHIRTGHCKLYSLGSS HDLGENLVLRNFYQSVTKAAIAMD GGSLEI
DVFIEPDEFELTIATVNERRLKAEIENRTPEMA

>d1ei9a_ c.69.1.13 (A:) Palmitoyl protein thioesterase 1 {Cow (*Bos taurus*)}

DPPAPLPLVIWHGMGDSCCNPLSMGAIKKMVEKKIPGIHVLSLEIGKTLREDVENSFFLVNSQVTT
VCQILAKDPKLQQGYNAMGFSQGGQFLRAVAQRCPSPPMVN LISVGGQH QGVFGLPRCPGESSHICD

FIRKTLNAGAYNKAIQERLVQAEYWHDPREDIYRNHSIFLADINQERGVNESYKKNLMALKKFVMV
KFLNDTIVDPVDSEWFGFYRSGQAKETIPLQESTLYTQDRLGLKAMDKAGQLVFLALEGDHLQLSEE
WFYAHIIIPFLE

>d1auoa_ c.69.1.14 (A:) Carboxylesterase {*Pseudomonas fluorescens*}

MTEPLILQPAKPADACVIWLHGLGADRYDFMPVAEALQESLLTTRFVLPQAPTRPVTINGGYEMPS
WYDIKAMSPARSISLEELEVSAKMVTDLIEAQKRTGIDASRIFLAGFSQGGAVVFHTAFINWQGPLGG
VIALSTYAPTFGDELELSASQQRIPALCLHGQYDDVVQNAMGRSAFEHLKSRGVTVTWQEYPMGHE
VLPQEIHDI GAWLAARLG

>d1fj2a_ c.69.1.14 (A:) Acyl protein thioesterase 1 {Human (*Homo sapiens*)}

MDPEFMSTPLPAIVPAARKATAAVIFLHGLDGTGHGWAEAFAGIRSSHIIKYPHAPVRPVTLNMNV
AMPSWFDIIGLSPDSQEDESIGKQAAENIKALIDQEVKNGIPSNRIILGGFSQGGALSLYTALTQQKL
AGVTALSCWLPLRASFPQGPPIGGANRDISILQCHGDCDPLVPLMFGSLTVEKLTNLNPNANVTFKTYE
GMMHSSCQEMMDVKQFIDKLLPPI

>d1qlwa_ c.69.1.15 (A:) A novel bacterial esterase {*Alcaligenes* sp.}

VPKTPAGPLTSLGQGSFFVGGRDVTSETLSLSPKYDAHGTVTVDQMYVRYQIPQRAKRYPITLIHGCC
LTGMTWETTPDGRMGWDEYFLRKGYSTYVIDQSGRGRSATDISAINAVKLGKAPASSLPDLFAAGHE
AAWAIFRFGPRYPDAFKDTQFPVQAQAEWQQMVPDWLGSMPNPTVANLSKLAIKLDGTVLLS
HSQSGIYPFQTAAMNPKGITAIUSVEPGCEPKPEDVKPLTSIPVLVFGDHIEEFPRWAPRLKACHAFI
DALNAAGGKQLMSLPALGVHGNHMMMQDRNNLQVADLILDWIGRNTA

>d1jfra_ c.69.1.16 (A:) Lipase {*Streptomyces exfoliatus*}

NPYERGPAPTNASIEASRGPYATSQTSVSSLVASGFGGGTIYYPTSTADGTFGAVVISPGFTAYQSSIAW
LGPRLASQGFVVFTIDTNTTLDQPDSRGRQLLSALDYLTQRSSVRTRVDATRLGVMGHSMGGGSLE
AAKSRISLKAAPLGTWNTDKTWPPELRTPTLVVGADGDTVAPVATHSKPFYESLPGSLDKAYLELRG
ASHFTPNTSDTTIAKYSISWLKRFIDSDTRYEQFLCPIPRPSLTIAEYRGTCPHTS

>d1tca_ c.69.1.17 (-) Triacylglycerol lipase {Yeast (*Candida antarctica*), form b}

LPSGSDPAFSQPKSVLDAGLTCQGASPSVSKPILLVPGTGTGPQSFDSNWIPSTQLGYTPCWISPP
PFMLNDTQVNTEYMVNAITALYAGSGNNKLPVLTWSQGGLVAQWGLTFFPSIRSKVDRLMAFAPDY
KGTVLGAPLDALAVSAPSVWQQTTGSALTTALRNAGGLTQIVPTTNLYSATDEIVQPQVNSPLDSSY
LFNGKNVQAQAVCGPLFVIDHAGSLTSQFSYVVGSRALRSTTGQARSADYGITDCNPLPANDLTPEQK
VAAAALLAPAAAIVAGPKQNCPELMPYARPFVAVGKRTCSGIVTP

>d3tgl_ c.69.1.17 (-) Triacylglycerol lipase {*Rhizomucor miehei*}

GIRAATSQEINELTYTTLANSYCRVTPGATWDCIHCDATEDLKIIKTWSTLIYDTNAMVARGDSE
KTIYIVFRGSSSIRNWIADLTFVPVSYPVSGTKVHKGLDSYGEVQNELVATVLDQFKQYPSYKVAVT
GHSLGGATVLLCALDLYQREEGLSSSNLFLYTQGPVGDPAFANYVVSTGIPYRRTVNERDIVPHLPP
AAFGLFHAGEEYWITDNSPETVQVCTSDLETSDCSNSIVPFTSVLDHLSYFGINTGLCT

>d1tia_ c.69.1.17 (-) Triacylglycerol lipase {*Penicillium camembertii*}

DVSTSELQDFEFWVQYAAASYEADYTAQVGDKLSCKGNCPEVEATGATVSYDFSDSTITDTAGYIA
VDHTNSAVVLAFRGYSVRNWWADATFVHTNPLGCDGCLAELGFWSSWKLVRDDIIKELKEVVAQN
PNYELVVVGHSLGAAVATLAATDLRGKGYPSAKLYAYASPRVGNAAALAKYITAQGNFRFTHTNDPVP
KLPLLSMGYVHVSPEYWITSPNNATVSTSDIKVIDGDVSFDGNTGTGLPLLTDFEHIWYFVQVDAG
KG

>d1tib_ c.69.1.17 (-) Triacylglycerol lipase {*Thermomyces (Humicola) lanuginosa*}

EVSQDLFNQFNLFQYSAAYCGKNNAPAGTNTCTGNACPEVEKADATFLYSFEDSGVGDVTGFL
ALDNTNKLIVLSFRGSRSIENWIGNLNFIDLKEINDICSGCRGHGFTSSWRSVADTLRQKVEDAVRE

HPDYRVVFTGHSLGGALATVAGADLRNGYDIDVFSYGAPRVGNRAFAEFLTVQTTGGLYRITHHTNDI
VPRLPPREFGYSHSSPEYWIKSGTLVPTVRNDIVKIEGIDATGGNNQPNIPDIPAHLLWYFGLIGTCL
>d1lgya_ c.69.1.17 (A:) Triacylglycerol lipase {Rhizopus niveus}
KVVAATTAQIQEFTKYAGIAATAYCRSVVPGNKWDCVQCQKWVDPGKIITFTSLLSDTNGYVLRSD
KQKTIYLVFRGTNSFRSAITDIVFNFSYKPVKGAHVHAGFLSSYEQVVNDYFPVVQEQLTAHPTYKVI
VTGHSLGGAQALLAGMDLYQREPRLSPKNLSIFTVGGPRVGNPTFAYYVESTGIPFQRTVHKRDIVPH
VPPQSFGLHPGVESWIKSGTSNVQICTSEIETKDCSNSIVPFTSILDHLSYFDINEGSCS
>d1thg_ c.69.1.17 (-) Type-B carboxylesterase/lipase {Fungus (Geotrichum candidum),
ATCC 34614}
EAPTAVLNGNEVISGVLEGKVDTFKGIPIFADPPLNDRFKHPQPFTGSYQGLKANDFSPACMQLDPG
NSLTLDDKALGLAKVIPEEFRGLYDMAKGTVMNEDCLYLNVFRPAGTKPDAKLPMVMWYGGAF
VYGSSAAYPGNSYVKESINMGQPVVVFSINYRTGPFGLGGDAITAEGNTNAGLHDQRKGLEWVSDN
IANFGGDPDKVMIFGESAGAMSVAHQLIAYGGDNTYNGKKLFHSAILQSGGPLYHDSVSGPDISYN
RFAQYAGCDTSASANDTLECLRSKSSSVLHDAQNSYDLKDLFGLLPQFLGFGPRPDGNIIPDAAYELF
RSGRYAKVPYISGNQEDEGTAFAPVALNATTPHVKKWLQYIFYDASEASIDRVLSLYPQTLVSGSPFR
TGILNALTPQFKRVAAILSDMLFQSPRRVMLSATKDVNRWTYLSTHLHNLVFPGLTFHGNELIFQFN
VNIGPANSYLRYFISFANHDPNVGTNLLQWDQYTDGKEMLEIHMTDNVMRTDDYRIEGISNFET
DVNLYG
>d1lpp_ c.69.1.17 (-) Type-B carboxylesterase/lipase {Fungus (Candida rugosa), formerly
Cylindracea}
APTATLANGDTITGLNAIINEAFLGIPFAEPPVGNLRFKDPVPYSGSLDGQKFTSYGPSCMQQNPEGT
YEENLPKAALDLMQSKVFEAVSPSEDCLTINVVRPPGKAGANLPVMLWIFGGGFVGGTSTFPP
AQMITKSIAMGKPIIHVSVNYRVSSWGFLAGDEIKAEGSANAGLKDQRLGMQWVADNIAAFGGDPT
KVTIFGESAGSMSVMCHILWNDGDNTYKPKPLFRAGIMQSGAMVPSDAVDGIYNEIFDLLASNAGC
GSASDKLA CLRGVSSDTLEDATNNTPGFLAYSSLRLSYLPRPDGVNITDDMYALVREGKYANIPVIIGD
QNDEGTFFGTSSLNVTTDAQAREYFKQSFVHASDAEIDTLMTAYPGDITQGSFPDGTGILNALTPQFKR
ISAVLGDGLFTLARRYFLNHYTGGTKYSFLSKQLSGLPVLGTFHSNDIVFQDYLLGSGSLIYNNAFIAFA
TDLDPNTAGLLVKWPEYTSSSQSGNNLMMINALGLYTGKDNFRTAGYDALFSNPPSFFV
>d1clea_ c.69.1.17 (A:) Type-B carboxylesterase/lipase {Candida cylindracea, cholesterol
esterase}
APTAKLANGDTITGLNAIINEAFLGIPFAEPPVGNLRFKDPVPYSGSLNGQKFTSYGPSCMQQNPEGT
FEENLGKTALDLMQSKVFQAVLPQSEDCLTINVVRPPGKAGANLPVMLWIFGGGFVGGTSTFPPA
QMVTKSVLMGKPIIHVAVNYRVASWGFLAGDDIKAEGSGNAGLKDQRLGMQWVADNIAFGGDP
KVTIFGESAGSMSVLCHLIWNDGDNTYKPKPLFRAGIMQSGAMVPSDPVDGTYGNEIYDLFVSSAGC
GSASDKLA CLRSSDSTLLDATNNTPGFLAYSSLRLSYLPRPDGKNITDDMYKLVRDYGKYASVPVIIG
DQNDEGTVFLGSSLNVTTNAQARAYFKQSFHASDAEIDTLMAAYPDITQGSFPDGTGIFNAITPQFK
RISAVLGDALFIHARRYFLNHFQGGTKYSFLSKQLSGLPIMGTFHANDIVWQDYLLGSGSVIYNNAFI
AFATDLPNTAGLLVNWPKYTSSSQSGNNLMMINALGLYTGKDNFRTAGYDALMTNPPSFFV
>d1i6wa_ c.69.1.18 (A:) Lipase A {Bacillus subtilis}
HNPVVMVHIGGASFNFAIKSYLVSQGWSRDKLYAVDFWDKTGTNYNNGPVLRSRVQKVLDETGA
KKVDIVAHSMGGANTLYYIKNLDGGNKVANVVTLGGANRLTTGKALPGTDPNQKILYTSIYSSADMI
VMNYLSRLDGARNVQIHGVGHIGLLYSSQVNSLIKEGLNGGGQNTN
>d4lipd_ c.69.1.18 (D:) Lipase {Burkholderia cepacia (formerly Pseudomonas cepacia)}
DNYAATRYPIILVHGLTGTDKYAGVLEYWYGIQEDLQQRGATVYVANLSGFQSDDGPNGRGEQLLAY

VKTVLAATGATKVNLVGHSQGGLTSRYVAAVAPDLVASVTTIGTPHRGSEFADFVQGVLAYDPTGLSS
TVIAAFVNVFGILTSSSNNTNQDALAALKTLTTAQAATYNQNYPSAGLGAPGSCQTGAPTETVGGNT
HLLYSWAGTAIQPTISVFGVTGATDTSTIPLVDPANALDPSTLALFGTGTVMVNRGSGQNDGVVSKCS
ALYQVLTSTSYKWNHLDEINQLLGVRGANAEDPVAVIRTHANRLKLAGV

>d1ex9a_ c.69.1.18 (A:) Lipase {Pseudomonas aeruginosa}

STYTQTKYPIVLAHGMLGFDNIGVDYWFGIPALRRDGAQVYVTEVSQLDTSEVRGEQLLQVVEEI
VALSGQPKVNLIGHSHGGPTIRYVAAVRPDLIASATSVGAPHKGSDTADFLRQIPPGSAGEAVLSGLVN
SLGALISFLSSGSTGTQNSLGSLESLNSEGAARFNAKYPQGIPTSACGEGAYKVNQVSYSSWSGSSPLT
NFLDPSDAFLGASSLTFKNGTANDGLVGTCSHLMVIRDNYRMNHLDEVNQVFGLTSLFETSPVSV
YRQHANRLKNASL

>d1cvl_ c.69.1.18 (-) Lipase {Chromobacterium viscosum}

ADTYAATRYPVILVHGLAGTDKFANVVDYWYGIQSDLQSHGAKVYVANLSGFQSDDGPNRGEQLLA
YVKQVLAATGATKVNLIHSGQGGLTSRYVAAVAPQLVASVTTIGTPHRGSEFADFVQDVLKTDPTGLS
STVIAAFVNVFGTLVSSSHNTDQDALAALRLTTAQTATYNRNFPSAGLGAPGSCQTGAATETVGGSQ
HLLYSWGGTAIQPTSTVLGVTGATDTSTGTLVDVANVTDPSLALLATGAVMINRASGQNDGLVSRCS
LFGQVISTSYHWNHLDEINQLLGVRGANAEDPVAVIRTHVNRRLKQGV

>d1hpla2 c.69.1.19 (A:1-336) Pancreatic lipase, N-terminal domain {Horse (Equus caballus)}

NEVCYERLGCFSDDSPWAGIVERPLKILPWSPEKVNTRFLLYTNENPDNFQEIVADPSTIQSSNFNTG
RKTRFIIHGFIDKGEESWLSTMCQNMFKVESVNCICVDWKSGSRTAYSQASQNVIRIVGAEVAYLVGVL
QSSFDYSPSNVHIHSHLGSAAAGEAGRRTNGAVGRITGLDPAEPCFQGTPELVRLDPSDAQFVDVIH
TDIAPFIPNLGFGMSQTAGHLDFFPNGGKEMPGCQKNVLSQIVDIDGIWQGTTRDFAACNHLRSYKYY
TDSILNPDGFAGFSCASYSDFANKCFPCSSEGCPQMGHYADRFPGRTKGVGQLFYLNLTGDASNFA

>d1etha2 c.69.1.19 (A:1-336) Pancreatic lipase, N-terminal domain {Pig (Sus scrofa)}

SEVCFPRLGCFSDDAPWAGIVQRPLKILPWSPKDVTDFLLYTNQNNYQELVADPSTITNSNFRM
DRKTRFIIHGFIDKGEEDWLSNICKNLFKVESVNCICVDWKGGRTGYTQASQNIRIVGAEVAYFVEV
LKSSLGYSPSNVHVIGHSLGSHAAGEAGRRTNGTIERITGLDPAEPCFQGTPELVRLDPSDAKFVDVIH
TDAAPIPNLGFMSQTVGHLDFFPNGGKQMPGCQKNILSQIVDIDGIWEGTRDFVACNHLRSYKYY
ADSILNPDGFAGFPCASYNVFTANKCFPCPSEGCPQMGHYADRFPGKTNGVSQVFLNTGDASNFA

>d1lppb2 c.69.1.19 (B:1-336) Pancreatic lipase, N-terminal domain {Human (Homo sapiens)}

KEVCYERLGCFSDDSPWSGITERPLHILPWSPKDVNTRFLLYTNENPNNFQEVAADSSSISGSNFKT
NRKTRFIIHGFIDKGEENWLANVCKNLFKVESVNCICVDWKGGRTGYTQASQNIRIVGAEVAYFVEF
LQSAFGYSPSNVHVIGHSLGAHAAGEAGRRTNGTIGRITGLDPAEPCFQGTPELVRLDPSDAKFVDVI
HTDGAPIVNLGFGMSQVVGHLDFFPNGGVEMPGCKKNILSQIVDIDGIWEGTRDFAACNHLRSYKY
YTDSIVNPDGFAGFPCASYNVFTANKCFPCPSGGCPQMGHYADRYPGKTNDVVGQKFYLDTGASNF

>d1gpl_2 c.69.1.19 (1-336) Pancreatic lipase, N-terminal domain {Guinea pig (Cavia porcellus)}

AEVCYSHLGCFSDEKPWAGTSQRPIKSLPSDPKINTRFLLYTNENQNSYQLITATDIATIKASNFNLN
RKTRFIIHGFDTSGENSWLSDMCKNMFQVEKVNICVDWKGGSKAQYSQASQNIRVVGAEVAYLVQ
VLSTSLNYAPENVHIHSHLGAHTAGEAGKRLNGLVGRITGLDPAEYPFQDTPEEVRLDPSDAKFVDV
IHTDISPILPSLGFMSQKVGHMDFFPNGGKDMPGCKTGISCNHHRSIEYYHSSILNPEGFLGYPCAS
YDEFQESGCFPCPAKGCPCMGHFADQYPGKTNAVEQTFLLNTGASDNFT

>d1rp1_2 c.69.1.19 (1-336) Pancreatic lipase, N-terminal domain {Dog (Canis familiaris)}

KEVCYEQIGCFSDAEPWAGTAIRPLKVLPWSPERIGTRFLLYTNKNPNNFQTLPSDPSTIGASNFQT

DKKTRFIIHGFIDKGEENWLLDMCKNMFKVVEVNCICVDWKKGSQTSYTAANNVVRVGAQVAQM
LSMLSANYSYSPSQVQLIGHSLGAHVAGEAGSRTPGLGRITGLDPVEASFQGTPEEVRDPTDADFVD
VIHTDAAPLIPFLGFGTSQQMGHLDFPNGGEEMPGCKKNALSQIVDLDDGIWEGTRDFVACNHLRSY
KYYESILNPDGFASYPCASYRAFESNKCFCPDQGPCQMGHYADKFAQKYFLNTGDSSNFA

>d1bu8a2_c.69.1.19 (A:1-336) Pancreatic lipase, N-terminal domain {Rat (Rattus norvegicus)}

KEVCYGHLCFSNDKPWAGMLQRPLKIFPWSPEIDTRFLLYTNENPNNYQKISATEPDTIKFSNFQ
LDRKTRFIVHGFIDKGEDGWLLDMCKKMFQVEKVNICVDWRRGSRTEYTQASYNTRVVGAEIAFL
VQVLSTEMGYSPENVHLIGHSLGAHVGEAGRRELEGHVGRITGLDPAEPCFQGLPEEVRDPSDAMF
VDVIHTDSAPIPYLGFQMSQKVGHLDFPNGGKEMPGCQKNILSTIVDINGIWEGTQNFVACNHLRS
YKYASSILNPDGFLGYPCSSYEKQNDCFPCPEEGCPKMGHYADQFEGKTATVEQTVYLNTGDSDG
NFT

>d1qj4a_c.69.1.20 (A:) Hydroxynitrile lyase {Rubber tree (Hevea brasiliensis)}

AFAHFVLIHTICHGAWIWHKLKPLLEALGHKVTALDLAASGVDPRQIEEIGSFDEYSEPLLTFLALP
PGEKVLVGESECGGLNIAIAADKYCEKIAAAVFHNSVLPDTEHCPSYVVDKLMVFPDWKDTTYFTY
TKDGKEITGLKLGFTLLRENLYTLCGPEEYELAKMLTRKGSFLQNILAKRPFFTKEGYGSIKIYVWT
DQDEIFLPEFQLWQIENYKPKDKVYKVEGGDHKLQLTKTKEIAEILQEVAADTYN

>d1e89a_c.69.1.20 (A:) Hydroxynitrile lyase {Cassava (Manihot esculenta)}

PISKMVTAFVLIHTICHGAWIWHKLKPALERAGHKVTALDMAASGIDPRQIEQINSFDEYSEPLLT
LEKLPQGEKVIIVGEACAGLNIAIAADRYVDKIAAGVFHNSLLPDTVHSPSYTVEKLESFPDWRDTE
YFTFTNITGETITMMLKLGVLLENLFTKCTDGEYELAKMVMRKGSFLQNVLAQRPKFTEKGYGSIK
KVYIWTQDKIFLPDFQRWQIANYPDKVYVQVGGDHKLQLTKTEEVAHILQEVADAYA

>d1keza_c.69.1.22 (A:) Erythromycin polyketide synthase {Saccharopolyspora erythraea}

SSALRDGYRQAGVSGRVSYLDLLAGLSDFREHFDDGSDGFSLDLVDMAADGPGVTVICAGTAAISGP
HEFTRLGALRGIAPVRAVPQGYEEGEPLSSMAAAVAQADAVIRTQGDKPFVAVGHSAGALMAY
ALATELLDRGHPPRGVVLIDVYPPGHQDAMNAWLEELTATLFDRETVMDDTRLTALGAYDRLTGQ
WRPRETGLPTLLVSAGEPMGPWPDDSWKPTWPFHDTVAVPGDHFTMVQEHADAIARHIDAWLG
GG

>d2masa_c.70.1.1 (A:) Inosine-uridine nucleoside N-ribohydrolase, IU-NH {Crithidia fasciculata}

AKKIILDCDPLDDAVAILLAHGNPEIELLAITTVVGNQTLAKVTRNAQLVADIAGITGVPIAAGCDKP
LVRKIMTAGHIHGESGMGTVAYPEAFKKNKVDERRHAVNLIIDLVMSEPKTITLVPTGGLTNIAMAARL
EPRIVDRVKEVVLMMGGYHEGNATSVAEFNIIIDPEAAHIVFNESWQVTMVGLDLTHQALATPPILQR
VKEVDTNPARFMLEIMDYTKIYQSNRYMAAAVHDPKAVAYVIDPSVMTTERVPVDIELTGKLTG
MTVADFRNPRPEHCHTQVAVKLDKFEKFWGLVLDALERIGDP

>d1ezra_c.70.1.1 (A:) Nucleoside hydrolase {Leishmania major}

PRKIILDCDPIDDAVAIFLAHGNPEIELLAITTVVGNQSLEKVTQARLVADVAGIVGVPVAAGCTKP
LVRGVRNASHIHGETGMGNVSYPPEFKTKLDRHAVQLIIDLIMSHEPKTITLVPTGGLTNIAMAVRL
EPRIVDRVKEVVLMMGGYHTGNASPVAEFNVFIDPEAAHIVFNESWNVMTMVGLDLTHLALATPAVQ
KRVREVGTKPAAFMLQILDYTKVYEKEHDTYGVKVDPCAVAYVIDPTVMTTERVPVDIELNGALTT
GMTVADFRYPRPKNCRTQVAVKLDKFDKFWCLVIDALERIGDP

>d1hoza_c.70.1.1 (A:) Inosine-adenosine-guanosine preferring nucleoside hydrolase {Trypanosoma vivax}

GSAKNVVLDHGDGNLDDFVAMVLLASNTEKVRILIGALCTDADCFVENGFNVTGKIMCLMHNHNNMLP

LFPIGKSAATAVNPFPKEWRCLAKNMDDMPILNIPENVELWDKIKAEENEKYEGQQLLADLVMNSEE
KVTICVTGPLSNVAWCIDKYGEKFTSKVEECVIMGGAVDVRGNVFLPSTDGTAEWNIYWDPASAKT
VFGCPGLRRIMFSLDSTNTVPVRSYVQRFGEQTNFLLSILVGTMWAMCTHCELLRDGDGYAWDA
LTAAYVVDQKVANVDPVPIDVVVDKQPNEGATVRTDAENYPLTFVARNPEAEFFLDMLLSARAC
>d1ra9_ c.71.1.1 (-) Dihydrofolate reductase, prokaryotic type {Escherichia coli}
MISLIAALAVDRVIGMENAMPWNLPADLAWFKRNTLDKPVIMGRHTWESIGRPLPGRKNILSSQP
GTDDRVTWVKSVDIAIACGDVPEIMVIGGGRVYEQLPKAQKLYLTHIDAEVEGDTHFPDYEPDD
WESVFSEFHDADAQNSHSHSYCFEILERR
>d3dfr_ c.71.1.1 (-) Dihydrofolate reductase, prokaryotic type {Lactobacillus casei}
TAFLWAQNRNGLIGKDGHLPPDDLHYFRAQTVGKIMVVGRRTYESFPKRPLPERTNVVLTHQ
EDYQAQGAVVVHDVAAVFAYAKQHLDQELVIAGGAQIFTAFKDDVDTLVTRLAGSFEGDTKMIPLN
WDDFTKVSSRTVEDTNPALHTHTYEVWQKKA
>d1df7a_ c.71.1.1 (A:) Dihydrofolate reductase, prokaryotic type {Mycobacterium
tuberculosis}
MVGLIWAQATSGVIGRGGDIPWRLPEDQAHFREITMGHTIVMGRRTWDSLPAKVRPLPGRNNVLS
RQADFMASGAEVVGSLEEALTSPEWVWVIGGGQVYALALPYATRCEVTEVDIGLPREAGDALAPVLDE
TWRGETGEWRFSRSLRRLYRHSYHRS
>d1d1ga_ c.71.1.1 (A:) Dihydrofolate reductase, prokaryotic type {Thermotoga maritima}
AKVIFVLAMDVSGKIASVESWSSFEDRKNFRKITTEIGNVVMGRITFEEIGRPLPERLNVVLTTRPK
TSNNPSLVFFNGSPADVVKFLEGKGYERVAVIGGKTVFTEFLREKLVDELFTVEPYVFGKIPFFDEF
EGYFPLKLEMRRLNERGTLFLKYSVE
>d1vdra_ c.71.1.1 (A:) Dihydrofolate reductase, prokaryotic type {Haloferax volcanii}
ELVSVAALAENRVIGRDGELPWPSIPADKKQYRSRIADDPVVLGRTTFESMRDDLPGSAQIVMSRSER
SFSVDTAHRASVEEAVIDAASLDAETAYVIGGAAIYALFQPHLDRMVLSRVPGEYEGDTYYPEWDA
AEWELDAETDHEGFTLQEWVRS
>d8dfr_ c.71.1.1 (-) Dihydrofolate reductases, eukaryotic type {Chicken (Gallus gallus)}
VRSLNSIVAVCQNMIGKDGKGNLPPPLRNEYKYFQRMTSTSHVEGKQNAVIMGKKTWFSIPEKNRP
LKDRINIVLSRELKEAPKGAHYLSKSLDDALALLDSPELKSKVDMVWVWVGGTAVYKAAMEKPINHRL
FVTRILHEFESDTFFPEIDYKDFKLLTEYGPVADIQEEDGIQYKFEVYQKSV
>d1hfq_ c.71.1.1 (-) Dihydrofolate reductases, eukaryotic type {Human (Homo sapiens)}
VGSLNCIVAVSQNMIGKNGDLPWPLRNLNESRYFQRMTTSSVEGKQNLVIMGKKTWFSIPEKNRP
LKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTEQPELANKVDMVWVWVGGSSVYKEAMNHPGHLK
LFVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSDVQEEKGIKYKFEVYEKND
>d1dyr_ c.71.1.1 (-) Dihydrofolate reductases, eukaryotic type {Fungus (Pneumocystis
carinii)}
NQKSLTLIVALTTSYGIGRSNSLPWKLKKEISYFKRVTSFVPTFDSFESMNVMGRKTWESIPLQF
RPLKGRINVVITRNESLDLNGIHSKSLDHALELLYRTYGSESSVQINRIFVIGGAQLYKAAMDHPKL
DRIMATIIYKDIHCDVFFPLKFRDKWSSVWKKEKHSDESWSVGTKVPHGKINEDGFDYEFEMWT
RDL
>d1aoea_ c.71.1.1 (A:) Dihydrofolate reductases, eukaryotic type {Yeast (Candida albicans)}
MLKPNVAIIAALKPALGIGYKGMPPWRLRKEIRYFKDVTTRTTKPNTRNAVIMGRKTWESIPQKFR
PLPDRLNILSRSYENEIIDDNIHASSIESSLNLVSDVERVFIIGGAEIYNELINNSLVSHLLITEIEHPSP
ESIEMDTFLKFPLESWTKQPKSELQKFGVDTVLEDDIKEGDFTYNYTLWTRK
>d1ekqa_ c.72.1.2 (A:) Hydroxyethylthiazole kinase (THZ kinase, ThiK) {Bacillus subtilis}

MDAQSAAKCLTAVRRHSPLVHSITNNVVTNFTANGLLALGASPMAYAKEEVADMAKIAGALVLNIG
TLSKESVEAMIIAGKSANEHGVPVILDPVGAGATPFRTESARDIIREVRLAAIRGNAAEIAHTVGVTD
WLIKGVDAGEGGGDIIRLAQQAQKLNTVIAITGEVDVIADTSHVYTLHNGHKLLTKVTGAGCLLTSV
VGAFCAVEENPLFAAIAAISSYGVAALAAQQTADKGPFSFQIELLNKLSTVTEQDVQEWATIERV

>d1jxha_ c.72.1.2 (A:) 4-amino-5-hydroxymethyl-2-methylpyrimidine phosphate kinase
(HMP-phosphate kinase, ThiD) {Salmonella typhimurium}

MQRINALTIAGTDPSSGAGIQADLKTFSALGAYGCSVITALVAENTCGVQSVYRIEPDFVAAQLDSVFS
DVRIDTTKIGMLAETDIVEAVAERLQRHHVRNVVLDTVMLAKSGDPLLSPSAIETLRVRLLPQVSLIT
PNLPEAAAALLDAPHARTEQEMLAQGRALLAMGCEAVLMKGGHLEDAQSPDWLFTREGEQRFSA
VNTKNTHGTGCTLSAALAAALRPRHRSWGETVNEAKAWLSAALAAQADTLEVGKIGIPVHHFHAWW

>d1rkd_ c.72.1.1 (-) Ribokinase {Escherichia coli}

AGSLVVLGSINADHILNLQSFPTPGETVTGNHYQVAFGGKGANQAVAAGRSGANIAFIACGDDSIGES
VRQQLATDNIDITPVSVIKGESTGVALIFVNGEGENVIGIHAGANAALSPALVEAQRERIANASALLMQ
LESPLESVMAAAKIAHQNTIVALNPAPARELPDELLALVDIITPNETEAEKLTGIRVENDEDAKAA
QVLHEKGIRTVLITLGSRGVWASVNGEGQRPVGFVRVQAVDTIAAGDTFNGALITALLEEKPLPEAIRF
AHHAAIAVTRKGAQSPWPWREEIDAFLDRQR

>d1bx4a_ c.72.1.1 (A:) Adenosine kinase {Human (Homo sapiens)}

VRENILFGMGNPLLDISAVVDKDFLDKYSLKPNDQILAEDKHKELFDELVKKFKVEYHAGGSTQNSI
KVAQWMIQQPHKAATFFGCIGIDKFGELKRKAAEAHVDAHYEYQNEQPTGTCAACITGDNRS
LIANLAAANCYKKEKHLDLKKNWMLVEKARVCYIAGFFLTVSPESVLKVAHHASENNRIFTLNLSAPFISQ
FYKESLMKVMPPYVDILFGNETEAATFAREQGFETKDIKEIAKKTQALPKMNSKRQRVIFTQGRDDT
IMATESEVTAFVLDQDQKEIIDTNGAGDAFVGGFLSQLVSDKPLTECIRAGHYAASIIIRRTGCTFPEK
PDFH

>d1dgya_ c.72.1.1 (A:) Adenosine kinase {Toxoplasma gondii}

GPMRVFAIGNPILDLVAEVPSSFLDEFLLKRGDATALATPEQMRIYSTLDQFNPTSLPGGSALNSVRV
QKLLRKPGSAGYMGAIADDPRGQVLKELCDKEGLATRFMVPAGQSTGTCAVLINEKERTLCTHLGAC
GSFRIPENWTTFASGALIFYATAYTLTATPKNALEVAGYAHGIPNAIFTLNLSAPFCVELYKDAMQSL
LHTNILFGNEEEFAHLAKVHNLVAAEKVALSVANKEHAVEVCTGALRLLTAGQNTGATKLVVMTRG
HNPVIAAEQTADGTVVVHEVGPVVAEKIVDTNGAGDAFVGGFLYGLSQGKTVKQCIMCGNACAQ
DVIQHVGFSLSF

>d1gc5a_ c.72.1.3 (A:) ADP-dependent glucokinase {Archaeon Thermococcus litoralis}

MKESLKDRIRLWKRLYNVAFENALNAIPNVKGVLLAYNTNIDAIKYLDADDLEKRVTEKGEKVF
EIIENPPEKISSIEELLGGILRSIKLGKAMEWVFESEEVRRYLREWGWDELRIQQAGIMANLLGGVYRIP
TIVHVPQNPKLQAEFLVDGPIYVPVFEGNKLKLVHPKDAIAEEEEELIHYIYEFPRGFQVFDVQAPREN
RFIANADDYNARVYMRREFREGFEEITRNVELAIISGLQVLKEYYPDGTTYKDVLDREVESHNLNRY
NVKSHFEFAYTANRRVREALVELLPKFTSVGLNEVELASIMEIIGDEELAKEVLEGHIFSVIDAMNVL
MDETGIERIHFTYGYLALTQYRGEEVRDALLFASLAAAAMKGNLERIEQIRDALSVPTNERAIV
LEEELEKEFTEFENGLIDMVDRLAFVPTKIVASPKSTVIGIGDTISSSAFVSEFGMRKR

>d2uaga3 c.72.2.1 (A:94-297) UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase MurD
{Escherichia coli}

DIELFCREAQAPIVAITGNSGKSTVTTLVGEMAKAAGVNVGVGGNIGLPALMLLDDECELYVLELSSF
QLETTSSLQAVAATILNVTEDHMDRYPFGLQYRAAKLRIYENAKVCVNNADDALTMPIRGADERCV
SFGVNMGDYHLNHQQGETWLRVKGEKVLNVKEMKLSGQHNYTNALALALADAAGLPRASSLKA
LTTFT

>d1e8ca3 c.72.2.1 (A:88-337) UDP-N-acetylmuramyl tripeptide synthetase MurE {Escherichia coli}

QLNERLSALAGRFYHEPSDNLRLVGVGTGTNGKTTTTQLLAQWSQLLGEISAVMGTVGNLLGKVIPT
ENTTGSVAVDVQHELAVLDQGATFCAMEVSSHGLVQHRVAALKFAASVFTNLSRDHLDYHGDMEHY
EAAKWLLYSEHHCGQAIINADDEVGRRWLAKLPDAVAVSMEDHINPNCHGRWLKATEVNYHDSGA
TIRFSSSWGDEIESHLMGAFNVSNLLLALATLLALGYPLADLLKTAARLQP

>d1gg4a4 c.72.2.1 (A:82-312) UDP-murNac-tripeptide D-alanyl-D-alanine-adding enzyme MurF {Escherichia coli}

DTRLAFGELAAWVRQQV PARVVALTGSSGKTSVKEMTAAILSQCNTLYTAGNLNNDIGVPMTLRL
TPEYDYAVIELGANHQGEIAWTVSLTRPEAALVNNLAAAHLEGFGLAGVAKAKGEIFSGLPENGLAI
MNADNNDWLNWQSVIGSRKVWRFPNAANSDFATNIHVTSHGTEFTLQTPGSDVLLPLPGRH
NIANALAAAALSMSGATLDAIKAGLANLKA

>d1jbwa2 c.72.2.2 (A:1-296) Folylpolylglutamate synthetase {Lactobacillus casei}

MNYTETVAYIHSFRLAKTGDHRRILLHALGNPQQQGRYIHVTGTNGKGSAAANIAHVLEASGLT
VGLYTSFIMRFNERIMIDHEPIPDAALVNAVAFVRAALERLQQQADFNVTTEFITALAYWYFRQR
QVDVAVIEVGIGGDTSTNVITPVVSVLVEALDHQKLLGHTITAIKHKAGIIRKIPVVTGNLVPDA
AAVVAAKVATTGSQWLRDFDRDFSVPKAKLHGWGQRFTYEDQDGRISDLEVPLVGDYQQRNMAIAIQ
TAKVYAKQTEWPLTPQNIRQGLAASH

>d1jzta_ c.104.1.1 (A:) Hypothetical protein YNL200c (YNU0_YEAST) {Baker's yeast (Saccharomyces cerevisiae)}

LKVVS SKLAAEIDKELMGPQIGFTLQQLMELAGFSVAQAVCRQFPLRGKTETEKGKHVFVIAGPGNN
GGDGLVCARHLKLFYGNPVVFPKRSERTEFYKQLVHQLNFFKVPVLSQDEGNWLEYLKPEKTL CIV
DAIFGFSFKPPMREPFGKIVEELCKVQNIPIVSDVPTGWDVDKGPISQPSINPAVLVSLVTPKPCSSH
IRENQTTTHYVGGRFIPRDFANKFGFEPFGYESTDQILKL

>d1b7ba_ c.73.1.1 (A:) Carbamate kinase {Enterococcus faecium}

GKKMVVALGGNAILSNDASAHAAQQALVQTSAYLVHLIKQGHRLIVSHGNPQVGNLLLQQAADSE
KNPAMPLDTCVAMTQSGISYWLSNALNQLNKAGIKKQVATVLTQVVVDPADAEAFKNPTKPIGPFLT
EAEAKEAMQAGAIKFEDAGRGRKVVPSPKPIDIHEAETINTLIKNDIITISCGGGGIPVVGQELKGV E
AVIDKDFASEKLAELVDADALVILTGVVVCINYGKPKDEKQLTNVTVAELEEYKQAGHFAPGSMLPKIE
AAIQFVESQPNKQAIITSLENLGSMSGDEIVGTVV

>d1e19a_ c.73.1.1 (A:) Carbamate kinase {Archaeon Pyrococcus furiosus}

GKRVVIALGGNALQQRGQKGSYEEMDNVRKTARQIAEIIARGYEVVITHGNGPQVGSLLLHMDAG
QATYGIPAQPM DVAGAMSQGWIGYMIQQALKNELRKRGMKKVVTIITQTIVDKNDPAFQNPTKPV
GPFYDEETAKRLAREKGWIVKEDSGRGWRRVVPSPDPKGHVEAETIKKLV ERGVIVIASGGGVPVIL
EDGEIKGVEAVIDKDLAGEKLAEEVNADIFMILTDVNGAALYGYTEKEQWLREVKVEELRKYEEGH
FKAGSMGPKVLAIRFIEWGGERAIIAHLEKAVEALEGKTGTQVLP

>d1eqja1 c.105.1.1 (A:77-310) 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain {Bacillus stearothermophilus}

QSLTRINIAIREGEFDRNETFLAAMNHVKQHGTSLHLFGLLSDGGVHSHIHLYALLRLAAKEGVKR
VYIHGFLDGRDVG PQTAPQYIKELQEKIKEYGVEIATLSGRYYSMDRDKRWDRVEKAYRAMVYGE G
PTYRDPLECIEDSYKHGIYDEFVLPSVIVREDGRPVATI QDNDAIIFYNFRPDRAIQISNTFTNDFRE
FDRGPKHPKHLFFVCLTHFSETVAGYVAFKP

>d1eqja2 c.76.1.3 (A:3-76,A:311-510) 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain {Bacillus stearothermophilus}

KKPVALIILDGFALRDETYGNAVAQANKPNFDRIWNEYPHTTLKACGEAVGLPEGQMGNSEVGHNLN
IGAGRIVYXTNLDNTIGEVLSQHGLRQLRIAETEKYPHVTFMMSGGREEEFPGEDRILINSPKVPTYD
LKPEMSAYEVT DALLKEIEADKYDAILNYANPDMVGHSGKLEPTIKAVEAVDECLGKVV DAILAKGG
IAIITADHGNADVLTPDGKPKQTAHTTNPVPIVTKKGIKLRDGGILGDLAPTMLDLLGLPQPKEMT
GKSLIV

>d1ed8a_c.76.1.1 (A:) Alkaline phosphatase {Escherichia coli}

TPEMPVLENRAAQGDITAPGGARRLTGDQTAALRDSLSKPAKNIILLIGDGMGDSEITAARNYAEGA
GGFFKGDALPLTGQYTHYALNKKTKGPDYVTDASAATAWSTGVKTYNGALGVDIHEKDHPTILEM
AKAAGLATGNVSTAELQDATPAALVAHVTSRKCYGPSATSEKCPGNALEKGGKGSITEQLLNARADVT
LGGGAKTFAETATAGEWQGKTLREQAQARGYQLVSDAASLNSVTEANQQKPLLGLFADGNMPVVRW
LGPKATYHGNIDKPAVCTPNPQRNDSVPTLAQMTDKAIELLSKNEKGFLLQVEGASIDKQDHAAN
PCGQIGETVDLDEAVQRALEFAKKEGNTLVIVTADHAHASQIVAPDTKAPGLTQALNTKDGAVMVM
SYGNSEEDSQEHTGSQRLIAAYGPHAANVVGLTDQTDLFYTMKAALGLK

>d1ew2a_c.76.1.1 (A:) Alkaline phosphatase {Human (Homo sapiens)}

IIPVEEENPDFWNREAAEALGAACKLQPAQTAANKLIIFLGDGMGVSTVTAARILKGQKDKLGPPEIP
LAMDRFPYVALSKTYNVDKHVPDSGATATAYLCGVKGNFQTIGLSAAARFNQCNTTRGNEVISVMN
RAKKAGKSVGVTTRVQHASPAGTYAHTVNRNWYSADVPASARQEGCQDIATQLISNMDIDVILG
GGRKYMFRMGTPDPEYPDDYSQGGTRLDGKNLVQEWLAKRQGARYVWNRTELMQASLDPSVTHL
MGLFEPGDMKYEIHRDSTLDPSLMEMTEAALRLLSRNPRGFFLVEGGRIDHGHESRAYRALTETI
MFDDAIERAGQLTSEEDTSLVTDHSHVFSFGGYPLRGSSIFGLAPGKARDRKAYTVLLYGNPGYV
LKDGARPDVTESESGSPEYRQQSAVPLDEETHAGEDVAVFARGPQAHLVHGVEQTFIAHVMAFAA
CLEPYTACDLAPP

>d1auk_c.76.1.2 (-) Arylsulfatase A {Human (Homo sapiens)}

RPPNIVLIFADDLGYGDLGCGHPSSTTPNLDQLAAGGLRFTDFYVPSLCTPSRAALLTGRLPVRMG
MYPGVLVPSRRGGLPLEEVTVAEVLAAARGYLTGMAGKWHLGVGPEGAFLPPHQGFHRFLGIPYSHD
QGQCQNLTFCFPATPCDGGCDQGLVPIPLLANSVEAQPWPWLPGLEARYMAFAHDLMAAQRQDRP
FFLYYASHHTHYQFSGQSFAERSGRGPFGLDMLDAAVGTLMTAIGDLGLEETLVIFTADNGPET
MRMSRGGCSGLLRGCKGTTYEGGVREPALAFWPGHIAPGVTHELASSDLLPTLAALAGAPLPNVT
LDGFDLSPLLLGTGKSPRQSLFFYPSYPDEVRGVFAVRTGKYKAHFFTQGSASDTTADPACHASSL
TAHEPPLLYDLKDPGENYNLLGGVAGATPEVLQALKQLQLLKAQLDAAVTFGPSQVARGEDPALQIC
CHPGCTPRPACCHCP

>d1fsu_c.76.1.2 (-) Arylsulfatase B (4-sulfatase) {Human (Homo sapiens)}

SRPPLVFLADDLGNWVDFHGSRI RTPHLDALAAGGVLLDNYTQPLXTPSRSQLLTGRYQIRTG
LQHQIWPQCQPCVPLDEKLLPQLLKEAGYTTMVGKWHLGMRYRKECLPTRRGFDYFGYLLGSED
YYSHERCTLIDALNVTRCALDFRDGEEVATGYKNMYSTNIFTKRAIALITNHPPEKPLFLYLALQSVH
EPLQVPEEYLKPYDFIQDKNRHHYAGMVSLMDEAVGNVTAALKSSGLWNNTVFIFSTDNGGQTLG
GNNWPLRGRKWSLWEGGVRGVGFVASPLLKQKGVKNRELIHISDWLPTLVKLARGHTNGTKPLDG
FDVWKTISEGSPRIELLNIDPNFVDSSPCPRNSMAPAKDSSLPEYSAFNSTVHAAIRHGNWKL
LTGYPGCGYWFPPPSQYNVSEIPSSDPPTKTLWLFDIDRDPEERHDL SREYPHIVTKLLSRLQFYHKK
SVPVYFPAQDPRCDPKATGVWGPWM

>d1hdha_c.76.1.2 (A:) Arylsulfatase B (4-sulfatase) {Pseudomonas aeruginosa}

KRPNFLVIVADDLGFSDIGAFGGIATPNLDALAIAGLRLTDFHTASTCSPTRSMMLTGTDHIIAGIGT
MAEALTELEGKPGYEGHLNERVVALPELLREAGYQTLMAGKWHLGLKPEQTPHARGFERSFSLLP
GAANYHGFEPYDESTPRILKGTALYVEDERYLDTLPEGFYSSDAFGDKLLQYLKERDQSRPFFAYL

PFSAPHWPLQAPREIVEKYRGRYDAGPEALRQERLARLRELKELGLVEADVEAHPVLALTREWEALEDE
ERAKSARAMEVYAAMVERMDWNIGRVVDYLRRQGELDNTFVLFMSDNGAEGALLEAFPKFGPDL
GFLDRHYDNSLENIGRANSYVWYGPRWAQAATAPSRLYKAFTTQGGIRVPALVRYPRLSRQGAISHA
FATVMDVTPTLLDLAGVRHPGKRWRGREIAEPRGRSWLGLWLSGETEAAHDENTVTGWELFGMRA
IRQGDWKAVYLPAPVGPATWQLYDLARDPGEIHDLADSQPGKLAELIEHWKRYVSETGVV

>d1k30a_ c.112.1.1 (A:) Glycerol-3-phosphate (1)-acyltransferase {Cushaw squash
(Cucurbita moschata)}

SHSRKFLDVRSEEELLSCIKKETEAGKLPPNVAAGMEELYQNYRNAVIESGNPKADEIVLSNMTVALD
RILLDVEDPFVSSHKAIREPFDYIFGQNYIRPLIDFGNSFVGNLSLFKDIEEKLQQGHNVVLISNH
QTEADPAIISLLEKTNPYIAENTIFVAGDRVLADPLCKPFSIGRNLCVYSKHKMFDIPELTETKRKA
NTRSLKEMALLLRGGSQLIWIAPSGGRDRPDSTGEWYPAPFDASSVDNMRRLIQHSDVPGHLFPL
ALLCHDIMPPPSQVEIEIGEKRVIAFNGAGLSVAPEISFEEIAATHKNPEEVREAYSKALFDSVAMQYN
VLKTAISGKQGLGASTADVLSQPW

>d1e4bp_ c.74.1.1 (P:) L-fucose-1-phosphate aldolase {Escherichia coli}

MERNKLARQIIDTCLMTRLGLNQGTAQVSVRYQDGLMPTGIPYEKLTESHIVFDGNGKHEEGK
LPSSEWRFHMAAYQSRPDANAVVHNHAVHCTAVSILNRSIPAIHYMIAAAGGNSIPCAPYATFGTREL
SEHVALALKNRKATLLQHHGLIACEVNLEKALWLAHEVEVLAQLYLTTLAITDPVPLSDEEIAVVLE
KF

>d1jdia_ c.74.1.1 (A:) L-ribulose-5-phosphate 4-epimerase {Escherichia coli}

MLEDLKRQVLEANLALPKHNLVTLTWGNVSAVDRERGVFVIKPSGVDYSIMTADDMVVVSIETGEV
VEGAKKPSDTPHRLLYQAFPSIGGIVHTHSRHATIWAQAGQSIPATGTTHADYFYGTIPCTRKMTD
AEINGEYEWETGNVIVETFEKQGIDAAQMPGVLVHSHGPFPAWGKNAEDAVHNAIVLEEVAYMGIFC
RQLAPQLPDMQQTLLNKHYLRKH

>d1j9la_ c.106.1.1 (A:) SurE homolog TM1662 (TM107 ?) {Thermotoga maritima}

MRILVTNDDGIQSKGIIVLAELLSEEHEVFVAPDKERSATGHSITIHVPLWMKKVFISERVVAYSTTG
TPADCVKLAYNVVMDKRVDLIVSGVNRGPNMGMDILHSGTVSGAMEGAMMNIPSIAISSANYESP
FEGAARFLIDFLKEFDLSLLDPFTMLNINVPAGEIKGWRFRTRQSRRRWNDYFEERVSPFGEKYYWM
MGEVIEDDDRRDDVDYKAVREGYVSITPIHPFLTNEQCLKKLREVYD

>d1cja2 c.75.1.1 (A:142-721) Cytosolic phospholipase A2 catalytic domain {Human (Homo sapiens)}

PDLRFSMALCDQEKTFRQQRKEHIRESMKLLGPKNSEGLHSARDVPVAVILGSGGGFRAMVGFSG
VMKALYESGILDCATYVAGLSGSTWYMSTLYSHPDFPEKGPEEINEELMKNVSHNPLLLLTPQKVKR
YVESLWKKKSSGQPVFTFDIFGMLIGETLIHNRMNTLSSSLKEKVNTAQCPPLFTCLHVKPDVSEL
MFADWVEFSPYEIGMAKYGTFMAPDLFGSKFFMGTVVKKYEENPLHFLMGVWGSFAFSILFNRLG
VSGSQRGSTMEELENITTKHIVSNDSSDDESHEPKGTENEDAGSDYQSDNQASWIHRMIMALV
SDSALFNTRERAGKVHNFMLGLNLNTSYPLSPLSDFATQDSFDDDELDAAVADPDEFERIYEPLDV
KSKKIHVVDGLTFNLPLPYLILRPQRGVDLIISDFDSARPSDSSPPFKELLAEKWAKMKNLPPFKIDP
YVFDREGLKECYVFKPNPDMEKDCPTIIHFVLANINFRKYKAPGVPRETEEEKEIADFDFDDPESP
FSTFNFQYPNQAFKRLHDLMHFNLTNNIDVIKEAMVESIEYRRQ

>d1xaa_ c.77.1.1 (-) 3-isopropylmalate dehydrogenase, IPMDH {Thermus thermophilus}

MKVAVLPGDGIGPEVTEAALKVLRALDEAEGGLAYEVFPFGGAIDAFAFGEPPPEPTRKGVEEAEAV
LLGSVGPKWDGLPRKIRPETGLLSLRKSQDLFANLRPAKVFPGLERLSPLKEEIARGVDVLIVRELT
GGIYFGEPRGMSEAEAWNTERYSKPEVERVARVAFAARKRRKHVVSVDKANVLEVGFEFWRKTVE
EVGRGYPDVALEHQYVDAMAMHLVRSRPARFDVVVTGNIFGDILSDLASVLPGLSGLLPSASLGRGTPV

FEPVHGSAPDIAGKGIANPTAAILSAMMMLEHAFGLVELARKVEDAVAKALLETPPPDLGGSAGTEA
FTATVLRHLA

>d1xad_ c.77.1.1 (-) 3-isopropylmalate dehydrogenase, IPMDH {Chimera (Thermus
thermophilus) and (Bacillus subtilis)}

MKVAVLPGDGIGPEVTEAALKVLRALDEAEGGLAYEVFPFGGAAIDAFGEPPPEPTRKGVEEAEAV
LLGSVGGPKWDQNPREL RPEKGLLSIRKQLDLFANLRPVKVFESLSDASPLKKEYIDNVDFVIVRELT
GGIYFGEPRGMSEAEAWNTERYSKPEVERVARVAFEAARKRRKHVVSVDKANVLEVGFEFWRKTVE
EVGRGYPDVALEHQYVDAMAMHLVRSRPARFDVVVTGNIFGDILSDLASVLPGLSGLLPSASLGRGTPV
FEPVHGSAPDIAGKGIANPTAAILSAMMMLEHAFGLVELARKVEDAVAKALLETPPPDLGGSAGTEA
FTATVLRHLA

>d2ayqa_ c.77.1.1 (A:) 3-isopropylmalate dehydrogenase, IPMDH {Bacillus coagulans}

MKMKLAVLPGDGIGPEVMDAAIRVLKTVLDNDGHEAVFENALIGGAAIDEAGTPLPEETLDICRRSD
AILLGAVGGPKWDHNPASLRPEKGLLGLRKEMGLFANLRPVKAYATLLNASPLKRREVENVDLVIVR
ELTGGLYFGRPSERRGPGENEVVDTLAYTREEIERIIEKAFQLAQIRRKKLASVDKANVLESSRMWRE
IAEETAKKYPDVELSHMLVDSTSMQLIANPGQFDVIVTENMFGDILSDEASVITGSLGMLPSASLRSD
RFGMYEPVHGSAPDIAGQGANPLGTVLSAALMLRYSFGLEKEAAAIEKAVDDVLQDGYCTGDLQV
ANGKVSTIELTDRLIEKLN

>d1a05a_ c.77.1.1 (A:) 3-isopropylmalate dehydrogenase, IPMDH {Thiobacillus
ferrooxidans}

MKKIAIFAGDGIGPEIVAAARQVLDAVDQAAHLGLRCTEGLVGGAAALDASDDPLPAASLQLAMAADA
VILGAVGGPRWDAYPPAKRPEQGLLRKGLDLYANLRPAQIFPQLLDASPLRPELVRDVLVRELT
GDIYFGQPRGLEVIDGKRRGFNTMVYDEDEIRRIAHVAFRAAQRRKQLCSVDKANVLETTTRLWRE
VVTEVARDYPDVRLSHMYVDNAAMQLIRAPAQFDVLLTGNMFGDILSDEASQLTGSIGMLPSASLGE
GRAMYEPIHGSAPDIAGQDKANPLATILSVAMMLRHSLNAEPWAQRVEAAVQRVLDQGLRTADIAA
PGTPVIGTKAMGAAVNALNLK

>d1cnza_ c.77.1.1 (A:) 3-isopropylmalate dehydrogenase, IPMDH {Salmonella typhimurium}

MSKNYHIAVLPGDGIGPEVMAQALKVMDAVRSRFRMRITTSHYDVGGIAIDNHGHPLPKATVEGCE
QADAILFGSVGGPKWENLPPESQPERGALLPLRKHFKLFSNLRPAKLYQGLEAFCLRADIAANGFDI
LCVRELTGGIYFGQPKGREGSGQYEKAFDTEVYHRFEIERIARIAFESARKRRRKVTSIDKANVLQSSI
LWREIVNDVAKTYPDVELAHMYIDNATMQLIKDPSQFDVLLCSNLFGLDILSDECAMITGSMGMLPSA
SLNEQGFLYEPAGGSAPDIAGKNIANPIAQILSLALLLRYSLDANDAATAIEQAINRALEEGVRTGDL
ARGAAAVSTDEMGIARYVAEGV

>d1cm7a_ c.77.1.1 (A:) 3-isopropylmalate dehydrogenase, IPMDH {Escherichia coli}

MSKNYHIAVLPGDGIGPEVMTQALKVLDVAVRNRFAMRITTSHYDVGGAAIDNHGQPLPPATVEGCE
QADAVLFGSVGGPKWEHLPPDQQPERGALLPLRKHFKLFSNLRPAKLYQGLEAFCLRADIAANGF
DILCVRELTGGIYFGQPKGREGSGQYEKAFDTEVYHRFEIERIARIAFESARKRRHKVTSIDKANVLQS
SILWREIVNEIATEYDPVELAHMYIDNATMQLIKDPSQFDVLLCSNLFGLDILSDECAMITGSMGMLPS
ASLNEQGFLYEPAGGSAPDIAGKNIANPIAQILSLALLLRYSLDADDAACAIERAINRALEEGIRTGDL
ARGAAAVSTDEMGIARYVAEGV

>d1iso_ c.77.1.1 (-) Isocitrate dehydrogenase, ICDH {Escherichia coli}

SKVVVPAQGGKITLQNGKLNVPENPIIPYIEGDGIGVDVTPAMLVVDAAVEKAYKGERKISWMEIYT
GEKSTQVYGQDVWLPAETLDLIREYRVAIKGPLTTPVGGGIRSLNVALRQELDLYICLRPVRYQQGTPS
PVKHPELTD MVIFRENSEDIYAGIEWKADSADA EKVIKFLREEMGVKKIRFPEHCIGIKPMSEEGTK
RLVRAAIEYAIANDRDSVTLVHKGNIMKFTTEGAFKDWGYQLAREEFGGELIDGGPWLKVKNPNTGK

EIVIKDVIADAFLLQILLRPAEYDVIAACMNLNGDYISDALAAQVGGIGIAPGANIGDEYALFEATHGTAP
DIAGQDKANPGSIIILSAEMMLRHMGWTEAADLIVKGMEGAINAKTVTKDFESLMDGAKLLKCSEFG
DAIENM

>d1hqa_c.77.1.1 (A:) Isocitrate dehydrogenase, ICDH {*Bacillus subtilis*}

MAQGEKITVSNGLNVPNNPIIPFIEGDGTGPDWNAASKVLEAAVEKAYKGEKKITWKEVYAGEKA
YNKTGEWLPAETLDVIREYFIAIKGPLTPVGGGIRSLNVALRQELDLFVCLRPVRYFTGVPSPVKRPE
DTDMVIFRENTEDIYAGIEYAKGSEEVQKLISFLQNELNVNKIRFPETSGIGIKPVSEEGTSRLVRAAID
YAIEHGRKSVTLVHKGKIMKFTGAFKNWGYELAEKEYGDKVFTWAQYDRIAEQKDAANKAQS
EAEAGKIIKDSIADIFLQILTRPNEFDVVATMNLNGDYISDALAAQVGGIGIAPGANINNYETGHAIF
EATHGTAPKYAGLDKVNPSVILSGVLLLEHLGWNEAADLVIKSMEKTIASKVVVYDFARLMDGATE
VKCSEFGHEELIKNMD

>d1ekxa1 c.78.1.1 (A:1-150) Aspartate carbamoyltransferase catalytic subunit {*Escherichia coli*}

ANPLYQKHIISINDLSRDDNLVLATAAKLKNPPELLKHKVIASCFEASTRTRLSFETSMHRLGAS
VVGFSDSANTSLGKKGETLADTISVISTYVDAIVMRHPQEGAARLATEFSGNVPVLNAGDGSNQHPT
QTLLDLFTIQETQG

>d1ekxa2 c.78.1.1 (A:151-310) Aspartate carbamoyltransferase catalytic subunit {*Escherichia coli*}

RLDNLHVAMVGDLYKGRVHSLTQALAKFDGNRFYFIAPDALAMPQYILDMLDEKGIASLHSSIEE
VMAEVDILYMTRVQKERLDPSEYANVKAQFVLRASDLHNAKANMKVLHPLPRVDEIATDVKTPH
AWYFQQAGNGIFARQALLALVLRDLVL

>d2atca2 c.78.1.1 (A:151-305) Aspartate carbamoyltransferase catalytic subunit {*Escherichia coli*}

RLNNLHVAMVGDLYKGRVHSLTQALAKFDGNRFYFIAPDALAMPEYILDMLDEKGIASLHSSIEE
VMTRVQKERLDPSEYABVKAQFLVRANSLGGLHNAKMNKVLHPLPRVDEIATDVKTPHAWYFQ
QAGNGIFARQALLALVLRDLVL

>d2at2a1 c.78.1.1 (A:1-144) Aspartate carbamoyltransferase catalytic subunit {*Bacillus subtilis*}

MKHLTTMSELSTEEIKDLLQTAQELKSGKTDNQLTGKFAANLFFEPSTRTRFSFEVAEKKLGMNVLN
LDGTSTSVQKGETLYDTIRTLESIGVDVCVIRHSEDEYYEELVSQVNIPILNAGDGCQHPQSLDLDM
TIYEEFNT

>d2at2a2 c.78.1.1 (A:145-295) Aspartate carbamoyltransferase catalytic subunit {*Bacillus subtilis*}

FKGLTVSIHGDIKHSRVARNAEVLTRLGARVLFSGPSEWQDEENTFGTYVSMDEAVESSDVVMLLRI
QNERHQSAVSQEGYLNKYGLTVERAERMKRHAIIMHPAPVNRGVEIDDSLVESEKSRIFKQMKNGVF
IRMAVIQCALQTNVCR

>d1dxha1 c.78.1.1 (A:1-150) Ornithine transcarbamoylase {*Pseudomonas aeruginosa*}

AFNMHNRNLLSLMHHSTRELRYLLDLRDLKRAKYTGTEQQHLKRKNIALIFEKTSTRTRCAFEVA
AYDQGANVTYIDPNSSQIGHKESMKDTARVLGRMYDAIEYRGFKQEIVEELAKFAGVPVFNGLTDEY
HPTQMLADVLTMRHSD

>d1dxha2 c.78.1.1 (A:151-335) Ornithine transcarbamoylase {*Pseudomonas aeruginosa*}

KPLHDISYAYLGDARNMGNLLLLIGAKLGMVRIAAPKALWPHDEFVAQCKKFAEESGAKLTLTED
PKEAVKGVDFVHTDVVWSMGPVEAWGERIKELLPYQVNMEIMKATGNPRAKFMHCLPAFHNSE
TKVGKQIAEQPNLANGIEVTEDVFESPNIAFEQAENRMHTIKAILVSTLADI

>d1duvg1 c.78.1.1 (G:1-150) Ornithine transcarbamoylase {Escherichia coli}
 SGFYHKKHFLKLLDFTPAELNSLLQLAAKLIKADKKSQKKEAKLTGKNIALIFEKSDSTRTRCSFEVAAYD
 QGARVTYLGPSSQIGHKESIKDTARVLGRMYDGIQYRGYQEIIVETLAEYASVPVWNGLTNEFHPT
 QLLADLLTMQEHLPG

>d1duvg2 c.78.1.1 (G:151-333) Ornithine transcarbamoylase {Escherichia coli}
 KAFNEMTLVYAGDARNMGNMSEAAALTEGLDLRLVAPQACWPEAALVTECRALAQNGGNITLT
 EDVAKGVEGADFIYTDVWVSMGEAKEKWAERIALREYQVNSKMMQLTGNPEVKFLHCLPAFHDD
 QTTLGKKMAEEFGLHGGMEVTDEVFESAASIVFDQAENRMHTIKAVMVATLSK

>d1a1s_1 c.78.1.1 (1-150) Ornithine transcarbamoylase {Archaeon Pyrococcus furiosus}
 VVSLAGRDLCLQDYTAEEIWTILETAKMFKIWQKIGKPHRLLEGKTLAMIFQKPSTRTRVSEFVAM
 AHLGGHALYLNQDLQLRRGETIADTARVLSRYVDAIMARVYDHKDVEDLAKYATVPVINGLSDFSH
 PCQALADYMTIWEKKG

>d1a1s_2 c.78.1.1 (151-313) Ornithine transcarbamoylase {Archaeon Pyrococcus furiosus}
 TIKGVKVVYVGDGNNVAHSLMIAGTKLGADVVPATPEGYEPDEKVIKWAENAAESGGSFELLHDP
 VKAVKADAVIYTDVWASMGQEAEEERRKIFRPFQVKNKDLVKHAKPDYMFMHCLPAHRGEEVTD
 VIDSPNSVVDQAENRLHAQKAVLALVMGGIK

>d1otha1 c.78.1.1 (A:34-184) Ornithine transcarbamoylase {Human (Homo sapiens)}
 KVQLKGRDLLTLKNFTGEEIKYMLWLSADLKFRIKQKGEYPLLLQKSLGMIFEKRSTRTRLSTETGF
 ALLGGHPCFLTTQDIHLGVNESLTDARVLSMADAVLARVYKQSDLDLTAKEASIPINGLSDLYHPI
 QILADYTLQEHYS

>d1otha2 c.78.1.1 (A:185-354) Ornithine transcarbamoylase {Human (Homo sapiens)}
 SLKGLTSLWIGDGNNILHSIMMSAAKFGMHLQAATPKGYEPDASVTKLAEQYAKENGTKLLLTNDPL
 EAAHGGNVLITDTWISMGREEEKKRLQAFQGYQVTMKTAKVAASDWTFLHCLPRKPEEVDDEVF
 YSPRSLVFEAENRKWTIMAVMVSLLDYSPQLQKPKF

>d1b74a1 c.78.2.1 (A:1-105) Glutamate racemase {Aquifex pyrophilus}
 MKIGIFDSGVGGLTVLKAIRNRYRKVDIVYLGDTARVPYGIRSKDTIIRYSLECAFLKDKGVDIIVVAC
 NTASAYALERLKEINVPVFGVIEPGVKEALKKSR

>d1b74a2 c.78.2.1 (A:106-252) Glutamate racemase {Aquifex pyrophilus}
 NKKIGVIGTPATVKSGAYQRKLEEGADVFAKACPLFAPLAEGLLEGEITRKVVEHYLKEFKGKIDTL
 ILGCTHYPLKKEIKFLGDAEVVDSSEALSLSLHNFIKDDGSSSLELFFTDLSPNLQFLIKLILGRDYP
 VKLAEGVF

>d1qopb_ c.79.1.1 (B:) Tryptophan synthase, beta-subunit {Salmonella typhimurium}
 TTLLNPYFGEFGGMYVPQILMPALNQLEEFVSAQKDPEFQAQFADLLKNYAGRPTALTKCQNITAG
 TRTTLYLKRELLHGGAHKTNQVLGQALLAKRMGKSEIIAETGAGQHGVASALASALLGLKCRIYMG
 AKDVERQSPNVFRMLMGAEVIPVHSGSATLKDACNEALRDWSGSYETAHYMLGTAAGPHPYPTIV
 REFQRMIGEETKAQILDKEGRLPDAVIACVGGGSNAIGMFADFINDTSVGLIGVEPGGHGIETGEHGA
 PLKHGRVGIYFGMKAPMMQTADGQIEESYSISAGLDFPSVGPQHAYLNSIGRADYVSITDDEALEAFK
 TLCRHEGIIPALESSHALAHALKMMREQPEKEQLLVNLSGRGDKDIFTVHDIL

>d1fcja_ c.79.1.1 (A:) O-acetylserine sulfhydrylase (Cystein synthase) {Salmonella typhimurium}
 SKIYEDNSLTIGHTPLVRLNRIGNRILAKVESRNPFSVSKRIGANMIWDAEKRGVLPKGVLEVEPT
 NGNTGIALAYVAAARGYKLTMPETMSIERRKLLKALGANLVLTEGAKGMKGAIQKAAEEIVASDPQK
 YLLLQQFSNPANPEIHEKTTPGPEIWEDTDGQVDVVISGVTGGTTLTGVTTRYIKGTGKTDLITVAVEP
 TDSPVIAQALAGEEIKPGPHKIQQIGAGFIPGNLDLKLIDKVVGITNEEAISTARRLMEEEGILAGISSG

AAVAAALKLQEDESFTNKNIVVILPSSG

>d1tdj_1 c.79.1.1 (5-335) Allosteric threonine deaminase N-terminal domain {Escherichia coli}

QPLSGAPEGAEYLRAVLRAPVYEEAAQVTPLQKMEKLSRLDNVILVKREDRQPVHSFKLRGAYAMM
AGLTEEQKAHGVITASAGNHAQGVAFSSARLGVKALIVMPTATADIKVDAVRGFGGEVLLHGANFDE
AKAKAIELSQQGFTWVPPFDHPMVIAGQGTLALELLQQDAHLDRVFVPGGGGLAAGVAVLIKQL
MPQIKVIAVEAEDSACLKAALDAGHPVDLPRVGLFAEGVAVKRIGDETFRLCQEYLLDDIITVDSDAICA
AMKDLFEDVRAVAEPSGALALAGMKKYIALHNIRGERLAHILSGANVNFHGLRYVSERCCELGE

>d1e5xa_ c.79.1.1 (A:) Threonine synthase {Mouse-ear cress (Arabidopsis thaliana)}

IETAVKPPHRTEDNIRDEARRNRSNAVNPFSAKYVPFNAAPGSTESYSLDEIVYRSRSGGLLDVEHD
MEALKRFDGAYWRDLFDSRVGKSTWPYGGVWSKKEWVLPEIDDDDIVSAFEGNSNLFWAERFGK
QFLGMNDLWVKHCGISHTGSFKDLGMTVLVSQVNRLRKMGRPVGVCSTGDTSAALSAYCASAG
IPSIVFLPANKISMAQLVQPIANGAFVLSIDTDFDGCMLKIREITAELPIYLANSLNLRLEGQKTAIEI
LQQFDWQVPDWWVIVPGGNLGNIFYKGFKMCQELGLVDRIPRMVCAQAANANPLYLHYKSGWKD
FKPMTASTTFASAIQIGDPVSDRAVYALKKCNVIVEEATEEELMDAMAQADSTGMFICPHTGVALTA
LFKLRNQGVIAPTDRTVVVSTAHLKFTQSKIDYHSNAIPDMACRFSNPPVDVKADFGAVMDVLKSY
LGSNTLTS

>d1f2da_ c.79.1.1 (A:) 1-aminocyclopropane-1-carboxylate deaminase {Yeast (Hansenula saturnus)}

AGVAKFAKYPLTFGSPISNLNRLSQHLGSKVNVYAKREDCNSGLAFGGNKLKLEIYVPDIVEGDYT
HLVSIGGRQSNQTRMVAALAAKLGKKCVLIQEDWVPIPEAEKDVYNRVGNIELSRIMGADVRVIEDG
FDIGMRKSFANALQELEDAGHKPYPIPAGCSEHKYGGGLGFVGFADDEVINQEVELGIKFDKIVCCVTG
STTAGILAGMAQYGRQDDVIAIDASFSEKTKEQTLRIANNTAKLIGVEHEFKDFTLDRFAYPCYGV
PNEGTEIAIRTCAEQEGVLTDPVYEGKSMQGLIALIKEDYFKPGANVLYVHLGGAPALSAYSSFFPTKT
A

>d1jbqa_ c.79.1.1 (A:) Cystathionine beta-synthase {Human (Homo sapiens)}

WIRPDAPSRTCWQLGRPASESPHHHTAPAKSPKILPDILKIGDTPMVRINKIGKKFGLKCELLAKCE
FFNAGGSVKDRISLRMIEDAERDGTLPKPGDTIIEPTSGNTGIGLALAAAVRGYRCIIVMPEKMSSEKV
DVLRALGAEIVRTPTNARFDSPEHVGVAVRLKNEIPNSHILDQYRNASNPLAHYDTTADEILQQCD
GKLDMLVASVGTGGTITGIARKLKEKCPGCRIGVDPEGSILAEPEELNQTEQTTYEVEGIGYDFIPTVL
DRTVVDKWFKSNDEEAFTFARMLIAQEGLLCGSAGSTVAVAVKAAQELQEGQRCVVILPDSVRNY
MTKFLSDRWMLQKGF

>d1jeoa_ c.80.1.3 (A:) Probable 3-hexulose-6-phosphate isomerase Mj1247 {Archaeon Methanococcus jannaschii}

LEELDIVSNLILKKFYTNDEWKNKLDLIDRIKAKKIFIFGVGRSGYIGRCFAMRLMHLGFKSYFV
GETTTPSYEKDDLLILISGSRTESVLTVAKKAKNINNNIIAIVCECGNVVEFADLTIPLEVKKSKYLPM
GTTFEETALIFLDLVIAEIMKRLNLDESEIIRHCNLL

>d1moq_ c.80.1.1 (-) "Isomerase domain" of glucosamine 6-phosphate synthase (GLMS) {Escherichia coli}

GDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSELGPNADLLSKVEHIQILACGTSYNSGMVS
RYWVESLAGIPCDVEIASEFRYRKSARRNSLMTLSQSGETADTLAGLRLSKELGYLGLSLAICNVPGS
SLVRESDLALMTNAGTEIGVASTKAFTTQLTVLLMLVAKLSRLKGLDASIEHDIVHGLQALPSRIEQM
LSQDKRIEALAEDFSDKHHALFLGRGDQYPIALEGALKLKEISYIHAEAYAAGELKHGPLALIDADMP
VIVVAPNNELLEKLKSNIEEVRARGGQLYVFADQDAGFVSSDNMHIIEMPHVEEVIAPIFYTVPLQLL

AYHVALIKGTDVDQPRNLAKSVTVE

>d1g98a_c.80.1.2 (A:) Phosphoglucose isomerase, PGI {Rabbit (*Oryctolagus cuniculus*)}

AALTRNPQFQKLQQWHREHGSELNLRHLFDTDKERFNHFSLTLNTNHGHILLDYSKNLVTEVMH
MLLDLAKSRGVEAARESMFNKEKINSTEDRAVLHVALRNRNTPIVVDGKDVMPVNVKVLDMKA
FCQVRVSGDWKGYTGKTITDVINIGIGGSDLGPLMVTEALKPYSSGGPRVWFVSNIDGTHIAKTLACL
NPESLFIASKTFTTQETITNAKTAKDWFLLSAKDPSTVAKHFVALSTNTAKVKEFGIDPQNMFEF
WDWVGGRYSLWSAIGLSIALHVGFDNFEQLLSGAHWMDQHFRTTPELKNAPVLLAMLGIWYINCF
GCETQAVLPYDQYLHRFAAYFQQGDMESNGKYITKSGARVDHQTGPVWGEPTNGQHAFYQLIHQ
GTKMIPCDFLIPVQTQHPIRKGLHHKILLANFLAQTEALMKGKSTEEARKELQAAGKSPEDLMKLLP
HKVFEGNRPTNSIVFTKLTFFILGALIAMYEHKIFVQGVVWDINSFDQWGVELGKQLAKKIEPELDG
SSPVTSHDSSTNGLINFIKQQREAK

>d1iata_c.80.1.2 (A:) Phosphoglucose isomerase, PGI {Human (*Homo sapiens*)}

AALTRDPQFQKLQQWYREHRSELNLRRLFDANKDRFNHFSLTLNTNHGHILVDYSKNLVTEEDVMR
MLVDLAKSRGVEAARERMFNKEKINYTEGRAVLHVALRNRNTPILVDGKDVMPVNVKVLDMKKS
FCQVRVSGDWKGYTGKTITDVINIGIGGSDLGPLMVTEALKPYSSGGPRVWYVSNIDGTHIAKTLAQL
NPESLFIASKTFTTQETITNAETAKEWFLQAADKPSAVAKHFVALSTNTTKVKEFGIDPQNMFEF
WDWVGGRYSLWSAIGLSIALHVGFDNFEQLLSGAHWMDQHFRTTPELKNAPVLLALLGIWYINCF
GCETHAMLPYDQYLHRFAAYFQQGDMESNGKYITKSGTRVDHQTGPVWGEPTNGQHAFYQLIH
QGTKMIPCDFLIPVQTQHPIRKGLHHKILLANFLAQTEALMRGKSTEEARKELQAAGKSPEDLERLL
PHKVFEGNRPTNSIVFTKLTFFMLGALVAMYEHKIFVQGIWDINSFDQWGVELGKQLAKKIEPELD
GSAQVTSHDASTNGLINFIKQQREARV

>d1c7qa_c.80.1.2 (A:) Phosphoglucose isomerase, PGI {*Bacillus stearothermophilus*}

AISFDYSNALPFMQENELDYLFSEFVKAHHMLHERKGGSDFLGWVDWPIRYDKNEFSRIKQAAER
IRNHSDALVVIGIGGSYLGARAAIEALSHTFHNQMNDTTQIYFAGQNISSTYISHLLDVLEGKDLINVI
SKSGTTTEPAIAFRIFRDYMEKKYKKEARKRIYVTTDRTKGALKKLADQEGYETFVIPDNIGGRYSV
LTAVGLLPIAVAGLNIDRMMEGAASAYHKYNNPDLLTNEYSQYAAVRNILYRKGAIELLVNYEPSLHY
VSEWWKQLFGESEKDKQGLFPASVDFTTDLHSMGQYVQEGRRNIETVLHVKKPQIELTIQEDPE
NIDGLNFLAGKTLDEVNKKAFQGTLLAHVDGGVPNLIVELDEMNEYTFGEMVYFFEKACGISGHL
GVNPFDPQGV EAYKKNMFALLGKPGFEDEKAALMKRL

>d1eu1a2_c.81.1.1 (A:4-625) Dimethylsulfoxide reductase (DMSO reductase) {*Rhodobacter sphaeroides*}

ANGEVMSGCHWGVFKARVENGRAVAFEPWDKDPAPSHQLPGVLDSIYSPTRIKYPMVRREFLEKGV
NADRSTRGNGDFVRVTWDEALDLVARELKRQESYGTGTFGGSYGWKSPGRLHNCQVLMRRALN
LAGGFVNSSGDYSTAAAQIIMPHVMGTLEVYEQQTAWPVVVENTDLMVFWAADPMKTNEIGWVIP
DHGAYAGMKALKEKGTTRVIAINPVRTETADYFGADVSPRPQTDVALMLGMAHTLYSEDLHDKDFL
ENCTTGFDLFAAYLTGESDGPKEAEWAAEICGLPAEQIRELARSFVAGRTMLAAGWSIQRMHGEG
AHWMLVTLASMIQIGLPGGGFGLSYHYSNGGSPTS DGPALGGISDGGKAVEGAAWLSESGATSIPCA
RVVDMLLNPGGEFQFNGATATYPDVKLAYWAGGNPFAHHQDRNRMLKAWEKLET FIVQDFQWTA
TARHADIVLPATTSYERNDIESVGDYSNRILAMKKVVDPLYEARSDYDIFAALAERLGKGAEFTEGR
DEMGWISSFYEA AVKQAEFKNVAMP SFEDFWSEGIVEFPITEGANFVRYADFREDPLFNPLGTPSGL
IEIYSKNIEKMGYDDCPAHPTWMEPA

>d1dmr_2_c.81.1.1 (3-625) Dimethylsulfoxide reductase (DMSO reductase) {*Rhodobacter capsulatus*}

LANGTVMMSGSHWGVFTATVENGRATAFTPWEKDPHPSPMLAGVLDSIYSPTRIKYPMVRREFLEKGV

VNADRSTRGNGDFVRVSWDQALDLVAAEVKRVEETYGPEGVFGGSYGWKSPGRLHNCTTLLRRML
TLAGGYVNGAGDYSTGAAQVIMPHVVGTLLEVYEQQTAWPVLAENTEVMVFWAADPIKTSQIGWVIP
EHGAYPGLEALKAKGKTKVIVIDPVRTKTVEFFGAEHITPKPQTDVAIMLGMAHTLAEDLYDKDFIA
NYTSGFDKFLPYLDGETDSTPKTAEWAEGISGVAETIKELARLFESKRTMLAAGWSMQRMHHGEQ
AHWMLVTLASMLGQIGLPGGGFGLSYHYSGGGTPSTSGPALAGITDGGAAATKGPEWLAASGASVIPV
ARVVDMLENPGAEFDFNGTRSKFPDVKMAYWVGGNPFVHHQDRNRMVKAWEKLETFFVHDFQ
WTPPTARHADIVLPATTSYERNDIETIGDYSNTGILAMKKIVEPLYEARSDYDIFAABAERLGKGAEFTE
GKDEMGWIKSFYDDAAKQKGAAGVQMPAFDAFWAEGIVEFPVTDGADFVRYASFREDPLLNPLGT
PTGLIEIYSKNIKMGYDDCPAHPTWMEPL

>d1aa6_2 c.81.1.1 (1-564) Formate dehydrogenase H {*Escherichia coli*}

MKKVVTVCPCYASGCKINLVVDNGKIVRAEAAQGKTNQGTLCCLKGYGWDFINDTQILTPRLKTPMI
RRQRGGKLEPVSWEALNYVAERLSAIEKEYGPDAIQTGSSRGTGNETNYVMQKFARAVIGTNNV
DCCARVCHGPSVAGLHQSVGNAMSNAINENIDNTDLVFFVGYNPADSHPIVANHVINAKRNGAKIIVC
DPRKIETARIADMHIALKNGSNIALLNAMGHVIEENLYDKAFVASRTEGFEEYRKIVEGYTPESVEDI
TGVSASEIRQAARMYAQAASAILWGMGVTQFYQGVETVRSLSLAMLGKPHAGVNPVRGQN
NVQGACDMGALPDTYPGYQYVKDPANREKFAKAWGVESLPAHTGYRISELPHRAAHGEVRAAYIMG
EDPLQTDALSAVRKAFEDLELVIVQDIFMKTASAADVILPSTSWGEHEGVFTAADRGFQRFFKAV
EPKWDLKTDWQIIEIATRMGYPMHYNNQEIWDELRLHLCPDFYGATYEKMGELGFIQWPCRDTS
DADQGTSYLFKEKFDTPNGLAQFFTCDWVA

>d1tmo_2 c.81.1.1 (5-631) Trimethylamine N-oxide reductase {*Shewanella massilia*}

NEDEWLTTGSHFGAFKMKRKNGVIAEVKPFDLDKYPTDMINGIRGMVYNPSRVRYPMVRLDFLLK
GHKSNTHQRGDFRFRVVTWWDKALTLFKHSLDEVQTQYGPSGLHAGQTGWRATGQLHSSTSHMQR
AVGMHGNVYKKGIDYSTGAGQTILPYVLGSTEVYAQGTSWPLILEHSDTIVLWSNDPYKNLQVGN
AETHESFAYLAQLKEKVKQKIRVISIDPVVTKTQAYLGCEQLVNPQTDVTLMLAIAHEMISKKLYD
DKFIQGYSLGFEEFVPMGTDKGVAKTPEWAAPICGVEAHVIRDLAKTLVKGRQFMMGWCIQRQ
QHGEQPYWMAAVLATMIGQIGLPGGGISYGHYSSIGVSSGAAAPGAFPRNLDENQKPLFSSDFK
GASSTIPVARWIDAILEPGKTIDANGSKVVYPDIKMMIFSGNPNWNHHQDRNRMKQAFHKLECVVT
VDVNWATCRFSDIVLPACTTYERNDIDVYGAYANRILAMQKMVEPLFDSLSDFEIFTRFAAVLGE
KEYTRNMGEMEWLETLYNECKAANAGKFEMPDFATFWKQGYVHFGDGEVWTRHADFRNDPEIN
PLGTPSGLIEIFSRKIDQFGYDDCKGHPTWMEKT

>d1g8ka2 c.81.1.1 (A:4-682) Arsenite oxidase large subunit {*Alcaligenes faecalis*}

NDRITLPPANAQRNMTCHFICVGCYHVKWPELEEGGRAPEQNALGLDFRKQLPPLAVTLTPAM
TNVVEHGDGARYDIMVVPDKACVVNSGLSSTRGGKMASYMYTPTGDGKERLSAPRYAADEWVDT
TWDHAMALYAGLIKKTLDKDGPGQVFFSCFDHGGAGGGFENTWGTGKLMFSAIQTPMVRHNRPA
YNSECHATREMGIGELNNAYEDAQLADVIWSIGNNPYESQTNYFLNHWLPLNLQGATTSKKKERFPN
ENFPQARIIFVDPRETSPVAIARHVAGNDRVLHLAIEPGTDALFNGLFTYVVEQGWDKPFIEAHTK
GFDDAVKTNRLSLDECSNITGVPVDMLKRAAEWSYKPKASGQAPRTMHAYEKGIWGNNDNYVIQSA
LLDLVIATHNVGRRGTGCVRMGGHQEGYTRPPYPGDKKIYIDQELIKGGRIMTWWGCNNFQTSNN
AQALREAILQRSIVKQAMQKARGATTEEMVDVIYEATQNGGLFVTSINLYPTKLAEEAHLMLPAAH
PGEMNLTSMNGERRIRLSEKFMPPGTAMADCLIAARIANALRDMYQKDGKAEMAAQFEGFDWK
TEEDAFNDGFRRAGQPGAPAIQSQQGSTGHLVTDRLRKSNGNVQLPVVSWDESKGLVGTMLYT
EGKFDTDDGKAHFKPAPWNG

>d2napa2 c.81.1.1 (A:4-600) Dissimilatory nitrate reductase (NAP) {*Desulfovibrio desulfuricans*}

RPEKWVKGVCRYCGTGCGVLVGVKDGKAVAIQGNPNNHNAGLLCLKGSLLIPVLNSKERVTQPLVRR
HKGGKLEPVSWEALDLMASFRSSIDMYGPNVVAWYGSQCCLTEESYVANKIFKGGFGTNNVDGN
PRLCMASAVGGYVTSFGKDEPMGTYADIDQATCFFIIGSNTSEAHVFLFRRIARRKQVEPGVKIIVADP
RRTNTSRIADMHVAFRPGTDLAFMHSMWVVIINEELDNPRFWQRYVNFMDAEGKPSDFEGYKAF
ENYRPEKVAEICRVPVEQIYGAARAFSAATMSLWCMGINQRVQGVFANNLIHNLHLITGQICRPGA
TSFSLTGQPNACGGVRDGGALSHLLPAGRAIPNAKHRAEMEKLWGLPEGRIAPEPGYHTVALFEALG
RGDVKMIICETNPAHTLPNLNKVHKAMSHPEFIVCIEAFPDAVTLEYADLVLPFAFWCERDGVY
CGERRYSLTEKAVDPPGQCRPTVNTLVEFARRAGVDPQLVNFNAEDVWNEWRMVSKGTTYDFW
GMTRELRKESGLIWPCSEDPGTSRVRGQDPCVPADHPDRFFFGKPDGRAVIWMRPAK
>d1ad3a_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Rat (Rattus
norvegicus)}

SISDTVKRAREAFNSGKTRSLQFRIQQLEALQRMINENLKSISGALASDLGKNEWTSYEEVAHVLEE
LDTTIKELPDWAEDEPVAKTRQTQQDDLYIHSEPLGVVLVIGAWNYPFNLTIQPMVGAVAAGNAVIL
KPSEVSGHMADLLATLIPQYMDQNLVYLVVKGVPETTELLKERFDHIMYTGSTAVGKIVMAAAKHL
TPVTLELGGKSPCYVDKDCDLVACRRIAWGKFMNSGQTCVAPDYILCDPSIQNQIVEKLLKSLKDF
YGEDAKQSRDYGRIINDRHFQRVKGLIDNQVAHGGTWDQSSRYIAPTILVDVDPQSPVMQEEIFGP
VMPIVCVRSLEEAIQFINQREKPLALYVFSNNEKVIKMAIETSSGGVTANDVIVHITVPTLPGGGVGN
SGMGAYHGKKSFFETFSHRSCLVKSLNNEEAHKARYPPSPA

>d1bi9a_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Rat (Rattus norvegicus),
retinal type II}

MASLQLPSPTPNLEIKYTKIFINNEWQNSESGRVFPCNPATGEQVCEVQEADKVDIDKAVQAARL
AFSLGSVWRRMDASERGRLLDKLADLVERDRATLATMESLNGGKPFQAFYIDLQGVIKTLRYAG
WADKIHGMTIPVDGDYFTFRHEPIGVCGQIIPWNFPLLMFTWKIAPALCCGNTVVIKPAEQTPLSA
LYMGALIKEAGFPPGVVNILPGYGPTAGAAIASHIGIDKIAFTGSTEVGKLIQEAAGRSNLKRVTLLEGG
KSPNIFADADLDYAVEQAHQGVFFNQGCCTAGSRIFVEESIYEEFVKRSVERAKRRIVGSPFDPTTE
QGPQIDKKQYNKILELIQSGVAEGAKLECGGKGLGRKGFIEPTVFSNVTDDMRIAKEEIFGPVQEILR
FKTMDEVIERANNSDFGLVAAVFTNDINKALMVSSAMQAGTVWINCYNALNAQSPFGGFKMSGNG
REMGEFGLREYSEVKTVTVKIPQKNS

>d1ag8a_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Cow (Bos taurus),
mitochondrial}

VPTPNQQPEVLYNQIFINNEWHDAVSKKTFPTVNPSTGDVICHVAEGDKADVDRVKAARAAAFQLG
SPWRRMDASERGRLLNRLADLIERDRTYLAALETLDNGKPYIISYLVLDLDMVLKCLRYAGWADKY
HGKTIPIDGDYFSYTRHEPVGVCGQIIPWNFPLLMQAWKLGALATGNVVMKVAEQTPLTALYVAN
LIKEAGFPPGVVNIPGFGPTAGAAIASHEDVDKVAFTGSTEVGHLIQVAAGKSNLKRVTLEIGGKSPN
IIMSDADMWAVEQAHFALFFNQGCCAGSRTFVQEDIYAEFVRSVARAKSRVVGPNPFSRTEQG
PQVDETQFKKVLGYIKSGKEEGLKLLCGGAAADRGYFIQPTVFGDLQDGMTIAKEEIFGPVMQILKF
KSMEEVGRANNSKYGLAAAVFTKDLKANYLSQALQAGTVWVNCYDVFGAQPFGGKLSGSGRE
LGEYGLQAYTEVKTVTVRVPQKNS

>d1cw3a_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Human (Homo sapiens),
mitochondrial}

AVPAPNQQPEVFCNQIFINNEWHDAVSRKTFPTVNPSTGEVICQVAEGDKEDVDKAVKAARAAAFQL
GSPWRRMDASHRGRLNRLADLIERDRTYLAALETLDNGKPYVISYLVLDLDMVLKCLRYAGWADK
YHGKTIPIDGDFSYTRHEPVGVCGQIIPWNFPLLMQAWKLGALATGNVVMKVAEQTPLTALYVA
NLIKEAGFPPGVVNIPGFGPTAGAAIASHEDVDKVAFTGSTEIGRVIQVAAGSSNLKRVTLELGGKSP

NIIMSDADMDWAVEQAHFALFFNQGQCCAGSRTFVQEDIYDEFVRSVARAKSRVVGPNPFDKTE
QGPQVDETQFKKILGYINTGKQEGAKLLCGGGIAADRGYFIQPTVFGDVQDGMTIAKEEIFGPVMQIL
KFKTIEEVVGRANNSTYGLAAAVFTKDLKANYLSQALQAGTVWVNCYDVFGAQSPFGGYKMSGSG
RELGEYGLQAYTEVKTVTVKVPQKNS

>d1bxsa_c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Sheep (*Ovis aries*)}

DVPAPLTNLQFKYTKIFINNEWSSVSGKKFPVFNPAATEEKLCEVEEGDKEDVDKAVKAARQAFQIG
SPWRTMDASERGRLLNKLADLIERDRLLLATMEAMNGGKLFNSAYLMDLGGCIKTLRYCAGWADKI
QGRTPMDGNFFTYTRSEPVGCGQIIPWNFLLMFLWKIGPALSCGNTVVVKPAEQTPLTALHMGS
LIKEAGFPPGVNIVPGYGPTAGAAISSHMDVDKVAFTGSTEVEGKLIKEAAGKSNLKRVSLELGGKSPC
IVFADADLDNAVEFAHQGVFYHQGCCIAASRLFVEESYDEFVRRSVERAKKYVLGNPLTPGVSQGP
QIDKEQYKILDLIESGKKEGAKLECGGGPWGNKGYFIQPTVFSVTDMMRIAKEEIFGPVQQIMKFK
SLDDVIKRANNTFYGLSAGIFTNDIDKAITVSSALQSGTVWVNCYSVSAQCPFGGFKMSGNGRELG
EYGFHEYTEVKTVTIKISQKNS

>d1a4sa_c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Baltic cod (*Gadus callarias*)}

AQLVDSMPSASTGSVVVTDLDLNYWGGRIKSKDGATTEPVFEPATGRVLCQMVP CGAEEVDQAVQS
AQAAYLKWSKMAGIERSRVMLEAARIERRRDNIAKLEVINNGKTITEAEYDIDAAWQCIEYYAGLAP
TLSGQHIQLPGGAFAYTRREPLGVCAGILAWNYPFMIAAWKCAPALACGNAVVFVKPSPMTPVTGVIL
AEIFHEAGVPVGLVNVVQGAETGSLCHHPNVAKVSFTGSVPTGKKVMEMSAKTVKHVTLELGGK
SPLLIFKDCELENAVRGALMANFLTQGGVCTNGTRVVFVQREIMPQFLEEVVKRTKAIVVGDPLLTET
RMGGLISKPQLDKVLGFVAQAKKEGARVLCGGEPLTPSDPKLKNYFMSPCVLDNCRDDMTCVKEE
IFGPVMSVLPFDTEEEVLQRANNTTFGLASGVFTRDISRAHRVAANLEAGTCYINTYSISPVEVPFGG
YKMSGFGRENGQATVDYYSQLKTIVIVEMGDVDSL

>d1euha_c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {*Streptococcus mutans*}

TKQYKNYVNGEWKLSENEIKIYEPASGAELGSVPAMSTEEVDYVYASAKKAQPAWRALSYIERAAYL
HKVADILMRDKEKIGAILSKEVAKGYKSAVSEVVRTAEIINYAAEEGLRMEGEVLEGGSFEEAASKKIA
VVRREPVLVLAISPFNYPVNLGSKIAPALIAGNVIAFKPPTQGSISGLLLAEFAEAGLPAGVFNTIT
GRGSEIGDYIVEHQAVNFNFTGSTGIGERIGKMAGMRPIMLELGGKDSAIVLEDADLELTAKNIIAGA
FGYSGQRCTAVKRVLMESVADELVEKIREKVLALTIGNPEDDADITPLIDTKSADYVEGLINDANDK
GATALTEIKREGNLICPILFDKVTDMRLAWEEPFGVPLPIIRVTSVEEAIEISNKSEYGLQASIFTNDF
PRAFGIAEQLEVGTVHINNKTQRGTDNFPFLGAKKSGAGIQGVKYSIEAMTTVKS VVFDIK

>d1ez0a_c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {*Vibrio harveyi*}

TDNVFIATNAFTGEALPLAFPVHTEVEVNQAATAAAKVARDFRRLNNSKRASLLRTIASSEARSDD
IARAHLETALPEVRLTGEIARTANQLRFLADVNSGSYHQAILDTPNPTRAPLPKPDIRRQQIALGPV
AVFGASNFLAFSAAGGDTASALAAGCPVIVKGHTAHPGTSQIVAEICIEQALKQEQLPQAIFTLQGN
QRALGQALVSHPEIKAVGFTGSVGGGRALFNLAHERPEPIPFYGELGAINPTFIFPSAMRAKADLADQ
FVASMTMGCGQFCTKPGVVFALNTPETQAFIETAQSLIRQSPSTLLTPGIRDSYQSQVVSRSDDGID
VTFSQAESPCVASALFVTSSENWRKHPAWEEEEIFGPQSLIVVCENVADMLSLSEMLAGSLTATI HATE
EDYPQVSQLIPRLEEIAGRLVFNGWPTGVEVGAMVHGGPYPASTHSASTSVGAEAIHRWLRPVAYQ
ALPESLLPDSLKAENPLEIARAVDGKAA

>d1k75a_c.82.1.2 (A:) L-histidinol dehydrogenase HisD {*Escherichia coli*}

NTIIDWNSCTAEQQRQLLMRPAISASESITRTVNDILDNVKARGDEALREYSAKFDKTTVTALKVSAE
EIAAASERLSDELKQAMAVAVKNIETFHTAQKLPPVDVETQPGVRCQQVTRPVASVGLYIPGGSAPLF
STVLMLATPASIAGCKKVVLCSPPIADEILYAAQLCGVQDVFNVGGAQAIAALAFGTESVPKVDKIFG

PGNAFVTEAKRQVSQRDGAIDMPAGPSEVLVIADSGATPDFVASDLLSQAHEGPDSSQVILLTPAAD
MARRVAEAEVERQLAELPRAETARQALNASRLIVTKDLAQCEISNQYGPEHLIIQTRNARELVDSITS
AGSVFLGDWSPESAGDYASGTNHVLPPTYGYTATCSSLGLADDFQKRMTVQELSKEGFSALASTIETLAA
AERLTAHKNAVTLRVNALKEQA

>d1aco_2 c.83.1.1 (2-528) Aconitase, first 3 domains {Cow (Bos taurus)}

RAKVAMSHFEPHEYIRYDLEKNIDIVRKRLNRPLTLSEKIVYGHLLDDPANQEIERGKTYLRLRPDRV
AMQDATAQMAMLQFISSGLPKVAVPSTIHCDHLIEAQLGGKDLRRAKDINQEVYNFLATAGAKYGV
GFWRPGSGIIHQIILENYAYPGVLLIGTDSHTPNGGGLGGICIGVGGADAVDVMAGIPWELKCPKVIGV
KLTGSLSGWTSPKDVILKVAGILTVKGGTGAIVEYHGPVDSISCTGMATICNMGAEIGATTSVFPYNH
RMKKYLSKTGRADIANLADEFKDLVPSGCHYDQLIEINLSELKPHINGPFTPDLAHPVAEVGSVA
EKEGWPLDIRVGLIGSCTNSSYEDMGRSAAVAKQALAHGLKCKSQFTITPGSEQIRATIERDGYAQLV
RDVGGIVLANACGPCIGQWDRKDIKKGEKNTIVTSYRNFTGRNDANPETHAFVTSPEIVTALAIAAG
TLKFNPETDFLTGKDGKKFKLEAPDADELPRAEFDPGQDTYQHPPKDSSGQR

>d3pmga1 c.84.1.1 (A:1-190) Phosphoglucomutase {Rabbit (Oryctolagus cuniculus)}

VKIVTVKTKAYPDQKPGTSGLRKRKRVVQSSSTNYAENFIQSIISTVEPAQRQEATLVVGGDGRFYMKE
AIQLIVRIAAAANGIGRLVIGQNGILSTPAVSCIIRKIKAIIGGIILTASHNPPGGPNGDFGIKFNISNGGPAPE
AITDKIFQISKTIIEEYAIKCPDLKVDLGVLGKQQFDLENKFKPFTVEIVDS

>d3pmga2 c.84.1.1 (A:191-303) Phosphoglucomutase {Rabbit (Oryctolagus cuniculus)}

VEAYATMLRNIFDFNALKELLSGPNRLKIRIDAMHGTVVGPYVKKILCEELGAPANSAVNCVPLEDFGG
HHPDPNLTYAADLVETMKSGEHDFGAAFDGDGDRNMILGKHGFFV

>d3pmga3 c.84.1.1 (A:304-420) Phosphoglucomutase {Rabbit (Oryctolagus cuniculus)}

NPSDSVAVIAANIFSIPYFQQTGVRGFARSMPTSGALDRVANATKIALYETPTGWKFFGNLMDASKLS
LCGEESFGTGSNDHIREKDWAVLAWLSILATRKQSVEDILKDHWHKFG

>d1kfia1 c.84.1.1 (A:3-205) Exocytosis-sensitive phosphoprotein, pp63/parafusin
{Paramecium tetraurelia}

QVIPAPRVQVTQPYAGQKPGTSGLRKKVSEATQPNYLENFVQSIFNTRKDELKPKNVLFVGGDGRY
FNRQAIFSIIRLAYANDISEVHVGQAGLMSTPASSHYIRKVNNEEVGNCIGGIILTASHNPPGKHEGDFGI
KFNVRTGAPAPEDFTDQIYTHTTKIKEYLTVDYEFEKHINLDQIGVYKFEGRLEKSHFEVKVVD

>d1kfia2 c.84.1.1 (A:206-323) Exocytosis-sensitive phosphoprotein, pp63/parafusin
{Paramecium tetraurelia}

VQDYTQLMQKLFDFDLKGLFSNKDFSFRFDGMHGVAGPYAKHIFGTLGCSKESLLNCDPSEDFGG
GHPDPNLTYAHDVLELLDIHKKKDVGTVPQFGAACDGDADRNMILGRQFFV

>d1kfia3 c.84.1.1 (A:324-443) Exocytosis-sensitive phosphoprotein, pp63/parafusin
{Paramecium tetraurelia}

TPSDSLAVIAANANLIFKNGLLGAARSMPTSGALDKVAANKIKLFETPTGWKFFGNLMDAGLINLC
GEESFGTGSNDHIREKDWAVLAWLTIHAHKNKNTDHFVTVEEIVTQYWQQFG

>d1k2yx1 c.84.1.1 (X:5-154) Phosphomannomutase/phosphoglucomutase {Pseudomonas
aeruginosa}

KAPTLPASIFRAYDIRGVVGDTLTAETAYWIGRAIGSESLARGEPCVAVGRDGRLSGPELVKQLIQGLVD
CGCQVSDVGMVPTPVLYAANVLEGGKSGVMLTGAHNPPDYNGFKIVVAGETLANEQIQALRERIEKN
DLASGVGSVEQVD

>d1k2yx2 c.84.1.1 (X:155-258) Phosphomannomutase/phosphoglucomutase {Pseudomonas
aeruginosa}

ILPRYFKQIRDDIAMAKPMKVVVDCGNGVAGVIAPQLIEALGCSVIPLYCEVDGNFPNHPDPGKPEN

LKDLIAKVKAEADLGLAFDGDGDRVGVVTTNTGTII

>d1k2yx3 c.84.1.1 (X:259-367) Phosphomannomutase/phosphoglucomutase {*Pseudomonas aeruginosa*}

YPDRLMLFAKDVSRNPGADIIFDVKCTRRLIALISGYGGRPVMWKTGHSLIKKKMKETGALLAGE
MSGHVFFKERWFGFDDGIYSAARLLEILSQDQRDSEHVFSAF

>d1k2yx4 c.84.1.1 (X:368-463) Phosphomannomutase/phosphoglucomutase {*Pseudomonas aeruginosa*}

PSDISTPEINITVTEDSKFAIEALQRDAQWEGNITTLDGVRVDYPKGWGLVRASNTTPVLVLRFEA
DTEEELERIKTVFRNQLKAVDSSLPVPF

>d1fuia2 c.85.1.1 (A:1-355) L-fucose isomerase, N-terminal and second domains {*Escherichia coli*}

MKKISLPKIGIRPVIDGRRMGVRESLEEQTMMNAKATAALLTEKLRHACGAAVECVISDTCIAGMAE
AAACEEFSSQNVGLTITVTPWCYCGSETIDMDPTRPKAIWGFNGTERPGAVYLAAALAAHSQKIP
AFSIYGHVDVQDADDTSPADVEEKLLRFARAGLAVASMKGKSYLSLGGVSMGIAGSIVDHNFFESWLG
MKVQAVDMTELRRRIDQKIYDEAELEMALAWADKNFRYGEDENNKQYQRNAEQSRAVLRESLLMA
MCIRDMMQGNKSLADIGRVEESLGYNAIAAGFQQQRHWTQYPNGDTAEAILNSSFDWNGVREPF
VVATENDSLNGVAMLMGHQLTGT

>d1fw8a_ c.86.1.1 (A:) Phosphoglycerate kinase {*Baker's yeast (Saccharomyces cerevisiae)*}

SKYSLAPVAKELQSLGKDVTFNLDCVGPEVEAAVKASAPGSVILLENLRYHIEEEGSRKVDGQKVK
SKEDVQKFRHELSSLADVYINDAFGTAHRAHSSMVGFDLPQRAAGFLEKELKYFGKALENPTRPFL
AILGGAKVADKIQLIDNLLDKVDSIIIGGGMAFTFKKVLLENTEIGDSIFDKAGAEIVPKLMEKAKAGV
EVLVLPVDFIADAFSADANTKTVDKEGIPAGWQGLDNGPESRKLFAATVAKAKTIVWNGPPGVFEF
EKFAAGTKALLDEVVKSSAAGNTVIIGGGDTATVAKKYGVTDKISHVSTGGGASLELLEGGKELPGVAF
LSEKSLSSKLSVQDLDLKDKRVFIRVDFNVPLDGKKITSNQRIVAALPTIKYVLEHHPRYVVLASHL
GRPNGERN

>d1qpg_ c.86.1.1 (-) Phosphoglycerate kinase {*Baker's yeast (Saccharomyces cerevisiae)*}

SLSSKLSVQDLDLKDKRVFIRVDFNVPLDGKKITSNQRIVAALPTIKYVLEHHPRYVVLASHLQPNG
ERNEKYSAPVAKELQSLGKDVTFNLDCVGPEVEAAVKASAPGSVILLENLRYHIEEEGSRKVDGQK
VKASKEDVQKFRHELSSLADVYINDAFGTAHRAHSSMVGFDLPQRAAGFLEKELKYFGKALENPT
RPFLAILGGAKVADKIQLIDNLLDKVDSIIIGGGMAFTFKKVLLENTEIGDSIFDKAGAEIVPKLMEKAK
AKGVEVLPVDFIADAFSADANTKTVDKEGIPAGWQGLDNGPESRKLFAATVAKAKTIVWNGPPG
VFEFKFAAGTKALLDEVVKSSAAGNTVIIGGGDTATVAKKYGVTDKISHVSTGGGASLELLEGGKELP
GVAFLSEK

>d1php_ c.86.1.1 (-) Phosphoglycerate kinase {*Bacillus stearothermophilus*}

MNKKTIRDVDVRGKRVFCRVDFNVPMEQGAITDDTRIRAALPTIRYLIEHGAKVILASHLGRPKGKV
VEELRLDAVAKRLGELLERPVAKTNEAVGDEVKAAVDRLNEGDVLLLENVRFYPGEEKNDPELAKA
FAELADLYVNDAFGAHRAHASTEGIAHYLPAVAGFLMEKELEVLGKALSNPDRPFTAIIGGAKVKD
KIGVIDNLEKVDNLIIGGLAYTFVKALGHVGVKSLLEEDKIELAKSFMEKAKEKGVRFYMPVDVVV
ADRFANDANTKVVPIAIPADWSALDIGPKTRELYRDVIRESKLVVWNGPMGVFEMDAFAHGTKAI
AEALAEALDTSYVIGGGDSAAAVEKFLADKMDHISTGGGASLEFMEGKQLPGVVALEDK

>d1vpe_ c.86.1.1 (-) Phosphoglycerate kinase {*Thermotoga maritima*}

EKMTIRDVDLKGKRVIMRVDFNVPVKDGVVQDDTRIRAALPTIKYALEQGAKVILLSHLGRPKGEPS
PEFSLAPVAKRSELLGKEVKFVPAVVGDEVKAVEELKEGEVLLLENTRFHPGETKNDPELAKFWA
SLADIHVNDAFGTAHRAHASNVGIAQFIPSVAGFLMEKEIKFLSKVTYNPEKPYVVVLGGAKVSDKIG

VITNLMEKADRILIGGAMMFTFLKALGKEVGSRRVEEDKIDLAKELVEKAKEKGV EIVLPVDAVIAQK
IEPGVEKKVVRIDDGIPEGWMGLDIGPETIELFKQKLSDAKTVVWNGPMGVFEIDDFAEGTKQVALA
IAALTEKGAITVVGGGDSAAAVNKFGLKDFSHVSTGGGASLEFLEGKELPGIASMRIKKA

>d16pk_ c.86.1.1 (-) Phosphoglycerate kinase {Trypanosoma brucei}

EKKSINECDLKGKKVLIRVDFNVPVKNKGITNDYRIRSALPTLKKVLTEGGSCVLM SHLGRPKGIPMA
QAGKIRSTGGVPGFQQKATLKPVAKRLESELLRPVTFAPDCLNAADVSKMSPGDVVLLENVRFYKE
EGSKKAKDREAMAKILASYGDVYISDAFGTAHRDSATMTGIPKILGNGAAGYLMEKEISYFAKVLGNP
PRPLVAIVGGAKVSDKIQLLDNMLQRIDYLLIGGAMAYTFLKAQGY SIGKSKCEESKLEFARSLLKKA E
DRKVQVILPIDHVCHTEFKAVDSPLITEDQNIPEGHMALDIGPKTIEKYVQTIGKCKSAIWN GPMGVF
EMVPYSKGTFAIAKAMGRGTHEHGLMSIIGGGDSASAAELSGEAKRMSHVSTGGGASLELLE GKTLP
GVTVLDDK

>d1hdia_ c.86.1.1 (A:) Phosphoglycerate kinase {Pig (Sus scrofa)}

NKLTLDKLNKGVKRVVMRVDNFNPM AAAQITNNARIKAAVPSIKFCLDDGAKSVVLM SHLGRPDGS
PMPDKYSLQPVAELKSALGKAVLFLKDCVGP AVEKACADPAAGSVILLENLRFHVEE EGKGDASG
NKAAGEPAKIKAFRASLSALGDVYVND AFGTAHRAHSSMVGVNLPKKAGAF LMKKELNYFAAAAES
PERPFLAILGGAKVADKIQLINMLDKVNEMIIGGGMAFTFLKVLNNMEIGTSLFDEAGKKIVKNLM
SKAAANGVKITL PVDFVTADKFDEQAKIGQATVASGIPAGWMGLDCGPKSSAKYSEAVARAKQIVWN
GPVGVFEWEAFAQGTKALMDEVVKATSRGCIT IIGGGDTATCCA KWNTEDNVSHVSTGGGASLELLE
GKVLPGVDALSNV

>d1jixa_ c.87.1.1 (A:) beta-Glucosyltransferase (DNA-modifying) {Bacteriophage T4}

MKIAIINMGNNVINFKTVPSSETIYLFKVIS EMLNVDIISLKNGVYTKSFDEVDVNDYDR LIVVNSSI
NFFGGKPNLAILSAQKFM AKYKSKIYYLFTDIRLPFSQSWPNVKNRPWAYLYTEEELLIKSPIKVISQ G
INLDIAKAAHKKVDNVIEFEYFPIEQYKIHMND FQLSKPTKKTL DVIYGGSF RSGQRESKMVEFLFDT
GLNIEFFGNAREKQFKNPYPWTKAPVFTG KIPMNMVSEKNSQAIAALIIGDKNYNDNFITLRVWE
TMASDAVMLIDEEFDTKHRIINDARFYVNNRA ELIDRVNELKHS DVLRKEMLSIQHDILNKTRAKK
AEWQDAFKKAIDL

>d1f0ka_ c.87.1.2 (A:) Peptidoglycan biosynthesis glycosyltransferase MurG {Escherichia coli}

KRLMVMAGGTGGHVFPGLAVAHHLMAQGWQVRWLGTADRMEADLVPKHGIEIDFIRISGLRGKI
KALIAAPLRIFNAWRQARAIMKAYKPDVVLGMGGYVSGPGGLAAWSLGIPVVLHEQNGIAGLTNKW
LAKIATKVMQAFPGA FPNAEVVGNPVRTDVLALPLPQQRLAGREGPVRVLLVGGSQGARILNQTMP
QVAAKLGDSVTIWHQSGKGSQQSVEQAYAEAGQPQHKVTEFIDDMAAAYAWADV VVCRSGALTVSEI
AAAGLPALFVPFQHKDRQQYWNALPLEKAGAAKII EQPQLSVD AVANTLAGWSRETLLTMAERARA
ASIPDATERVANEVSRVARAL

>d1f6da_ c.87.1.3 (A:) UDP-N-acetylglucosamine 2-epimerase {Escherichia coli}

MKVLTVFGTRPEAIKMAPLVHALAKDPFF EAKVCVTAQHREMLDQVLKLF SIVPDYDLNIMQPGQG
LTEITCRILEGLKPILAEFKPDVVLVHGDT TTTTLATSLAAFYQRIPVGHVEAGLRTGDLYSPWPEE ANR
TLTGHLAMYHFSPTETS RQNLLRENVADSRIFITGNTVIDALLWVRDQVMSSDKLRSELAANYPFID
PDKKMILVTGHRRESFGRGFEEICHALADIATTHQDIQIVYPVHLNPNVREPVN RILGHVKNVILIDP
QEYLPFVWLMNHAWLILTDSSG IQEEAPSLGKPVLMRDTTERPEAVTAGTVRLVGTDKQRIVEEV
TRLLKDENEYQAMSRAHNPYGDGQACSRILEALKNNRISL

>d1iira_ c.87.1.5 (A:) UDP-glucosyltransferase GtfB {Amycolatopsis orientalis}

MRVLLATCGSRGDTEPLVALAVRVRDLGADVRMCAPPDCAERLAEVGVPHVPVGP SARAPIQRAKPL
TAEDVRRFTTEAIATQFDEIPAAAEGCAA VVTTGLLAAAIGVRSVAEKL GIPYFYAFHCPSYVPSPPYP

PPPLGEPSTQDTIDIPAQWERNNSAYQRYGGLNSHRDAIGLPPVEDIFTFGYTDHPWVAADPVLA
PLQPTDLDAVQTGAWILPDERPLSPELAFLDAGPPPVYLGFGSLGAPADAVRVAIDAIRAHGRRVIL
SRGWADLVLPDDGADCFAIGEVDNHQVLFGRVAAVIHHGGAGTTHVAARAGAPQILLPQMADQPYA
GRVAELGVGVAHDGPIPTFDSLAAALATALTPETHARATAVAGTIRTDGAAVAARLLLDVAVSRE

>d1em6a_ c.87.1.4 (A:) Glycogen phosphorylase {Human (Homo sapiens)}

ENVAELKKSFNRLHFTLVKDRNVATTRDYFALAHTVRDHLVGRWIRTQQHYDDKCPKRVYLSL
EFYMGRTLQNTMINLGLQNACDEAIYQLGLDIEELEEIEEDAGLNGGLGRLAACFLDSMATLGLAA
YGYGIRYEGIFNQKIRDGWQVEEADDWLRYPNPWEKSRPEFMLPVHFGYKVEHTNTGKWKWIDTQ
VVLALPYDTPVPGYMNNTVNTMRLWSARAPNDFNLRDFNVGDYIQAVLDRNLAENISRVLYPNDN
FFEGKELRLKQEFVVAATLQDIIRRFKASKFGSTRGAGTVFDFPDQVAIQLNDRNLAENISRVLYPNDN
VDIEKLPWSKAWELTQKTFAYTNHTVLPALERWVVDLVEKLLPRHLEIIEINQKHLDRIVALFPK
DVDRLRRMSLIEEESKRINMAHLCIVGSHAVNGVAKIHSDIVKTKVFKDFSELEPDKFQNKTNGITP
RRWLLLCNPLAELIAEKIGEDYVKDLSQLTKLHSLGDDVFLRELAKVKQENKLFQFLETEYKV
KINPSSMFDVQVKRIHEYKRQLLNCLHVITMYNRIKDPKLFVPRTVIIGGKAAPGYHMAKMIKLI
TSVADVNNNDPMVGSGLKLVIFLENYRVSLAEKVIPATDLSEQISTAGTEASGTGNMKFMLNGALTIGT
MDGANVEMAEAGEENLFIIFGMRIDDVAALDKKGYEKEYEALPELKLVIDQIDNGFFSPKQPDFL
KDIINMLFYHDFKVFADYEAYVKCQDKVSQLYMNPKAWNTMVLKNAASGKFSDDRTIKEYAQNI
WNVEPS

>d1a8i_ c.87.1.4 (-) Glycogen phosphorylase {Rabbit (Oryctolagus cuniculus)}

QEKRKQISVRLAGVENVTELKKNFNRLHFTLVKDRNVATPRDYFALAHTVRDHLVGRWIRTQQ
HYEYKDPKRIYYLSLEFYMGRTLQNTMVNLAENACDEATYQLGLDMEELEEIEEDAGLNGGLGR
LAACFLDSMATLGLAAYGYGIRYEFIFNQKICGGWQMEEADDWLRYPNPWEKARPEFTLPVHFGY
RVEHTSQGAKWVDTQVVLAMPYDTPVPGYRNNVNTMRLWSAKAPNDFNLKDFNVGGYIQAVLD
RNLAENISRVLYPNDNFFEGKELRLKQEFVVAATLQDIIRRFKSSKFGCRDPVRTNFDAFPDKVAIQ
LNDTHPSLAPELMRVLDLERLDWDKAWEVTVKTCAYTNHTVIPEALERWVHLLLETLLPRHLQI
IYEINQRFLNRVAAAFPGDVDRLRRMSLVEEGAVKRINMAHLCAAGSHAVNGVARIHSEILKKTIFKD
FYELEPHKFQNKTNGITPRRWLVLCNPLAELIAERIGEEYISDLQLRKLLSYVDDEAFIRDVAVK
QENKLFKFAAYLERYKVHINPNSLFDVQVKRIHEYKRQLLNCLHVITLYNRIKKEPNKFVPRTVMIG
GKAAPGYHMAKMIKLIITAIGDVVNHDPVVGDRLRVIFLENYRVSLAEKVIPAADLSEQISTAGTEASG
TGNMKFMLNGALTIGTMDGANVEMAEAGEENFFIFGMRVEDVDRLDQRGYNAQEYYDRIPELRQ
IIEQLSSGFFSPKQPDFKDIVNMLMHHDFKVFADYEYVKCQERVSALYKNPREWTRMIRNIAT
SGKFSDDRTIAQYAREIHWGVEPSRQRLP

>d1yga_ c.87.1.4 (A:) Glycogen phosphorylase {Baker's yeast (Saccharomyces cerevisiae)}

TRRLTGFLPQEIKSIDTMIPLLSRALWNKHQVKKFNKAEDFQDRFIDHVETTLARSLYNCDDMVAYE
AASMSIRDNLVIDWNKTQQKFTTRDPKRVYLSLEFLMGRALDNALINMKIEDPEDPAASKGKPRE
MIKALDELGFKLEDVLDQEPDAGLNGGLGRLAACFVDSMATEGIPAWGYGLRYEYGIFAQKIIDGY
QVETPDYWLNSGNPWEIERNEVQIPVTFYGYVDRPEGGKTTLSASQWIGGERVLAVAYDFPVPFGK
TSNVNLRLLWQARPTTEFDLNKFNNGDYKNSVAQQQRAESITAVLYPNDNFAQKELRLKQYFW
CAASLHDILRRFKSKRPWTEFPDQVAIQLNDRNLAENISRVLYPNDNFAQKELRLKQYFW
YTNHTVMQEALEKWPRLFGHLLPRHLEIIEINQKHLDRIVALFPK
MAFLAIVGSHKVNGLVHSELIKTTIFKDFIKFYGPSKFNVTNGITPRRWLQANPSLAKLISETL
NDPTEEYLLDMAKLTQLEKYVEDKEFLKKNVQVKNKIRLVDLIKKENDGVDIINREYLDLDFD
MQVKRIHEYKRQQLNVFGIYRYLAMKNMLKNGASIEEVARKYPRKVSIFGGKSAPGYMAKLIKLI
NCVADIVNNDSEIEHLLKVVVADYVNSKAEIIPASDLSEHISTAGTEASGTSNMKFVMNGGLIIGTV

DGANVEITREIGEDNVFLFGNLSERVEELRYNHQYHPQDLPSSLDSVLSYIESGQFSPENPNEFKPLV
DSIKYHGDYYLVSDDFESYLATHELVDQEFHNQRSEWLKKSVLSLANVGGFFSSDRICIEEYSDTIWNVE
PVT

>d1qm5a_ c.87.1.4 (A:) Maltodextrin phosphorylase (MALP) {*Escherichia coli*}

SQPIFNDKQFQEALSQRWQRYGLNSAAEMTPRQWWLAVSEALAEMLRAPFAKPVANQRHVNYIS
MEFLIGRLTGNNLLNLGWYQDVQDSLKAYDINLTDLLEEEIDPALGNGGLGRLAACFLDSMATVQGS
ATGYGLNYQYGLFRQSFVDGKQVEAPDDWHRSNYPWFRHNEALDVQVGIGGKVTKDGRWEPEFTI
TGQAWDLPVVGYRNGVAQPLRLWQATHAHPFDLTKFNDGDFLRAEQQGINA EKLTKVLYPNDNHT
AGKKLRLMQQYFQCACSVADILRRHHLAGRKLHELADYEVIQLNDTHPTIAIPELLRVLIDEHQMSW
DDAWAITSKTFAYTNHTLMPEALERWDVKLVKGLLPRHMQIINEINTRFKTLVEKTWPGEKVWA
KLAVVHDKQVHMANLCVVGFAVNGVAALHSDLVVKDLFPEYHQLWPNKFHNVTNGITPRRWIKQ
CNPALAAALLDKSLQKEWANDLDQLINLEKFADDAKFRDQYREIKQANKVRLAEFVKVRTGIEINPQA
IFDIQIKRLHEYKRQHLNLLHILALYKEIRENPQADRVPRVFLFGAKAAPGYLAKNIIFAINKVADVIN
NDPLVGDGLKVVFLPDYCVSAAEKLIPAADISEQISTAGKEASGTGNMKLALNGALTVGTLGDGANVEI
AEKVGEENIFIFGHTVEQVKAILAKGYDPVKWRKKDKVLDAVLKELESGKYSYDGDKHAFDQMLHSI
GKQGGDPYLVMAFVAAYVEAQKQVDVLYRDQEAWTRAILNTARCGMFSSDRSIRDYQARIWQAKR

>d4ecaa_ c.88.1.1 (A:) Asparaginase type II {*Escherichia coli*}

LPNITILATGGTIAGGDSATKSNYTVGKVGVENLVNAVPLKDIANVKGEQVVNIGSQMDMNDNVWL
TLAKKINTDCDKTDGDFVITHGVDTMEETAYFLDLTVKCDKPVVMVGAMRPSTSMSADGPFNLNAV
VTAADKASANRGLVVMNDTVLDGRDVTKTNTTVDVATFKSVNYGPLGYIHNGKIDYQRTPARKHTS
DTPFDVSKLNELPKVGIVNYANASDLPKALVDAGYDGVISAGVGNGLYKSVFDLATAAKTGTAV
VRSSRVPTGATTQDAEVD DAKYGFVASGTLNPKARVLLQLALTQTKDPQQIQIFNQY

>d1wsaa_ c.88.1.1 (A:) Asparaginase type II {*Wolinella succinogenes*}

KPQVITLATGGTIAGSGESSVKSSYSAGAVTVDKLLAAVPAINDLATIKGEQISSIGSQEMTGKVVWKL
AKRVNELLAQKETEAVIITHGTDMEETAFFLNLTVKSQKPVVVGAMRPGSSMSADGPMNLNAV
NVAINKASTNKGVVVMNDEIHAAREATKLNTTAVNAFASPNTGKIGTVYYGKVEYFTQSVRPHTLA
SEFDISKIEELPRVDILYAHPPDDTDVLVNAALQAGAKGIIHAGMGNGNPFPLTQNALEKAAKSGVVVA
RSSRVGSGSTTQAEVDDKGLGFVATESLNPKARVLLMLALTKTSDREAIQKIFSTY

>d1jsra_ c.88.1.1 (A:) Asparaginase type II {*Erwinia chrysanthemi*}

LPNIVILATGGTIAGSAATGTQTTGYKAGALGVDTLINAVPEVKKLANVKGEQFSNMASENMTGDVV
LKLSQRVNELLARDDVDGVDVITHGTDVVEESAYFLHLTVKSDKPVVFAAMRPATAISADGPMNLE
AVRVAGDKQSRGRGVMVINDRIGSARYITKTNASTLDTFRANEEGYLGVIIIGNRIYYQNRIDKLHTT
RSVFDVRGLTSLPKVDILYGYQDDPEYLYDAAIQHGVKIVYAGMGAGSVSVRGIAGMRKALEKGVVV
MRSTRTGNGIVPPDEELPGLVSDSLNPAHARILLMLALTRTSDPKVIQEFHTY

>d1agx_ c.88.1.1 (-) Glutaminase-asparaginase {*Acinetobacter glutaminasificans*}

KNNVVIVATGGTIAGAGASSTNSATYSAKVPVDALIKAVPQVNDLANITGIQALQVASESITDKELLS
LARQVNDLVKPSVNGVVITHGTDMEETAFFLNLVVHTDKPIVLVGSMPSTALSADGPLNLYSAV
ALASSNEAKNKGVMVLMNDSIFAARDVTKGINIHTHAFVSQWGALGTLVEGKPYWFRSSVKKHTN
NSEFNIEKIQGDALPGVQIVYGSNDMMPDAYQAFKAGVKAIHAGTGNGSMANYLVPEVRKLHDEQ
GLQIVRSSRVAQGFVLRNAEQPDDKYGWIAAHDLPQKARLLMALALTKTNDAKEIQNMFWNY

>d4pgaa_ c.88.1.1 (A:) Glutaminase-asparaginase {*Pseudomonas sp.*, 7A}

KLANVVILATGGTIAGAGASAANSATYQAAKVGVDKLIAGVPELADLANVRGEQVMQIASESITNDDL
LKLKGRVAELADSNVDGIVITHGTDLEETAYFLNLVQKTDKPIVVVGSMPRGTAMSADGMLNLYN
AVAVASNKDSRGGKVLVTMNDIEIQSGRDVSKSINIKTEAFKSAWGPLGMVVEGKSYWFRLPKRHT

VNSEFDIKQISSLPQVDIAYSYGNVTDTAYKALAQNGAKALIHAGTGNGSVSSRVVPALQQLRKNGTQI
IRSSHVNQGGFVLRNAEQPDDKNDWVVAHDLNPEKARILAMVAMTKTQDSKELQRIFWEY

>d1pfa_ c.89.1.1 (A:) Phosphofructokinase {Escherichia coli}

MIKKIGVLTSGGDAPGMNAAIRGVRSALTEGLEVMGIYDGYLGLYEDRMVQLDRYSVSDMINRGGT
FLGSARFPEFRDENIRAVAIENLKKRGIDALVIGGDGSYMGAMRLTEMGFPCIGLPGTIDNDIKGTD
YTIGFFTALSTVVEAIDRLRDTSSSHQRISVVEVMGRYCGDLTLAAAIAAGGCEFVVVPEVEFSREDLVN
EIKAGIAKGGKHAIVAITEHMCVDVDELAHFIEKETGRETRATVLGHIQRGGSPVPYDRILASRMGAYAI
DLLLAGYGGRCVGIQNEQLVHHDIIDAENMKRPFKGDWLDCAKKLY

>d3pfa_ c.89.1.1 (-) Phosphofructokinase {Bacillus stearothermophilus}

MKRIGVLTSGGDSPGMNAAIRSVVRKAIYHGVEVYGVYHYAGLIAGNIKKLEVGDVGDIIHRGGTILY
TARCFEFTKEEGQKKGIEQLKKGHIQGLVIGGDGSYQGAKKLTEHGFPCVGVPGTIDNDIPGTDFTIG
FDTALNTVIDAIDKIRDTATSHERTYVIEVMGRHAGDIALWSGLAGGAETILPEADYDMNDVIARLK
RGHERGKKHSIIVAEGVGSVDFGRQIQEATGFETRVTVLGHVQRGGSPAFDRVLASRLGARAVEL
LLEGKGGRCVGIQNNQLVDHDIAEALANKHTIDQRMYSKELSI

>d1cbf_ c.90.1.1 (-) Cobalt precorrin-4 methyltransferase CbiF {Bacillus megaterium}

GLVPRGSHMKLYIIGAGPGDPLITVKGLKLLQQADVLYADSLVSQDLIAKSKPGAEVLTAGMHLE
EMVGTMLDRMREGKVVVRVHTGDPAMYGAIMEQMVLLKREGVDIEIVPGVTSVFAAAAAAEALTE
IPDLTQTIVLTRAEGRTPVPEFEKLTDLAKHKCTIALFLSSTLTKKVMKEFINAGWSEDTPVVVVYKA
TWPDEKIVRTTVKDLDDAMRTNGIRKQAMILAGWALDP

>d1i74a_ c.107.1.1 (A:) Manganese-dependent inorganic pyrophosphatase (family II)
{Streptococcus mutans}

SKILVFGHQNPDSDAIGSSMAYAYLKRQLGVDAQAVALGNPNEETAFLVDYFGIQAPPVVKSAQAEGA
KQVILTDHNEFQQSIADIREVEVVEVDHHRVANFETANPLYMRLEPVGSSASSIVYRKYKENGVAIPK
EIAGVMLSGLISDTLLLKSPTHASDPVAEADLAKIAGVDLQEYGLAMLKAGTNLASKTAAQLVDIDA
KTFELNGSQVRAQVNTVDINEVLERQNEIEEAIKASQAANGYSDFVLMITDILNSNSEILALGNNTD
KVEAAFNFTLKNNAFLAGAVSRKKQVVPQLTESFNG

>d1k20a_ c.107.1.1 (A:) Manganese-dependent inorganic pyrophosphatase (family II)
{Streptococcus gordonii}

SKILVFGHQNPDSDAIGSSYAFAYLAREAYGLDTEAVALGEPNEETAFLVDYFGVAAPRVITSAKAEGA
EQVILTDHNEFQQSVADIAEVEVYGVVDHHRVANFETANPLYMRLEPVGSSASSIVYRMFKEHSVAVSK
EIAGLMLSGLISDTLLLKSPTHPTDKAIAPELAEAGVNL EEYGLAMLKAGTNLASKSAEELIDIDAK
TFELNGNNVRVAQVNTVDIAEVLERQAEIEAAIEKAIADNGYSDFVLMITDIINSNSEILAIGSNMDKV
EAAFNFLVLENNHAFLAGAVSRKKQVVPQLTESFNA

>d1k23a_ c.107.1.1 (A:) Manganese-dependent inorganic pyrophosphatase (family II)
{Bacillus subtilis}

MEKILIFGHQNPDTDTICSAIAYADLKNKLGFAEPVRLGQVNGETQYALDYFKQESPRLVETAANEV
NGVILVDHNERQQSIKDIEEVQVLEVIDHHRVANFETAEPYLYRAEPVGCTATILNKMYKENNVKIEK
EIAGLMLSIAISDLSLLFKSPTCTDQDVAAAKELAEIAGVDAEYGLNMLKAGADLSKKTVEELISLDAK
EFTLGSKKVEIAQVNTVDIEDVKKRQAELEAVISKVVAEKNDLFLLVITDILENDSLALAIAGNEAAKV
EKAFNVTLENNTALLKGVVSRKKQVVPVLTAM

>d1ayl_1 c.91.1.1 (228-540) Phosphoenolpyruvate (PEP) carboxykinase (ATP-oxaloacetate
carboxy-liase) {Escherichia coli}

IASMHCASANVGEKGDVAVFFGLSGTGKTTLSTDPKRRLIGDDEHGWDDDGVFNFEFGCYAKTIKLSK
EAEPEIYNAIRRDALLENVTVREDGTIDFDDGSKTENTRVSYPIYHIDNIVKPVSKAGHATKVIFLTAD

AFGVLPPVSRILTADQTQYHFLSGFTAKLAGTERGITEPTPTFSACFGAAFLSLHPTQYAEVLVKRMQA
AGAQAQYLVNTGWNGTGKRISIKDTRAIIDAILNGSLDNAETFTLPMFNLAIPTELPGVDTKILDPRNT
YASPEQWQEKAE TLAKLFIDNFDKYTDTPAGAALVAAGPKL

>d1ii2a1 c.91.1.1 (A:201-523) Phosphoenolpyruvate (PEP) carboxykinase (ATP-oxaloacetate
carboxy-liase) {Trypanosoma cruzi}

HLCMHASANVGKQGDVTVFFGLSGTGKTTLSADPHRNLIGDDEHVWTD RGVFNIEGGCYAKAIGLN
PKTEKDIYDAVRFGAVAENCVLDRKRTGEIDFYDESICKNTRVAYPLSHIEGALSKAIAGHPKNVIFLTN
DAFGVMPVARL TSAQAMFWFVMGYTANVPGVEAGGTRTARPIFSSCFGGPFLVRHATFYGEQLAE
KMQKHNSRVWLLNTGYAGGRADRGAKRMPLRVTRAIIDAIHDGTLDRTEYEEYPGWGLHIPKYVA
KVPEHLLNPRKAWKDVRQFNETSKELVAMFQESFSARFAAKASQEMKSAVPRYVEFA

>d1khba1 c.91.1.1 (A:260-622) Cytosolic phosphoenolpyruvate carboxykinase
(GTP-hydrolysing) {Human (Homo sapiens)}

WLAEHMLVLGITNPEGEKKYLAAAFPSACGKTNLAMMNPSLPGWKVECVGDDIAWMKFDAQGH
RAINPENGFFGVAPGTSVKTNPNAIKTIQKNTIFTNVAETSDGGVYWEGIDEPLASGVTTISWKNKE
WSSEDGEPCAHNSRFCTPASQCPIIDAAWESPEGVPIEGIIIFGGRRPAGVPLVYEALSWQHGVFVGA
AMRSEATAAAEHKGIIMHDPFAMRPFYNGFYNGKYLAHWLSMAQHAAKLPKIFHVNWFRKDKEG
KFLWPGFGENSRLVLEWMFNDRIDGKASTKLTPIGYIPKEDALNLKGLGHINMMELFISISKEFWDKEV
EDIEKYLVDQVNADLPCEIEREILALKQRISQM

>d1jb1a_ c.91.1.2 (A:) HPr kinase HprK C-terminal domain {Lactobacillus casei}

ERRSMHGVLVDIYGLGLVITGDSGVGKSETALELVQRGHRLIADDRVDVYQQDEQTIVGAAPPILSHL
LEIRGLGIIDVMNLFAGAVREDTTISLIVHLENWTPDKTFDRLGSGEQTLIFDVPVPKITVPVKVG
RNLAIHIEVAAMNFRAKSMGYDATKTFEKNLNHLIEH

>d1ayl_2 c.109.1.1 (1-227) Phosphoenolpyruvate (PEP) carboxykinase (ATP-oxaloacetate
carboxy-liase) {Escherichia coli}

MRVNGLTPQELEAYGISDVHDIYNPSYDILLYQEELDPSLTGYERGVLTNLGAVAVDTGIFTGRSPKD
KYIVRDDTTRDTFWWADKGGKNDNKPLSPETWQHLKGLVTRQLSGKRLFVVDAFCGANPDTRLS
VRFITEVAWQAHFVKNMFIRPSDEELAGFKPDFIVMNGAKCTNPQWKEQGLNSENFVAFNLTERM
QLIGGTWYGGEMKKGMFMSMMNYLLPLKG

>d1ii2a2 c.109.1.1 (A:2-200) Phosphoenolpyruvate (PEP) carboxykinase (ATP-oxaloacetate
carboxy-liase) {Trypanosoma cruzi}

PPTIHRNLLSPELVQWALKIEKDSRLTARGALAVMSYAKTGRSPLDKRIVDTDDVRENVDWGKVN
KLSEESFARVRKIAKEFLDTREHLFVVD CFAGHDERYRLKVRVFTTRPYHALFMRDMLIVPTPEELA
TFGEPDYVIYNAGECKADPSIPGLTSTTCVALNFKTREQVILGTEYAGEMKKGILTMFELMPQMN

>d1khba2 c.109.1.1 (A:10-259) Cytosolic phosphoenolpyruvate carboxykinase
(GTP-hydrolysing) {Human (Homo sapiens)}

NLSAKVVQGSLSLDPQAVREFLENNALCQPDHIHICDGSEEENGRLLGQMEEGILRRLKKYDNC
WLALDPRDVARIESKTVIVTQEQRDTVPIPKTGLSQLGRWMSEEDFEKAFNARFPGCMKGRMYY
IPFSMGLPSLSKIGIELTDSPIVVASMRIMTRMGTPVLEALGDGEFVKCLHSVGCPLPLQKPLVNN
WPCNPELTIAHLPDRREIISFGSGYGGNSLLGKKCFALRMASRLAKEEG

>d1doza_ c.92.1.1 (A:) Ferrochelatase {Bacillus subtilis}

SRKKMGLLMAYGTPYKEEDIERYTHIRGRKPEPEMLQDLKDRYEAIIGISPLAQITEQQAHNLE
QHLNEIQDEITFKAYIGLKHIEPIEDAVAEMHKDGITEAVSIVLAPHFSTFSVQSYNKRakeEAEKLG
GLTITSVESWYDEPKFVTYWVDRVKETYASMPEDERENAMLIVSAHSLPEKIKEFGDPYPDQLHESA
KLIAEGAGVSEYAVGWQSEGNTDPDWLGPVQDLTRDLFEQKGYQAFVYVPGFVADHLEVLVDND

YECKVVTDDIGASYRPEMPNAKPEFIDALATVVLLKKLGR

>d1hrka_ c.92.1.1 (A:) Ferrochelatase {Human (Homo sapiens)}

RKPKTGILMLNMGGPETLGDVHDFLLRFLDRDLMTLPIQNKLAPFIAKRLTPKIQEQYRRIGGGSPI
KIWTSKQGEQGMVKKLDELSPNTAPHKYYIGFRYVHPLTEEAIEEMERDGLERAI AFTQYPQYSCSTTG
SSLNAIYRYNQVGRKPTMKWSTIDRWPTHLLLIQCFADHILKELDHFPLEKRSEVVILFSAHSLPM
SVVNRGDPYPQEVSATVQKVMERLEYCNPYRLVWQSKVGPMPWLGQPQTDESIGLGCERGRKNILLV
PIAFTSDHIETLYELDIEYSQVLAKECGVENIRRAESLNGNPLFSKALADLVHSHIQSNELCSKQLTLCSC
PLCVNPVCRETKSFFTSQQL

>d1qgoa_ c.92.1.2 (A:) Cobalt chelatase CbiK {Salmonella typhimurium}

KKALLVVSFGTSYHDTCEKNIVACERDLAASCPDRDLFRAFTSGMIIRKLRQRDGDIDTPLQALQKL
AAQGYQDVAIQSLHIINGDEYEKIVREVQLLRPLFTRRLTLGVPLLSHNDYVQLMQALRQQMPSLRQT
EKVVFMGHGASHHAFAYACLDHMMTAQRFPARVGAVESYPEVDILIDSLRDEGVTGVHLMPLMLV
AGDHAINDMASDDGDSWKMRFNAAIPATPWLSGLGENPAIRAMFVAHLHQALNM

>d1efdn_ c.92.2.1 (N:) Periplasmic ferric siderophore binding protein FhuD {Escherichia coli}

GIDPNRIVALEWLPVELLLLALGIVPYGVADTINYRLWVSEPPPLPDSVIDVGLRTEPNLELLTEMKPSF
MVWSAGYGPSPPEMLARIAPGRGFNFSDGKQPLAMARKSLTEMADLLNLQSAAEETHLAQYEDFIRSM
KPRFVKRGARPLLLTTLIDPRHMLVFGPNSLFQEILDEYGI PNAWQGETNFWGSTAVSIDRLAAYKD
VDVLCFDHNSKMDALMATPLWQAMPFVRAGRFQRPVAVWVFGATLSAMHFVRVLDNAIG

>d1toaa_ c.92.2.2 (A:) Periplasmic zinc binding protein TroA {Treponema pallidum}

GKPLVVTTIGMIADAVKNIAQGDVHLKGLMGPGVDPHLYTATAGDVEWLG NADLILYNGLHLETKM
GEVFSKLRGSRVVAVSETIPVSQRSLSEAEFDPHVWFDVKLWSYSVKAVYESLCKLLPGKTREFTQ
RYQAYQQQLDKL DAYVRRKAQSLPAERRVLTAHDAFGYFSRAYGFEVKGLQGVSTASEASA HDMQE
LAAFIAQRKLP AIFISSIPHKNVEALRDAVQARGHVQIGGELFSDAMGDAGTSEGTYVGMVTHNID
TIVAALAR

>d1psza_ c.92.2.2 (A:) Pneumococcal surface antigen PsaA {Pneumococcus (Streptococcus pneumoniae)}

KKDTTSGQKLKVVATNSIIADITKNIAGDKIDLHSIVPIGQDPHEYEPLPEDVKKTSEADLIFYNGINL
ETGGNAWFTKLVENAKKTENKDYFAVSDGVDVIYLEGQNEKGKEDPHAWLNLENGIIFAKNIAKQL
SAKDPNNKEFEYKLNKEYTDKLDKLDKESKDKFNKIPAEKKLIVTSEGAFKYFSKAYGVPSAYIWEIN
TEEEGTPEQIKTLVEKLRQTKVPSLFEVSSVDDRPMKTVSQDTNIPYAIQIFTDSIAEQGKEGDSYSS
MMKYNLDKIAEGLAK

>d1mioa_ c.92.2.3 (A:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Clostridium pasteurianum}

SENKDEILEKYIPKTKKTRSGHIVIKTEETPNPEIVANTRTVPGIITARGCAYAGCKGVVMGPIKDMV
HITHGPIGCSFYTWGGRRF KSKPENGTGLNFNEYVFSTDMQESDIVFGGVNKLKDAIHEAYEMFHPA
AIGVYATCPVGLIGDDILAVAATASKEIGIPVHAFSCEGYKGVSSAGHHIANNTVMTDIIGKGNKEQK
KYSINVLGEYNIGDAWEMDRVLEKIGYHV NATLTGDATYEKVQNA DKADLNLVQCHR SINYIAEM
METKYGIPWIKCNFIGVDGIVETLRDMAKCFDDPELTKRTEEVI AEEIAAIQDDL DYFKEKLQGTAC
LYVGGSRSHTYMNLKSFVDSLVAGFEFAHRDDYEGREVIPTIKIDADSKNIPEITVTPDEQKYRVVI
PEDKVEELK KAGVPLSSYGGMMKEMHDG TILIDDMNHHDMEVVLEKLPDMFFAGIKEKFVIQKG
GVLSKQLHSYDYN GPYAGFRGVVNF GHELVNGIYTPAWKMITPPWKKASSES

>d1miob_ c.92.2.3 (B:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Clostridium pasteurianum}

LDATPKEIVERKALRINPAKTCQPVGAMYAALGIHNCLPHSHGSQGCCSYHRTVLSRHFKEPAMAST
SSFTEGASVFGGGSNIKTAVKNIFSLYNPDIIAVHTTCLSETLGDDLPTYISQMEDAGSIPEGKLVHTN
TPSYVGSHTVGFANMVQGIVNYLSENTGAKNGKINVIPGFVGPADMREIKRLFEMDIPYIMFPDTS
GVLGDPTTGEYKMYPEGGKIEDLKDTGNSDLTSLGYSASDLGAKTLEKKCKVPFKTLRTPIGVSAT
DEFIMALSEATGKEVPASIEEERGQLIDLMDAQQYLQGKKVALLGDPDEIILSKFIIELGAIPKYVVT
GTPGMKFQKEIDAMLAEGIEGSKVKVEGDFFDVHQWIKNEGVDLLISNTYGKFIAREENIPFVRFG
FPIMDRYGHYYPKVGKGAIRLVEEITNVILDKIERECTEEDFEVVV

>d2mina_ c.92.2.3 (A:) Nitrogenase iron-molybdenum protein, alpha and beta chains
{Azotobacter vinelandii}

SREEVESLIQEVLEVYPEKARKDRNKHLAVNDPAVTQSKKCIISNKKSQPGLMTIRGCAYAGSKGVVW
GPIKDMIHSHGPGVCGQYSRAGRNNYYIGTTGVNAFVTMNFSTDFQEKDIVFGGDKKLAKLIDEVE
TLFPLNKGISVQSECPIGLIGDDIESVSKVKAELSKTIVPVRCEGFRGVSQSLGHHIANDAVRDWVLG
KRDEDTTFASTPYDVAIIGDYNIGGDAWSSRILLEEMGLRCVAQWSGDGSSIEIELTPKVKLNLVHCYR
SMNYISRHMEEKYGIPWMEYNFFGPTKTIESLRAIAAKFDESIQKKCEEVIKYPKPEWEAVVAKYRP
RLEGKRVMLYIGGLRPRHVIGAYEDLGMEVVGTGYEFAHNDDYDRTMKEMGDSTLLYDDVTGYEFE
EFVKRIKPDIGSGIKEKFIQKMGIPFREMHSWDYSGPYHGFDFGFAIFARDMDMTLNNPCWKKLQ
APWE

>d2minb_ c.92.2.3 (B:) Nitrogenase iron-molybdenum protein, alpha and beta chains
{Azotobacter vinelandii}

SQQVDKIKASYPLFLDQDYKDMMLAKKRDGFEEKYPQDKIDEVFQWTTTKEYQELNFQREALTVNPA
KACQPLGAVLCSLGFANTLPYVHGSQGCVAIFRYSYFNHRHFREPVSVCVSDSMTEDAAVFGGQQNMKD
GLQNCKATYKPDMAVSTTCMAEVIGDDLNAFINNSKKEGFIPDEFVPPFAHTPSFVGSHTVGDWN
MFEGIARYFTLKSMDKVVGSNKKINIVPGFETYLGFRVVIKRMSEMGGVYSLSDPPEEVLDTPAD
GQFRMYAGTTQEEMKDAPNALNTVLLQPWHLEKTKKFVEGTWKHEVPKLNIPMGLDWTDEFL
MKVSEISGQPIPASLTKERGLVDMMTDSHTWLHGKRFALWGDPDFVMGLVKFLELCEPVLHLC
HNGNKRWKAVDAILAASPYGKNATVYIGKDLWHLRSLVFTDKPDFMIGNSYGGFIQRDTLHKGKE
FEVPLIRIGFPIFDRHHLHRSTTLGYEGAMQILTTLVNSILERLDEETRGMQATDYNHDLVR

>d1qgua_ c.92.2.3 (A:) Nitrogenase iron-molybdenum protein, alpha and beta chains
{Klebsiella pneumoniae}

TNATGERNLALIQEVLEVPETARKERRKHMVSDPKMKSVGKCIISNRKSQPGVMTVRGCAYAGS
KGVVFGPIKDMAHISHGPGVCGQYSRAGRNNYYTGVSGVDSFGTLNFTSDFQERDIFGGDKKLSKLI
EEMELLFPLTKGITIQSECPVGLIGDDISAVANASSKALDKPVPVVRCEGFRGVSQSLGHHIANDVVRD
WILNNREGQPFETTPYDVAIIGDYNIGGDAWASRILLEEMGLRVVAQWSGDGLVEMENTPFVKLNL
VHCYRSMNYIARHMEEKHQIPWMEYNFFGPTKIAESLRKIADQFDDTIRANAEAVIARYEGQMAAII
AKYRPRLEGRKVLVLYMGLRPRHVIGAYEDLGMEIIAAGYEFANDDYDRTLPLDKEGTLFFDASS
YELEAFVKALKPDLIGSGIKEKYIFQKMGVPPFRQMHSWDYSGPYHGYDGFDFGFAIFARDMDMTLNNPAW
NELTAPWL

>d1qgub_ c.92.2.3 (B:) Nitrogenase iron-molybdenum protein, alpha and beta chains
{Klebsiella pneumoniae}

SQTIDKINSCYPLFEQDEYQELFRNKRQLEEAHDAQRVQEVFAWTTTAEYEALNFRREALTVDPKA
CQPLGAVLCSLGFANTLPYVHGSQGCVAIFRYSYFNHRHFKEPIACVSDSMTEDAAVFGGNNMNLGL
QNASALYKPEIIAVSTTCMAEVIGDDLQAFIANAKKDGFDSSIAVPHAHTPSFIGSHVTGWDNMFEG
FAKTFTADYQGGQPKLPLNLVTFETYLGFRVVLKRMMEQMAVPCSLSDPSEVLDTPADGHYRM
YSGGTTQEMKEAPDAIDTLLLQPWQLLKSQKVVQEMWNQPATEVAIPLGLAATDELLMTVSQLSG

KPIADALTLERGRLVDMMLDSHTWLHGKFKGLYGDPDFVMGLTRFLELGCEPTVILSHNANKRWQ
KAMNKMLDASPYGRDSEVFINDLWHFRSLMFTRQPDFMIGNSYGKFIQRDTLAKGKA FEVPLIRL
GFPLFDRHHLHRQTTWGYEGAMNIVTTLVNAVLEKLDSDTSQLGKTDYSFDLVR

>d1jr2a_ c.113.1.1 (A:) Uroporphyrinogen III synthase (U3S, HemD) {Human (Homo sapiens)}

MKVLLLKDAKEDDCGQDPYIRELGLYGLEATLIPVLSFEFLSLPSFSEKLSHPEDYGGGLIFTS PRAVEA
AELCLEQNNKTEVWERSLKEKWNASVYVVG NATASLVSKIGLDTEGETCGNAEKLA EYICSRESSA
LPLLFPCGNL KREILPKALKDKGIAMESITVYQTV AHPGIQGNLNSYYSQQGVPASITFFSPSGLTYSLK
HIQELSGDNIDQIKFAAIGPTTARALAAQGLPV SCTAESPTPQALATGIRKALQ

>d2dri_ c.93.1.1 (-) D-ribose-binding protein {Escherichia coli, strain k-12}

KDTIALVVSTLNNPFFVSLKDG AQKEADKLGYNLVVLD SQNNPAKELANVQDLTVRGT KILLINPTDS
DAVGNV KMANQANIPVITLDRQATKGEV VSHIASDNVLGGKIAGDYIAKKAGEGAKVIELQGIAGTS
AARERGE GFQQA VA AHKFNVLASQPADFDRIKGLNVMQNLLTAHPDVQAVFAQNDEMALGALRAL
QTAGKSDVMVVGFDGTPDGEKAVNDGKLAATIAQLPDQIGAKGVETADKVLKGEKVQAKYPVDLKL
VVKQ

>d8abp_ c.93.1.1 (-) L-arabinose-binding protein {Escherichia coli}

NLKLGF LVKQPEEPWFQTEWKFADKAGKDLGFEVIKIAVPDGEKTLNAIDSLAASGAKGFVICTPDP
KLGSAIVAKARGYDMKVI AVDDQFVNAK GKPMDTVPLVMLAATKIGERQQELYKEMQKRGWDVK
ESAVMAITANELDTARRRTTG SMDALKAAGFPEKQIYQVPTKSN DIPGAFDAANSMLVQHPEVKHW
LIVGMNDSTVLGGV RATEGQGFKAADIIGINGVD AVSELSKAQATGFYGSLLPSPDVHGYKSEMLY
NWWAKDVEPPKFTEVTDVVLITRDNFKEELEKKGLGK

>d1rpja_ c.93.1.1 (A:) D-allose-binding protein {Escherichia coli}

AAEYAVVLKTL SNPFWVDMKKGIEDEAKTLGVSVDIFASPSEGDFQS QQLFEDLSNKNYKGI AFAPL
SSVNLVMPVARAWKKGIYLVNLDEKIDMDNLK KAGGNVEAFVTTDNVAVGAKGASFIIDKLGAEGGE
VAIEGKAGNASGEARRNGATEAFKKASQIKL VASQPADWDRIKALDVATNVLQRNPNIKAIY CANDT
MAMGVAQAVANAGKTGKVLVVGTDGIPEAR KMVEAGQMTATVAQNPADIGATGLKLMVDAEKSGK
VIPLDKAPEFKLVDSILVTQ

>d2gbp_ c.93.1.1 (-) Galactose/glucose-binding protein {Escherichia coli}

ADTRIGVTIYKYDDNFMSVVRKAIEQ DAKAAPDVQLLMNDSQNDQSKQNDQIDVLLAKGVKALAIN
LVDPAAGTVIEKARGQNPV VVFFNKEPSRKALDSYDKAYYVGTDSKESGIIQGD LIAKHWAANQG
WDLNKDGGIQFVLLKGEPGHPDAEARTTYVIKELNDKGIKTEQLQLDTAMWDTAQAKDKMDAWL
SGPNANKIEVVIANN DAMAMGAVEALKAHNKSSIPVFGVDALPEALALVKSGALAGTVLNDANNQA
KATFDLAKNLADGKGAADGTNWKIDNKVVRVPYVGV DKNLAEFSK

>d1gca_ c.93.1.1 (-) Galactose/glucose-binding protein {Salmonella typhimurium, strain lt2}

ADTRIGVTIYKYDDNFMSVVRKAIEKDGKSAPDVQLLMNDSQNDQSKQNDQIDVLLAKGVKALAIN
LVDPAAGTVIEKARGQNPV VVFFNKEPSRKALDSYDKAYYVGTDSKESGVIQGD LIAKHWAANQG
WDLNKDGGIKIYVLLKGEPGHPDAEARTTYVVKELNDKGIKTEQLALDTAMWDTAQAKDKMDAWL
SGPNANKIEVVIANN DAMAMGAVEALKAHNKSSIPVFGVDALPEALALVKSGAMAGTVLNDANNQA
KATFDLAKNLAEKGAADGTSWKIENKIVRVPYVGV DKNLSEFTQK

>d1pea_ c.93.1.1 (-) Amide receptor/negative regulator of the amidase operon (AmiC)
{Pseudomonas aeruginosa}

PLIGLLFSETGVTADIERSQRYGALLAVEQLNREGGVGRPIETLSQDPGGDPDRYRLCAEDFIRNRG
VRFLVGCYMSHTRKAVMPVVERADALLCYPTPYEGFEYSPNIVYGGPAPNQNSAPLAAYLIRHYGER
VVFIGSDYIYPRESNHVMRHLRQHGGTVLEEIYIPLYP SDDDLQRAVERIYQARADVVFSTVVGTT

AELYRAIARRYGDGRRPPIASLTTSEAEVAKMESDVAEGQVVVAPYFSSIDTPASRAFVQACHGFFPEN
ATITAWAEAAAYWQTLLLGRAAQAGNWRVEDVQRHLYDIDIDAPQGPVRRVERQNNHSRLSSRIAEI
DARGVFQVRWQSPEPIRPPDYVVVHNLDDW

>d1jx6a_ c.93.1.1 (A:) Quorum-sensing signal (autoinducer-2) binding protein LuxP {Vibrio
harveyi}

GYWGYQEFLDEFPEQRNLTNALSEAVRAQPVPLSKPTQRPIKISVVYPGQQVSDYWVRNIASF EKRL
YKLNINYQLNQVFTRPNADIKQQSLSLMEALKSKSDYLIFTLDTTRHRKFVEHVLDSTNTKLILQNIT
TPVREWDKHQPFLYVGFDAEGSRELATEFGKFFPKHTYYSVLYFSEGYISDVRGDTFIHQVNRDNN
FELQSAYYTKATKQSGYDAAKASLAKHPDVFYACSTDVALGAVDALAELGREDIMINGWGGGSAE
LDAIQKGDLDITVMRMNDDTGIAMAEAIKWLDLEDKPVPTVYSGDFEIVTKADSPERIEALKKRAFR
YSD

>d1dbqa_ c.93.1.1 (A:) Purine repressor (PurR), C-terminal domain {Escherichia coli}

KSIGLLATSEAAAYFAEIIIEAVEKNCQKGYTLILGNAWNNLEKQRAYLSMMAQKRVDGLLVMCSEYP
EPLLAMLEEYRHIPMVVMDWGEAKADFTDAVIDNAFEGGYMAGRYLIERGHREIGVIPGLERNTG
AGRLAGFMKAMEEAMIKVPESWIVQGDPEPEGYRAMQQILSQPHRPTAVFCGGDIMAMGALCAA
DEMGLRVPQDVSILGYDNVRNARYFTPALTTIHQPDKSLGETAFNMLLDRIVNKREEPQSIEVHPRLI
ERRSVADGPFDRYRR

>d1jyea_ c.93.1.1 (A:) Lac-repressor (lacR) core (C-terminal domain) {Escherichia coli}

LLIGVATSSLALHAPSQIVAAILSRADQLGASVVVSMVERSGVEACKTAVHNLLAQRVSGLIINYPLDD
QDAIAVEAACTNVPALFLDVSDQTPINSIIFSHEDGTRLGVEHLVALGHQQIALLAGPLSSVSARLRLA
GWHKYLTRNQIQPIAEREGDWSAMSGFQQTMQMLNEGIVPTAMLVANDQMALGAMRAITESGLR
VGADISVVGYYDDTEDSSCYIPPLTTIKQDFRLLGQTSVDRLQLSQGQAVKGNQLLPVSLVKKRKTTLAP

>d1tlfa_ c.93.1.1 (A:) Lac-repressor (lacR) core (C-terminal domain) {Escherichia coli}

LLIGVATSSLALHAPSQIVAAIKSRADQLGASVVVSMVERSGVEACKAAVHNLLAQRVSGLIINYPLD
DQDAIAVEAACTNVPALFLDVSDQTPINSIIFSHEDGTRLGVEHLVALGHQQIALLAGPLSSVSARLRL
AGWHKYLTRNQIQPIAEREGDWSAMSGFQQTMQMLNEGIVPTAMLVANDQMALGAMRAITESGL
RVGADISVVGYYDDTEDSSCYIPPLTTIKQDFRLLGQTSVDRLQLSQGQAVKGNQLLPVSLVKKRKTTLA
PNTQTASPRALADSLMQLARQVSRL

>d1byka_ c.93.1.1 (A:) Trehalose repressor, C-terminal domain {Escherichia coli}

SDKVVAVIIVTRLDLSENLAVQTMLPAFYEQGYDPIMMESQFSPQLVAEHLGVLKRRNIDGVVLFGFT
GITEEMLAHWQSSVLRLARDAKGFASVCYDDEGAIKILMQRLYDQGHRNISYLGVPHSVTTGKRRH
EAYLAFCKAHKLHPVAALPGLAMKQGYENVAKVITPETTALLCATDTLALGASKYLQEQRIDTLQLA
SVGNTPLMKFLHPEIVTVDPGYAEAGRQAACQLIAQVTGRSEPQQIIPATLS

>d2liv_ c.93.1.1 (-) Leucine-, isoleucine-, valine-binding (LIV) protein {Escherichia coli}

EDIKVAVVGAMSGPVAQYGDQEFTGAEQAVADINAKGGIKGNKLQIAKYDDACDPKQAVAVANKVVN
DGIKYVIGHLCSSSTQPASDIYEDEGILMITPAATAPELTARGYQLILRTTGLSDSQGPTAAKYILEKVK
PQRIAIHVHDKQYGEGLARAVQDGLKKNANVVFFDGITAGEKDFSTLVARLKKENIDFVYGGYHP
EMGQILRQARAAGLKTQFMGPEGVANVLSNIAGESAEGLLVTKPKNYDQVPANKPIVDAIKAKKQD
PSGAFVWTTTYAALQSLQAGLNQSDPAEIAKYLKANSVDTVMGPLTWDEKGLKGFEGVFDWHA
NGTATDAK

>d2lbp_ c.93.1.1 (-) Leucine-binding protein {Escherichia coli}

DDIKVAVVGAMSGPIAQWGIMEFNQAEQAIKDINAKGGIKGDKLVGVEYDDACDPKQAVAVANKIVN
DGIKYVIGHLCSSSTQPASDIYEDEGILMISPGATAPELTARGYQHIMRTAGLDSSQGPTAAKYILETVK
PQRIAIHVHDKQYGEGLARAVQDGLKKNANVVFFDGITAGEKDFSAIARLKKENIDFVYGGYYPE

MGQMLRQARSVGLKTQFMGPEGVGNASLSNIAGDAAEGMLVTMPKRYDQDPANQGIVDALKADKK
DPSGPYVWITYAAVQSLATALERTGSDEPLALVKDLKANGANTVIGPLNWDEKGLKGFDFGVFQW
HADGSSTKAK

>d1dp4a_c.93.1.1 (A:) Hormone binding domain of the atrial natriuretic peptide receptor
{Rat (*Rattus norvegicus*)}

SDLTVAVVLPLTNTSYPWSWARVGPVELALARVKARPDLLPGWTVRMVLGSSENAAGVCSDTAAP
LAAVDLKWEHSPAVFLGPGCVYSAAPVGRFTAHWVRVPLLTAGAPALGIGVKDEYALTTRTGPSHVKL
GDFVTALHRRLGWEHQALVLYADRLGDDRPCFFIVEGLYMRVRERLNITVNHQEFVEGDPDHYPKL
LRAVRRKGRVIYICSSPDAFRNLMLLALNAGLTGEDYVFFHLDVFGQSLKSAQGLVPQKPWERGDGQ
DRSARQAFQAAKIITYKEPDNPEYLEFLKQLKLLADKKFNFTVEDGLKNIIPASFDGLLLYVQAVTE
TLAQGGTVTDGENITQRMWNRSFQGVGTGYLKIDRNGDRDTRDFSLWMDMPETGAFRVVLNYNGTS
QELMAVSEHKLYWPLGYPPPDVPCGCF

>d1jdp_a_c.93.1.1 (A:) Hormone binding domain of the atrial natriuretic peptide receptor
{Human (*Homo sapiens*)}

EALPPQKIEVLVLLPQDDSYLFSLTRVRPAIEYALRSVEGNGTGRRLLPPGTRFQVAYEDSDCGNRALF
SLVDRVAAARGAKPDLILGPVCEYAAAPVARLASHWDLPMLSAGALAAGFQHKDSEYSHLTRVAPAY
AKMGEMMLALFRHHHWSRAALVYSDDKLERNCYFTLEGVHEVFQEEGLHTSIYSFDETKDLDED
IVRNIQASERVVIMCASSDTIRSIMLVHRHGMTSGDYAFFNIELFNSSSYGDGSWKRGDKHDFAKQ
AYSSLQTVTLLRRTVKPEFEKFSMEVKSSVEKQGLNMEDYVNMFVEGFHDAILLYVLALHEVLRAGYS
KKDGGKIIQQTWNRTFEGIAGQVSIDANGDRYGFVSIAMTDVEAGTQEVIGDYFGKEGRFEMRP

>d1ewka_c.93.1.1 (A:) Metabotropic glutamate receptor subtype 1 {Rat (*Rattus norvegicus*)}

RSVARMDGDVIIGALFSVHHQPPAEKVPERKCGEIREQYGIQRVEAMFHTLDKINADPVLLPNITLGS
EIRDSCWHSSVALEQSIIEFIRDSLISIRDEKDGLNRCLPDGQTLPPGRTKKPIAGVIGPGSSVAIQVN
LLQLFDIPQIAYSATSIDLSDKTLYKYFLRVVPSDTLQARAMLDIVKRYNWTYVSAVHTEGNYGESGM
DAFKELAAQEGLCIAHSKIYSNAGEKSFDRLLRKLRLRERLPKARVVVCFCEGMTVRGLLSAMRRLGV
VGEFSLIGSDGWADRDEVIEGYEVEANGGITIKLQSPVRSFDDYFLKLRDLTNTNRNPFPEFWQHR
FQCRLPGHLENPNFKVCTGNESLEENYVQDSKMGFVINAIYAMAHGLQNMHHALCPGHVGLCD
AMKPIDGRKLLDFLIKSSFVGSGEVWFDEKGDAPGRYDIMNLQYTEANRYDYVHVGTWHEGVLN
IDDYKI

>d1jeta_c.94.1.1 (A:) Oligo-peptide binding protein (OPPA) {*Salmonella typhimurium*}

ADVPAQVQLADKQTLVRNNGSEVQSLDPHKIEGVPESNVSRDLFEGLLISDVEGHPSGVAEKWENK
DFKVWTFHLRENAKWSGTPVTAHDFVYSWQRLADPNTASPYASYLQYGHIANIDDIAGKKPATD
LGVKALDDHTFEVTLSEPVYFYKLLVHPSVSPVKSAREKFGDKWTQPANIVTNGAYKLNWVVN
ERIVLERNPQYWDNAKTVINQVTYLPISSEVTDVNRYSGEIDMTYNNMPIELFQKLKKEIPNEVRV
DPYLCTYYYYEINNQKAPFNDVRVRTALKLALDRDIIVNKVKNQGDLPAYSYTPPYTDGAKLVEPEWF
KWSQQKRNEEAKKLLAEAGFTADKPLTFDLYNTSDLHKKLAIAVASIWKKNLGVNVNLENQEWK
TFLDTRHQGTDFVARAGWCADYNEPTSFLNTMLSDSSNNTAHYKSPAFDKLIADTLKVADDTQRSE
LYAKAEQQLDKDSAIVPYYYYVNARLVKPWVGGYTGKDLNIIYVKNLYIIKH

>d1pda_1_c.94.1.1 (3-219) Porphobilinogen deaminase (hydroxymethylbilane synthase),
N-terminal domain {*Escherichia coli*}

DNLVRIATRQSPLALWQAHYVKDKLMASHPLVVELVPMVTRGDVILDTPLAKVGGKGLFVKELEV
ALLENRADIHAVHSMKDVPEFPQGLGLVTICEREDPRDAFVSNNYDSLALPAGSIVGTSSLRRQCQL
AERRPDLIIRSLRGNVGTRLSKLDNGEYDAIILAVAGLKRLGLESRIRAALPPEISLPAVGQGAVGIECR
LDDSRRELLAAL

>d1lst_ c.94.1.1 (-) Lysine-,arginine-,ornithine-binding (LAO) protein {Salmonella typhimurium}

ALPQTVRIGTDTTYAPFSSKDAKGEFIGFDIDLGNEMCKRMQVKCTWVASDFDALIPSLKAKKIDAIIS
SLSITDKRQQEIAFSDKLYAADSRLIAAKGSP IPTLES LK GK HVGVLQGSTQEAYANDNWRTKGV DV
VAYANQDLIYSDLTAGRLDAALQDEVAASEGFLKQPAGKEYAFAGPSVKDKKYFGDGTGVGLRKDDT
ELKAAFDKALTEL RQDGT YDKMAKKY FDFNVYGDK

>d1sbp_ c.94.1.1 (-) Sulphate-binding protein {Salmonella typhimurium}

KDIQLLNVSYP TRELYEQYNKAFSAHWKQETGDNVVIDQSHGGSGKQATSVINGIEADTVTLALAY
DVNAIAERGRIDKNWIKRLPDD SAPYTSTIVFLVRKGNPKQIHDWNDLIKPGVSVITPNPKSSGGAR
WNYLAAWGYALHHNNNDQAKAEDFVKALFKNVEVLDSGARGSTNTFFVERGIGDVLIAWENEALLA
TNELGKDKFEIVTPSESILAEPTVSVVDKVV EKKDTKAVAEAYLK YLSPEGQEIAAKNFYRPRDADV
AKKYDDAFPKLKLFTIDEVFGGWAKAQKDH FADGGTFDQISK

>d1ixh_ c.94.1.1 (-) Phosphate-binding protein {Escherichia coli}

EASLTGAGATFPAPVYAKWADTYQKETGNKVNYQGIGSSGVKQIIANTVDFGASDAPLSDEKLAQE
GLFQFP TVIGGVVLAVNIPGLKSGELVLDGKTLGDIYLGKIKKWDDEAIAKLN PGLKLP SQNI AVRR
ADGSGTSFVFTSYLAKVNEEWKNNVGTGSTVKWPIGLGGKGN DGIAAFVQRLPGAIGYVEYAYAKQN
NLAYTKLISADGKPVSPTEENFANAAGADWSKTFAQDLTNQKGEDAWPITSTTFILIHKDKKPEQ
GTEVLKFFDWAYKTGAKQANDLDYASLPDSVVEQVRAAWKTNIKDSSGKPLY

>d3mbp_ c.94.1.1 (-) D-maltodextrin-binding protein, MBP {Escherichia coli}

KIEEGKLV I WINGDKGYNGLAEVGKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPDII FWAHDRF
GGYAQSGLLAEITPDKAFQDKLYPFTWDAVRYNGKLIAYPIAVEALS LIYNKDLLPNP PKTWEEIPAL
DKELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENGYDIKDVGV DNAGAKAGLTF LVDLIKN
KHMNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSKVNYGVTVLPTFKGQPSKPFVGVLSAGIN
AASPNKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRI AATMENAQKGEIMP NIP
QMSAFWYAVRTAVINAASGRQTVDEALKDAQTRITK

>d1elja_ c.94.1.1 (A:) D-maltodextrin-binding protein, MBP {Archaeon Pyrococcus furiosus}

MKIEEGKVVIWHAMQPNELEVFQSLAE EYMALCPEVEIVFEQKPNLE DALKAAIPTGQGPDLFIWA
HDWIGKFAEAGLLEPID EYVTE DLLNEFAPMAQDAMQYKGHYYALPFAAETVAIIYNKEMVSEPPKT
FDEMKAIMEKYYDPANEKYGI AWPINAYFISAIAQAFGGYYFDDKTEQPGLDKPETIEGFKFFFTEIW
PYMAPTGDYNTQQSIFLEGRAPMMVNGPWSINDVKKAGINFGVVPLPPIIKDGKEYWPRPYGGVKL
IYFAAGIKNKDAAWKFAKWLTTSEESIKTLALELGYIPVLT KVLD DPEIKNDPV IYGFQAVQHAYLM
PKSPKMSAVWGGVDGAIN EILQDPQNADIEGILK KYQQEILNNMQ

>d1eu8a_ c.94.1.1 (A:) D-maltodextrin-binding protein, MBP {Archaeon Thermococcus litoralis}

IEEGKIVFAVGGAPNEIEYWKGVIAEF EKYPGVTVELKRQATDTEQRRLDLVNALRGKSSDPDVFL
MDVAWLGGQFIASGWLEPLDDYVQKDN YDLSVFFQSVINLADKQGGKLYALPVYIDAGLLYR KDLLE
KYGYSKPPETWQELVEMAQKIQSGERETNP NFWGFWVWQGKQYEGLV CDFVEYVY SNGGSLGEFKD
GKWVPTLNKPENVEALQFMVDLIHKYKISPPNTYTEMTEEPVRLMFQQGNAAFERNWPYAWGLH
NADDSPVKGKGVAPLPHFPGHKSAA TLGGWHIGISKYS DNKALAWEFVKFVESYSVQKGFAMNLG
WNPGRVDVYDDPAVVS KSPHLKELRAV FENA VPRPIV PYPQLSEIIQKYVNSALAGKISPQEALDKA
QKEAEELVKQ

>d3thia_ c.94.1.1 (A:) Thiaminase I {Paenibacillus thiaminolyticus}

ITLKVAIYPYVPDPARFQA AVLDQWQRQEPGVKLEFTDWD SYADPPDDLDFVLD SIFLSHFVDAG
YLLPFGSQDIDQAEDVLPFALQGA KRNGEVYGLPQILCTNLLFYRK GDLKIGQVDNIYELYKKIGTSHS

EQIPPPQNKGLLINMAGGTTKASMYLEALIDVTGQYTEYDLLPPLDPLNDK VIRGLRLLINMAGEKP
SQYVPEDGDAYVRASWFAQGS GRAFIGYSESMRMGDYAEQVRFKPISSSAGQDIPLFYSDVVSNS
KTAHPELAKKLANVMASADTVEQALRPQADGQYPQYLLPARHQVYEALMQDYPIYSELAQIVNKPS
NRVFR LGPEVRTWLKDAKQVLPEALG

>d1mrp_ c.94.1.1 (-) Ferric-binding protein {Haemophilus influenzae}

DITVYNGQHKEAATAVAKAFEQETGIKVTLNSGKSEQLAGQLKEEGDKTPADV FYTEQTATFADLSE
AGLLAPISEQTIQQTAAQKGVPLAPKKDWIALSGRSRVVVDHTKLSEKDMEKSVLDYATPKWKGKIG
YVSTSGAFLEQVVALSKMKGDKVALNWLKGLKENGKLYAKNSVALQAVENGEVPAALINNYWYNL
AKEKGVENLKSRLYFVRHQDPGALVSYSGAAVLKASKNQAEAKFVDFLASKKQEQALVAARAEYPL
RADVVS PFNLEPYEKLEAPVVSATTAQDKEHAIKLIEEAGLK

>d1d9ya_ c.94.1.1 (A:) Ferric-binding protein {Neisseria gonorrhoeae}

DITVYNGQHKEAAQAVADAFTRATGIKVKLNCAKGDQLAGQIKEEGSRSPADV FYSEQIPALATLSAA
NLLEPLPASTINETRGKGVVAAKDWVALSGRSRVVVDTRKLSEKDLEKSVLN YATPKWKNRIGY
VPTSGAFLEQIVAIKLGEEAALKWLKGLKEYGKPYAKNSVALQAVENGEIDAALINNYWHAFAR
EKGVQNVHTRLNFRHRDPGALVTYSGAAVLKSSQNKDEAKKFVAF LAGKEGQRALTAVRAEYPLN
PHVVSTFNLEPIAKLEAPQVSATTVSEKEHATRLL EQAGMK

>d1dpe_ c.94.1.1 (-) Dipeptide-binding protein {Escherichia coli}

KTLVYCSEGSPEGFNPLFISGTTYDASSVPLYNRLVEFKIGTTEVIPGLAEKWEVSE DGKTYTFHLRK
GVKWHDNKEFKPTRELNADDVVSFDRQKNAQNPYHKVSGGSYEFEGMGLPELISEVKKVDDNT
VQFVLTRPEAPFLADLAMDFASILSKEYADAMMKAGTPEKLDLNP IGTGPFQLQYQKDSRIRYKAF
DGYWGTQKPIDTLVFSITPDASVRYAKLQKNECQVMPYPNPADIARMKQDKSINLMEMPGLNVGYL
SYNVQKKPLDDVKVRQALTYAVNKDAIKAVYQGAGVSAKNLIPPTMWGYND DVQDYTDPEKAKA
LLKEAGLEKGFSDLWAMPVQRPYNPNARRMAEMIQADWAKVGVQAKIVTYEWGEYLKRAKDGE
HQTVMMGWTGDNGDPDNFFATEFSCAASEQGSNYSKWCYKPFEDLIQPARATDDH NKRVELYKQA
QVVMHDQAPALIIAHSTVFEPVRKEVKGYVVDPLGKHHFENVSIE

>d1hsla_ c.94.1.1 (A:) Histidine-binding protein {Escherichia coli}

AIPQKIRIGTPTYAPFESKNAQGELVGFIDDLAKELCKRINTQCTFVENPLDALIPSLKAKKIDAIMSS
LSITEKRQEQEIAFTDKLYAADSRLVAKNSDIQPTVASLKGKRVGVLQGT TQETFGNEHWAPKGIEIVS
YQGQDNIYSDLTAGRIDAAFQDEVAASEGFLKQPVGKDYKFGGPAVKDEKLFVGTGMGLRKEDNEL
REALNKAF AEMRADGTYEKLAKKYFDFDVYGG

>d1pot_ c.94.1.1 (-) Spermidine/putrescine-binding protein PotD {Escherichia coli}

NNTLYFYNWTEYVPPGLLEQFTKETGIKVIYSTYESNETMYAKLKYKDGAYDLVVPSTYYYVDKMRK
EGMIQKIDKSKLTNFSNLDPDMLNKPFDPNNDYSIPYIWGATAIGVNGDAVDPKSVTSWADLWKPE
YKGSLLLTDDAREVFQMALRKLGYSGNTTDPKEIEAAYNELKKLMPNVAAFN SDNPANPYMEGEVN
LGMWNGSAFVARQAGTPIDVVWPKEGGIFWMSLAIPANAKNKEGALKLINFLLRPDVAKQVAETI
GYPTPNLAARKLLSPEVANDKTLYPDAETIKNGEWQNDVGAASSIYEEYYQKLKAG

>d1a99a_ c.94.1.1 (A:) Putrescine receptor (PotF) {Escherichia coli}

QKTLHIYNWSDYIAPD TVANFEKETGIKVVDVFD SNEVLEGKLMAGSTGFDLVVPSASFLERQLTA
GVFQPLDKSKLPEWKNLDPELLKLVAKHDPDNKFAMPYMWATTGIGYNVDKVKAVLGENAPVDS
WDLILKPENLEKLSGVSFLDAPEEVFATVLN YLGKDPNSTKADDYTG PATDLLLKL RPNIRYFHSS
QYINDLANGDICVAIGWAGDVWQASNR AKEAKNGVNVSF SIPKEGAMAFFDV FAMPADAKNKDEA
YQFLNYLLRPDVVAHISDHV FYANANKAATPLVSAEVRENPGIYPPADVRAKLF TLKVQDPKIDRVR
TRAWTKVKSG

>d1wdna_ c.94.1.1 (A:) Glutamine-binding protein {Escherichia coli}

KLVVATDTAFVPPFEFKQGDLYVGFVDLWAAIAKELKLDYELKPMDFSGIIPALQTKNVDLALAGITI
TDERKKAIDFSDGYKSGLLVMVKANNNDVKSVDLDGKVVAVKSGTGSVDYAKANIKTKDLRQFP
NIDNAYMELGTNRADAVLHDTNPNILYFIKTAGNGQFKAVGDSLEAQYGIAPFKGSDELDRKVNAL
KTLRENGTYNEIYKKWFGTEPK

>d1ftka_ c.94.1.1 (A:) Glutamate receptor ligand binding core {Rat (*Rattus norvegicus*),
GluR2}

KTVVVTTILESPYVMMKKNHEMLEGNERYEGYCVDLAAEIAKHCGFKYKLTIVGDGKYGARDADTK
IWNMGVGVGKADIAIAPLITLVREEVIDFSKPFMSLGLSISIMIKKPGTDGNPIESAEDLSKQTEIAY
GTLDSGSTKEFFRRSIAVFDKMWTYMRSAEPSVFRVTTAEGVARVRKSKGKYAYLLESTMNEYIEQ
RKPCDTMKVGGNLDKSGYGIATPKGSSLGNVNLAVLKLNEQGLLDKLNKWWYDKGEC

>d1ii5a_ c.94.1.1 (A:) Glutamate receptor ligand binding core {*Synechocystis* sp., GluR0}

GSAMALKVGVGNPPFVYFYGEGKNAAF TGISLDVWRAVAESQKWNSEYVRQNSISAGITAVAEGELD
ILIGPISVTPERAAIEGITFTQPYFSSGIGLLIPGTATPLFRSVGDLKNKEVAVVRD TTAVDWANFYQAD
VRETNNLTAATLLQKKQVEAVMFDRPALIYYTRQNPNLNLEVTEIRVSLEPYGFVLKENSPLQKTIN
VEMLNLLYSRVIAEFTERWLG

>d1amf_ c.94.1.1 (-) Molybdate-binding protein, ModA {*Escherichia coli*}

GKITVFAAASLTNAMQDIATQFKKEKGV DVVSSFASSTLARQIEAGAPADLFISADQKWMDYAVDK
KAIDTATRQTLGNSLVVAPKASVQKDF TIDSKTNWTSLLNGGRLAVGDPEHVPAGIYAKEALQKL
GAWDTLSPKLAPAEDVRGALALVERNEAPLGIVYGSDAVASKGVKVVATFPEDSHKKVEYPVAVVEG
HNNATVKAFYDYLGKGPQAAEIFKRYGFTIK

>d1atg_ c.94.1.1 (-) Molybdate-binding protein, ModA {*Azotobacter vinelandii*}

ELKVVVTATNFLGTLEQLAGQFAKQTGHAVVISSGSSGPVYAQIVNGAPYNVFFSADEKSPEKLDNQG
ALPGSRFTYAIGKLVLSAKPGLVDNQGKVLGNGWRHIAISNPQIAPYGLAGTQVLTHLGLLDKLT
QERIVEANSVQAHSQTASGAADLGFVALAQIIQAAAKIPGSHWFPPANYEPIVQQA VITKSTAEKA
NAEQFMSWMKGPKAVAIKAAGYVLPQ

>d1al3_ c.94.1.1 (-) Cofactor-binding fragment of CysB {*Klebsiella aerogenes*}

TWPKDGS LYVATHTHTQARYALPGVIKGFIERPRVSLHMHQGSPTQIAEAVSKGNADFAIATEALHLY
DDLVMPCYHWNRSIVVTPEHPLATKGSVSIEELAQYPLVTYTFGFTGRSELDTAFNRAGLTPRIVFT
ATDADVIKTYVRLGLGVGVIASMAVDPVSDPDLVKLDANGIFSHSTTKIGFRRSTFLRSYMYDFIQR
APHLTRD VVDTAVALRSNEDIEAMFKDIKLEPK

>d1i6aa_ c.94.1.1 (A:) Hydrogen peroxide-inducible genes activator OxyR, regulatory domain
{*Escherichia coli*}

ETMSGPLHIGLIPTVGPYLLPHIIPMLHQTFPKLEMYLHEAQTHQLLAQLDSGKLD AVILALVKESEA
FIEVPLFDEPMLLAIYEDHPWANREAVPMADLAGEKLLMLEDGHCLRDQAMGFCFEAGADEDTHF
RATSLETLRNMVAAGSGITLLPALAVPPERKRDRGVVYLP AIKPEPRRTIGLVYRPGSPLRSRYEQLAEA
IRARMDGHFD

>d1kwha_ c.94.1.1 (A:) Alginate-binding periplasmic protein AlgQ2 {*Sphingomonas* sp.}

KEATWVTDKPLTLKIHMFRDKWVWDENWPVAKESFRLTNVKLQSVANKAATNSQE QFNLMMA
SGDLPDVVGGDNLKDKFIQYQEGAFVPLNKLIDQYAPHIKAFFKSHPEVERAIKAPDGNIFYFIPYVP
DGVVARGYFIREDWLKKNLKPQNIDELYTVLKAFKEKDPNGNGKADEV PFIDRHPDEVFRLVNF
WGARSSGSDNYMDFYIDNGRVKHPWAETAFRDGMKHVAQWYKEGLIDKEIFTRKAKAREQMFGG
NLGGFTHDWFASMTFNEGLAKTVPGFKLIPIAPPTNSKGQRWEEDSRQKVRPDGWAITVKNKNP
VETIKFFDFYFSRPGRDISNFGVPGVTYDIKNGKAVFKDSVLKSPQPVNNQLYDMGAQIPIGFWDY
DYERQWTTPEAQAGIDMYVKGKYVMPGFEGVNM TREERAIYDKYWADVRTYMYEMGQAWVMGT

KDVDKTWDEYQRQLKLRGLYQVLQMMQQAYDRQYKN

>d1cb6a2 c.94.1.2 (A:1335-1691) Lactoferrin {Human (Homo sapiens)}

EEEVAARRARVWVCAVGEQELRKCQWSGLSEGSVTCSSASTTEDICIALVLKGEADAMSLDGGYVYT
AGKCGLVPLAENYKSSQSSDPDPCVDRPVEGYLAVAVVRRSDTSLTWNSVKGKKSCHTAVDRTAG
WNIPMGLLFNQTGSCKFDEYFSQSCAPGSDPRSNLCALCIGDEQGENKCVPNSENERYGYTGAFRCL
AENAGDVAFVKDVTVLQNTDGNNEAWAKDLKLADFALLCLDGKRKPVTEARSCHLAMAPNHAV
VSRMDKVERLQVLLHQQAKFGRNGSDCPDKFCLFQSETKNLLFNDNTECLARLHGKTTYEKYLG
QYVAGITNLKCKSTSPLEACEFLRK

>d1lct_ c.94.1.2 (-) Lactoferrin {Human (Homo sapiens)}

RSVQWCAVSNPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQAIENRADAVTLDGGFIYEAGLA
PYKLRPVAAEVYGTERRPRTHYYAVAVVKKGGSFQLNELQGLKSCHTGLRRTAGWNVPIGTLRPFLN
WTGPPEPIEAAVARFFSASCVPGADKGFQPNLCRLCAGTGENKCAFSSQEPYFSYSGAFKCLRDGAGD
VAFIRESTVFEDLSDEAERDEYELCPDNTRKPVDFKDKCHLARVPSHAVVARSVNGKEDAIWNLLR
QAQEKFGKDKSPKFQFLGSPSGQKDLLFKDSAIGFSRVPFRIDSGLYLGSYFTA

>d1lgb_ c.94.1.2 (C:) Lactoferrin {Human (Homo sapiens)}

HYYAVAVVKKGGSFQLNELQGLKSCHTGLRRTAGWNVPIGTLRPFLNWTGPPEPIEAAVARFFSASC
VPGADKGFQPNLCRLCAGTGENKCAFSSQEPYFSYSGAFKCLDGAGDVAFIRESTVFEDLSDEAERD
EYELCPDNTRKPVDFKDKCHLAR

>d1ce2a1 c.94.1.2 (A:1-333) Lactoferrin {Domestic water buffalo (Bubalus arnee bubalis)}

APRKNVRWCTISQPEWLKCHRWQWRMCKLGAAPSITCVRRASVLECIIRAITEKKADAVTLDGGMVF
EAGRPYKLRPVAAEYGTKEPQTHYYAVAVVKKGSNFQLDQLQGRNSCHTGLGRSAGWNIPMGIL
RPYLSWTESLEPLQGAFAKFFSASCVPVDRQAYPNLCQLCKGEGENQCACSPREPYFGYSGAFKCLQ
DGAGDVAFVKETTVFENLPEKADRQYELLCLNTRAPVDAFKECHLAQVPSHAVVARSVDGKEDL
IWKLLSQAQEKFGKNSGSFQFLGSPPGQRDLLFKDSALGFLRIPSKVDSALYLGSRYLTAALKNLRE

>d1ce2a2 c.94.1.2 (A:334-689) Lactoferrin {Domestic water buffalo (Bubalus arnee bubalis)}

TAAEVQARRARVWCAVGPPEEQKCKQWSQSQGIVTCATASTTDDICIALVLKGEADALSLDGGYIY
TAGKCGLVPLAENRKSSKHSLLDCVLRPTEGYLAVAVVKKANEGLTWNSLKGKKSCHTAVDRTAG
WNIPMGLIANQTGSCAFDEFFSQSCAPGADPKSRLCALCAGDDQGLDKCVPNSEKEYGYTGAFRCL
AEDVGDVAFVKNDTVWENTNGESTADWAKNLNREDFRLLCLDGTRKPVTEAQSCHLAVAPNHAV
VLSERAAHVEQVLLHQQALFGENGKNCVDFKFLKSETKNLLFNDNTECLAKLGGRPTEEYELGT
EYVTAIANLKKCSTSPLEACAFLTR

>d1b1xa1 c.94.1.2 (A:1-333) Lactoferrin {Horse (Equus caballus)}

APRKSVRWCTISPAEAAKCAKFQRNMKKVRGSPVSCIRKTSSEFCIQAIANKADAVTLDGGGLVYEAG
LHPYKLRPVAAEVYQTRGKQTRYAVAVVKKGSGFQLNQLQGVKSCHTGLGRSAGWNIPIGTLRPY
LNWTGPPEPLQKAVANFFSASCVPADGKQPNLCRLCAGTEADKACSSQEPYFGYSGAFKCLENG
AGDVAFVKDSTVFENLPDEAERDKYELCPDNTRKPVDAFKECHLARVPSHAVVARSVDGREDLIW
KLLHRAQEEFGRNKSSAFQFLGSTPGEQDLLFKDSALGFVRIPSQIDSGLYLGANYLTATQNLRE

>d1b1xa2 c.94.1.2 (A:334-689) Lactoferrin {Horse (Equus caballus)}

TAAEVAARRERVWCAVGPPEERKCKQWSDVSNRKVACASASTTEECIALVLKGEADALNLDGGFIY
VAGKCGLVPLAENQKSNAPDCVHRPPEGYLAVAVVRKSDADLTWNSLSGKKSCHTGVGRTAA
WNIPMGLLFNQTGSCKFDKFFSQSCAPGADPQSSLCALCVGNNENENKMPNSEERYGYTGAFRC
LAEKAGDVAFVKDVTVLQNTDGNSEPWAKDLKQEDFELLCLDGTRKPVAAEAESCHLARAPNHAV
VSQSDRAQHLKVLFLQDQFGGNGPDCPGKFLKSETKNLLFNDNTECLAELQGKTTYEQYLG
EYVTSITNLRRCSSPPLLEACAFLRA

>d1dtza1 c.94.1.2 (A:1-333) Lactoferrin {Arabian camel (Camelus dromedarius)}
ASKKSVRWCTTSPAESKKCAQWQRRMKKVRGPSVTCVKKTSRFECIQAISTEKADAVTLDGGGLVYD
AGLDPYKLRPIAAEVYGTENQPQTHYYAVAIKKGTNFQLNQLQGLKSCHTGLGRSAGWNIPMGLLR
PFLDWTGPPEPLQKAVAKFFSASCVPCVDGKEYPNLCQLCAGTGENKCACSSQEPYFGYSGAFKCLQ
DGAGDVAFVKDSTVFESLPAKADRDQYELLCPNNTRKPVDAFQECHLARVPSHAVVARSVNGKEDL
IWKLLVKAQEKFRGKPSAFQLFGSPAGQKDLLFKDSALGLLRIPKKIDSGLYLGSNYITAIRGLRE
>d1dtza2 c.94.1.2 (A:334-689) Lactoferrin {Arabian camel (Camelus dromedarius)}
TAAEVELRRAQVWCAVGSDEQLKCQEWSRQSNQSVVCATASTTEDCIALVLKGEADALSLDGGYIYI
AGKCGLVPLAESQSQSPSSGLDCVHRPVKGYLAVAVVRKANDKITWNSLRGKKSCHTAVDRTAGW
NIPMGPLFKD TDSCRDFEFSQSCAPGSDPRSKL CALCAGNEEGQLKCVPNSSERLYGYTGAFRCLAE
NVGDVAFVKDVTVL DNTDGGKTEQWAKDLKLGDFELLCLNGTRKPVTEAESCHLPVAPNHAVVSRI
DKVAHLRQVLLRQQAHFGRNGEDCPGKFLFQSKTKNLLFNDNTECLAKLQGKTTYDEYLG PQYVT
AIAKLRR CSTSPLEACAFLMR
>d1dot_1 c.94.1.2 (1-334) Ovotransferrin {Duck (Anas platyrhynchos)}
APPKTTVRWCTISSAEKKCNLKDHMQQERVTLSCVQKATYLDCAKISNNEADAISLDGGQVFEA
GLAPYKLPKPIAAEVYERSGGSTTSYYAVAVVKKGTDFMIKDLRGKTSCHTGLGRSAGWNIPIGTLIHR
EDIEWEGIESGISEQAVAKFFSASCVPGATIEQKLCRQCKGDAKTCLRN GPYSGYSGAFQCLKDGKG
DVAFVKHTTVQENAPEEKDEYELLCLDGSRQPVD SYKTCNWARVA AHAVVARDDSKIDDIWSFLGM
QAYSLGVDTTSD FHLFGPPGKKDPVLKDLLFKDSAIMLKRVP ELMDSQLYLGFEYYS AIQSLRKD
>d1dot_2 c.94.1.2 (335-686) Ovotransferrin {Duck (Anas platyrhynchos)}
QLTVGPRENKIQWCAVGKDEKSKDRWSVVSNGEVECTILDDNKDCIVKITKGEADAISLDGGFVYT
AGVCGLVPVVGESYED ETQCSKDEEQPAYF AVAVVKKSSAITWNNLQ GKKSCHTAVGRTAGWNIPM
GLIHNKTGSCDFDDYFSEGCAPGSPNSRLCKLCQSGENLLEKCVASSHEKYYGYTGALRCLVEQGD
VAFIKHSTVGENVSGSNKDDWAKGLTRDDFELLCTNGKRAKTM DYKTC HLAKVP THAVVARPEKA
NKIRELLEGQEKLFG LHGTEKERFMMFQSQTKDLLFKALTKCLV KLRQGITYKEFLGDEYYASVASLN
TCNPSDLLQVCTFLEDK
>d1gv8a_ c.94.1.2 (A:) Ovotransferrin {Duck (Anas platyrhynchos)}
SYYAVAVVKKGTDFMIKDLRGKTSCHTGLGRSAGWNIPIGTLIHRGDIEWEGIESGSVEQAVAKFFSAS
CVPGATTEQKLCRQCKGDAKTCLRNAPYSGYSGAFQCLKDGKGDVAFVKHTTVQENAPEEKDEYE
LLCLDGTRQPVD SYKTCNWARVAA
>d1ieja_ c.94.1.2 (A:) Ovotransferrin {Chicken (Gallus gallus)}
KSVIRWCTISSPEEKCNLRLDTQQRISLTCVQKATYLDCAKAIANNEADAITLDGGQVFEAGLAPY
KLKPIAAEVYEHTEGSTTSYYAVAVVKKGTEFTVNDLQ GKTSCHTGLGRSAGWNIPIGTLHARGAIE
WEGIESGSVEQAVAKFFSASCVPGATIEQKLCRQCKGDPKTKCARNAPYSGYSGAFHCLKDGKGDVAF
VKHTTVNENAPDQKDEYELLCLDGSRQPVDNYKTCNWARVA AHAVVARDDNKVEDIWSFLSKAQS
DFGVDTKSD FHLFGPPGKKDPVLKDLLFKDSAIMLKRVP SLMDSQLYLGFEYYS AIQSMR
>d1iq7a_ c.94.1.2 (A:) Ovotransferrin {Chicken (Gallus gallus)}
RIQWCAVGKDEKSKDRWSVVSNGDV ECTVVD ETKDCI IKIMKGEADA VALDGGGLVYTAGVCGLVPV
MAERYDDESQCSKTDERPASYFAVAVARKDSNVNWN NLKGKKSCHTAVGRTAGWVIPMGLIHNRTG
TCNFDEYFSEGCAPGSPNSRLCQLCQSGGIPPEKCVASSHEKYFGYT GALRCLVEKGDVAFIQHSTV
EENTGGKKNKADWAKNLQMDDFELLCTDGRRANVM DYREC NLAEVPTHAVVVRPEKANKIRD LLE
RQEKRFVNGSEKSKFMMFESQNKDLLFKDLTKCLFKVREGTTYKEFLGDKFYTVISSLKT CNPSDI
LQMCSFLEGG
>d1jnfa1 c.94.1.2 (A:3-334) Transferrin {Rabbit (Oryctolagus cuniculus)}

EKTVRWCAVNDHEASKCANFRDSMKKVLPEDGPRIICVKKASYLDCIKAIAAHEADAVTLDAGLVHE
AGLTPNNLKPVVAEFYGSKENPKTFYYAVALVKKGSNFQLNELQGKKSCHTGLGRSAGWNIPIGLLLC
DLPEPRKPLEKAVASFFSGSCVPCADGADFPQLCQLCPGCGCSSVQPYFGYSGAFKCLKDGLGDVAFV
KQETIFENLPSKDERDQYELLCLDNTRKPVDEYEQCHLARVPSHAVVARSVDGKEDLIWELLNQAQ
EHFGKDKSGDFQLFSSPHGKNLLFKDSAYGFFKVPPrMDANLYLGYEYVTAVRNLRGICPDP

>d1jnf2 c.94.1.2 (A:335-676) Transferrin {Rabbit (*Oryctolagus cuniculus*)}

LQDECKAVKWCALGHHERLKCDEWSVTSGGLIECESAETPEDCIAKIMNGEADAMSLDGGYVYIAG
QCGLVPVLAENYESTDCKKAPEEGYLSVAVVKKSNPDINWNNLEGGKKSCHTAVDRTAGWNIPMGLL
YNRINHCRFDEFFRQGCAPGSQKNSSLCELCVGPSVCAPNNREGYYGYTGAFRCLVEKGDVAFVKSQ
TVLQNTGGRNSEPWAKDLKEEDFELLCLDGTTRKPVSEAHNCHLAKAPNHAVVSRKDKAACVKQKL
LDLQVEFGNTVADCSSKFCMFHSKTKDLLFRDDTKCLVDRGKNTYEKYL GADYIKAVSNLRKCSTS
RLLEACTFHKH

>d1tfd_ c.94.1.2 (-) Transferrin {Rabbit (*Oryctolagus cuniculus*)}

VRWCAVNDHEASKCANFRDSMKKVLPEDGPRIICVKKASYLDCIKAIAAHEADAVTLDAGLVHEAGL
TPNNLKPVVAEFYGSKENPKTFYYAVALVKKGSNFQLNELQGKKSCHTGLGRSAGWNIPIGLLYCDLP
EPRKPLEKAVASFFSGSCVPCADGADFPQLCQLCPGCGCSSVQPYFGYSGAFKCLKDGLGDVAFVQKQ
TIFENLPSKDERDQYELLCLDNTRKPVDEYEQCHLARVPSHAVVARSVDGKEDLIWELLNQAQEHF
GKDKSGDFQLFSSPHGKNLLFKDSAYGFFK

>d1a8e_ c.94.1.2 (-) Transferrin {Human (*Homo sapiens*)}

DKTVRWCAVSEHEATKQCQFRDHMKSVIPSDGPSVACVKKASYLDCIRAIAANEADAVTLDAGLVYD
AYLAPNNLKPVVAEFYGSKEDPQTFYYAVAVVKKDSGFQMNQLRGKKSCHTGLGRSAGWNIPIGLLY
CDLPEPRKPLEKAVANFFSGSCAPCADGTDGDFPQLCQLCPGCGCSTLNQYFGYSGAFKCLKDGAGDVA
FVKHSTIFENLANKADRQYELLCLDNTRKPVDEYKDCHLAQVPSHTTVVARSMMGGKEDLIWELLNQ
AQEHFGKDKSKEFQLFSSPHGKDLLFKDSAHGFLKVPPrMDAKMYLGYEYVTAIRNLREGTC

>d1h76a1 c.94.1.2 (A:3-333) Transferrin {Pig (*Sus scrofa*)}

QKTVRWCTISNQEANKCSSFRENMSKAVKNGPLVSCVKKSSYLDCIKAIRDKEADAVTLDAGLVFEA
GLAPYNLKPVVAEFYQKDNPQTHYYAVAVVKKGSNFQWNQLQGKRSCHTGLGRSAGWIIPMGLLY
DQLPEPRKPIEKAVASFFSSSCVPCADPVNFPKLCQQCAGKGAEKACSNHEPYFGYAGAFNCLKEDA
GDVAFVKHSTVLENLPDKADRQYELLCRDNTRRPVDDYENCYLAQVPSHAVVARSVDGQEDSIWE
LLNQAQEHFGRDKSPDFQLFSSSHGKDLLFKDSANGFLKIPSKMDSLYLGYQYVTALRNREE

>d1h76a2 c.94.1.2 (A:342-687) Transferrin {Pig (*Sus scrofa*)}

ECKKVRWCAIGHEETQKCDAWSINSGGKIECVSAENTEDCIAKIVKGEADAMSLDGGYIYIAGKCLV
PVLAENYKTEGENCVNTPEKGYLAVAVVKKSSGPDLNWNNLKGKKSCHTAVDRTAGWNIPMGLLY
NKINSCKFDQFFGEGCAPGSQRNSSLCALCIGSERAPGRECLANNHERYYGYTGAFRCLVEKGDVAFV
KDQVVQNTDGNKDDWAKDLKQMDFELLCQNGAREPVDNAENCHLARAPNHAVVARDKVT
VAEELLKQQAQFGRHVTDSSSFCMFKSNTKDLLFRDDTQCLARVGKTTYESYLGADYITAVANLRK
CSTSKLLEACTFHSA

>d1afwa1 c.95.1.1 (A:25-293) Thiolase {Baker's yeast (*Saccharomyces cerevisiae*)}

KNSLLEKRPEDVVIVAANRSAIGKGFKGAFKDVNTDYLLYNFLNEFIGRFPEPLRADLNLIIEVACGN
VLNVGAGATEHRAACLASGIPYSTPFVALNRQCSSGLTAVNDIANIKIKVGQIDIGLALGVESMTNNYK
NVNPLGMISSEELQKNREAKKCLIPMGITNENVAANFKISRKQDEFAANSYQKAYKAKNEGLFEDE
ILPIKLPDGSICQSDGPRPNVTAESLSSIRPAFIKDRGTTTAGNASQVSDGVAGVLLARRSVANQ

>d1afwa2 c.95.1.1 (A:294-417) Thiolase {Baker's yeast (*Saccharomyces cerevisiae*)}

LNLPLVGRYIDFQTVGVPPEIMGVGPAYAIKPVLEATGLQVQDIDIFEINEAFAAQALYCIHKLGLDLNK

VNPRGGAIALGHPLGCTGARQVATILRELKKDQIGVVSMCIGTGMGAAAIIFIKE
>d1qfla1 c.95.1.1 (A:4-268) Biosynthetic thiolase {*Zoogloea ramigera*}
SIVIASAARTAVGSFNQAFANTPAHELGATVISAVLERAGVAAGEVNEVILGQVLPAGEGQNPARGAA
MKAGVPQEATAWGMNQLCGSGLRAVALGMQIATGDASIIVAGGMESMSMAPHCAHLRGGVKMGD
FKMIDTMIKDGLTDAFYGYHMGTTAENVAKQWQLSRDEQDAFAVASQNKAEAAQKDGFRKDEIVP
FIVKGRKGDITVDADEYIRHGATLDSMAKLRPAFDKEGTVTASNAGLNDGAAAALLMSEAEASRRG
>d1qfla2 c.95.1.1 (A:269-392) Biosynthetic thiolase {*Zoogloea ramigera*}
IQPLGRIVSWATVGVDPKVMGTGPIPASRKALERAGWKIGDLDLVEANEFAAAQACAVNKDLGWDP
SIVNVNGGAIAGHPIGASGARILNTLLFEMKRRGARKGLATLCIGGGMGVAMCIESL
>d1ek4a1 c.95.1.1 (A:1-253) Beta-ketoacyl-ACP synthase I {*Escherichia coli*}
MKRVVITGLGIVSSIGNNQEVLASLREGRSGITFSQELKDSGMRSHVWGNVKLDTTGLIDRKKVVRF
MSDASIYAFLSMEQAIADAGLSPEAYQNNPRVGLIAGSGGGSPRFQVFGADAMRGPRGLKAVGPYVV
TKAMASGVSACLATPFKIHGVNYSISSASATSAHCIGNAVEQIQLGKQDIVFAGGGEELCWEMACEFD
AMGALSTKYNDTPEKASRTYDAHRDGFVIAGGGGMVVVEELEHALARGAHI
>d1ek4a2 c.95.1.1 (A:254-406) Beta-ketoacyl-ACP synthase I {*Escherichia coli*}
YAEIVGYGATSDGADMVAPSGEGAVRCMKMAMHGVDTPIDYLNHGTSTPVGDKELAAIREVFGD
KSPAISATKAMTGHSGLAAGVQEAIYSLLMLEHGFIAPSINIEELDEQAAGLNIVTETTTDRELTVMSSN
SFGFGGTNATLVMRKLKD
>d1kas_1 c.95.1.1 (2-251) Beta-ketoacyl-ACP synthase II {*Escherichia coli*}
KRRVVVTGLGMLSPVGNTVESTWKALLAGQSGISLIDHFDTSAYATKFAGLVKDFNCEDIISRKEQRK
MDAFIQYGIVAGVQAMQDSGLEITEENATRIGAAIGSGIGGLGIEENHTSLMNGGPRKISPFVFPSTIV
NMVAGHLTIMYGLRGPISISIATACTSGVHNIGHAARIAYGDADVMVAGGAEKASTPLGVGGFGAARA
LSTRNDNPQAASRPWDKERDGFVLGDGAGMLVLEEYEHAKKRG
>d1kas_2 c.95.1.1 (252-412) Beta-ketoacyl-ACP synthase II {*Escherichia coli*}
KIYAELVGFMSDDAYHMTSPPENGAGAALAMANALRDAGIEASQIGYVNAHGTSTPAGDKAEAQAV
KTIFGEAASRVLVSSTKSMTGHLLGAAGAVESIYSILALRDQAVPPTINLDNPDEGCDLDFVPHEARQ
VSGMEYTLCSNFGFGGTNGSLIFKKI
>d1e5ma1 c.95.1.1 (A:6-255) Beta-ketoacyl-ACP synthase II {*Synechocystis* sp.}
KKRVVVTGLGAIPTIGNTLQDYWQGLMEGRNGIGPITRFDASDAQCRFGGEVKDFDATQFLDRKEA
KRMDRFCHFAVCASQQAINDAKLVINELNADEIGVLIGTGIGGLKVLEDQQTILLDKGSPRCSPFMIP
MMIANMASGLTAINLGAKPNNCTVTACAAGSNAIGDAFRLVQNGYAKAMICGGTEAAITPLSYAGFA
SARALSFRNDDPLHASRPFDKDRDGFVMGEGSGILILEELESALARGA
>d1e5ma2 c.95.1.1 (A:256-416) Beta-ketoacyl-ACP synthase II {*Synechocystis* sp.}
KIYGEMVGYAMTCDAYHITAPVPDGRGATRAIAWALKDSGLKPEMVSYINAHGTSTPANDVTETRAI
KQALGNHAYNIAVSSTKSMTGHLLGGSGGIEAVATVMAIAEDKVPPTINLENPDPECDLDYVPGQSR
ALIVDVALSNSFGFGGHNVTLAFKKYQ
>d1hnja1 c.95.1.1 (A:1-174) Ketoacyl-ACP synthase III (FabH) {*Escherichia coli*}
MYTKIIGTGSYLPEQVRTNADLEKMVDTSDEWIVTRTGIRERHIAAPNETVSTMGFEAATRAIEMAG
IEKDQIGLIVVATTSATHAFPSAACQIQSMLGKCPAFDVAAACAGFTYALSVADQYVKSGAVKYALV
GSDVLARTCDPTDRGTIIIFGDGAGAAVLAASEEPI
>d1hnja2 c.95.1.1 (A:175-317) Ketoacyl-ACP synthase III (FabH) {*Escherichia coli*}
ISTHLHADGSYGELLTLPNADRVNPNESIHLTMAGNEVFKVAVTELAHIVDETLAANNLDRSQLDWL
VPHQANLRIISATAKKGMSMDNVVVTLDHRHGNTSAASVPCALDEAVRDGRIKPGQLVLEAFGGGF
TWGSALVRF

>d1hzpa1 c.95.1.1 (A:-10-174) Ketoacyl-ACP synthase III (FabH) {Mycobacterium tuberculosis}

MTEIATTSGARVGLLSVGAYRPERVVTNDEICQHIDSSDEWIYTRTGIKTRRFAADDESAASMATEA
CRRALSNAGLSAADIDGVIVTTNTHFLQTPPAAPMVAASLGAKGILGFDLSAGCAGFGYALGAAADMI
RGGGAATMLVVGTEKLSPTIDMYDRGNCFIFADGAAAVVGETPFQGI

>d1hzpa2 c.95.1.1 (A:175-317) Ketoacyl-ACP synthase III (FabH) {Mycobacterium tuberculosis}

GPTVAGSDGEQADAIRQDIDWITFAQNPSGPRPFVRLGPAVFRWAAFKMGDVGRRAMDAAGVRP
DQIDVFVPHQANSRINELLVKNLQLRPDAVVANDIEHTGNTSAASIPLAMAELLTTGAAKPGDLALLI
GYGAGLSYAAQVVRM

>d1bi5a1 c.95.1.2 (A:1-235) Chalcone synthase {Alfalfa (Medicago sativa)}

MVSVSEIRKAQRAEGPATILAIQTANPANCVESQSTYPDFYFKITNSEHKTELKEKFQRMCDKSMIKRR
YMYLTEEILKENPNVCEYMAPSLDARQDMVVVEVPRLGKEAAVKAIKEWGPQSKITHLIVCTTSGV
DMPGADYQLTKLLGLRPYVKRYMMYQQGAFAGGTVLRLAKDLAENNKGARVLVVCSEVTAVTFRGP
SDTHLDSLVLGQALFGDGAAALIVGSDPVPEIEKP

>d1bi5a2 c.95.1.2 (A:236-389) Chalcone synthase {Alfalfa (Medicago sativa)}

IFEMVWTAQTIAPDSEGAIDGHLREAGLTFHLLKDVPGIVSKNITKALVEAFEPLGISDYNISIFWIAHP
GGPAILDQVEQKLALKPEKMNATREVLSEYGNMSSACVLFILDEMRRKSTQNGLKTTGEGLEWGV
FGFGPGLTIETVVLRSVAI

>d1ee0a1 c.95.1.2 (A:20-235) Pyrone synthase (PyS, chalcone synthase 2) {Gerbera hybrida}

GLATILAIQTATPPNCVAQADYADYYFRVTKSEHMVDLKEKFKRICEKTAIKKRYLALTEDYLQENPT
MCEFMAPSLNARQDLVVTGVPMLGKEAAVKAIDEWGLPKSKITHLIFCTTAGVDMPGADYQLVKLL
GLSPSVKRYMLYQQGAAAGGTVLRLAKDLAENNKGSRLVIVCSEITAILFHGPNENHLDSLVAQALFG
DGAAALIVGSGPHL

>d1ee0a2 c.95.1.2 (A:236-395) Pyrone synthase (PyS, chalcone synthase 2) {Gerbera hybrida}

AVERPIFEIVSTDQITLPDTEKAMKLHLREGGLTFQLHRDVPLMVAKNIENAAEKALSPLGITDWNS
VFWMVHPGGRAILDQVERKLNKEDKLRASRVLSEYGNLISACVLFIDEVVRKRSMAGKSTTGEG
LDCGVLFVFGPGMTVETVVLRSVRVT

>d1feha1 c.96.1.1 (A:210-574) Fe-only hydrogenase, catalytic domain {Clostridium pasteurianum}

HMDRVKNALNAPEKHVIVAMAPSVRASIGELFNMFGVDVTGKIYTALRQLGFDKIFDINFGADMTI
MEEATELVQRIENNGPFPMFTSCCPGWVQAENYPELLNLSAKSPQQIFGTASKTYPPSISGLDP
KNVFTVTVMPCSTSKKFEADRPQMEKDGLRDIDAVITTRERAKMIKDAKIPFAKLEDSEADPAMGEY
SGAGAIFGATGGVMEAAALRSKDFAEAELEDIEYKQVRGLNGIKEAEVEINNNKYNVAVINGASNLF
KFMKSGMINEKQYHFIEVMACHGGCVNGGGQPHVNPDKLEKVDIKKVRASVLYNQDEHLSKRKSH
ENTALVKMYQNYFGKPGEGRAHEILHFYK

>d1hfel1 c.96.1.1 (L:87-398) Fe-only hydrogenase larger subunit, C-domain {Desulfovibrio desulfuricans}

WVPEVEKCLKDGKVKCIAMPAPAVRYALGDAFGMPVGSVTTGKMLAALQKLGFAHCWDTEFTADV
TIWEEGSEFVERLTKKSDMPLPQFTSCCPGWQKYAETYPPELLPHFSTCKSPIGMNGALAKTYGAER
MKYDPKQVYTVSIMPICIAKKYEGLRPELKSSGMRDIDATLTTRELAYMIKKAGIDFAKLPDGKRDSL
MGESTGGATIFGVTGGVMEAAALRFAYEAVTGKKPDSWDFKAVRGLDGIKEATVNVGGTDVKVAVVH
GAKRFKQVCDVVKAGKSPYHFIEYMACPGGCVCVGGGQPVMPGVLEAM

>d1aln_1 c.97.1.1 (1-150) Cytidine deaminase {Escherichia coli}
MHPRFQTAFAQLADNLQSALEPILADKYFPALLTGEQVSSLKSATGLDEDALAFALLPLAAACARTPL
SNFNVGAIARGVSGTWYFGANMEFIGATMQQTVHAEQSAISHAWLSGEKALAAITVNYTPCGHCRQ
FMNELNSGLDLRIHLP

>d1aln_2 c.97.1.1 (151-294) Cytidine deaminase {Escherichia coli}
GREAHALRDYLPDAFGPKDLEIKTLLMDEQDHGYALTGDALSQAAIAAANRSHMPYSKSPSGVALEC
KDGRIFSGSYAENAAFNPPLPPLQGALILLNLKGYDYPDIQRAVLAEKADAPLIQWDATSATLKALGC
HSIDRVLLA

>d1g8ma2 c.97.2.1 (A:201-593) AICAR transformylase domain of bifunctional purine
biosynthesis enzyme ATIC {Chicken (Gallus gallus)}
GVSQPLRLRYGMNPHQSPAQLYTTTRPKLPLTVVNGSPGFINLCDALNAWQLVKELKQALGIPAAASF
HVSPAGAAVGIPLSEEEAQVCMVHDLHKTTLPLASAYARSRGADRMSSFGDFIALSDICDVPTAKIISR
EVSDGVVAPGYEEALKILSKKNGGYCVLQMDPNYEPDDNEIRTYGLQLMQKRNNAVIDRSLFKN
IVTKNKTLPESAVRDLIVASIAVKYTQNSVVCYAKDGQVIGIGAGQQSRIHCTRLAGDKANSWWLRH
HPRVLSMKFKAGVKRAEVSNAIDQYVTGTIGEDDLVKWQAMFEEVPAQLTEAEKKQWIAKLTAVS
LSSDAFFPFRDNDRAKRIGVQFIVAPSGSAADDEVVIEACNELGITLIHTNLRLFHH

>d1rgea_d.1.1.1 (A:) RNase Sa {Streptomyces aureofaciens}
DVSGTVCLSALPPEATDTLNLIASDGPFPYSQDGVVFNRESVLPTQSYGYYHEYTVITPGARTRGTR
RIITGEATQEDYYTGDHYATFSLIDQTC

>d1fus_d.1.1.1 (-) RNase F1 {Fusarium moniliforme}
ESATTCGSTNYSASQVRAAANAACQYYQNDDTAGSSTYPHTYNNYEGFDFPVDGPYQEFPIKSGGVY
TGGSPGADRVVINTNCEYAGAITHTGASGNNFVGCSTN

>d1i0va_d.1.1.1 (A:) RNase T1 {Aspergillus oryzae}
ACDYTCGSNCYSSSDVSTAQAAGYKLHEDGETVGSNSYPHKYNNYEGFDFSVSSPYEWPILSSGDVY
SGGSPGADRVVFNENNQLAGVITHTGASGNNFVECT

>d1rtu_d.1.1.1 (-) RNase U2 {Ustilago sphaerogena}
CDIPQSTNCGGNVYSNDDINTAIQALDDVANGDRPDNYPHQYYXEASEDITLCCGSGPWSEFPLVY
NGPYSSRDNYVSPGPDRVIYQNTTGEFCATVTHTGAASYDGFTQCS

>d1a2pa_d.1.1.1 (A:) Barnase/Binase {Bacillus amyloliquefaciens}
VINTFDGVADYLQTYHKLPDNYITKSEAQALGWVASKGNLADVAPGKSIGGDIFSNREGKLPKSGR
TWREADINYTSGFRNSDRILYSSDWLIYKTTDHYQTFTRIR

>d1goua_d.1.1.1 (A:) Barnase/Binase {Bacillus intermedius}
AVINTFDGVADYLIRYKRLPNDYITKSQASALGWVASKGDLAEVAPGKSIGGDVFSNREGRLPSAGSR
TWREADINYVSGFRNADRLVYSSDWLIYKTTDHYATFTRIR

>d2rbia_d.1.1.1 (A:) Barnase/Binase {Bacillus intermedius}
VINTFDGVADYLIRYKRLPNDYITKSQASALGWVASKGNLAEVAPGKSIGGDVFSNREGRLPSASGRT
WREADINYVSGFRNADRLVYSSDWLIYKTTDNYATFTRIR

>d1rds_d.1.1.1 (-) RNase Ms {Molsin (Aspergillus saitoi)}
ESCEYTCGSTCYWSSDVSAKAKGYSLYESGDTIDDPHEHYHDYEGFDFPVSGTYEYPIMSDYDVYT
GGSPGADRIVFNGDDELAVITHHTGASGDDFVACSSS

>d0rst_d.1.1.1 (-) RNase St {Streptomyces erythreus}
QAPCGDTSGFEEVRLADLPPEATDTYELIEKGGYPYPEDGTVFENREGILPDCAEGYYHEYTVKTPS
GDDRGARRFVVGDDGGEYFYTEDHYESFRLTIVN

>d1aqza_d.1.1.1 (A:) Ribotoxin {Fungus (Aspergillus restrictus), restrictocin}

ATWTCINQQLNPKTNKWEDKRLLYSQAKAESNSHHAPLSDGKTGSSYPHWFTNGYDGNGLIKGR
TPIKFGKADCDRPPKHSQNGMGKDDHYLLEFPTFPDGHDKFDSKPKENPGPARVIYTYPNKVFC
GIVAHQRGNQGDRLRCSH

>d1de3a_d.1.1.1 (A:) Ribotoxin {Fungus (*Aspergillus giganteus*), alpha-Sarcin}

AVTWTCLNDQKNPKTNKYETKRLLYNQKAESNSHHAPLSDGKTGSSYPHWFTNGYDGDGKLPK
GRTPIKFGKSDCDRPPKHSKDGNGKTDHYLLEFPTFPDGHDKFDSKPKENPGPARVIYTYPNKV
FCGIIAHTKENQGELKLC SH

>d1cnsa_d.2.1.1 (A:) Plant class II chitinase {Barley (*Hordeum vulgare*)}

SVSSIVSRAQFDRMLLRNDGACQAKGFYTYDAFVAAAAAFSGFGTTGSADVQKREVA AFLAQT SHE
TTGGWATAPDGAFAWGYCFKQERGASSDYCTPSAQWPCAPGKRYGRGPIQLSHNYNYGPAGRAIG
VDLLANPDLVATDATVSFKTAMWFWMTAQP PKSSHAVIVGQWSPSGADRAAGRVPGFGVITNIIN
GGIECGHGQDSRVADRIGFYKRYCDILGVGYGNLDCYSQRPFA

>d1dxja_d.2.1.1 (A:) Plant class II chitinase {Jack bean (*Canavalia ensiformis*)}

DVGSVIDASLFDQLLKH RNDPAC EGKGFYSYNAFVTAARSFGGFGTTGDTNTRKREVA AFLAQT SHE
TTGGAAGSPDGPYAWGYCFVTERDKSNKYCDPGT PCPAGKSYGRGPIQLTHNYNYA QAGRALGV DL
INNPDLVARDAVISFKTAIWFWMT PQGNKPSCHDVITNRWTPSAADVAANRTPGFGVITNIINGGIE
CGRGPSPASGDRIGFYKRYCDVLHLSYGNLNCRDQRPF GG

>d1lsg_1 d.2.1.2 (1-144) Lysozyme {Chicken (*Gallus gallus*)}

MKVFGRC ELAAAMKRHGLDN YRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWW
CNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCR L
QQHHLGGAKQAGDV

>d3lzt_d.2.1.2 (-) Lysozyme {Chicken (*Gallus gallus*)}

KVFGRC ELAAAMKRHGLDN YRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWC
NDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCR L

>d1jse_d.2.1.2 (-) Lysozyme {Turkey (*Meleagris gallopavo*)}

KVYGRCELAAAMKRLGLDN YRGYSLGNWVCAAKFESNFNT THATNRNTDGSTDYGILQINSRWWC N
DGRTPGSKNLCNIPCSALLSSDITASVNCAKKIASGGNGMNAWVAWRNRCKGTDVHAWIRGCR L

>d1hhl_d.2.1.2 (-) Lysozyme {Guinea fowl (*Numida meleagris*)}

KVFGRC ELAAAMKRHGLDN YRGYSLGNWVCAAKFESNFNSQATNRNTDGSTDYGV LQINSRWWC
NDGRTPGSRNLCNIPCSALQSSDITATANCAKKIVSDGDGMNAWVAWRKHCKGTDV RVVWIKGCR L

>d1ghla_d.2.1.2 (A:) Lysozyme {Pheasant (*Phasianus colchicus*)}

GKVYGRCELAAAMKRMGLDN YRGYSLGNWVCAAKFESNFNTGATNRNTDGSTDYGILQINSRWW
CNDGRTPGSKNLCHIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRKHCKGTDVNVWIRGCR L

>d1jsf_d.2.1.2 (-) Lysozyme {Human (*Homo sapiens*)}

KVFERCELARTLKR LGMDGYRGISLANWMCLAKWESGYNTRATNYNAGDRSTDYGIFQINSRYWC
NDGKTPGAVNACHLSCSALLQDN IADAVACAKRVVRDPQGIRAWVAWRNR CQNRDVRQYVQGGCV

>d2eql_d.2.1.2 (-) Lysozyme {Horse (*Equus caballus*), milk}

KVFSKCEL AHKLAQEMDGF GGYS LANWVCM AEYESNFNTRAFNGKNANGSSDYGLFQLNNKWW
CKDNKRSSSNACNIMCSKLLDENIDDDISCAKRVVRDPKGMSAWKAWVKHCKDKDLSEYLASCNL

>d1qqya_d.2.1.2 (A:) Lysozyme {Dog (*Canis familiaris*), milk}

MKIFSKCELARKL KSMGMDGF HGYS LANWVCM AEYESNFNTQAFNGRNSNGSSDYGIFQLNSKW
WCKSNSHSSANACNIMCSKFLDDNIDDDIACAKRVVKDPNGMSAWVAWVKHCKGKDL SKYLASCN

L

>d1jug_d.2.1.2 (-) Lysozyme {Australian echidna (*Tachyglossus aculeatus*)}

KILKKQELCKNLVAQGMNGYQHITLPNWVCTAFHESSYNTRATNHNTDGSTDYGILQINSRYWCHD
GKTPGSKNACNISCCKLLDDITDDLKCAKKIAGEAKGLTPWVAVWKSCKRGHDLSKFKC
>d1lmq_ d.2.1.2 (-) Lysozyme {Rainbow trout (Oncorhynchus mykiss)}
KVYDRCELARALKASGMDGYAGNSLPNWVCLSKWESSYNTQATNRNTDGSTDYGIFQINSRYWCD
DGRTPGAKNVCGIRCSQLLTDLTVAIRCAKRVVLDPNGIGAWVAVRLHCQNQDLRSYVAGCGV
>d1gd6a_ d.2.1.2 (A:) Lysozyme {Silkworm (Bombyx mori)}
KTFTRCGLVHELKRGHGFEEENLMRNWVCLVEHESSRDTSK'TNTNRNGSKDYGLFQINDRYWCSKGA
SPGKDCNVKCSLLTDDITKAAKCAKKIYKRHRFDAWYGWKNHCQGSLPDISSC
>d1iiza_ d.2.1.2 (A:) Lysozyme {Tasar silkworm (Antheraea mylitta)}
KRFTRCGLVNELRKQGFENLMRDWVCLVENESARYTDKIANVNKNGSRDYGLFQINDKYWCSKG
STPGKDCNVTCSQLLTDITVASTCAKKIYKRTKFDASGWDNHCNHSNPDISSC
>d1alc_ d.2.1.2 (-) alpha-Lactalbumin {Baboon (Papio cynocephalus)}
KQFTKCELSQNLIDIDYGRALPELICTMFHTSGYDTQAIVENDESTYGLFQISNALWCKSSQPQS
RNICDITCDKFLDDDITDDIMCAKKILDIKGIDYWIAHKALCTEKLEQWLCEK
>d1b9oa_ d.2.1.2 (A:) alpha-Lactalbumin {Human (Homo sapiens)}
KQFTKCELSQLLKIDIDYGGIALPELICTMFHTSGYDTQAIVENDESTYGLFQISNKLWCKSSQVPQS
RNICDISCDKFLDDDITDDIMCAKKILDIKGIDYWLAAHKALCTEKLEQWLCEKL
>d1hfx_ d.2.1.2 (-) alpha-Lactalbumin {Guinea pig (Cavia porcellus)}
KQLTKCALSHELNDLAGYRDITLPEWLCIIFHISGYDTQAIKNSDHKEYGLFQINDKDFCESSTTVQS
RNICDISCDKLLDDDITDDIMCVKILDIKGIDYWLAAHKPLCSKLEQWYCEAQ
>d1fkqa_ d.2.1.2 (A:) alpha-Lactalbumin {Goat (Capra hircus)}
MEQLTKCEVFQKLKDLKDYGGVSLPEWVCVAFHTSGYDTQAIQNNDESTYGLFQINNKIWCKDDQ
NPHSRNICNISCDFLDDDITDDIVCAKKILDKVGINYWLAHKALCSEKLDQWLCEKL
>d1f6ra_ d.2.1.2 (A:) alpha-Lactalbumin {Cow (Bos taurus)}
EQLTKCEVRFELKDLKGYGGVSLPEWVCTTFHTSGYDTQAIQNNDESTYGLFQINNKIWCKDDQN
PHSSNICNISCDFLDDDITDDIMCVKILDIKVGINYWLAHKALCSEKLDQWLCEKL
>d1j8wa_ d.2.1.2 (A:) alpha-Lactalbumin {Mouse (Mus musculus)}
TELTCKVSHAIKMDGYQGISLLEWTCVLFHTSGYDSQAVVNDNGSTEYGLFQISERFWCKSSSEFP
ESENICGISCDFLDDDELDDIVCAKKIVAIGIDYWKAYKPMCEKLEQWRCEKP
>d169la_ d.2.1.3 (A:) Phage T4 lysozyme {Bacteriophage T4}
MNIFEMLRIDEGLRLKIYKDTEGYTIGIGHLLTKSPSLNAAKSELDKAIGRNCNGVITKDEAEKLFN
QDVDAAVRGILRNAKLPVYDSLDAVRRCALINMVFQMGETGVAGFTNSLRMLQQKRWDAAAAAL
AAAAWAAATPNRAKRVTTFRTGTWDAYK
>d174la_ d.2.1.3 (A:) Phage T4 lysozyme {Bacteriophage T4}
MNIFEMLRIDEGLRLKIYKDTEGYTIGIGHLLAAAADLAAAKAALAAAIGRNTNGVITKDEAEKLF
NQDVDAAVRGILRNAKLPVYDSLDAVRRRAALINMVFQMGETGVAGFTNSLRMLQQKRWDEAAVN
LAKSRWYNQTPNRAKRVTTFRTGTWDAYKNL
>d176la_ d.2.1.3 (A:) Phage T4 lysozyme {Bacteriophage T4}
MNIFEMLRIDEGLRLKIYKDTEGYTIGIGHLLTKVDGNSNAAKSELDKAIGRNTNGVITKDEAEKLFN
QDVDAAVRGILRNAKLPVYDSLDAVRRRAALINMVFQMGETGVAGFTNSLRMLQQKRWDEAAVNL
AKSRWYNQTPNRAKRVTTFRTGTWDAYKNL
>d189l_ d.2.1.3 (-) Phage T4 lysozyme {Bacteriophage T4}
MNLFEMLRIDEGLRLKIYKDTEGYTIGIGHLLTKSPDLNVAKSELDKAIGRNCNGVITKDEAEKLFN
QDVDAAVRGILRNPKLPVYDSLDAVRRCALINMVFQMGETGVAGFTDSLRLMLQQKRWDEAAANL

AKSRWYNQTPDRAKRVITTFRTGTWDAYKNL
>d191l_ d.2.1.3 (-) Phage T4 lysozyme {Bacteriophage T4}
MNIFEMLRIDEGLRLKIYKDTEGYTIGIGHLLTKSPSLNAAKSELDKAIGRACAGAITKDEAEKLFNQ
DVDAAVRGILRNAKLKPVYDSLDAVRRCALINMVFQMGETGVAGFTNSLRMLQQKRWDAAAAALA
KSRWYNQTPNRAKRVITTFRTGTWDAYK
>d192l_ d.2.1.3 (-) Phage T4 lysozyme {Bacteriophage T4}
MNIFEMLRIDEGLRLKIYKDTEGYTIGIGHLLTKSPSLAAAKAALAAAIGRNTNGVITKDEAEKLFN
QDVDAAVRGILRNAKLKPVYDSLDAVRRALINMVFQMGETGVAGFTNSLRMLQQKRWAAAAAAL
AKSRWYNQTPNRAKRVITTFRTGTWDAYK
>d217l_ d.2.1.3 (-) Phage T4 lysozyme {Bacteriophage T4}
MNIFEMLRIDEGLRLKIYKDTEGYTIGIGHLLTKSPSLNAAKEELDKAIGRNTNGVITKDEAEKLFN
QDVDAAVRGILRNAKLKPVYDSLDAVRRALINMVFQMGETGVAGFTNSLRMLQQKRWDEAAVNL
AKSRWYNQTPNRAKRVITTFRTGTWDAYK
>d1k28a3 d.2.1.3 (A:130-345) Tail-associated lysozyme gp5, catalytic domain
{Bacteriophage T4}
NVLNQGGEVGYDSSSNVIQDSNLDTAINPDDRPLSEIPTDDNPNSMAEMLRRDEGLRLKVYWDT
EGYPTIGIGHLIMKQPVRDMAQINKVLSKQVGREITGNPGSITMEEATTLFERDLADMQRDIKSHSK
VGPVWQAVNRSRQMALENMAFQMGVGGVAKFNTMLTAMLAGDWEKAYKAGRDSLWYQQTKGRA
SRVTMIILTGNLESYGVEVKT
>d1am7a_ d.2.1.4 (A:) Lambda lysozyme {Bacteriophage lambda}
MVEINNQRKAFLDMLAWSEGTDNGRQKTRNHGYDVIVGGELFTDYSHPKLVTLNPKLKSTGAG
RYQLLSRWWDAYRKQLGLKDFSPKSQDAVALQQIKERGALPMIDRGDIRQAIDRCSNIWASLPGAGY
GQFEHKADSLIAKFKEAGGTVR
>d153l_ d.2.1.5 (-) Lysozyme {Goose (Anser anser anser)}
RTDCYGNVNRIDTTGASCKTAKPEGLSYCGVSASKKIAERDLQAMDRYKTIHKVGEKLCVEPAVIAGI
ISRESHAGKVLKNGWGDGRNGFGLMQVDKRSKPKQGTWNGEVHITQGTTLINFIKTIQKKFPSWT
KDQQKGGISAYNAGAGNVRSYARMDIGTTHDDYANDVVARAQYKQHG
>d1qsaa2 d.2.1.6 (A:451-618) 70 kDa soluble lytic transglycosylase, SLT70 {Escherichia coli}
LAYNDLFKRYTSGKEIPQSYAMAIARQESAWNPKVKSPV GASGLMQIMPGTATHTVKMFSIPGYSSP
GQLLDPETNINIGTSLYQYVYQQFGNNRIFSSAAYNAGPGRVRTWLGNSAGRIDAFAVESIPFSETRG
YVKNVLAIDAYYRYFMGDKPTLMSATEWGRY
>d1qusa_ d.2.1.6 (A:) 36 kDa soluble lytic transglycosylase, SLT35 {Escherichia coli}
MVEPQHNMVMGGDFANNPNAQQFIDKMNKHFDRQQLQEILSQAKRLDSVLRMLMDNQAPTTS
VKPPSPNGAWLRYRKKFITPDNVQNGVFWNQYEDALNRAWQVYGPPEIIVGIIGVETRWGRV
MGKTRILDALATLSFNYPRAEYFSGELETFLMARDEQDDPLNLKGSFAGAMGYGQFMPSSYKQYA
VDFSGDGHINLWDPVDAIGSVANYFKAHGWVKGQVAVMANGQAPGLPNGFKTKYSISQLAAAGLT
PQQPLGNHQASLLRLDVGTGYQYWYGLPNFYTTITRYNHSTHYAMAVWQLGQAVALARVQ
>d1chka_ d.2.1.7 (A:) Endochitinase {Streptomyces sp., strain N174}
AGAGLDDPHKKEIAMELVSSAENSSLDWKAQYKYIEDIGDGRGYTGGIIGFCSGTGDMLELVQHYTD
LEPGNILAKYLPALKKVNGSASHSLGTPFTKDWATAAKDTVFQQAQNDERDRVYFDPVAVSQAQAD
GLRALGQFAYYDAIVMHGPGNDPTSFGGIRKTAMKKARTPAQGGDETTYLNGFLDARKAAMLTEAA
HDDTSRVDTEQRVFLKAGNLDLNPPLKWKTYGDPYVINS
>d1qgia_ d.2.1.7 (A:) Endochitinase {Bacillus circulans}
ASPDDNFSPETLQFLRNNTGLDGEQWNNIMKLINKPEQDDLNWIKYYGYCEDIEDERGYTIGLFGA

TTGSRDTHPDGPDFKAYDAAKGASNPSADGALKRLGINGKMKGSILEIKDSEKVFCEGKIKKLQND
AAWRKAMWETFYNVYIRYSVEQARQRGFTSAVTIGSFVDTALNQGATGGSDTLQGLLARSGSSSNE
KTFMKNFHAKRTLVDVDTNKYNKPPNGKNRVKQWDTLVDMGKMNKLVNDSEIAQVTDWEMK

>d1aec_ d.3.1.1 (-) Actinidin {Chinese gooseberry or kiwifruit (*Actinidia chinensis*)}
LPSYVDWRSAGAVVDIKSQGECGGCWAFSAIATVEGINKIVTGVLSLSEQELIDCGRTQNTRGCNGG
YITDGFQFIINNGGINTEENYPYTAQDGECDVALQDQKYVTIDTYENVPYNNEWALQTAVTYQPVSV
ALDAAGDAFKQYSSGIFTGPCGTAIDHAVTIVGYGTEGGIDYWIVKNSWDTTWGEEGYMRILRNVGG
AGTCGIATMPSYPVKY

>d2act_ d.3.1.1 (-) Actinidin {Chinese gooseberry or kiwifruit (*Actinidia chinensis*)}
LPSYVDWRSAGAVVDIKSQGECGGCWAFSAIATVEGINKITSGSLISLSEQELIDCGRTQNTRGCDGGY
ITDGFQFIINDGGINTEENYPYTAQDGDVALQDQKYVTIDTYENVPYNNEWALQTAVTYQPVSV
LDAAGDAFKQYASGIFTGPCGTAVDHAIVIVGYGTEGGVDYWIVKNSWDTTWGEEGYMRILRNVGG
AGTCGIATMPSYPVKY

>d1ppn_ d.3.1.1 (-) Papain {Papaya (*Carica papaya*)}
IPEYVDWRQKGAVTPVKNQGSCGSCWAFSAVVTIEGIIKIRTGNLNEYSEQELDCDRRSYGCNGGYP
WSALQLVAQYGIHYRNTYPYEGVQRYCRSREKGPYAAKTGVRQVQPYNEGALLYSIANQPVSVVLE
AAGKDFQLYRGGIFVGPCGNKVDHAVAAGVYGPYILIKNSWGTGWGENGYIRIKRGTGNSYGVCGLY
TSSFYPVKN

>d1pcia_ d.3.1.1 (A:) Caricain (protease omega) {Papaya (*Carica papaya*)}
LTSTERLIQLFNSWMLNHNKIFYENVDEKLYRFEIFKDNLNYIDETNKKNSYWLGLNEFADLSNDE
FNEKYVGLIDATIEQSYDEEFINEDIVNLPENVDWRKKGAVTPVRHQGSCGSCWAFSAVATVEGINK
IRTGKLVELSEQELVDCERRSHGCKGGYPPYALEYVAKNGIHLRSKYPYKAKQGTCAKQVGGPIVKT
SGVGRVQPNNEGNLLNAIAKQPVSVVVEKGRPFQLYKGGIFEGPCGTKVDGAVTAVGYGKSGGKGYI
LIKNSWGTAWGEGYIRIKRAPGNSPGVCGLYKSSYPTKN

>d1ppo_ d.3.1.1 (-) Caricain (protease omega) {Papaya (*Carica papaya*)}
LPENVDWRKKGAVTPVRHQGSCGSCWAFSAVATVEGINKIRTGKLVELSEQELVDCERRSHGCKGGY
PPYALEYVAKNGIHLRSKYPYKAKQGTCAKQVGGPIVKTSGVGRVQPNNEGNLLNAIAKQPVSVV
ESKGRPFQLYKGGIFEGPCGTKVDHAVTAVGYGKSGGKGYILIKNSWGTAWGEGYIRIKRAPGNSPG
VCGLYKSSYPTKN

>d1yal_ d.3.1.1 (-) Chymopapain {Papaya (*Carica papaya*)}
YPQSIDWRAKGAVTPVKNQGACGSCWAFSTIATVEGINKIVTGNLLELSEQELVDCDKHSYGCCKGGY
QTTSLQYVANNGVHTSKVYPYQAKQYKCRATDKPGPKVKITGYKRVPSNCETSFLGALANQPLSVLV
EAGGKPFQLYKSGVFDGPGCTKLDHAVTAVGYGTSKGKGYILIKNSWGPNWGEGKGYMRLKRQSGNS
QGTGCVYKSSYPPFKGFA

>d1gece_ d.3.1.1 (E:) Glycyl endopeptidase {Papaya (*Carica papaya*)}
LPESVDWRAKGAVTPVKHQGYCESCWAFSTVATVEGINKIKTGNLVELSEQELVDCDLQSYGCNRY
QSTSLQYVAQNGIHLRAKYPYIAKQQTCRANQVGGPKVKITNGVGRVQSNNEGSLNIAIAHQPVSVV
ESAGRDFQNYKGGIFEGSCGTKVDHAVTAVGYGKSGGKGYILIKNSWGPNGWGENGYIRIRRASGNSPG
VCGVYRSSYPIKN

>d1cqda_ d.3.1.1 (A:) Proline-specific cysteine protease {Ginger rhizome (*Zingiber officinale*)}
LPDSIDWRENGAVVPVKNQGGCGSCWAFSTVAAVEGINQIVTGDLSLSEQQLVDCTTANHGCRGG
WMNPAFQFIVNNGGINSEETYPYRGQDGCINSTVNAPVVSIDSYENVP SHNEQSLQKAVANQPVSVT
MDAAGRDFQLYRSGIFTGSCNISANHALTVVGYGTENDKDFWIVKNSWGNWGESGYIRAERNIEN

PDGKCGITRFASYPVKK

>d3gcb_ d.3.1.1 (-) Bleomycin hydrolase {Baker's yeast (*Saccharomyces cerevisiae*), Gal6}
AFQGAMASSIDISKINSWNKEFQSDLTHQLATTVLKKNYNADDALLNKTRLQKQDNRFVNTVSTDS
TPVTNQKSSGRAWLFAATNQLRLNLVSELNLKEFELSQAYLFFYDKLEKANYFLDQIVSSADQDIDS
RLVQYLLAAPTEDGGQYSMFLNLVKKYGLIPKDLYGDLPYSTTASRKWNSLLTTKLREFAETLRTALK
ERSADDSIIVTLREQMQREIFRLMSLFMDIPPVQPNEQFTWEYVDKDKKIHTIKSTPLEFASKYAKLD
PSTPVSLINDPRHPYGLIKIDRLGNVLGGDAVIYLNVDNETLSKLVVKRLQNNKAVFFGSHTPKFM
DKKTGVMDIELWNYPAIGYNLPQKASRIRYHESLMTHAMLITGCHVDETSKLPRLRYVENSWGKD
SGKDGLYVMTQKYFEEYCFQIVVDINELPKELASKFTSGKEEPVLPIWDPMGALA

>d2cb5a_ d.3.1.1 (A:) Bleomycin hydrolase {Human (*Homo sapiens*)}
SSSGLNSEKVAALIQLNSDPQFVLAQNVGTTHDLLDICLKRATVQRAQHVFQHAVPQEGKPITNQK
SSGRSWIFSCLNVMRLPFMKKLNIEEFESQSYLFFWDKVERCYFFLSAFVDTAQRKEPEDGRLVQF
LLMNPANDGGQWDMLVNIVEKYGVIPKCFPESYTTEATRRMNDILNHKMREFCIRLRNLVHSGAT
KGEISATQDVMMEEIFRVVICLGNPPETFTWEYRDKDKNYEKIGPITPLEFYREHVKPLFNMEDKI
CLVNDPRPQHKHNKLYTVEYLSNMVGGKRTLYNNQPIDFLKMMVAASIKDGEAVWFGCDVKGKHN
SKLGLSDMNLVDHELDFVSLKNMKAERLTFGESLMTHAMTFTAVSEKDDQDGAFTKWRVENS
WGEDHGHKGYLCMTDEWFSEYVYEVVDRKHVPEEVLAVLEQEPILPAWDPMGALA

>d1f2aa_ d.3.1.1 (A:) Cruzain {*Trypanosoma cruzi*}
APAAVDWRARGAVTAVKDQGCSCWAFSAIGNVEQWFLAGHPLTNLSEQMLVSCDKTDSGCSG
GLMNNAFEWIVQENNGAVYTEDSYPYASGEGISPPCTTSGHTVGATITGHVELPQDEAQAIAWLAVN
GPVAVAVDASSWMTYTGGVMTSCVSEQLDHGVLVGYNDSAAVPYWIINKNSWTTQWGEEGYIRIAK
GSNQCLVKEEASSAVVG

>d3pbh_ d.3.1.1 (-) (Pro)cathepsin B {Human (*Homo sapiens*)}
MRSRPSFHPLSDELVNYVKNRNTTWQAGHNFYNVDMSYLKRLCGTFLGGPKPPQRMFTEDLKL
ASFDAREQWPQCPTIKEIRDQGSCGSCWAFGAVEAISDRICHTNAHVSVEVSAEDLLTCCGSMCGDG
CNGGYPAEAWNFWRKGLVSGGLYESHVGCPRYSIPPCEHHVNGSRPPCTGEGDTPKCSKICEPGYS
PTYKQDKHYGYNYSVSNSEKDIMAEIYKNGPVEGAFSVYSDFLLYKSGVYQHVTGEMMGHAIKIL
GWGVENGTPYWLANSWNTDWDNGFFKILRGQDHCIESEVVAGIPRTD

>g1huc.1 d.3.1.1 (A;B:) (Pro)cathepsin B {Human (*Homo sapiens*)}
LPASFDAREQWPQCPTIKEIRDQGSCGSCWAFGAVEAISDRICHTNXVSVEVSAEDLLTCCGSMCGD
GCNGGYPAEAWNFWRKGLVSGGLYESHVGCPRYSIPPCEHHVNGSRPPCTGEGDTPKCSKICEPGY
SPTYKQDKHYGYNYSVSNSEKDIMAEIYKNGPVEGAFSVYSDFLLYKSGVYQHVTGEMMGHAIKIL
GWGVENGTPYWLANSWNTDWDNGFFKILRGQDHCIESEVVAGIPRTD

>d1mira_ d.3.1.1 (A:) (Pro)cathepsin B {Rat (*Rattus norvegicus*)}
SDDMINYINKQNTTWQAGRNFYNVDISYLKKLKCGTVLGGPKLPERVGFSEDINLPESFDAREQWSN
CPTIAQIRDQGSCGSSWAFGAVEAMSDRICHTNGRVNVEVSAEDLLTCCGIQCGDGCNGGYPGAW
NFWTRKGLVSGGVYNHSHIGCLPYTIPPCEHHVNGARPPCTGEGDTPKCNKMCEAGYSTSYKEDKHY
GYTSYSVSDSEKEIMAEIYKNGPVEGAFTVFSDFLTYKSGVYKHEAGDVMGGHAIKILGWGIENGVPY
WLANSWNADWDNGFFKILRGENHCGIESEIVAGIPRTQYWGFR

>d1thea_ d.3.1.1 (A:) (Pro)cathepsin B {Rat (*Rattus norvegicus*)}
LPESFDAREQWSNCPPTIAQIRDQGSCGSCWAFGAVEAMSDRICHTNGRVNVEVSAEDLLTCCGIQCG
DGCNGGYPGAWNFWRKGLVSGGVYNHSHIGCLPYTIPPCEHHVNGARPPCTGEGDTPKCNKMCEA
GYSTSYKEDKHYGYTSYSVSDSEKEIMAEIYKNGPVEGAFTVFSDFLTYKSGVYKHEAGDVMGGHAIR
ILGWGIENGVPYWLANSWNADWDNGFFKILRGENHCGIESEIVAGIPRT

>d1qdqa_d.3.1.1 (A:) (Pro)cathepsin B {Cow (Bos taurus)}
LPESFDAREQWPNCPTIKEIRDQGSCGSCWAFGAVEAISDRICHSNGRVNVEVSAEDMLTCCGGEGC
DGCNGGEPGAWNFWTKKGLVSGGLYNHSHVGCGRPYSIPPCEHHVNGSRPPCTGEGDTPKCSKTCEP
GYSPSYKEDKHFGCSSYSVANNEKEIMAEIYKNGPVEGAFSVYSDFLLYKSGVYQHVSGEIMGGHAIRI
LGWGVENGTPYWLANSWNTDWGDNGFFKILRGQDHCGIESEIVAGMPCT

>d1cs8a_d.3.1.1 (A:) (Pro)cathepsin L {Human (Homo sapiens)}
SLTFDHSLEAQWTKWKAMHNRLYGMNEEGWRRRAVWEKNMKMIELHNQEYREGKHSFTMAMNA
FGDMTSEEFRQVMNGFQNRKPRKGVFQEPLFYEAAPRSVDWREKGYVTPVKNQGCQGCSCWAFSAT
GALEGQMFRKTGRLISLSEQLVDCSGPQGNQEGCNGGLMDYAFQYVQDNGGLDSEESYPYEATEESC
KYNPKYSVANDAGFVDIPKQEKALMKAVATVGPISVAIDAGHESFLFYKEGIYFEPDCSSEDMDHGVL
VVGYGFESESDNNKYWLKNSWGEEWGMGGYVKMAKDRRNHCGIASAASYPTV

>g1icf.1 d.3.1.1 (A:,B:) (Pro)cathepsin L {Human (Homo sapiens)}
APRSVDWREKGYVTPVKNQGCQGCSCWAFSATGALEGQMFRKTGRLISLSEQLVDCSGPQGNQEGC
GGLMDYAFQYVQDNGGLDSEESYPYEATEESCKYNPKYSVANDTGFVDIPKQEKALMKAVATVGPIS
VAIDAGHESFLFYKEGIYFEPDCSSEDMDHGVLVVGYGFESESDNNKYWLKNSWGEEWGMGGYVK
MAKDRRNHCGIASAASYPTV

>d1mema_d.3.1.1 (A:) (Pro)cathepsin K {Human (Homo sapiens)}
APDSVDYRKKGYVTPVKNQGCQGCSCWAFSSVGALEGQLKKKTGKLLNLSPQNLVDCVSENDGCGGG
YMTNAFQYVQKNRGIDSEDAYPYVQGEESCMYNPTGKAAKCRGYREIPEGNEKALKRAVARVGPVSV
AIDASLTSFQFYKGVYDESCNSDNLNHAFLAVGYGIQKGNKHWHIKNWSWGENWGNKGYILMARN
KNNACGIANLASFPKM

>d7pcka_d.3.1.1 (A:) (Pro)cathepsin K {Human (Homo sapiens)}
LYPEEILDTHWELWKKTHRKQYNNKVD EISRRLIWEKNLKYISIHNL EASLGVHTYELAMNHLGDM
TSEEVVQKMTGLKVPLSHSRNDTLYIPEWEGRAPDSVDYRKKGYVTPVKNQGCQGCSCWAFSSVGA
LEGQLKKKTGKLLNLSPQNLVDCVSENDGCGGGYMTNAFQYVQKNRGIDSEDAYPYVQGEESCMYN
PTGKAAKCRGYREIPEGNEKALKRAVARVGPVSV AIDASLTSFQFYKGVYDESCNSDNLNHAFLAV
GYGIQKGNKHWHIKNWSWGENWGNKGYILMARNKNNACGIANLASFPKM

>d8pcha_d.3.1.1 (A:) (Pro)cathepsin K {Pig (Sus scrofa)}
YPPSMDWRKKGNFVSPVKNQGCQGCSCWTFSTTGALESVAIATGKMLSLAEQQLVDCAQNFNNHG
CQGGLPSQAF EYIRYNGKIMGEDTYPYKQDDHCKFQPDKAI AFVKD VANITMND E EAMVEAVALY
NPVSFAFEVTNDFL MYRKGIYSSTSCHKTPDKVNHAFLAVGYGEENGIPYWIVKNSWGPQWGMNG
YFLIERGKNMCGLAACASYPIPLV

>d1fh0a_d.3.1.1 (A:) (Pro)cathepsin V {Human (Homo sapiens)}
LPKSVDWRKKGYVTPVKNQKQCGSCWAFSATGALEGQMFRKTGKLVSLSEQLVDCSRPQGNQGC
NGGF MARAFQYVKENGGLDSEESYPYAVDEICKYRPENVAQDTGFTV VAPGKEKALMKAVATVG
PISVAMDAGHSS FQFYKSGIYFEPDCSSKNLDHGVLVVGYGFE GANS DSKYWLKNSWGP EWGSN
GYVKIAKDKNHCGIATAASYPNV

>d1deua_d.3.1.1 (A:) (Pro)cathepsin X {Human (Homo sapiens)}
RGQTCYRPLRGDGLAPLGRTTYPRPHEYLSPADLPKSWDWRNVDGVNYASITRNQHIPQYCGSCWA
HASTSAMADRINIKRKGAWPSTLLSVQNVIDCGNAGSCEGGNDLSVWDYAHQHGPDETCNNYQAK
DQECDKFNQCGTCNEFKECHAIRNYTLWRVGDYGSLSGREKMMAEIYANGPISCGIMATERLANYT
GGIYAEYQDTTYINHVVSVAGWGISDGTEYWIVRNSWGEPWGERGWL RIVTSTYKDGKGARYNLAI
EEHCTFGDPIV

>d1ef7a_d.3.1.1 (A:) (Pro)cathepsin X {Human (Homo sapiens)}

LPKSWDWRNV DGVNYASITRNQHIPQYCGSCWAHASTSAMADRINIKRKGAWPSTLLSVQNVIDCG
NAGSCEGGNDLSVWDYAHQHGIPEDETCNNYQAKDQECDKFNQCGTCNEFKECHAIRNYTLWRVGD
YGSLSGREKMMAEIYANGPISCGIMATERLANYTGGIYAEYQDTTYINHVVSVAGWGISDGT EYWIVR
NSWGEPWGERGWLRIVTSTYKDGKGARYNLAIEEHCTFGDPIV

>d1cv8_ d.3.1.1 (-) Staphopain {Staphylococcus aureus}

NEQYVNKLENFKIRETQGNNGWCAGYTM SALLNATYNTNKYHAEAVMRFLHPNLQGGQFQFTGLT
PREMIYFGQTQGRSPQLLRMTTYNEVDNLT KNNKGIAILGSRVESRNGMHAGHAMAVVGNAKLN
NGQEVIWIWNPWDNGFMTQDAKNNVIPVSN GDHYQWYSSYGY

>d1dkia_ d.3.1.1 (A:) Streptococcal pyrogenic exotoxin B {Streptococcus pyogenes}

LDKVN LGGELSGSNMYVYNISTGGFVIVSGDKRSPEILGYSTSGSFDVNGKENIASFMESYVEQIKENK
KLDSTYAGTAEIKQPVVKSLLDSKGIHYNQGNPYNLLTPVIEKVKPGEQSFVGGQHAATGSVATATAQI
MKYHNYPNKGLKDYTYTLSSNPNFYFNHPKNLFAAISTRQYNWNNILPTYSGRESNVQKMAISELMA
DVGISVDMDYGPSSGSAGSSRVQRALKENFGYNQSVHQINRGDFSKQDWEAQIDKELSQNPVYQ
GVGKVGGHAFVIDGADGRNFYHVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVGIK
P

>d1qmya_ d.3.1.2 (A:) FMDV leader protease {Foot-and-mouth disease virus}

MELTYLNGEKKTFYSRPNHDAWLNAILQLFRYVEEPPFDWVYSSPENLTLEAIKQLEDLTGLELH
EGGPPALVIWNIKHLHTGIGTASRPSEV CVVDGTDMSLADFHAGIFLKGQEHAVFACVTSNGWYAI
DDEDFYPWTPDPSDVLVFPYD

>d1qola_ d.3.1.2 (A:) FMDV leader protease {Foot-and-mouth disease virus}

MELTYLNGEKKTFYSRPNHDAWLNAILQLFRYVEEPPFDWVYSSPENLTLEAIKQLEDLTGLELH
EGGPPALVIWNIKHLHTGIGTASRPSEV CVVDGTDMSLADFHAGIFLKGQEHAVFACVTSNGWYAI
DDEDFYPWTPDPSDVLVFPYDQEPLNGEWKAKVQRKLL

>d1kful3 d.3.1.3 (L:2-355) Calpain large subunit, catalytic domain (domain II) {Human (Homo sapiens)}

AGIAAKLAKDREAAEGLGSHERAIKYLNQDYEARNECLEAGTLFQDPSFPAIPALGFKELGPYSSK
TRGMRWKRPTEICADPQFIIGGATRTDICQ GALGDCWLLAAIASLTLN EEILARVVPLNQSFQENYAG
IFHFQFWQYGEWVEVVDDRLPTKDGELLFVHSAEGSEFWSALLEKAYAKINGCYEALSGGATTEG
FEDFTGGIAEWYELKPPPNLFKIIQKALQKGSLLGCSIDITSAADSEAITFQKLVKGHAYSVTGAEV
ESNGSLQKLIRIRNPWGEVETGRWVNDNCPSWNTIDPEERERLRRHEDGEFWMFSDFLRHYSR
LEICNLTPDTLTSPTYK

>d1df0a3 d.3.1.3 (A:2-355) Calpain large subunit, catalytic domain (domain II) {Rat (Rattus norvegicus)}

AGIAMKLAKDREAAEGLGSHERAIKYLNQDYETLRNECLEAGALFQDPSFPALPSSLGFKELGPYSSK
TRGIEWKRPT EICADPQFIIGGATRTDICQ GALGDSWLLAAIASLTLN EEILARVVPLDQSFQENYAGI
FHFQFWQYGEWVEVVDDRLPTKDGELLFVHSAEGSEFWSALLEKAYAKINGCYEALSGGATTEGF
EDFTGGIAEWYELRPPPNLFKIIQKALEKGSLLGCSIDITSAADSEAVTYQKLVKGHAYSVTGAEVE
SSGSLQKLIRIRNPWQVEWTGKWNDCPSWNTVDPEVRANLTERQEDGEFWMFSDFLRHYSR
LEICNLTPDTLTCDSYK

>d1f13a4 d.3.1.4 (A:191-515) Transglutaminase catalytic domain {Human (Homo sapiens)}

DAVYLDNEKEREYVLDIGVIFYGEVNDIKTRSWSYGQFEDGILDTCLYVMDRAQMDLSGRGNPIK
VSRVGSAMVNAKDD EGVLVGSDNIYAYGVPPSAWTGSVDILLEYSSEN PVRYGQCWVFAVGFNT
FLRCLGIPARIVTNYFSAHDNDANLQMDIFLEEDGNVNSKLTKDSVWNYHCWNEAWMTRPDLVPG
FGGWQAVDSTPQENS DGMYRCGPASVQAIKHGHVCFQFDAPFVFAEVNSDLIYITAKKDGT HVVEN

VDATHIGKLIVTKQIGGDGMMDITDTYKFQEGQEEERLALETALMYGAKKPLNTEGVMKSR
>d1g0da4_d.3.1.4 (A:141-461) Transglutaminase catalytic domain {Red sea bream (Chrysophrys major)}

DMVYLPDESKLQEYVMNEDGVIYMGTDWYIRSIPWNYGQFEDYVMDICFEVLDNSPAALKNSEMD
IEHRSDPVYVGRITAMVNSNGDRGVLTRWEEPYTDGVAPYRWTGSPILQQWSKAGVRPVKYGQ
CWVFAAVACTVLRCLGIPTRPITNFASAHDVDGNLSVDFLLNERLESLSRQSDSSWNFHCWVES
WMSREDLPEGNDGWQVLDPTPQELSDGEFCCGPCPVAAIKEGNLGVKYDAPFVFAEVNADTIYWIV
QKDGQRRKITEDHASVGNISTKSVYGNHREDVTLHYKYPEGSQKEREVYKKAGRRVT

>d1e2ta_d.3.1.5 (A:) Arylamine N-acetyltransferase {Salmonella typhimurium}

HMTSFLHAYFTRLHCQPLGVPTVEALRTLHLAHNCAIPFENLDVLLPREIQLDETALEEKLLYARRG
GYCFELNGLFERALRDIGFNVRSLGRVILSHPASLPPRTHRLLLVDVEDEQWIADVGGGQTLTAPL
RLQAEIAQQTPHGEYRLMQEGSTWILQFRHHEHWQSMYCFDLGVQQQSDHVMGNFWSAHW PQS
HFRHLLMCRHLPDGGKLLTNFHFTRYHQHAVEQVNVDPVPSLYQLLQQQFGLGVNDVKHGFT
EAELA AVMAAF

>d1uch_d.3.1.6 (-) Ubiquitin C-terminal hydrolase UCH-13 {Human (Homo sapiens)}

RWLPLEANPEVTNQLKQLGLHPNWQFVDVYGMPELLSMVPRPVCAVLLLFPITEKEYEVRTEEE
EKIKSQGDVTSSVYFMKQTISNACGTIGLIHAIANNKDKMHFESGSTLKKFLEESVMSPEERARYL
ENYDAIRVTHE TSAHEGQTEAPSIDEKVDLHFIALVHVDGHLYELDGRKPPINHGGETSDETLLEDAI
EVCKKFMERDPDELRFNAIALSAA

>d1cmxa_d.3.1.6 (A:) Ubiquitin C-terminal hydrolase UCH-13 {Synthetic, based on Saccharomyces cerevisiae sequence}

RAVVPIESNPEVFTNFAHKLGLKNEWAYFDIYSLTEPELLAFLPRPVKAIVLLFPINEDRKSSTSQQIT
SSYDVIWFKQSVKNACGLYAILHSLSNQSLLEPGSDLDNFLKSQSDTSSSKNRFDDVTTDQFVLNVI
KENVQTFSTGQSEAPEATADTNLHYITYVEENGGIFELDGRNLSGPLYLGKSDPTATDLIEQELVRVRV
ASYMENANEEDVNLNFAMLGLGPN

>d1avpa_d.3.1.7 (A:) Human adenovirus 2 proteinase {Mastadenovirus H2}

MGSEQELKAIKDLGCGPYFLGTYDKRFPGFVSPHKLACAIVNTAGRETGGVHWMAFAWNPRSKT
CYLFEPFGFSDQRLKQVYQFEYESLLRRSAIASSPDRICITLEKSTQSVQGPNSAACGLFCCMFLHAFAN
WPQTPMDHNPTMNLITGVPNSMLNSPQVQPTLRRNQEQLYSFLERHSPYFRSHSAQIRSATSFCHL
KNM

>d1euva_d.3.1.7 (A:) Ulp1 protease C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

GSLVPELNEKDDDQVQKALASRENTQLMNRDNIEITVRDFKTLAPRRWLNDTIIIEFFMKYIEKSTPN
TVAFNSFFYTNLSERGYQGVRRWMKRKKTQIDKLDKIFTPINLNQSHWALGIIDLKKTIGYVDSLS
NGPNAMSFALTDLQKYVMEESKHTIGEDFDLIHLDCPQQPNGYDCGIYVCMNTLYGSADAPLDFDY
KDAIRMRRFIAHLILTALK

>d7ceib_d.4.1.1 (B:) DNase domain of colicin E7 {Escherichia coli}

RNKPGKATGKGKPVNNKWLNNAGKDLGSPVPDRIANKLRDKEFKSFDDFRKKFWEEVSKDPELSK
QFSRNNNDRMKVGKAPKTRTQDVSGKRTS FELHHEKPISQNGGVYDMDNISVVT PKRHIDIH

>d1emvb_d.4.1.1 (B:) DNase domain of colicin E9 {Escherichia coli}

MESKRNKPGKATGKGKPVGDKWLD DAGKDSGAPIPDRIADKLRDKEFKSFDDFRKAVWEEVSKDP
ELSKNLNPSNKSSVSKGYSPFTPKNQVGGRKVYELHHDKPISQGGEVYDMDNIRVTT PKRHIDIH

>d1ql0a_d.4.1.2 (A:) Sm endonuclease {Serratia marcescens}

SIDNCAVGCPTGGSSKVSIVRHAYTLNNNSTTKFANVWVAYHITKDT PASGKTRNWKTD PALNPADTL

APADYTGANAALKVDRGHQAPLASLAGVSDWESLNYLSNITPQKSDLNQGAWARLEDQERKLIDRA
DISSVYTVTGPLYERDMGKLPGTQKAHTIPSAYWKVIFINNSPAVNHYAAFLFDQNTPKGADFCQFR
VTVDEIEKRTGLIIWAGLPDDVQASLKSXKPGVLPPELMGCKN

>d1a73a_ d.4.1.3 (A:) Intron-encoded homing endonuclease I-PpoI {Slime mold (Physarum polycephalum)}

ALTNAQILAVIDSWEETVGFVITHHVPLGGGLQGLHLCYEIPLAAPYGVGFAKNGPTRWQYKRTI
NQVVHRWGSHTVPFLLEPDNINGKTCTASHLCHNTRCHNPLHLCWESLDDNKGRNWCPGPNNGC
VHAVVCLRQGPLYGPGATVAGPQQRGSHFVV

>d1e7la2 d.4.1.5 (A:1-103) Recombination endonuclease VII, C-terminal and dimerization domains {Bacteriophage T4}

MLLTGKLYKEEKQKFYDAQNGKCLICQRELNPDVQANHLDDHDLNGLNGPKAGKVRGLLCNLCDAAEG
QMKHKFNRSGLKGQVDYLEWLENLLTYLKSQDYTQNN

>d1dy5a_ d.5.1.1 (A:) Ribonuclease A (also ribonuclease B, S) {Cow (Bos taurus)}

KETAAAKFERQHMDSSSTAASSSNYCNQMMKSRNLTKDRCKPVNTFVHESLADVQAVCSQKNVAC
KNGQTNQYQSYSTMSITDCRETGSSKYPNCAYKTTQANKHIIIVACEGNPYVPVHFDASV

>d1h8xa_ d.5.1.1 (A:) Ribonuclease A (also ribonuclease B, S) {Cow (Bos taurus)}

KESAAAKFERQHMDSGNSPSSSSTYCNQMMRRRNMTQGRCKPVNTFVHEPLVDVQNVCFQEKVTC
KNGQGNQYKSNSSMHITDCRLTNGSRYPNCAYRTSQKERHIIIVACEGSPYVPVHFDASVE

>d1rbd_ d.5.1.1 (-) Ribonuclease A (also ribonuclease B, S) {Cow (Bos taurus)}

SSSNYCNQMMKSRNLTKDRCKPVNTFVHESLADVQAVCSQKNVACKNGQTNQYQSYSTMSITDCRE
TGSSKYPNCAYKTTQANKHIIIVACEGNPYVPVHFDASV

>g1d5d.1 d.5.1.1 (A:,B:) Ribonuclease A (also ribonuclease B, S) {Cow (Bos taurus)}

KETAAAKMERQHLDXNYCNQMMKSRNLTKDRCKPVNTFVHESLADVQAVCSQKNVACKNGQTN
CYQSYSTMSITDCRETGSSKYPNCAYKTTQANKHIIIVACEGNPYVPVHFDASV

>d1e21a_ d.5.1.1 (A:) Ribonuclease A (also ribonuclease B, S) {Human (Homo sapiens), des1-7}

AFQRQHMDSDSSPSSSSTYCNQMMRRRNMTQGRCKPVNTFVHEPLVDVQNVCFQEKVTCCKNGQG
NCYKSNSSMHITDCRLTNGSRYPNCAYRTSPKERHIIIVACEGSPYVPVHFDASVE

>d1rraa_ d.5.1.1 (A:) Ribonuclease A (also ribonuclease B, S) {Rat (Rattus norvegicus)}

AESSADKFKRQHMDTEGPKSSPTYCNQMMKRQGMKTKGCKPVNTFVHEPLEDVQAICSQGQVTC
KNGRNNCHKSSSTLRITDCRLKSSKYPNCDYTTTDSQKHIIIACDGNPYVPVHFDASV

>d1onc_ d.5.1.1 (-) P-30 protein {Frog (Rana pipiens)}

EDWLTFQKKHITNTRDVCNDIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTSEFYLSDC
NVTSRPCKYKLLKSTNKFCVTCENQAPVHFVGVGSC

>d1bc4_ d.5.1.1 (-) Cytotoxic ribonuclease {Bullfrog (Rana catesbeiana)}

ENWATFQQKHIINTPIINCNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNVLSTTRFQLN
TCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP

>d11bga_ d.5.1.1 (A:) Seminal ribonuclease {Cow (Bos taurus)}

KESAAAKFERQHMDSGNSPSSSSTYCNLMCCRKMTQGKCKPVNTFVHESLADVQAVCSQKKVTC
KNGQTNQYQSKSTMRTDCRETGSSKYPNCAYKTTQVEKHIIIVACGGKPSVPVHFDASV

>d1b6va_ d.5.1.1 (A:) Hybrid between ribonuclease A and seminal ribonuclease {Cow (Bos taurus)}

KETAAAKFERQHMDSSSTAASSSNYCNQMMKSRNLTKDRCKPVNTFVHESLADVQAVCSQKKVTC
KNGQTNQYQSKSTMRTDCRETGSSKYPNCAYKTTQANKHIIIVACGGKPYVPVHFDASV

>d1dyta_d.5.1.1 (A:) Eosinophil cationic protein (ECP), ribonuclease 3 {Human (Homo sapiens)}

RPPQFTRAQWFQAIQHISLNPPRCTIAMRAINNYRWRCKNQNTFLRRTTFANVVNVCGNQSIRCPHNR
TLNCHRSRFRVPLHCDLINPGAQNISNCRYADRPGRRFYVVACDNRDPRDSPRYPPVVPVHLDTTI

>d1hi2a_d.5.1.1 (A:) Eosinophil-derived neurotoxin (EDN) {Human (Homo sapiens)}

MKPPQFTWAQWFETQHINMTSQQCTNAMQVINNYQRRCKNQNTFLLTTFANVVNVCGNPNMTC
PSNKTRKNCHHSGSQVPLIHCNLTTPSPQNISNCRYAQTAPANMFYIVACDNRDQRRDPPQYPPVVPVH
LDRII

>d1rnfa_d.5.1.1 (A:) Ribonuclease 4 {Human (Homo sapiens)}

MQDGMYQRFLRQHVHPEETGGSDRYCNLMMQRRKMTLYHCKRFNTFIHEDIWNIRSICSTTNIQC
KNGKMNCHGEGVVKVTDICRDTGSSRAPNCRYRAIASTRRVVIACEGNPQVPVHFDG

>d1b1ia_d.5.1.1 (A:) Angiogenin {Human (Homo sapiens)}

EDNSRYTHFLTQHYDAKPKGRDDRYCESIMRRRGLTSPCKDINTFIHGNKRSIKAICENKNGNPHRE
NLRISKSSFQVTTCKLHGGSPWPPCQYRATAGFRNVVACENGLPVHLDQSIFRRP

>d1agi_d.5.1.1 (-) Angiogenin {Cow (Bos taurus)}

AQDDYRYIHFLTQHYDAKPKGRNDEYCFNMMKNRRLTRPCKDRNTFIHGNKNDIKAICEDRNGQP
YRGDLRISKSEFQITICKHKGGSSRPPCRYGATEDSRVIVVGCENGLPVHFDESFITPRH

>d1ag2_d.6.1.1 (-) Prion protein domain {Mouse (Mus musculus)}

GLGGYMLGSAMSRPMIHFNDWEDRYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQH
TVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYY

>d1b10a_d.6.1.1 (A:) Prion protein domain {Golden hamster (Mesocricetus auratus)}

LGGYMLGSAMSRPMMHFGNDWEDRYRENMNRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQH
TVTTTTKGENFTETDIKIMERVVEQMCTTQYQKESQAYYDG

>d1fo7a_d.6.1.1 (A:) Prion protein domain {Human (Homo sapiens)}

LGGYMLGSAMSRPIIHFSDYEDRYRENMHRYPNQVYYRPMDEYSNQNNFVHDCVNITIKQHTVT
TTTTKGENFTKTDVKMMERVVEQMCITQYERESQAYYQRGSS

>d1i4ma_d.6.1.1 (A:) Prion protein domain {Human (Homo sapiens)}

GAVVGGGLGGYMLGSAMSRPIIHFSDYEDRYRENMHRYPNQVYYRPMDEYSNQNNFVHDCVNITI
KQHTVTTTTKGENFTETDVKMMERVVEQMCITQYERESQAYY

>d1dwya_d.6.1.1 (A:) Prion protein domain {Cow (Bos taurus)}

GLGGYMLGSAMSRPLIHFSDYEDRYRENMHRYPNQVYYRPVDQYSNQNNFVHDCVNITVKEHT
VTTTTKGENFTETDIKMMERVVEQMCITQYQRESQAYYQ

>d1i17a_d.6.1.1 (A:) Prion-like protein Doppel {Mouse (Mus musculus)}

RVAENRPGAFIKQGRKLDIDFGAEGNRYAANYWQFPDGIYYEGCSEANVTKEMLVTSCVNATQAA
NQAEFSSREKQDSKLRVLRWRLIKEICSAKHCDFWLARGAA

>d1e01a_d.7.1.1 (A:) Membrane-bound lytic murein transglycosylase D, MltD {Escherichia coli}

DSITYRVRKGDSSIAKRHGVMRWNSTANLQPGDKLTLFVK

>d1hywa_d.186.1.1 (A:) Head-to-tail joining protein W, gpW {Bacteriophage lambda}

MTRQEELAAARAALHDLMTGKRVATVQKDGRRVEFTATSVSDLKKYIAELEVTGMTQ

>d1ejra_d.8.1.1 (A:) Urease, gamma-subunit {Klebsiella aerogenes}

MELTPREKDKLLLFTAALVAERRLARGLKLNPESVALISAFIMEGARDGKSVASLMEEGRHVLTREQ
VMEGVPEMIPDIQVEATFPDGSKLVTVHNPII

>d4ubpa_d.8.1.1 (A:) Urease, gamma-subunit {Bacillus pasteurii}

MHLNPAEKEKQLIFLASELLRRKARGLKLNYPEAVAIITSFIMEGARDGKTVAMLMEEGKHVLRD
DVMEGVPEMIDDIQAEATFPDGTGLVTVHNPIS
>d1e9ya2 d.9.1.1 (A:1-105) Urease, gamma-subunit {Helicobacter pylori}
MKLTPKELDKMLHYAGELAKKRKEKGIKLNVEAVALISAHIMEEARAGKKTAAELMQEGRTLLK
PDDVMDGVASMIHEVGIAMFPDGTGLVTVHTPIEANGK
>d1qe6b_ d.9.1.1 (B:) Interleukin-8, IL-8 {Human (Homo sapiens)}
AKECRCQCIKTYSKPFHPKFIKELRVIESGPCCANTEIIVKLSDGRELCLDPKENWVQRVVEKFLKRA
ENS
>d3il8_ d.9.1.1 (-) Interleukin-8, IL-8 {Human (Homo sapiens)}
LRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRELCLDPKENWVQRVVEKFLKRAENS
>d1plfa_ d.9.1.1 (A:) Platelet factor 4, PF4 {Cow (Bos taurus)}
LQCVCCLKTTSGINPRHISSEVIGAGLHCPSPQLIATLKTGRKICLDQQNPLYKKIIRLLKS
>d1pfma_ d.9.1.1 (A:) Platelet factor 4, PF4 {Human (Homo sapiens)}
MSAKELRCQCVKTTTSQVRPRHITSLEVIKAGPHCPTAQLIATLKNRGIKICLDLQAPLYKKIIRLLKS
>d1rhpa_ d.9.1.1 (A:) Platelet factor 4, PF4 {Human (Homo sapiens)}
DLQCLCVKTTTSQVRPRHITSLEVIKAGPHCPTAQLIATLKNRGIKICLDLQAPLYKKIIRLLKS
>d1mgsa_ d.9.1.1 (A:) Melanoma growth stimulating activity (MGSA) {Human (Homo
sapiens)}
ASVATELRCQCLQTLQGIHPKNIQSVNVKSPGPHCAQTEVIATLKNRGIKICLDLQAPLYKKIIRLLKS
DKSN
>d1roda_ d.9.1.1 (A:) IL-8/MGSA chimeric protein CIL-8M {Human (Homo sapiens)}
SAKELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRELCLDPASPIVKKIIRLLKS
SN
>d1huna_ d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Human (Homo sapiens),
1-beta}
APMGSDPPTACCFSTYRQIPQNFIAAYFETSSQCSKPGVIFLTKRSRQVCADPSEEWVQKYVSDLELSA
LN
>d1b50a_ d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Human (Homo sapiens),
1-alpha}
SLAADTPTACCFSTYRQIPQNFIAAYFETSSQCSKPGVIFLTKRSRQVCADPSEEWVQKYVSDLELSA
>d1ha6a_ d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Mouse (Mus musculus),
ccl20/mip-3a}
ASNYDCCLSYIQTPLPSRAIVGFTRQMADEACDINAIIFHTKKRKSVCADPKQNWVKRAVNLVSLRV
KKM
>d1cm9a_ d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Kaposi's sarcoma herpes
virus, VMIP-II}
SWHRPDKCCLGYQKRPLPQVLLSSWYPTSQLCSKPGVIFLTKRGRQVCADKSKDWVKKLMQQLPVT
AR
>d1b3aa_ d.9.1.1 (A:) RANTES (regulated upon activation, normal T-cell expressed and
secreted) {Human (Homo sapiens)}
PYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNPAVVVTRKNRQVCANPEKKWVREYINSLEMS
>d1doka_ d.9.1.1 (A:) Monocyte chemoattractant protein-1 (MCP-1, MCAF) {Human (Homo
sapiens)}
MQPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWWQDSMDHL

DKQT
>d1esra_ d.9.1.1 (A:) Monocyte chemoattractant protein-2 (MCP-2) {Human (Homo sapiens)}
EPDSVSIPITCCFNVINRKIPIQRLESYTRITNIQCPKEAVIFKTQRGKEVCADPKERWVRDSMKHLDQ
IFQNLKP
>d1el0a_ d.9.1.1 (A:) CC chemokine I-309 {Human (Homo sapiens)}
SKSMQVPFSRCCFSFAEQEIPLRAILCYRNTSSICSGNEGLIFKLKRGKEACALDTVGVVQRHRKMLRH
CPSKRK
>d1eot_ d.9.1.1 (-) Eotaxin {Human (Homo sapiens)}
GPASVPTTCCFNLANRKIPLQRLESYRRITSGKCPQKAVIFKTKLAKDICADPKKKWVQDSMKYLDQ
KSPTPKP
>d1eiha_ d.9.1.1 (A:) Eotaxin-2 {Human (Homo sapiens)}
VVIPSPCCMFFVSKRIPENRVVSYQLSSRSTCLKAGVIFTTKKGQSCGDPKQEWVQRYMKNLDAKQ
KKASPR
>d1j9oa_ d.9.1.1 (A:) Lymphotactin {Human (Homo sapiens)}
VGSEVSDKRTCVSLLTQRLPVSRIKTYTITEGSLRAVIFITKRGLKVCADPQATWVRDVVRSMDRKS
NTRNNMIQTKPTGTQSTNTAVTLTG
>d1bo0_ d.9.1.1 (-) Monocyte chemoattractant protein-3 (MCP-3) {Human (Homo sapiens)}
QPVGINTSTTCCYRFINKKIPKQRLESYRRTTSSHCPCREAVIFKTKLDKEICADPTQKWVQDFMKHL
DKKTQTPKL
>d1b2ta_ d.9.1.1 (A:) Chemokine domain of fractalkine {Human (Homo sapiens)}
MQHHGVTKCNITCSKMTSKIPVALLIHYQQNQASCGKRAIILETRQHRLFCADPKEQWVKDAMQHL
DRQAAALTRNG
>d1f2la_ d.9.1.1 (A:) Chemokine domain of fractalkine {Human (Homo sapiens)}
VTKCNITCSKMTSKIPVALLIHYQQNQASCGKRAIILETRQHRLFCADPKEQWVKDAMQHLDRO
>d1tvxa_ d.9.1.1 (A:) Neutrophil-activating peptide-2 (NAP-2) {Human (Homo sapiens)}
LRCLCIKTTSGIHPKNIQSLEVIGKGTNCNQEVIATLKDGRKICLDPDAPRIKKIVQKLAGD
>d1tvxb_ d.9.1.1 (B:) Neutrophil-activating peptide-2 (NAP-2) {Human (Homo sapiens)}
DSDLYAELRCLCIKTTSGIHPKNIQSLEVIGKGTNCNQEVIATLKDGRKICLDPDAPRIKKIVQKLAG
D
>d1a15a_ d.9.1.1 (A:) Stromal cell-derived factor-1 (SDF-1) {Human (Homo sapiens)}
KPVLSYRCPFRFFESHVARANVKHLKILNTPACALQIVARLKNNNRQVCIDPKLKWIQEYLEKALN
>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)}
SYRCPFRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQEYLEKALN
>d1mi2a_ d.9.1.1 (A:) Macrophage inflammatory protein-2 {Mouse (Mus musculus)}
AVVASELRQCCLKTLPRVDFKNIQSLSVTPPGPHCAQTEVIATLKGQKVCCLDPEAPLVQKIIQKILNK
GKAN
>d2hcc_ d.9.1.1 (-) Chemokine hcc-2 (macrophage inflammatory protein-5) {Human (Homo sapiens)}
HFAADCTSISYQSIPCSLMKSYFETSSECSKPGVIFLTKKGRQVCAKPSGPGVQDCMKKLPYSI
>d1qnka_ d.9.1.1 (A:) Gro beta {Human (Homo sapiens)}
TELRCQCLQTLQGIHLKNIQSIVKVKSPGPHCAQTEVIATLKNQKACLNPASPMVKKIIEKMLKNGK

SN

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

MDRFHATSADCCISYTPRSIPCSLLESYFETNSECSKPGVIFLTKKGRRFCANPSDKQVQVCMRMLKL
DTRIKTRKN

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

ATVKFKYKGEKEVDISKIKKVVWRVGMISFTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKK

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

MVKVKFKYKGEKEVDTSKIKKVVWRVGMVSFTYDDNGKTGRGAVSEKDAPKELLDMLARAEREK
K

>d1ap0_ d.9.2.2 (-) Modifier protein 1 (M31, HP1 beta) {Mouse (Mus musculus)}

HMVEEVLEEEEEYVVEKVLDRRVVKGKVEYLLKWKGFSDNTWEPEENLDCPDLIAEFLQSQK
TAHETDKS

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

HMKEESEKPRGFARGLEPERIIGATDSSGELMFLMKWKSDEADLVPAKEANVKCPQVVISFYEERL
TWH

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

QVENYDSWEDLVSSIDTIERKDDGTLEIYLTWKNGAISHHPSTITNKKCPQKMLQFYESHL

>d1g6za_ d.9.2.2 (A:) Histone methyltransferase clr4 chromo domain {Fission yeast (Schizosaccharomyces pombe)}

ISSPKQEEYEVEVERIVDEKLDNRNGAVKLYRIRWLNYSRSRTWEPPENLSGCSAVLAEWKRRKRRLKG
SNS

>d1bb8_ d.10.1.1 (-) DNA-binding domain from tn916 integrase {Enterococcus faecalis}

EKRRDNRGRILKTGESQRKDGRLYKYIDSFGEQPVVYSWKLVAIDRVPAGKRDCISLREKIAELQKD
IHD

>d1gcca_ d.10.1.2 (A:) GCC-box binding domain {Mouse-ear cress (Arabidopsis thaliana)}

KHYRGVRQRPWGKFAAEIRDPAKNGARVWLGTFTAEDAALAYDRAAFMRGRSALLNFPLRV

>d1qk9a_ d.10.1.3 (A:) Methyl-CpG-binding protein 2, MECP2 {Human (Homo sapiens)}

ASASPKQRRSIIRDGPYDDPTLPEGWTRKLRKQKSGRSAGKYDVYLINPQGKAFRSKVELIAYFE
KVGDTSLDPNDFDFTVTGRGSGSGC

>d1d9na_ d.10.1.3 (A:) Methylation-dependent transcriptional repressor MBD1/PCM1 {Human (Homo sapiens)}

MAEDWLDCPALGPGWKRREVFVKSGATCGRSPTYQSPGDRIRSKVELTRYLGPACDLTLFDFKQ
GILCYPAPK

>d1k25a1 d.11.1.1 (A:632-692) Penicillin-binding protein 2x (pbp-2x), c-terminal domain {Streptococcus pneumoniae}

TESSYAMPSIKDISPGELAEALRRNIVQPIVVGTTGKIKETSVEEGTNLAPNQVLLLSK

>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}

QQSPYPMPVSKDISPGDLAEELRRNLVQPIVVGTTGKIKNSSAEEGKNLAPNQVLLLSK

>d1qmea2 d.11.1.1 (A:693-750) Penicillin-binding protein 2x (pbp-2x), c-terminal domain

{*Streptococcus pneumoniae*}

AEEVPDMYGWTKETAETLAKWLNIELEFQSGSTVQKQDVRANTAIDIKKITLTLGD
>d1jj2r_ d.12.1.1 (R:) Ribosomal protein L23 {Archaeon *Haloarcula marismortui*}
SWDVIKHPHVTEKAMNDMDFQNKLQFAVDDRASKGEVADAVEEQYDVTVEQVNTQNTMDGEKK
AVVRLSEDDDAQEVASRI

>d1ffki_ d.12.1.2 (I:) Ribosomal protein L15e {Archaeon *Haloarcula marismortui*}
MKSMYAYIREAWKRPYEGYVGEMLMWHRLQKWRREPAVVRI PRPTRLDRARALGYKAKKGIIVRV
RIRRGRRATRPNKGRKSKMMVNRPRKKNLQWIAEERANRKYPNMEVLNSYWVGEDGRYKW
FEVILVDRDHAIKSDPQLSWVSRTRGRVYRGLTSAGRKARGLRRKGRGAEKVRPSLRANFRKKRR
>d1jj2l_ d.12.1.2 (L:) Ribosomal protein L15e {Archaeon *Haloarcula marismortui*}
ARSAYSYIREAWKRPKEGQIAELMWHRMQEWNEPAVVRIERPTRLDRARSLGYKAKQGIIVRVA
IRKGSRRTRFNKGRRSKRMMVNRITRKKNIQRIAEERANRKFNLRLVNSYSVGEDGRHKWHEVI
LIDPDHAIKSDQLSWISRTRHRLRTRFGLTSAGRRRCRLRGQKQKSEKVRPSLRVNGAKA
>d4rhn_ d.13.1.1 (-) Histidine triad nucleotide-binding protein (HINT) {Rabbit (*Oryctolagus cuniculus*)}
RPGGDTIFGKIIRKEIPAKIIFEDDQCLAFHDISPQAPTHFLVIPKKHISQISAAEDADESLLGHLMIIVGK
KCAADLGLKKGYRMVVNEGSDGGQSVYHVHLHVLGGRQMNWPPG
>d1fit_ d.13.1.1 (-) FHIT (fragile histidine triad protein) {Human (*Homo sapiens*)}
SFRFGQHLIKPSVFLKTELSFALVNRKPVVPGHVLVCP LRPVERFHDLRPDEVADLFQTTQRVGTVV
EKHFHGTSLTFSMQDGPEAGQTVKHVHVHVLPRKAGDFHRNDSIYEELQKHKEDFPASWRSEEE
MAAEAAALRVYFQ
>d1kpf_ d.13.1.1 (-) Protein kinase C inhibitor-1, PKCI-1 {Human (*Homo sapiens*)}
DTIFGKIIRKEIPAKIIFEDDRCLAFHDISPQAPTHFLVIPKKHISQISVAEDDDESLLGHLMIIVGKCAA
DLGLNKGYRMVVNEGSDGGQSVYHVHLHVLGGRQMHWPPG
>d1emsa1 d.13.1.1 (A:281-440) NIT-FHIT fusion protein, C-terminal domain {Nematode
(*Caenorhabditis elegans*)}
RSDLYTLHINEKSSETGGLKFARFNIPADHIFYSTPHSFVFNLPVTDGHVLPSPKRVVPRLTDLTD
ETADLFIVAKKVQAMLEKHHNVTSTTICVQDGKDAGQTVPHVHIHILPRRAGDFGDNEIYQKLASHD
KEPERKPRSNEQMAEEAVVYRNLN
>d1guqa1 d.13.1.2 (A:2-177) Galactose-1-phosphate uridylyltransferase {*Escherichia coli*}
TQFNPVDHPHRRYNPLTGQWILVSPHRAKRPWQGAQETPAKQVLP AHPDCFLCAGNVRVTGDKN
PDYTGTYVFTNDFAAALMSDTPDAPESHDP LMRCSARGTSRVICFSPDHSKTLPELSVAALTEIVKT
WQEQTAE L GKTYPWVQVFENKGAAMGCSNPHPGGQIWANSFLPN
>d1guqa2 d.13.1.2 (A:178-348) Galactose-1-phosphate uridylyltransferase {*Escherichia coli*}
EAEREDRLQKEYFAEQKSPMLVDYVQRELADGSRTVVETEHWLAVVPYWAAWPFETLLLPAKAVL
RITDLTDAQRSDLALAKKLTSTRYDNLFCQSFYPSMGWHGAPFNGEENQHWQLHAHFYPPLLRSAT
VRKFMVGYEMLAETQRDLTAEQAERLRAVSDIHFRESGV
>d1jyaa_ d.198.1.1 (A:) YopE chaperone SycE {*Yersinia pestis*}
YSFEQAITQLFQQLSLSIPDTIEPVIGVKVGEFACHITEHPVQGILMFTLPSLDNNDKETLLSHNIFSQ
DILKPILSWDEVGHPVLWNRQPLNSLDNNSLYTQLEMLVQGAERLQ
>d1k6za_ d.198.1.1 (A:) YopE chaperone SycE {*Yersinia pestis*}
SFEQAITQLFQQLSLSIPDTIEPVIGVKVGEFACHITEHPVQGILMFTLPSLDNNDKETLLSHNIFSQD
ILKPILSWDEVGHPVLWNRQPLNSLDNNSLYTQLEMLVQGAERLQTSSLSIPPRFSHH
>d1jyoa_ d.198.1.1 (A:) Virulence effector SptP secretion chaperone SicP {*Salmonella*}

typhimurium}

LQAHQDIIANIGEKLGLPLTFDDNNQCLLLDSDIFTSIEAKDDIWLLNGMIPLSPVCGDSIWRQIMV
INGELAAANEGTLAYIDAAETLLLIHAITDLTNTYHIIISQLESFVNQQEALKNILQEYAKV

>d1k3ea_d.198.1.1 (A:) Secretion chaperone CesT {Escherichia coli}

MSSRSELLLEKFAEKIGISISFNENRLCSFAIDEIYYISLSDANDEYMMIYGVCGKFPTDNSNFALEIL
NANLWFAENGGPYLCYEAGAQSLLLALRFPLDDATPEKLENEIEVVVKSMENLYLVLHNQGITLENE
HMKIEEISS

>d1k3sa_d.198.1.1 (A:) Secretion chaperone SigE {Salmonella enterica}

MESLLNRLYDALGLDAPEDPELLIIDDGIQVYFNESDHTLEMCCPFMPLPDDILTQHFRLNNTSAV
TIGADADNTALVALYRLPQTSTEEEEALTGFELFISNVKQLKEHYA

>d1k8kf_d.198.2.1 (F:) ARPC4 (20 kDa subunit) {Cow (Bos taurus)}

TATLRPYLSAVRATLQAALCLENFSSQVVERHNKPEVEVRSSKELLQPVTISRNEKEKVLIEGSINSV
RVSIYVQADEIEKILCHKFMRFMMRAENFFILRRKPVVEGYDISFLITNFHTEQMYKHKLVDFVIH
FMEEIDKEISEMKLSVNARARIVAEFLKNF

>d1k8kd1_d.198.2.1 (D:1-120) ARPC2 (34 kDa subunit) {Cow (Bos taurus)}

MILLEVNRIIEETLALKFENAAAGNKPEAVEVTFADFDGVLVYHISNPNGDKTKVMVSISLKFYKELQ
AHGADELLKRVYGSYLVNPESGYNVSLLYDLENLPASKDSIVHQAGMLKRNC

>d1k8kd2_d.198.2.1 (D:121-284) ARPC2 (34 kDa subunit) {Cow (Bos taurus)}

FASVFEKYFQFQEEGKEGENRAVIHYRDEETMYVESKKDRVTVVVFSTVFKDDDDVVIGKVFMQEFK
EGRRASHTAPQVLFVSHREPPLELKDTDAAVGDNIGYITFVLFPRHTNASARDNTINLIHTFRDYLHY
HIKCSKAYIHTRMRAKTSDFLKVLRARPDA

>d1kafa_d.199.1.1 (A:) DNA-binding C-terminal domain of the transcription factor MotA
{Bacteriophage T4}

MEITSDMEEDKDLMLKLLDKNGFVLKKEIYRSNYLAILEKRTNGIRNFEINNNNGNMRIFGYKMME
HHIQKFTDIGMSCKIAKNGNVYLDIKRSAENIEAVITVASEL

>d1dar_3_d.14.1.1 (476-599) Elongation factor G (EF-G), domain IV {Thermus thermophilus}

VGKQPQVAYRETITKPVDFEGKFIQGTGGRGYGHVKIKVEPLPRGSGFEFVNAIVGGVIPKEYIPAVQK
GIEEAMQSGPLIGFPVVDIKVTLYDGSYHEVDSSEMAFKIAGSMAIKEAVQKGD

>d1pkp_1_d.14.1.1 (78-148) Ribosomal protein S5, C-terminal domain {Bacillus
stearothermophilus}

GTTIPHEVIGHFGAGEIILKPASEGTGVIAGGPARAVLELAGISDILSKSIGSNTPINMVRATFDGLKQL
K

>d1fjge1_d.14.1.1 (E:74-154) Ribosomal protein S5, C-terminal domain {Thermus
thermophilus}

GTIPHEIEVEFGASKIVLKPAPGTGVIAGAVPRAILELAGVTDILTKELGSRNPINIAYATMEALRQLR
TKADVERLRKG

>d1fjgi_d.14.1.1 (I:) Ribosomal protein S9 {Thermus thermophilus}

EQYYGTGRRKEAVARVFLRPGNGKVTVNGQDFNEYFQGLVRAVAALEPLRAVDALGRFDAYITVRGG
GKSGQIDAIKLGARALVQYNPDYRAKLPGLFLTRDARVVERKKYKHKARRAPQYSKR

>d1a6f_d.14.1.2 (-) RNase P protein {Bacillus subtilis}

AHLKRNRLKKNEDFQVFKHGTSVANRQFVLYTLDQPENDELRVGLSVSKKIGNAVMRNRIRKRI
RQAFLEEKERLKEKDYIIIARKPASQLTYEETKKSLLQHLFRKSSLYK

>d1d6ta_d.14.1.2 (A:) RNase P protein {Staphylococcus aureus}

MLLEKAYRIKKNADFQRIYKKGHSVANRQFVVYTCNNKEIDHFRLGISVSKKLGNAVLRNKIKRAIRE

NFKVHKSHILAKDIIVIARQPAKDMTTLQIQNSLEHVLKIAKVFNKKIK
>d1b63a1 d.14.1.3 (A:217-331) DNA mismatch repair protein MutL {Escherichia coli}
GTAFLEQALAEWQHGDLTLRGWVADPNHTTPALAEIQYCYVNGRMMRDRLINHAIRQACEDKLG
DQQPAFVLYLEIDPHQVDVNVHPAKHEVRFHQSRVLVHDFIYQGVLSVLQ
>d1h7sa1 d.14.1.3 (A:232-365) DNA mismatch repair protein PMS2 {Human (Homo sapiens)}
GQKQLQSLIPFVQLPPSDSVCEEYGLSCSDALHNLFYISGFISQCTHGVGRSSTDRQFFFINRRPCDPA
KVCRLVNEVYHMYNRHQYPFVVLNISVDSECVDINVTDPKRQILLQEEKLLAVLKTSLIGMFDS
>d1ei1a1 d.14.1.3 (A:221-392) DNA gyrase B {Escherichia coli}
GIKAFVEYLNKNKTIPIHPNIFYFSTEKDGIGVEVALQWNDGFQENIYCFTNNIPQRDGGTHLAGFRA
AMTRTLNAYMDKEGYSKKAKVSATGDDAREGLIAVVSVKVPDPKFSSQTKDKLVSSEVKSASAVEQQM
NELLAEYLLNPTDAKIVVGKIIDAARAREAAARRAREMT
>d1e3ha2 d.14.1.4 (A:3-151) Polynucleotide phosphorylase/guanosine pentaphosphate
synthase (PNPase/GPSI), domains 1 and 4 {Streptomyces antibioticus}
NETHYAEVIDNGAFGTRTIRFETGRLARQAAGSAVAYLDDDTMVLSATTASKNPKDQLDFFPLTVD
VEERMYAAGKIPGSFFRREGRPSEDAILTCLRIDRPLRPSFKKGLRNEIQVVATIMALNPDHLYDVVAI
NAASASTQLAGLP
>d1e3ha3 d.14.1.4 (A:346-482) Polynucleotide phosphorylase/guanosine pentaphosphate
synthase (PNPase/GPSI), domains 1 and 4 {Streptomyces antibioticus}
TDIRTLAAEVEAIPRVHGSALFERGETQILGVTTLNMLRMEQQDLTLPVTRKRYMHNYNFPYVSVG
ETGRVGSPPKREIGHGALAERAIVPVLPTREEFPYAIRQVSEALGSNGSTSMGSVCASTMSLLNAGVP
LK
>d1h72c1 d.14.1.5 (C:5-167) Homoserine kinase {Archaeon Methanococcus jannaschii}
MKVRVKAPCTSANLGVGFDVFGCLCKEYPDVIEVEAIDDKEIHIEVDDKNIPTDPDKNVAGIVAKKMI
DDFNIGKGVKITIKKGVKAGSGLGSSAASSAGTAYAINELFKLNLDKLKLVDYASYGELASSGAKHADN
VAPAIFFGFTMVTNYEPLVHLHIPID
>d1fi4a1 d.14.1.5 (A:3-190) Mevalonate 5-diphosphate decarboxylase {Baker's yeast
(Saccharomyces cerevisiae)}
VYTASVTAPVNIATLKYWGKRDTKLNLPNTSSISVTLTSDDLRDLTSAATAPEFERDTLWLNAGEPHSI
DNERTQNCLRDLRQLRKEMESKDASLPTLSQWKLHIVSENNFPTAAGLASSAAGFAALVSAIAKLYQ
LPQSTSEISRIARKGSGSACRSLFGGYVAWEMGKAEDGHDSMAVQIADSSDWP
>d1c3ta_ d.15.1.1 (A:) Ubiquitin {Human (Homo sapiens)}
MQLFVKTLTGKTLTVELEPSDTVENLAKAKIQDKEGIPPDQQLIFAGKQLEDGRTLSDYNLQKESTIH
LVLRLRGG
>d1gjza_ d.15.1.1 (A:) Ubiquitin {Human (Homo sapiens)}
GSMQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQLIFAGKQLE
>d1ubi_ d.15.1.1 (-) Ubiquitin {Human (Homo sapiens)}
MQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQLIFAGKQLEDGRTLSDYNIQKESTLHL
LVLRLRGG
>d1ud7a_ d.15.1.1 (A:) Ubiquitin {Human (Homo sapiens)}
MQVFLKTLTGKTVTIEVEPSDTVENFKAKIQDKEGIPPDQQLIFAGKQLEDGRTLSDYNIQKESTIHL
LVLRLRGG
>d1a5r_ d.15.1.1 (-) SUMO-1 (smt3 homologue) {Human (Homo sapiens)}
GMSDQEAKPSTEDLGDKKEGEYIKLVIGQDSSEIHFVKVMTTHLKKLKESYCRQGVPMNSLRF

FEGQRIADNHTPKELGMEEEDVIEVYQEQTGGHSTV

>d1euvb_ d.15.1.1 (B:) SUMO-1 (smt3 homologue) {Baker's yeast (Saccharomyces cerevisiae)}

PETHINLKVSDGSSEIFFKIKKTTPLRRLMEAFARQKGEMDSLRFYDGIQADQTPEDLDMEDN
DIIEAHREQIGG

>d1ndda_ d.15.1.1 (A:) Nedd8 {Human (Homo sapiens)}

MLIKVKTLTGKEIEIDIEPTDKVERIKERVEEKEGIPPQQQLIYSGKQMNDEKTAADYKILGGSVLHL
VLALR

>d1vcba_ d.15.1.1 (A:) Elongin B {Human (Homo sapiens)}

MDVFLMIRRHKTTIFTDAKESSTVFELKRIVEGILKRPPDEQRLYKDDQLDDGKTLGECGFTSQTA
RPQAPATVGLAFRADDTFEALCIEPFSSPPE

>d1bt0a_ d.15.1.1 (A:) Rub1 {Mouse-ear cress (Arabidopsis thaliana)}

MLIKVKTLTGKEIEIDIEPTDTIDRIKERVEEKEGIPPVQQQLIYAGKQLADDKTAKDYNIEGGSVLHL
LAL

>d1h8ca_ d.15.1.2 (A:) Fas-associated factor 1, Faf1 {Human (Homo sapiens)}

NAEPVSKLRIRTPSGEFLERRFLASNKLQIVDFVASKGFPWDEYKLLSTFPRRDVTQLDPNKSLEEV
KLFPPQETLFLEAKE

>d1i42a_ d.15.1.2 (A:) p47 {Rat (Rattus norvegicus)}

KASSILINEAEPTTNIQIRLADGGRLVQKFNHSHRISDIRLFIVDARPAMAATSFVLMTTFPNKELAD
ENQTLKEANLLNAVIVQRLT

>d1eo6a_ d.15.1.3 (A:) Golgi-associated ATPase enhancer of 16 kD, Gate-16 {Cow (Bos taurus)}

MKWMFKEDHSLEHRCVESAKIRAKYPDRVPVIVEKVSQIVDIDKRKYLVPSPDITVAQFMWIIRKR
IQLPSEKAIFLVDKTVPQSSLTMGQLYEKEKDEDGFLYVAYSGENTFG

>d1gnua_ d.15.1.3 (A:) GABA(A) receptor associated protein GABARAP {Human (Homo sapiens)}

MKFVYKEEHPFEKRRSEGEKIRKKYPDRVPVIVEKAPKARIGDLDRKKYLVPSPDLTVGQFYFLIRKRI
HLRAEDALFFVNNVIPPTSATMGQLYQEHHEEDFFLYIAYSDESUYGL

>d1ef1a3 d.15.1.4 (A:4-87) Moesin {Human (Homo sapiens)}

TISVRVTTMDAELEFAIQPNTTGKQLFDQVVKTIGLREVWFFGLQYQDTKGFSTWLKLNKKVTAQD
VRKESPLLKFKRAKFYPE

>d1gc7a3 d.15.1.4 (A:1-87) Radixin {Mouse (Mus musculus)}

MPKPINVRVTTMDAELEFAIQPNTTGKQLFDQVVKTIVGLREVWFFGLQYVDSKGYSTWLKLNKKV
TQQDVKKENPLQFKFRAKFFPE

>d1gg3a3 d.15.1.4 (A:1-81) Erythroid membrane protein 4.1R {Human (Homo sapiens)}

MHCKVSLDDTVYECVVEKHAKGQDLLKRVCEHLNLEEDYFGLAIWDNATSKTWLDSAKEIKKQ
VRGVPWNFTFNVKFYP

>d1h4ra3 d.15.1.4 (A:20-103) Merlin {Human (Homo sapiens)}

KTFTVRIVTMDAEMEFNCEMKWKGKDLFDLVCRTLGLRETWFFGLQYTIKDTVAVLKMDDKKVLD
HDVSKEEPVTFHFLAKFYPE

>d1c1yb_ d.15.1.5 (B:) c-Raf1 RBD {Human (Homo sapiens)}

SNTIRVFLPNKQRTVVNVRNGMSLHDCLMKALKVRGLQPECCAUFRLLEHKGKKARLDWNTDAA
SLIGEELQVDFL

>d1lfda_ d.15.1.5 (A:) Ral guanosine-nucleotide exchange factor, RalGDS {Rat (Rattus

norvegicus}}
GDCCIIRVSLDVDNGNMYKSILVTSQDKAPT VIRKAMDKHNLEDEPEDYELLQIISEDHKLKIPENA
NVFYAMNSAANYDFILKKR
>d1raxa_ d.15.1.5 (A:) Ral guanosine-nucleotide exchange factor, RalGDS {Human (Homo sapiens}}
QQVGDCCIIRVSLDVDNGNMYKSILVTSQDKAPAVIRKAMDKHNLEEEEPEDYELLQILSDDRKLKIP
ENANVFYAMNSTANYDFVLKKRTFT
>d1rlf_ d.15.1.5 (-) RalGDS-like factor, Rlf {Mouse (Mus musculus}}
GSSDCRIIRVQMELGEDGSVYKSILVTSQDKAPSVISRVLKKNNRDSAVASEFELVQLLPGDRELTIPHS
ANVFYAMDGASHDFLLRQRR
>d1ef5a_ d.15.1.5 (A:) Rgl {Mouse (Mus musculus}}
EDTCHIRISVEDNNGNMYKSIMLTSQDKTPAVIQRAMSKHNLESDPAEEYELVQVISEDKELVIPDSAN
VFYAMNSQVNFDFILRKKN
>d1e8xa3 d.15.1.5 (A:142-321) Phosphoinositide 3-kinase (PI3K) {Pig (Sus scrofa}}
AASEETLAFQRQLNALIGYDVT DVS NVHDDELEFTRRRRLVTPRMAEVAGRDPKLYAMHPWVTSKPL
PEYLLKKITNNCFVIVHRSTTSQTIKVSADDTPGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVC
GRDEYLVGETPIKNFQWVRQCLKNGEIIHLVLDTPDPALDEVRKE
>d1e8ya3 d.15.1.5 (A:143-322) Phosphoinositide 3-kinase (PI3K) {Human (Homo sapiens}}
MSEESQAFQRQLTALIGYDVT DVS NVHDDELEFTRRGLVTPRMAEVASRDPKLYAMHPWVTSKPLP
EYLWKKIANNCIFVIVHRSTTSQTIKVSPDDTPGAILQSFFTKMAKKKSLMDIPESQSEQDFVLRVCGR
DEYLVGETPIKNFQWVRHCLKNGEIIHVLDTPDPALDEVRKEE
>d1i35a_ d.15.1.5 (A:) Protein kinase byr2 {Yest (Schizosaccharomyces pombe}}
CILRFIACNGQTRAVQSRGDYQKTLAIALKKFSLEDASKFIVCVSQSSRIKLITEEEFKQICFNSSSPERD
RLIIVPKEKPCPSFEDLRRSWEIE
>d1d4ba_ d.15.2.1 (A:) Cell death-inducing effector B (CIDE-B), N-terminal domain {Human (Homo sapiens}}
MEYLSALNPSDLLRSVSNISSEFGRRVWTSAPPPQRPFVCDHKRTIRKGLTAATRQELLAKALETLL
LNGVLT LVLEEDGTAVDSEDFQLLEDDTCLMVLQSGQSWSPTRSGVLHHHHHH
>d1c9fa_ d.15.2.1 (A:) Caspase-activated DNase (CAD), DFF40, N-terminal domain {Mouse (Mus musculus}}
MCAVLRQPKCVKLRALHSACKFGVAARSCQELLRKGCVRFQLPMPGSRLCLYEDGTEVTDDCFGLP
NDAELLLLTAGETWHGYVSD
>d1ibxa_ d.15.2.1 (A:) Caspase-activated DNase (CAD), DFF40, N-terminal domain {Human (Homo sapiens}}
MLQKPKSVKLRALRSPRKFVAGRSCQEVLRKGC LRFQLPERGSRLCLYEDGTELTEDYFPSVPDNA
ELVLLTLGQAWQGH
>d1f2ri_ d.15.2.1 (I:) Inhibitor of caspase-activated DNase (ICAD), DFF45, N-terminal domain {Mouse (Mus musculus}}
MELSRGASAPDPDDVRPLKPCLLRRNHSRDQHGVAASSLEELRSKACELLAIDKSLTPITLVLAEDGT
IVDDDDYFLCLPSNTKFVALACNEKWTYNSD
>d1ibxb_ d.15.2.1 (B:) Inhibitor of caspase-activated DNase (ICAD), DFF45, N-terminal domain {Human (Homo sapiens}}
SGEIRTLKPCLLRRNYSREQHGVAASCLEDLRSKACDILAIKSLTPVTLVLAEDGTIVDDDDYFLCLP
SNTKFVALASNEKWAYNNSD

>d1ip9a_ d.15.2.2 (A:) Bud emergence mediator Bemp1 {Baker's yeast (*Saccharomyces cerevisiae*)}

GAMGSSTSLKTTTKIKFYKDDIFALMLKGDTTYKELRSKIAPRIDTDNFKLQTKLFDGSGEIKTDS
QVSNIIQAKLKISVHDI

>d1fm0d_ d.15.3.1 (D:) Molybdopterin synthase subunit MoaD {*Escherichia coli*}

MIKVLFFAQVRELVGTDVAADFPTVEALRQHMAAQSDRWALALEDGKLLAAVNQTLVSFDHPL
TDGDEVAFPPVTGG

>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*}

MVIGMKFTVITDDGKKILESGAPRRIKDVLGELEIPIETVVVKKNGQIVIDEEEIFDGDHIEVIRVIYGG

>d1czpa_ d.15.4.1 (A:) 2Fe-2S ferredoxin {*Cyanobacterium* (*Anabaena* sp.), pcc 7119 and 7120}

ATFKVTLINAEAGTKHEIEVPPDDEYILDAAEEQGYDLPFSCRAGACSTCAGKLVSGTVDQSDQSFLDD
DQIEAGYVLTVCVAYPTSDVVIQTHKEEDLY

>d1frd_ d.15.4.1 (-) 2Fe-2S ferredoxin {*Cyanobacterium* (*Anabaena* sp.), pcc 7119 and 7120}

ASYQVRLINKKQDIDTTIEIDEETTILDGAEENGIELPFSCSHSGSCSSCVGKVVVEGEVDQSDQIFLDDE
QMKGFFALLCVTYPRSNCTIKTHQEPYLA

>d4fxc_ d.15.4.1 (-) 2Fe-2S ferredoxin {*Spirulina platensis*}

ATYKVTLINAEAGINETIDCDDDTYILDAAEEAGLDLPYSCRAGACSTCAGTITSGTIDQSDQSFLDDD
QIEAGYVLTVCVAYPTSDCTIKTHQEEGLY

>d1fxia_ d.15.4.1 (A:) 2Fe-2S ferredoxin {*Cyanobacterium* (*Aphanothece sacrum*)}

ASYKVTLKTPDGDNVITVPDDEYILDVAEEEGLDLPYSCRAGACSTCAGKLVSGPAPDEDQSFLDDD
QIQAGYILTCVAYPTGDCVIETHKEEALY

>d1dox_ d.15.4.1 (-) 2Fe-2S ferredoxin {*Synechocystis* sp., pcc 6803}

ASYTVKLITPDGESSIECSDDTYILDAAEEAGLDLPYSCRAGACSTCAGKITAGSVDQSDQSFLDDDQI
EAGYVLTVCVAYPTSDCTIETHKEEDLY

>d2cjn_ d.15.4.1 (-) 2Fe-2S ferredoxin {*Synechococcus elongatus*}

ATYKVTLVLRPDGSETTIDVPEDEYILDVAEEQGLDLPFSCRAGACSTCAGKLLGEVVDQSDQSFLDDD
QIEKGFVLTVCVAYPRSDCKILTQEEELY

>d1awd_ d.15.4.1 (-) 2Fe-2S ferredoxin {*Chlorella fusca*}

YKVTLKTPSGEETIECPEDTYILDAAEEAGLDLPYSCRAGACSSCAGKVESGEVDQSDQSFLDDAQM
KGFVLTVCVAYPTSDVTILTHQEAALY

>d1fra_ d.15.4.1 (A:) 2Fe-2S ferredoxin {*Equisetum arvense*}

AYKTVLKTSPGFTLDVPEGTTLIDAAEEAGYDLPFSCRAGACSSCLGKVVSGSVDESEGSFLDDGQM
EEGFVLTCAIPESDLVIETHKEEELF

>d1doi_ d.15.4.1 (-) 2Fe-2S ferredoxin {Archaeon *Haloarcula marismortui*}

PTVEYLNIEVVDNNGWDMYDDDDVFGEASDMDLDDDEDYGSLEVNEGEYILEAAEAQGYDWPFCR
AGACANCAAIIVLEGDIDMDMQILSDEEVEDKNVRLTCIGSPDADEVKIVYNAKHLDYLQNRVI

>d1e0za_ d.15.4.1 (A:) 2Fe-2S ferredoxin {Archaeon *Halobacterium halobium*}

PTVEYLNIEYTLDDQGWDMDDDDLFKAADAGLDGEDYGTMEVAEAGEYILEAAEAQGYDWPFCR
AGACANCASIVKEGEIDMDMQILSDEEVEEKDVRLTCIGSPADEVKIVYNAKHLDYLQNRVI

>d1pfd_ d.15.4.1 (-) 2Fe-2S ferredoxin {Parsley (Petroselinum crispum)}
ATYNVKLITPDGEVEFKCDDDDVYVLDQAEEEGIDIPYSCRAGSCSSCAGKVVSGSIDQSDQSFLDDEQ
MDAGYVLTCHAYPTSDVVIETHKEEEIV

>d1a70_ d.15.4.1 (-) 2Fe-2S ferredoxin {Spinach (Spinacia oleracea)}
AAYKVTLVPTGNVEFQCPDDVYILDAAEEEGIDLPYSCRAGSCSSCAGKLTGSLNQDDQSFLDDDD
QIDEGWVLTCAAYPVSDVTIETHKKEELTA

>d1gaqb_ d.15.4.1 (B:) 2Fe-2S ferredoxin {Maize (Zea mays)}
ATYNVKLITPEGEVELQVPDDVYILDQAEEEDGIDLPYSCRAGSCSSCAGKVVSGSVDQSDQSYLDDGQ
IADGWVLTCHAYPTSDVVIETHKEEELTGA

>d1e9ma_ d.15.4.1 (A:) Ferredoxin VI {Rhodobacter capsulatus}
AKIIFIEHNGTRHEVEAKPGLTVMEAARDNGVPGIDADCGGACACSTCHAYVDPAWVDKLPKALPTE
TDMIDFAYEPNPATSRLTCQIKVTSLLDGLVVHLPEKQI

>d1put_ d.15.4.1 (-) Putidaredoxin {Pseudomonas putida}
SKVVVYVSHDGTTRRLQDVADGVSLMQAAVSNGIYDIVGDCGGSASCATCHVYVNEAFTDKVPAANERE
IGMLECVTAELKPNRLCCQIIMTPELDGIVVDVPDRQW

>d1b9ra_ d.15.4.1 (A:) Terpredoxin {Pseudomonas sp.}
PRVVFIDEQSGEYAVDAQDQSLMEVATQNGVPGIVAECGGSCVCATCRIEIEDAWVEIVGEANPDEN
DLLQSTGEPMTAGTRLSCQVFIDPSMDGLIVRVPLPA

>d1ayfa_ d.15.4.1 (A:) Adrenodoxin {Cow (Bos taurus)}
KITVHFINRDGETLTTKGKIGDSLDDVVVQNNLDIDGFGACEGTLACSTCHLIFEQHIFEKLEAITDEE
NDMLDLAYGLTDRSRLGCQICLTKAMDNMTVRVP

>d1feha2 d.15.4.2 (A:1-126) Fe-only hydrogenase, N-terminal domain {Clostridium
pasteurianum}
MKTIHNGVQFNTDEDTTILKFARDNNIDISALCFLNNCNDINKCEICTVEVEGTGLVTACDTLIEDG
MIINTNSDAVNEKIKSRISQLLDIHEFKGPCNRRENCEFLKLVIKYKARASKPFLP

>d1hlra2 d.15.4.2 (A:1-80) Aldehyde oxidoreductase, N-terminal domain {Desulfovibrio
gigas}
MIQKVITVNGIEQNLVDAEALLSDVLRQQLGLTGKVGCEQGCGACSVILDGKVVVRACVTKMKRV
ADGAQITTEIEGVG

>d1dgja2 d.15.4.2 (A:1-80) Aldehyde oxidoreductase, N-terminal domain {Desulfovibrio
desulfuricans}
METKTLIVNGMARRLLVSPNDLLVDVLRSQLQLTSVKVCGCGKQCGACTVILDGKVVVRACIHKMSRVA
ENASVTTLEGIG

>d1fo4a2 d.15.4.2 (A:3-92) Xanthine oxidase, N-terminal domain {Cow (Bos taurus)}
ADELVFFVNGKVKVEKNADPETLLAYLRRKLGLRGTKLGCGECCGACTVMLSKYDRLQDKIIHFS
ANACLAPICTLHHVAVTTVEGIG

>d1jroa2 d.15.4.2 (A:1-84) Xanthine dehydrogenase chain A, N-terminal domain
{Rhodobacter capsulatus}
MEIAFLLNGETRRVRIEDPTQSLELLRAEGLTGTKEGCNEGDCGACTVMIRDAAGSRVNAACLMLL
PQIAGKALRTIEGIAAP

>d1qj2a2 d.15.4.2 (A:3-81) Carbone monoxide (CO) dehydrogenase iron-sulfur protein,
N-domain {Pseudomonas carboxydovorans}
KAHIELTINGHPVEALVEPRTLLIHFIREQQNLTGAHIGCDTSHCGACTVDLDGMSVKSCMFAVQAN
GASITTEIGMA

>d1ffva2 d.15.4.2 (A:3-81) Carbone monoxide (CO) dehydrogenase iron-sulfur protein, N-domain {Hydrogenophaga pseudoflava}
 KKIITVNVNGKAQEKAVEPRTLLIHFLREELNLTGAHIGCETSHCGACTVDIDGRSVKSCSTHLAVQCD
 GSEVLTVGLA

>d2pia_3 d.15.4.2 (224-321) Phthalate dioxygenase reductase, C-terminal domain {Pseudomonas cepacia, db01}
 SFGATNTNARENTPFTVRLSRSGTSFEIPANRSILEVLRDANVRVPSSCESGTCGCKTALCSGEADHR
 DMVLRDDEKGTQIMVCVSRKSAELVLDL

>d1fumb2 d.15.4.2 (B:1-105) Fumarate reductase iron-sulfur protein, N-terminal domain {Escherichia coli}
 AEMKNLKIEVVRYNPEVDTAPHSAFYEVYPYDATTSLLDALGYIKDNLAPDLSYRWSCRMAICGSCGM
 MVNNVPKLACKTFLRDYTDGMKVEALANFPIERDLVVD

>d1qlab2 d.15.4.2 (B:1-106) Fumarate reductase iron-sulfur protein, N-terminal domain {Wolinella succinogenes}
 MGRMLTIRVFKYDPQSAVSKPHFQEQYKIEEAPSMTIFIVLNMIRETYDPDLNFDVFCRAGICGSCGM
 MINGRPSLACRTLTKDFEDGVITLLPLPAFKLIKDLSVD

>d1jq4a_ d.15.4.2 (A:) Methane monooxygenase reductase N-terminal domain {Methylococcus capsulatus}
 MQRVHTITAVTEDGESLRFECRSDDEVITAALRQNIFLMSSCREGGCATCKALCSEGDYDLKGC SVQA
 LPPEEEEEGLVLLCRTYPKTDLEIELPYTH

>d1ssn_ d.15.5.1 (-) Staphylokinase {Staphylococcus aureus}
 SSSFDKGGYKKGDASYFEPTGPYLMVNVTVGVDKGNELLSPHYVEFPIKPGTTLTKEKIEYYVEWA
 LDATAYKEFRVVELDPSAKIEVTTYDKNKKKEETKSPITEKGFVVPDLSEHIKNPGFNLIKVVIEKK

>d2sak_ d.15.5.1 (-) Staphylokinase {Staphylococcus aureus}
 SYFEPTGPYLMVNVTVGVDKGNELLSPHYVEFPIKPGTTLTKEKIEYYVEWALDATAYKEFRVVELDP
 SAKIEVTTYDKNKKKEETKSPITEKGFVVPDLSEHIKNPGFNLIKVVIEKK

>d1bmlc1 d.15.5.1 (C:12-148) Streptokinase {Streptococcus equisimilis}
 SVNNSQLVSVAGTVEGTNQDISLKF FEIDLTSRPAHGGKTEQGLSPKSKPFATDSGAMPHKLEKADL
 LKAIQEQLIANVHSNDDYFEVIDFASDATITDRNGKVYFADKDGSVTLPTQPVQEFLLSGHVRVRPYK
 E

>d1bmlc3 d.15.5.1 (C:285-372) Streptokinase {Streptococcus equisimilis}
 DPFDRSHLKLFTIKYVDVNTNELLKSEQLLTASERNLDFRDLYDPRDKAKLLYNLDAFGIMDYTLT
 GKVEDNHDDTNRIITVYMGKR

>d1c4pc_ d.15.5.1 (C:) Streptokinase {Streptococcus equisimilis}
 KPIQNQAQSV DVEYTVQFTPLNPDDDFRPGDKLTKLLKTLAIGDTITSQELLAQAQSILNKTHPGYTI
 YERDSSIVTHDNDIFRTILPMDQEFTYHVKNREQAYEINKKSGLN EENNTDLISEKYYVLKKG

>d1qgra_ d.15.5.1 (A:) Streptokinase {Streptococcus equisimilis}
 IQNQAQSV DVEYTVQFTPLNPDDDFRPGDKLTKLLKTLAIGDTITSQELLAQAQSILNKNHPPGYTIYE
 RDSSIVTHDNDIFRTILPMDQEFTYRVKNREQAYRINKKSGLN EENNTDLISEKYYVLKKGKPYDP
 FD

>d1esfa2 d.15.6.1 (A:121-233) Staphylococcal enterotoxin A, SEA {Staphylococcus aureus}
 EEKKVPINLWLDGKQNTVPLETVKTNKKNVTVQELDLQARRYLQEKYNLYNSDVFDGKVQRGLIVF
 HTSTEPVNYDLFGAQQQSNTLLRIYRDNKTINSENMHIDIYLYTS

>d1i4pa2 d.15.6.1 (A:121-239) Staphylococcal enterotoxin C2, SEC2 {Staphylococcus aureus}

NHFDNGNLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEFNSSPYETGYIKF
IENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDKSKSVKIEVHLTTKNG
>d3tss_2 d.15.6.1 (94-194) Toxic shock syndrome toxin-1 (TSST-1) {Staphylococcus aureus}
LPTPIELPLKVKVHGKDSPLKYWPKFDKKQLAISTLDFKIRHQLTQTHGLYRSSDKTGGYWKITMND
GSTYQSDLSKKFEYNTEKPPINIDEIKTIEAEIN
>d1sebd2 d.15.6.1 (D:127-235) Staphylococcal enterotoxin B, SEB {Staphylococcus aureus}
DKYRSITVRVFEDGKNLLSFDVQTNKKKQVTAQELDYLRHYLVKNKKLYETGYIKFIENENSWFYDM
MPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLT
>d3seb_2 d.15.6.1 (122-238) Staphylococcal enterotoxin B, SEB {Staphylococcus aureus}
NGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKQVTAQELDYLRHYLVKNKKLYEFNNSPYETGYIK
FIENENSWFYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLTTKK
>d1enfa2 d.15.6.1 (A:102-213) Staphylococcal enterotoxin H, SEH {Staphylococcus aureus}
EKLAQERVIGANVWVDGIQKETELIRTNKKNVTLQELDIKIRKILSDKYKIYYKDSEISKGLIEFDMKT
PRDYSFDIYDLKGENDYEIDKIYEDNKTLSDDISHIDVNLTY
>d1an8_2 d.15.6.1 (96-208) Streptococcal superantigen Spe-C {Streptococcus pyogenes}
NKVNHKLLGNLFISGESQQLNKNKIILEKDIVTFQEIDFKIRKYLMDNYKIYDATSPYVSGRIEIGTKD
GKHEQIDLFDSNEGTRSDIFAKYKDNRIINMKNFSHFDIYLEK
>d1et9a2 d.15.6.1 (A:96-204) Streptococcal superantigen Spe-H {Streptococcus pyogenes}
EKKEIKVPVNVWDKSKQPPMFITVKNPKVTAQEVDIKVRKLLIKKYDIYNNREQKYSKGTVTLDL
NSGKDIVFDLYYFNGDFNSMLKIYSNNERIDSTQFHVDVSI
>d1eu3a2 d.15.6.1 (A:97-209) Streptococcal superantigen Smez-2 {Streptococcus pyogenes}
TSIPKNIPVNLWINGKQISVPYNEISTNKT'TVTAQEIDLKVRKFLIAQHQLYSSGSSYKSGRLVFHTND
NSDKYSFDLFYVGYRDKESIFKVYKDNKSFNIDKIGHLDIEIDS
>d1bxta2 d.15.6.1 (A:120-234) Streptococcal superantigen SSA {Streptococcus pyogenes}
QIEGKFPNITVKVYEDNENILSFDIT'TNKKQVTVQELDCKTRKILVSRKNLYEFNNSPYETGYIKFIESS
GDSFWYDMMPAPGAIFDQSKYLMYNDNKTVSSSAIAIEVHLTKK
>d1fnua2 d.15.6.1 (A:108-221) Streptococcal pyrogenic exotoxin A1 {Streptococcus
pyogenes}
GNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYTIDNKQLYTNGPSKYETGYIKFIP
KNKESFWFDFPEPEFTQSKYLMYKDNETLDNKTQSIEVYLTTK
>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}
MTTFKLIINGKTLKGEITIEAVDAAEAIEKIFKQYANDNGIDGEWTYDDATKTFTVTE
>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}

ELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWVWYDDATKTFTVTEMVTE
VPVA
>d1qkza_ d.15.7.1 (A:) Immunoglobulin-binding protein G, different constituent domains
{Streptococcus sp., group G}
VTTYKLVINGKTLKGETTTKAVDAATAEKVFKQYANDNGVDGEWYDDATKTFTVTEK
>d2igd_ d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains
{Streptococcus sp., group G}
MTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWVWYDDATKTFTVTE
>d2igg_ d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains
{Streptococcus sp., group G}
LTPAVTTYKLVINGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWYDDATKTFTVTEKPE
>d1heze_ d.15.7.1 (E:) Immunoglobulin light chain-binding domain of protein L
{Peptostreptococcus magnus}
EVTIKVNLIFADGKIQTAEFKGTFEEATAEAYRYADLLAKVNGEYTDLEDGGNHMNIKFA
>d1hz6a_ d.15.7.1 (A:) Immunoglobulin light chain-binding domain of protein L
{Peptostreptococcus magnus}
HHAMEEVTIKANLIFANGSTQAEFKGTFEKATSEAYAYADTLKKDNGEWTVDVADKGYTLNIKFAG
>d1jmla_ d.15.7.1 (A:) Immunoglobulin light chain-binding domain of protein L
{Peptostreptococcus magnus}
MHHHHHHGMEEVTIKANLIFANGSTQAEFKGTFEKATSEAYAYADTLKKDNGEWTVDVVPAKAYTL
NIKFAG
>d1k52a_ d.15.7.1 (A:) Immunoglobulin light chain-binding domain of protein L
{Peptostreptococcus magnus}
MHHHHHHHAMEEVTIKANLIFANGSTQAEFKGTFEKATSEAYAYADTLKKDNGEWTVDVADGGYT
LNIKFAG
>d1kh0a_ d.15.7.1 (A:) Immunoglobulin light chain-binding domain of protein L
{Peptostreptococcus magnus}
EEVTIKANLIFANGSTQAEFKGTFEKALSEVLAYADTLKKDNGEWTVIDKRVTNGVILNIKFAG
>d2ptl_ d.15.7.1 (-) Immunoglobulin light chain-binding domain of protein L
{Peptostreptococcus magnus}
ENKEETPETPETDSEEEVTIKANLIFANGSTQAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADK
GYTLNIKFAG
>d1tif_ d.15.8.1 (-) Translation initiation factor IF3, N-terminal domain {Bacillus
stearothermophilus}
KDFIINEQIRAREVRLIDQNGDQLGIKSKQEALEIAARRNLDLVLVAPNAKPPVCRIMDYGKFRFEQQ
KKEKEARK
>d1f52a1 d.15.9.1 (A:1-100) Glutamine synthetase, N-terminal domain {Salmonella
typhimurium}
SAEHLVLTMLNEHEVKFVDLRFTDTKGKEQHVTIPAHQVNAEFFEKGKMGFDGSSIGGWKGINESDMV
LMPDASTAVIDPFFADSTLIIRCDILEPGTLQGY
>d1coy_2 d.16.1.1 (319-450) Cholesterol oxidase {Brevibacterium sterolicum}
GNNGNIMVGRANHMWDATGSKQATIPTMGIDNWADPTAPIFAEIAPLPAGLETYVSLYLAIKTNPER
ARFQFNSGTGKVDLTWAQSQNQKIDMAKKVFDKINQKEGTIYRTDLFGVYKYTWGDDFTYHPLG
>d1ijha2 d.16.1.1 (A:319-450) Cholesterol oxidase {Streptomyces sp.}

GPNGNIMTARANHMWNPTGAHQSSIPALGIDAWDNSDSSVFAEIAPMPAGLETWVSLYLAIKPNPQ
 RGTFFVYDAATDRAKLNWTRDQNAVNAAKALFDRINKANGTIYRYDLFGTQLKAFADDFCYHPL
 G
 >d1k0ia2 d.16.1.2 (A:174-275) p-Hydroxybenzoate hydroxylase (PHBH) {Pseudomonas
 aeruginosa}
 LKVFERVYPFGWLGLLADTPPVSHELIYANHPRGFALCSQRSATRSQYYVQVPLSEKVEDWSDERFW
 TELKARLPSEVAEKLVTGPSLEKSIAPLRSFVVEP
 >d1foha4 d.16.1.2 (A:241-341) Phenol hydroxylase {Soil-living yeast (Trichosporon
 cutaneum)}
 GEQTDYIWGVLDVAVPASNFPDIRSRAIHSAESGSIIMIPRENNLVRFYVQLQARAEEKGGRVDRTKFT
 PEVVIANAKKIFHPYTFDVQQLDWFTAYHIGQR
 >d1an9a2 d.16.1.3 (A:195-287) D-amino acid oxidase {Pig (Sus scrofa)}
 LQPGRGQIHKVDAPWLKNFIITHDLERGIYNSPYIIPGLQAVTLGGTFQVGNWNEINNIQDHNTIWEQ
 CCRLEPTLKDIAKIVGEYTGFRPVRP
 >d1c0pa2 d.16.1.3 (A:1194-1288) D-amino acid oxidase {Yeast (Rhodotorula gracilis)}
 AEPIRQQTVLVKSPCKRCTMDSSDPASPAYIIPRPGGEVICGGTYGVGDWDLVSNPETVQRILKHCLRL
 DPTISSDGTIEGIEVLRHNVGLRPAR
 >d1el8a2 d.16.1.3 (A:218-321) Sarcosine oxidase {Bacillus sp., strain b0618}
 LQPYRQVVGFFESDESKYSNDIDFPGMVEVPNGIYYGFPSFGGCGCLKLGYHTFGQKIDPDTINREFG
 VYPEDESNLRAFLEEYMPGANGELKRGAVCMYTKTL
 >d1i8ta2 d.16.1.7 (A:245-313) UDP-galactopyranose mutases {Escherichia coli}
 EYRSLKFETERHEFPNFQGNVINFDTANVPYTRIIEHKHFDYVETKHTVVTKEYPLEWKVGDEPY
 YPV
 >d1cf3a2 d.16.1.4 (A:325-520) Glucose oxidase {Aspergillus niger}
 NLQDQTTATVRSRITSAGAGQGQAAWFATFNETFGDYSEKAHELLNTKLEQWAEAVARGGFHNTT
 ALLIQYENYRDWIVNHNVAISELFLDTAGVASFDVWDLPLPFRGYVHILDKDPYLHFFAYDPQYFLN
 ELDLLGQAAATQLARNISNSGAMQTYFAGETIPGDNLAYDADLSAWTEYIPYHFRPNYHGVGT
 >d1gpea2 d.16.1.4 (A:329-524) Glucose oxidase {Penicillium amagasakiense}
 NMQDQTTTTVSSRASSAGAGQQAFFANFTETFGDYAPQARDLLNTKLDQWAEETVARGGFHNV
 TALKVQYENYRNWLLDEDVAFELFMDTEGKINFDLWDLIPFTRGSVHILSSDPYLWQFANDPKFF
 LNEFDLLGQAAASKLARDLTSQGAMKEYFAGETLPGYNLVQATLSQWSDYVLQNFRPNWHAVSS
 >d1b5qa2 d.16.1.5 (A:294-405) Polyamine oxidase {Maize (Zea mays)}
 DMAVYTKIFLKFPRKFWPEGKGREFFLYASSRRGYGVWQEFKQYDPANVLLVTVTDEESRRIEQQ
 SDEQTKAEIMQVLRKMFPGKDVPDATDILVPRWWSDRFYKGTFSN
 >d1f8ra2 d.16.1.5 (A:320-432) L-amino acid oxidase {Malayan pit viper (Calloselasma
 rhodostoma)}
 HYRSGTKIFLTCTTKFWEDDGIHGGKSTTDLPSRFIYYPNHNFTNGVGVIIAYGIGDDANFFQALDFK
 DCADIVFNDLSLIHQLPKKDIQSFCYPSVIQKWSLKYAMGGITT
 >d1gosa2 d.16.1.5 (A:290-401) Monoamine oxidase B {Human (Homo sapiens)}
 PLGSVIKICIVYYKEPFWRKKDYCGTMIIDGEEAPVAYTLDDTKPEGNYAAIMGFILAHKARKLARLTK
 EERLKKLCELYAKVLGSLEALEPVHYEKNWCEEQYSGGCYTTY
 >d1d5ta2 d.16.1.6 (A:292-388) Guanine nucleotide dissociation inhibitor, GDI {Cow (Bos
 taurus)}
 RKAGQVIRIICLSHPKNTNDANSCQIIPQNQVNRKSDIYVCMISYAHNVAAQKGYIAIASTTVETTD

PEKEVEPALGLLEPIDQKFVAISDLYE

>d1mola_ d.17.1.1 (A:) Monellin, B & A chains together {Serendipity berry (Dioscoreophyllum cumminsii)}

GEWEIIDIGPFTQNLGKFAVDEENKIGQYGRLLTFNKVIRPCMKKTIYENEREIKGYEYQLVYASDKLF
RADISEDYKTRGRKLLRFNGPVPPP

>d1eqka_ d.17.1.2 (A:) Phytocystatin {Japanese rice (Oryza sativa), subsp. japonica, oryzacystatin-I}

MSSDGGPVLGGVEPVGNENDLHLVDLARFAVTEHNKKANSLLFEKLVSVKQQVAVAGTLYYFTIEVK
EGDAKKLYEAKVWEKPWMDFKELQEFKPVASANA

>d1cewi_ d.17.1.2 (I:) Cystatin {Chicken (Gallus gallus)}

GAPVPVDENDEGLQRALQFAMA EYNRASNDKYSSRVVRVISAKRQLVSGIKYILQVEIGRTTCKPKSSG
DLQSCFEHDEPEMAKYTTCTFVVYSIPWLNQIKLLESKCQ

>d1dvd_ d.17.1.2 (-) Cystatin A (stefin A) {Human (Homo sapiens)}

MIPGGLSEAKPATPEIQEIVDKVKPQLEEKTNETYGKLEAVQYKTQVVAGTNYIYKVRAGDNKYMHL
KVFKSLPGQNE DLVLTGYQVDKNKDDDELTFG

>d1stfi_ d.17.1.2 (I:) Cystatin B (stefin B) {Human (Homo sapiens)}

MMSGAPSATQPATAETQHIADQVRSQLEEKYNKKFPVFKAVSFKSQVVAGTNYFIKVVHVGDEDFVHL
RVFQSLPHENKPLTLSNYQTNKAKHDELTYF

>d1g96a_ d.17.1.2 (A:) Cystatin C {Human (Homo sapiens)}

VGGPMDASVEEEGVRRALDFAVGEYNKASNDMYHSRALQVVRARKQIVAGVNYFLDVELGRTTCTK
TQP NLNCPFH DQPHLKRKAFCSFQIYAVPWQGTMTLSKSTCQDA

>d1oaca2 d.17.2.1 (A:91-185) Copper amine oxidase, domains 1 and 2 {Escherichia coli}

KRPHPLNALTAEIKQAVEIVKASADFKPNTRFTEISLLPPDKEAVWAFALENKPVQPRKADVIML
DGKHIEAVVDLQNNKLLSWQPIKDAHG

>d1oaca3 d.17.2.1 (A:186-300) Copper amine oxidase, domains 1 and 2 {Escherichia coli}

MVLLDDFASVQNIINNSEEFAAAVKKGITDAKKVITPLTVGYFDGKDGLKQDARLLKVISYLDVGD
GNYWAHPHENLVAVVDLEQKKIVKIEEGPVVPVPM TARPFDGRDRVA

>d1ksia2 d.17.2.1 (A:6-98) Copper amine oxidase, domains 1 and 2 {Pea seedling (Pisum sativum)}

VQHPLDPLTKEEFLAVQTIVQNKYPISNNRLAFHYIGLDDPEKDHVLR YETHPTLV SIPRKIFVVAIIN
SQTHEILINLRIRSIVSDNIHNGY

>d1ksia3 d.17.2.1 (A:99-206) Copper amine oxidase, domains 1 and 2 {Pea seedling (Pisum sativum)}

GFPILSVDEQSLAIKLPKYPPFIDSVKKRGLNLSEIVCSSFTMGWFGEEKNVRTVRLDCFMKESTVN
IYVRPITGITIVADLDMKIVEYHDRDIEAVPTAENT EYQ

>d1av4_2 d.17.2.1 (9-96) Copper amine oxidase, domains 1 and 2 {Arthrobacter globiformis}

ASPFRLASAGEISEVQGILRTAGLLGPEKRIAYLGVLPARGAGSEAEDRRFRVFIHDSVSGARPQEVTV
SVTNGTVISAVELDTAATG

>d1av4_3 d.17.2.1 (97-211) Copper amine oxidase, domains 1 and 2 {Arthrobacter globiformis}

ELPVLEEEFEVVEQLLATDERWLKALAARNLDVSKVRVAPLSAGVFEYAEERGRRLRGLAFVQDFP
EDSAWAHPVDGLVAYVDVVSKEVTRVIDTGVPVPAEHGNYTDPELTG

>d1a2va2 d.17.2.1 (A:18-115) Copper amine oxidase, domains 1 and 2 {Yeast (Hansenula polymorpha)}

PARPAHPLDPLSTAEIKAATNTVKSIFAGKKISFNTVTLREPAKAYIQWKEQGGPLPPRLAYVILE
AGKPGVKEGLVDLASLSVIETRALETVQPI
>d1a2va3 d.17.2.1 (A:116-236) Copper amine oxidase, domains 1 and 2 {Yeast (Hansenula polymorpha)}
LTVEDLCSTEEVIRNDPAVIEQCVLGIPANEMHKVYCDPWTIGYDERWGTGKRLQALVYYRSDDED
DSQYSHPLDFCPIVDTEEEKVIFIDIPNRRRKVSKHKHANFYPPKHMIEKVGAMR
>d1eeja2 d.17.3.1 (A:1-60) Disulfide bond isomerase, DsbC, N-terminal domain {Escherichia coli}
DDAAIQQLAKMGIKSSDIQPAPVAGMKTVLTNSGVLYITDDGKHIIQGPMYDVSGTAPV
>d3stda_ d.17.4.1 (A:) Scytalone dehydratase {Fungus (Magnaporthe grisea)}
GEITFSDYLGLMTCVYEWADSYDSKDWDRLRKYIAPTLRIDYRSFLDKLWEAMPAAEFVGMVSSKQ
VLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKID
GVWKFAGLKPDIRWGEFDFDRIFEDGRETFG
>d1ouna_ d.17.4.2 (A:) Nuclear transport factor-2 (NTF2) {Rat (Rattus norvegicus)}
GDKPIWEQIGSSFIQHYYQLFDNDRTQLGAIYIDASCLTWEGQQFQGKAAIVEKLSSLPFQKIQHSITA
QDHQPTPDSCHISMVVGQLKADEDPIMGFQHMFLLKNINDAWVCTNDMFRLALHNF
>d1jkg_a_ d.17.4.2 (A:) NTF2-related export protein 1 (p15) {Human (Homo sapiens)}
ASVDFKTYVDQACRAAEFVNVYYTTMDKRRRLSRLYMGATLVWNGNAVSGQESLSEFFEMLPS
SEFQISVVDCCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNTVWKIASDCFRF
QDWAS
>d1jkg_b_ d.17.4.2 (B:) NTF2-like domain of Tip associating protein, TAP {Human (Homo sapiens)}
APPCKGSYFGTENLKSILVHFLQYYAIYDSGDRQGLLDAYHDGACCSLSIPFIPQNPARRSSLAIEYFKD
SRNVKCLKDPTLRFLLKHTRLNVVAFLNELPKTQHDVNSFVVDISAQTSTLLCFSVNGVFKEVDGK
SRDSLRAFTRTFIAPVANSGLCIVNDELVFRNASSEIQRAFAMPAPT
>d1qja_ d.17.4.3 (A:) Delta-5-3-ketosteroid isomerase, steroid delta-isomerase, KSI
{Comamonas testosteroni and Pseudomonas testosteroni}
MNTPEHMTAVVQRYVAALNAGDLGIVALFADDATVENPVGSEPRSGTAAIREFYANSLKLPLAVEL
TQEVRAVANEAAFAFIVSFYQGRKTVVAPIDHFRFNGAGKVVSMRALFGEKNIHAGA
>d1ea2a_ d.17.4.3 (A:) Delta-5-3-ketosteroid isomerase, steroid delta-isomerase, KSI
{Pseudomonas putida}
NLPTAQEVQGLMARFIELVDVGDIQVQMYADDATVEDPFGQPPIHGREQIAAFYRQGLGGGKVVRA
CLTGPVRASHNGCGAMPFRVEMVWNGQPCALDVIDVMRFDEHGRIQTMQAYWSEVNLV
>d1eg9b_ d.17.4.4 (B:) Naphthalene 1,2-dioxygenase beta subunit {Pseudomonas putida}
MINIQEDKLVSADAEIILRFFNCHDSALQQEATLLTQEAHLLDIQAYRAWLEHCVGSEVQYQVISR
ELRAASERRYKLNAMNVYENFQQLKVRVEHQLDPQNWGNSPKLRFTRFITNVQAAMDVNDKE
LLHIRSNVILHRARRGNQVDVFAAREDKWKRGEVGRKLVQRFVDYPERILQTHNLMVFL
>d1euic_ d.17.5.1 (C:) Uracil-DNA glycosylase inhibitor protein {Bacteriophage pbs2}
QLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMMLLTSDAPEYKPWALVIQDSNGENKIK
ML
>d1ugia_ d.17.5.1 (A:) Uracil-DNA glycosylase inhibitor protein {Bacteriophage pbs2}
TNLSDIIEKETGKQLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMMLLTSDAPEYKPWAL
VIQDSNGENKIKML
>d1pcf_a_ d.18.1.1 (A:) Transcriptional coactivator PC4 C-terminal domain {Human (Homo

sapiens}}

AMFQIGKMYVSVRDFKGVKVLIDIREYWMDPEGEMKPKGRKGISLNPEQWSQLKEQISDIDDAVRKL
>d1jb0d d.187.1.1 (D:) Photosystem I subunit PsuA {Synechococcus elongatus}
TTLTGQPPLYGGSTGGLLSAADTEEKYAITWTSPEQVFEMPTAGAAVMREGENLVYFARKEQCLAL
AAQQLRPRKINDYKIYRIFPDGETVLIHPKDGVPPEKVNKGREAVNSVPRSIGQNPNSQLKFTGKKP
YDP

>d3frua2 d.19.1.1 (A:1-178) Fc (IgG) receptor, alpha-1 and alpha-2 domains {Rat (Rattus norvegicus)}

AEPRLPLMYHLAAVSDSLTGLPSFWATGWLGAQYLYNNLRQEADPCGAWIWENQVSWYWEKE
TTDLKSKEQLFLEAIRTENQINGTFTLQGLLGCCELAPDNSSLPTAVFALNGEEFMRFNPRTGNWSG
EWPETDIVGNLWMKQPEAARKESEFLLTSCPERLLGHLERGRQNLEW

>d1cd1a2 d.19.1.1 (A:7-185) CD1, alpha-1 and alpha-2 domains {Mouse (Mus musculus)}

NYTFRCLQMSSFANRSWSRTDSVWVLGDLQTHRWSNDSATISFTKPKWSQGKLSNQQWEKQHM
QVYRVSFTRDIQELVKMMSPKEDYPIEIQLSAGCEMYPGNASESFLHVAFAQGKYVVRFWGTSWQTV
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}

LQNHTFLHTVYQCQDGSVGLSEAYDEDQLFFDFSQNTRVPRLPEFADWAQEQGDAILFDKEFCE
WMIQQIPKLDGKIPV

>d1hdmb2 d.19.1.1 (B:3-87) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DM}

FVAHVESTCLDDAGTPKDFTYCISFNKDLLTCWDPEENKMAPCNLANVLSQHNLNPKDTLMQRL
NGLQNCATHTQPFWGSNTNR

>d1aqdb2 d.19.1.1 (B:4-92) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR1}

RPRFLWQLKFECHFFNGTERVRLLERCIYNQEESVRFSDVGEYRAVTELGRPDAEYWNSQKDLLE
QRRAAVDTYCRHNYGVGESFTVQ

>d1bx2b2 d.19.1.1 (B:3-92) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR2}

TRPRFLWQPKRECHFFNGTERVFLDRYFYNQEESVRFSDVGEFRAVTELGRPDAEYWNSQKDIL
EQARAAVDTYCRHNYGVVESFTVQ

>d1fv1a2 d.19.1.1 (A:3-81) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR2}

EEHVIIQAEFYLNPDQSGEFMFDGDEIFHVDMAKKETVWRLEEFGRFASFQAQALANIAVDKA
NLEIMTKRSNYTP

>d1fv1b2 d.19.1.1 (B:1-92) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR2}

GDTRPRFLQDKYCHFFNGTERVFLHRDIYNQEEDLRFSDVGEYRAVTELGRPDAEYWNSQK
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}

PRFLEYSTSECHFFNGTERVRYLDRYFHNQEENVRFDSDVGEFRAVTELGRPDAEYWNSQKDLLEQ
KRGRVDNYCRHNYGVVESFTVQ

>d1d5zb2 d.19.1.1 (B:1-92) MHC class II, N-terminal domains of alpha and beta chains

{Human (Homo sapiens), HLA-DR4}
GDTRPRFLEQVKHECHFFNGTERVRFDRYFYHQEEYVRFSDVGEYRAVTELGRPDAEYWNSQK
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}
VADHVASYGVNLYQSYGSPSGQYSHEFDGDEEFYVDLERKETVWQLPLFRRFRFPDPQFALTNIAVLK
HNLNIVIKRSNSTAATN
>d1jk8b2 d.19.1.1 (B:3-94) MHC class II, N-terminal domains of alpha and beta chains
{Human (Homo sapiens), HLA-DQ8}
SPEDFVYQFKGMCYFTNGTERVRLVTRYIYNREEYARFSDVGVYRAVTPPLGPPAAEYWNSQKEVLE
RTRAEELDTVCRHNYQLELRTTTLQRR
>d1iaka2 d.19.1.1 (A:1-81) MHC class II, N-terminal domains of alpha and beta chains
{Mouse (Mus musculus), I-AK}
IEADHVGSYGITVYQSPGDIGQYTFEFDGDELFIYVDLDDKKETVWMLPEFAQLRRFEPQGGQNIATG
KHNLEILTKRSNSTP
>d1iakb2 d.19.1.1 (B:5-92) MHC class II, N-terminal domains of alpha and beta chains
{Mouse (Mus musculus), I-AK}
GSFVHQFQPCYFTNGTQRIRLVIRYIYNREEYVRFSDVGEYRAVTELGRPDAEYWNKQYLERTRA
ELDTVCRHNYEKTETPTSLR
>d1fnga2 d.19.1.1 (A:1-81) MHC class II, N-terminal domains of alpha and beta chains
{Mouse (Mus musculus), I-EK}
IKEEHTIIQAEFYLLPDKRGEFMDFDGDGDEIFHVDIEKSETIWRLEEFKAFASFEAQGALANIAVDKA
NLDVMKERSNNTP
>d1fn gb2 d.19.1.1 (B:4-92) MHC class II, N-terminal domains of alpha and beta chains
{Mouse (Mus musculus), I-EK}
RPWFLEYCKSECHFYNGTQRVRLVRYFYFNLEENLRFSDVGEFRAVTELGRPDAENWNSQPEFLE
QKRAEVDTVCRHNYEIFDNFLVP
>d1i3rb2 d.19.1.1 (B:1-120) MHC class II, N-terminal domains of alpha and beta chains
{Mouse (Mus musculus), I-EK}
GKKVITAFNEGLKGGGSLVGGGSGGGSRPWFLEYCKSECHFYNGTQRVRLVRYFYFNLEENLRFSD
SDVGEFRAVTELGRPDAENWNSQPEFLEQKRAEVDTVCRHNYEIFDNFLVPRR
>d2iadb2 d.19.1.1 (B:5-93) MHC class II, N-terminal domains of alpha and beta chains
{Mouse (Mus musculus), I-AD}
RHFVQFKGECYFTNGTQRIRLVTRYIYNREEYVRYDSDVGEYRAVTELGRPDAEYWNSQPEILERT
RAEVDTACRHNIEGPEPTSTSLR
>d1es0a2 d.19.1.1 (A:1B-82) MHC class II, N-terminal domains of alpha and beta chains
{Mouse (Mus musculus), I-A(G7)}
DIEADHVGFGYFTVYQSPGDIGQYTHEFDGDELFIYVDLDDKKKTWVRLPEFGQLILFEPQGGQNIAA
EKHNLGILTKRSNFTPA
>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)}
RHFVHQFKGECYFTNGTQRIRLVTRYIYNREEYLRFDSDVGEYRAVTELGRHSAEYWNKQYLERTRA
ELDTACRHNIEETEVPSTSLR
>d1k8ia2 d.19.1.1 (A:11-92) MHC class II, N-terminal domains of alpha and beta chains

{Mouse (Mus musculus), H2-DM}
QNHTFRHTLFCQDGIPNIGLSEYDEDELFSFDFSQNTRVPRLPDFAEWAQGGDASAIAFDKSFCE
MLMREVSPKLEGQIP
>d1k8ib2 d.19.1.1 (B:1-94) MHC class II, N-terminal domains of alpha and beta chains
{Mouse (Mus musculus), H2-DM}
GFVAHVESTCVLNDAGTPQDFTYCVSFNKDLLACWDPDVGKIVPCEFGVLSRLAEIISNILNEQESLIH
RLQNGLQDCATHTQPFWDVLTHRTR
>d1i4fa2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-A2.1}
GSHSMRYFFTSVSRPGRGEPRIAIVGYVDDTQFVRFSDAASQRMEPRAPWIEQEGPEYWDGETRK
VKAHSQTHRVDLGLTRGYYNQSEAGSHTVQRMYGCDVGSWDRFLRGYHQYAYDGKDYIALKEDLRS
WTAADMAAQTTKHKWEAAHVAEQLRAYLEGTCVEWLRRYLENGKETLQR
>d1hsaa2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-B2705}
GSHSMRYFHTSVSRPGRGEPFITVGYVDDTLFVRFSDAASPREEPRAPWIEQEGPEYWDRETQIC
KAKAQTDREDLRTLRRYYNQSEAGSHTLQNMYGCDVGPDRLLRGYHQDAYDGKDYIALNEDLSS
WTAADTAAQITQRKWEAARVAEQLRAYLEGECVEWLRRYLENGKETLQR
>d1hsba2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-AW68}
GSHSMRYFYTSVSRPGRGEPRIAIVGYVDDTQFVRFSDAASQRMEPRAPWIEQEGPEYWDRNTR
NVKAQSQTDRVDLGLTRGYYNQSEAGSHTIQMMYGCDVGSWDRFLRGYRQDAYDGKDYIALKEDLR
SWTAADMAAQTTKHKWEAAHVAEQWRAYLEGTCVEWLRRYLENGKETLQR
>d1agda2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-B0801}
GSHSMRYFDTAMSRPGRGEPFISVGYVDDTQFVRFSDAASPREEPRAPWIEQEGPEYWDRNTQI
FKTNTQTDRESLRNLRGYYNQSEAGSHTLQSMYGCDVGPDRLLRGHNQYAYDGKDYIALNEDLRS
WTAADTAAQITQRKWEAARVAEQDRAYLEGTCVEWLRRYLENGKDTLER
>d1a1na2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-B*3501}
GSHSMRYFYTAMSRPGRGEPRIAIVGYVDDTQFVRFSDAASPRTEPRPPWIEQEGPEYWDRNTQI
FKTNTQTYRESLRNLRGYYNQSEAGSHIIQRMYGCDLGPDRLLRGHDQSAYDGKDYIALNEDLSS
WTAADTAAQITQRKWEAARVAEQLRAYLEGLCVEWLRRYLENGKETLQR
>d1e27a2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-B*5101}
GSHSMRYFYTAMSRPGRGEPRIAIVGYVDDTQFVRFSDAASPRTEPRAPWIEQEGPEYWDRNTQI
FKTNTQTYRENLRALRYYNQSEAGSHTWQTMYGCDVGPDRLLRGHNQYAYDGKDYIALNEDLSS
WTAADTAAQITQRKWEAAREAEQLRAYLEGLCVEWLRRHLENGKETLQR
>d1efxa2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-CW3}
GSHSMRYFYTAVSRPGRGEPHFIIVGYVDDTQFVRFSDAASPRGEPRAPWVEQEGPEYWDRETQK
YKRQAQTDRVSLRNLRGYYNQSEAGSHIIQRMYGCDVGPDRLLRGYDQYAYDGKDYIALNEDLRS
WTAADTAAQITQRKWEAAREAEQLRAYLEGLCVEWLRRYLKNGKETLQR
>d1qqda2 d.19.1.1 (A:2-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-CW4}

SHSMRYFSTSVSWPGRGEPFIAVGYVDDTQFVRFSDAASPRGEPREPWVEQEGPEYWDRETQK
YKRQAQADRVNLRKLRGYYNQSEDSHTLQRMFGCDLGPDRLLRGYNQFAYDGGDYIALNEDLRS
WTAADTAAQITQRKWEAAREAEQRRAYLEGTCVEWLRRYLENGKETLQR
>d1mhea2 d.19.1.1 (A:2-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-E}
SHSLKYFHTSVSRPGRGEPFISVGYVDDTQFVRFNDAAASPRMVPAPWMEQEGSEYWDRETRS
ARDTAQIFRVNLRRLRGYYNQSEAGSHTLQWMHGCELGPDRRFLRGYEQFAYDGGDYIALNEDLRS
WTAVDTAAQISEQKSNDAEAEHQRAYLEDTCVEWLHKYLEKGGKETLLH
>d1de4a2 d.19.1.1 (A:4-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), hemochromatosis protein Hfe}
RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFDHESRRVEPRTPWVSSRISSQMWLQLSQSLK
GWDHMFVDFWTFIMENHNHNSKESHTLQVILGCEMQEDNSTEGYWKYGYDGDHLEFCPDTLDW
RAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQLLELGRGVLG
>d1fzka2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), H-2KB}
GPHSLRYFVTAVSRPGLGEPYMEVGYVDDTEFVRFSDAENPRYEPRARWMEQEGPEYWERETQ
KAKGNEQSFVRDLRLLGYYNQSKGGSHTIQVISGCEVGS DGRLLRGYQYAYDGGDYIALNEDLKT
WTAADMAALITKHKWEQAGAAEYRAYLEGTCVEWLRRYLKNGNATLLR
>d1jpfa2 d.19.1.1 (A:2-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), H-2DB}
PHSMRYFETAVSRPGLLEPRYISVGYVDNKEFVRFSDAENPRYEPRAPWMEQEGPEYWERETQK
AKGQEQWFRVSLRNLLGYYNQSAGGSHTLQMSGCDLGS DWRLLRGYLQFAYEGRDYIALNEDLKT
WTAADMAAQITRRKWEQSGAAEHYKAYLEGECEVEWLHRYLKNGNATLLR
>d1mhca2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), H-2M3}
GSHSLRYFHTAVSRPGRGEPQYISVGYVDDVQFQRCDSEIEIPRMEPRAPWMEKERPEYWKELKLK
VKNIAQSARANLRTLRYYNQSEGGSHILQWMVSCVGPDMRLLGAHYQAAYDGS DYITL NEDLSS
WTAVDMVSQITKSRLESAGTAEYFRAYVEGECELELLHRFLRNGKEILQR
>d1ld9a2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), H-2LD}
GPHSMRYFETAVSRPGLGEPYISVGYVDNKEFVRFSDAENPRYEPQAPWMEQEGPEYWERITQI
AKGQEQWFRVNLRLTLLGYYNQSAGGHTLQWMYGCDVGS DGRLLRGYEQFAYDGGDYIALNEDLK
TWTAAADMAAQITRRKWEQAGAAEYRAYLEGECEVEWLHRYLKNGNATLLR
>d1qo3a2 d.19.1.1 (A:2-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), H-2DD}
SHSLRYFVTAVSRPGLGEPYMEVGYVDNTEFVRFSDAENPRYEPRARWIEQEGPEYWERETRRRA
KGNEQSFVRDLRTALRYYNQSAGGSHTLQWMAGCDVES DGRLLRGYWQFAYDGGDYIALNEDLKT
WTAADMAAQITRRKWEQAGAAERDRAYLEGECEVEWLHRYLKNGNATLLR
>d1k8da2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), IB QA-2}
GQHSLQYFHTAVSRPGLGEPWFISVGYVDDTQFVRFSDAENPRMEPRARWMEQEGPEYWERETQ
IAKGHEQSFRLRTAQSYYNQSKGGSHTLQWMYGCDMGSDGRLLRGYLQFAYEGRDYIALNEDLK
TWTAVDMAAQITRRKWEQAGIAEKDQAYLEGTCMQLRRYLELGGKETLLR
>d1ed3a2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Rat (Rattus

norvegicus), RT1-AA}
 GSHSLRYFYTAVSRPGLGEPFRIAVGYVDDTEFVRFSDAENPRMEPRARWMEREGPEYWEQQTRI
 AKEWEQIYRVDLRTLRYGYYNQSEGGSHTIQEMYGCDVGS DGSLLRQDAYDGRDYIALNEDLKT
 WTAADFAAQITRNKWERARYAERLRLAYLEGTCVEWLSRYLELGKETLLR
 >d1zaga2 d.19.1.1 (A:5-183) Zinc-alpha-2-glycoprotein, ZAG {Human (Homo sapiens)}
 DGRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNSKDRKSQPMGLWRQVEGMEDWKQDSQL
 QKAREDIFMETLKDIVEYYNDSNGSHVLQGRFGCEIENNRSSGAFWKYYYDGDYIEFNKEIPAWVP
 FDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYSKNILDR
 >d1hyrc2 d.19.1.1 (C:0-180) MHC I homolog {Human (Homo sapiens), Mic-a}
 MEPHSLRYNLTVLSWDGVSQSGFLTEVHLDGQPFLRCRQKCRAPQGGWAEDVLGNKTWDRET
 RDLTGNGKDLRMTLAHIKDQKEGLHSLQEIRVCEIHEDNSTRSSQHFYYDGELFLSQNLETKEWTM
 PQSSRAQTLAMNVRNFLKEDAMKTKTHYHAMHADCLQELRRYLKSGVVLRR
 >d1c16a2 d.19.1.1 (A:1-180) MHC I homolog {Mouse (Mus musculus), t22}
 GSHSLRYFYTAVSRPGLGEPWFIIVGYVDDMQVLRFSKKEETPRMAPWLEQEEADNWEQQTRIVTI
 QGQLSERNLMTLVHFYFNKSMDDSHTLQWLQGC DVEPDRHLCLWYNQLAYDSEDLPTLNENPSSCT
 VGNSTVPHISQDLKSHCSDLLQKYLEKGERLL
 >d1exua2 d.19.1.1 (A:4-176) Class I MHC-related Fc receptor {Human (Homo sapiens)}
 HLLSLYHLTAVSSPAPGTPAFVWVGWLGPPQYLSYNSLRGEAEPGAWVWENQVSWYWEKETTDL
 RIKEKLFLEAFKALGGKGPYTLQGLLGC ELGPDNTSVPTAKFALNGEEFMNFDLKQGTWGGDWPEA
 LAISRWQQQDKAANKELTFLFSCPHRLREHLERGRGNLEW
 >d1kcg_c d.19.1.1 (C:) Class I MHC-related molecule Ulbp3 {Human (Homo sapiens)}
 DAHSLWYNFTIHLPRHGQQWCEVQSQVDQKNFLSYDCGSDKVLSMGHLEEQLYATDAWGKQLEM
 LREVGQRLRLELADTELEDFTPSGPLTLQVRMSCECEADGYIRGSWQFSFDGRKFLFDSSNNRKT
 VVHAGARRMKEKWEKDSGLTTFFKMVS MRDCKSWLRDFLMHRKKRLE
 >d1jfma_ d.19.1.1 (A:) NK cell ligand RAE-1 beta {Mouse (Mus musculus)}
 DAHSLRCNLTIKDPTPADPLWYEAKCFVGEILHLHLSNINKTMTSGDPGETANATEVKKCLTQPLKNL
 CQKLRNKVSNKVDTHKTNNGYPHLQVTMIYPSQGRTPSATWEFNISDSYFFTFY TENMSWRSAN
 DESGVIMNKWKDDGEFVKQLKFLIHECSQKMDEFLKQSKEK
 >d2aak_ d.20.1.1 (-) Ubiquitin conjugating enzyme {Arabidopsis thaliana}
 MSTPARKRLMRDFKRLQQDPPAGISGAPQDNNIMLWNAVIFGPDTPWDGGTFKLSLQFSEYDYPN
 KPPTVRFVSRMFHPNIYADGSICLDILQNWSPYIDVAAILTSIQSLLCDPNPNSPANSEARMYSESK
 REYNRRVRDVVEQSWT
 >d1fzya_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces
 cerevisiae), ubc1}
 SRAKRIMKEIQAVKDDPAAHITLEFVSESDIHHLKGTFLGPPGTPYEGGKFVVDIEVPM EYFPKPPKM
 QFDTKVYHPNISSVTGAICLDILKNAWSPVITLKSALISLQALLQSPEPNDPQDAEVAQH YLRDRESF
 NKTAALWTRLYAS
 >d1ayza_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces
 cerevisiae), ubc2 (RAD6)}
 STPARRRLMRDFKRMKEDAPPGVSASPLPDNVMVWNAMIIGPADTPYEDGTFRLLLEFDEEYPNK
 PPHVKFLSEMFPNVYANGEICLDILQNRWTPTYDVASILT SIQSLFNDPNPASPANVEAATLFKDHK
 SQYVKRVKETVEKSWEDDMD
 >d1qcqa_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces
 cerevisiae), ubc4}

MSSSKRIAKELSDLERDPPTSCSAGPVGDDLYHWQASIMGPADSPYAGGVFFLSIHFPTDYPFKPPKIS
FTTKIYHPNINANGNICLDILKDQWSPALTLKVVLSICSLLTDANPDDPLVPEIAHIYKTRPKYEAT
AREWTKKYAV

>d2ucz_ d.20.1.1 (-) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae), ubc7}

SKTAQKRLKELQQLIKDSPPGIVAGPKSENNIFIWDCLIQPPDTPYADGVFNKLEFPKDYPLSPPK
LTFTPSILHPNIYPNGEVCISILHSPGDDPNMYELAEERWSPVQSVKILLSVMSMLSEPNIESGANID
ACILWRDNRPEFERQVKLSILKSLGF

>d1jata_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae), ubc13}

AASLPKRIIKETEKLVSDPVPGITAEPHDDNLRVFQVTIEGPEQSPYEDGIFELELYLPDDYPMEAPKV
RFLTKIYHPNIDRLGRICLDVLTNWSPALQIRTVLLSIQALLASPNDPLANDVAEDWIKNEQGAK
AKAREWTKLYAKKKP

>d1j7db_ d.20.1.1 (B:) Ubiquitin conjugating enzyme {Human (Homo sapiens), ubc13}

AGLPRRIKETQRLLAEPVPGIKAEPDESNAFYFHVVIAGPQDSPFEGGTFKLELFLPEEYPMAPKV
RFMTKIYHPNVDKLGRICLDILKDKWSPALQIRTVLLSIQALLSAPNDPLANDVAEQWKTNEAQA
IETARAWTRLYAMN

>d1jatb_ d.20.1.1 (B:) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae), mms2}

SKVPRNFRLLLEELEKGEKGFPESCSYGLADSDITMTKWNGTILGPPHSNHENRIYSLSIDCGPNYP
DSPPKVTFISKINLPCVNPTTGEVQTFHFLRDWKRAYTMETLLDLRKEMATPANKKLRQPKEGE
TF

>d1j7da_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Human (Homo sapiens), mms2}

GVKVPNFRLLLEELEEGQKGVGDGTVSWGLEDDEDMTLTRWTGMIIGPPRTNYENRIYSLKVECGP
KYPEAPPSVRFVTKINMNGINSSGMVDARSIPVLAKWQNSYSIKVVLQELRRLMMSKENMKLPQP
PEGQTYNN

>d1c4zd_ d.20.1.1 (D:) Ubiquitin conjugating enzyme {Human (Homo sapiens), ubch7}

SRRLMKELEEIRKCGMKNFRNIQVDEANLLTWQGLIVPDNPPYDKGAFRIEINFPAEYFPKPPKITFK
TKIYHPNIDEKGQVCLPVISAEENWKPATKTDQVIQSLIALVNDPQPEHPLRADLAEYSKDRKKFCK
NAEFTKKY

>d1u9aa_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Human (Homo sapiens), ubc9}

LNMSGIALSRLAQERKAWRKDHPFGFVAVPTKNPDGTMNLMNWECAIPGKKGTPWEGGLFKLRM
LFKDDYPSPPCKKFEPPLFHPNVYPSGTVCLSILEEDKDWPAITIKQILLGIQELLNEPNIQDPAQA
EAYTIYCQNRVEYEKRVRAQAKKFAPS

>d1i7ka_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Human (Homo sapiens), ubch10}

PVGKRLQQELMTLMMSGDKGISAFPESDNLFKWVGTIHGAAGTVYEDLRYKLSLEFPSGYPNAPT
VKFLTPCYHPNVDTQGNISLDILKEKWSALYDVRTILLSIQSLLGEPNIDSPLNTHAAELWKNPTAFK
KYLQETYSKQVT

>d2e2c_ d.20.1.1 (-) Ubiquitin conjugating enzyme {Clam (Spisula solidissima), E-2C}

MTTSKERHSVSKRLQQLRLLMSGDPGITAFPDGDNLFKWVATLDGPKDVTYVESLKYKLTLEFPSPD
YPYKPPVVKFTTPCWHPNVDQSGNICLDILKENWTASYDVRTILLSLQSLGEPNNASPLNAQAAD
MWSNQTEYKKVLHEKYKTAQSDK

>d1bwza1 d.21.1.1 (A:1-130) Diaminopimelate epimerase {Haemophilus influenzae}

MQFSKMHLGNDVVDGVTQNVFFTPETIRRLANRHCGIGFDQLLIVEAPYDPELDFHYRIFNAD

GSEVSQCGNGARCFARFVTLKGLTNKKDISVSTQKGNMVLTVKDMNQIRVNMGEPIWEPKIPF
>d1bwza2 d.21.1.1 (A:131-274) Diaminopimelate epimerase {Haemophilus influenzae}
TANKFEKNYILRTDIQTVLCGAVSMGNPHCVVQVDDIQATANVEQLGPLESHERFPERVNAGFMQII
NKEHIKLRVYERGAGETQACGSGACA AVAVGIMQGLLNNNVQVDLPGGSLMIEWNGVGHPLYMTGE
ATHIYDGFITL

>d1h6ra_ d.22.1.1 (A:) Green fluorescent protein, GFP {Jellyfish (Aequorea victoria)}
SKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLT LKFIVTTGKLPVPWPPTLVTTTFAYGLQ
CFARYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI
LGHKLEYNYN SHCVYIVADKQKNGIKVNFKIRHNIEDG SVQLADHYQQNTPIGDGPVLLPDNHLYCY
QSALS KDPNEKRDMVLLLEFVTAAGITH

>d2emd_ d.22.1.1 (-) Green fluorescent protein, GFP {Jellyfish (Aequorea victoria)}
ELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLT LKFICTTGKLPVPWPPTLVTTLSYGVQCFSR
YPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGH
KLEYNYN SHNVYIMADKQKNGIKVNFKIRHNIEDG SVQLADHYQQNTPIGDGPVLLPDNHYLSTQS
ALS KDPNEKRDMVLLLEFVTAAGIT

>d1ggxa_ d.22.1.1 (A:) Red fluorescent protein (fp583 or dsred(clontech)) {Coral (Discosoma
sp.)}
VIKEFMRFKVRMEGT VNGHEFEIEGEGEGRPYEGHNTV KLVTKGGPLPFAWDILSPQFQYGSKVY
VKHPADIPDYK KLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIYKVKFIGVNFPSDGPVMQK
KTMGWEASTERLYPRDGV LKGEIHKALKLKDGGHYLV EFKSIYMAKKPVQLPGY YVDSKLDITSHN
EDYTIVEQYERTEGRHHLFL

>d1gl4a1 d.22.1.2 (A:399-631) Domain G2 of nidogen-1 {Mouse (Mus musculus)}
GSPQRVNGKVKGRIFV GSSQVPVFENTDLHSYVVMNHGRSYTAISTIPETVGYSL LPLAPIGGIIGW
MFAVEQDGFKN GFSITGGEFTRQAEVTF LGHPGKLV LKQQFSGIDEHGHLTISTELEGRVPQIPYGAS
VHIEPYTELYHYSSSVITSSSTREYTVMEPDQDGAAPSHTHIYQWRQTITFQECAHDDARPALPSTQQ
LSVDSV FVLYNKEERILRYALSNSIGPVR

>d1c8za_ d.23.1.1 (A:) Transcriptional factor tubby, C-terminal domain {Mouse (Mus
musculus)}
GSVDIEVQDLEEFALRPAPQGITIKCRITRD KKGMDRGMFPTYFLHLDREDGKKVFLLAGRKRKSK
TSNYLISVDPTDL SRGGDSYIGKLR SNLMGTKFTVYDNGVNPQKASSSTLESGLTRQELAAVCYETNV
LGFKGPRKMSVIVPGMNMVHERVCIRPRNEHETLLARWQNKNTESI ELQNKTPVWNDTQSYVL
NFHGRVTQASVKNFQIIHGNDPDYIVMQFGRVAEDVFTMDYNYPLCALQAF AIALSSFDSKLACE

>d2pil_ d.24.1.1 (-) Pilin {Gc (Neisseria gonorrhoeae)}
FTLIELMIVIAIVGILAAVALPAYQDY TARAQVSEAILLAEGQKSAVTEYYLNHGKWPENNTSAGVASP
PSDIKGYVKEVEVKNGVVTATMLSSGVNNEIKGK KLSLWARRENGSVKWF CGQPVTRTDDDTVAD
AKDGKEIDTKHLPSTCRDNF DAK

>d1hpwa_ d.24.1.1 (A:) Pilin {Pseudomonas aeruginosa}
ALEGTEFARAQ LSEAMTLASGLKTKVSDIF SVDGSCPANTAATAGIEKDTDINGKYVAKVTTGGTAAA
SGGCTIVATMKASDVATPLRGKTLTLTLGNADKGSYTWACTSNADNKYLPKTCQTATTTTP

>d1dzoa_ d.24.1.1 (A:) Pilin {Pseudomonas aeruginosa, type IV pilin, pak pilin}
GTEFARSEGASALASVNPLKTTVEEALSRGWSVKS GTGTEDATKKEVPLGVAADANKLGTIALKPDP
ADGTADITLFTMGAGPKNKGKIITLRTAADGLWKCTSDQDEQFIPK GCSR

>d1p32a_ d.25.1.1 (A:) Acidic mitochondrial matrix protein p32 {Human (Homo sapiens)}
MHTDGDKAFVDFLSDEIKEERKI QKHKTLPKMSGGWELELNGTEAKLVRKVAGEKITVTFNINNSIP

PTFDGEEEPSQGQKVEEQPELTSTPNFVVEVIKNDGKKALVLDCHYPEDEVGQEDEAESDIFSIRE
VSFQSTGESEWKDNTNYTLNTDSLWDALYDHLMDFLADRGVNDNTFADELVELSTALEHQEYITFLED
LKSFVKSQ

>d1bkf_ d.26.1.1 (-) FK-506 binding protein (FKBP12), an immunophilin {Human (Homo sapiens)}

GVQVETISPGDGRTFPKRGQTCVVHYTGMLLEDGKKFDSSRDKNKPFKFMLGKQEVIRGWEEGVAQ
MSVGQRAKLTISPDYAYGATGVPGIIPPHATLVFDVELLKE

>d1c9ha_ d.26.1.1 (A:) Calcineurin (FKBP12.6) {Human (Homo sapiens)}

GVEIETISPGDGRTFPKKGQTCVVHYTGMLQNGKKFDSSDRNKPFRIGKQEVIKGFEEGAAQMS
LGQRAKLTCTPDVAYGATGHPGVIPP NATLIFDV ELLNLE

>d1yat_ d.26.1.1 (-) Calcineurin (FKBP12.6) {Baker's yeast (Saccharomyces cerevisiae)}

SEVIEGNVKIDRISPGDGATFPKTGDLVTIHYTG TLENGQKFDSSVDRGSPFQCNI GVGQVIKGDVGI
PKLSVGEKARLTIPGYAYGPRGFPLIPP NSTLVFDV ELLKVN

>d1pbk_ d.26.1.1 (-) FKBP25 {Human (Homo sapiens)}

PKYTKSVLKKGDKTNFPKKGDVVHCWYTGTLQDGT VFD TNIQTS AKKKKNAKPLSFKVGVGK VIRG
WDEALLTMSKGEKARLEIEPEWAYGKKGQPD AKIPPNAKLT FEVELVDID

>d1rot_ d.26.1.1 (-) FKBP59-I, N-terminal domain {Rabbit (Oryctolagus cuniculus)}

GVDISPKQDEGLVKVIKREGTGTETPMIGDRV FVHYTGWLLDGT KFDSSLDRKDKFSFDL GKGEVIK
AWDIAVATMKVGELCRITCKPEYAYGSAGSPP KIPP NATLVFEV E LFEFKG

>d1pina2 d.26.1.1 (A:45-163) Mitotic rotamase PIN1, domain 2 {Human (Homo sapiens)}

GKNGQGEPARVRCSHLLVKHSQSRPSSWRQEKIT RTTKEEALELINGYIQKIKSGEEDFESLASQFSD
CSSAKARGDLGAFSRGQM QPFEDASFALRTGEMSGPVFT DSGIHIL RTE

>d1eq3a_ d.26.1.1 (A:) Parvulin {Human (Homo sapiens), hpar14}

NAVKVRHILCEKHGKIMEAMEKLKSGMRFNEVA AQYSEDKARQGGDLGWMTRGSMVGP FQEAAF
ALPVSGMDKPVFTDPPVKT KFGYHIIMVEGRK

>d1fd9a_ d.26.1.1 (A:) Macrophage infectivity potentiator protein (MIP) {Legionella pneumophila}

TDKDKLSYSIGADLGKNFKNQGIDVNPEAMAKGM QDAMSGAQLALTEQQMKDVLNKFQKDLMAK
RTAEFNKKADENKVKGEAFLTENKNKPGVVVLP SGLQYKVINSGNGVKPGKSDT VTVEYTGR LIDGT
VFDSTEKTGK PATFQVSQVIPGWTEALQLMPAGST WEIYVPSGLAYGPRSVGGPIGN ETLIFKIHLIS
VKKS

>d1grj_2 d.26.1.2 (80-158) GreA transcript cleavage factor, C-terminal domain {Escherichia coli}

MPNNGRVIFGATVTVLNLDSDEEQTYRIVGDDEADFKQNLISVNSPIARGLIGKEEDDVVIKTPGGE
VEFEVIKVEYL

>d3eipa_ d.26.2.1 (A:) Colicin E3 immunity protein {Escherichia coli}

GLKLDLTFWFDKSTEDFKGEEYSKDFGDDGSVMESLGV PFKDNV NNGCFDVIAEWVPLLQPYFNHQI
DISDNEYFVSFDYRDGDW

>d1edqa3 d.26.3.1 (A:444-516) Chitinase A {Serratia marcescens}

YGRGWTGVNGYQNNIPFTGTATGPVKGTWENGIVDYRQIAGQFMSGEWQTYT DATAEAPYVFKPST
GDLITFD

>d1goia3 d.26.3.1 (A:292-379) Chitinase B {Serratia marcescens}

YGRAFKGVSGNGGQYSSHSTPGEDPYPSTDYWL VGCEECVRDKDPRIAS YRQLEQMLQGN YGYQR
LWNDKTKTPYLYHAQNGLFV TY

>d1d2ka2 d.26.3.1 (A:293-354) Chitinase 1 {Fungus (Coccidioides immitis)}
YGRAFASTDGIGTSFNGVGGGSWENGVWDYKDMPPQGAQVTELEDIAASYSYDKNKRYLISY

>d1e9la2 d.26.3.1 (A:267-336) Chitinase-like lectin ym1 {Mouse (Mus musculus)}
YGHTEFILDPSKTGIGAPTISTGPPGKYTDESGLLAYEVCFTFLNEGATEVWDAPQEVPIAYQGNWEW
GY

>d1fjgp_ d.27.1.1 (P:) Ribosomal protein S16 {Thermus thermophilus}
MVKIRLARFGSKHNPHYRIVVTDARRKRDKGYIEKIGYYDPRKTTDPDWLKV DVERARYWLSVGAQP
TDTARRLLRQAGVFRQE

>d1fjgs_ d.28.1.1 (S:) Ribosomal protein S19 {Thermus thermophilus}
PRSLKKGVFVDDHLLLEKVLELNAKGEKRLIKTWSRRSTIVPEMVGHTIAVYNGKQHVPVYITENMV
GHKLGEFAPTRTYRGHGK

>d1qkha_ d.28.1.1 (A:) Ribosomal protein S19 {Thermus thermophilus}
GVFVDDHLLLEKVLELNAKGEKRLIKTWSRRSTIVPEMVGHTIAVYNGKQHVPVYITENMVGHKLGE
FAPTRTY

>d1jj2w_ d.29.1.1 (W:) Ribosomal protein L31e {Archaeon Haloarcula marismortui}
ERVVTIPLRDARAEPNHKRADKAMILIREHLAKHFSVDEDAVRLDPSINEAAWARGRANTPSKIRVR
AARFEEEEGEAIVEAE

>d1b33n_ d.30.1.1 (N:) Allophycocyanin linker chain (domain) {Mastigocladus laminosus}
GRLFKITACVPSQTRIRTQRELQNTYFTKLVPYENWFREQRIQKMGGKIVKVELATGKQGINTGLA

>d1qcsa2 d.31.1.1 (A:86-201) C-terminal domain of NSF-N, NSF-Nc {Hamster (Cricetulus
griseus)}
DKAKQCIGTMTIEIDFLQKKNIDSNPYDTDKMAAEFIQQFNNQAFSVGQQLVFSFNDKLFGLLVKDIE
AMDPSILKGE PASGKRQKIEVGLVVGNSQVAF EKAENSSLNLIGKAKT

>d1cr5a2 d.31.1.1 (A:108-210) C-terminal domain of NSF-N, NSF-Nc {Baker's yeast
(Saccharomyces cerevisiae), sec18p}
SGKQSYLGSIDISFRARGKAVSTVFDQDELAKQFVRCYESQIFSPTQYLIMEFQGHFFDLKIRNVQAI
DLGDIEPTSAVATGIETKGILTQQTQINFFKGR

>d1cz4a2 d.31.1.1 (A:92-185) C-terminal domain of VAT-N, VAT-Nc {Archaeon
Thermoplasma acidophilum}
TEIAKKVTLAPIIRKDQRLKFGEGIEEYVQRALIRPML EQDNISVPGLTLAGQTGLLFKVVKTLP SKV
PVEIGEETKIEIREEPASEVLEEGG

>d1e32a3 d.31.1.1 (A:107-200) Membrane fusion atpase p97 domain 2, P97-Nc {Mouse
(Mus musculus)}
DVKYGKRIHVLPIDDTVEGITGNLFEVYLKPYFLEAYRPIRKGDFLVRGGMRAVEFKV VETDPSPYCI
VAPDTVIHCEGEPIKREDEEESLNE

>d1qipa_ d.32.1.1 (A:) Glyoxalase I (lactoylglutathione lyase) {Human (Homo sapiens)}
GGLTDEAALSCCSDADPSTKDFLLQQTMLRVKDPKKS LDFYTRVLG MTLIQKCDFPIMKFSLYFLAYE
DKNDIPKEKDEKIAWALS RKATLELTHNWGTEDDETQSYHNGNSDPRGFGHIGIAVPDVYSACKRF
EELGVKFKVKKPDDGKMKGLAFIQDPDGYWIEILNPNKMATLM

>d1f9za_ d.32.1.1 (A:) Glyoxalase I (lactoylglutathione lyase) {Escherichia coli}
MRL LHTMLRVGDLQRSIDFYTKVLGMKLLRTSENPEYKYS LAFVGYGPETEEAVIELTYNWGV DKYE
LGTAYGHIALSVDNAAEACEKIRQNGGNVTREAGPVKGGTTVIAFVEDPDGYKIELIEEKDAGRGLGN

>d1qtoa_ d.32.1.2 (A:) Bleomycin resistance protein, BRP {Streptomyces verticillus}
MVKFLGAVPVLTAVDVPANVSFVVDTLGF EKDFGDRDFAGVRRGD IRLHISRTEHQIVADNTSAWIE

VTDPDALHEEWARAVSTDYADTSGPAMTPVGGESPAGREFAVRDPAGNCVHFTAGE
>d1byla_d.32.1.2 (A:) Bleomycin resistance protein, BRP {Streptoalloteichus hindustanus}
FMAKLTSAVPVLTARDVAGAVEFWTDRLGFSRDFVEDDFAGVVRDDVTLFISAVQDQVVPDNTLAW
VWVRGLDELYAEWSEVVSTNFRDASGPAMTEIGEQPWGREFALRDPAGNCVHFVAE
>d1ecsa_d.32.1.2 (A:) Bleomycin resistance protein, BRP {Klebsiella pneumoniae}
TDQATPNLPSRDFDSTAIFYERLGFIVFRDAGWMILQRGDLMEFFAHPGLDPLASWFSCCLRLD
DLAEFYRQCKSVGIQETSSGYPRIHAPELQGWGGTMAALVDPDGTLLRLIQNEL
>d1jc4a_d.32.1.4 (A:) Methylmalonyl-CoA epimerase {Propionibacterium shermanii}
NEDLFICIDHVAYACPDADASKYYQETFGWHELHREENPEQGVVEIMMAPAAKLTEHMTQVQVM
APLNDESTVAKWLAKHNGRAGLHHMAWRVDDIDAVSATLRERGVQLLYDEPKLGTGGNRINFMHP
KSGKGVLIELTQYPK
>d1gdga1 d.32.1.3 (A:1-132) 2,3-Dihydroxybiphenyl dioxygenase (DHBD, BPHC enzyme)
{Pseudomonas sp.}
SIERLGYLGFVAVKDVPAWDHFLTKSVGLMAAGSAGDAALYRADQRAWRIAVQPGELDDLAYAGLEV
DAAALERMADKLRQAGVAFTRGDEALMQRKVMGLLCLQDPFGLPLEIYYGPAEIFHEPFLPSAP
>d1gdga2 d.32.1.3 (A:133-288) 2,3-Dihydroxybiphenyl dioxygenase (DHBD, BPHC enzyme)
{Pseudomonas sp.}
VSGFVTGDQGIGHFVRCVPDTAKAMAFYTEVLGFVLSIDIQMGPEVPAHFHLCNCRHHTIALA
AFPIPKRIHFMQLQANTIDVGYAFDRLDAAGRITSLGRHTNDQTLSEFYADTPSPMIEVEFGWGPR
TVDSWTVARHSRTAMWGHKSV
>d1han_1 d.32.1.3 (2-132) 2,3-Dihydroxybiphenyl dioxygenase (DHBD, BPHC enzyme)
{Burkholderia cepacia (formerly Pseudomonas cepacia)}
SIRSLGYMGFAVSDVAAWRSFLTQKGLMEAGTTDNGDLFRIDSRWRIAVQQGEVDDLAFAGYEVA
DAAGLAQMADKLRQAGIAVTTGDASLARRRGVTGLITFADPFGLPLEIYYGASEVFEEKPFLPGA
>d1han_2 d.32.1.3 (133-289) 2,3-Dihydroxybiphenyl dioxygenase (DHBD, BPHC enzyme)
{Burkholderia cepacia (formerly Pseudomonas cepacia)}
AVSGFLTGEQGLGHFVRCVPDSDKALAFYTDVLFQQLSDVIDMKGPDVTVPAYFLHCNERHHTLAI
AAFPLPKRIHFMLEVASLDDVGFADRVADGLITSTLGRHTNDHMVSFYASTPSGVEVEYGWSAR
TVDRSWVVVRHDSPPMWWGHKSVR
>d1mpya1 d.32.1.3 (A:1-145) Catechol 2,3-dioxygenase (metapyrocatechase) {Pseudomonas
putida, mt2}
MNKGVMRPGHVQLRVLDMSKALEHYVELLGLIEMDRDDQGRVYLKAWTEVDKFSVLVLEADEPG
MDFMGFKVVEDALRQLERDLMAYGCAVEQLPAGELNSCGRRVRFQAPSGHHFELYADKEYTGKW
GLNDVNPEAWPRDLKG
>d1mpya2 d.32.1.3 (A:146-307) Catechol 2,3-dioxygenase (metapyrocatechase)
{Pseudomonas putida, mt2}
MAAVRFDHALMYGDELPATYDLFTKVLGFYLAEQVLDENGTRVAQFLSLSTKAHDVAFIHHPEKGR
LHHVSFHFLETWEDLLRAADLISM TDTSIDIGPTRHGLTHGKTIYFFDPSGNRNEVFCGGDYNYPDHK
PVTWTTDQLGKAIFYHDRILNERFMTVLT
>d1cxa1 d.32.1.3 (A:4-153) 4-hydroxyphenylpyruvate dioxygenase, HppD {Pseudomonas
fluorescens}
YENPMGLMGFEFIEFASPTPGTLEPIFEIMGFTKVATHRSKNVHLYRQGEINLILNNEPNSIASYFAAE
HGPSVCGMAFRVKDSQKAYNRALELGAQPIHIDTGPMEINLPAIKGIGGAPLYLIDRFEGEGSSIIDIDF
VYLEGVERNVPV

>d1cxa2 d.32.1.3 (A:154-356) 4-hydroxyphenylpyruvate dioxygenase, HppD {*Pseudomonas fluorescens*}

AGLKVIDHLTHNVYRGRMVYWANFYEKLFNFREARYFDIKGEYTGTLTSKAMSAPDGMIRIPLNEESS
KGAGQIEEFLMQFNNEGIIQHVAFLTDDLKTKWDALKKIGMRFMTAPPDTTYEMLEGRLPDHGEPV
DQLQARGILLDGSSEVGDKRLLLQIFSETLMGPVFFEFIQKRGDDGFGEGNFKALFESIERDQVRRGV
LAT

>d1fx3a_ d.33.1.1 (A:) Bacterial protein-export protein SecB {*Haemophilus influenzae*}

QPVLQIQRIYVKDVSFEAPNLPHIFQEQWKPKLGFDLSTETTQVGDDLYEVVLNISVETTLEDSDGVA
FICEVKQAGVFTISGLEVDQMAHCLTSQCPNMLFPYARELVSNLVNRGTFPALNLSPVNFDALFVEYM
NRQQAEN

>d1bm8_ d.34.1.1 (-) DNA-binding domain of Mlu1-box binding protein MBP1 {Baker's yeast (*Saccharomyces cerevisiae*)}

QIYSARYSGVDVYEFIHSTGSIMKRKKDDWVNATHILKAANFAKAKRTRILEKEVLKETHEKVQGGF
GKYQGTWVPLNIAKQLAEKFSVYDQLKPLDFD

>d1dk0a_ d.35.1.1 (A:) Heme-binding protein A (HasA) {*Serratia marcescens*}

AFSVNYDSSFGGYSIHLYLQWASTFGDVNHTNGNVTDANSGGFYGGSLSGSQYAISSTANQVTAFVA
GGNLTYYTLFNEPAHTLYGQLDLSLFGDGLSGGDTSPYSIQVPDVSFGGLNLSLQAQGHGDDVHVVV
GLMSGDTGALETALNGILDDYGLSVNSTFDQVAAATA

>d1eyqa_ d.36.1.1 (A:) Chalcone isomerase {Alfalfa (*Medicago sativa*)}

SITAITVENLEYPVAVTSPVTGKSYFLGGAGERGLTIEGNFIKFTAIGVYLEDIAVASLAAKWGKSSEE
LLETLDYRDIISGPFELIRGSKIRELSGPEYSRKVMENCVAHLKSVGTYGDAEAEAMQKFAEAFKP
VNFPPGASVFYRQSPDGILGLSFSPDTSIPEKEAALIENKAVSSAVLETMIGEHAHVSPDLKRCLAARLP
ALLNE

>d1b3ob2 d.37.1.1 (B:112-159) Type II inosine monophosphate dehydrogenase {Human (*Homo sapiens*)}

QGFITDPVVLSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRVLGIIIS

>d1jr1a2 d.37.1.1 (A:113-155) Type II inosine monophosphate dehydrogenase {Chinese hamster (*Cricetulus griseus*)}

GFITDPVVLSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRVL

>d1jr1a3 d.37.1.1 (A:178-232) Type II inosine monophosphate dehydrogenase {Chinese hamster (*Cricetulus griseus*)}

IMTKREDLVVAPAGITLKEANEILQRSKKGKLPVNNDELVAIARTDLKKNRD

>d1zfja2 d.37.1.1 (A:95-158) Type II inosine monophosphate dehydrogenase {*Streptococcus pyogenes*}

NGVIIDPFFLTPEHKVSEAEELMQRYSRISGVPIVETLANRKLVGIIITNRDMRFISDYNAPISEH

>d1zfja3 d.37.1.1 (A:159-220) Type II inosine monophosphate dehydrogenase {*Streptococcus pyogenes*}

MTSEHLVTAAVGTDLETAERILHEHRIEKLPLVDNSGRLSGLITIKDIEKVIEFPAAKDEF

>d1bvqa_ d.38.1.1 (A:) 4-hydroxybenzoyl-CoA thioesterase {*Pseudomonas* sp., CBS-3}

ARSITMQRIEFGDCDPAGIVWYPNYHRWLDAASRNYFIKCGLPWRQTVVERGIVGTPIVSCNASF
VCTASYDDVLTETCIKEWRRKSFVQRHSVSRTTPGGDVQLVMRADEIRVVFAMNDGERLRAIEVPAD
YIELC

>d1mkaa_ d.38.1.2 (A:) beta-Hydroxydecanol thiol ester dehydrase {*Escherichia coli*}

VDKRESYTKEDLLASGRGELFGAKGPQLPAPNMLMMDRVVVKMTETGGNFDDKGYVEAELDINPDW

FFGCHFIGDPVMPGCLGLDAMWQLVGFYLGWLGEGEGKGRALGVGEVKFTGQVLPTAKKVTYRIHFK
RIVNRRLIMGLADGEVLVDGRLIYTASDLKVGLFQDTSAF
>d1c8ua1 d.38.1.3 (A:2-115) Thioesterase II (TesB) {Escherichia coli}
SQALKNLLTLLNLEKIEEGLFRGQSEDLGLRQVFGGQVVGQALYAAKETVPEERLVHSFHSYFLRPGD
SKKPIIYDVETLRDGNSFSARRVAAIQNGKPIFYMTASFQAPEAGF
>d1c8ua2 d.38.1.3 (A:116-286) Thioesterase II (TesB) {Escherichia coli}
EHQKTMPSAPAPDGLPSETQIAQSLAHLPLPVLDKFKICDRPLEVRPVEFHNPLKGHVAEPHRQVWI
RANGSVPDDLRVHQYLLGYASDLNPLVALQPHGIGFLEPGIQIATIDHSMWFHRPFLNEWLLYSV
ESTSASSARGFVRGEFYTDGVLVASTVQEGVMRNHN
>d1cmia_d.39.1.1 (A:) Dynein light chain 8 (DLC8) {Human (Homo sapiens)}
KAVIKNADMSEEMQQDSVECATQALEKYNIEKDIAAHIKKEFDKKYNPTWHCIVGRNFGSYVTHET
KHFIYFYLQVAILLKFSG
>d1csei_d.40.1.1 (I:) Eglin C {Leech (Hirudo medicinalis)}
KSFPEVVGKTVDAQAREYFTLHYPQYNVYFLPEGSPVTLDLRYNRVRVFNPGTNNVNHVPHVG
>d1egl_d.40.1.1 (-) Eglin C {Leech (Hirudo medicinalis)}
TEFGSELKSFPEVVGKTVDAQAREYFTLHYPQYDVYFLPEGSPVTLDLRYNRVRVFNPGTNNVNHVP
HVG
>d1ypci_d.40.1.1 (I:) Chymotrypsin inhibitor CI-2 {Barley (Hordeum vulgare)}
MKTEWPELVGKSVAAAKKVLQDKPEAQIIVLPVGTIVTMEYRIDRVRLFVDKLDNIAQVPRVG
>d2snii_d.40.1.1 (I:) Chymotrypsin inhibitor CI-2 {Barley (Hordeum vulgare)}
LKTEWPELVGKSVEEAKKVLQDKPEAQIIVLPVGTIVTMEYRIDRVRLFVDKLDNIAEVPRVG
>g1cq4.1 d.40.1.1 (A:,B:) Chymotrypsin inhibitor CI-2 {Barley (Hordeum vulgare)}
KTEWPELVGKSVEEAKKVLQDKPEAQIIVLPVGTIVXYRIDRVRLFVDKLDNIAQVPRVG
>d1tin_d.40.1.1 (-) Trypsin inhibitor V {Pumpkin (Cucurbita maxima)}
SSCPGKSSWPHLVGVGGSVAKAIERQNPVKAIVILEEGTPVTKDFRCNRVRIWVNKRGLVSPPRIG
>d1dwma_d.40.1.1 (A:) Trypsin inhibitor LUTI {Flax (Linum usitatissimum)}
SRRCPGKNAWPELVGKSGNMAAATVERENRNHAIVLKEGSAMTKDFRCDRVWVIVNDHGVVTSV
PHIT
>d1jv2b3 d.200.1.1 (B:606-690) Integrin beta tail domain {Human (Homo sapiens)}
DACTFKKECKVECKKFDREPYMTENTCNRYCRDEIESVKELKDTGKDAVNCTYKNEDDCVVRVQYYE
DSSGKSILYVVEEPECPKG
>d1hlra3 d.41.1.1 (A:194-310) Aldehyde oxidoreductase, domain 3 {Desulfovibrio gigas}
DYGADLGLKMPAGTLHLAMVQAKVSHANIKGIDTSEALTMPGVHSVITHKDVKGKNRITGLITFPTN
KGDGWRPILCDEKVFQYGDICALVCADSEANARAAAEEKVKVDLEELPAY
>d1dgja3 d.41.1.1 (A:194-310) Aldehyde oxidoreductase, domain 3 {Desulfovibrio
desulfuricans}
EFGADAALRMPENTLHLALAQAKVSHALIKGIDTSEAEKMPGVYKVLTHKDVKGKNRITGLITFPTN
KGDGWERPILNDSKIFQYGDALAIVCADSEANARAAAEEKVKFDLELLPEY
>d1fiqc1 d.41.1.1 (C:571-694) Xanthine oxidase, domain 5 (?) {Cow (Bos taurus)}
DTVGRPLPHLAAAMQASGEAVYCCDIPRYENELFLRLVTSTRAHAKIKSIDVSEAQKVPGFVCFLSAD
DIPGSNETGLFNDET VFAKDTVTCVGHII GAVVADTPEHAERAAHVVKVTYEDLPA
>d1fo4a3 d.41.1.1 (A:537-694) Xanthine oxidase, domain 5 (?) {Cow (Bos taurus)}
KLDPTYTSATLLFQKHPPANIQLFQEVPNGQSKEDTVGRPLPHLAAAMQASGEAVYCCDIPRYENEL
FLRLVTSTRAHAKIKSIDVSEAQKVPGFVCFLSADDIPGSNETGLFNDET VFAKDTVTCVGHII GAVVA

DTPEHAERAAHVVKVTYEDLPA

>d1jrob1 d.41.1.1 (B:2-123) Xanthine dehydrogenase chain B, N-terminal domain {*Rhodobacter capsulatus*}

SVGKPLPHDSARAHVTGQARYLDDLPCPANTLHLAFLGLSTEASAAITGLDLEPVRESPGVIAVFSTAAD
LPHDNDASPAPSPEPVLATGEVHFVVGQPIFLVAATSHRAARIAARKARITYAPR

>d1qj2b1 d.41.1.1 (B:10-146) Carbon monoxide (CO) dehydrogenase molybdoprotein, N-domain {*Pseudomonas carboxydovorans*}

TSAERA EK LQGMGCKRKRVEDIRFTQGKGNVDDVKLPGMLFGDFVRSSH AHARIKSIDTSKAKAL
PGVFAVLTAADLKPLNLHYMPTLAGDVQAVLADEKVL FQNQEVAFVVA KDRYVAADAIELVEVDYEP
LPVL

>d1ffvb1 d.41.1.1 (B:7-146) Carbon monoxide (CO) dehydrogenase molybdoprotein, N-domain {*Hydrogenophaga pseudoflava*}

DAEARELALAGMGASRLRKEDARFIQKGNVDDIKMPGMLHMDIVRAPIAHGRIKKIHKDAALA
MPGVHAVLTAEDLKPLKLHWMPPTLAGDVA AVLAD EKVHFQMQEVAI VIADDRYIAADAVEAVKVEY
DEL PVVIDP

>d1qapa2 d.41.2.1 (A:8-129) Quinolinic acid phosphoribosyltransferase, N-terminal domain {*Salmonella typhimurium*}

DDRRDALLERINLDIPAAVAQALREDLGGEVDAGNDITAQLLPADTQAHATVITREDGVFCGKRWVE
EVFIQLAGDDVRLTWHVDDGDAIHANQTVFELQGPVRLTGTALNFVQTLSG

>d1qpoa2 d.41.2.1 (A:2-116) Quinolinic acid phosphoribosyltransferase, N-terminal domain {*Mycobacterium tuberculosis*}

GLSDWELAAARAAIARGLDEDLRYGPDVTTLATVPASATTTASLV TREAGVVAGLDVALLTLNEVLG
TNGYRVLDRVEDGARVPPGEALMTLEAQTRGLLTAERTMLNLVGHLSG

>d2tpt_3 d.41.3.1 (336-440) Thymidine phosphorylase {*Escherichia coli*}

TAMLT KAVYADTEGFVSEMDTRALGM AVVAMGGRRQASDTIDYSVGFTDMARLGDQVDGQRPLA
VIHAKDENNWQEAAKAVKAAIKLADKAPESTPTVYRRISE

>d1brwa3 d.41.3.1 (A:331-433) Pyrimidine nucleoside phosphorylase {*Bacillus stearothermophilus*}

KAA Y TSTVTAAADGYVAEMAADDIGTAAMWLGAGRAK KEDVIDLAVGIVLHKKIGDRVQKGEALATI
HSNRPDVLDVKEKIEAAIRLSPQPVARPPLIYETIV

>d1ffkf_d.41.4.1 (F:) Ribosomal protein L10e {*Archaeon Haloarcula marismortui*}

KPGA HFRNSIKPAYTRREYISGIPGKIAQFKMGNNAGPTYP AQVENVVEKPVQIRHNALEAARNA
ANRFVQNSGAAANYKFRIRKFPFHVIREQDGDGM RAPFGKSVGTAARSHGANHDFIAWVNPDP AV
EFAWRRAYMKVTPTVNIDSSPAGNA

>d1jj2h_d.41.4.1 (H:) Ribosomal protein L10e {*Archaeon Haloarcula marismortui*}

KPGAMYRNSSKPAYTRREYISGIPGKIAQFDMGNNAGPTYP AQVELVVEKPVQIRHNALEAARVA
ANRYVQNSGAAANYKFRIRKFPFHVIRENKA AAAAAAAAAA ADGM RAPFGKPVGTAAARVHGANHIFI
AWVNPDPNVEEAWRRAKMKVTPTINIDSSPAGNA

>d1fm0e_d.41.5.1 (E:) Molybdopterin synthase subunit MoeE {*Escherichia coli*}

AETKIVVGPQPFSGEY P WLAERDEDGAVVTFTGKVRNHN LGDSVNALTLEHYPGMTEKALAEIV
DEARNRWPLGRVTVIHRIGELWPGDEIVFVGVTSAHRSSAFEAGQFIMDY LKTRAPFWKREATPEG
DRWVEARESDQQA AKRW

>d1buoa_d.42.1.1 (A:) Promyelocytic leukemia zinc finger (PLZF) protein BTB domain {*Human (Homo sapiens)*}

MGMIQLQNPSHPTGLLCKANQMRLAGTLCDDVIMVDSQEFHAHRTVLACTSKMFEILFHRNSQHY
TLDFLSPKTFQQILEYAYTATLQAKAEDLDDLLYAAEILEIEYLEEQCLKMLETIQ
>d1vcbb_ d.42.1.1 (B:) Elongin C {Human (Homo sapiens)}
MYVKLISSDGHEFIVKREHALTSGTIKAMLSGPGQFAENETNEVNFREIPSHVLSKVCMYFTYKVRT
NSSTEIPEFPIAPEIALELLMAANFLDC
>d1hv2a_ d.42.1.1 (A:) Elongin C {Baker's yeast (Saccharomyces cerevisiae)}
MSQDFVTLVSKDDKEYEISRSAAMISPTLKAMIEGPFRESKGRIELKQFDSHILEKAVEYLNYNLKYS
GVSEDDDEIPEFEIPTMSLELLLAADYLSI
>d1a68_ d.42.1.2 (-) Shaker potassium channel {California sea hare (Aplysia californica)}
ERVVINVSGLRFETQLKTLNQPDTLLGNPQKRNRYYDPLRNEYFFDRNRPSFDAILYFYQSGGRLR
RPVNVPLDVFSEEIKFYELG
>d1t1da_ d.42.1.2 (A:) Shaker potassium channel {California sea hare (Aplysia californica)}
ERVVINVSGLRFETQLKTLNQPDTLLGNPQKRNRYYDPLRNEYFFDRNRPSFDAILYFYQSGGRLR
RPVNVPLDVFSEEIKFYELGENAFERYREDEGF
>d3kvt_ d.42.1.2 (-) kv3.1 voltage-gated potassium channel {California sea hare (Aplysia californica)}
ENRVIINVGIRHETYKATLKKIPATRLSRLTEGMLNYDPVLNEYFFDRHPGVFAQIINYRSGKLHYP
TDVCGPLFEELEFWGLDSNQVEPCCWMTYTAHR
>d1exbe_ d.42.1.2 (E:) KV1.1 {Rat (Rattus norvegicus)}
CERVVINISGLRFETQLKTLAQFPNTLLGNPKKRMRYFDPLRNEYFFDRNRPSFDAILYFYQSGGRLR
RPVNVPLDMFSEEIKFYELGEEA
>d1dsxa_ d.42.1.2 (A:) Kv1.2 {Rat (Rattus norvegicus)}
ERVVINISGLRFEVQLKTLAQFPETLLGDPKPKRMRYFDPLRNEYFFDRNRPSFDAILYFYQSGGRLRR
PVNVPLDIFSEEIRFYELG
>d1qdva_ d.42.1.2 (A:) Kv1.2 {Rat (Rattus norvegicus)}
ERVVINISGLRFETQLKTLAQFPETLLGDPKPKRMRYFDPLRNEYFFDRNRPSFDAILYFYQSGGRLRR
PVNVPLDIFSEEIRFYELGEEAMEMFREDEG
>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}
DVLGSYQHGARIGVLVAAKGADEELVKHIAMHVAASKPEFIKPEDVSAEVVEKEYQVQLDIAMQSGK
PKEIAEKMVEGRMCKFTGEVSLTGQPFVMEPSKTVGQLLKEHNAEVTGFIRFEVGEIEKVETDFAA
EVAAMSKQS
>d1efub4 d.43.1.1 (B:55-139) Elongation factor Ts (EF-Ts), dimerisation domain
{Escherichia coli}
VAADGVIKTKIDGNYGIILEVNCQTDVFAKDAGFQAFADKVLDAAVAGKITDVEVLKAQFEEERVALV
AKIGENINIRRVAALEG
>d1tfe_ d.43.1.1 (-) Elongation factor Ts (EF-Ts), dimerisation domain {Thermus
thermophilus}
AREGIIGHYIHHNQRVGVLVELNCETDFVARNELFQNLAKDLAMHIAMMNPYVSAEEIPAELEKE
RQIYIQAALNEGKPPQIAEKIAEGRLLKYLEEVVLEEQPFVKDDKVKVKELIQQAIAKIGENIVRRFC
RFELGA
>d1i0ha2 d.44.1.1 (A:91-205) Mn superoxide dismutase (MnSOD) {Escherichia coli}

GTTLQGD LKAAIERDFGSDNFKA EF EKA AASRFGSGWAWLV LKGD KLAVVSTANQDSPLMGEAIS
GASGFPIMGLDVWEHAYFLKFQNRDPDIKEFWNVVNWDEAAARFAAKK
>d1mnga2 d.44.1.1 (A:93-203) Mn superoxide dismutase (MnSOD) {Thermus thermophilus}
GGAKEPVGELKKAIDEQGGFQALKEKLTQAAMGRFGSGWAWLVKDPFGKLVSTPNQDNPVME
GFTPIVGIDVWEHAYYLKYQNRADY LQAIWNVLNWDVAEEFFKKA
>d1ap6a2 d.44.1.1 (A:84-198) Mn superoxide dismutase (MnSOD) {Human (Homo sapiens)}
NNGGEPKGELLEAIKRDFGSFDKFKEKLTAA SVGVQGSWGWLGFNKERGHLQIAACPNDPLQGT
TGLIPLLIGIDVWEHAYYLQYKNVRPDY LKAIWNVINWENVTERYMACKK
>d1kkca2 d.44.1.1 (A:98-213) Mn superoxide dismutase (MnSOD) {Aspergillus fumigatus}
EKSGGGKIDQAPVLKAAIEQRWGSFDKFDAFN TLLGIQGSWGWLVTGDGPKGKLDITTTTHDQDP
VTGAAPVFGVDMWEHAYYLQYLNDKASYAKGIWNVINWAEAEENRYIAGDK
>d1dt0a2 d.44.1.1 (A:84-197) Fe superoxide dismutase (FeSOD) {Pseudomonas ovalis}
AGGQPTGALADAINA AFGSFDKFKEEFTKTSVGTFGSGWGWL VKKADGSLALASTIGAGCPLTIGDT
PLLTCDVWEHAYYIDYRNL RPKYVEAFWNLVNWAFVAEQFEGKTYKV
>d3sdpa2 d.44.1.1 (A:84-190) Fe superoxide dismutase (FeSOD) {Pseudomonas ovalis}
DAGGQPTGALADAINA AFGSFDKFKEEFTKTSVGTFGSGWAWLVKADGSLALCSTIGAGAPLTSGDT
PLLTCDVWEHAYYIDYRNL RPKYVEAFWNLVNWAFVAEEG
>d1isaa2 d.44.1.1 (A:83-192) Fe superoxide dismutase (FeSOD) {Escherichia coli}
NAGGEPTGKVAEIAASFGSFADFKAQFTDAAIKNFGSGWTWLVKNSDGKLAIVSTS NAGTPLTTDA
TPLLTVDVWEHAYYIDYRNARPGYLEHFWALVNWEFVAKNLAA
>d1idsa2 d.44.1.1 (A:86-199) Fe superoxide dismutase (FeSOD) {Mycobacterium
tuberculosis}
NNGDKPTGELAAAIADAFGSFDKFRAQFHAAATTVQGSWAALGWDTLGNKLLIFQVYDHQTNFP
LGIVPLLLLDMWEHAFYLQYKNVKVDFAKAFWNVVNWADVQSR YAAATS
>d1coja2 d.44.1.1 (A:91-212) Fe superoxide dismutase (FeSOD) {Aquifex pyrophilus}
GGKGPESEALKKKIEEDIGGLDACTNELKAAAMAFRGWAILGLDIFSGRLVVNGLDAHN VYNTGLIP
LIVIDTYEHAYYVDYKKNRPPYIDAFFKNINWDV VNERFEKAMKAYEALKDFIK
>d1sssa2 d.44.1.1 (A:93-208) Fe superoxide dismutase (FeSOD) {Archaeon Sulfolobus
solfataricus}
PSGKGGGKPGGALADLINKQYGSFDRFKQVFTETANSLPGTGWAVLYDTE SGNLQIMTFENHFQN
HIAEIPILILDEFEHAYYLQYKNKRADYVNAWWNVVNWDAAEKKLQKYL
>d1b06a2 d.44.1.1 (A:93-210) Fe superoxide dismutase (FeSOD) {Archaeon Sulfolobus
acidocaldarius}
PAGKGGGKPGGALADLIDKQYGSFDRFKQVFSANSLPGSGWTVLYYDNESGNLQIMTVENHFMN
HIAELPVILIVDEFEHAYYLQYKNKRGDYLN AWWNVVNWDDAEKRLQKYLNK
>d1bsma2 d.44.1.1 (A:87-201) Cambialistic superoxide dismutase {Propionibacterium
shermanii}
SAPERPTDELGAAID EFFGSFDNMKAQFTAAATGIQGSGWASLVWDPLGKRINTLQFYDHQNNLPA
GSIPLLQLDMWEHAFYLQYKNVKGDYVKS WNVVNWDDVALRFSEARVA
>d1qnna2 d.44.1.1 (A:85-191) Cambialistic superoxide dismutase {Porphyromonas
gingivalis}
KGGAPKGLGEAIDKQFGSFEKFKEEFNTAGTTLFGSGWVWLASDANGKLSIEKEPNAGNPVRKGL
NPLLGFVDVWEHAYYLTYQNRADHLKDLWSIVDWDIVESRY
>d1ctf_ d.45.1.1 (-) Ribosomal protein L7/12, C-terminal domain {Escherichia coli}

EFDVILKAAGANKVAVIKAVRGATGLGLKEAKDLVESAPAALKEGVSKDDAEALKKALEEAGAEVEV
K
>d1dd3a2 d.45.1.1 (A:58-128) Ribosomal protein L7/12, C-terminal domain {Thermotoga
maritima}
EFDVVLKSFQGNKIQVIKVVREITGLGLKEAKDLVEKAGSPDAVIKSGVSKEEAEIKKKLEEAGAEVE
LK
>d1ekta_ d.46.1.1 (A:) Transcription-state regulator AbrB, the N-terminal DNA recognition
domain {Bacillus subtilis}
MKSTGIVRKVDELGRVVIPIELRRTLGLIAEKDALEIYVDDEKIILKKYKPNMT
>d1mmsa2 d.47.1.1 (A:8-70) Ribosomal protein L11, N-terminal domain {Thermotoga
maritima}
QIKLQLPAGKATPAPPVGPALGQHGVNIMEFCKRFNAETADKAGMILPVVITVYEDKSFTFII
>d2reb_2 d.48.1.1 (269-328) RecA protein, C-terminal domain {Escherichia coli}
NFYGELVDLGVKEKLIKAGAWYSYKGEKIGQGKANATAWLKDNPETAKEIEKKVRELLL
>d1g19a2 d.48.1.1 (A:270-329) RecA protein, C-terminal domain {Mycobacterium
tuberculosis}
SREGSLIDMGVDQGLIRKSGAWFTYEQEQLGQGENARNFLVENADVADIEKKIKEKLG
>d1e8oa_ d.49.1.1 (A:) Signal recognition particle alu RNA binding heterodimer, SRP9/14
{Human (Homo sapiens)}
PQYQTWEEFSRAAEKLYLADPMKARVVLKYRHSDGNLCVKVTDLCLVYKTDQAQDVKKIEKFHS
QLMRLMVA
>d1e8ob_ d.49.1.1 (B:) Signal recognition particle alu RNA binding heterodimer, SRP9/14
{Human (Homo sapiens)}
VLESEQFLTELTRLFQKCRSTSGSVYITLKKYDGRTPKIPKKGTVVEGFEPADNKLLRATDGGKKISTV
VSSKEVNKFQMAYSNLLRANMDGLK
>d1914_ d.49.1.1 (-) Signal recognition particle alu RNA binding heterodimer, SRP9/14
{Mouse (Mus musculus)}
MVLESEQFLTELTRLFQKCRSSGSVFITLKKYDGRTPKIPKSSVEGLEPAENKLLRATDGGKRKIST
VVSSKEVNKFQMAYSNLLRANMDGLKKRDKKNKSKKSKPAQGGEQKLISEEDDSAGSPMPQFQTW
EEFSRAAEKLYLADPMKVRVVLKYRHVDGNLCIKVTDLCLVYRTDQAQDVKKIEKFHSQLMRLM
VAKESRNV
>d1di2a_ d.50.1.1 (A:) Double-stranded RNA-binding protein A, second dsRBD {Xenopus
laevis}
MPVGSQELAVQKGWRLPEYTVAQESGPPHKREFTITCRVETVETGSGTSKQVAKRVAAEKLLTKF
KT
>d1ekza_ d.50.1.1 (A:) Staufen, domain III {Fruit fly (Drosophila melanogaster)}
MDEGDKKSPISQVHEIGIKRNMTVHFVKVLRREGPAHMKNFITACIVGSIVTEGEGNGKKVSKKRAAE
KMLVELQKL
>d1stu_ d.50.1.1 (-) Staufen, domain III {Fruit fly (Drosophila melanogaster)}
PISQVHEIGIKRNMTVHFVKVLRREGPAHMKNFITACIVGSIVTEGEGNGKKVSKKRAAEKMLVELQK
L
>d1qu6a1 d.50.1.1 (A:1-90) dsRNA-dependent protein kinase pkr {Human (Homo sapiens)}
GSHMEMAGDLSAGFFMEELNTYRQKQGVVLKYQELPNSGPPHRRFTFQVIIDGREFPEGEGRSKK
EAKNAAAKLAVEILNKEKKAVSPL

>d1qu6a2 d.50.1.1 (A:91-179) dsRNA-dependent protein kinase pkr {Human (Homo sapiens)}
LLTTTNSSEGLSMGNYIGLINRIAQKKRLTVNYEQCASGVHGPEGFHYKCKMGQKEYSIGTGSTKQEA
KQLAAKLAYLQILSEETGSGC

>d1pkp_2 d.50.1.2 (4-77) Ribosomal S5 protein, N-terminal domain {Bacillus stearothermophilus}
INPNKLELEERVVAVNRVAKVVKGGRRRLRFSALVVVGDKNHVGFGTGKAQEVPEAIRKAIEDAKKN
LIEVPIV

>d1fjge2 d.50.1.2 (E:5-73) Ribosomal S5 protein, N-terminal domain {Thermus thermophilus}
DFEEKMILIRRTARMQAGRRFRFGALVVVGDQRVGLGFGKAPEVPLAVQKAGYYARRNMVEVP
LQN

>d1ah5_2 d.50.2.1 (220-313) Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain {Escherichia coli}
NHHETALRVTAERAMNTRLEGGCQVPIGSYAELIDGEIWLRLALVGAPDGSQIIRGERRGAPQDAEQM
GISLAEELLNNGAREILAEVYNGDAPA

>d1pda_2 d.50.2.1 (220-307) Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain {Escherichia coli}
NHHETALRVTAERAMNTRLEGACQVPIGSYAELIDGEIWLRLGLVGAPDGSQIIRGERRGAPQDAEQM
GISLAEELLNNGAREILAEVY

>d1dq3a2 d.50.3.1 (A:336-414) PI-Pfui intein middle domain {Archaeon Pyrococcus furiosus}
GNFGLPLNFNAFKEWASEYGVFVKTSQTIAIINDERISLGQWHTRNRVSKAVLVKMLRKLIEATK
DEEVKRMLHLIE

>d1jida_d.201.1.1 (A:) SRP19 {Human (Homo sapiens)}
AARSPADQDRFICIYPAYLNNKKTIAEGRRIPISKAVENPTATEIQDVCSAVGLNVFLEKNKMYSEW
NRDVQYRGRVRVQLKQEDGSLCLVQFPSRKSVMLYAAEMIPKLKTR

>d1dt4a_d.51.1.1 (A:) Neuro-oncological ventral antigen 1, nova-1, KH3 {Human (Homo sapiens)}
MKDVVEIAPENLVGAILGKGGKTLVEYQELTGCRIQISKKGFLPGTRNRKVTITGTPAATQAAQYLI
TQRI

>d1dtja_d.51.1.1 (A:) Neuro-oncological ventral antigen 2, nova-2, KH3 {Human (Homo sapiens)}
MKELVEMAVPENLVGAILGKGGKTLVEYQELTGARIQISKKGFLPGTRNRRVTITGSPAATQAAQYLI
SQRVT

>d1ec6a_d.51.1.1 (A:) Neuro-oncological ventral antigen 2, nova-2, KH3 {Human (Homo sapiens)}
MKELVEIAPENLVGAILGKGGKTLVEYQELTGARIQISKKGFLPGTRNRRVTITGSPAATQAAQYLIS
QRVTYEQGVRASNPQKV

>d1vig_d.51.1.1 (-) Vigilin, KH6 {Human (Homo sapiens)}
INRMDYVEINIDHKFHRHLIGKSGANINRIKDQYKVSVRIPDSEKSNLIRIEGDPQGVQAKRELLEL
AS

>d2fmr_d.51.1.1 (-) Fragile X protein, KH1 {Human (Homo sapiens)}
ASRFHEQFVREDLMGLAIGTHGANIQARKVPGVTAIDLDEDTCTFHIGEDQDAVKKARSFLE

>d1khma_d.51.1.1 (A:) HnRNP K, KH3 {Human (Homo sapiens)}
GSPNSYGD LGGPIITTQVTIPKDLARSIIGKGGQRIKQIRHESGASIKIDE PLEGESEDRIITITGTQDQIQN
AQYLLQNSVKQYSGKFF

>d1k1ga_d.51.1.1 (A:) RNA splicing factor 1 {Human (Homo sapiens)}
TRVSDKVMIPQDEYPEINFVGLLIGPRGNTLKNIEKECNAKIMIRGKGSVKEGKVGVRKDGQMLPGED
EPLHALVTANTMENVKKAVEQIRNILKQGIETPEDQNDLRKMQLRELARLNGTLR

>d2proc1 d.52.1.1 (C:18-85) Alpha-lytic protease prodomain {Lysobacter enzymogenes}
IFPTQLPQYLQTEKLARTQAAAIEREFGAQFAGSWIERNEDGSFKLVAATSGARKSSTLGGVEVRNVR

>d3proc1 d.52.1.1 (C:6-85) Alpha-lytic protease prodomain {Lysobacter enzymogenes}
PQLKFAMQRDLGIFPTQLPQYLQTEKLARTQAAAIEREFGAQFAGSWIERNEDGSFKLVAATSGARK
SSTLGGVEVRNVR

>d3proc2 d.52.1.1 (C:86-163) Alpha-lytic protease prodomain {Lysobacter enzymogenes}
YSLKQLQSAMEQLDAGANARVKGVSPLDGVQSWYVDPRSNAVVKVDDGATDAGVDFVALSGAD
SAQVRIESSPGKL

>d1gpma3 d.52.2.1 (A:405-525) GMP synthetase, C-terminal, dimerisation domain
{Escherichia coli}
GPGLGVRVLGEVKKEYCDLLRRADAIFIEELRKADLYDKVSQAFTVFLPVRVSGVMGDGRKYDWWVS
LRAVETIDFMTAHWAHLPYDFLGRVSNRIINEVNGISRVVYDISGKPPATIEWE

>d1fjgc1 d.52.3.1 (C:2-106) Ribosomal protein S3 N-terminal domain {Thermus
thermophilus}
GNKIHPIGFRLGITRDWESRWYAGKKQYRHLLLEDQRIRGLLEKELYSAGLARVDIERAADNVAVTV
HVAKPGVVIGRGERIRVLREELAKLTGKNVALNVQEV

>d1egaa2 d.52.3.1 (A:183-295) GTPase Era C-terminal domain {Escherichia coli}
DYITDRSQRFMASEIIREKLMRFLGAELPYSVTVEIERFVSNERGGYDINGLILVEREQKKMVIGNKG
AKIKTIGIEARKDMQEMFEAPVHLELWVKVSGWADDERALRSL

>d1hh2p2 d.52.3.1 (P:199-276) Transcription factor NusA, C-terminal domains {Thermotoga
maritima}
RVPEFVIGLМКLEIPEVENGIVEIKAIAREPGVRTKVAVASNDPNVDPIGACIGEGGSRIAAILKELKGE
KLDVLKWS

>d1hh2p3 d.52.3.1 (P:277-344) Transcription factor NusA, C-terminal domains {Thermotoga
maritima}
DDPKQLIANALAPATVIEVEILDKENKAARVLVPPTQLSLAIGKGGQNARLAAKLTGWKIDIKPIMNL

>d1k0ra2 d.52.3.1 (A:184-262) Transcription factor NusA, C-terminal domains
{Mycobacterium tuberculosis}
THPNLVRKLFSLVEPEIADGSVEIVAVAREAGHRSKIAVRSNVAGLNAKGACIGPMGQVRNVMSELS
GEKIDIIDYDD

>d1k0ra3 d.52.3.1 (A:263-329) Transcription factor NusA, C-terminal domains
{Mycobacterium tuberculosis}
DPAFVAVANALSPAKVVSVIDQTARAARVVVPDFQLSLAIGKEGQNARLAARLTGWRIDIRGDAPP

>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 {Thermus
thermophilus}

QNPNSAPLVAQRVAEQIERRFAVRRRAIKQAVQVRMESGAKGAKVIVSGRIGGAEQARTEWAAQGRV
PLHTLRANIDYGFALARTTYGVLGVKAYIFLGEV
>d1hh2p4 d.202.1.1 (P:1-126) Transcription factor NusA, N-terminal domain {Thermotoga
maritima}
MNIGLLEALDQLEEEKGISKEEVIPILEKALVSAYRKNFGNSKNVEVVIDRNTGNIKVYQLLEVVEEVE
DPATQISLEEAKKIDPLAEVGSIVKKELNVKNFGRIAAQTAKQVLIQRIRELEKEKQ
>d1k0ra4 d.202.1.1 (A:-4-99) Transcription factor NusA, N-terminal domain
{Mycobacterium tuberculosis}
VSRHRMNIDMAALHAIEVDRGISVNELLETIKSALLTAYRHTQGHQTDARIEIDRKTGVVRIARETD
EAGNLISEWDDTPEGFGRIAATTARQVMLQFRDAE
>d1onea2 d.54.1.1 (A:1-141) Enolase {Baker's yeast (Saccharomyces cerevisiae)}
AVSKVYARSVYDSRGNPTVEVELTTEKGVFRSIVPSGASTGVHEALEMRDGDKSKWMGKGV LHAVK
NVNDVIAPAFVKANIDVKDQKAVDDFLISLDGTANKSKLGANAILGVSLAASRAAAAENKVPYKHL
ADLSKSKT
>d1pdz_2 d.54.1.1 (1-139) Enolase {Lobster (Homarus vulgaris)}
SITKVFARTIFDSRGNPTVEVDLYTSKGLFRAAVPSGASTGVHEALEMRDGDKSKYHGKSVFNAVKN
VNDVIVPEIHKSLKVTQQKECDEFMCKLDGTENKSSLGANAILGVSLAICKAGAAELGIPLYRHIANL
ANY
>d1e9ia2 d.54.1.1 (A:1-139) Enolase {Escherichia coli}
SKIVKIIGREIIDS RGNPTVEAEVHLEGGFVGMAAAPSGASTGSREALELRDGDKSRLFGKGVTKAVAA
VNGPIAQALIGKDAKDQAGIDKIMIDLGTENKSKFGANAILAVSLANAKAAAAAKGMPLYEHIAEL
NGT
>d1bqg_2 d.54.1.1 (12-143) D-glucarate dehydratase {Pseudomonas putida}
GAPVITDLKVVVAVGHDSMLLNLSGAHGPLFTRNII L TDSSGHVGVGEVPGGEGIRKTLEDARHLII
NQSIGNYQSLLNKVRNAFADRVDGGRGLQTFDLRIAVHAVTAVESALLDLLGQHLQVPVAALLG
>d1ec7a2 d.54.1.1 (A:5-137) D-glucarate dehydratase {Escherichia coli}
FTTPVVTEMQVIPVAGHDSMLMNLGAHAPFFTRNIVIIKDNSGHTGVGEIPGGEKIRKTLEDAIPLV
VGKTLGEYKNVLTIVRNTFADR DAGGRGLQTFDLRTTIHVVTGIEAAML DLLGQHLGVNVASLLG
>d1fhua2 d.54.1.1 (A:1-99) O-succinylbenzoate synthase {Escherichia coli}
MRSAQVYRWQIPMDAGVVLDRRRLKTRDGLYVCLREGERE GWGEISPLPGFSQETWEEAQSVLLA
WVNNWLAGDCELPQMPSVAFGVSCALAE LDTLP
>d1muca2 d.54.1.1 (A:4-130) Muconate-lactonizing enzyme (cis muconate cycloisomerase)
{Pseudomonas putida}
ALIERIDAIIVDLPTIRPHK LAMHTMQQT LVVLRVRCSDGVEGIGEATTIGGLAYGYESPEGIKANID
AHLAPALIGLAADNINAAMLKLDK LAKGNTFAKSGIESALLDAQGKRLGLPVSELLGG
>d2mnr_2 d.54.1.1 (3-132) Mandelate racemase {Pseudomonas putida}
EVLITGLRTRAVNVPLAYPVHTAVGT VGTAPLV LIDLATSAGVVGHSYLFAYTPVALKSLKQLDDMA
AMIVNEPLAPVSLEAMLAKRFCLAGYTG LIRMAAAGIDMAAWDALGKVHETPLVKLLGANAR
>d2chr_2 d.54.1.1 (1-126) Chlormuconate cycloisomerase {Alcaligenes eutrophus}
MKIDAIEAVIVDVPTKRPIQMSITTVHQQSYVIVRVYSEGLVGVGEGGSVGGPVWSAECAETIKIIVER
YLAPHL LGTDAFNVSGALQTMARAVTGNASAKAAVEMALLDLKARALGV SIAELLGG
>d1jpdx2 d.54.1.1 (X:-2-113) L-Ala-D/L-Glu epimerase {Escherichia coli}
GSHMRTVKVFEEAWPLHTPFVIARGSRSEARVVVELEEEGIKGTGECTPYPRYGESDASVMAQIMS
VVPQLEKGLTREELQKILPAGAARNALDCALWDLAARRQQQSLADLIGI

>d1jpma2 d.54.1.1 (A:1-125) L-Ala-D/L-Glu epimerase {*Bacillus subtilis*}
MKIIRIETSRIAVPLTKPFKTALRTVYTAESVIVRITYDSGAVGWGEAPPTLVITGDSMDSIESAIHHVL
KPALLGKSLAGYEAILHDIQHLLTGNMSAKAAVEMALYDGWAQMCGLPLYQMLGG

>d1kca2 d.54.1.1 (A:1-160) beta-Methylaspartase {*Clostridium tetanomorphum*}
MKIVDVLCTPGLTGFYFDDQRAIKKGAGHDGFTYTGSTVTEGFTQVRQKGESISVLLVLEDGQVAHG
DCAAVQYSGAGGRDPLFLAKDFIPVIEKEIAPKLGREITNFKPMAEEFDKMTVNGNRLHTAIRYGIT
QAILDAVAKTRKVTMAEVIRDEYNP

>d1kkoa2 d.54.1.1 (A:1-160) beta-Methylaspartase {*Citrobacter amalonaticus*}
MKIKQALFTAGYSSFYFDDQQAIKNGAGHDGFIYTGDPVTPGFTSVRQAGECVSVQLILENGAVAVGD
CAAVQYSGAGGRDPLFLAEHFIPFLNDHIKPLLEGRDVAFLPNARFFDKLRIDGNLLHTAVRYGLSQ
ALLDATALASGRLKTEVVCDEWQL

>d1bxea_ d.55.1.1 (A:) Ribosomal protein L22 {*Thermus aquaticus*, subsp. *Thermus thermophilus*}
MEAKAIARYVRISPRKVRVLVVDLIRGKSLEEARNILRYTNKRGAYFVAKVLESAAANAVNNHDMLED
RLYVKAAYVDEGPALKRVLPRARGRADIKKRTSHITVILGEK

>d1jj2q_ d.55.1.1 (Q:) Ribosomal protein L22 {*Archaeon Haloarcula marismortui*}
GISYSVEADPDTTAKAMLRERQMSFKHSKAIAREIKGKTAGEAVDYLEAVIEGDQVPVFKQHNSGVG
HKSKVDGWDAGRYPEKASKAFLDLENVGNADHQGFDGEAMTIKHVAAHKVGEQQGRKPRAMG
RASAWNSPQVDVELILEEP

>d1gd8a_ d.188.1.1 (A:) Prokaryotic ribosomal protein L17 {*Thermus thermophilus*}
SSHRLALYRNQAKSLLTHGRITTTVPKAKELRGFVDHLIHLAKRGLHARRLVLRDLQDVKLVRKLF
DEIAPRYRDRQGGYTRVLKLAERRRGDGAPLALVELVE

>d1oela3 d.56.1.1 (A:137-190,A:367-409) GroEL {*Escherichia coli*}
PCSDSKAIAQVGTISANSDETGVKLIAEAMDKVGKEGVITVEDGTGLQDELVDVXERVAKLAGGVAVI
KVGAAATEVEMKEKKARVEDALHATRAAVEE

>d1ioea3 d.56.1.1 (A:137-190,A:367-409) GroEL {*Paracoccus denitrificans*}
PVNDSSEVAQVGTISANGESFIGQQAIEAMQRVGNEGVTVEENKGMETEVEVVXERVAKLAGGVAVI
RVGGMTEIEVKERKDRVDDALNATRAAVQE

>d1a6da3 d.56.1.2 (A:146-214,A:368-403) Thermosome {*Archaeon Thermoplasma acidophilum*}
TDDATLRKIALTALSGKNTGLSNDFLADLVVKAVNAVAEVRDGTIVDTANIKVDKKNNGGSVNDTQF
ISXAVSILIRGGTDHVVSEVERALNDAIRVVAITKEDGK

>d1a6db3 d.56.1.2 (B:145-215,B:368-403) Thermosome {*Archaeon Thermoplasma acidophilum*}
GADEKALLLKMAQTSLNSKSASVAKDKLAEISYEAVKSVAEALRDGKYYVDFDNIQVVKKQGGAIDDT
QLINXKAVSILVRGETEHVVDEMERSITDSLHVVASALEDG

>d1h6ha_ d.189.1.1 (A:) p40phox NADPH oxidase {*Human (Homo sapiens)*}
AVAQQLRAESDFEQLPDDVAISANIADIEEKRGFTSHFVVFVIEVKTGGSKYLIYRRYRQFHALQSKLE
ERFGPDSKSSALACTLPTLPKVVYGVKQIEAEMRIPALNAYMKSLLSPLVWVLMDEDVRIFYQSPY
DSEQVP

>d1gd5a_ d.189.1.1 (A:) p47phox NADPH oxidase {*Human (Homo sapiens)*}
GSMGDTFIRHIALLGFEKRFVPSQHYYVMFLVKWQDLSEKVVYRRFTEIYEFHKTLEMFPIEAGAI
NPENRIIPLPAPKWFDGQRAAENRQGTLECYSTLMSLPTKISRCPHLLDFFKVRPDDLKLP

>d1ji8a_ d.203.1.1 (A:) DsrC, the gamma subunit of dissimilatory sulfite reductase {*Archaeon*

Pyrobaculum aerophilum}

MPVKCPGEYQVDGKKVILDEDCFMQNPEDWDEKVAEWLARELEGIQKMTEEHWKLVKYLREYW
ETFGTCPPIKMVTKETGFSLEKIYQLFPSGPAHGACKVAGAPKPTGCV

>d1ghha_ d.57.1.1 (A:) DNA damage-inducible protein DinI {Escherichia coli}
MRIEVTIAKTSPLPAGAILAGELSRRIQYAFPDNEGHVSVRYAAANNLSVIGATKEDKQRISEILQE
TWESADDWFVSE

>d1fxd_ d.58.1.1 (-) Ferredoxin II {Desulfovibrio gigas}
PIEVNDDCMACEACVEICPDVFEMNEEGDKAVVINPDSLDCVVEAIDSCPAEAIVRS

>d1dura_ d.58.1.1 (A:) Ferredoxin II {Peptostreptococcus asaccharolyticus}
AYVINDSCIACGACKPECPVNCIQEGSIYADADSCIDCGSCASVCPVGAPNPED

>d1fca_ d.58.1.1 (-) Ferredoxin II {Clostridium acidi-urici}
AYVINEACISCGACEPECPVDAISQGGSRVIDADTCIDCGACAGVCPVDAPVQA

>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}
ALMITDECINCDVCEPECPNGAISQGDETYVIEPSLCTECVGHYETSQCVEVCPVDCIIKDP SHEETED
ELRAKYERITG

>d7fd1a_ d.58.1.2 (A:) Ferredoxin {Azotobacter vinelandii}
AFVVTDNCIKCKYTDCEVCPVDCFYEGPNFLVIHPDECIDCALCEPECPAQAI FSEDEVPEDMQEFI
QLNAELAEVWPNITEKKDPLPDAEDWDGKGLQHLE

>d1bc6_ d.58.1.2 (-) Ferredoxin {Bacillus schlegelii}
AYVITEPCIGTKDASCVEVCPVDCIHEGEDQYYIDPVCIDCGACEAVCPVSAIYHEDFVPEEWKSYIQ
KNRDFFKK

>d1h98a_ d.58.1.2 (A:) Ferredoxin {Thermus thermophilus}
PHVICEPCIGVKDQSCVEVCPVECIYDGGDQFYIHPEECIDCGACVPACPVNAIYPEEDVPEQWKSYIE
KNRKLGL

>d1xer_ d.58.1.3 (-) Ferredoxin {Archaeon Sulfolobus sp.}
GIDPNYRTNRQVVGHEHSGHKVYGPVEPPKVLGIHGTIVGVDFDLCIADGSCINACPVNVFQWYDTPG
HPASEKKADPVNEQACIFCMACVNVCPVAAIDVKPP

>d1vjw_ d.58.1.4 (-) Ferredoxin {Thermotoga maritima}
MKVRVDADACIGCGVCENLCPDVFQLGDDGKAKVLQPETDLPCA KDAADSCPTGAISVE

>d1fxra_ d.58.1.4 (A:) Ferredoxin I {Sulfate-reducing bacteria (Desulfovibrio africanus)}
ARKFYVDQDECIACESCVEIAPGAFAMDPEIEKAYVKDVEGASQEEVEEAMDTCPVQCIHWEDE

>d1iqza_ d.58.1.4 (A:) Ferredoxin {Bacillus thermoproteolyticus}
PKYTIVDKETCIACGACGAAAPDIYDYDEDGIAVYVTLDDNQGIVEVPDILIDDMDAFEGCPTDSIKV
ADEPFDGDPNKFE

>d1jb0c_ d.58.1.4 (C:) Photosystem I iron-sulfur protein PsaC {Synechococcus elongatus}
AHTVKIYDTCIGCTQCVRACPTDVLEMVPWDGCKAGQIASSPRTEDCVGCKRCETACPTDFLSIRVYL
GAETTRSMGLAY

>d1feha3 d.58.1.5 (A:127-209) Fe-only hydrogenase, second domain {Clostridium
pasteurianum}
KDKTEYVDERSKSLTVDRTKLLCGRCV NACGKN TETYAMKFLNKNKGTIIGA EDEKCFDDTNCLLC

GQCIIACPVAALSEKS

>d1hfel2 d.58.1.5 (L:2-86) Fe-only hydrogenase larger subunit, N-domain {Desulfovibrio desulfuricans}

SRTVMERIEYEMHTPDPKADPKLHFVQIDEAKCIGCDTCSQYCPTAAIFGEMGEPHSIPHIEACINC
GQCLTHCPENAIYEAQS

>d1keka5 d.58.1.5 (A:669-785) Pyruvate-ferredoxin oxidoreductase, PFOR, domain V {Desulfovibrio africanus}

TSQFEKRGVAINVPQWVPENCIQCNQCAFVCPHSAILPVLAKEEELVGAPANFTALEAKGKELKGYKF
RIQINTLDCMGCNCADICPPKEKALVMQPLDTQRDAQVPNLEYAARIP

>d1h7wa5 d.58.1.5 (A:845-1017) Dihydropyrimidine dehydrogenase, C-terminal domain {Pig (Sus scrofa)}

ELQGWGQSPGTESHQKGPVPRIAEELMGKKLPNFGPYLEQRKKIIAEEKMRLKEQNAAFPPLERK
PFIPKKPIPAIKDVIGKALQYLGTGELSNIQVVAVIDEEMCINCCKCYMTCNDSGYQAIQFDPETHL
PTVTDCTGCTLCLSVCPHDCIRMVSRTPPYEPKRGL

>d1jnrb_ d.58.1.5 (B:) Adenylylsulfate reductase B subunit {Archaeon Archaeoglobus fulgidus}

PSFVNPEKCDGCKALERTACEYICPNLMTLDKEKMKAYNREPDMCWECYSCVKMCPQGAIIDVRG
YVDYSPLGGACVPMRGTSIDIMWTVKYRNGKVLRFKFAIRTPWGSIQPFEGFPPEPTEEALKSELLAG
EPEIIGTSEFPQVKKKA

>d1d09b1 d.58.2.1 (B:1-100) Aspartate carbamoyltransferase {Escherichia coli}

MTHDNKLQVEAIKRGTVIDHIPAQIGFKLLSLFKLTETDQRITIGLNLPSGEMGRKDLIKIENTFLSED
QVDQLALYAPQATVNRIDNYEVVGKSRPSLP

>d2atcb1 d.58.2.1 (B:1-100) Aspartate carbamoyltransferase {Escherichia coli}

MTHNDKLQVAEIKRGTVINHIPAEIGFKLLSLFKLTETDQRITIGLNLPSGEMGRKDLIKIENTFLSED
EVDELALYAPQATVNRINDYEVVGKSRPSLP

>d1pca_2 d.58.3.1 (4A-99A) Procarboxypeptidase A {Pig (Sus scrofa)}

KEDFVGHQVLRISVDDEAQVQKVELEDLEHLQLDFWRGPARPGFPIDVRVPPFSIQAVKVFLEAHG
IRYTIMIEDVQLLLDEEQEQMFASQGR

>d1pyta_ d.58.3.1 (A:) Procarboxypeptidase A {Cow (Bos taurus)}

KEDFVGHQVLRITAADAEVQTVKELEDLEHLQLDFWRGPGQPGSPIDVRVPPPSLQAVKVFLEAHG
IRYRIMIEDVQSLLEEQEQMFASQSR

>d1aye_2 d.58.3.1 (4A-99A) Procarboxypeptidase A {Human (Homo sapiens)}

LETFVGQVLEIVPSNEEQIKNLLQLEAQEHLQLDFWKSPTTPGETAHVRVPPVNVQAVKVFLESQG
IAYSIMIEDVQVLLDKENEMLFNRRR

>d1nsa_2 d.58.3.1 (7A-95A) Procarboxypeptidase B {Pig (Sus scrofa)}

FEGEKVFRVNVEDENDISELHELASTRQIDFWKPDSVTQIKPHSTVDFRVKAEDILAVEDFLEQNEL
QYEVLINNLRVLEAQFDSVSR

>d1pba_ d.58.3.1 (-) Procarboxypeptidase B {Pig (Sus scrofa)}

HHSGEHFEGEKVFRVNVEDENDISELHELASTRQIDFWKPDSVTQIKPHSTVDFRVKAEDILAVEDF
LEQNELQYEVLINN

>d1spbp_ d.58.3.2 (P:) Subtilisin prosegment {Bacillus amyloliquefaciens}

EKKYIVGFKQTMSTMSAAKKKDVISEKGGKQKQFKYVDAASATLNEKAVKELKKDPSVAYVEEDH
VAHAY

>d1scjb_ d.58.3.2 (B:) Subtilisin prosegment {Bacillus subtilis}

EKKYIVGFKQTMSAMSSAKKKDVISQKGGKVEKQFKYVNAAAATLDEKAVKELKKDPSVAYVEEDHI
AHEY

>d1itpa_ d.58.3.2 (A:) Proteinase A inhibitor 1, POIA1 {Oyster mushroom (Pleurotus
ostreatus)}

GSAGKFVIFKNDVSEDKIRETKDEVIAEGGTITNEYNMPGMKGFAGELTPQSLTKFQGLQGLDIDSIE
EDGIVTTQ

>d1mli_ d.58.4.1 (-) Muconalactone isomerase {Pseudomonas putida}

MLFHVKMTVKLPVDMDDPAKATQLKADEKELAQRLQREGTWRHLWRIAGHYANYSVFDVPSVEAL
HDTLMQLPLFPYMDIEVDGLCRHPSSIHSDDR

>d2pii_ d.58.5.1 (-) PII (product of glnB) {Escherichia coli}

MKKIDAIKPKFLDDVREALAEVGITGMTVTEVKGFGFRQKGHTELYRGAEYMVDFLPKVKIEIVVPD
DIVDTCVDTHIRTAQTGKIGDGKIFVFDVARVIRIRTGEEDDAI

>d1gnka_ d.58.5.1 (A:) PII-homolog GlnK {Escherichia coli}

MKLVTVIIPKFLDREALSSIGIQGLTVTEVKGFGFRQKHAELYRGAEYSVNFLPKVKIDVAIADDQ
LDEVIDIVSKAAYTGKIGDGKIFVAELQRVIRIRTGEADEAAL

>d1nuea_ d.58.6.1 (A:) Nucleoside diphosphate kinases {Human (Homo sapiens)}

ANLERTFIAIKPDGVQRGLVGEIHKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFFPGLVKYMN
SGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSDSVKSAEKEISLWFKP
EELVDYKSCAHDWVYE

>d1ehwa_ d.58.6.1 (A:) Nucleoside diphosphate kinases {Human (Homo sapiens), NDK4}

HMGTRERTLVAVKPDGVQRRLVGDVIQRFERRGFTLVGMKMLQAPESVLAEHYQDLRRKPFYPALIR
YMSSGPVVAMVWEGYNVVRASRAMIGHTDSAEAAPGTIRGDFSVHISRNVIHASDSVEGAQREIQL
WFQSSELVSW

>d1be4a_ d.58.6.1 (A:) Nucleoside diphosphate kinases {Cow (Bos taurus)}

ANSERTFIAIKPDGVQRGLMGEIHKRFEQKGFRLVAMKFMRASEDLLKEHYIDLKDRPFFAGLVKYM
HSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSDSVESAKEIALLWFR
PEELVNYKSCAQNWIYE

>d1hlwa_ d.58.6.1 (A:) Nucleoside diphosphate kinases {Dictyostelium discoideum}

VNKERTFLAVKPDGVARGLVGEIARYEKKGFVLVGLKQLVPTKDLAESHYAHEKRPFFGGLVSFITS
GPVVAMVFEKGKVASARLMIGVTNPLASAPGSIRGDFGVDVGRNIIAGSDSVESANREIALWFKPEE
LLEVKPNPNLYE

>d1nsqa_ d.58.6.1 (A:) Nucleoside diphosphate kinases {Drosophila melanogaster}

AANKERTFIMVKPDGVQRGLVKGKIERFEQKGFKLVALKFTWASKELLEKHYADLSARPFFPGLVNY
MNSGPVVPMVWEGLNVVKTGRQMLGATNPADSLPGTIRGDFCIQVGRNIIHGSDAVESAKEIALLW
FNEKELVTWTPAAKDWIYE

>d1nhkl_ d.58.6.1 (L:) Nucleoside diphosphate kinases {Myxococcus xanthus}

AIERTLSIIPKPDGLEKGVIGKIISRFEKGLKPVAIRLQHLSQAQAEQFYAVHKARPFKDLVQFMISGP
VVLVLEGENAVLANRDIMGATNPAQAAGTIRKDFATSIDKNTVHGSDSLENAKIEIAYFFRETEIH
SYPYQ

>d1ha1_1 d.58.7.1 (8-92) Nuclear ribonucleoprotein A1, RNP A1, UP1 {Human (Homo
sapiens)}

EPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCVVMRDPNTRKSRGFGFVYATVEEVDAAMNA
RPHKVDGRVVEPKRAVSRE

>d1ha1_2 d.58.7.1 (99-180) Nuclear ribonucleoprotein A1, RNP A1, UP1 {Human (Homo

sapiens}}
AHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRGSGKKRGFAFVTFDDHDSVDKIVIQY
HTVNGHNCEVRKAL
>d2up1a2 d.58.7.1 (A:99-190) Nuclear ribonucleoprotein A1, RNP A1, UP1 {Human (Homo sapiens}}
GAHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRGSGKKRGFAFVTFDDHDSVDKIVIQK
YHTVNGHNCEVRKALSKQEMASAS
>d1fht_ d.58.7.1 (-) Splicesomal U1A protein {Human (Homo sapiens}}
AVPETRPNHTIYINNLNEKIKKDELKKSLEYAIFSQFGQILDILVSRSLKMRGQAFVIFKEVSSATNALRS
MQGFPPFYDKPMRIQYAKTDSDIIAKMGTFVERDRKREKRKPKSQE
>d1nrca_ d.58.7.1 (A:) Splicesomal U1A protein {Human (Homo sapiens}}
TRPNHTIYINNLNEKIKKDELKKSLEYAIFSQFGQILDILVSRSLKMRGQAFVIFKEVSSATNALRSMQG
FPFYDKPMRICYAKTD
>d1urna_ d.58.7.1 (A:) Splicesomal U1A protein {Human (Homo sapiens}}
AVPETRPNHTIYINNLNEKIKKDELKKSLEYAIFSQFGQILDILVSRSLKMRGQAFVIFKEVSSATNALR
SMQGFPPFYDKPMRIQYAKTDSDIIAKMGTFVERDRKREKRKPKSQE
>d2u1a_ d.58.7.1 (-) Splicesomal U1A protein {Human (Homo sapiens}}
MAPAQPLSENPPNHILFLTNLPEETNELMLSMLFNQFPGFKEVRLVPRHDI AFVEFDNEVQAGAA
RDALQGFKITQNNAMKISFAKK
>d1a9nb_ d.58.7.1 (B:) Splicing factor U2B" {Human (Homo sapiens}}
IRPNHTIYINNMNDKIKKEELKRSLEYAIFSQFGHVVDIVALKTMKMRGQAFVIFKELGSSTNALRQLQ
GFPFYGKPMRIQYAKTDSDIISKMRG
>d1u2fa_ d.58.7.1 (A:) Splicing factor U2AF 65 KDa subunit {Human (Homo sapiens}}
ARRLYVGNIPFGITEEAMMDFNAQMRLGGLTQAPGNPVLAVQINQDKNFALFRSVDETTQAMA
FDGIIFQGQSLKIRRP HDYQPLPG
>d2u2fa_ d.58.7.1 (A:) Splicing factor U2AF 65 KDa subunit {Human (Homo sapiens}}
AHKLFIGGLPNYLNDQVKELLSFGPLKAFNLVKDSATGLSKGYAFCEYVDINVTDQAIAGLNGMQL
GDKLLVQRASVGAKNA
>d1b7fa1 d.58.7.1 (A:123-204) Sex-lethal protein {Drosophila melanogaster}
SNTNLIVNYLPQDMTDRELYALFRAIGPINTCRIMRDYKTGYSYGYAFVDFDFTSEMDSQRAIKVLNGIT
VRNKRLKVSYPARPG
>d1b7fa2 d.58.7.1 (A:205-289) Sex-lethal protein {Drosophila melanogaster}
GESIKDTNLYVTNLPRITDDQLDTIFGKYGSIVQKNILRDKLTGRPRGVAFVRYNKREEAQE AISALN
NVIPEGGSQPLSVRLA
>d1sxl_ d.58.7.1 (-) Sex-lethal protein {Drosophila melanogaster}
MSYARPGGESIKDTNLYVTNLPRITDDQLDTIFGKYGSIVQKNILRDKLTGRPRGVAFVRYNKREEA
QE AISALN NVIPEGGSQPLSVRLAEH GK
>d1d8za_ d.58.7.1 (A:) Hu antigen C (Huc) {Mouse (Mus musculus}}
MDSKTNLIVNYLPQNMTQDEFKSLFGSIGDIESCKLVRDKITGQSLGYGFVNYS DPNDADKAIN TLN
GLKLQTKTIKVSYPARSSASIR
>d1d9aa_ d.58.7.1 (A:) Hu antigen C (Huc) {Mouse (Mus musculus}}
DANLYVSGLPKTM SQEMEQ LFSQYGRITSRILLDQATGVS RGVGFIRFDKRIEAE EAIKGLNGQKPL
GAAEPITVKFANNPSQ
>d1fxla1 d.58.7.1 (A:37-118) Hu antigen D (Hud) {Human (Homo sapiens}}

SKTNLIVNYLPQNMTQEEFRSLFGSIGEIESCKLVRDKITGQSLGYGFVNYIDPKDAEKAINTLNGLRL
QTKTIKVSYPARPS
>d1fxla2 d.58.7.1 (A:119-203) Hu antigen D (Hud) {Human (Homo sapiens)}
SASIRDANLYVSGLPKMTQKELEQLFSQYGRITSRILVDQVTGVSARGVGFIRFDKRIEAEAAIKGLNG
QKPSGATEPITVKFA
>d1hd1a_ d.58.7.1 (A:) Heterogeneous nuclear ribonucleoprotein d0 {Human (Homo
sapiens)}
KMFIGGLSWDTTKKDLKDYFSKFGEVVDCTLKLDPITGRSRGFGFVLFKESVSKVMDQKEHKLN
GKVIDPKRA
>d2msta_ d.58.7.1 (A:) Neural RNA-binding protein Musashi-1 {Mouse (Mus musculus)}
KIFVGGSLVNTTVEDVKHYFEQFGKVDDAMLMFDKTTNRHRGFGFVTFESEDIVEKVCIEHFHEIN
NKMVECKKA
>d1cvja1 d.58.7.1 (A:11-90) Poly(A)-binding protein {Human (Homo sapiens)}
ASLYVGDLPDVTTEAMLYEKFPAGPILSIRVCRDMITRRSLGYAVVNFQPPADAERALDTMNFVVIK
GKPVIRIMWSQRD
>d1cvja2 d.58.7.1 (A:91-179) Poly(A)-binding protein {Human (Homo sapiens)}
PSLRKSGVGNIFIKNLKSIDNKALYDTFSAFGNILSCKVVCDENGSKGYGFVHFETQEAAERAIEKM
NGMLLNDRKVFVGRFKSRKER
>d1qm9a1 d.58.7.1 (A:1-110) Polypyrimidine tract-binding protein {Human (Homo
sapiens)}
MGNSVLLVSNLNPVTPQSLFILFGVYGDVQRVKILFNKKENALVQMADGNQAQLAMSHLNGHKL
HGKPIRITLSKHQNVQLPREGQEDQGLTKDYGNSPLHRFKKPGS
>d1qm9a2 d.58.7.1 (A:111-198) Polypyrimidine tract-binding protein {Human (Homo
sapiens)}
KNFQNIFFPSATLHLSNIPPSVSEEDLKVLFSSNGGVVKGFKFFQKDRKMALIQMGSVEEAVQALIDL
HNHDLGENHHLRVSFSKSTI
>d1fj7a_ d.58.7.1 (A:) Nucleolin {Golden hamster (Mesocricetus auratus)}
GSHMLEDPVEGSESTTPFNLFIGNLNPKNKSVKVAELKVAISELFAKNDLAVVDVVRTGTNRKFGYVDFES
AEDLEKALELTGLKVFVGFNEIKLEKPKGRDGTGRC
>d1fjca_ d.58.7.1 (A:) Nucleolin {Golden hamster (Mesocricetus auratus)}
SHMLEDPCTSKKVRARTLLAKNLSFNITEDELKEVFEDALEIRLVSQDGKSKGIAYIEFKSEADAEEK
NLEEKQGAIEIDGRSVSLYYTGEKGGTRG
>d1fjeb1 d.58.7.1 (B:1-91) Nucleolin {Golden hamster (Mesocricetus auratus)}
GSHMVEGSESTTPFNLFIGNLNPKNKSVKVAELKVAISELFAKNDLAVVDVVRTGTNRKFGYVDFESAEDL
EKALELTGLKVFVGFNEIKLEKPKGR
>d1fjeb2 d.58.7.1 (B:92-175) Nucleolin {Golden hamster (Mesocricetus auratus)}
DSKKVRAARTLLAKNLSFNITEDELKEVFEDALEIRLVSQDGKSKGIAYIEFKSEADAEEKNLEEKQGA
EIDGRSVSLYYTGEK
>d1h6kx_ d.58.7.1 (X:) CBP20, 20KDa nuclear cap-binding protein {Human (Homo sapiens)}
KSCTLYVGNLSFYTTTEEQIYELFSKSGDIKKIIMGLDKMTACGFCFVEYYSRADAENAMRYINGTRL
DRIIRTDWDAG
>d1fo1a2 d.58.7.2 (A:123-191) mRNA export factor tap {Human (Homo sapiens)}
TIPYGRKYDKAWLLSMIQSKCSVPFTPIEFHYENTRAQFFVEDASTASALKAVNYKILDRENRRISIII
>d1ft8a2 d.58.7.2 (A:118-199) mRNA export factor tap {Human (Homo sapiens)}

NWFKITIPYGRKYDKAWLLSMIQSKCSVPFTPIEFHYENTRAQFFVEDASTASALKAVNYKILDRENRRISIIINSSAPPHT

>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)}

RGGAGTSQDGTSKNWFKITIPYGRKYDKAWLLSMIQSKSSVPFTPIEFHYENTRAQFFVEDASTASALKAVNYKILDRENRRISIIINSSAPPHTI

>d1jmta_ d.58.7.3 (A:) U2AF35 (35 KDa subunit) {Human (Homo sapiens)}

SQTIALLLNIYRNPQNSSQSADGLRSAVSDVEMQEHYDEFFEEVFTEEMEEKYGEVEEMNVCDNLGDHLVGNVYVKFRREEDA EKAVIDLNNRWFNGQPIHAELSP

>d1dbda_ d.58.8.1 (A:) Papillomavirus-1 E2 protein {Bovine papillomavirus type 1}

RRTTNDGFHLLKAGGSCFALISGTANQVKCYRFRVKKNHRHRYENCTTTWFTVADNGAERQGGQAQILITFGSPSQRQDFLKHVPLPPGMNISGFTASLDF

>d2bopa_ d.58.8.1 (A:) Papillomavirus-1 E2 protein {Bovine papillomavirus type 1}

SCFALISGTANQVKCYRFRVKKNHRHRYENCTTTWFTVADNGAERQGGQAQILITFGSPSQRQDFLKHVPLPPGMNISGFTASLDF

>d1a7ge_ d.58.8.1 (E:) Papillomavirus-1 E2 protein {Human papillomavirus type 31}

ATTPIIHLKGDANILKCLRYRLSKYKQLYEQVSSTWHWTCTDGKHKNAIVTLTYISTSQRDDFLNTVVIPNTVSVSTGYMTI

>d1by9_ d.58.8.1 (-) Papillomavirus-1 E2 protein {Human papillomavirus type 16}

TTPIVHLKGDANTLCLRYRFFKKHCTLYTAVSSTWHWTGHNVKHKSAIVTLTYDSEWQRDQFLSQVKIPKTITVSTGFMS

>d1f9fa_ d.58.8.1 (A:) Papillomavirus-1 E2 protein {Human papillomavirus type 18}

HMTPIIHLKGDNRSLKCLRYRLRKHS DHYRDISSTWHWTGAGNEKTGILTVTYHSETQRTKFLNTVAIPDSVQILVGYMTM

>d1b3ta_ d.58.8.1 (A:) Epstein barr virus nuclear antigen-1 (ebna1) {Epstein-Barr virus}

KGGWFGKHRGQGGSNPKFENIAEGLRALLARSHVERTTDEGTWVAGVFVYGGSKTSLYNLRRGTALAIQCRLTPLSRLPFGMAPGPGPQPGPLRESIVCYFMVFLQTHIFAEVLKDAIKDLVMTKPAPTCNIRVTVCSFDDGVDLP

>d1vhib_ d.58.8.1 (B:) Epstein barr virus nuclear antigen-1 (ebna1) {Epstein-Barr virus}

PKFENIAEGLRALLARSHVERTTDEGTWVAGVFVYGGSKTSLYNLRRGTALAIQCRLTPLSRLPFGMAPGPGPQPGPLRESIVCYFMVFLQTHIFAEVLKDAIKDLVMTKPAPTCNIRVTVCSFDDGVDLP

>d3rubl2 d.58.9.1 (L:22-147) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Tobacco (Nicotiana tabacum), variant turkish samsun}

LYYTPPEYQTKD TDILAAFRVTPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLTSLDRYKGRICYRIERVVGEKDQYIAYVAYPLDLFEEGSVTNMFTSIVGNVFGFKALRALRLEDLRIPPAYVKT

>d1bura2 d.58.9.1 (A:12-147) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Spinach (Spinacia oleracea)}

EFKAGVKDYKLYYTPPEYETLTDILAAFRVSPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLTNLDRYKGRICYHIPEVAGEENQYICYVAYPLDLFEEGSVTNMFTSIVGNVFGFKALRALRLEDLRIPPAYVKT

T

>d1bwva2 d.58.9.1 (A:7-149) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Galdieria partita}

RIKNSRYESGVIPIYAKMGYWNPDYQVKD TDVLALFRVTPQPGVDPIEAAA AVAGESSTATWTTVVWT

DLLTAADLYRAKAYKVDQVPNNPEQYFAYIAYELDLFEEGSIANLTASIIGNVFGFKAVKALRLEDMRL
PLAYLKTFQ

>d1gk8a2 d.58.9.1 (A:7-149) Ribulose 1,5-bisphosphate carboxylase-oxygenase
{Chlamydomonas reinhardtii}

TKAGAGFKAGVKDYRLTYTPDYVVVVDLILAAFRMTPQPGVPPEECGAAVAESSTGTWTTVWT
DGLTSLDRYKGRCYDIEPVPGEDNQYIAYVAYPIDLFEEGSVTNMFTSIVGNVFGFKALRALRLEDLRI
PPAYVKTFV

>d1bxna2 d.58.9.1 (A:22-150) Ribulose 1,5-bisphosphate carboxylase-oxygenase
{Alcaligenes eutrophus}

YKMGYWDGDYVPKDTDLLALFRITPQDGVDPVEAAA AVAGESSTATWTVVWTDRLTACDMYRAK
AYRVPVPNNPEQFFCYVAYDLSLFEEGSIANLTASIIGNVFSFKPIKAARLEDMRFPVAYVKT

>d1rbla2 d.58.9.1 (A:9-147) Ribulose 1,5-bisphosphate carboxylase-oxygenase
{Synechococcus sp., strain pcc 6301}

SAAGYKAGVKDYKLTYYTPDYTPKDTDLLAAFRFSPQPGVPADEAGAAIAAESSTGTWTTVWTDLL
TDMDRYKKGKCYHIEPVAGEENSYFAFIAYPLDLFEEGSVTNILTSIVGNVFGFKAIRSLRLEDIRFPVAL
VKT

>d5ruba2 d.58.9.1 (A:2-137) Ribulose 1,5-bisphosphate carboxylase-oxygenase
{Rhodospirillum rubrum}

DQSSRYVNLALKEEDLIAGGEHVLCAIYMKPKAGYGYVATAAHFAAESSTGTNVEVCTTDDFTRGVD
ALVYEVDARELTKIAYPVALFDRNITDGKAMIASFLTMTMGNNQGMGDVEYAKMHDFYVPEAYRAL
FD

>d1geha2 d.58.9.1 (A:12-136) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Archaeon
Thermococcus kodakaraensis}

YVDKGYEPSKRRDIIAVFRVTPAEGYTIEQAAGAVAAESSTGTWTTLYPWYEQERWADLSAKAYDFH
DMGDGSWIVRIAYPFHAFEEANLPGLLASIAGNIFGMKRVKGLRLEDLYFPEKLIREF

>d2acy_ d.58.10.1 (-) Acylphosphatase {Cow (Bos taurus)}

AEGDTLISVDYEIFGKVGQVFFRKYTQAEKKLGLVGVVQNTDQGTVQQLQGPASKVRHMQEWL
ETKGPSKSHIDRASFHNEKIVKLDYTDYFQIVK

>d1aps_ d.58.10.1 (-) Acylphosphatase {Horse (Equus caballus)}

STARPLKSVDYEVFGRVQGVCFRMYAEDEARKIGVVGWVKNKTSKGTVTGQVQGPPEEKVNSMKSWLS
KVGSPSSRIDRTNFSNEKTISKLEYSNFSVRY

>d1i1ga2 d.58.37.1 (A:62-141) LprA {Archaeon Pyrococcus furiosus}

YSLVTITGVDTKPEKLFVEAEKLEKEYDFVKELYLSSGDHMIMAVIWAKDGEDLAEIISNKIGKIEGVTK
VCPAILEKLLK

>d1dar_4 d.58.11.1 (600-689) Elongation factor G (EF-G), domains III and V {Thermus
thermophilus}

VILEPIMRVEVTTPEEYMGDVGDLNARRGQILGMEPRGNAQVIRAFVPLAEMFGYATDLRSKTQGR
GSFVMFFDHYQEVPKQVQEKLK

>d1fnma4 d.58.11.1 (A:404-482) Elongation factor G (EF-G), domains III and V {Thermus
thermophilus}

VPEPVIDVAIEPKTKADQEKLSQALARLAEEDPTFRVSTHPETGQTIISGMGELHLEIIVDRKREFKV
DANVGKPQVA

>d1b64_ d.58.12.1 (-) Guanine nucleotide exchange factor (GEF) domain from elongation
factor-1 beta {Human (Homo sapiens)}

MLVAKSSILLDVKPWDDDETDMAKLEECVRSIQADGLVWGSSKLVVPVGYGIKKLQIQCVVEDDKVGTD
MLEEQITAFEDYVQSMDVAAFNKI
>d1f60b_ d.58.12.1 (B:) Guanine nucleotide exchange factor (GEF) domain from elongation
factor-1 beta {Baker's yeast (*Saccharomyces cerevisiae*)}
PAAKSIVTLDVKPWDDDETNEEMVANVKAIEMEGLTWGAHQFIPIGFIGIKKLQINCVVEDDKVSLDD
LQQSIEEDEDHVQSTDIAAMQKL
>d1gh8a_ d.58.12.1 (A:) aEF-1beta {Archaeon *Methanobacterium thermoautotrophicum*}
MGDVVATIKVMPESPVDLEALKKEIQERIPEGTELHKIDEPIAFGLVALNVMVVVGDAEGGTEAA
EESLSGIEGVSNIETDVRRLM
>d1b7yb4 d.58.13.1 (B:682-775) Phenylalanyl-tRNA synthetase {*Thermus thermophilus*
(*Thermus aquaticus*)}
LAFQDPSRHAAFRDLAVVVPAPTPYGEVEALVREAAGPYLESALFDLYQGPPLEGHKSLAFHLRF
RHPKRTLREDEVEEAVSRVAEALRAR
>d1jjcb4 d.58.13.1 (B:682-785) Phenylalanyl-tRNA synthetase {*Thermus thermophilus*
(*Thermus aquaticus*)}
LAFQDPSRHAAFRDLAVVVPAPTPYGEVEALVREAAGPYLESALFDLYQGPPLEGHKSLAFHLRF
RHPKRTLREDEVEEAVSRVAEALRARGFGLRGLDTP
>d1loua_ d.58.14.1 (A:) Ribosomal protein S6 {*Thermus thermophilus*}
MRRYEVNIVLNPNDQSQLALEKEIIQRAAENYGARVEKVEELGLRRLAYPIAKDPQGYFLWYQVEM
PEDRVNDLARELRIRDNVRRVMVKSQEPF
>d1qjha_ d.58.14.1 (A:) Ribosomal protein S6 {*Thermus thermophilus*}
MRRYEVNIVLNPNDQSQLALEKEIIQRALENYGARVEKVAILGLMVLAYPIAKDPQGYFLWYQVEM
PEDRVNDLARELRIRDNVRRVMVKS
>d1fjgj_ d.58.15.1 (J:) Ribosomal protein S10 {*Thermus thermophilus*}
KIRIKLRGFDHKTLDASAQKIVEAARRSGAQVSGPIPLPTRVRRFTVIRGPFKHKDSREHFELRTHNR
LVDIINPNRKTIEQLMTLDLPTGVEIEIKT
>d1fa0a1 d.58.16.1 (A:352-523) Poly(A) polymerase, C-terminal domain {Baker's yeast
(*Saccharomyces cerevisiae*)}
NDFFFRYKFFYLEITAYTRGSDEQHLKWSGLVESKVRLLVMKLEVLGKIAHPFTKPFESSYCCPTED
DYEMIQDKYGSHKTETALNALKLVTDENKEEESIKDAPKAYLSTMYIGLDFNIENKKEKVDIHIPCTE
FVNLCSFNEDYGDHKVFNALALRFVKGYDLPDEVFD
>d1f5aa1 d.58.16.1 (A:365-498) Poly(A) polymerase, C-terminal domain {Cow (*Bos taurus*)}
PNFFQKYKHIVLLASAPTEKQRLEWVGLVESKIRILVGSLEKNEFITLAHVNPQSFAPKENPDKEE
FRTMWVIGLVFKKTENSENLSVDLTYDIQSFTDTVYRQAINSKMFEVDMKIAAMHVKRKQLHQLLP
>d1afj_ d.58.17.1 (-) Mercuric ion binding protein MerP {*Shigella flexneri*}
ATQTVTLAVPGMTCAACPITVKKALSKEGVSQVDVGFEEKREAVVTFDDTKASVQKLTATADAGYP
SSVKQ
>d1fvqa_ d.58.17.1 (A:) Copper transporter domain ccc2a {Baker's yeast (*Saccharomyces*
cerevisiae)}
AREVILAVHGMTCSACTNTINTQLRALKGVTCKDISLVTNECQVTYDNEVTADSIKEIIEDCGFDCEIL
RDS
>d1aw0_ d.58.17.1 (-) Menkes copper-transporting ATPase {Human (*Homo sapiens*)}
LTQETVINIDGMTCSVCVQSIIEGVIKPKGVKSIRVSLANSNGTVEYDPLLTSPETLRGAIEDMGFDAT
LSD

>d1cc8a_ d.58.17.1 (A:) ATX1 metallochaperone protein (ATOX1) {Baker's yeast (Saccharomyces cerevisiae)}

AEIKHYQFNVVMTCGSCGAVNKVLTKLEPDVSKIDISLEKQLVDVYTTLPYDFILEKIKKKTGKEVRSQ
KQL

>d1fe0a_ d.58.17.1 (A:) ATX1 metallochaperone protein (ATOX1) {Human (Homo sapiens), HAH1}

PKHEFSVDMTCGGCAEAVSRVLNKLGGVKYDIDLPNKKVCIESEHSMDTLLATLKKTKGKTVSYLGL

>d1cpza_ d.58.17.1 (A:) Copper chaperone {Enterococcus hirae}

AQEFVSKGMSCNHCVARIEEAVGRISGVKKVKVQLKKEKAVVKFDEANVQATEICQAINELGYQAEVI

>d1k0va_ d.58.17.1 (A:) Copper chaperone {Bacillus subtilis, CopZ}

MEQKTLQVEGMSQCVCVAVETSQVGLDGVSAVHVNLEAGKVDVSFDADKVSVDIADAIEDQGYD
VAKIEGR

>d1qupa2 d.58.17.1 (A:2-73) Copper chaperone for superoxide dismutase, N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

TTNDTYEATYAIPMHCENCVNDIKACLKNVPGINSLNFDIEQQIMSVESSVAPSTIINTLRNCGKDAII
RGA

>d1gmua2 d.58.38.1 (A:71-138) Urease metallochaperone UreE, C-terminal domain {Klebsiella aerogenes}

DEEVSVVRCDPFMLAKACYALGNRHVPLQIMPGEALRYHHDHVLDDMLRQFGLTVTFGQLPFEPEA
GA

>d1eara2 d.58.38.1 (A:75-142) Urease metallochaperone UreE, C-terminal domain {Bacillus pasteurii}

LEKVYVIKQTMQEMGKMAFEIGNRHTMCIIEDDEILVRYDKTLEKLIDEVGVSYEQSERRFKPEPK
Y

>d1psda3 d.58.18.1 (A:327-410) Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain {Escherichia coli}

FPEVSLPLHGRRMLMHIHENRPGVLTALNKIFAEQGVNIAAQYLQTSAQMGYVVIDIEADEDVAEKAL
QAMKAIPGTIRARLLY

>d1tdj_2 d.58.18.2 (336-423) Allosteric threonine deaminase C-terminal domain {Escherichia coli}

QREALLAVTIPEEKGSFLKFCQLLGGRSVTEFNRYFADAKNACIFVGVRLSRGLEERKEILQMLNDGG
YSVVDLSDDMAKLVHRYMV

>d1tdj_3 d.58.18.2 (424-514) Allosteric threonine deaminase C-terminal domain {Escherichia coli}

GGRPSHPLQERLYSFEFPESPGALLRFLNTLGTYWNISLFHYRSHGTDYGRVLA AFELGDHEPDFET
RLNELGYDCHDETNNPAFRFFLAG

>d1phza1 d.58.18.3 (A:19-115) Phenylalanine hydroxylase N-terminal domain {Rat (Rattus norvegicus)}

GQETS YIEDNSNQNGAISLIFSLKEEVGALAKVLR LFEENDINLTHIESRPSRLNKDEYEFFTYLDKRT
KPVLGSIKSLRNDIGATVHELSDRDEK

>d1cg2a2 d.58.19.1 (A:214-326) Carboxypeptidase G2, dimerisation domain {Pseudomonas sp., strain rs-16}

SGIAYVQVNITGKASHAGAAPELGVNALVEASDLVLR TMNIDDKAKNLRFNW TIAKAGNVSNIIPASA
TLNADVRYARNEDFDAAMKTLEERAQQKLP EADV KIVIVTRGRPA

>d1dqaal d.58.20.1 (A:587-703) NAD-binding domain of HMG-CoA reductase {Human (Homo sapiens)}
GMTRGPVVRPRACDSAEVKAWLETSEGFVAVIKEAFDSTSRFARLQKLHTSIAGRNLIRFQSRSGDA
MGMNMISKGTEKALSKLHEYFPEMQILAVSGNYCTDKKPAAINWIEGRG

>d1qaxa1 d.58.20.1 (A:111-220) NAD-binding domain of HMG-CoA reductase {Pseudomonas mevalonii}
LMHAQVQIVGIQDPLNARLSLLRRKDEIHELNRKDQLLNSLGGGCRDIEVHTFADTPRGPMLVAHLI
VDVRDAMGANTVNTMAEAVAPLMEAITGGQVRLRILSNLADL

>d1ekra_ d.58.21.1 (A:) Molybdenum cofactor biosynthesis protein C, MoaC {Escherichia coli}
GEAHMVDVSAKAETVREARAEAFVTMRSETLAMIIDGRHHKGDVFATARIAGIQAARTWDLIPLC
HPLMLSKVEVNLQAEPEHNRVRIETLCRLTGKTVEMEALTAASVAALTIYDMCKAVQKDMVIGPVR
LLAKSGGKSGDFK

>d1f3va_ d.58.22.1 (A:) TRADD, N-terminal domain {Human (Homo sapiens)}
HEEWVGSAYLFEVSSLDKVVLSDAYAHPQKQVAVYRALQAALAESGGSPDVLQMLKIHRSDPQLIVQ
LRFCEGRQPCGRFLRAYREGALRAALQRSLAALAQHSVPLQLELRAGAERLDALLADEERCLSCILA
QQPDRLRDEELAELEDALRNKCG

>d1mla_2 d.58.23.1 (128-197) Probable ACP-binding domain of malonyl-CoA ACP
transacylase {Escherichia coli}
GTGAMAAIIGLDDASIAKACEEAAEGQVSPVNFNSPGQVVIAGHKEAVERAGAACKAAGAKRALPL
PVS

>d1ffgb_ d.58.24.1 (B:) CheY-binding domain of CheA {Escherichia coli}
PRRIISRLKAGEVDLLEELGHLTTLTDVVKGADSLSAILPGDIAEDDITAVLCFVIEADQITFETV

>d1kp6a_ d.58.25.1 (A:) Killer toxin KP6 alpha-subunit {Smut fungus (Ustilago maydis)}
NNAFCAGFGLSCKWECWCTAHGTGNELRYATAAGCGDHLSKSYDARAGHCLFSDDLRNQFYSHCS
SLNNNMSCRSLSK

>d1h72c2 d.58.26.1 (C:168-300) Homoserine kinase, C-terminal domain {Archaeon
Methanococcus jannaschii}
FKLDILIAIPNISINTKEAREILPKAVGLKDLVNNVKGACGMVYALYNKDKSLFGRYMMSDKVIEPVRG
KLIPNYFKIKEEVKDKVYGITISGSGPSIIAFPKEEFIDEVENILRDYYENTIRTEVGGKVEVV

>d1fi4a2 d.58.26.2 (A:191-393) Mevalonate 5-diphosphate decarboxylase {Baker's yeast
(Saccharomyces cerevisiae)}
QMKACVLVVS DIKKDVSSTQGMQLTVATSELFKERIEHVVPKRFEVVRKAIVEKDFATFAKETMMD
SNSFHATCLDSFPPIFYMNDTSKRIISWCHTINQFYGETIVAYTFDAGPNAVLYYLAENESKLF AFIYKL
FGSVPGWDKKFTTEQLEAFNHQFESSNFTARELDLELQKDVARVILTQVSGSPQETNESLIDAKTGL

>d1regx_ d.58.27.1 (X:) Translational regulator protein regA {Bacteriophage T4}
MIEITLKKPEDFLKVKETLTRMGIANNKDKVLYQSCHILQKKGLYIVHFKEMLRMDGRQVEMTEE
DEVRRDSIAWLLLEDWGLIEIVPGQRTFMKDLTNNFRVISFKQKHEWKLVPKYTIGN

>d1fvga_ d.58.28.1 (A:) Peptide methionine sulfoxide reductase {Cow (Bos taurus)}
KIVSPQEALPGRKEPLVVAAKHHVNGNRTVEPFPEGTQMAVFGMGCFWGAERKFWTLKGVYSTQV
GFAGGYTPNPTYKEVCSGKTGHAEVVRVVFQPEHISFEELLKVFWEHNDPTQGMRQGNHGSQYR
SAIYPTSAEHVGAALKSKEDYQKVLSEHGFLITTDIREGQTFYYAEDYHQYLSKDPDGYC

>d1ff3a_ d.58.28.1 (A:) Peptide methionine sulfoxide reductase {Escherichia coli}
SLFDKHLVSPADALPGRNTPMPVATLHAVNGHSMTNVPDGM EIAIFAMGCFWGVVERLFWQLPGV

YSTAAGYTGGYTPNPTYREVCSGDTGHAEAVRIVYDPSVISYEQLLQVFWENHDPAQGMRQGNHDG
TQYRSAIYPLTPEQDAAARASLERFQAAMLAADDDRHITEIANATPFYEAEDDHQQYLHKNPYGYC
GIGGIGVCLPPEA

>d1ff3c_ d.58.28.1 (C:) Peptide methionine sulfoxide reductase {Escherichia coli}
LVSPADALPGRNTPMPVATLHAVNGHSMTNVPDGMEDIAIFAMGCFWGVVERLFWQLPGVYSTAAGY
TGGYTPNPTYREVCSGDTGHAEAVRIVYDPSVISYEQLLQVFWENHDPAQGMRQGNHDGTQYRSAI
YPLTPEQDAAARASLERFQAAMLAADDDRHITEIANATPFYEAEDDHQQYLHK

>d1azsa_ d.58.29.1 (A:) Adenylyl cyclase VC1, domain C1a {Dog (Canis familiaris)}
DMMFHKIYIQKHDNVSILFADIEGFTSLASQCTAQLVMTLNELFARFDKLAENHCLRIKILGDCYY
CVSGLPEARADHAHCCVEMGMDMIEAISLVREMTGVNVNMRVGIHSGRVHCGVLGLRWQFDVW
SNDVTLANHMEAGGKAGRIHITKATLSYLNQDYEVEPGCGGERNAYLKEHSIETFLIL

>d1azsb_ d.58.29.1 (B:) Adenylyl cyclase IIC1, domain C2a {Rat (Rattus norvegicus)}
HQS YDCVCMFASIPDFKEFYTESDVNKEGLECLRLLEIIADFDDLLSKPKFSGVEKIKTIGSTYMAA
TGLSAIPSQEHAQEPERQYMHIGTMVEFAYALVGKLDAINKHSFNDFKLRVGINHGPVIAGVIGAQKP
QYDIWGNTVNVASRMDSTGVLDKIQVTEETSLILQTLGYTCTCRGIINVKGKGLDKTYFVNT

>d1fx2a_ d.58.29.1 (A:) Receptor-type monomeric adenylyl cyclase {Trypanosome
(Trypanosoma brucei), different isoform}
NNNRAPKEPTDPVTLIFTDIESSTALWAAHPDLMPDAVAHHRMVRSLIGRYKCYEVKTVGDSFMI
ASKSPFAAVQLAQELQLCFLHHDWGTNALDDSYREFEEQRAEGECEYTPPTAHMDPEVYSRLWNG
LRVRVGIHTGLCDIRHDEVTKGYDYYGRTPNMAARTESVANGGQVLMTHAAYMSLSAEDRKQIDVT
ALGDVALRGVSDPVKMYQLNTVPSRNFAALRLDREYFD

>d1fx4a_ d.58.29.1 (A:) Receptor-type monomeric adenylyl cyclase {Trypanosome
(Trypanosoma brucei), different isoform}
DNDSAPKEPTGPVTLIFTDIESSTALWAAHPDLMPDAVATHHRLIRSLITRYECYEVKTVGDSFMIAS
KSPFAAVQLAQELQLCFLRLDWETNAVDES YREFEEQRAEGECEYTPPTASLDPEVYSRLWNGLRVR
VGIHTGLCDIRYDEVTKGYDYYGRTSNMAARTESVANGGQVLMTHAAYMSLSGEDRNQLDVTTLGA
TVLRGVPEPVRMYQLNAVPGRNFAALRLDR

>d1eqoa_ d.58.30.1 (A:) 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK
{Escherichia coli}
TVAYIAIGSNLASPLEQVNAALKALGDIPESHILTVSSFYRTPPLGPQDQPDYLNAAVALETSLAPEELL
NHTQRIELQQGRVKAERWGPRTLDDIMLFGNEVINTERLTVPHYDMKNRGMFLWPLFEIAPELV
FPDGEMLRQILHTRAFDKLNKW

>d1cbka_ d.58.30.1 (A:) 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK
{Haemophilus influenzae}
MITAYIALGSNLNTPVEQLHAALKAISQLSNTHLVTTSSFYKSKPLGPQDQPDYVNAVAKIETELSPLK
LLELQRIENEQGRVRLRRWGERTLDDLILLYGNEIIQNERLTIPHYDMHNREFVIVPLFEIASDLVLP
NSQIITELVKQFADHKMIKLNLP

>d1gpja3 d.58.39.1 (A:1-143) Glutamyl tRNA-reductase catalytic, N-terminal domain
{Archaeon Methanopyrus kandleri}
MEDLVS VGITHKEAEVEELEKARFESDEAVRDIVESFGLSGSVLLQTSNRVEVYASGARDRAEELGDL
IHDDAWVKRGSEAVRHFRVASGLESMMVGEQEILRQVKKAYDRAARLGTLDALKIVFRRRAINLGK
RAREETRI

>d1hbnc_ d.58.31.1 (C:) Methyl-coenzyme M reductase gamma chain {Archaeon
Methanobacterium thermoautotrophicum}

AQYYPGTTKVAQNRRNFCNPEYELEKLEISDEDVVKILGHRAPGEEYPSVHPPLEEMDEPEDAIRE
MVEPIDGAKAGDRVRYIQFTDSMYFAPAQPYVRSRAYLCRYRGADAGTSLGRQIETREDRDLEKISKE
LLETFFDPARSGVRGKSVHGHSLRLDEDGMMFDMMLRRQIYNKDTGRVEMVKNQIGDELDEPVDL
GEPLDEETLMEKTTIYRVDGEAYRDDVEAVEIMQRIHVLRSQGGFNL
>d1e6vc_ d.58.31.1 (C:) Methyl-coenzyme M reductase gamma chain {Archaeon
Methanopyrus kandleri}
FYYPGETDVAENRRKYMNPNYELKKLREIPDEDIVRLMGHREPGEYPSVHPPLEEMEEPECPIREL
VEPTEGAKAGDRIRYIQFTDSVYFAPIHPYIRARMYMWRYRGVDTGSLSGRQIIEVRERDLEKIAKEL
LETEIFDPARSGVRGATVHGHALRLDENGLMLHALRRYRLNEETGEVEYVKDQVGIELDEPIPVGAP
ADEDDLKERTTIYRIDGTPYREDEELLQVVQRIHELRTLAGEYRPEE
>d1e6yc_ d.58.31.1 (C:) Methyl-coenzyme M reductase gamma chain {Archaeon
Methanosarcina barkeri}
AYERQYYPGATSVAANRRKHMSGKLEKLEISDEDLTAVLGHRAPGSDYPSTHPPLEEMGEPACSTR
ENVAATPGAAAGDRVRYIQFADSMYNAPATPYFRSYFAAINFRGVDPGTLGSRQIVEARERDMEQCA
KVQMETEITDHALAGVRGATVHGHSVRLQEDGVMFDMMLDRRLENGTIIMDKDQVAIPLDRKVDL
GKPMSEEAARKRTTIYRVDNVAFRDDAEVVEVWHRIFDQRTKFGFQPK
>d1hbna2 d.58.31.2 (A:2-269) Alpha chain {Archaeon Methanobacterium
thermoautotrophicum}
ADKLFINALKKKFEESPEEKTTFFYTLGGWKQSERKTEFVNAGKEVAAKRGIPQYNPDIGTPLGQRV
LMPYQVSTTDTYVEGDDLHFVNNAAMQQMWDDIRRTVIVGLNHAHAVIEKRLGKEVTPETITHYL
ETVNHAMPGAADVQEHMVETHPALVADSYVKVFTGNDEIADEIDPAFVIDINKQFPEDQAETLKA
VGDGIWQVVRIPRTIVSRTCDGATTSRWSAMQIGMSMISAYKQAAGEAATGDFAYA AKHAEVIHMGTY
LPV
>d1e6va2 d.58.31.2 (A:8-272) Alpha chain {Archaeon Methanopyrus kandleri}
LFMKALKEKFEESPEEKYTKFYIFGGWKQSERKKEFKEWADKIVEERGVPHYNPDIGVPLGQRKLM
SYQVSGTDVFEVGGDDLTFVNNAAMQQMWDDIRRTVIVGMDTAHRVLERRLGKEVTPETINEYMET
LNHALPGGAVVQEHMVEIHPGLTWDCYAKIITGDLELADEIDDKFLIDIEKLPPEEQAEQLIKAIGNR
TYQVCRMPTIVGHVCDGATMYRWAAMQIAMSFCAYKIAAGEAAVSDFAFASKHAEVINMGEMLPA
>d1e6ya2 d.58.31.2 (A:1002-1283) Alpha chain {Archaeon Methanosarcina barkeri}
AADIFSKFKDMEVKFAQEFGSNKQTGGDITDKTAKFLRLGPEQDPRKVEMIKAGKEIAEKRGIAFY
NPMHSGAPLGQRAITPYTISGTDIVCEPDDLHYVNNAAMQQMWDDIRRTCIVGLDMAHETLEKR
LGKEVTPETINHYLEVLNHAMPGAADVQEMMVETHPALVDDCYVKVFTGDDALADEIDKQFLIDIN
KEFSEEQAQIKASIGKTSWQAIHIPTIVSRTTDGAQTSRWAAMQIGMSFISAYAMCAGEAAVADLSF
AAKHAALVSMGEMLPA
>d1hbna2 d.58.31.2 (B:2-188) Beta chain {Archaeon Methanobacterium
thermoautotrophicum}
AKFEDKVDLYDDRGNLVEEQVPLEALSPLRNPAIKSIVQGIKRTVAVNLEGIENALKTAKVGGPACKI
MGRELDLDIVGNAESIAAAKEMIQVTEDDDTNVELLGGGKRALVQVPSARFDVAAEYSAAPLVAT
AFVQAIINEFDVSMYDANMVKAAVLGRYPQSVEYMGANIATMLDIPQKLEGP
>d1e6vb2 d.58.31.2 (B:7-189) Beta chain {Archaeon Methanopyrus kandleri}
DTVDLYDDRGNCVAAEVPIEVLSPMRNEAIQSIVNDIKRTVAVDLEGIENALQATVGGKGMKIPGRE
MDVDIVDNAEIADEIEKMIRVYQDDDTNVEPMYDGRLLVQLPSERVKVMADPYSGLTQAGMAV
VHAIDVCEVDMWDANMVKAAVFGRYPQTIDYFGGNVASMLDVPMKQEGV
>d1e6yb2 d.58.31.2 (B:2002-2185) Beta chain {Archaeon Methanosarcina barkeri}

SDTVDIYDDRGLLESNVDIMSLAPTRNAAIQSIIMDTKRSVAVNLAGIQGALASGKMGKGRQILGR
GLNYDIVGNADAIAENVKKLQVDEGDDTNVIKVKGGKSLLIQSPKSRIIAGADFMSATTVGAAAVTQ
TIMDMFGTDPYDAPIVKSASVWGSYPQTMMDLGGQVQGILSIPQNEGL

>d1e8ga1 d.58.32.1 (A:274-560) Vanillyl-alcohol oxidase {Fungus (Penicillium
simplicissimum)}

GGYQSYLITLPKDGDLKQAVDIIRPLRLGMALQNVPTIRHILLDAAVLGDKRSYSSRTEPLSDEELDKI
AKQLNLGRWNFYGALYGPEPIRRVLWETIKDAFSAIPGVKFFYPEDTPENSVLRVRDKTMQGIPTYD
ELKWIDWLPNGAHLFFSPIAKVSGEDAMMAYVTKKRCQEAGLDFIGTFTVGMREMHHIVCIVFNK
KDLIQKRKVQWLMRTLDDCAANGWGEYRTHLAFMDQIMETYNWNNSSFLRFNEVLKNAVDPNG
IIAPGKSGVWPSQYSHVTWKL

>d1diqa1 d.58.32.1 (A:243-521) Flavoprotein subunit of p-cresol methylhydroxylase
{Pseudomonas putida}

PVFKPFEVIFEDEADIVEIVDALRPLRMSNTIPNSVVIASLWEAGSAHLTRAQYTTTEPGHTPDSVIKQ
MQKDTGMGAWNLYAALYGTQEQVDVNWKIVTDVFKLKGKGRIVTQEEAGDTQPFKYRAQLMSGVP
NLQEFGLYNWRGGGSMWFAPVSEARGSECKQAAMAKRVLHXYGLDYVAEFIVAPRDMHHVIDV
LYDRTNPEETKRADACFNELLDEFEKEGYAVYRVNTRFQDRVAQSYGPVKKRLEHAIKRAVDPNNIL
APGRSGIDLNNDF

>d1f0xa1 d.58.32.2 (A:274-567) D-lactate dehydrogenase {Escherichia coli}

KNQQVFYIGTNQPEVLTEIRRHILANFENLPVAGEYMHRDIYDIAEKYKDTFLMIDKLGTDKMPFF
FNLKGRTDAMLEKVKFFRPHFTDRAMQKFGHLFPSHLPFRMKNWRDKYEHLLKLMAGDGVGE
AKSWLVDFYKQAEQDFVCTPEEGSKAFLHRFAAAGAAIRYQAVHSDEVEDILALDIALRRNDTEWY
EHLPEIDSQVLVHKLYYGHFMCYVFHQDYIVKKGVDVHALKEQMLELLQQRGAQYPAEHNVGHLYK
APETLQKFYRENDPTNSMNP GIGKTSKRKNW

>d1i19a1 d.58.32.3 (A:274-613) Cholesterol oxidase {Brevibacterium sterolicum}

FRQRCQSYTDIPWRELFAPKGADGRTFEKFAESGGAEAIWYPPFTEKPWMKVWTVSPTKPDSSNE
VGSLGSAGSLVGKPPQAREVSGPYNYIFSDNLPEPITDMIGAINAGNPGIAPLFGPAMYEITKLGLAAT
NANDIWGWSKDVQFYIKATTLRLTEGGAVVTSRANIATVINDFTEWFHERIEFYRAKGEFPLNGPV
EIRCCGLDQAADVQVPSVGPPTISATRPRPDHPDWDVAIWLNLVGVPGTPGMFEFYREMEQWMRS
HYNNDATFRPEWSKGFAPDPYTDNDIVTNKMRATYIEGVPTTENWDTARARYNQIDPHRVF
TNGFMDKLLP

>d1ftra1 d.58.33.1 (A:1-148) Formylmethanofuran:tetrahydromethanopterin
formyltransferase {Archaeon Methanopyrus kandleri}

MEINGVEIEDTFAEAFEAKMARVLITAASHKWAMIAVKEATGFGTSVIMCPAEAGIDCGYVPPEETPD
GRPGVTIMIGHNDEDELKEQLLDRIGQCVMTAPTASAFDAMPEAEKEDEDRVGYKLSFFGDGYQEE
DELDGRKVWVKIPVV

>d1ftra2 d.58.33.1 (A:149-296) Formylmethanofuran:tetrahydromethanopterin
formyltransferase {Archaeon Methanopyrus kandleri}

EGEFIVEDSFGITTVAGGNFYIMAESQPAGLQAAEAAVDAIKGVEGAYAPFPGGIVASASKVSKQYD
FLPASTNDAYCPTVEDNELPEGVKCVYEIVINGLNEEAVKEAMRVGIEAACQPGVVKISAGNFGGKL
GQYEIHLHDLF

>d1qd1a1 d.58.34.1 (A:2-180) Formiminotransferase domain of
formiminotransferase-cyclodeaminase. {Pig (Sus scrofa)}

SQLVECVPNFSEGNQEVDAISRVAQTGCVLLDVDSGPSTNRTVYTFVGRPEDVVEGALNAARA
AYQLIDMSRHHGEHPRMGALDVCPFIPVRGVTMDECVRCAQAFGQRLAEELGVPVYLYGEEARTAG

RQSLPALRAGEYEALPEKLNKQAEWAPDFGPSAFVPSWGATVAGARK

>d1qd1a2 d.58.34.1 (A:181-326) Formiminotransferase domain of formiminotransferase-cyclodeaminase. {Pig (*Sus scrofa*)}

FLLA FNINLLSTREQAHRIALDLREQGRGKDQPGRLKKVQAIGWYLDEKNLAQVSTNLLDFEVTGL
HTVFEETCREAQELSLPVVGSQVLVGLVPLKALLDAAAFYCEKENLFLQDEHRIRLVVNRLGLDSLAP
FKPKERIEEYL

>d1dj0a1 d.58.35.1 (A:7-114) Pseudouridine synthase I {*Escherichia coli*}

PPVYKIALGIEYDGSKYGWQRQNEVRSVQEKLEKALSQVANEPITVFCAGRTDAGVHGTGQVVHFE
TTALRKDAAWTLGVNANLPGDIAVRWVKTVPDDFHARFSAT

>d1dj0a2 d.58.35.1 (A:115-270) Pseudouridine synthase I {*Escherichia coli*}

ARRYRYIIYNHRLRPAVLSKGVTHFYEPLDAERMHRAAQCLLGENDFTSFRAVQCQSRTPWNRVMH
INVTRHGYPYVVVDIKANAFVHHMVRNIVGSLMEVGAHNQPESWIAELLAAKDRTLAAATAKAEGLY
LVAVDYPDRYDLPKPPMGPLFLAD

>d1k8wa1 d.58.35.2 (A:9-73) Pseudouridine synthase II TruB {*Escherichia coli*}

MDINGVLLLDKPGQMSSNDALQVKRIYNANRAGHTGALDPLATGMLPICLGEATKFSQYLLDSD

>d1k8wa2 d.58.35.2 (A:74-312) Pseudouridine synthase II TruB {*Escherichia coli*}

KRYRVIARLQRTDTSADGQIVEERPVTFSAEQLAAALDTRFGDIEQIPSMYSALKYQGGKLYEYAR
QGIEVPREARPITVYELLFIRHEGNELELEIHCSTGYIRTIIDDLGEKLGCGAHVIYLRRLAVSKYPVE
RMVTLEHLRELVEQAEQQDIPAAELLDPLLMPMDSPASDYPVNLPLTSSVYFKNGNPVRTSGAPLE
GLVRVTEGENGKFIGMGEIDDEGRVAPRRLVVEY

>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*}

IGWVKGIDDNWHLTLFIENGRILDYPARPLKTGLLEIAKIHKGDFRITANQNLIAGVPESEKAKIEKIA
KESGLMNAV

>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*}

MHALVQLRGEVNMHTDIQDTLEMLNIHHVNHCTLVPETDAYRGMVAKVNDVFAFGEPSQETLETV
LATRAEPLGDDADVDDEWVAEHTDYDDISGLAFALLSEETTTLREQGLSPTLRLHPPRGHGDGVKHP
VKEGGQLGKHDTEGIDDLLEAMR

>d1fw9a_ d.190.1.1 (A:) Chorismate lyase {*Escherichia coli*}

SHPALTQLRALRYSKEIPALDPQLLDWLLLEDSMTRKFEQQGKTVSVTMIREGFVEQNEIPEELPLL
KESRYWLREILLSADGEPWLAGRTVVPVSTLSGPELALQKLGKTPLGRYLFTSSTLTRDFIEIGRDAGL
WGRSRLRLSGKPLLLTELFLPASPLY

>d1bowa_ d.60.1.1 (A:) Multidrug-binding domain of transcription activator BmrR {*Bacillus subtilis*}

RLGEVFLVDEEEIRIIQTEAEGIGPENVLNASYSKLLKFFIESADGFTNNSYGATFSFQPYTSIDEMTYR
HIFTPVLTNKQISSITPDMEITTPKGRYACIAYNFSPEHYFLNLQKLIKIADRQLTVVSDVYELIPIHY
SPKKQEEYRVMKIRIL

>d1d5ya3 d.60.1.2 (A:122-294) Rob transcription factor, C-terminal domain {*Escherichia coli*}

EFTMPEHKFVTLEDTPVIGVTSYSCSLEQISDFRHEMRYQFVHDFLGNAPTIPPVLYGLNETRPSQ
DKDDEQEVFYTTALAQQADGYVLTGHPVMLQGGYVMFTYEGLGTGVQEFILTVYGTCTMPMLNLT

RRKGQDIERYYP AEDAKAGDRPINLRCELLIPRRKLAAA
>d1jh6a_ d.61.1.1 (A:) tRNA splicing product Appr>p cyclic nucleotide phosphodiesterase {Thale cress (Arabidopsis thaliana)}
MEEVKKDVYSVWALPDEESEPRFKKLMEALRSEFTGPRFVPHVTVAVSAYLTADEAKKMFESACDG
LKAYTATVDRVSTGTTTTFFQCVFLLLQTTPEVMEAGEHCKNHFNCSSTTTPYMPHLSLLYAELETEEEK
NAQEKAYTLDSSLGLSFRNLRLALCKTDTEDKTLETWETVAVCNLNP
>d1f32a_ d.62.1.1 (A:) Pepsin inhibitor-3 {Pig roundworm (Ascaris suum)}
FLFSMSTGPFICTVKDNQVFVANLPWTMLEGDDIQVGKEFAARVEDCTNVKHDMPAPTCTKPPPFPG
PQDMKMFNFVGC SVLGNKLFIDQKYVRDLTAKDHAEVQTFREKIAAFEEQQENQPPSSGMPHGAVP
AGGLSPPPPPSFCTV
>d1d8ia_ d.63.1.1 (A:) mRNA triphosphatase CET1 {Baker's yeast (Saccharomyces cerevisiae)}
HMYRNVPIWAQKWKPTIKALQSINVKDLKIDPSFLNIIPDDDLTKSVQDWVYATIYSIAPELRSFIELE
MKFGVIIDAKGPD RVNPPVSSQCVFTELD AHLTPNIDASLFKELSKYIRGISEVTENTGKFSIIESQTRD
SVYRVGLSTQRPRFLRMSTDIKTGRVGFIEKRHVAQLLLYSPKDSYDVKISLNLELPVPDNDPPEKY
KSQSPISERTKDRVSYIHNSCTRIDITKVENHNQNSKSRQSETTHEVELEINTPALLNAFDNITNDS
KEYASLIRTF LNNGTIHRRKLSSLSY
>d2if1_ d.64.1.1 (-) Eukaryotic translation initiation factor eIF-1 (SUI1) {Human (Homo sapiens)}
MRGSHHHHHHTDPMSAIQNLHSFDPFADASKGDDLLPAGTEDYIHIRIQQRNGRKTLLTTVQGIADD
YDKKKLVKAFKKK FACNGTVIEHPEYGEVIQLQGDQRKNICQLVEIGLAKDDQLKVHGF
>d1d1ra_ d.64.1.1 (A:) YciH {Escherichia coli}
KGDGVVRIQRQTSGRKKGKGVCLITGVLDLDAELTKLAAELKKKCGCGGAVKDGVIIEIQGDKRDLLKSL
LEAKGMKVKLAGGLE
>d1lbu_2 d.65.1.1 (84-213) Zn²⁺ DD-carboxypeptidase, C-terminal, catalytic domain {Streptomyces albus G}
VNFTYAE LNRCNSDWSGGKVSAA TARANALVTMWKLQAMRHAMGDKPITVNGGFRSVTCNSNVG
GASNSRHM YGHAADLGAGSQGFCALQAARNHGFTEILGPGYPGHNDHHTHVAGGDGRFWSAPSCG
I
>d1vhh_ d.65.1.2 (-) Sonic hedgehog {Mouse (Mus musculus)}
KLTPLAYKQFIPNVAEKT LGASGRYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDK
LNALAISVMNQWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTS DRDRSKYGM LARLAVEAGF
DWVYYESKAHIHCSVKAENSVAAK
>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}
GRYIGPVCRLCRREGVKLYLKGERCYSPKCAMERRPYPPGQH GQKRARRPSDYAVRLREKQKLRRYI
GISERQFRNLFEEASKKKGVTGSVFLGLLESRLDNVVYRLGFAVSRRQARQLVRHGHITVNGRRVDLP
SYRVRPGDEIAVAEKSRNLELIRQNLEAMKGRKVG PWLSLDVEGMKGKFLRLPDREDLALPVQENL
VIEFYSR
>d1c06a_ d.66.1.2 (A:) Ribosomal protein S4 {Bacillus stearothermophilus}
MKLSEYGLQLQE KQKLRHMYGVNERQFRKTFEEAGKMPGKHGENFMILLESRLDNLVYRLGLART
RRQARQLVTHGHILVDGSRVNIPSYRVKPGQTI AVREKSRNLQVIKEALEANNYPDYLSFDPEKMEG

TYTRLPERSELPAEINEALIVEFYSR

>d1dm9a_d.66.1.3 (A:) Heat shock protein 15 kD {Escherichia coli}

PAVEVRLDKWLWAARFYKTRALAREMIEGGKVHYNGQRSKPSKIVELNATLTLRQGNDETRVIVKA
ITEQRRPASEAALLYEETAESVEKREKMALARKLNALT

>d1qf6a3_d.67.1.1 (A:63-241) Threonyl-tRNA synthetase (ThrRS), second 'additional'
domain {Escherichia coli}

KDEEGLEIIRHSCAHLGHAIKQLWPHTKMAIGPVIDNGFYDVLDRTLTQEDVEALEKRMHELA
EKNYDVIKKKVSWEHARETFANRGESYKVSILDENIAHDDKPGLYFHEEYVDMCRGPHVPMRFC
HHFKLMKTAGAYWRGDSNNKMLQRIYGTAWADKKALNAYLQRLEAAK

>d1f7ua3_d.67.2.1 (A:2-135) Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional'
domain {Baker's yeast (Saccharomyces cerevisiae)}

ASTANMISQLKKLSIAEPAVAKDSDHPDVNIVDLMRNYISQELSKISGVDSSLIFPALEWTNTMERGDL
LIPIRLRIKGANPKDLAVQWAEKFGDGFLEKVEANGPFIQFFNPQFLAKLVIPDILTRKEDYG

>d1iq0a3_d.67.2.1 (A:1-96) Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional'
domain {Thermus thermophilus}

MLRRALEEAIAQALKEMGVPVRLKVARAPKDKPGDYGVPLFALAKELRKPPQAIQELKDRLPLPEF
VEEAVPVGGLNFRLRTEALLREALRPA

>d1dd5a_d.67.3.1 (A:) Ribosome recycling factor, RRF {Thermotoga maritima}

VNPFKEAKEKMKRTLEKIEDELKRMRTGKPSAILEEIKVDYYGVPTPVNQLATISISEERTLVIKPW
DKSVLSLIEKAINASDLGLNPINDGNVIRLVFSPPTTEQREKVVKKAKEIVEEGKIAIRNIRREILKKIK
EDQKEGLIPEDDAKRENEIQKLTDEFIEKLDEVFIEKKEEIMEF

>d1eh1a_d.67.3.1 (A:) Ribosome recycling factor, RRF {Thermus thermophilus}

MTLKELYAETRSHMQKSLEVLEHNLGLRTGRANPALLHLKVEYYGAHVPLNQTATVTPDPRTL
VQSWDQNALKAIEKAIRSDGLNPNKGDALYINIPPLTEERRKDLVRAVRQYAEGRVAIRNIRRE
ALDKLKLAKELHLSSEDETKRAEAEIQKITDEFIAKADQLAEKKEQEILG

>d1ek8a_d.67.3.1 (A:) Ribosome recycling factor, RRF {Escherichia coli}

MISDIRKDAEVRMDKCVEAFKTQISKIRTGRASPSLLDGIVVEYYGTPTPLRQLASVTVEDSRTLKIN
FDRSMSPAVEKAIMASDLGLNPNSAGSDIRVPLPPLTEERRKDLTKIVRGEAEQARVAVRNVRRDAN
DKVKALLKDKSEDDRRSQDDVQKLTDAAIKKIEAALADKEAELMQF

>d1ge9a_d.67.3.1 (A:) Ribosome recycling factor, RRF {Aquifex aeolicus}

MIKELEDIFKEAEKDMKAVEYYKNEIAGLRTSRASALVEEIKVEYYGSKVPIKQLGTISVPEHNQIV
IQVWDQNAVPAIEKAIREELNLPNTVQGNVIRVTLPLTEERRRELVRLLHKITEEARVVRNVRRRE
AKEMIEELEGESEDEKKRALERLQKLTDKYIDEINKLMEAKEKEIMSV

>d1j98a_d.185.1.2 (A:) Autoinducer-2 production protein LuxS {Bacillus subtilis}

VESFELDHNAVVPYVRHCGVHKVGTGVDVVKFDIRFCQPNKQAMKPDTHLEHLLAFTIRSHAE
KYDHFDIIDISPMGCQTGYLVVSGETTSAEIVDLLEDTMKEAVEITEIPAANEKQCGQAKLHDLEGA
KRLMRFWLSQDKEELLKVF

>d1inna_d.185.1.2 (A:) Autoinducer-2 production protein LuxS {Deinococcus radiodurans}

NVESFDLDHTKVKAPYVRLAGVKTTPKGDQISKYDLRFLQPNQGAIDPAAIHTLEHLLAGYMRDHL
EGVVDVSPMGCRTGMYMAVIGEPDEQGMKAFEAALKDTAGHDQPIPGVSELECGNYRDHDLAAA
RQHARDVLDQGLKVQETILL

>d1j6wa_d.185.1.2 (A:) Autoinducer-2 production protein LuxS {Haemophilus influenzae}

LLDSFKVDHTKMNAVRIAKTMLTPKGDNITVFDLRFICIPNKEILSPKGIHTLEHLFAGFMRDHLN
GDSIEIIDISPMGCRTGFYMSLIGTPNEQKVSEAWLASMQDVLGVQDQASIPELNIYQCGSYTEHSLED

AHEIAKNVIARGIGVKNEDLSLDN

>d1j6xa_ d.185.1.2 (A:) Autoinducer-2 production protein LuxS {*Helicobacter pylori*}
MKMNVESFNL DHTKVKAPYVRIADRKKGVNGDLIVKYDVRFKQPNRDHMDMPSLHLSLEHLVAEII
RNHANYVVDWSPMGCQTGFYLTVLNHDNYTEILEVLEKTMQDVLKAKEVPASNEKQCGWAANHT
LEGAQNLARAFLDKRAEWSEVG

>d1hr6b1 d.185.1.1 (B:24-245) Mitochondrial processing peptidase (MPP) beta chain
{*Baker's yeast (Saccharomyces cerevisiae)*}
PGTRTSKLPNGLTIATEYIPNTSSATVGFVDAGSRAENVKNNGTAHFLEHLAFKGTQNRPQQGIELEI
ENIGSHLNAYTSRENTVYYAKSLQEDIPKAVDILSDILTKSVLDNSAIERERDVIRESSEVDKMYDEV
VFDHLHEITYKQDQLGRTILGPIKNIKISITRTDLKDYITKNYKGD RMVLAGAGAVDHEKLVQYAQKYF
GHVPKSESPVPLGSPR

>d1hr6b2 d.185.1.1 (B:246-462) Mitochondrial processing peptidase (MPP) beta chain
{*Baker's yeast (Saccharomyces cerevisiae)*}
GPLPVFCRGERFIKENTLPTTHIAIALEGVSW SAPDYFVALATQAIVGNWDRAIGTGTNSPSPLAVAA
SQNGSLANSYMSFSTSYADSGLWGM YIVTDSNEHNVRLIVNEILKEWKRIKSGKISDAEVNRAKAQL
KAALLSLD GSTAIVEDIGRQVVTGKRLSPEEVFEQVDKITKDDIIMWANYRLQNKPVSMVALGNT
STV PNVSYIEEKL NQ

>d1hr6a1 d.185.1.1 (A:14-233) Mitochondrial processing peptidase (MPP) alpha chain
{*Baker's yeast (Saccharomyces cerevisiae)*}
ARTDNFKLSSLANGLK VATSNTPGHF SALGLYIDAGSRFEGRN LKGCTHILDRLAFKSTEHVEGRAM
AETLELLGGNYQCTSSREN LMYQASVFNQDVGKMLQLMSETVRF PKITEQELQEQLSAEYEI DEV
WMKPELVLP ELLHTAAYSGETLGSPLICRGLIPSISKYLLDYRNKFYTPENTVAAFVGPHEKALEL
TGKYLGDWQSTHPPITKK

>d1hr6a2 d.185.1.1 (A:234-470) Mitochondrial processing peptidase (MPP) alpha chain
{*Baker's yeast (Saccharomyces cerevisiae)*}
VAQYTTGGESCIPPAPVFGNLP ELFHIQIGFEGLPIDHPDIYALATLQTLLGGGGSFSAGGPGKGMYSRLY
THVLNQYYFVENCVAFNHSYS DSGIFGISLSCIPQAAPQAVEVIAQQMYNTFANKDLRLTEDEV SRAK
NQLKSSLLMNLESKLVELED MGRQVLMHGRKIPVNEMISKIEDLKPDDISRVAEMIFTGNVNNAGN
GKGRATVVMQGD RGSFGDVENVLKAYGLGNSSS

>d1be3a1 d.185.1.1 (A:1-233) Cytochrome bc1 core subunit 1 {*Cow (Bos taurus)*}
TATYAQALQSV PETQVSQLDNGLRVASEQSSQPTCTVGWVIDAGSRYESEKNNGAGYFVEHLAFKGT
KNRPGNALEKEVESMG AHLNAYSTREHTAYYIKALSKDLPKAVELLADIVQNC SLEDSQIEKERDVIL
QELQENDTSMRDVVFNYLHATAFQGTPLAQSVEG PSENV RKLRSRADL TEYLSRHYKAPRMV LAAAG
GLEHRQLLDLAQKHFSGLSGTYDEDAVPTLSP

>d1be3a2 d.185.1.1 (A:234-446) Cytochrome bc1 core subunit 1 {*Cow (Bos taurus)*}
CRFTGSQICHREDGLPLAHVAIAVEGPGWAHPDNVALQVANAIIGHYDCTYGGGAHLSSPLASIAATN
KLCQSFQTFNICYADTGLLGAHFVCDHMSIDMMFVLQGGQWMRLCTSATESEVLRGKNLLRNALVS
HLDGTTVPCE DIGRSLTYGRRIP LAEWESRIA EVDARVVREVC SKYFYDQCPAVAGFGPIEQLPDYN
RIRSGMFWLRF

>d1bcca1 d.185.1.1 (A:4-232) Cytochrome bc1 core subunit 1 {*Chicken (Gallus gallus)*}
YAQALQSV PETQVSQLDN GVRVASEQSSQPTCTVGWVIDAGSRYESEKNNGAGYFLEHLAFKGTKNR
PQNALEKEVESMG AHLNAYSSREHTAYYIKALSKDVPKAVELLADIVQNC SLEDSQIEKERDVIVREL
QENDTSMREVVFN YLHATAFQGTGLAQSVEG PSENI RKLRSRADL TEYLSHTHYTAPRMV LAAAGGVE
HQQLELAQKHFGGVPFTYDDDAVPTLS

>d1bcca2 d.185.1.1 (A:233-445) Cytochrome bc1 core subunit 1 {Chicken (Gallus gallus)}
KCRFTGSQIRHREDGLPLAHVAIAVEGPGWAHPDLVALQVANAIIGHYDRTYGGGLHSSSPLASIAVT
NKLCQSFQTFSCYSETGLFGFYVCDRMSIDMMFVLQGGQWMRLCTSISESEVLRGKNFLRNALVS
HLDGTTVPCEDIGRELLTYGRRIPLEEWEERLAEVDARMVREVCSKYIYDQCPAVAGPGPIQLPDYN
RIRSGMFWLR

>d1ezva1 d.185.1.1 (A:27-239) Cytochrome bc1 core subunit 1 {Baker's yeast
(Saccharomyces cerevisiae)}
AEVTQLSNGIVVATEHNPAHTASVGVVFGSAAENENPNNGVSNLWKNIFLSKENSAAVAKEGLALS
SNISRDFQSYIVSSLPGSTDKSLDFLNQSFQQKANLLSSSNFEATKKSVLKQVQDFEDNDHPNRVLE
HLHSTAFQNTPLSLPTRGTLESLENLVADLESFANNHFLNSNAVVTGNIKHEDLVNSIESKNLSL
QTGTKPVLKK

>d1ezva2 d.185.1.1 (A:240-456) Cytochrome bc1 core subunit 1 {Baker's yeast
(Saccharomyces cerevisiae)}
KAAFLGSEVRLRDDTLPKAWISLAVEGEPVNSPNYFVAKLAAQIFGSYNAFEPASRLQGIKLLDNIQE
YQLCDNFNFHFSLSYKDSGLWGFSTATRNVTMIDDLIHFTLKQWNRLTISVTDTEVERAKSLLKLQLG
QLYESGNPVNDANLLGAEVLKGSKLSLGEAFKKIDAITVKDKAWAGKRLWDQDIAIAGTGQIEGLL
DYMIRSDMSMMRW

>d1be3b1 d.185.1.1 (B:21-235) Cytochrome bc1 core subunit 2 {Cow (Bos taurus)}
PQDLEFTRLPNGLVIASLENYAPASRIGLFIKAGSRYENSNNLGTSHLLRLASSLTTKGASSFKITRGIE
AVGGKLSVTSTRENMAYTVECLRDDVDILMEFLNVTTAPEFRRWEVAALQPQLRIDKAVALQNPQ
AHVIENLHAAAYRNALANSLYCPDYRIGKVTPELVHDYVQNHFTSARMALIGLVSHPVLKQVAEQF
LNIRGGLGLSGA

>d1be3b2 d.185.1.1 (B:236-439) Cytochrome bc1 core subunit 2 {Cow (Bos taurus)}
KAKYHGGEIREQNGDSLVAALVAESAAIGSAEANAFSVLQHVLGAGPHVKRGSNATSSLYQAVAKGV
HQPFDVSAFNASYSDSGLFGFYTISQAASAGDVIKAAYNQVKTIAQGNLSNPDVQAAKNKLKAGYLM
SVESSEGFLDEVGSQLAAGSYTPPSTVLQQIDAVADADVINAACKFVSRKSMASGNLGHTPPFIDE
L

>d1bccb1 d.185.1.1 (B:18-235) Cytochrome bc1 core subunit 2 {Chicken (Gallus gallus)}
PPHPQDLEITKLPNGLVIASLENYSPGSTIGVFIKAGSRYENSNNLGTSHLLRLASSLTTKGASSFKITR
GIEAVGGKLSVESTRENMAYTVECLRDDVEILMEFLNVTTAPEFRPWEVADLQPQLKIDKAVAFQN
PQTHVIENLHAAAYRNALADSLYCPDYRIGKVTVELHDFVQNHFTSARMALVGLGVSHPVLKNAE
QLLNIRGGLGLSGA

>d1bccb2 d.185.1.1 (B:236-439) Cytochrome bc1 core subunit 2 {Chicken (Gallus gallus)}
KAKYRGGEIREQNGDSLVAALVAESAAIGGAEANAFSVLQHVLGANPHVKRGLNATSSLYQAVAKGV
HQPFDVSAFNASYSDSGLFGFYTISQAAYAGQVIKAAYNQVKTIAQGNVSNENVQAAKNKLKAKYLM
SVESSEGFLEEVGSQLAAGSYNPPSTVLQQIDAVADADVINAACKFVSRQKSMASGNLGHTPPFVD
EL

>d1ezvb1 d.185.1.1 (B:17-218) Cytochrome bc1 core subunit 2 {Baker's yeast
(Saccharomyces cerevisiae)}

LTVSARDAPTKISTLAVKVHGGSRATKDGVAHLLNRFNFQNTNTRSALKLVRESELLGGTFKSTLDR
EYITLKATFLKDDLPYYVNALADVLYKTAFKHELTESVLPAAARYDYAVAEQCPVKSADQLYAITFRK
GLGNPLLYDGVERVSLQDIKDFADKVYTKENLEVSGENVVEADLKRFDVDESLLSTLPAGKSLVSK

>d1ezvb2 d.185.1.1 (B:219-368) Cytochrome bc1 core subunit 2 {Baker's yeast
(Saccharomyces cerevisiae)}

SEPKFFLGEENRVRFIGDSVAAIGIPVNKASLAQYEVLANYLTSALSELSGLISSAKLKDFTDGGGLFTLF
VRDQDSAVVSSNIKKIVADLKKGKDLSPAINYTKLKNVQNESVSSPIELNFDVAVKDFKLGKFNVAV
GDVSNLPYLDEL

>d1tig_ d.68.1.1 (-) Translation initiation factor IF3, C-terminal domain {Bacillus
stearothermophilus}

INVKEVRLSPTIEEHDFNTKLRNARKFLEKGDVKATIRFKGRAITHKEIGQRVLDRLSEACADIAVV
ETAPKMDGRNMFLVLAPKND

>d2ifea_ d.68.1.1 (A:) Translation initiation factor IF3, C-terminal domain {Escherichia coli}
VIQVKEIKFRPGTDEGDYQVKLRSLIRFLEEGDKAKITLRFGRGREMAHQIGMEVLNRVKDDLQELA
VVESFPTKIEGRQMIMVLAPKKKQ

>d1i96v_ d.68.1.1 (V:) Translation initiation factor IF3, C-terminal domain {Thermus
thermophilus}

EVKSIKFRVKIDEHDYQTKLGHKIRFLQEGHKVKVTIMFRGREVAHPELGERILNRVTELDKDLAVV
EMKPEMLGRDMNMLLAPVK

>d1dcja_ d.68.3.1 (A:) SirA {Escherichia coli}

MTDLFSSPDHTLDALGLRCPEPVMVRKTVRNMQPGETLLIADDPATTRDIPGFCTFMEHELVAK
ETDGLPYRYLIRKGG

>d1jdqa_ d.68.3.2 (A:) Hypothetical protein TM0983 {Thermotoga maritima}

GSSHHHHHSSGLVPRGSHMAKYQVTKTLDVRGEVCPVPDVETKRALQNMKPGEILEVWIDYPMS
KERIPETVKKLGHEVLEIEEVPSEWKIYIKVK

>d1qmha2 d.68.2.1 (A:5-184,A:280-338) RNA 3'-terminal phosphate cyclase, RPTC
{Escherichia coli}

MIALDGAQGGGGQILRSALSLSMITGQPFTITSIRAGRAKPGLLRQHLTAVKAATEICGATVEGAELG
SQRLFRPGTVRGGDYRFAIGSAGSCTLVLQTVLPALWFADGSPSRVEVSGGTDNPSAPPADFIRRVLE
PLLAKIGIHQQTLLRHGFYPAGGGVVATEVSPVASFNTLQLGXAVGEYLADQLVLPALAGAGEFTV
AHPSCHLLTNIAVVERFLPVRFSLIETDGVTRVSI

>d1uae_ d.68.2.2 (-) UDP-N-acetylglucosamine enolpyruvyl transferase (EPT, MurA, MurZ)
{Escherichia coli}

MDKFRVQGPTKLQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDVDTSMKLLSQLGAKVERN
GSVHIDARDVNVFCAPYDLVKTMRASIWALGPLVARFGQGQVSLPGGCTIGARPVDLHISGLEQLGAT
IKLEEGYVKASVDGRLKGAHIVMDKVSVGATVTIMCAATLAEGTTHIENAAREPEIVDTANFLITLGA
ISGQGTDRIVIEGVERLGGGVYRVLPDRIETGTFLVAAAISRKIIICRNAQPDTLDAVLAKLRDAGADIE
VGEDWISLDMHGKRPKAVNVRTAPHPAFPTDMAQFTLLNLVAEGTGFITETVFENRFMHVPELSR
MGAHAEIESNTVICHGVEKLSGAQVMATDLRASASLVLAGCIAEGTTVVDRIYHIDRGYERIEDKLRA
LGANIERVKG

>d1ejda_ d.68.2.2 (A:) UDP-N-acetylglucosamine enolpyruvyl transferase (EPT, MurA, MurZ)
{Enterobacter cloacae}

MDKFRVQGPTRLQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDIDTTMKLLTQLGTVKVERX
GSVWIDASNVNNFSAPYDLVKTMRASIWALGPLVARFGQGQVSLPGGCAIGARPVDLHIFGLEKLGA
EIKLEEGYVKASVNGRLKGAHIVMDKVSVGATVTIMSAATLAEGTTHIENAAREPEIVDTANFLVALG
AKISGQGTDRITIEGVERLGGGVYRVLPDRIETGTFLVAAAISGGKIVCRNAQPDTLDAVLAKLREAGA
DIETGEDWISLDMHGKRPKAVTVRTAPHPAFPTDMAQFTLLNLVAEGTGVITETIFENRFMHVPE
LIRMGAEIESNTVICHGVEKLSGAQVMATDLRASASLVLAGCIAEGTTVVDRIYHIDRGYERIEDKL
RALGANIERVKG

>d1g6sa_ d.68.2.2 (A:) 5-enol-pyruvyl shikimate-3-phosphate(EPSP) synthase {Escherichia coli}

MESLTLQPIARVDGTINLPGSKSVSNRALLLAALAHGKTVLTNLLDSDVVRHMLNALTALGVSYTLSD
DRTRCEIIGNGGPLHAEGALELFLGNAGTAMRPLAALCLGSNDIVLTGEPKMERPIGHLVDALRLG
GAKITYLEQENYPPLRLQGGFTGGNVDDVDSVSSQFLTALLMTAPLAPEDTVIRIKGDLVSKPYIDITL
NLMKTFGVEIENQHYQQFVVKGGQSYQSPGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQG
DIRFADVLEKMGATICWGDDYISCTRGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRNIYNWR
VKETDRLFAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFSLVALSDTPVTILD
PKCTAKTFPDYFEQLARISQAA

>d1imua_ d.204.1.1 (A:) Ribosome binding protein Y (HI0257, YfiA homologue) {Haemophilus influenzae}

MTLNITSKQMDITPAIREHLEERLAKLGKWQTLISPHFVLNKPNGFSVEASIGTPLGNLLASATSD
DMYKAINVEEEKLERQLNKLQHKSESRRADERLKDSFEN

>d1tola2 d.69.1.1 (A:125-216) C-terminal domain of Tola {Escherichia coli}

SGADINNYAGQIKSAIESKFYDASSYAGKTCTLRILKLPDGMMLLDIKPEGGDPALCQAALAAAKLAKIP
KPPSQAVYEVFKNAPLDFKPAAL

>d1kpta_ d.70.1.1 (A:) Virally encoded KP4 toxin {Ustilago maydis, P4 strain}

LGINCRGSSQCGLSGGNLMVRIRDQACGNQGQTWCPGERRAKVCGTGNSISAYVQSTNNCISGTEAC
RHLTNLVNHGCRVCGSDPLYAGNDVSRGQLTVNYVNSC

>g1kve.1 d.70.1.2 (A,B:) SMK toxin {Halotolerant yeast (Pichia farinosa)}

WSLRWRMQSTTIAAIAAGCSGAATFGGLAGGIVGCIAAGILAILQGFEVNWNGGGGDRSNPVXGEA
TTIWVGGADEAIDKGTSPSKNDLQNMADLAKNGFKGHQGVACSTVKDGNKDVYMIKFSLAGGSND
PGGSPCSDD

>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}

RIPTDPTMYRFYEMLQVYGTTLKALVHEKFGDGIISAINFKLDVKKVADPEGGERAVITLDGKYLP
PF

>d3rubs_ d.73.1.1 (S:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Tobacco (Nicotiana tabacum), variant turkish samsun}

MQVWPPINKKKYETLSYLPDLSQEQLLSEVEYLLKNGWVPCLEFETEHEGFVYRENNKSPGYDGRY
WTMWKLPFMFGCTDATQVLAEEVEAKKAYPQAWIRIIGFDNVRQVQCISFIAYKPEGY

>d1burs_ d.73.1.1 (S:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Spinach (Spinacia oleracea)}

MQVWPILGMKKYETLSYLPPLTTEQLLAEVNYLLVNNWVPCLEFEVKDGFVYREHLKSPGYDGRY
WTMWKLPFMFGCTDPAQVLNELEECKKAYPDAFIRIIGFDNKRQVQCISFIAYKPAY

>d8ruci_ d.73.1.1 (I:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Spinach (Spinacia oleracea)}

MQVWPILNLKKYETLSYLPPLTTDQLARQVDYLLNKNWVPCLEFETDHGFVYREHHNSPGYYDGR
YWTMWKLPFMFGCTDPAQVLNELEECKKEYPNAFIRIIGFDSNREVQCISFIAYKPAY

>d1bwvs_ d.73.1.1 (S:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Galdieria partita}

VRITQGTFSFLPDLTDEQIKKQIDYMISKKLAIGIEYTNDIHPRNAYWEIWGLPLFDVTDPAAVLFEIN
ACRKARSNFYIKVVGFSVIRGIESTIISFIVNRPKHEPGFNLMRQEDKRSIKYTIHSYESYKPEDERY

>d1gk8i_ d.73.1.1 (I:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Chlamydomonas reinhardtii}

MVWTPVNNKMFETFSYLPPLTDEQIAAQVDYIVANGWIPCLEFAEADKAYVSNESAIRFGSVSCLYY
DNRYWTMWKLPFMFGCRDPMQVLRREIVACTKAFPDAYVRLVAFDNQKQVQIMGFLVQRP

>d1bxni_ d.73.1.1 (I:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Alcaligenes eutrophus}

MRITQGTFSFLPELTDEQITKQLEYCLNQGWAAGLETTDDPHPRNTYWEMFGLPMFDLRDAAGILM
EINNARNTFPNHYIRVTAFDSTHTVESVMSFIVNRPADEPGFRLVLRQEEPGRTLRYSESYSYA

>d1rblm_ d.73.1.1 (M:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Synechococcus sp., strain pcc 6301}

SMKTLPKERRFETFSYLPPLSDRQIAAQIEYMIEQGFFHPLIEFNEHSNPEEFYWTMWKLPFACAAP
QQVLDEVRECRSEYGDYIRVAGFDNIKECQTSSFIVHRPGR

>d1dcpa_ d.74.1.1 (A:) Pterin-4a-carbinolamine dehydratase (PCD)/dimerization cofactor of HNF1 (DCoH) {Rat (Rattus norvegicus)}

HRLSAEERDQLLPNLRAVGWNELEGRDAIFKQFHFKDFNRAFGFMTRVALQAEKLDHHPWFNVY
NKVHITLSTHECAGLSERDINLASFIEQVAVSMT

>d1xxaa_ d.74.2.1 (A:) C-terminal domain of arginine repressor {Escherichia coli}

LKNLVLDDIDYNDVAVVIHTSPGAAQLIARLLDSLGAEGILGTIAGDDTIFTTPANGFTVKDLYEAILL
F

>d1b4ba_ d.74.2.1 (A:) C-terminal domain of arginine repressor {Bacillus stearothermophilus}

ALVDVFIKLDGTGNLLVLRTPGNAHAIGVLLDNLDWDEIVGTICGDDTCLIIICRTPKDAKKVSNQLL
SML

>d1f9na2 d.74.2.1 (A:79-149) C-terminal domain of arginine repressor {Bacillus subtilis}

ALMDAFVKIDSASHMIVLKTMPGNAQAIGALMDNLDWDEMMGTICGDDTILIIICRTPEDTEGVKNR
LLELL

>d1i50k_ d.74.3.2 (K:) RPB11 {Baker's yeast (Saccharomyces cerevisiae)}

MNAPDRFELFLLGEGESKLIKIDPDTKAPNAVITFEKEDHTLGNLIRAELLNDRKVLFAAYKVEHPF
FARFKLRIQTTEGYDPKDALKNACNSIINKLGALKTNFETEWNLQTL

>d1bdfa1 d.74.3.1 (A:2-52,A:179-232) RNA polymerase alpha {Escherichia coli}

QGSVTEFLKPRLVLDIEQVSSTHAKVTLEPLERGFHTLGNALRAILLSSMPXPVERIAYNVEAARVEQ
RTDLDKLVIEMETNGTIDPEEAIRRAATILAEQLEAFV

>d1i6va1 d.74.3.1 (A:6-49,A:173-229) RNA polymerase alpha {Thermus aquaticus}

LKAPVFTATTQGDHYGEFVLEPLERGFVTLGNPLRRILLSSIPXVRRVAFQVEDTRLGQRTDLDKL
TLRIWTDGSVTPLEALNQAVAILKEHLNYFANPE

>d1i50c1 d.74.3.1 (C:3-41,C:173-268) RPB3 {Baker's yeast (Saccharomyces cerevisiae)}

EEGPQVKIREASKDNVDFILSNVDLAMANSLRRVMIAEIXAAAIEFEYDPWNKLKHTDYWYEQDSA
KEWPQSKNCEYEDPPNEGDPFDYKAQADTFYMNVESVGSIPVDQVVVRGIDTLQKKVASILLALTQ
MDQD

>d1c0aa2 d.74.4.1 (A:288-420) Prokaryotic AspRS, insert domain {Escherichia coli}

NPMELTDVADLLKSVEFAVFAFPANDPKGRVAALRVPGGASLTKRQIDEYGNFVKIYGAAGLAYIKVN
ERAKGLEGINSPVAKFLNAEIIEDILDRATAAQDGMIFFGADNKKIVADAMGALRLKVGKDLGLT

>d1g51a2 d.74.4.1 (A:295-414) Prokaryotic AspRS, insert domain {Thermus thermophilus}

FGLELKEVGPLFRQSGFRVQEAESVKALALPKALSKEVAELEEVAKRHKAQGLAWARVEEGGFSG

GVAKFLEPVREALLQATEARPGDTLLFVAGPRKVAATALGAVRLRAADLLGLK
>d1a79a2 d.75.1.1 (A:9-82) tRNA splicing endonuclease EdnA, N-terminal domain
{Archaeon Methanococcus jannaschii}
KITGLLDGDRVIVFDKNGISKLSARHYGNVEGNFLSLSLVEALYLINLGWLEVKYKDNKPLSFEELYEY
ARNVE
>d1ewqa4 d.75.2.1 (A:1-120) DNA repair protein MutS, domain I {Thermus aquaticus}
MEGMLKGGEGPGLPPLQYVELRDQYDPDYLLLFQVGFYECFGEDAERLARALGLVLTHKTSKDFD
TPMAGIPLRAFEAYAERLLKMGFRLAVADQVEPAEEAEGLVRRREVTQLLTPGT
>d1e3ma4 d.75.2.1 (A:2-116) DNA repair protein MutS, domain I {Escherichia coli}
SAIENFDAHTPMMQQYLRLKAQHPEILLFYRMGDFYELFYDDAKRASQLLDISLTKRGASAGEPIPM
AGIPYHAVENYLAKLVNQGESVAICEQIGDPATSKGPVERKVVRIVTP
>d1e3mb4 d.75.2.1 (B:14-116) DNA repair protein MutS, domain I {Escherichia coli}
MQQYLRLKAQHPEILLFYRMGDFYELFYDDAKRASQLLDISLTKRGASAGEPIPMAGIPYHAVENYL
AKLVNQGESVAICEQIGDPATSKGPVERKVVRIVTP
>d1gyfa_d.76.1.1 (A:) GYF domain from cd2bp2 protein {Human (Homo sapiens)}
DVMWEYKWENTGDAELYGPFTSAQMOTWVSEGYFPDGVYCRKLDPPGGQFYNSKRIDFDLYT
>d1jg5a_d.205.1.1 (A:) GTP cyclohydrolase I feedback regulatory protein, GFRP {Rat (Rattus
norvegicus)}
PYLLISTQIRMEVGPTMVGDEHSDPELMQQLGASKRRVLGNNFYEYVNDPPRIVLDKLECRGFRVL
SMTGVGQTLVWCLHKE
>d1iq4a_d.77.1.1 (A:) Ribosomal protein L5 {Bacillus stearothermophilus}
MNRLKEKYLNEVVPALMSKFNYKSIMQVPKIEKIVINMGVGDVAVQNPKALDSAVEELTLIAGQRPVV
TRAKKSIAGFRLRQGMPIGAKVTLRGERMYEFLDKLISVSLPRARDFRGVSKKSFDDGRGNYTLGIKEQ
LIFPEIDYDKVNVKVRGMDIVIVTTANTDEEARELLALLGMPFQK
>d1jj2d_d.77.1.1 (D:) Ribosomal protein L5 {Archaeon Haloarcula marismortui}
FHEMREPRIEKVVVHMIGHGGDLANAEDILGEITGQMPVRTKAKRTVGEFDIREGDPGAKVTL
RDEMAEEFLQALPLAELATSQFDDTGNFSFGVEEHTEFPSQEYDPSIGIYGLDVTVNLRPGYRVAK
RDKASRSIPTKHRLNPADAVAFIESTYDVEV
>d1eika_d.78.1.1 (A:) RNA polymerase subunit RBP5 (RNA polymerase subunit H)
{Archaeon Methanobacterium thermoautotrophicum}
MKREILKHQLVPEHVILNESEAKRVLKELDAHPEQLPKIKTTDPVAKAIGAKRGDIVKIIRKSPTAEF
VTYRLVQD
>d1hmja_d.78.1.1 (A:) RNA polymerase subunit RBP5 (RNA polymerase subunit H)
{Archaeon Methanococcus jannaschii}
PKHEIVPKEEVEEILKRYNIKIQLPKIYEDDPVIQEIGAKEGDVVRVIRKSPTAGVSIAYRLVIKRI
>d1dzfa2 d.78.1.1 (A:144-215) Eukaryotic RPB5 C-terminal domain {Baker's yeast
{Saccharomyces cerevisiae}}
ITHHELVPKHIRLSSDEKRELLKRYRLKESQLPRIQRADPVALYLGLKRGEVVKIIRKSETSGRYASYRI
CM
>d1qkla_d.78.1.2 (A:) RPB6 {Human (Homo sapiens)}
MSDNEDNFDGDDFDDVEEDEGLDDLENAEEEGQENVEILPSGERPQANQKRITTPYMTKYERARV
LGTRALQIAMCAPVMVELEGETDPLLIAMKELKARKIPIIIRRYLPDGSYEDWGVDELIITD
>d1i50f_d.78.1.2 (F:) RPB6 {Baker's yeast (Saccharomyces cerevisiae)}
KAIPKDQRATTPYMTKYERARILGTRALQISMNAPVFDLEGETDPLRIAMKELAEKKIPLVIRRYLP

DGSFEDWSVEELIVDL

>d1qu9a_d.79.1.1 (A:) Conserved 'hypothetical' protein YjgF {Escherichia coli}
SKTIATENAPAAIGPYVQGVLDLGNMIITSGQIPVNPKTGEVPADVAAQARQSLDNVKAIVEAAGLKVG
DIVKTTVFVKDLNDFATVNATYEAFFTEHNATFPARSCVEVARLPKDVKIEIEIAIVRR

>d1qd9a_d.79.1.1 (A:) Purine regulatory protein YabJ {Bacillus subtilis}
TKAVHTKHAPAAIGPYSQGIIVNNMFYSSGQIPLTPSGEMVNGDIKEQTHQVFSNLKAVLEEAGASFE
TVVKATVFIADMEQFAEVNEVYGYFDTHKPARSCVEVARLPKDALVEIEVIALVK

>d1jd1a_d.79.1.1 (A:) Highdosage growth inhibitor YER057cp (YEO7_YEAST) {Baker's yeast
(Saccharomyces cerevisiae)}
TTLTPVICESAPAAAASYSHAMKVNNLIFLSGQIPVTPDNKLVEGSIADKAEQVIQNIKNVLEASNSL
DRVVKVNIPLADINHFAEFNSVYAKYFNTHKPARSCVAVALPLGVDMEMEAIAAER

>d1dbfa_d.79.1.2 (A:) Chorismate mutase {Bacillus subtilis}
MMIRGIRGATTVERDTEEEILQKTKQLEKIIIEENHTKPEDVVQMLLSATPDLHAVFPAKAVRELSG
WQYVPVTCMQEMDVTGGLKCCIRVMMTVQTDVPQDQIRHVYLEKAVVLRPDLSTKNTL

>d1fnja_d.79.1.2 (A:) Chorismate mutase {Bacillus subtilis}
MIRGIRGATTVERDTEEEILQKTKQLEKIIIEENHTKPEDVVQMLLSATPDLHAVFPAKAVRELSGW
QYVPVTCMQEMDVTGGLKCSIKVMMTVQTDVPQDQIRHVYLEKAVVLR

>d1jy8a_d.79.5.1 (A:) 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase IspF
{Escherichia coli}
MRIGHGFDVHAFGGEGPIIIGGVRIPIYEKGLLAHSDGDVALHALTDALLGAAALGDIGKLPDTPAF
KGADSRELLREAWRRIQAKGYTLGNVDVTIIAQAPKMLPHIPQMRVFIAEDLGCHMDDVNVKATTT
EKLGFTRGEGIACEAVALLI

>d1fsz_2 d.79.2.1 (232-356) Cell-division protein FtsZ {Archaeon Methanococcus jannaschii}
INVDFADV KAVMNNGLAMIGIGESDSEKRAKEAVSMALNSPLLDVDDIDGATGALIHVMGPEDLTLE
EAREVVATVSSRLDPNATIIWGATIDENLENTVRVLLVITGVQSRIEFTDTGLKRKKL

>d1tuba2 d.79.2.1 (A:246-440) Tubulin alpha-subunit {Pig (Sus scrofa)}
GALNVDLTFEQTNLVPYPRGHFPLATYAPVISA EKAYHEQLSVAEITNACFEPANQMVKCDPRHGKY
MACCLLYRGDVVPKDVNAAIATIKTKRTIQFVDWCPTGFKVGINYEPPTVVPGGDLAKVQRAVCMLS
NTTAIAEAWARLDHKFDL MYAKRAFVHWYVGE GMEEGEFSEAREDMAALEKDYEEVGVDSV

>d1tubb2 d.79.2.1 (B:246-437) Tubulin beta-subunit {Pig (Sus scrofa)}
GQLNADLRKLAVNMVFPRLHFFMPGFAPLTSRGSQYRALTVP ELTQQMFDAKNMMAACDPRHG
RYLTVA AVFRGRMSMKEVDEQMLNVQNKSSYFVEWIPNNVKTAVCDIPRGLKMSATFIGNSTAIQ
ELFKRISEQFTAMFRRKAFLHWYTGEGMDEMEFTEAESNMNDLVSEYQQYQD

>d1ck9a_d.79.3.1 (A:) Eukaryotic ribosomal protein L30 (L30e) {Baker's yeast
(Saccharomyces cerevisiae)}
APVKSQESINQKLALVIKSGKYTLGYKSTVKSLRQGKSKLIIIAANTPVL RKSELEYAMLSKTKVYYF
QGGNNELGTAVGKLF RVGVVSILEAGDSDILTTLA

>d1jj2f_d.79.3.1 (F:) Ribosomal protein L7ae {Archaeon Haloarcula marismortui}
PVYVDFDVPADLEDDALEALEVARDTGAVKKG TNETTKSIEGSAELVFVAEDVQPEEIVMHIPELA
DEKGVPFIFVEQQDDLGHAAGLEVGSAAA AVTDAGAAATVLEEIADKVEELR

>d1e7ka_d.79.3.1 (A:) Spliceosomal 15.5kd protein {Human (Homo sapiens)}
ADVNP KAYPLADAHLTKKLLDLVQSCNYKQLRKGANEATKTLNRGISEFIVMAADAEPLEIHLPL
LCEDKNVPYVFRSKQALGRACGVS RPVIACSVTIKEGSQLKQIQSIQSIERLLV

>d1dt9a2 d.79.3.2 (A:277-422) C-terminal domain of eukaryotic peptide chain release factor

subunit 1, ERF1 {Human (Homo sapiens)}

NVKFIQEKKLIGRYFDEISQDTGKYCFGVEDTLKALEMGAVEILIVYENLDIMRYVLHCQGTEEEKILY
 LTPEQEKDKSHFTDKETGQEHELIESMPLLEWFANNYKKFGATLEIVTDKSQEGSQFVKGFGGIGGIL
 RYRVDFQGM

>d1clia1 d.79.4.1 (A:5-170) Aminoimidazole ribonucleotide synthetase (PurM) N-terminal
 domain {Escherichia coli}

TLSYK DAGVDIDAGNALVGRIKGVVKKTRRPEVMGGLGGFGALCALPQKYREPVLVSGTDGVTGL
 RLAMDLKRHDTIGIDLAMCVNDLVVQGAEPLFFLDYYATGKLDVDTASAVISGIAEGCLQSGCSLVG
 GETAEMPGMYHGEDYDVAGFCVGVVEKSEII

>d1clib1 d.79.4.1 (B:1021-1170) Aminoimidazole ribonucleotide synthetase (PurM)
 N-terminal domain {Escherichia coli}

ALVGRIKGVVKKTRRPEVMGGLGGFGALCALPQKYREPVLVSGTDGVTGLRLAMDLKRHDTIGIDL
 VAMCVNDLVVQGAEPLFFLDYYATGKLDVDTASAVISGIAEGCLQSGCSLVGGETAEMPGMYHGEDY
 DVAGFCVGVVEKSEII

>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}

PIAQIHILEGRSDEQKETLIREVSEAIRSLDAPLTSVRVIITEMAKGHFGIGGELASKVRR

>d1otga_ d.80.1.2 (A:) 5-carboxymethyl-2-hydroxymuconate isomerase (CHMI) {Escherichia
 coli}

PHFIVECSDNIREEADLPGLFAKVNPTLAATGIFPLAGIRSRVHWVDTWQMADGQHDYAFVHMTLK
 IGAGRSLESRQQAGEMLFELIKTHFAALMESRLLALSFEIEELHPTLNFKQNNVHALFK

>d1gd0a_ d.80.1.3 (A:) Microphage migration inhibition factor (MIF) {Human (Homo
 sapiens)}

PMFIVNTNVPRASVPDGFSELSTQQLAQATGKPPQYIAVHVVPDQLMAFGGSSEPCALCSLHSIGKIG
 GAQNRSYSKLLCGLLAERLRISPDRVYINYYDMNAANVGWNNSTFALEHH

>d1fim_ d.80.1.3 (-) Microphage migration inhibition factor (MIF) {Rat (Rattus norvegicus)}

PAFIVNTNVPRASVPEGFSELSTQQLAQATGKPAQYIAVHVVPDQLMTFSGTSDPCALCSLHSIGKIGG
 AQNRNYSKLLCGLSDRLHISPDRVYINYYDANA

>d1mfia_ d.80.1.3 (A:) Microphage migration inhibition factor (MIF) {Mouse (Mus
 musculus)}

PMFIVNTNVPRASVPEGFSELSTQQLAQATGKPAQYIAVHVVPDQLMTFSGTNDPCALCSLHSIGKIG
 GAQNRSYSKLLCGLSDRLHISPDRVYINYYDMNAANVGWNGSTFA

>d1hfoa_ d.80.1.3 (A:) Microphage migration inhibition factor (MIF) {Trichina (Trichinella
 spiralis)}

PIFTLNTNIKATDVPSDFLSSTSALVGNILSKPGSYVAVHINTDQQLSFGGSTNPAAFGLMSIGGIEPS
 RNRDHS AKLFDHLNNTKLGIPKNRMYIHVNLNGDDVGVNGTTF

>d1dpta_ d.80.1.3 (A:) D-dopachrome tautomerase {Human (Homo sapiens)}

PFLELDTNLPANRVPAGLEKRLCAAASILGKPADRVNVTVRPGLAMALSGSTEPQAQLSISSIGVVGT
 AEDNRSHSAHFEEFLTKELALGQDRILIRFFPLESWQIGKIGTVMTFL

>d1gado2 d.81.1.1 (O:149-312) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
 {Escherichia coli}

CTTNCLAPLAKVINDNFGIIEGLMTTVHATTATQKTVDGPSHKDWRGGRGASQNIIPSSTGAAKAVG
 KVLPELNGKLTGMAFRVPTPNVSVVDLTVRLEKAATYEQIKA AVKAAAEGEMKGVLYTEDD VVST

DFNGEVCTSVFDAKAGIALNDNFVKLVSWYD

>d1gd1o2 d.81.1.1 (O:149-312) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
{*Bacillus stearothermophilus*, nca 1503}

CTTNCLAPFAKVLHEQFGIVRGMMTTVHSYTNDQRILDLPHKDLRRARAAAESIIPPTTTGAAKAVAL
VLPELKGKLNMGAMRVPTPNVSVVDLVAELEKEVTVEEVNAALKAAAEGELKGILAYSEEPLVSRDY
NGSTVSSTIDALSTMVIDGKMKVVSWSYD

>d1cero2 d.81.1.1 (O:149-312) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
{*Thermus aquaticus*}

CTTNLAPVMKVLLEEAFGVEKALMTTVHSYTNDQRLDLPHKDLRRARAAAINIIPPTTTGAAKATA
LVLPSLKGRFDGMALRVPTATGSISDITALLKREVTAEVNAALKAAAEGPLKGILAYTEDEIVLQDIV
MDPHSSIVDAKLTALGNMVKVFAWYD

>d1hdgo2 d.81.1.1 (O:149-312) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
{*Thermotoga maritima*}

CTTNSIAPIVKVLHEKFGIVSGMLTTVHSYTNDQRVLDLPHKDLRRARAAAIVNIIPPTTTGAAKAVALV
VPEVKGKLDGMAIRVPTPDGSITDLTVLVEKETTVVEEVNAVMEATEGRLKGIIGYNDEPIVSSDIIGT
TFSGIFDATITNVIGGKLVKVASWYD

>d1b7go2 d.81.1.1 (O:139-300) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
{*Archaeon Sulfolobus solfataricus*}

CNTTALLRTICTVNVKSKVEKVRATIVRRAADQKEVKKGPINSLVPDPATVPSHHAKDVNSVIRNLDI
ATMAVIAPTTLMHMHFINITLKDVEKKDILSVLENTPRIVLISSKYDAEATAELVEVARDLKRDRND
IPEVMIFSDSIYVKDDEVMLMYAVHQ

>d1cf2o2 d.81.1.1 (O:139-303) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
{*Archaeon Methanothermus fervidus*}

SCNTTGLCRTLKLPHDSFGIKKVRVIVRRGADPAQVSKGPINAIIPNPKLPSHHGPDVKTVDINID
TMAVIVPTTLMHQHNMVEVEETPTVDDIIDVFEDTPRVILISAEDGLTSTAEIMEYAKELGRSRNDL
FEIPVWRESITVVDNEIYYMQAVHQESD

>d1ggaa2 d.81.1.1 (A:165-333) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
{*Trypanosoma brucei brucei*, glycosome}

CTTNCLAPLVHVLVKEGFGISTGLMTTVHSYTATQKTVDGVSVDKWRGGRAAALNIIPSTTGAAKAV
GMVIPSTQKGLTGMAFRVPTADSVVDLTFIATRDTSIKEIDAALKRASKTYMKNILGYTDEELVSAD
FISDRSSIYDSKATLQNNLPNERFFKIVSWYD

>d1i32a2 d.81.1.1 (A:166-334) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
{*Leishmania mexicana*}

CTTNCLAPIVHVLTKENFGIETGLMTTIHSYTATQKTVDGVSLKDWRRGGRAAAVNIIPSTTGAAKAVG
MVIPSTKGLTGMSFRVPTPDVSVVDLTFRATRDTSIQEIDKAIKAAQTYMKGILGFTDEELVSADFI
NDRSSVYDSKATLQNNLPGEKRFFKIVSWYD

>d1dssg2 d.81.1.1 (G:149-312) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
{*Lobster (Palinurus versicolor)*}

CTTNCLAPVAKVLHENFEIVEGLMTTVHAVTATQKTVDGPSAKDWRRGGRAAQNIIPSTTGAAKAV
GKVIPELDGKLTGMAFRVPTPNVSVVDLTVRLGKECSYDDIKAAMKAASEGPLQGVLYTDEDDVSC
DFTGDNRSSIFDAKAGIQLSKTFVKVVSWSYD

>d3gpdg2 d.81.1.1 (G:151-314) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
{*Human (Homo sapiens)*}

CTTNCLAPLAKVIHDHFGIVEGLMTTVHAITATQKTVDSPSGKLWRGGRAAQNLIPASTGAAKAVG

KVIPELDGKLTGMAFRVPTANVSVLDLTCRLEKPAKYDDIKKVVKEASEGPLKGILGYTEDEVVSDDF
NGSNHSSIFDAGAGIELNDTFVKLWSWYD
>d1jn0a2 d.81.1.1 (A:149-312) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
{Spinach (*Spinacia oleracea*)}
CTTNCLAPFVKVLDQKFGIIGTMTTTHSYTGDQRLLDASHRDLRRARAACLNIVPTSTGAAKAVAL
VLPQLKGLNGIALRVPTPNVSVVDLVVQVSKKTFEEVNAAFRESADQELKGILSVCDEPLVSIDFRC
TDVSSSTIDSSLTMVMGDDMVKVIWYD
>d1gl3a2 d.81.1.1 (A:134-354) Aspartate beta-semialdehyde dehydrogenase {*Escherichia coli*}
NCTVSLMLMSLGGLFANDLVWVSVATYQAASGGGARHMRLLTQMGLHYGHVADELATPSSAILDI
ERKVTTLTRSGELPVDNFGVPLAGSLIPWIDKQLDNGQSREEWKGQAETNKILNTSSVIPVDGLCVR
VGALRCHSQAFTIKLKKDVS IPTVEELLA AHNPWAKVVPNDREITMRELTPAAVTGTLTPVGRLRK
LNMGPFLSAFTVGDQLLWG
>d1ebfa2 d.81.1.2 (A:151-340) Homoserine dehydrogenase {*Baker's yeast (Saccharomyces cerevisiae)*}
PIISFLREIITGDEVEKIEGIFSGTLSYIFNEFSTSQANDVKFSDVVKVAKKLGYTEPDPRDDLNLGLDV
ARKVTIVGRISGVEVESPTSFVQSLIPKPLESVKSADEFLEKLSDYDKDLTQLKKEAATENKVLRFIG
KVDVATKSVSVGIEKYDYSHPFASLKGSDNVISIKTKRYTNPVVIQGAGAG
>d1e5qa2 d.81.1.2 (A:125-391) Saccharopine reductase {*Rice blast fungus (Magnaporthe grisea)*}
LDPGIDHLYAIKTIEEVHAAGGKIKTFLSYCGGLPAPESSDNPLGYKFSWSSRGVLLALRNAASFYKDG
KVTNVAGPELMATAKPYFIYPGFVAVPNRDSTPYKERYQIPEADNIVRGTLRYQGFPQFIKVLVDIG
FLSDEEQPFLKEAIPWKEATQKIVKASSASEQDIVSTIVSNATFESTEEQKRIVAGLKWLGIFSDKKIT
PRGNALDTLCATLEEKMQFEGERDLVMLQHKFEIENKDGSRTRTSSLCEYGAPIGSGG
>d1f06a2 d.81.1.3 (A:119-268) Diaminopimelic acid dehydrogenase (DAPDH)
{*Corynebacterium glutamicum*}
WDPGMFSINRVYAAAVLAHQHTFWGPGLSQGHSDALRRIPGVQKAVQYTLPSDALEKARRGEA
GDLTGKQTHKRQCFVADAADHERIENDIRTMPDYFVGYEVEVNFIDEATFDSEHTGMPHGHHVIT
TGDTGGFNHTVEYILKLD
>d1dih_2 d.81.1.3 (131-240) Dihydrodipicolinate reductase {*Escherichia coli*}
VGVNVMLKLEKAAKVMGDYTDIEIIEAHRHKVDAPSGTALAMGEAIAHALDKDLKCAVYSREG
HTGERVPGTIGFATVRAGDIVGEHTAMFADIGERLEITHKASSR
>d1k5ha3 d.81.1.3 (A:126-274) 1-deoxy-D-xylulose-5-phosphate reductoisomerase
{*Escherichia coli*}
ESLVTGRLFMDAVKQSKAQLLPVDSEHNAIFQSLPQPIQHNLGYADLEQNGVVSILLTGSGGPFRET
PLRDLATMTPDQACRHPNWSMGRKISVDSATMMNKGLEYIARWLFNASASQMEVLIHPQSVIHS
MVRYQDGSVLAQLGEP
>d1gcua2 d.81.1.4 (A:129-246) Biliverdin reductase {*Rat (Rattus norvegicus)*}
MEEFEFLRREVLGKELLKGLRFTASPLEEERFGFPAFSGISRLTWLVSLFGELSLISATLEERKEDQY
MKMTVQLETQNKGLLSWIEEKGPGLKRNRYVNFQFTSGSLEEVPSVGVN
>d1h6da2 d.81.1.5 (A:213-374) Glucose-fructose oxidoreductase {*Zymomonas mobilis*}
DPMNRAAVKLIRENLGKLG MVTTDNSDVMQNDPAQQWRLRRELAGGGSLMDIGIYGLNGTRYL
LGEEPIEVRAITYSDPNDRFVEVEDRIIWQMRFRSGALSHGASSYSTTTTSRFSVQGDKAVLLMDP
ATGYYQNLISVQTPGHANQSMMPQFIMPAN

>d1dpga2 d.81.1.5 (A:182-412,A:427-485) Glucose 6-phosphate dehydrogenase {Leuconostoc mesenteroides}

KEMVQNIAALRFGNPIFDAAWNKDYIKNVQVTLSEVLGVEERAGYYDTAGALLDMIQNHTMQIVG
WLAMEKPESFTDKDIRAAKNAAFNALKIYDEAEVNKYFVRAQYGAGDSADFKPYLEELDVPADSKN
NTFIAGELQFDLPRWEGVPPFYVRSKRLAAKQTRVDIVFKAGTFNFGSEQEAQEAVLSIIIDPKGAIEL
KLNKSVEDAFNTRTIDLGWTVSDEDKKNTPXGSNFADWNGVSIWKFVDAISAVYTADKAPLETY
KSGSMGPEASDKLLAANGDAWVFKG

>d1qkia2 d.81.1.5 (A:200-434,A:450-511) Glucose 6-phosphate dehydrogenase {Human (Homo sapiens)}

DHYLGKEMVQNLMLVRFANRIFGPIWNRDNIACVILTFKEPFGTEGRGGYFDEFGIIRDVMQNHLLQ
MLCLVAMEKPASTNSDDVRDEKVKVLKCISEVQANNVVLGQYVGNPDGEGEATKGYLDDPTVPRGS
TTATFAAVVLYVENERWDGVPFILRCGKALNERKAEVRLQFHDVAGDIFHQQCKRNELVIRVQPNEA
VYTKMMTKKPGMFFNPEESELDTYGNRYKNVLPXMHFVRSDELLEAWRIFTPLLHQIELEKPKP
IPYIYSGRGPTEADELMKRVGFQYEGTYKVVN

>d1oaca4 d.82.1.1 (A:5-90) Copper amine oxidase, domain N {Escherichia coli}

AHMVPMDKTLKEFGADVQWDDYAQLFTLIKDGAYVKVKGPAQTAIVNGQPLALQPVVMKDNKA
WVSDTFINDVFQSGLDQTFQVE

>d1ekga_ d.82.2.1 (A:) C-terminal domain of frataxin {Human (Homo sapiens)}

LDETTYERLAEETLDSLAEFFEDLADKPYTFEDYDVSFGSGVLTVKLGGDLGTYVINKQTPNKQIWL
SSPSSGPKRYDWTGKNWVYSHDGVSLHELLAAELTKALKTKLDLSSLAYSGK

>d1ew4a_ d.82.2.1 (A:) CyaY {Escherichia coli}

MNDSEFHRLADQLWLTIEERLDDWDGSDIDCEINGGVLITTFENGSKIHNQEPHQLVWLATKQG
GYHFDLKGDEWICDRSGETFWDLLEQAATQQAGETVSFR

>d1ewfa1 d.83.1.1 (A:1-217) Bactericidal permeability-increasing protein, BPI {Human (Homo sapiens)}

VNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYSDFKIKHLGKGHYSFYSDIREFQLPSSQIS
MVPNVGLKFSISNANIKISGKWKAQKRFLKMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSSCS
HINSVHVHISKSKVGWLIQLFHKKIESALRNKMNSQVCEKVTNSVSSELQPYFQTLPMVKIDSVAGI
NYGLVAPPATTA

>d1ewfa2 d.83.1.1 (A:218-456) Bactericidal permeability-increasing protein, BPI {Human (Homo sapiens)}

ETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHDRMVYLGSLDYFFNTAGLVYQEAGVLKMTLRD
DMIPKESKFRLLTKFFGTFLPEVAKKFPNMKIQHVSASTPPHLSVQPTGLTFYPAVDVQAFVLPNS
ALASLFLIGMHTTGSMEVSAESNRLVDELKLDRLLELKHNSNIGFPVVELLDIMNYIVPILVLPVNE
KLQKGFPLPTPARVQLYNVVLQPHQNFLFGADVYK

>d1ihra_ d.191.1.1 (A:) Dimeric C-terminal domain of membrane protein TonB {Escherichia coli}

ARAQALRIEQVKVDFDVTDPGRVDNVQILSAKPANMFEREVKNAMRRWRYEPGKPGSGIVVNILF
KINGTTE

>d2sici_ d.84.1.1 (I:) Subtilisin inhibitor {Streptomyces albogriseolus, s-3253}

YAPSALVLTVGKVSATTAAPERAVTLTCAPGPGSHPAAGSACADLAAVGGDLNALTRGEDVMCPM
VYDPVLLTVDGVWQGKRVSYERVFSNECEMNAHGSSVFAF

>d1e6ta_ d.85.1.1 (A:) MS2 virus coat protein {Bacteriophage MS2}

ASNFTQFVLVDNGGTGDVTVAPSNFANGVAEWISSNSRSQAYKVTCSVRQSSAQRNKYTIKVEVPKV

ATQTVGGVELPVAAWRSYLNMEITPIFATNSDCELIVKAMQGLLKDGNPIPSAIAANSIGY
>d1unaa_d.85.1.1 (A:) GA coat protein {Bacteriophage GA}
ATLHSFVLVDNGGTGNVTVPVPSNANGVAEWLSNNSRSQAYRVTASYRASGADKRKYTIKLEVPKIV
TQVVNGVELPVSAAWKAYASIDLTPIFAATDDVTVISKSLTGLFKVGNPIAEAISSQSGFYA
>d1frsa_d.85.1.1 (A:) fr coat protein {Bacteriophage FR}
ASNFEFVLVDNGGTGDVKVAPSNFANGVAEWISSNRSQAYKVTCSVRQSSANNRKYTVKVEVPKV
ATQVQGGVELPVAAWRSYMNMEITPIVFATNDDCALIVKALQGTFTGNPIATAIAANSIGY
>d1qbea_d.85.1.1 (A:) Qbeta coat protein {Bacteriophage Qbeta}
AKLETVTGLNIGKDGKQTLVLNPRGVNPTNGVASLSQAGAVPALEKRVTVSQSRSNRKKNYKVQVK
IQNPTACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVRTELAALLASPLLDIAIDQLNPAY
>d1dwna_d.85.1.1 (A:) PP7 coat protein {Bacteriophage PP7}
SKTIVLSVGEATRRTLTEIQSTADRQIFEEKVGPLVGRRLRLTASLRQNGAKTAYRVNLKLDQADVDCST
SVCGELPKVRYTQVWSHDVTIVANSTEASRKSLYDLTKSLVATSQVEDLVNVLVPLGR
>d1ej1a_d.86.1.1 (A:) Translation initiation factor eIF4e {Mouse (Mus musculus)}
KHPLQNRWALWFFKNDKSKTWQANLRLISKFDTVEDFWALYNHIQLSSNLMPGCDYSLFKDGIEP
MWEDEKNKRGRWLITLTKQRRSDDLDFWLETLLCLIGESFDDYSDDVCGAVNVRAKGDKIAI
WTTECENRDAVTHIGRVYKERLGLPPKIVIGYQSHADTATKSGSTTKNRFV
>d1ap8_d.86.1.1 (-) Translation initiation factor eIF4e {Baker's yeast (Saccharomyces cerevisiae)}
MSVEEVSKKFEENVSVDDTTATPKTVLSDSAHFDVKHPLNTKWTWYTKPAVDKSESWSDLLRPV
TSFQTVVEEFWAIQNIPEPHELPLKSDYHVFNRDVRPEWEDEANAKGGKWSFQLRGKADIDELWL
RTLLAVIGETIDEDDSQINGVVLIRKGGNKFALWTKSEDKEPLLIRIGGKFKQVLKLTDDGHLEFFPH
SSANGRHPQPSITL
>d3grs_3 d.87.1.1 (364-478) Glutathione reductase {Human (Homo sapiens)}
YNNIPTVVFSHPPIGTVGLTEDEAIHKYGIENVKTYSTSTFTPMYHAVTKRKTCKVMKMCANKEEKV
VGIHMQLGCDLEMLQGFVAVKMGATKADFDNTVAIHPTSSEELVTLR
>d1gesa3 d.87.1.1 (A:336-450) Glutathione reductase {Escherichia coli}
YSNIPTVVFSHPPIGTVGLTEPQAREQYGDQVKVYKSSFTAMYTAVTTHRQPCRMKLVCGVSEEKIV
GIHGIGFGMDEMLQGFVAALKMGATKKDFDNTVAIHPTAAEEFVTMR
>d1feca3 d.87.1.1 (A:358-485) Trypanothione reductase {Crithidia fasciculata}
HTKVACAVFSIPPMGVCYVEEDAACKYDQVAVYESSFTPLMHNISGSTYKFMVRIVTNHADGEVL
GVHMLGDSSPEIISVAICLKMGAISDFYNTIGVHPTSAAEELCSMRTPAYFYEKGRVEK
>d1aoga3 d.87.1.1 (A:358-487) Trypanothione reductase {Trypanosoma cruzi}
DHTRVASAVFSIPPIGTCGLIEEVASKRYEVVAVYLSSTFTPLMHKVS GSKYKTFVAKIITNHS DGTVLGV
HLLGDNAP EIIQGIGICLKNAKISDFYNTIGVHPTSAAEELCSMRTPSYYYVKGEKMEKP
>d1h6va3 d.87.1.1 (A:367-499) Mammalian thioredoxin reductase {Rat (Rattus norvegicus)}
YDNVPTTVFTPLEYGCCGLSEEKAVEKFGREENIEVYHSFFWPLEWTVPSRDNNKCYAKVICNLKDN
ERVVGFHVLGPNAGEVTQGFAAALKCGLTKQLDSTIGIHPVCAEIFTTLSVTKRSGGDILQSGCCG
>d1nhp_3 d.87.1.1 (322-447) NADH peroxidase {Enterococcus faecalis}
GVQGSGLAVFDYKFASTGINEVMAQKLGKETKAVTVVEDYLMDFNPKQKAWFKLVYDPETTQIL
GAQLMSKADLTANINAIQAKMTIEDLAYADFFFQPAFDKPWNIINTAALEAVKQER
>d1d7ya3 d.87.1.1 (A:309-405) NADH-dependent ferredoxin reductase, BphA4
{Pseudomonas sp., KKS102}
TAPGYAELPWYWS DQAGALRIQVAGLASGDEEIVRGEVSLDAPKFTLIELQKGRIVGATCVNNARDFAP

LRRLAVGAKPDRAALADPATDLRKLAAA

>d1lv_3 d.87.1.1 (336-458) Dihydrolipoamide dehydrogenase {*Pseudomonas putida*}
PAAIAAVCFDPEVVVVGKTPEQASQQGLDCIVAQFPFAANGRAMSLESKSGFVRVARRDNHLILG
WQAVGVAVSELSTAFASQLEMGACLEDVAGTIHAHPTLGEAVQEALRALGHALHI

>d1lpfa3 d.87.1.1 (A:349-472) Dihydrolipoamide dehydrogenase {*Pseudomonas fluorescens*}
YDLIPSVIYTHPEIAWVGKTEQTLKAEGVEVNVGTFPFAASGRAMAANDTTGLVKVIADAKTDRVLG
VHVIGPSAAELVQGAIGMEFGTSAEDLGMMVFSHPTLSEALHEAALAVNGHAIHIA

>d3lada3 d.87.1.1 (A:349-472) Dihydrolipoamide dehydrogenase {*Azotobacter vinelandii*}
YDLIPAVIYTHPEIAGVGKTEQALKAEGVAINVGVFPFAASGRAMAANDTAGFVKVIADAKTDRVLGV
HVIGPSAAELVQGAIAEMFGTSAEDLGMMVFAHPALSEALHEAALAVSGHAIHVA

>d1ebda3 d.87.1.1 (A:347-461) Dihydrolipoamide dehydrogenase {*Bacillus stearothermophilus*}
AIPAVVFSDEPCASVGYFEQAKDEGIDVIAAKFPFAANGRALALNDTDGFLKLVVRKEDGVIIGAQII
GPNASDMIAELGLAIEAGMTAEDIALTIHAHPTLGEIAMEAAEVAL

>d1ojt_3 d.87.1.1 (471-598) Dihydrolipoamide dehydrogenase {*Neisseria meningitidis*}
ARVIPGVAYTSPEVAWVGETELSAKASARKITKANFPWAASGRAIANGCDKPFKLIFFDAETGRIIGG
GIVGPNGGDMIGEVCIAIEMGCCAADIGKTIHPHPTLGESIGMAAEVALGTCTDLPPQKK

>d1jeha3 d.87.1.1 (A:356-478) Dihydrolipoamide dehydrogenase {*Baker's yeast (Saccharomyces cerevisiae)*}
YNNIPSVMYSHPEVAWVGKTEEQVKEAGIDYKIGKFPFAANSRAKTNQDTEGFVKILIDSKTERILGA
HIIGPNAGEMIAEAGLALAYGASAEVARVCHAHPTLSEAFKEANMAAYDKAIHC

>d1dxla3 d.87.1.1 (A:348-470) Dihydrolipoamide dehydrogenase {*Garden pea (Pisum sativum)*}
YDKVPGVVYTNPEVASVGKTEEQVKETGVEYRVGKFPFMANSRAKAIDNAEGLVKIIAEKETDKILG
VHIMAPNAGELIHEAAIALQYDASEDIARVCHAHPTMSEAIKEAAMATYDKPIHI

>d1fda3 d.87.1.1 (A:328-401) Flavocytochrome c sulfide dehydrogenase, FCSD, flavin-binding subunit {*Purple phototrophic bacterium (Chromatium vinosum)*}
PGTPSYLNTCYSILAPAYGISVAAIYRPNADGSAIESVPSGGVTPVDAPDWVLEREVQYAYSWYNNIV
HDTFG

>d1qj2c1 d.87.2.1 (C:178-285) Carbon monoxide (CO) dehydrogenase flavoprotein, C-terminal domain {*Pseudomonas carboxydovorans*}
GHGYAYEKLRKIGDYATAAAVVLMSGGKCVTASIGLTVANTPLWAEAGKVLVGTALDKPALDK
AVALAEAITAPASDGRGPAEYRTKMAGVMLRRAVERAKAR

>d1ffvc1 d.87.2.1 (C:178-287) Carbon monoxide (CO) dehydrogenase flavoprotein, C-terminal domain {*Hydrogenophaga pseudoflava*}
GTGWAYEKLRKRTGDWATAGCAVVMRSGNTVSHIRIALTNVAPTALRAEAAEAALLGKAFTKEAV
QAAADAAIAICEPAEDLRGDADYKTAMAGQMVKRALNAAWARCA

>d1fo4a4 d.87.2.1 (A:415-531) Xanthine oxidase, domain 4 (?) {*Cow (Bos taurus)*}
DEFFSAFKQASREDDIAKVTGMRVLFQPGSMQVKELALCYGGMADRTISALKTTQKQLSKFWNE
KLLQDVCAGLAEELSPDAPGGMIEFRRTLTLSSFFFKFYLTVLKKGKDS

>d1jroa3 d.87.2.1 (A:346-462) Xanthine dehydrogenase chain A, domain 4 {*Rhodobacter capsulatus*}
PGLRCYKLSKRFQDISAVCGCLNLTGSKIETARIAFGGMAGVPKRAAAFEAALIGQDFREDTIAA

ALPLLAQDFTPLSDMRASAAYRMNAAQAMALRYVRELSGEAVAVLEVMP
>d1srsa_d.88.1.1 (A:) Serum response factor (SRF) core {Human (Homo sapiens)}
TRGRVKIKMEFIDNKLRRYTTFSKRKTGIMKKAYELSTLTGTQVLLLVASETGHVYTFATRKLQPMIT
SETGKALIQTCLNSPD
>d1mnmma_d.88.1.1 (A:) MCM1 transcriptional regulator {Baker's yeast (Saccharomyces cerevisiae)}
QKERRKIEIKFIENKTRRHVTFSKRKHGIMKKAFELSVLTGTQVLLLVSETGLVYTFSTPKFEPIVTQ
QEGRNLIQAACLNAPDD
>d1egwa_d.88.1.1 (A:) Mef2a core {Human (Homo sapiens)}
GRKKIQITRIMDERNRQVTFTRKRFGLMCKAYELSVLCDCEIALIIFNSSNKLQYASTDMDKVLLKY
TEY
>d1tbd_d.89.1.1 (-) The origin DNA-binding domain of SV40 T-antigen {Simian virus 40}
GSKVEDPKDFPSELLSFLSHAVFSNRTLACFAIYTTKEKAALLYKIMEKYSVTFISRHNNSYNHNILFF
LTPHRHRVSAINNYAQKLCCTFSFLICKGVNKEYLMYSALTRDPFVIEESLPGGLKEHDFNPES
>d1f08a_d.89.1.2 (A:) Replication initiation protein E1 {Bovine papillomavirus}
GSRATVFKLGLFKSLFCLSFHDITRLFKNDKTTNQQWVLAVFGLAEVFFEASFELKKQCSFLQMOK
RSHEGGTCAVYLICFNTAKSRETVRNLMANMLNVREECLMLQPPKIRGLSALFWFKSSSPATLKH
GALPEWIRAQTTLN
>d1nox_d.90.1.1 (-) NADH oxidase {Thermus thermophilus, HB8}
PVLDAKTAALKRRSIRRYRKDPVPEGLLREILEAALRAPSAWNLQPWRIVVVRDPATKRALREAAFG
QAHVEEAPVVLVLYADLEDALAHLEVIHPGVQGERREAQKQAIQRAFAAMGQEARKAWASGQSYI
LLGYLLLLLEAYGLGSPMLGFDPERVRAILGLPSRAAIPALVALGYPAAEGYPSHRLPLERVVLR
>d1bkja_d.90.1.1 (A:) Flavin reductase P (NADPH:FMN oxidoreductase) {Vibrio harveyi}
NNTIETILAHRSIRKFTAVPITDEQRQTIIQAGLAASSSSMLQVVSIVRVTDSEKRNELAQFAGNQAYV
ESAAEFLVFCIDYQRHATINPDVQADFTELTLIGAVDSGIMAQNCLLAAESMGLGGVYIGGLRNSAAQ
VDELLGLPENSAVLFMCLGHPDQNPVVKPRLPAHVVVHENQYQELNLDIQQSYDQTMQAYYASRT
SNQKLSTWSQEVGTGKLAGE SRPHILPYLNSKGLAKR
>d1vfra_d.90.1.1 (A:) Flavin reductase P (NADPH:FMN oxidoreductase) {Vibrio fischeri}
THPIIHDLNRYTSKKYDPSKKVSQEDLAVLLEALRLSASSINSQPWKFIVIESDAAKQRMHDSFANM
HQFNQPHIKACSHVILFANKLSYTRDDYDVVLSKAVADKRITEEQKEAAFASFKEVFNCDENGEHK
AWTKPQAYLALGNALHTLARLNIDSTTMEGIDPELLSEIFADELKGYECHVALAIGYHHPSEDYNASL
PKSRKAFEDVITIL
>d1kqba_d.90.1.1 (A:) Nitroreductase {Enterobacter cloacae}
DIISVALKRHSTKAFDASKKLTAEAEKIKTLLQYSPSSTNSQPWHFIVASTEEGKARVAKSAAGTYVF
NERKMLDASHVVVFCAKTAMDDAWLERVVDQEEADGRFNTPEAKAANKGRTYFADMHRVDLK
DDDQWMAKQVYLVNFGNLLGVGAMGLDAVPIEGFDAAILDEEFGLKEKGFTSLVVVVPVGHHSVEDF
NATLPKSRLPLSTIVTEC
>d1icra_d.90.1.1 (A:) Nitroreductase {Escherichia coli, minor form}
DIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVAKSAAGNYVF
NERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKGRKFFADMHRKDLH
DDAEWMAKQVYLVNFGNLLGVAALGLDAVPIEGFDAAILDAEFGLKEKGYTSLVVVVPVGHHSVEDF
NATLPKSRLPQNITLTEV
>d1f5va_d.90.1.1 (A:) Nitroreductase {Escherichia coli, oxygen-insensitive form}
MTPTIELICGHRHSIRHFTDEPISEAQREAIINSARATSSSSFLQCSSIIRITDKALREELVTLTGGQKHVA

QAAEFWVFCADFNRLQICPDAQLGLAEQLLLGVVDTAMMAQNALIAAESLGLGGVYIGGLRNNIE
AVTKLLKLPQHVLPLFGLCLGWPADNPDLPKRLPASILVHENSYQPLDKGALAQYDEQLAEYYLTRG
SNNRRDTWSDHIRRTIIKESRPFILDYLHKQGWATR
>d1dt9a3_d.91.1.1 (A:5-142) N-terminal domain of eukaryotic peptide chain release factor
subunit 1, ERF1 {Human (Homo sapiens)}
PSAADRNVEIWKIKLIKSLEAARGNGTSMISLIIPPKDQISRVAKMLADEFGTASNIKSRVNRSLVGLG
AITSVQQRLKLYNKVPPNGLVVYCGTIVTEEGKEKKVNIDFEPFKPINTSLYLCDNKFHTEALTALLSD
>d1c7ka_d.92.1.1 (A:) Zinc protease {Streptomyces caespitosus}
TVTVTYDPSNAPSFQQEIANAAQIWNSSVRNVQLRAGGNADFSYYEGNDSRGSYAQTDGHGRGYIFL
DYQQNQYDSTRVTAHETGHVLGLPDHYQGPCSELMSSGGGPGPCTNPYPNAQERSRVNALWANG
>d1g12a_d.92.1.12 (A:) Fungal zinc peptidase {Grifola frondosa}
TYNGCSSSEQSALAAAASAAQSYVAESLSYLQHTAATPRYTTWFGSYISSRHSTVLQHYTDMNSND
FSSYSFDCTCTAAGTFAYVYPNRFQTVYLCGAFWKAPTTGTDSQAGTLVHESSHFRNGGKDYAYG
QAAAKSLATMDPKAVMNADNHEYFSENNPAQS
>d1eb6a_d.92.1.12 (A:) Fungal zinc peptidase {Aspergillus oryzae, deuterolysin}
TEVTDCKGDAESSLTALSNAAKLANQAAEAAESGDESKFEEYFKTTDQQTRTTVAERLRRAVAKEAG
STSGGSTTYHCNDPYGYCEPNVLAYTLPSKNEIANCDIYYSELPLAQKCHAQDQATTTLHEFTHAPG
VYQPGTEDLGYGYDAATQLSAQDALNNADSYALYANAIELKC
>d1ezm_d.92.1.2 (-) Elastase {Pseudomonas aeruginosa}
AEAGGPGGNQKIGKYTYGSDYGLIVNDRCEMDDGNVITVDMNSSTDDSKTTPFRFACPTNTYKQV
NGAYSPLNDAHFFGGVVFKLYRDWFGTSPHLTKLYMKVHYGRSVENAYWDGTAMLFGDGATMFYP
LVSLDVAHEVSHGFTEQNSGLIYRGQSGGMNEAFSDMAGEAAEFYMRGKNDFLIGYDIKKGSGALR
YMDQPSRDGRSIDNASQYYNGIDVHHSSGVYNRAFYLLANSPGWDTRKAFEVFVDANRYWTATS
NYNSGACGVIRSAQNRNYSAADVTRAFSTVGVTCF
>d8tlne_d.92.1.2 (E:) Thermolysin {Bacillus thermoproteolyticus}
ITGTSTVGVGRGVLGDQKNINTTYSTYYYLQDNTRGDGIFTYDAKYRTTLPGLSWADADNQQFFASYD
APAVDAHYYAGVTYDYKKNVHNRLSYDGNNAAIRSSVHYSGYNNAFWNGSEMVMYGDGDGQTFIPL
SGGIDVVAHELTHAVTDYTAGLIYQNESGAINAISDIFGTLVEFYANKNPDWEIGEDVYTPGISGDSL
RSMSPAKYGDPDHYSKRYTGTQDNGGVHINSIINKAAYLISQGGTHYGVSVVIGIRDKLGKIFYRA
LTQYLTPSNTSFLRAAAVQSATDLYGSTSQEVASVKQAFDAVGVK
>d1npc_d.92.1.2 (-) Neutral protease {Bacillus cereus, strain dsm 3101}
VTGTNKVGTGKGVLDGDKSLNTTSLGSSYYLQDNTRGATIFTYDAKNRSTLPGTLWADADNVFNAA
YDAAAVIDAHYYAGKTYDYKATFNRSINDAGAPLKSTVHYGSNNYNNAFWNGSQMVYGDGDGVTF
TSLGGIDVIGHELTHAVTENSNNLIYQNESGALNEAISDIFGTLVEFYDNRNPDWEIGEDIYTPGKAG
DALRMSDPTKYGDPDHYSKRYTGSSDNGGVHTNSGIINKQAYLLANGGTHYGVTVTGIGDKLGA
IYYRANTQYFTQSTTFSQARAGAVQAAADLYGANSAAVAVKQSFSAVGVN
>d1bqba_d.92.1.2 (A:) Aureolysin {Staphylococcus aureus}
AAATGTGKGVLDGDKDININSIDGGFSLEDLTHQGKLSAYNFNDQTGQATLITNEDENFVKDDQRAG
VDANYYAKQTYDYKNTFGRESYDNHGSPIVSLTHVNHYGGQDNRNNAAWIGDKMIYGDGDGRTF
TNLSGANDVVAHEITHGVTQQTANLEYKQSGALNESFSDVFGYFVDEDFLMGEDVYTPGKEGDA
LRSMSPNQFQPSHMKDYVYTEKDNGGVHTNSGIPNKAAYNVIQAIGKSKSEQIYYRALTEYLTSN
SNFKDLKDALYQAAKDLYEQQTAEQVYEAWNEVGVE
>d1hs6a3_d.92.1.13 (A:209-460) Leukotriene A4 hydrolase catalytic domain {Human (Homo
sapiens)}

LESRQIGPRTLWSEKEQVEKSAYEFSETESMLKIAEDLGGPYVWGQYDLLVLPPSPFYGGMENPCL
TFVTPTELLAGDKSLSNVIAHEISHSWTGNLVTNKTWDHFWLNEGHTVYLERHICGRLFGEKFRHFN
ALGGWGELQNSVKTFGETHPFTKLVVDLTDIDPDVAYSSVPYEKGFALLFYLEQLLGGPEIFLGLKA
YVEKFSYKSITDDWKFDFLYSYFKDKVDVNLQVDWNAWLYSPGLPPIKPNY

>d1dmta_d.92.1.4 (A:) Neutral endopeptidase (neprilysin) {Human (Homo sapiens)}
GICKSSDCIKSAARLIQNMDATTEPCTDFFKYACGGWLKRNVIPETSSRYGNFDILRDELEVVLKVDL
QEPKTEDIVAVQKAKALYRSCINESAIDSRGGEPLKLLPDIYGWPVATENWEQKYGASWTAEKAI
QLNSKYGKKVLINLFGVTDKNSVNHVIHIDQPRGLPSRDYECTGIYKEACTAYVDFMISVARLIR
QEERLPIDENQLALEMNKVMLEKEIANATAKPEDRNDPMLLYNKMTLAQIQNFSLEINGKPFWS
LNFTNEIMSTVNISITNEEDVVVYAPEYLTKLKPIITKYASARDLQNLMSWRFIMDLVSSLSR
TYKESR NAFRKALYGTSETATWRRCANVYNGNMENAVGRLYVEAAFAGESKHVVEDLIAQIREVFIQTLDDL
TWMDAETKKRAEEKALAIKERIGYPDDIVSNDNKLNNLEYELNYKEDEYFENIIQNLKFSQSKQLKK
LREKVDKDEWISGAAVVNAFYSSGRNQIVFPAGILQPPFFSAQSNLNYGGIGMVIGHEITHGFDDN
GRNFNKDGLVDWWTQQSASNFKEQSQCVMVYQGNFSDWLAGGQHLNGINTLGENIADNGGLGQ
AYRAYQNYIKKNGEEKLLPGLDLNHKQLFFLNFAQVWCGTYRPEYAVNSIKTDVHSPGNFRIIGTLQ
NSAEFSEAFHCRKNSYMNPEKKCRVW

>d1i1ip_d.92.1.5 (P:) Neurolysin (endopeptidase 24.16) {Rat (Rattus norvegicus)}
MSSYTAAGRNVLRWDLSPQIKTRTEQLIAQTKQVYDVTGIALKEVITYENCLQVLADIEVITYIVERT
MLDFPQHVSSDREVRAASTEADKLSRFDIEMSMREDVFQRIVHLQETCDLEKIKPEARRYLEKSIK
MGKRNLHLSEHIRNEIKSMKKRMSELCIDFNKLNEDDTSLVFSKAELGALPDDFIDSLEKTDEDK
YKVTLYPHYFPVMKKCCVPETRRKMEMAFHTRCKQENTAILQQLPLRAQVAKLLGYNTHADFV
LELNTAKSTSRVA AFLDLSQKLKPLGEAEREFILSLKKKECEERGFEYDGKINAWDLHYMTQTEE
LKYSVDQESLKEYFPIEVVTEGLLSIYQELLGLSFEQVPDAHVWNKSVSLYTVKDKATGEVLGQFYLD
LYPREGKYNHAACFGLQPGCLLPDGSRMMSVAALVVNFSQPVAGRPSLLRHDEVRTYFHEFGHVMH
QICAQTD FARFSGTNVETDFVEVPSQMLENWWVDVDSLRLKLSKHYKDGHPITDELLEKLVASRLVN
TGLLTRQIVLSKVDQSLHTNATLDAASEYAKYCTEILGVAATPGTNMPATFGHLAGGYDGGYYGYL
WSEVFSMDMFHSCFKKEGIMNPEVGMKYRNLLKPGGSLDGMDMLQNFLQREPNQKAFLMSRGL

>d1j7na1 d.92.1.14 (A:27-263) Anthrax toxin lethal factor, N- and C-terminal domains
{Bacillus anthracis}
ERNKTQEEHLKEIMKHIVKIEVKGEEAVKKEAAEKLEKVPDVLVEMYKAIGGKIYIVDGDITKHISL
EALSEDKKKIKDIYKGDALLHEHYVYAKEGYEPLVIQSSSEDYVENTEKALNVVYEIGKILSRDILSKIN
QPYQKFLDVLNTIKNASDSGDLLFTNQLKEHPTDFSVEFLEQNSNEVQEVFAKAFAYYIEPQHRD
VLQLYAPEAFNYMDKFNEQEINLSLEELKDQR

>d1j7na2 d.92.1.14 (A:551-773) Anthrax toxin lethal factor, N- and C-terminal domains
{Bacillus anthracis}
PKSKIDTKIQEAQLNINQEWNKALGLPKYTKLITFNVHNRYASNIVESAYLILNEWKNNIQSDLIKKV
TNYLVDGNGRFVFTDITLPNIAEQYTHQDEIYEQVHSGLYVPESRSILLHGPSKGVLELRNDSEGFHIE
FGHAVDDYAGYLLDKNQSDLVTNSKKFIDIFKEEGSNLTSYGRTEAEFFAEAFRLMHSTDHAERLK
VQKNAPKTFQFINDQIKFI

>d1lml_d.92.1.3 (-) Leishmanolysin {Leishmania major}
VVRDVNWGALRIAVSTEDLTPAYHCARVGQHVKD HAGAIVTCTAEDILTNEKRDILVKHLIPQAVQ
LHTERLKVQQVQGWKVTDMVGDICGDFKVPQAHITEGFSNTDFVMYVASVPSEEGVLAWATTCCQ
TFSDGHPAVGVINIPAANIASRYDQLVTRVVTHEMAHALGFSGPFEDARIVANVPNVRGKNFDPVPI
NSSTAVAKAREQYGCDTLEYLEVEDQGGAGSAGSHIKMRNAQDELMAPAAAAGYYTALTMAIFQDL

GFYQADFSKAEVMPWQGNAGCAFLTNKCMESVTPQWPAMFCNESEDAIRCPTSRLSLGACGVTRH
PGLPPYWQYFTDPSLAGVSAFMDYCPVVVPYSDGSCQRASEAHASLLPFNVFSDAARCIDGAFRPK
ATDGIVKSYAGLCANVQCDTATRYSVQVHGSNDYTNCTPGLRVELSTVSNAFEFGGYITCPPYVEVC
QGNVQAAKD

>d1kapp2 d.92.1.6 (P:1-246) Metallo protease, catalytic (N-terminal) domain {*Pseudomonas aeruginosa*, alkaline protease}

GRSDAYTQVDNFLHAYARGGDELVNGHPSYTVDQAAEQILREQASWQKAPGDSVLTLSYSFLTKPND
FFNTPWKYVSDIYSLGKFSAFSAQQQAQAKLSLQSWSDVTNIHFVDAGQGDQGLDFGNFSSSVGGA
AFAFLPDVPDALKGQSWYLINSSYSANVNPANGNYGRQTLTHEIGHTLGLSHPGDYNAGEGDPTYAD
ATYAEDTRAYSVMYSWEEQNTGQDFKQAYSSAPLLDDIAAIQKLY

>d1sat_2 d.92.1.6 (4-246) Metallo protease, catalytic (N-terminal) domain {*Serratia marcescens*}

TGYDAVDDLLHYHERGNGIQINGKDSFSNEQAGLFITRENQTWNGYKVFQGPVKLTFSPDYKFSST
NVAGDTGLSKFSAEQQAQAKLSLQSWADVANTFTEVAAGQKANITFGNYSQDRPGHYDYGTQAYAF
LPNTIWQGGDLGGQTWYNVNQSNVHKPATEDYGRQTFTHEIGHALGLSHPGDYNAGEGDPTYADV
TYAEDTRQFSLMSYWSETNTGGDNGGHYAAAPLLDDIAAIQHLY

>d3btaa3 d.92.1.7 (A:1-546) Botulinum neurotoxin {*Clostridium botulinum*, serotype A}

PFVVKQFNYKDPVNGVDIAYIKIPNVGQMPVKAFKIHNKIWVIPERDTFTNPEEGDLNPPPEAKQV
PVSYYDSTYLSTDNEKDNLYLKGVTKLFERIYSTDLGRMLLTSIVRGIPFWGGSTIDTELKVIDTNCINV
IQPDGYSRSEELNLVIIGPSADIIQFECKSFGHEVLNLTRNGYGSTQYIRFSPDFTFGFEESLEVDTNPL
LGAGKFATDPAVTLAHELHAGHRLYGIAINPNRVFKVNTNAYYEMSGLEVSFEELRTFGGHDAKFID
SLQENEFRLYYYNFKDIASTLNKAKSIVGTTASLQYMKNVFKEKYLLEDTSGKFSVDKLFKFKLYK
MLTEIYTEDNFVFKFVLRKTYLNFDFKAVFKINIVPKVNYTIYDGFNLRNTNLAANFNGQNTENN
MNFTKLKNFTGLFEFYKLLCVRGIITSKTKSLDKGYNKALNDLCIKVNNWDLFFSPSEDNFTNDLNK
GEEITSDTNIEAAEENISLDLIQQYYLTFNFDNEPENISIENLSSDIIGQLELMPNIERFPNGKKYELDK

>d1epwa3 d.92.1.7 (A:1-533) Botulinum neurotoxin {*Clostridium botulinum*, serotype B}

PVTINNFNYNDPIDNNNIIMPEPPFARGTGRYKAFKITDRIWIIPERYTFGYKPEDFNKSSGIFNRD
VCEYYDPDYLNNTDKKNIFLQTMIKLFNRIKSKPLGEKLEMIINGIPYLGDRRVPLEEFNTNIASVT
VNKLISNPGEVERKKGIFANLIIFGPGPVLNENETIDIGIQNHFASREGFGGIMQMKFCPEYVSFVNNV
QENKGASIFNRRGYFSDPALILMHELIHVLHGLYGKVDLPIVPNEKKFFMQSTDAIQAEELYTFGG
QDPSIITPSTDKSIYDKVLQFRGIVDRLNKLVCISDPNINININIKNFKDKYKFVEDSEGKYSIDVES
FDKLYKSLMFGFTETNIAENYKIKTRASYSFSDSLPPVKIKNLLDNEIYTIIEGFNISKDMEKEYRGQ
NKAINKQAYEEISKEHLAVYKIQMCKSVKAPGICIDVDNEDLFFIADKNSFSDLSKNERIEYNTQSN
YIENDFPINELILDLDLISKIELPSENTESLTFNVDVPPVYEQPAIKKIFTDE

>d1f83a_ d.92.1.7 (A:) Botulinum neurotoxin {*Clostridium botulinum*, serotype B}

PVTINNFNYNDPIDNNNIIMPEPPFARGTGRYKAFKITDRIWIIPERYTFGYKPEDFNKSSGIFNRD
VCEYYDPDYLNNTDKKNIFLQTMIKLFNRIKSKPLGEKLEMIINGIPYLGDRRVPLEEFNTNIASVT
VNKLISNPGEVERKKGIFANLIIFGPGPVLNENETIDIGIQNHFASREGFGGIMQMKFCPEYVSFVNNV
QENKGASIFNRRGYFSDPALILMHELIHVLHGLYGKVDLPIVPNEKKFFMQSTDAIQAEELYTFGG
QDPSIITPSTDKSIYDKVLQFRGIVDRLNKLVCISDPNINININIKNFKDKYKFVEDSEGKYSIDVES
FDKLYKSLMFGFTETNIAENYKIKTRASYSFSDSLPPVKIKNLLDNEIYTIIEGFNISKDMEKEYRGQ
NKAINKQAYEEISK

>d1ast_ d.92.1.8 (-) Astacin {European fresh water crayfish (*Astacus astacus*)}

AAILGDEYLWGGVPIPYTFAGVSGADQSAILSQMGQEELEKTCIRFVPRTTESDYVEIFTSVSGSCWSYVG

RISGAQVSLQANGCVYHGTHHELMHAIGFYHEHTRMDRDNYVTINYQNVDPMSMTSNFDIDTYSRY
VGEDYQYYSIMHYGKYSFSIQWGVLETIVPLQNGIDLTPYDKAHMLQTDANQINNLYTNECSL
>d4aig_ d.92.1.9 (-) Snake venom metalloprotease {Eastern diamondback rattlesnake
(Crotalus adamanteus), adamalysin II}
NLPQRYIELVVVADRRVFMKYNSDLNIIRTRVHEIVNIINEFYRSLNIRVSLTDLEIWSGQDFITIQSSSS
NTLNSFGEWRRERVLLTRKRHDNAQLLTAINFEGKIIGKAYTSSMCNPRSSVGIVKDHSPINLLVAVTM
AHELGHNLGMEHDGKDCLRGASLCIMRPGLTPGRSYEFSDDSMGYQKFLNQYKQPQCILNKP
>d1atla_ d.92.1.9 (A:) Snake venom metalloprotease {Western diamondback rattlesnake
(Crotalus atrox), atrolysin C}
LPQRYIELVVVADHRVFMKYNSDLNTIRTRVHEIVNFINGFYRSLNIHVSLTDLEIWSNEDQINIQSAS
SDTLNAFAEWRETDLLNRKSHDNAQLLTAIELDEETLGLAPLGTMCDPKLSIGIVQDHSPINLLMGV
TMAHELGHNLGMEHDGKDCLRGASLCIMRPGLTKGRSYEFSDDSMHYERFLKQYKQPQCILNKP
>d1buda_ d.92.1.9 (A:) Snake venom metalloprotease {Five-pace snake (Agkistrodon acutus),
acutolysin A}
FQRYMEIVIVVDHSMVKKYNGSDSIKAWVYEMINTITESYSYLKIDISLSGLEIWSGKDLIDVEASAG
NTLKSFGEWRAKDLIHRISHDNAQLLTATDFDGATIGLAYVASMCPKRSVGVIQDHSSVNRLVAITL
AHEMAHNLGVSHEGSCSCGGKSCIMSPSISDETIKYFSDCSYIQCRDYISKENPPCILN
>d1quaa_ d.92.1.9 (A:) Snake venom metalloprotease {Chinese five-pace snake (Agkistrodon
acutus), acutolysin C}
PAPQTSIELFLIVDHSYAKYNSNSSKITTTLKARVNIMNAIYSSLNLVITLSGIEMWSAADLITVQSSS
RNTLKLAFASWRETDLLKRTSNDNAQLLTATNFNGNTVGLAYLKTMCNSKYSVGLIQDHSAIPLLMVAV
TMAHELGHNLGMNHDGAGCSCATCIMAPVLSSGPAKSFSDCSKHQYQSFLTIIHKPQCLLN
>d1bkca_ d.92.1.10 (A:) TNF-alpha converting enzyme, TACE, catalytic domain {Human
(Homo sapiens)}
DPMKNTCKLLVADHRFYRYMGRGEESTTTNYLIELIDRVDDIYRNTAWDNAGFKGYGQIEQIRILK
SPQEVKPGKEKHYNMAKSYPNEEKDAWDVKMLLEQFSFDIAEEASKVCLAHLFTYQDFDMGTLGLA
YVGSPRANSHGGVCPKAYSPVGVKKNYLNGLTSTKNYGKTILTKEADLVTTHELGHNFGAEHDPD
GLAECAPNEDQGGKYVMYPIAVSGDHENNKMFQCSKQSIYKTIESKAQECFQER
>d1cgl_ d.92.1.11 (A:) Fibroblast collagenase (MMP-1) {Human (Homo sapiens)}
VLTEGNPRWEQTHLRYRIENYTPDLPRADVDHAIEKAFQLWSDVTPLTFTKVSEGGADIMISFVRGD
HRDNSPFDGPGGNLAHAFDPPGIGGDAHFDEDERWTNNFREYNLHRVAAHELGHSLGLSHSTDI
GALMYPSTYFSGDVQLAQDDIDGIQAIYGRSQNPVQ
>d1hfc_ d.92.1.11 (-) Fibroblast collagenase (MMP-1) {Human (Homo sapiens)}
PRWEQTHLTYRIENYTPDLPRADVDHAIEKAFQLWSNVTPLTFTKVSEGGADIMISFVRGDHRDNS
PFDGPGGNLAHAFQPPGIGGDAHFDEDERWTNNFREYNLHRVAAHELGHSLGLSHSTDIGALMY
PSYTFSGDVQLAQDDIDGIQAIYGRS
>d1fbl_2 d.92.1.11 (100-271) Fibroblast collagenase (MMP-1) {Pig (Sus scrofa)}
FVLTPGNPRWENTHLTYRIENYTPDLSREDVDRAIEKAFQLWSNVSPLTFTKVSEGGADIMISFVRG
DHRDNSPFDGPGGNLAHAFQPPGIGGDAHFDEDERWTKNFRDYNLYRVAHELGHSLGLSHSTDI
GALMYPNYIYTGDVQLSQDDIDGIQAIYGPSENVPVQPSG
>d1hova_ d.92.1.11 (A:) MMP-2 {Human (Homo sapiens)}
MYNFFPRKPKWDKNQITYRIIGYTPDLDPETVDDAFARAFQVWSDVTPLRFSRIHDGEADIMINFG
RWEHGDGYPFDGKDLLAHAFAPGTGVGGDSHFDDDELWTNTSANYSLFLVAAHEFGHAMGLEHS
QDPGALMAPIYTYTKNFRLSQDDIKGIQELYG

>d1i76a_d.92.1.11 (A:) Neutrophil collagenase (MMP-8) {Human (Homo sapiens)}
MLTPGNPKWERTNLTYRIRNYTPQLSEAEVERAIKDAFELWSVASPLIFTRISQGEADINIAFYQRDH
GDNSPFDGPNILAHAFQPGQGIGGDAHFDAEETWTNTSANYNLFLVAAHEFGHSLGLAHSSDPGA
LMYPNYAFRETSNYSLPQDDIDGIQAIYG

>d1qiba_d.92.1.11 (A:) Gelatinase A {Human (Homo sapiens)}
RKPKWQDKNQITYRIIGYTPDLDPETVDDAFARAFQVWSDVTPLRFSRIHDGEADIMINFRWEHGD
GYFPDGDGGLLAHAFAPGTGVGGDSHFDDDELWVSLGKGVGYSLFLVAAHEFGHAMGLEHSQDPGAL
MAPIYTYTKNFRLSQDDIKGIQELYGASP

>d1hy7a_d.92.1.11 (A:) Stromelysin-1 (MMP-3) {Human (Homo sapiens), fibroblast}
FRTPFGIPKWRKTHLTYRIVNYTPDLPKDAVDSAVEKALKVWEEVTPLTFSRLYEGEADIMISFAVRE
HGDFYFPDGPVLAHAYAPGPGINGDAHFDDEQWTKDTTGTNLFLVAAHEIGHSLGLFHSANTE
ALMYPLYHSLDLTRFRLSQDDINGIQSLYGGPPP

>d1mmq_d.92.1.11 (-) Matrilysin (MMP-9) {Human (Homo sapiens)}
YSLFPNSPKWTSKVVTYRIVSYTRDLPHITVDRLVSKALNMWGKEIPLHFRKVVWGTADIMIGFARG
AHGDSYFPDGPNTLAHAFAPGTGLGGDAHFDDEDERWTDGSSLGINFLYAATHELGHSLGMGHSSD
PNAVMYPTYGNGDPQNFKLSQDDIKGIQKLYGK

>d1hv5a_d.92.1.11 (A:) Stromelysin-3 (MMP-11) {Mouse (Mus musculus)}
MFVLSGGRWEKTDLTYRILRFPWQVLRQVRQTVAEALQVWSEVTPLTFTFVHEGRADIMIDFARY
WHGDNLPFDGPGGILAHAFPPKTHREGDVHFDYDETWTIGDNQGTDLLQVAAHEFGHVGLGLQHTT
AAKALMSPFYTFRYPLSLSPDDRRGIQHLYG

>d1jk3a_d.92.1.11 (A:) Macrophage elastase (MMP-12) {Human (Homo sapiens)}
GPVWRKHYITYRINNYTPDMNREDVDYAIRKAFQVWSNVTPLKFSKINTGMADILVVFARGAHGDF
HAFDGGKILAHAFGPGSGIGGDAHFDDEDEFWTTTHSGGTNLFLTAVHAIGHSLGLGHSSDPKAVMFP
TYKYVDINTFRLSADDIRGIQSLYG

>d830ca_d.92.1.11 (A:) Collagenase-3 (MMP-13) {Human (Homo sapiens)}
YNVFPRTLKWSKMNLYRIVNYTPDMTHSEVEKAFKAFKFWSDVTPLNFTRLHDGIADIMISFGI
KEHGDFYFPDGPSSLLAHAFPPGPNYGGDAHFDDEDETWTSSSKGYNLFLVAAHEFGHSLGLDHSKD
PGALMFPIYTYTGKSHFMLPDDDDVQGIQSLYGGPGDE

>d1cxva_d.92.1.11 (A:) Collagenase-3 (MMP-13) {Mouse (Mus musculus)}
YNVFPRTLKWSQTNLYRIVNYTPDMTHSEVEKAFKAFKFWSDVTPLNFTRIYDGTADIMISFGT
KEHGDFYFPDGPSSLLAHAFPPGPNYGGDAHFDDEDETWTSSSKGYNLFLVAAHEFGHSLGLDHSKD
PGALMFPIYTYTGKSHFMLPDDDDVQGIQFLYG

>d1bqqm_d.92.1.11 (M:) Membrane-type matrix metalloproteinase (CDMT1-MMP) {Human (Homo sapiens)}
IQGLKWQHNEITFCIQNYTPKVGEYATYEAIRKAFRWESATPLRFREVPYAYIREGHEKQADIMIFF
AEGFHGDSTPFDGEGGFLAHAYFPGPNIGGDTHFDSAEPWTVRNEIDLNGNDIFLVAVHELGHALGL
EHSSDPSAIMAPFYQWMDTENFVLPDDDRRGIQQLYGGES

>d1qba_4 d.92.2.1 (201-337) Bacterial chitinase, Domain 2 {Serratia marcescens}
SNADLQTLPAGALRGKIVTPMVKVHAQDADLRKGVLDLSTLVKPAADVVSQRFALLGVPVQTN
GYPIKTDIQPGKFKGAMAVSGAYELKIGKKEAQVIGFDQAGVIFYGLQSILSLVPSDGSQKIATLDASDA
PR

>d1jaka2 d.92.2.1 (A:8-150) beta-N-acetylhexosaminidase, N-terminal domain {Streptomyces plicatus}
DRKAPVRPTPLDRVIPAPASVDPGGAPYRITRGTHIRVDDREARRVGDYLDLRLPATGYRLPVTAH

GHGGIRLRLAGGPYGDGYRLDSSGAGVTITARKAAGLFHGVQTLRQLLPPAVEKDSAQPGPWLVAG
GTIEDTPR
>d1cwdl_d.93.1.1 (L:) p56-lck tyrosine kinase {Human (Homo sapiens)}
GSWFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNGEVVKHYKIRNLDNGGF
YISPRITFPGLHELVRHYTNASDGLCTRLSR
>d1lka_d.93.1.1 (A:) p56-lck tyrosine kinase {Human (Homo sapiens)}
LEPEPWFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNGEVVKHYKIRNLDN
GGFYISPRITFPGLHELVRHYTNASDGLCTRLSRPCQT
>d1bkl_d.93.1.1 (-) v-src tyrosine kinase {Rous sarcoma virus, Schmidt-ruppin strain a}
EEWYFGKITRRESESLNPNENPRGTFLVRESEETTKGAYCLSVSDFDNAKGLNVKHYKIRKLDSSGGFY
ITSRTQFSSLQQLVAYYSKHADGLCHRLTNVCPTSKEFIVTD
>d1shaa_d.93.1.1 (A:) v-src tyrosine kinase {Rous sarcoma virus, Schmidt-ruppin strain a}
AEEWYFGKITRRESERLLLNPENPRGTFLVRESEETTKGAYCLSVSDFDNAKGLNVKHYKIRKLDSSGG
FYITSRTQFSSLQQLVAYYSKHADGLCHRLTNVCPT
>d1a09a_d.93.1.1 (A:) c-src tyrosine kinase {Human (Homo sapiens)}
DSIQAEWYFGKITRRESERLLLNAENPRGTFLVRESEETTKGAYCLSVSDFDNAKGLNVKHYKIRKLD
SSGGFYITSRTQFNSLQQLVAYYSKHADGLCHRLTTCVCP
>d1g83a2_d.93.1.1 (A:142-245) Tyrosine kinase Fyn {Human (Homo sapiens)}
DSIQAEWYFGKLGKDAERQLLSFGNPRGTFLIRESEETTKGAYSLSIRDWDDMKGDHVKHYKIRKLD
DNGGYITTRAQFETLQQLVQHYSERAAAGLSSRLVVP
>d1ayaa_d.93.1.1 (A:) Tyrosine phosphatase Syp {Mouse (Mus musculus)}
MRRWFHPNITGVEAENLLLTRGVDGSFLARPSKSNPGDFTLSVRRNGAVTHIKIQNTGDYYDLYGGE
KFATLAELVQYYMEHHGQLKEKNGDVIELKYPLN
>d1fhs_d.93.1.1 (-) Growth factor receptor-bound protein 2 (GRB2) {Human (Homo
sapiens)}
GIEMKPHPWFFGKIPRAKAEEMLSKQRHDGAFLIRESEAPGDFSLSVKFGNDVQHFVKVLRDGAGK
YFLWVVKFNSLNELVDYHRSTSVSRNQQIFLRDIEQVPPQPTYVQA
>d1zfpe_d.93.1.1 (E:) Growth factor receptor-bound protein 2 (GRB2) {Human (Homo
sapiens)}
KPHPWFFGKIPRAKAEEMLSKQRHDGAFLIRESEAPGDFSLSVKFGNDVQHFVKVLRDGAGKYFLW
VVKFNSLNELVDYHRSTSVSRNQQIFLRDIEQ
>d1qca2_d.93.1.1 (A:146-248) Hemopoetic cell kinase Hck {Human (Homo sapiens)}
EEWFFKGISRKDAERQLLAPGNMLGSFMIRDSEETTKGSYSLSVRDYDPRQGDVTKHYKIRKLDNGGF
YISPRSTFSTLQELVDHYKKGNDGLCQKLSVPCMSS
>d1mil_d.93.1.1 (-) Shc adaptor protein {Human (Homo sapiens)}
GSQLRGEPWFHGKLSRREAEALLQLNGDFLVRSTTTTPGQYVLTGLQSGQPKHLLLDPEGVVVRTK
DHRFESVSHLISYHMDNHLPIISAGSELCLQQPVERKL
>d1qada_d.93.1.1 (A:) Phosphatidylinositol 3-kinase, p85-alpha subunit {Cow (Bos taurus)}
EDLPHHDEKTWNVGSNNRKAENLLRGKRDGTFLVRESSKQGCYACSVVVDGEVKHCVINKTATGY
GFAEPYNLYSSLKELVLHYQHTSLVQHNSLNVTLAYPVYA
>d1pica_d.93.1.1 (A:) Phosphatidylinositol 3-kinase, p85-alpha subunit {Human (Homo
sapiens)}
GSIPIHHDEKTWNVGSNNRKAENLLRGKRDGTFLVRESSKQGCYACSVVVDGEVKHCVINKTATGY
GFAEPYNLYSSLKELVLHYQHTSLVQHNSLNVTLAYPVYAQQRR

>d1fu6a_ d.93.1.1 (A:) Phosphatidylinositol 3-kinase, p85-alpha subunit {Rat (Rattus norvegicus)}
GMNNNMSLQDAEWYWGDISREEVNEKLRDTADGTFLVRDASTKMHGDYTLTLRKGGNNKSIKIFH
RDGKYGFSDPLTFNSVVELINHRYNESLAQYNPKLDVKLLYPVSKY

>d1ab2_ d.93.1.1 (-) Proto-oncogen tyrosine kinase {Human (Homo sapiens)}
GSGNSLEKHSWYHGPPVSRNAAEYLLSSGINGSFLVRESESSPGQRSISLRYEGRVYHYRINTASDGKLY
VSESRFNTLAELVHHHSTVADGLITTLHYPAPKRGHHRD

>d1a81a1 d.93.1.1 (A:9-137) Syk tyrosine kinase {Human (Homo sapiens)}
SANHLPPFFGNITREEAEDYLVQGGMSDGLYLLRQSRNYLGGFALSVAHGRKAHHTIERELNGTYAI
AGGRTHASPADLCHYHSQESDGLVCLLKKPFNRPPQGVQPKTGPFDLKENLIREYVVKQTNW

>d1a81a2 d.93.1.1 (A:138-262) Syk tyrosine kinase {Human (Homo sapiens)}
LQGQALEQAIISQKPQLEKLIATTAHEKMPWFHGGKISREESEQIVLIGSKTNGKFLIRARDNNGSYALC
LLHEGKVLHYRIDKDKTGKLSIPEGKGFDTLWQLVEHYSYKADGLLRVLTVPQCQKI

>d1a81e1 d.93.1.1 (E:9-117) Syk tyrosine kinase {Human (Homo sapiens)}
SANHLPPFFGNITREEAEDYLVQGGMSDGLYLLRQSRNYLGGFALSVAHGRKAHHTIERELNGTYAI
AGGRTHASPADLCHYHSQESDGLVCLLKKPFNRPPQGVQPKT

>d1a81e2 d.93.1.1 (E:152-262) Syk tyrosine kinase {Human (Homo sapiens)}
PQLEKLIATTAHEKMPWFHGGKISREESEQIVLIGSKTNGKFLIRARDNNGSYALC
LLHEGKVLHYRIDKDKTGKLSIPEGKGFDTLWQLVEHYSYKADGLLRVLTVPQCQKI

>d1csya_ d.93.1.1 (A:) Syk tyrosine kinase {Human (Homo sapiens)}
GSRRASVGSHEKMPWFHGGKISREESEQIVLIGSKTNGKFLIRARDNNGSYALC
LLHEGKVLHYRIDKDKTGKLSIPEGKGFDTLWQLVEHYSYKADGLLRVLTVPQCQKIGTQ

>d2plda_ d.93.1.1 (A:) Phospholipase C-gamma-1 {Cow (Bos taurus)}
GSPGIHESKEWYHASLTRAQAEHMLMRVPRDGAFLVRKRNEPNSYAISFRAEGKIKHCRVQQEGQT
VMLGNSEFDSLVDLISYYEKHPLYRKMMLRYPINEENSS

>d1blk_ d.93.1.1 (-) P55 Blk protein tyrosine kinase {Mouse (Mus musculus)}
GSVAPVETLEVEKWWFRTISRKDAERQLLAPMKNKAGSFLIRESESNKGAFSLVKDITQTQGEVVKHY
KIRSLDNGGYYISPRITFPTLQALVQHYSKKGDLGCQKLTLPVCVLA

>d2abl_2 d.93.1.1 (140-237) Abl tyrosine kinase {Human (Homo sapiens)}
SLEKHSWYHGPPVSRNAAEYLLSSGINGSFLVRESESSPGQRSISLRYEGRVYHYRINTASDGKLYVSS
SRFNTLAELVHHHSTVADGLITTLHYPAP

>d1jwoa_ d.93.1.1 (A:) Csk homologous kinase Chk {Human (Homo sapiens)}
LSLMPWFHGGKISGQEAQQPPEDGLFLVRESARHPGDYVLCVSFGRDVIHYRVLHRDGHHTIDEA
VFFCNLMDMVEHYSKDKGAICTKLVPRPKR

>d1bf5a3 d.93.1.1 (A:569-710) STAT-1 {Human (Homo sapiens)}
LLPLWNDGCIMGFISKERERALLKDQQPGTFLLRFSESSREGAITFTWVERSQNGGEPDFHAVEPYT
KKELSAVTFPDIIRNYKVMMAENIPENPLKYLYPNIDKDHAFGKYYSRGIKTELISVS

>d1bg1a3 d.93.1.1 (A:576-716) STAT3b {Mouse (Mus musculus)}
ILALWNEGYIMGFISKERERAILSTKPPGTFLLRFSSESSKEGGVTFTWVEKDISGSTQIQSVEPYTKQ
LNNMSFAEIIIMGYKIMDATNILVSPVLYLPDIPKEEAFGKYCRPESQEHPEADPGSAAPYLKTKFICV
TPF

>d2cbla3 d.93.1.1 (A:264-351) Cbl {Human (Homo sapiens)}
THPGYMAFLTYDEVKARLQKFIHKPGSYIFRLSCTRLGQWAIGYVTADGNILQTIPHNKPLFQALIDG
FREGFYLPDGRNQNPDLTG

>d2shpa2 d.93.1.1 (A:2-110) Tyrosine phosphatase shp-2 {Human (Homo sapiens)}
KSRWFHPNITGVEAENLLLTRGVDGSFLARPSKSNPGDLTLSVRRNGAVTHIKIQNTGDYYDLYGG
EKFATLAEVLQYYMEHHGQLKEKNGDVIELKYPLNCADPTSE

>d2shpa3 d.93.1.1 (A:111-218) Tyrosine phosphatase shp-2 {Human (Homo sapiens)}
RWFHGHLSGKEAEKLLTEKKGKHSFLVRESQSHPGDFVLSVRTGDDKGESNDGKSKVTHVMIRCQE
LKYDVGGGERFDSLTDLVEHYKKNPMVETLGTVLQKQPLNT

>d1d4ta_ d.93.1.1 (A:) The Xlp protein Sap {Human (Homo sapiens)}
MDAVAVYHGKISRETGEKLLLATGLDGSYLLRDESEVPGVYCLCVLYHGYIYTYRVSQTETGSWSAET
APGVHKRYFRKIKNLISAFQKPDQGIVIPQYYPVEK

>d1spha_ d.94.1.1 (A:) Histidine-containing phosphocarrier protein (HPr) {Bacillus subtilis}
AQKTFKVTADSGIHARPATVLVQTASKYDADVNGKTVNLKDIMGVMSLGIKGAIEITISASGAD
ENDALNALEETMKSEGLGE

>d1ptf_ d.94.1.1 (-) Histidine-containing phosphocarrier protein (HPr) {Enterococcus faecalis}
MEKKEFHIVAETGIHARPATLLVQTASKFNSDINLEYKGSVNLKSIMGVMSLGVGQSDVTITVDGA
DEAEGMAAIVETLQKEGLA

>d1opd_ d.94.1.1 (-) Histidine-containing phosphocarrier protein (HPr) {Escherichia coli}
MFEQEVTTAPNGLHTRPAAQFVKEAKGFTSEITVTSNGKSASAKDLFKLQTLGLTQGTVVTTISAEGE
DEQKAVEHLVKLMAELE

>d1pch_ d.94.1.1 (-) Histidine-containing phosphocarrier protein (HPr) {Mycoplasma capricolum}
AKFSAITDKVGLHARPASVLAKEASKFSSNITHANEKQGNLKSIMNVMAMAIKTGTEITIADGNDA
DQAIQAIKQTMIDTALIQQ

>d1zer_ d.94.1.1 (-) Histidine-containing phosphocarrier protein (HPr) {Staphylococcus aureus}
MEQNSYVIIDETGIHARPATMLVQTASKFDSIQLEYNGKKVNLKSIMGVMSLGVGKDAEITTYADGS
DESDAIQAISDVLSKEGLT

>d1qr5a_ d.94.1.1 (A:) Histidine-containing phosphocarrier protein (HPr) {Staphylococcus carnosus}
MEQQSYTIIDETGIHARPATMLVQTASKFDSIQLEYNGKKVNLKSIMGVMSLGVGKDAEITTYADGS
DEADAIQAITDVLSKEGLTE

>d1k1ca_ d.94.1.1 (A:) Crh, catabolite repression HPr-like protein {Bacillus subtilis}
VQQKVEVRLKTGLQARPAALFVQEANRFTSDVFLEKDGKKNVNAKSIMGLMSLAVSTGTEVTLIAQGE
DEQEALEKLAAYVQEEV

>d1jrma_ d.206.1.1 (A:) Hypothetical protein MTH637 {Archaeon Methanobacterium thermoautotrophicum}
VITMDCLREVGDDLLVNIEVSPASGKFGIPSYNEWKRKRIEVKIHSPQKGANREIIEKFSETFGRDVE
IVSGQKSRQKTIRIQGMGRDLFLKLVSEKFGLEIP

>d1iba_ d.95.1.1 (-) Glucose permease domain IIB {Escherichia coli}
MAPALVAAFVGGKENITNLDACITRLRVSADVSKVDQAGLKKLGAAGVVVAGSGVQAIFGTKSDNLK
TEMDEYIRNFG

>d1af5_ d.95.2.1 (-) DNA endonuclease I-CreI {Chlamydomonas reinhardtii}
KYNKEFLLYLAGFVDGDSIIAQIKPNQSYKFKHQLSLTFQVTQKTQRRWFLGKLVDEIGVGYVRDRG
SVSDYILSEIKPLHNFLTQLQPFLLKQKQANLVLKIIIEQLPLEVCTWVDQIAALNDS

>d1g9za_ d.95.2.1 (A:) DNA endonuclease I-CreI {Chlamydomonas reinhardtii}
NTKYNKEFLLYLAGFVDGDGSIIAQIKPNQSYKFKHQLSLTFQVTQKTQRRWFLLDKLVDEIGVGYVR
DRGSVSDYILSEIKPLHNFLTQLQPFLKQKQANLVLKIIELPSAKESPKFLEVCTWVDQIAALND
SKTRKTTSETVRAVLD

>d1b24a1 d.95.2.1 (A:7-99) I-dmoI {Archaeon Desulfurococcus mobilis}
VSGISAYLLGLIIGDGLYKLYKGNRSEYRVVITQKSENLKQHIAPLMQFLIDELNVKSKIQIVKGDT
RYELRVSSKKLYYYFANMLERIR

>d1b24a2 d.95.2.1 (A:100-179) I-dmoI {Archaeon Desulfurococcus mobilis}
LFNMREQIAFIKGLYVAEGDKTLKRLRIWNKKNKALLEIVSRWLNNLGVNNTIHLDDHRHGYYVVLNIS
LRDRIKFVHTILS

>d1dfaa2 d.95.2.2 (A:181-298) PI-SceI {Baker's yeast (Saccharomyces cerevisiae)}
PILYENDHFFDYMQKSKFHLTIEGPKVLAYLLGLWIGDGLSDRATFSVDSRDTSLMERTVEYAEKLN
CAEYKDRKEPQVAKTVNLYSKVVRGNGIRNNLNTENPLWDAIVGLGFLKD

>d1dfaa3 d.95.2.2 (A:299-415) PI-SceI {Baker's yeast (Saccharomyces cerevisiae)}
GVKNIPSFLSTDNIGTRETFLAGLIDSDGYVTDEHGKATIKTIHTSVRDGLVSLARSLGLVSVNAEPA
KVDMNGTKHKISYAIYMSGGDVLLNVLSKAGSKFRPAPAAFARE

>d1dq3a3 d.95.2.2 (A:129-226) PI-Pfui intein {Archaeon Pyrococcus furiosus}
PDGEDYKFIFDYWLAGFIAGDGCDFKYHSHVKGHEIYDRLRIYDYRIETFEIINDYLEKTFGRKYSIQ
KDRNIYYIDIKARNITSHYKLLLEGIDNG

>d1dq3a4 d.95.2.2 (A:227-335) PI-Pfui intein {Archaeon Pyrococcus furiosus}
IPPQILKEGKNAVLSFIAGLFDAGHVSNNKPGIELGMVNKRLIEDVTHYLNALGIKARIREKLRKDGID
YVLHVEEYSSLLRFYELIGKNLQNEEKREKLEKVLNSNHKG

>d1a8ra_ d.96.1.1 (A:) GTP cyclohydrolase I {Escherichia coli}
PSLSKEAALVHEALVARGLETPLRPPVHEMDNETRKSILAGHMTEIMQLLNDLADDSLMETPHRI
AKMYVDEIFSGLDYANFPKITLIENKMKVDEMVTVRDITLTSTCESHFVTIDGKATVAYIPKDSVIGLS
KINRIVQFFAQRQPQVQERLTQQILIALQTLGTTNNVAVSIDAVHYCVKARGIRDATSATTTTSLGGLFK
SSQNTRHEFLRAVRHHN

>d1is8a_ d.96.1.1 (A:) GTP cyclohydrolase I {Rat (Rattus norvegicus)}
RPRSEEDNELNLPNLAAAYSSILRSLGEDPQRQGLLKPWRAATAMQFFTKGYQETISDVLNDAIFD
EDHDEMIVVKDIDMFSMCEHHLVPFVGRVHIGYLPNKQVLGSLKLARIVEIYSRRLQVQERLTQKQIAV
AITEALQPAGVGVVIEATHMCMVMRGVQKMNSTVTSTMLGVFREDPKTREFLTLIRS

>d1b66a_ d.96.1.2 (A:) 6-pyruvoyl tetrahydropterin synthase {Rat (Rattus norvegicus)}
LRRRARLSRLVSFSASHRLHSPSLSAEENLKVFGKCNNPNGHGHNYKVVVTIHGEIDPVTGMVMNLT
DLKEYMEEAIMKPLDHKNLDDLVPYFADVVSTTENVAVYIWENLQRLLPVGALYKVKVYETDNNIV
VYKGE

>d1dhn_ d.96.1.3 (-) 7,8-dihidroneopterin aldolase {Staphylococcus aureus}
MQDTIFLKGMRFYGYHGALSAENEIGQIFKVDVTLKVDLSEAGRTDNVIDTVHYGEVFEEVKSIMEG
KAVNLEHLAERIANRINSQYNRMETKVRITKENPPPIPGHYDGVGIEIVRENK

>d1b9la_ d.96.1.3 (A:) 7,8-dihidroneopterin triphosphate epimerase {Escherichia coli}
AQPAAIIRIKNLRLRTFIGIKEEEINNRQDIVINVTIHYPADKARTSEDINDALNYRTVTKNIIQHVENN
RFSLLEKLTQDVLDIAREHHWVTYAEVEIDKLHALRYADSVSMTLWQR

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

E

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

>d1puc_ d.97.1.1 (-) suc1 {Fission yeast (*Schizosaccharomyces pombe*)}
SKSGVPRLLTASERERLEPFIDQIHYSPTYADDEYEYRHVMLPKAMLKAIPTDYFNPETGTLRILQEE
EWRGLGITQSLGWEMYEVHVPEPHILLFKREKD

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

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

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

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

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

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

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

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

>d1e3ha6 d.101.1.1 (A:483-578) Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domains 2 and 5 {*Streptomyces antibioticus*}
APVAGIAMGLISQINGETHYVALTDILGAEDAFGDMDFKVAGTKEFVTALQLDTKLDGIPASVLA
LQARDARLHILDVMMEAIDTPDEMSPN

>d1efnb_ d.102.1.1 (B:) Regulatory factor Nef {Human immunodeficiency virus type 1}
RPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQNYTPGPGVRY
LTFGWCYKLVPEPDKVEEANKGENTSLLHPVSLHGMDPPEREVLEWRFDLAFHHVARELHPE
YF

>d2nef_ d.102.1.1 (-) Regulatory factor Nef {Human immunodeficiency virus type 1}
AWLEAQEEEEVGFVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
PDWQNYTPGPGIRYPLTFGWCYKLVPEPEKLEANKDDPPEREVLEWRFDLAFHHMARELHPE

YFKNA

>d1cby_ d.103.1.1 (-) Mosquitocidal delta-endotoxin CytB {*Bacillus thuringiensis*, strain Kyushuensis}

CSAPIIRKPFKHIVLTVPSSDLNFNFTVFYVQPQYINQALHLANAFQGAIPLNLFNFEEKALQIANGI
PNSAIVKTLNQSVIQQTVEISVMVEQLKKIIQEVGLVINSTSFWNSVEATIKGTFNLDLDTQIDEAWIF
WHLSAHNTSYYYNLFISIQNEDTGAVMAVPLAFEVSV DVEKQKVLFFTIKDSARYEVKMKALTLV
QALHSSNAPIVDIFNVNNYLY

>d1seta2 d.104.1.1 (A:111-421) Seryl-tRNA synthetase (SerRS) {*Thermus thermophilus*, strain hb27}

VGGEEANREIKRVGGPPEFSFPPLDHVALMEKNGWWEPRISQVSGRSYALKGDLALYELALLRFAM
DFMARRGFLPMTLPSYAREKAFLGTGHFPAYRDQVWAIAETDLYLTGTAEVVNLALHSGEILPYEAL
PLRYAGYAPAFRSEAGSFGKDVRGLMRVHQFHKVEQYVLTEASLEASDRAFQELLENAEEILRLELPE
YRLVEVATGDMGPGKWRQVDIEVYLPSEGRYRETHSCSALLDWQARRANLRYRDPEGRVRYAYTLN
NTALATPRILAMLENHQLQDGRVRVPQALIPYMGKEVLEPCG

>d1e1oa2 d.104.1.1 (A:161-502) Lysyl-tRNA synthetase (LysRS) {*Escherichia coli*, gene lysU}

DQEVRYRQRYLDLIANDKSRQTFVVRSKILAAIRQFMVARGFMEVETPMMQVIPGGASARPFITHHN
ALDLDMYLRIAPELYLKRLVVGGERVFEINRNFNREGISVRHNPEFTMMELYMAYADYHDLIELTES
LFRTLAQEVLTGTTKVTYGEHVDFDGKPFKLTMR EAIKKYRPETDMADLDFDAKALAESIGITVE
KSWGLGRIVTEIFDEVAEAHLIQPTFITEYPAEVSPLARRNDVNPEITDRFEFFIGGREIGNGFSELND
AEDQAERFQEQVNAKAAGDDEAMFYDEYVTALEYGLPPTAGLGIGIDRMIMLFTNSHTIRDVILFP
AMRP

>d1bbua2 d.104.1.1 (A:161-502) Lysyl-tRNA synthetase (LysRS) {*Escherichia coli*, gene lysS}

DQEARYRQRYLDLISNDESRNTFKVRSQILSGIRQFMVNRGFMEVETPMMQVIPGGAAARPFITHH
NALDLDMYLRIAPELYLKRLVVGGERVFEINRNFNREGISVRHNPEFTMMELYMAYADYKDLIELT
ESLFRTLAQDILGKTEVTYGDVTLDFGKPFKLTMR EAIKKYRPETDMADLDFDSAKAIAESIGIHV
EKSWGLGRIVTEIFEEVAEAHLIQPTFITEYPAEVSPLARRNDVNPEITDRFEFFIGGREIGNGFSELN
DAEDQAQRFLDQVAADAGDDEAMFYDEYVTALEHGLPPTAGLGIGIDRMVMLFTNSHTIRDVIL
FPAMRP

>d1kmma2 d.104.1.1 (A:4-325) Histidyl-tRNA synthetase (HisRS) {*Escherichia coli*}

NIQAIRGMNDYLPGETAIWQRIEGLTKNVLGSYGYSEIRLPIVEQTPLFKRAIGEVTDVVEKEMYTFE
DRNGDSLTLRPEGTAGCVRAGIEHGLLYNQEQRLWYIGPMFRHERPQKGRYRQFHQLGCEVFGLQG
PDIDAELIMLTARWWRALGISEHVTLELNSIGSLEARANYRDALVAFLEQHKEKLEDEDCKRRMYTN
PLRVLDSKNPEVQALLNDAPALGDYLDEESREHFAGLCKLLESAGIAYTVNQRLVRGLDYNNRTVFE
WVTNSLGSQGTVCAGGRYDGLVEQLGGRATPAVGFAMGLERLVLVQAVNPEFKA

>d1qe0a2 d.104.1.1 (A:1-325) Histidyl-tRNA synthetase (HisRS) {*Staphylococcus aureus*}

MIKIPRGTQDILPEDSKKWRYIENQLDELMTFYNYKEIRTPIFESTDLFARGVDSTDVVQKEMYTF
KDKGDRSITLRPEGTA AVVRSYIEHKMQGNPNQPIKLYNGPMFRYERKQKGRYRQFNQFVGEAIGA
ENPSVDAEVLAMVMHIYQSFGKHLKLVINSVGDMSRKEYNEALVKHFEPVIHEFCSDCQSR LH TD
PMRILDCKVDRDKEAIKTAPRITDFLNEESKAYYEQVKAYLDDLGPYTEDPNLVRGLDYHTHTAFEL
MMDNPNYDGAITTLCGGGRYNGLLELLDGPSETGIGFALSIERLLLAL EEEGIELD

>d1h4vb2 d.104.1.1 (B:2-325) Histidyl-tRNA synthetase (HisRS) {*Thermus thermophilus*}

TARAVRGTKDLFGKELRMHQ RIVATARKVLEAAGALELVTPIFEETQVFEKGVGAATDIVRKEMFTF
QDRGGRSLTLRPEGTAAMVRAYLEHGMKVWPQPVRLWMAGPMFRAERPQKGRYRQFHQVNYEAL
GSENPILDAEAVVLLYECLKELGLRRLKVKLSSVGDPEDRARYNAYLREVLSPHREALSEDSKERLEE

NPMRILDSKSERDQALLKELGVRPMLDFLGEEARHLKEVERHLERLSVPYELEPALVRGLDYVVRT
AFEVHHEEIGAQSALGGGGRYDGLSELLGGPRVPGVGFAGFVERVALALEAEGFGLPE
>d1atia2 d.104.1.1 (A:1-394) Glycyl-tRNA synthetase (GlyRS) {Thermus thermophilus}
AASSLDELVALCKRRGFIFQSSEIYGGLQGVDYDGLGVELKNNLKQAWWRRNVYERDDMEGLDAS
VLTHRLVLHYSGHEATFADPMVDNRITKKRYRLDHLLEKEQPEEVLKRLYRAMEVEEENLHALVQAM
MQAPERAGGAMTAAGVLDPASGEPGDWTPPRYFNMMFQDLRGPRGGRGLLAYLRPETAQGIFVNF
KNVLDATSRKLGFGIAQIGKAFRNEITPRNFIFRVREFEQMEIEYFVRPGEDEYWHRYWVEERLKW
WQEMGLSRENLPYQQPPESSAHYAKATVDILYRFPHGSLELEGIAQRDFFDLGSHTKDQEALGITA
RVLRNEHSTQRLAYRDPETGKWFVPIEPSAGVDRGVLALLAEAFTREELPNGEERIVLKLKP
>d1b76a2 d.104.1.1 (A:1-394) Glycyl-tRNA synthetase (GlyRS) {Thermus thermophilus}
AASSLDELVALCKRRGFIFQSSEIYGGLQGVDYDGLGVELKNNLKQAWWRRNVYERDDMEGLDAS
VLTHRLVLHYSGHEATFADPMVDNAKARYWTPPRYFNMMFQDLRGPRGGRGLLAYLRPETAQGF
VNFKNVLDATSRKLGFGIAQIGKAFRNEITPRNFIFRVREFEQMEIEYFVRPGEDEYWHRYWVEERL
KWWQEMGLSRENLPYQQPPESSAHYAKATVDILYRFPHGSLELEGIAQRDFFDLGSHTKDQEALGI
TARVLRNEHSTQRLAYRDPETGKWFVPIEPSAGVDRGVLALLAEAFTREELPNGEERIVLKLKP
>d1qf6a4 d.104.1.1 (A:242-532) Threonyl-tRNA synthetase (ThrRS) {Escherichia coli}
RDHRKIGKQLDLYHMQEEAPGMVFWHNDGWTIFRELEVFRSKLKEYQYQEVKGFMMMDRVLWE
KTGHWDNYKDAMFTTSENREYCIKPMNCPGHVQIFNQGLKSYRDLPLRMAEFGSCHRNEPSGSL
HGLMRVRGFTQDDAHIFCTEEQIRDEVNGCIRLVYDMYSTFGFEKIVVKLSTRPEKRIGSDEMWDRA
EADLAVALEENNIPFEYQLGEGAFYGPKIEFTLYDCLDRAWQCGTVQLDFSLPSRLSASYVGEDNERK
VPVMIHRAILGSMERFIGILTEEFAGF
>d1eova2 d.104.1.1 (A:205-557) Aspartyl-tRNA synthetase (AspRS) {Baker's yeast
{Saccharomyces cerevisiae}}
PILLEDASRSEAEAEAAGLPVVNLDTRLDYRVIDLRTVTNQAIFRIQAGVCELFREYLATKKFTEVHT
PKLLGAPSEGGSSVFVETYFKGKAYLAQSPQFNKQLIVADFERVYEIGPVFRAENSNTHRHMTEFT
GLDMEMAFEEHYHEVLDLTLSELFVIFSELPKRFAHEIELVRKQYPVEEFKLPKDGKMVRLTYKEGIE
MLRAAGKEIGDFEDLSTENEKFLGKLVDRKYDITDFYILDKFPLEIRPFYTMPDPANPKYSNSYDFFM
RGEIILSGAQRIHDHALLQERMKAHGLSPEDPGLKDYCDGFSYGCPPHAGGGIGLERVVMFYLDLKN
IRRASLFPDRPKRLRP
>d1b8aa2 d.104.1.1 (A:104-438) Aspartyl-tRNA synthetase (AspRS) {Archaeon Pyrococcus
kodakaraensis}
PLPLDPTGKVKAEIDLRLNRRFMDLRRPEVMAIFKIRSSVFKAVRDRFFHENGFIHTPKIIATATEG
GTELFPMKYFEEDAFLAESPQLYKEIMMASGLDRVYEIAPIFRAEEHNTTRHLNEAWSIDSEMAFIE
DEEEVMSFLERLVAHAINYVREHNAKELDILNFELEEKPLPFRVSYDKALEILGDLGKEIPWGEDID
TEGERLLGKYMENENAPLYFLYQYPSEAKPFYIMKYDNKPEICRAFDFLEIRGVEISSGGQREHRHD
ILVEQIKEKGLNPESFEFYLKAFRYGMPHGGFGLGAERLIKQMLDLPNIREVILFPRDRRRLTP
>d1c0aa3 d.104.1.1 (A:107-287,A:421-585) Aspartyl-tRNA synthetase (AspRS) {Escherichia
coli}
VLPLDSNHVNTTEEARLKYRYLDLRRPEMAQRLKTRAKITSLVRRFMDDHGFLDIETPMLTKATPEG
ARDYLVP SRVHKGFYALPQSPQLFKQLLMMSGFDRIYQIVKCFRDEDLRADRQPEFTQIDVETSFM
TAPQVREVMALVRHLWLEVKVDLGDFFVMTFAEAERRYGSDKPDLRXDESKWAPLWVIDFPMF
EDDGEGGLTAMHHPFTSPKDMTAAELKAAPENAVANAYDMVINGYEVGGGSVRIHNGDMQQT VFG
ILGINEEQREKFGFLLDALKYGTPPHAGLAFGLDRLTMLLTGTDNIRDVIAFPKTTAAACLMT EAPS
FANPTALAELSIQVVK

>d1g51a3 d.104.1.1 (A:105-294,A:415-580) Aspartyl-tRNA synthetase (AspRS) {Thermus thermophilus}

TPPFPVDAGWRGEEKEASEELRLKYRYLDLRRRRMQENLRLRHRVIKAIWDFLDREGFVQVETPF
LTKSTPEGARDFLVPYRHEPGLFYALPQSPQLFKQMLMVAGLDRYFQIARCFRDEDLRADRQPDFTQ
LDLEMSFVEVEDVLELNERLMAHVFREALGVELPLFPRLSYEEAMERYGSDKPDLRXREGFRFLW
VVDFPLLEWDEEEEAWTYMHHPFTSPHPEDLPLEKDPGRVRALAYDLVLNGVEVGGGSIRIHDPR
LQARVFRLLGIGEEEQREKFGFFLEALEYGAPPHGGIAWGLDRLLALMTGSPSIREVIAFPKNKEGKD
PLTGAPSPVPEEQRLRELGLMVVRP

>d1jca_ d.104.1.1 (A:) Phenyl-tRNA synthetase (PheRS) alpha subunit, PheS {Thermus thermophilus and (Thermus aquaticus)}

RVDVSLPGASLFSGGLHPITLMERELVEIFRALGYQAVEGPEVESEFFNFDALNIPEHHPARDMWD
FWLTGEGFRLEGPLGEEVEGRLLLRTHTSPMQVRYMVAHTPPFRIVVPGRVFRFEQTDATHEAVFH
QLEGLVVGEGIAMAHKGAIELAQALFGPDSKVRFPVYFPFVEPGAQFAVWWPEGGKWLELGGA
GMVHPKVFQAVDAYRERLGLPPAYRGVTGFAFGLGVERLAMLRYGIPDIRYFFGGRLKFLEQFKGVL

>d1jcb5 d.104.1.1 (B:475-681) Phenyl-tRNA synthetase (PheRS) beta subunit, PheT, central domain {Thermus thermophilus (Thermus aquaticus)}

ALPAFFPAPDNRGVEAPYRKEQRLREVLGSGLFQEVYTYSFMDPEDARRFRLDPPRLLLLNPLAPEK
AALRTHLFPGLVRVLKENLDLDRPERALLFEVGRVFREREETHLAGLLFGEGVGLPWAKERLSGYFL
LKGYLEALFARLGLAFRVEAQAFPFLHPGVSGRVLVEGEEVGLGALHPEIAQELELPPVHLFELRLPL
PDKP

>d1hc7a2 d.104.1.1 (A:5-276) Prolyl-tRNA synthetase (ProRS) {Thermus thermophilus}

KGLTPQSQDFSEWYLEVIQKAELADYGPVVRTIVVRPYGYAIWENIQVLDRMFKETGHQNAFYPLF
IPMSFLRKEAEHVEGFSPELAVVTHAGGEELEPLAVRPTSETVIGYMWSKWIRSWRDLPLLNQW
GNVVRWEMRTRPFLRTSEFLWQEGHTAHATREEAEVEVRRMLSIYARLAREYAAIPVIEGLKTEKE
KFAGAVYTTTIEALMKDGKALQAGTSHYLGENTAFARAFDIKFQDRDLQVKYVHTTSWGLSWRFIGAI
MTHGDD

>d1g5ha2 d.104.1.1 (A:41-330) The aaRS-like accessory subunit of mitochondrial polymerase gamma, N-terminal domain {Mouse (Mus musculus)}

EALVDLCRRRHFLSGTPQQLSTAALLSGCHARFGPLGVELRKNLASQWWSSMVVFREQVFAVDSLH
QEPGSSQPRDSAFRLVSPESIREILQDREPSKEQLVAFLENLLKTSGKLRATLLHGALEHYVNCGLDV
NRKLPFGLAQIGVCFHPVSNQTPSSVTRVGEKTEASLVWFTPTRTSSQWLDFWLRHRLWWRK
FAMSPSNFSSADCQDELGRKGSKLYSFPWGKEPIETLWNLGDQELLHTYPGNVSTIQGRDGRKNV
VPCVLSVSGDVDLGLTAYLYDSFQL

>d12asa_ d.104.1.1 (A:) Asparagine synthetase {Escherichia coli}

AYIAKQRQISFVKSHFSRQLEERLGLIEVQAPILSRVGDGTQDNLSGAEKAVQVKVLPDAQFEVVH
SLAKWKRQTLGQHDFSAEGLYTHMKALRPDEDRLSPLHSVYVDQWDWERVMGDGERQFSTLKS
TVEAIWAGIKATEAAVSEEFGLAPFLPDQIHVHSQELLSRYPDLDAKGRERAIKDLGAVFLVGIGGK
LSDGHRHDVRAPDYDDWSTPSELGHAGLNGDILVWNPVLEDAFELSSMGRVADATLKHQALATG
DEDRLLEWHQALLRGEMPQTIGGGIGQSRLTMLLLQLPHIGVQAGVWPAAVRESVPSLL

>d1bia_3 d.104.1.2 (64-270) Biotin repressor/biotin holoenzyme synthetase, catalytic (central) domain {Escherichia coli}

IQLLNAKQILGQLDGGSAVLPVIDSTNQYLLDRIGELKSGDACIAEYQQAGRGRGRKWFSPFGANL
YLSMFWRLEQGPAAIIGLSLVIGIVMAEVLRLKLGADKVRVKWPNDLYLQDRKLAGILVELTGKTGDA
AQVIGAGINMAMRRVEESVVNQGWITLQEAGINLDRNTLAAMLIRELRAALELFEQGLAPYLSR

WEKLDN

>d1qtsa2 d.105.1.1 (A:825-938) Alpa-adaptin AP2, C-terminal subdomain {Mouse (Mus musculus)}

FFQPTEMASQDFQRWKQLSNPQQEVQNIKAKHPMDTEITKAKIIGFGSALLEEVDPNPANFVGA
GIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKDVTVSQRLCELLSEQF

>d1e42a2 d.105.1.1 (A:825-937) Beta2-adaptin AP2, C-terminal subdomain {Human (Homo sapiens)}

LFVEDGKMERQVFLATWKDIPNENELQFIKECHLNADTVSSKLQNNNVYTIAKRNVEGQDMLYQ
SLKLTNGIWILAELRIQPGNPNYTLCLKCRAPEVSQYIYQVYDSILKN

>d1c44a_ d.106.1.1 (A:) Sterol carrier protein 2 (SCP2) {Rabbit (Oryctolagus cuniculus)}

SSAGDGFKANLVFKEIEKKLEEEGEQFVKKIGGIFAFKVKDGGPGGKEATWVVDVKNKGKSVLPNSDK
KADCTITMADSDLLALMTGKMNPQSAFFQGKLGITGNMGLAMKLQNLQLQPGKAKL

>d1ikta_ d.106.1.1 (A:) SCP2-like domain of MFE-2 {Human (Homo sapiens)}

LQSTFVFEEIGRRLKDIGPEVVKKVNAVFEBWHITKGGNIGAKWTIDLKSGSGKVYQGPAGKAADTTII
LSEDEFMEVVLGKLDLPQKAFFSGRLKARGNIMLSQKLQMLKDYAKL

>d1eq6a_ d.107.1.1 (A:) Ran-binding protein mog1p {Baker's yeast (Saccharomyces cerevisiae)}

SMNNKEVELYGGAITTVVPPGFIDASTLREVPDTQEVYVNSRRDEEEFEDGLATNESIIVDLLETVDK
SDLKEAWQFHVEDLTELNGTTKWEALQEDTVQQGTFKFTGLVMEVANKWVGKPDLAQTVVIGVALIR
LTQFDTDVVISINVPLTKEEASQASNKELPARCHAVYQLLQEMVRKFHVVDTSLFA

>d1b87a_ d.108.1.1 (A:) Aminoglycoside 6'-N-acetyltransferase {Enterococcus faecium}

MISEFDRNNPVLKDQLSDLLRLTWPEEYGDSSAEEVEEMMNPERIAVAAVDQDELVGFIGAIPQYGI
TGWELHPLVVESSRRKNQIGTRLVNYLEKEVASRGGITIYLGTDLDLHGTTLSTQTDLYEHTFDKVASI
QNLREHPYEFYKLGKIVGVLPNANGWDPDIWMAKTIIPRPS

>d1bo4a_ d.108.1.1 (A:) Aminoglycoside 3-N-acetyltransferase {Serratia marcescens}

GIIRTCRLGPDQVKSMRAALDLFGREFGDVATYSQHQPDSYLGNNLRSKTFIALAAFDQEAUVGAL
AAYVLPKFEQPRSEIYIDLAVSGEHRROGIATALINLLKHEANALGAYVIYVQADYGGDDPAVALYTKL
G

>d1cm0a_ d.108.1.1 (A:) Histone acetyltransferase domain of P300/CBP associating factor, PCAF {Human (Homo sapiens)}

KVIEFHVVGNLSLQKPNKKILMWLVGLQNVFVSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGI
CFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHDILNFLTAYADEYAIGYFKKQGFSSKEI
KIPKTKYVGYIKDYEGATLMGCELNPRI

>d1ygha_ d.108.1.1 (A:) Catalytic domain of GCN5 histone acetyltransferase {Baker's yeast (Saccharomyces cerevisiae)}

KIEFRVNNNDNTKENMMVLTGLKNIFQKQLPKMPKEYIARLVYDRSHLSMAVIRKPLTVVGGITYRP
FDKREFAEIVFCAISSTEQVRGYGAHLMNHLKDYVRNTSNIKYFLTYADNYAIGYFKKQGFTEITLD
KSIWMGYIKDYEGGTLMQCSMLPRIRYLD

>d1qsta_ d.108.1.1 (A:) Catalytic domain of GCN5 histone acetyltransferase {Tetrahymena thermophila}

LDFDILTNDGTHRMKLLIDLKNIQSRQLPKMPKEYIVKLVFDRHHESMVILKNKQKQVIGGICFRQYK
PQRFAEVAFLAVTANEQVRGYGTRLMNKFCDHMQKQNIYLLTYADNFAIGYFKKQGFTEHRMPQ
EKWKGYIKDYDGGTLMCEYIHPYVDY

>d1qsmas_ d.108.1.1 (A:) Histone acetyltransferase HPA2 {Baker's yeast (Saccharomyces

cerevisiae}}
DNITVRFVTENDKEGWQRLWKSQDFYEVSFDDLDDFNFRFLDPNIKMWAAVAVESSEKIIGM
INFFNHMTTWDFDKKIYINDLYVDENSRVKGAGGKLIQFVYDEADKLGTPSVYWCCTDESNHRAQLL
YVKVGYKAPKILYKRKGY
>d1bob_ d.108.1.1 (-) Histone acetyltransferase HAT1 {Baker's yeast (Saccharomyces
cerevisiae}}
FKPETWTSSANEALRVSVIGENAVQFSPLFTYPIYGDSEKIYGYKDLIIHLAFDSVTFKPYVNVKYSAK
LGDDNIVDVEKKLLSFLPKDDVIVRDEAKWVDCFAERKTHNLSDFEKFVSEYSLNGEEFVYKSSL
VDDFARMHRRVQIFSLLFIEAANYIDETDPSWQIYWLLNKKTKELIGFVTTYKYWHYLGAKSFDE
DIDKKFRAKISQFLIFPPYQNKGHGSCLYEAIQSWLEDKSITEITVEDPNEAFDDLDRDNDIQRRLK
GYDAVFQKHSLSDEFLESSRSLKLEERQFNRLVEMLLLLNNS
>d1fy7a_ d.108.1.1 (A:) Histone acetyltransferase ESA1 {Baker's yeast (Saccharomyces
cerevisiae}}
ARVRNLNRIIMGKYEIEPWYFSPYPIELTDEDFIYIDDFTLQYFGSKKQYERYRKKCTLRHPPGNEIYR
DDYVSFFEIDGRKQRTWCRNLCLLSKFLDHKTLYYDVPFLFYCMTRRDELGHHLVGYFSKEKESA
DGYNVACILTLPQYQRMGYGKLLIEFSYELSKKENKVGSPKPLSDLGLLSYRAYWSDTLITLLVEHQK
EITIDEISSMTSMTTTDLHTAKTLNLRYYKGQHIFLNEDILDYRNRLKAKRRTIDPNRLIWKPP
>d1cjwa_ d.108.1.1 (A:) Serotonin N-acetyltransferase {Sheep (Ovis aries)}
HTLPANEFRCLTPEDAAGVFEIEREAFISVSGNCPLNLDVQHFLLTLCPELSLGFVVEGRLVAFIIGSL
WDEERLTQESLALHRPRGSAHLHALAVHRSFRQQGKGSVLLWRYLHHVGAQPAVRRAVLMCEDA
LVPFYQRFQFHPAGPCAIVVGSLSLTFTEMHCSL
>d1i12a_ d.108.1.1 (A:) Glucosamine-phosphate N-acetyltransferase GNA1 {Baker's yeast
(Saccharomyces cerevisiae}}
LPDGFYIRRMEEGDLEQVTETLKVLTTVGTITPESFCKLIKYWNEATVWVNDNEDKKIMQYNPMVIV
DKRTETVAATGNIIERKIIHELGLCGHIEDIAVNSKYQGQGLGKLLIDQLVTIGFDYGCYKIILDCDEKN
VKFYEKCGFSNAGVEMQIRK
>d1iica1 d.108.1.2 (A:34-218) N-myristoyl transferase, NMT {Baker's yeast (Saccharomyces
cerevisiae}}
AMKDHKFWRTQPVKDFDEKVVVEEGPIDKPKTPEDISDKPLPLSSFEWCSIDVDNKKQLEDVFLVLL
NENYVEDRDAGFRFNKYTEFFNWALKSPGWKDWVHIGVVRVETQKLVAFISAIPVTLGVRGKQVPS
VEINFLCVHKQLRSKRLTPVLIKEITRRVKNKCDIWHALYTAGIVLPAPVSTCR
>d1iica2 d.108.1.2 (A:219-455) N-myristoyl transferase, NMT {Baker's yeast (Saccharomyces
cerevisiae}}
YTHRPLNWKKLYEVDFTGLPDGHTTEEDMIAENALPAKTKTAGLRKLLKEDIDQVFELFKRYQSRFE
LIQIFTKEEFEHNFIGEESLPLDKQVIFSYYVEQPDGKITDFFSFYSLPFTILNNTKYKDLGIGYLYYYAT
DADFQFKDRFDPKATKALKTRLCELIYDACILAKNANMDVFNALTSQDNFLFLDDLKFGPGDGFLN
FYLFNYRAKPITGGLNPDNSNDIKRRSNVGVVML
>d1nmta1 d.108.1.2 (A:60-224) N-myristoyl transferase, NMT {Yeast (Candida albicans)}
EGPIDKLTPEVDPNDPLPLISDFEWSTLDIDDNLQLELYKLLYDNYVEDIDATFRFKYSHEFFQW
ALKPPGWRKDWVHGVVRVSTGKLVAFIAATPVTFKLNKSNKVIDSVEINFLCIHKKLRNRLAPVLI
KEITRRVKNQNIWQALYTGGSILPTPLTTCR
>d1nmta2 d.108.1.2 (A:225-451) N-myristoyl transferase, NMT {Yeast (Candida albicans)}
YQHRPINWSKLDHVGFSHLPPNQTKSSMVASYTLNPNPKLGLRPMTGKDVSTVLSLLYKYQERFDI
VQLFTEEEFKHWMLGHDENSNSNVVKSYYVEDENGIITDYFSYLLPFTVLDNAQHDELGIAYLFY

ASDSFEKPNYKKRLNELITDALITSKKFGVDVFNCLTCQDNTYFLKDCKFGSGDGLNYYLFNYRTFP
MDGGIDKKTKEVVEDQTSIGVLL

>d2vik_ d.109.1.1 (-) Villin, domain 1 (res. 1-126) {Chicken (Gallus gallus)}
VELSKKVTGKLDKTTPIGIQIWRIENMEMVPVPTKSYGNFYEGDCYVLLSTRKTGSGFSYNIHYWLK
NSSQDEQGAAAIYTTQMDEYLGSAVQHVREYVQGHESETFRAVYFKQGLIYKQGGVASGMK

>d1svy_ d.109.1.1 (-) Severin, domain 2 {Dictyostelium discoideum}
EYKPRLLHISGDKNAKVAEVPLATSSLNSGDCFLLDAGLTIYQFNGSKSSPQEKNAAEVARAIDAER
KGLPKVEVFCETDSDIPAEFWKLGGKGAIAAKH

>d1d0na2 d.109.1.1 (A:153-262) Gelsolin {Horse (Equus caballus)}
VPNEVVVQRLQVKRRVVRATEVPPVSWESFNNGDCFILDLGNNIYQWCGSKSNRFRERLQVSK
GIRDNERSGRAQVSVFEEGAEPEAMLQVLGPKPTLPEATEDTVK

>d1d0na3 d.109.1.1 (A:263-383) Gelsolin {Horse (Equus caballus)}
EDAANRKLAKLYKVSNGAGPMVSLVADENPFAQALRSEDCFILDHGKDGKIFVWKGKQANMEER
KAALKTASDFISKMDYPKQTQVSVLPEGGETPLFRQFFKNWRDPDQTEGLGLAYL

>d1d0na4 d.109.1.1 (A:384-532) Gelsolin {Horse (Equus caballus)}
SSHIAHVERVPFDAATLHTSTAMAAQHGMDDGTGQKQIWRVEGSNKVPVDPATYQGQFYGGDSYIIL
YNYRHGSRQGGIYNWQGAQSTQDEVAASAILTAQLDEELGGTPVQSRVVQKKEPAHLMSLFGGKP
MIVYKGGTSREGGQTA

>d1d0na5 d.109.1.1 (A:533-628) Gelsolin {Horse (Equus caballus)}
PASTRLFQVRASSGATRAVEIIPKAGALNSNDAFVLKTPSAAYLWVGAGASEAEKTGAQELLRVLRA
QPVQVAEGSEPDSEALGGKATYRTSP

>d1d0na6 d.109.1.1 (A:629-755) Gelsolin {Horse (Equus caballus)}
RLKDKKMDAHPRLFACSNKIGRFVIEEVPGEFMQEDLATDDVMLLDTWDQVFWVWGKDSQDEE
KTEALTSAKRYIDTDPAHRDRRTPITVVKQGFEPSPVGVWFLGWDDSYWSVDPLDRALAEAA

>d1d4xg_ d.109.1.1 (G:) Gelsolin {Human (Homo sapiens)}
VEHPEFLKAGKEPGLQIWRVEKFDLVPVPTNLYGDFFTGDAYVILKTVQLRNGNLQYDLHYWLGNE
CSQDESGAAAIYTVQLDDYLNGRAVQHVREYVQGFESATFLGYFKSGLKYYKGGVASGFK

>d1db0b1 d.109.1.1 (B:412-532) Gelsolin {Human (Homo sapiens)}
MDDDGTTGQKQIWRIEGSNKVPVDPATYQGQFYGGDSYIILYNYRHGGRQGGIYNWQGAQSTQDEVAA
SAILTAQLDEELGGTPVQSRVVQKKEPAHLMSLFGGKPMIYKGGTSREGGQTA

>d1db0b3 d.109.1.1 (B:629-742) Gelsolin {Human (Homo sapiens)}
RLKDKKMDAHPRLFACSNKIGRFVIEEVPGELMQEDLATDDVMLLDTWDQVFWVWGKDSQDEE
KTEALTSAKRYIETDPANRDRRTPITVVKQGFEPSPVGVWFLGWDDSYWS

>d1kcqa_ d.109.1.1 (A:) Gelsolin {Human (Homo sapiens)}
VVQRLFQVKGRRVVRATEVPPVSWESFNNGDCFILDLGNNIHWCGSNSNRYERLQVSKGIRDN
ERSGRARVHVSEEGTEPEAMLQVLGPKPALPAGTEDTA

>d1f7sa_ d.109.1.2 (A:) Cofilin (actin depolymerizing factor, ADF) {Plant (Arabidopsis
thaliana), ADF1}
ASGMAVHDDCKLRFLELKAKRTHRFIVYKIEEKQKQVVVEKVGQPIQTYEEFAACLPADDECRIYDF
DFVTAENCQKSKIFFIAWCPDIAKVRSKMIYASSKDRFKRELDGIQVELQATDPTE

>d1cfya_ d.109.1.2 (A:) Cofilin (actin depolymerizing factor, ADF) {Baker's yeast
(Saccharomyces cerevisiae)}
VAVADESLTAFNDLKLKGGKYLKFLGLNDAKTEIVVKETSTDPSYDAFLEKLPENDCLYAIYDFEYEIN
GNEGKRSKIVFFTWSPDTAPVRSKMVYASSKDALRRALNGVSTDVQGTDFSEVSYDSVLERVSR

>d1cnua_ d.109.1.2 (A:) Cofilin (actin depolymerizing factor, ADF) {Amoeba (Acanthamoeba castellanii), actophorin}

GIAVSDDCVQKFNELKLGHQHRYVTFKMNASNTEVVVEHVGGPNATYEDFKSQLPERDCRYAIFDY
EFQVDGGQRNKITFILWAPDSAPIKSKMMYTSTKDSIKKKLVGIQVEVQATDAAEISEDAVSERAKGD

>d1hqz1_ d.109.1.2 (1:) Cofilin-like domain of actin-binding protein abp1p {Baker's yeast (Saccharomyces cerevisiae)}

LEPIDYTTTHSREIDAEYLKIVRGSDPDTTWLIISPNAKKEYEPESTGSSFHDFLQLFDETKVQYGLARV
SPPGSDVEKIIIGWCPDSAPLKTRASFAANFAAVANNLFKGYHVQVTARDEDDLLENELLMKISNAA
GA

>d1ak7_ d.109.1.2 (-) Destrin {Human and pig (Homo sapiens) and (Sus scrofa)}

TMITPSSGNSASGVQVADEVCRIFYDMKVRKSTPEEIKRKKAVIFCLSADKKCIIVEEGKEILVGDVG
VTITDPFKHFVGMPEKDCRYALYDASFETKESRKEELMFFLWAPELAPLKSMMIYASSKDAIKKKFQ
GIKHECQANGPEDLNRACIAEKLGGSLIVAFEGCPV

>d1pne_ d.110.1.1 (-) Profilin (actin-binding protein) {Cow (Bos taurus)}

AGWNAYIDNLMADGTCQDAIVGYKDSPSVWAAVPGKTFVNITPAEVGILVGKDRSSFFVNGLTLGG
QKCSVIRDSLLQDGEFTMDLRTKSTGGAPT FNITVTMTAKTLVLLMGKEGVHGGMINKKCYEMASH
LRRSQY

>d1fil_ d.110.1.1 (-) Profilin (actin-binding protein) {Human (Homo sapiens), isoform I}

AGWNAYIDNLMADGTCQDAIVGYKDSPSVWAAVPGKTFVNITPAEVGVLVGKDRSSFFVNGLTLGG
QKCSVIRDSLLQDGEFSMDLRTKSTGGAPT FNVTVTKTDKTLVLLMGKEGVHGGMLINKKCYEMASH
LRRSQY

>d1d1ja_ d.110.1.1 (A:) Profilin (actin-binding protein) {Human (Homo sapiens), isoform II}

AGWQSYVDNLMCDGCCQEAAIVGYCDAYVWAATAGGVFQSITPIEIDMIVGKDRGFFTNGLTLGA
KKCSVIRDSLYVDGCTMDIRTKSQGGEPTYNVAVGRAGRALVIVMGKEGVHGGTLNKKAYELALYL
RRSD

>d1acf_ d.110.1.1 (-) Profilin (actin-binding protein) {Acanthamoeba castellanii}

SWQTYVDTNLVGTGAVTQAAILGLDGNTWATSAGFAVTPAQGTTLAGAFNNADAIRAGGFDLAGVH
YVTLRADDRSIYKGGKSSGVITVKT SKAILVGVYNEKIQPGTAANVVEKLADYLIQGGF

>d1f2ka_ d.110.1.1 (A:) Profilin (actin-binding protein) {Acanthamoeba castellanii}

SWQTYVDTNLVGTGAVTQAIIIGHDGNTWATSAGFAVSPANGAALANAFKDATAIRSNFELAGTRY
VTIRADDRSVYKGGKSGAVITVKT SKAILIGVYNEKIQPGTAANVVEKLADYLIQGGF

>d1ypra_ d.110.1.1 (A:) Profilin (actin-binding protein) {Baker's yeast (Saccharomyces cerevisiae)}

SWQAYTDNLIGTGKVDKAVIYSRAGDAVWATSGGLSLQPNEIGEIVQGFDPAGLQSNGLHIQGGKF
MLLRADDRSIYGRHDAEGVVCVVRTKQTVIIAHYPPTVQAGEATKIVEQLADYLIQGGF

>d1cqa_ d.110.1.1 (-) Profilin (actin-binding protein) {Birch (Betula verrucosa)}

SWQTYVDEHLMCDIDGQGEELAASAVGHDSVWAQSSFPQFKPQEITGIMKDFEEPGHLAPTGL
HLGGIKYMIQGEAGAVIRGKKGGGITIKKTGQALVFGIYEEPVTGQCNMVVERLGDYLIQGL

>d3nul_ d.110.1.1 (-) Profilin (actin-binding protein) {Mouse-ear cress (Arabidopsis thaliana)}

SWQSYVDDHLMCDVEGNHLTAAAILGQDGSVWAQSAKFPQLKPQEIDGIKKDFEEPGFLAPTGLFL
GGEKYMVIQGEQGA VIRGKKGGVTIKKTNQALVFGFYDEPMTGGQC NLVVERLGDYLIQGL

>d1g5ua_ d.110.1.1 (A:) Profilin (actin-binding protein) {Para rubber tree (Hevea brasiliensis), hev8}

SWQTYVDDHLMCDIDGHRLTAAAIIGHDGSVWAQSSSFPQFKSDEVAAMKDFDEPGSLAPTGLHL
GGTKYMIQGEPEGAVIRGKKGSGGITVKRTGQALIIGIYDEPLTPGQCNMIVERLGDYLLDQGL
>d1f5ma_ d.110.2.1 (A:) Hypothetical protein ykl069wp {Baker's yeast (Saccharomyces cerevisiae)}

STGFHHADHVNYSSNLNKEEILEQLLSYEGLSGDQVNWVCNLSNASSLIWHAYKSLAVDINWAGFY
VTQASEENTLILGPFQGVACQMIQFGKVCGTAASTKETQIVPDVVKYPGHIACDGETKSEIVVPIIS
NDGKTLGVIDIDCLDYEGFDHVDKEFLEKLAKLINKSCVF
>d3pyp_ d.110.3.1 (-) Photoactive yellow protein, PYP {Ectothiorhodospira halophila}
MEHVAFGSEDIENLAKMDDGQLDGLAFGAIQLDGDGNILQYNAAEGDITGRDPKQVIGKNFFKDV
APCTDSPEFYGKFKEGVASGNLNTMFEYTFDYQMTPTKVKVHMKKALS GDSYWVFKRV
>d1ew0a_ d.110.3.2 (A:) Histidine kinase FixL heme domain {Rhizobium meliloti}
GSHMLETEDVVRARDAHLRSILDTPDATVVSATDGTIVSFNAAVRQFGYAEVEVIGQNLRLMPE
PYRHEHDGYLQRYMATGEKRIIGIDRVVSGQRKDGSTFPMKLA VGEMRSGGERFFTFGIRDLT
>d1dp6a_ d.110.3.2 (A:) Histidine kinase FixL heme domain {Bradyrhizobium japonicum}
DAMIVIDGHGIIQLFSTAAERLFGWSELEAIGQNVNILMPEPDRSRHDSYISRYRTSDPHIIGRIVT
GKRRDGTTFPMHLSIGEMQSGGEPYFTGFVRDLTEHQQTQARLQEL
>d1bywa_ d.110.3.3 (A:) Erg potassium channel, N-terminal domain {Human (Homo sapiens)}

SRKFIANARVENCAVIYCNDGFCELCGYSRAEVMQRPCTCDFLHGPCTQRRAAAQIAQALLGAEER
KVEIAFYRKDGSCFLCLVDVVPVKNEDGAVIMFILNFEVMEK
>d1g28a_ d.110.3.4 (A:) Photoreceptor phy3 flavin-binding domain, lov2 {Maidenhair fern (Adiantum capillus-veneris)}

KSFVITDPRLPDNIIFASDRFLELTEYTRREEVLGNCRFLQGRGTD RKAVQLIRDAVKEQRDVTVQV
LNYTKGGRAFWNLFHLQVMRDENG DVQYFIGVQQEM
>d1ifqa_ d.110.4.1 (A:) Sec22b {Mouse (Mus musculus)}

SVLLTMIARVADGLPLAASMQEDEQSGRDLQYQSQAQQLFRKLNEQSPTRCTLEAGAMTFHYIIEQ
GVCYLVLCEAAFPKKLAFAYLEDLHSEFDEQH GKVPVTVSRPYSFIEFDTFIQKTKKLYI
>d1h8ma_ d.110.4.1 (A:) Synaptobrevin homolog 1 ykt6 {Baker's yeast (Saccharomyces cerevisiae)}

MRIYYIGVFRSGGEKALELSEVKDLSQFGFFERSSVGQFMFFAETVASRTGAGERQSIEEGNYIGHVY
ARSEGICGLITDKQYPVRPAYTLLNKILDEYLVAHPKEEWADV TETNDALKMKQLD TYISKYQDPSQ
ADA
>d1cfe_ d.111.1.1 (-) Pathogenesis-related protein 1 (PR1) {Tomato (Lycopersicon esculentum), P14a}

QNSPQDY LAVHNDARAQVGVGPM SWDANLASRAQNYANSRAGDCNLIHSGAGENLAKGGDFTGR
AAVQLWVSRPSYNYATNQCVGGKKCRHYTQVVWRNSVRLGCGRARC NNGWWFISCNYDPVGNW
IGQRPY
>d1qnxa_ d.111.1.1 (A:) Insect allergen 5 (AG5) {Yellow jacket (Vespula vulgaris), Ves v 5}

AEAEFNKYCKIKCLKGGVHTACKYGS LKPNCGNKVVVSYGLTKQEKQDILKEHNDFRQKIARGLETR
GNPGPQPPAKNMKNLWVND E LAYVAQVWANQCQYGHDT CRDVAKYQVGQ NVALTGSTAAKYDDP
VKLVKMWEDEVKDYNPKK KFSGNDFLKTGHYTMVWANTKEVGC GSIKYIQEKWHKHLYVCNYG
PSGNFKNEELYQTK
>d1a6ja_ d.112.1.1 (A:) Nitrogen regulatory bacterial protein Ila-ntr {Escherichia coli}

LQLSSVLNRECTRSRVHCQSKKRALEIISELAAKQLSLPPQVVF EAILTREKMGSTGIGNGIAIPHGKL

EEDTLRAVGVFVQLETPIAFDAIDNQPVDLLFALLVPADQTKTHLHTLSLVAKRLADKTICRRLRAAQ
SDEELYQIITDTE

>d1a3aa_d.112.1.1 (A:) Phosphotransferase IIa-mannitol {Escherichia coli}
LFKLGAEINFLGRKAATKEEAIKFAGEQLVKGGYVEPEYVQAMLDREKLTPTYLGESIAVPHGTVEAK
DRVLKTGVVFCQYPEGVRFGEEDDIARLVIGIAARNNEHIQVITSLTNALDDESVIERLAHTTSVDEV
LELLAGRK

>d1hynp_d.112.1.2 (P:) Erythrocyte membrane Band 3 {Human (Homo sapiens)}
KVYVELQELVMDEKNQELRWMEARWVQLEENLGENGAWGRPHLSHLTFWSSLELRRVFTKGTV
LLDLQETSLAGVANQLLDRFIFEDQIRPQDREELLRALLKXSHAGELEALGGVKPAVLTRSGDPSQP
LLPQHSSLETQLFCEQGDGGTEGHSPSGILEKIPPDSEATLVLVGRADFLEQPVLGFVRLQEAAELEAV
ELPVPPIRFLVLLGPEAPHIDYTLGAAATLMSERVFRIDAYMAQSRGELLHSLEGFLDCSLVLPPTD
APSEQALLSLVPVQRELLRRRYQ

>d1mut_d.113.1.1 (-) Nucleoside triphosphate pyrophosphorylase (MutT) {Escherichia coli}
MKKLQIAVGIIRNENNEIFITRRAADAHMANKLEFPGGKIEMGETPEQAVVRELQEEVGITPQHSLF
EKLEYEFPDRHITLWFVWVERWEGEPWGKEGQPGEWMSLVGLNADDFPPANEPVIAKLRKRL

>d1g0sa_d.113.1.1 (A:) ADP-ribose pyrophosphatase {Escherichia coli}
MLKPDNLPVTFGKNDVEIARETLYRGFFSLDLYRFRHRLFNGQMSHEVRREIFERGHAAVLLPFDP
VRDEVVLIQIRIAAYDTSETPWLLEMVAGMIEEGESVEDVARREAIEEAGLIVKRTKPVLSFLASPGG
TSERSSIMVGEVDATTASGIHGLADENEDIRVHVVSREQAYQWVEEGKIDNAASVIALQWLQLHHQA
LKNEWA

>d1jkna_d.113.1.1 (A:) Diadenosine tetraphosphate hydrolase {Narrow-leaved blue lupine (Lupinus angustifolius)}
GPLGSMDSPPEGYRRNVGICLMNNDKKIFAASRLDIPDAWQMPQGGIDEGEDPRNAAIRELREETG
VTSAEVIAEVPYWLTYDFPPKVREKLNQWGSWDWKGQAQKWFLFKFTGQDQEINLLGDGSEKPEFG
EWSWVTPEQLIDLTVFEFKKPVYKEVLSVFAPHL

>d1hx3a_d.113.1.2 (A:) Isopentenyl diphosphate isomerase {Escherichia coli}
EHVILLNAQGVPTGTLEKYAAHTADTRLHLAFSSWLFNAKGQLLVTRRALSCKAWPGVWTVNSVAG
HPQLGESNEDAVIRRCRYELGVEITPPESIYPDFRYRATDPSGIVENEVCPVFAARTTSALQINDDEVM
DYQWCDLADVLHGIDATPWAFSPWMVMQATNREARKRLSAFT

>d1hzta_d.113.1.2 (A:) Isopentenyl diphosphate isomerase {Escherichia coli}
LHLAFSSWLFNAKGQLLVTRRALSCKAWPGVWTVNSVCGHPQLGESNEDAVIRRCRYELGVEITPPES
IYPDFRYRATDPSGIVENEVCPVFAARTTSALQINDDEVMDYQWCDLADVLHGIDATPWAFSPWMV
MQATNREARKRLSAFTQLKL

>d1ush_1 d.114.1.1 (363-550) 5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain {Escherichia coli}
KIGETNGRLEGDRDKVRFVQTNMGRLLILAAQMDRTGADFVMSGGGIRDSIEAGDISYKNVLKVQPF
GNVVVYADMTGKEVIDYLTAVAQMKPDSGAYPQFANVSFVAKDGKLNLDLKIKGEPVDPKTYRMAT
LNFNATGGDGYPRLDNKPgyvntGFIDAEVLKAYIQKSSPLDVSVYEPKGEVSWQ

>d1hrua_d.115.1.1 (A:) Hypothetical protein YrdC {Escherichia coli}
NNLQRDAIAAAIDVLNEERVIAYPTEAVFGVCGDPDSETAVMRLLELKQRPVDKGLILIAANYEQLKP
YIDDTMLTDVQRETIFSRWPGPVTFVFPAPATTPRWLTGRFDSLAVRVTDHPLVVALCQAYGKPLVST
SANLSGLPPCRTVDEVRAQFGAAFPVVPGETGGRLNPSEIRDALTGELFR

>d1g57a_d.115.1.2 (A:) 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase,

RibB {Escherichia coli}

LLSSFQTPFERVENALAAALREGRGVMVLDDRENEGDMIFPAETMTVEQMALTIRHSGSIVCLCIT
EDRRKQLDLPMMVENNTSAYGTGFTVTIEAAEGVTTGVSAAADRITTVRAAIADGAKPSDLNRPQHV
FPLRAQAGGVLTRGGHTEATIDLMTLAGFKPAGVLCELTNDDGTMARAPECIEFANKHNMALVTIED
LVAYRQAHE

>d1dbxa_ d.116.1.1 (A:) Hypothetical protein HI1434 (YbaK homologue) {Haemophilus influenzae}

TPAIDLLKKQKIPFILHTYDHPNNQHFGEAAEKLGDIPNRSFKTLVAENGDQKKLACFVLATAN
MLNLKKAASIGVKKVEMADKDAQKSTGYLVGGISPLGQKKRVKTVINSTALEFETIYVSGGKRGLS
VEIAPQDLAKVLGAFTDIVDE

>d1qqqa_ d.117.1.1 (A:) Thymidylate synthase {Escherichia coli}

MKQYLELMQKVLDEGTQKNDRTGTGTLSEFGHQMRFNLDGFPVLTTRCHLRSIIHELLWFLQGD
TNIAYLHENNVTIWDEWADENGDLGPVYGKQWRAPPTPDGRHIDQITTVLNQLKNDPDSRRIIVS
AWNNGELDKMALAPCHAFFQFYVADGKLSQLYQRSCDVFLGLPFNIASYALLVHMMQAQCDELVG
DFVWTGGDTHLYSNHMDQTHLQLSREPRPLPKLIKRKPESIFDYRFEDFEIEGYDHPGKAPVAI

>d1tsy_ d.117.1.1 (-) Thymidylate synthase {Lactobacillus casei}

MLEQPYLDLAKKVLDEGHFKPDRTHGTYSIFGHQMRFDLSKGFLLTTRKVPFGLIKSELLWFLHG
DTNIRFLQHRNHIWDEWAFKWKVKSDEYHGPDMDFGHRSDKDEFAAVYHEEMAKFDDRVLH
DDAFAAKYGDGLVYGSQWRAPHTSKGDTIDQLGDVIEQIKTHPYSRKLIVSAWNPEDVPTMALPP
CHTLYQFYVNDGKLSLQYQRSADIFLGVFNIASYALLTHLVAHECGLEVGEFIHTFGDAHLYVNHLD
QIKEQLSRTPRPAPTQLNPKHDIFDFDMKDIKLLNYDPYPAIKAPVAV

>d1bkpa_ d.117.1.1 (A:) Thymidylate synthase {Bacillus subtilis}

TQFDKQYNSIIKDIINNGISDEEFDVRTKWDSDGTPAHTLSVISKQMRFDNSEVPILTTRKVAWKTAI
KELLWIWQLKSNVNDLNMGMVHIWDQWKQEDGTIGHAYGFQLGKKNRSLNGEKVDQVDYLLH
QLKNNPSSRRHITMLWNPDELAMALTPCVYETQWYVVKHGKHLHLEVRARSNDMALGNPFNVFQY
NVLQRMIAQVTGYELGEYIFNIGDCHVYTRHIDNLKIQMEREQFEAPELWINPEVKDFYDFTIDDFK
LINYKHGDKLLFEVAV

>d1tis_ d.117.1.1 (-) Thymidylate synthase {Bacteriophage T4}

MKQYQDLIKDIFENGYETDDRTGTGTIALFGSKLRWDLTKGFPAVTTKKLAWKACIAELIWFVLSGST
NVNDLRLIQHDSLIQGKTVDENYENQAKDLGYHSGELGPIYQKQWRDFGGVDQIIEVIDRIKKLPN
DRRQIVSAWNPALPKYMALPPCHMFYQFNVRNGYLDLQWYQRSVDVFLGLPFNIASYATLVHIVAK
MCNLIPGDLIFSGGNTHIYMNHVEQCKEILRREPKELCVLSGLPYKFRYLSTKEQLKYVLKLRPKD
FVLNNYVSHPPKGMMAV

>d1f28a_ d.117.1.1 (A:) Thymidylate synthase {Pneumocystis carinii}

NAEEQQYLNLVQYIINHGEDRPDRGTGTLVSVFAPSPLKFSRLRNKTFPLLTTRKRVFIRGVIEELLWFIR
GETDSLKLRKNIHIWDANGSREYLDISGLTKRQEGDLGPIYGFQWRHFGAEYIDCKTNYIGQGVQDQ
LANIIQKIRTSYDRRLILSAWNPADLEKMALPPCHMFQFYVHIPSNNHRPELSCQLYQRSMDGL
GVPFNIASYALLTCMAIHVCDLDPGDFIHVMGDCHYKDHIEALQQQLTRSPRPFTLSLNRSDIED
FTLDDFNIQNYHPYETIKMKMSI

>d2tsra_ d.117.1.1 (A:) Thymidylate synthase {Rat (Rattus norvegicus)}

QHGELQYLRQVEHIMRCGFKKEDRTGTGTLVSVFGMQARYSLRDEFPLLTTRKRVFVWKGVLEELLWFI
KGSTNAKELSSKGVRIWDANGSRDFLDSLGFSAEQEGDLGPVYGFQWRHFGADYKDMDSYSGQG
VDQLQKVIDTIKTNPDDRRRIIMCAWNPKDLPLMALPPCHALCQFYVNGELSCQLYQRSMDGLGV
PFNIASYALLTYMIAHITGLQPGDFVHTLGDHAIYLNHIEPLKIQLQREPRPFPKLRILRKVETIDDFK

VEDFQIEGYNPHTI

>d1hvya_d.117.1.1 (A:) Thymidylate synthase {Human (Homo sapiens)}

PPHGELQYLGGIQLHILRCGVRKDDRTGTGLSVFGMQARYSLRDEFPLTTKRVFVWKGVLEELLWFI
KGSTNAKELSSKGVKIWDANGSRDFLDSLGFSTREEGDLGPVYGFQWRHFGAEYRDMESDYSQGQV
DQLQRVIDTIKTNPDDRRRIIMCAWNPRDLPLMALPPCHALCQFYVVNSELSCLYQSRSGDMGLGVP
FNIASYALLTYMIAHITGLKPGDFIHTLGDAAHYLNHIEPLKIQQLQREPRPFPKLRILRKVEKIDDFKAE
DFQIEGYNPHTIKMEMAV

>d1b5ea_d.117.1.1 (A:) dCMP hydroxymethylase {Bacteriophage T4}

MISDSMTVEEIRLHLGLALKEKDFVVDKTVGKTIIEIGASFVADEPFIFGALNDEYIQRLEWYKSKSL
FVKDIPGETPKIWQQVASSKGEINSNYGWAIWSEDNYAQYDMCLAELGQNPDSRRGIMYTRPSMQ
FDYNKDGMSDFMCTNTVQYLIRDKKINAVVNMRSNDVVFGRNDYAWQKYVLDKLVSDLNAGDST
RQYKAGSIIWNVGSLHVYSRHFYLVDPHWKGTGETHISKKDY

>d1kq4a_d.207.1.1 (A:) Thy1 homologue {Thermotoga maritima, TM0449}

HMKIDILDKGFVELVDVMGNDSLAVRAARVSFDMGLKDEERDRHLIEYLMKHGHETPFEHIVFTFH
VKAPIFVARQWFRHRIASYNELSGRYSKLSYEFYIPSPERLEGYKTTIPPERVTEKISEIVDKAYRTYLE
LIESGVPREVARIVLPLNLYTRFFWTVNARSLMNFNLNLRADSHAQWEIQYALAIARIFKEKCPWTF
EAFLKYAYKGDIL

>d1lba_d.118.1.1 (-) Bacteriophage T7 lysozyme (Zn amidase) {Bacteriophage T7}

AKQRESTDAIFVHCSATKPSQNVGVREIRQWHKEQGWLDVGYHFIIKRDGTVEAGRDEMAVGS
GYNHNSIGVCLVGGIDDKGFDFANFTPAQMQLSRLSLVTLAKYEGAVLRAHHEVAPKACPSFDLKR
WWEKNELVTSDRG

>d1cyo_d.120.1.1 (-) Cytochrome b5 {Cow (Bos taurus)}

SKAVKYYTLEEIQKHNSKSTWLILHYKVYDLTKFLEEHPGGEEVLREQAGGDATENFEDVGHSTDA
RELSKTFIIGELHPDDRSKIT

>d1f03a_d.120.1.1 (A:) Cytochrome b5 {Cow (Bos taurus)}

AVKYYTLEEIQKHNSKSTWLILHYKVYDLTKFLEEHPGGEEVLRAQAGGDATANFEAVGHSTDARE
LSKTFIIGELHPDDR

>d1aqa_d.120.1.1 (-) Cytochrome b5 {Rat (Rattus norvegicus)}

KYYTLEEIQKHKDSKSTWVILHHKVYDLTKFLEEHPGGEEVLREQAGGDATENFEDVGHSTDAREL
SKTYIIGELHPDDRSKIA

>d1axx_d.120.1.1 (-) Cytochrome b5 {Rat (Rattus norvegicus)}

DKDVKYYTLEEIQKHKDSKSTWVILHHKVYDLTKFLEEHPGGEEVLREQAGGDATENFEDVGHSTD
ARELSKTYIIGELHPDDRSKIAKPSETL

>d1euea_d.120.1.1 (A:) Cytochrome b5 {Rat (Rattus norvegicus)}

DPAVYYRLEEVAKRNTAEETWMVIHGRVYDITRFLSEHPGGEEILLEQAGADATESFEDIGHSPDA
REMLKQYYIGDVHPNDLKP

>d1icca_d.120.1.1 (A:) Cytochrome b5 {Rat (Rattus norvegicus)}

DPAVYYRLEEVAKRNTSEETWMVIHGRVYDLTRFLSEHPGGEEVLREQAGADATESFEDVGHSPD
AREMLKQYYIGDVHPNDLKP

>d1do9a_d.120.1.1 (A:) Cytochrome b5 {Rabbit (Oryctolagus cuniculus)}

DKDVKYYTLEEIKKHNSKSTWLILHHKVYDLTKFLEEHPGGEEVLREQAGGDATENFEDVGHSTD
ARELSKTYIIGELHPDDRSKLSKPMETL

>d1cxya_d.120.1.1 (A:) Cytochrome b558 {Ectothiorhodospira vacuolata}

TLPVFTLEQVAEHHSPDCCWMAIHGKVYDLTPYVNPHPGAGMMLVWCGQESTEAWETKSYGEP

HSSLAARLLQRYLIGTL

>d1ltda2 d.120.1.1 (A:10-97) Flavocytochrome b2, N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

KISPAEVAKHNKPDDCWVINGVYVDLTRFLPNHPGGQDVIKFNAGKDVTAIFEPLHAPNVIDKYIA
PEKKLGPLQGSMPPELVCPPY

>d1soxa2 d.120.1.1 (A:3-93) Sulfite oxidase, N-terminal domain {Chicken (Gallus gallus)}

SYPEYTRREEVGRHRSPEERVVWTHGTDVDFVDFVELHPGGPDKILLAAGGALEPFWALYAVHGEP
HVLELLQYKVGELSPDEAPAAPDA

>d1vcc_ d.121.1.1 (-) Vaccinia DNA topoisomerase I, 9 kDa N-terminal fragment {Vaccinia virus, strain WR}

MRALFYKDGKLFDTNDFLNPVSDDNPAYEVLQHVKIPTHLTLDVWVVEQTWEEALTRLIFVGSDSKG
RRQYFYGKMHV

>d1amw_ d.122.1.1 (-) HSP90 {Baker's yeast (Saccharomyces cerevisiae)}

ASETFEFQAEITQLMSLIINTVYSNKEIFLRELISNASDALDKIRYKSLSDPKQLETEPDLFIRITPKPEQ
KVLEIRDSGIGMTKAELINNLGTIAKSGTKAFMEALSAGADVSMIGQFGVGFYSFLVADRVQVISKSN
DDEQYIWESNAGGSFTVTLDEVNERIGRGTILRLFLKDDQLEYLEEKRIKEVIKRHSEFVAYPIQLVVT
KEVE

>d1byqa_ d.122.1.1 (A:) HSP90 {Human (Homo sapiens)}

PMEEEEVETFAFQAEIAQLMSLIINTFYNSNKEIFLRELISNSSDALDKIRYETLTDPSKLDGSGKELHINL
IPNKQDRTLTIVDTGIGMTKADLINNLGTIAKSGTKAFMEALQAGADISMIGQFGVGFYSAYLVAEKV
TVITKHNDDEQYAWESSAGGSFTVRTDTGEPMGRGTVKILHLKEDQTEYLEERRIKEIVKKHSQFIG
YPITLFVE

>d1ei1a2 d.122.1.2 (A:2-220) DNA gyrase B {Escherichia coli}

SNSSDSSSIKVLKGLDAVRKRPGRMYIGDIDDGTGLHHMVFEVDNAIDEALAGHCKEIIVTIHADNSV
SVQDDGRGIPTGIHPEEGVSAAEVIMTVLHAGGKFDDNSYKVSGLHGVSVVNALSQKLELVIQRE
GKIHRQIYEHGVPQAPLAVTGETEKTGMTVRFWPSLETFTNVTEFEYEILAKRLRELSFLDSGVSIRL
RDKRDGKEDHFHYEG

>d1b63a2 d.122.1.2 (A:-2-216) DNA mismatch repair protein MutL {Escherichia coli}

SHMPIQVLPPQLANQIAAGEVVERPASVVKELVENSLDAGATRIDIIDIERGGAKLIRIRDNGCGIKKDE
LALALARHATSKIASLDDLEAIIISLGRGEALASISSVSRLLTSRTAEQQEAWQAYAEGRDMNVTVKP
AAHPVGTTLLEVLDLFYNTPARRKFLRTEKTEFNHIDEIIRRIALARFDVTINLSHNGKIVRQYRAVPE
GGQKERRLGAIC

>d1bkna2 d.122.1.2 (A:20-216) DNA mismatch repair protein MutL {Escherichia coli}

VERPASVVKELVENSLDAGATRIDIIDIERGGAKLIRIRDNGCGIKKDELALALARHATSKIASLDDLEAI
ISLGRGEALASISSVSRLLTSRTAEQQEAWQAYAEGRDMNVTVKPAAHPVGTTLLEVLDLFYNTPAR
RKFLRTEKTEFNHIDEIIRRIALARFDVTINLSHNGKIVRQYRAVPEGGQKERRLGAIC

>d1h7sa2 d.122.1.2 (A:29-231) DNA mismatch repair protein PMS2 {Human (Homo sapiens)}

GQVVLSTAVKELVENSLDAGATNIDLKLDYGVDLIEVSDNGCGVEEENFEGLTLKHHTSKIQEFA
DLTQVETFGFRGEALSSLCALSDVTISTCHASAKVGTMLFMDHNGKIIKTPYPRPRGTTVSVQQLFS
TLPVRHKEFQRNIKKEYAKMVQVLHAYCIISAGIRVSNQNLGQGRQPVVCTGGSPSIKENIGSVF

>d1bxda_ d.122.1.3 (A:) Histidine kinase domain of the osmosensor EnvZ {Escherichia coli}

TGQEMPMEMADLNAVLGEVIAAESGYEREIETALYPGSIEVKMHPLSIKRAVANMVVNAARYGNGW
IKVSSGTEPNRAWFQVEDDGPAGIAPEQRKHLFQPFVRGDSARTISGTGLGLAIVQRIVDNHNGMLEL

GTSERGGLSIRAWLPVPVTRAQGTKEG

>d1i58a_d.122.1.3 (A:) Histidine kinase CheA {*Thermotoga maritima*}

GSHMVPISFVFNFRPMVRDLAKKMNKEVNFIMRGEDTELDRTFVEEIGEPLHLLRNAIDHGIEP
KEERIAKGGKPPIGTLILSARHEGNNVVIEVEDDGRGIDKEKIIRKAIEKGLIDESKAATLSDQEILNFLF
VPGFSTKEKVSEVSGRGGVMDVVKNVVESSLNGSISIESEKDKGKVTIRLPLT

>d1id0a_d.122.1.3 (A:) Histidine kinase PhoQ domain {*Escherichia coli*}

RELHPVAPLLDNLTSALNKVYQRKGVNISLDISPEISFVGEQNDFVEVMGNVLDNACKYCLEFVEISA
RQTDEHLYIVVEDDGGPIPLSKREVIFDRGQRVDTLRPGQGVGLAVAREITEQYEGKIVAGESMLGGA
RMEVIFGRQH

>d1gkza2_d.122.1.4 (A:186-378) Branched-chain alpha-ketoacid dehydrogenase kinase (BCK)
{*Rat (Rattus norvegicus)*}

DFVGHICTRLSPKKIIEKWVDFARRLCEHKYGNAPVRVINGHVAARFPFIPMPLDYILPELLKNAMRA
TMESHLDTPYNVPDVVITIANNDVDLIIRISDRGGGIAHKDLDRVMDYHFTTAEASTQDPRISPLFGH
LDMHSGGQSGPMHGFGLPSTRAYAAYLGGSLQLQSLQIGITDVYLRRLRHIDGREE

>d1jm6a2_d.122.1.4 (A:1177-1366) Pyruvate dehydrogenase kinase {*Rat (Rattus norvegicus)*,
isozyme 2}

PKHIGSIDPNCVSDVVKDAYDMAKLLCDKYYMASPDLEIQEVNATNATQPIHMVYVPSHLYHMLFE
LFKNAMRATVESHESSLTPPIKIMVALGEEDLSIKMSDRGGGVPLRKIERLFSYMYSTAPTQPGTG
GTPLAGFGYGLPISRLYAKYFQDGLQFMEGFGTDAVIYKALSTDSVERLPVY

>d1ixma_d.123.1.1 (A:) Sporulation response regulatory protein Spo0B {*Bacillus subtilis*}

SDTALTNELIHLLGHSRHDWMNKLQLIKGNLSLQKYDRVFEMIEEMVIDAKHESKLSNLKTPHLAF
DFLTFNWKTHYMTLEYEVLGEIKDLSAYDQKLAKLMRKLHFLFDQAVSRESENHLTVSLQTDHPDR
QLILYLDHFHGAFAFDDIRQNGYEDVDIMRFEITSHECLIEIGL

>d1bola_d.124.1.1 (A:) Ribonuclease Rh {*Rhizopus niveus*}

SSCSSTALSCSNSANSNTCCSPEYGLVVLNMQWAPGYGPDNAFTLHGLWPKCSGAYAPSGGCDNSR
ASSIASVIKSKDSSLYNMMLTYWPSNQGNNNVFWSHEWSKHGTCVSTYDPCYDNYEEGEDIVDYF
QKAMDLSQYVNYKAFSSNGITPGGTYTATEMQSAIESYFGAKAKIDCSSGTLSDVALYFYVRGRDITY
VITDALSTGSCSGDVEYPTK

>d1bk7a_d.124.1.1 (A:) Ribonuclease MC1 {*Bitter melon (Momordica charantia)*}

FDSFWFVQWPPAVCSFQKSGSCPGSLRFTTIHGLWPPQSGTSLTNCPSGPFIDITKISHLQSQLNTL
WPNVLRANNQQFWSHEWTKHGTCSESTFNQAAYFKLAVDMRNNYDIIGALRPHAAGPNGRTKSR
QAIKGFLLKAKFGKFPGLRCRTDPQTKVSYLVQVACFAQDGSSTLIDCTRDTGANFIF

>d1dixa_d.124.1.1 (A:) RNase LE {*Tomato (Lycopersicon esculentum)*}

ASGSKDFDFYFVQWPGSYCDTKQSCCYPTTGKPAADFGIHGLWPNNDGTYPNSCDPNSPYDQS
QISDLISSMQNWPTLACPSGSGSTFWSHEWEKHGTCAESVLTNQHAYFKKALDLKNQIDLLSILQG
ADIHPDGESYDLVNIRNAIKSAIGYTPWICQNVQSGNSQLYQVYICVDGSGSSLIECFIPGGKCGTSI
EFPTF

>d1iqqa_d.124.1.1 (A:) S3-RNase {*Japanese pear (Pyrus pyrifolia)*}

YDYFQFTQQYLAVCNSNRTLCKDPPDKLFTVHGLWPSNMVGPDPKCPKIKNIRKREKLEHQLI
WPNVFDRTKNNLFWDKWEMKHGSCGYPTIDNENHYFETVIKMYISKKQNVSRILSKAKIEPDGKK
RALLDIENAIRNGADNKKPKLKCQKKGTTTELVEITLCSKSGEHFIDCPHPFEPISPHYCPTNNIKY

>d1g2ra_d.192.1.1 (A:) Hypothetical cytosolic protein SP0554 {*Streptococcus pneumoniae*}

RKIPLRKS SVSNEVIDKRDLRIVKNKEGQVFIDPTGKANGRGAYIKLDNAEAEAKKKKVFNRFS
MEVEESFYDELIAYVDHKVKRRELGLE

>d1c4ka3 d.125.1.1 (A:570-730) Ornithine decarboxylase C-terminal domain {Lactobacillus sp., strain 30a}

APLKQVLPISIYAANEERYNGYTIRELCQELHDFYKNNNTFTYQKRLFLREFFPEQGMLPYEARQEFIR
NHNKLVPLNKIEGEIALEGALPYPPGVFCVAPGEKWSETAVKYFTILQDGINNFPGFAPEIQGVYFKQ
EGDKVVAYGEVYDAEVAKNDDRYNN

>d1g61a_ d.126.1.1 (A:) Ribosome anti-association factor eIF6 (aIF6) {Archaeon Methanococcus jannaschii}

MIIRKYFSGIPTIGVLALTTEEITLLPIFLDKDDVNEVSEVLETKCLQTNIGGSSLVGSLSVANKYGLLLP
KIVEDEELDRIKNFLKENNLDLNVEIIKSKNTALGNLILTNDKGALISPELKDFKKDIEDSLNVEVEIG
TIAELPTVGSNAVVTNKGCLTHPLVEDDELEFLKSLFKVEYIGKGTANKGTTSVGACIIANSKGAVVGG
DTTGPELLIIEDALGL

>d1g62a_ d.126.1.1 (A:) Ribosome anti-association factor eIF6 (aIF6) {Baker's yeast (Saccharomyces cerevisiae)}

MATRTQFENSNEIGVFSKLTNTYCLVAVGGSENFYSAFEAELGDAIPIVHTTIAGTRIIGRMTAGNRRG
LLVPTQTTDQELQHLRNSLPDSVKIQRVEERLSALGNVICCNDYVALVHPDIDRETEELISDVLGVEV
FRQTISGNILVGSYCSLSNQGLVHPQTSVQDQEELSSLLQVPLVAGTVNRGSSVVGAGMVVNDYLAV
TGLDTTAPELSVIESIFRL

>d1jdw_ d.126.1.2 (-) L-arginine: glycine amidinotransferase {Human (Homo sapiens)}

CPVSSYNEWDPLEEVIVGRAENACVPPFTIEVKANTYEKYWPFYQKQGGHYFPKDHLKKAIAEIEE
MCNILKTEGVTVRRPDPIDWSLKYKTPDFESTGLYSAMPRDILIVVGNEIIEAPMAWRSRFFEYRAYR
SIIKDYFHRGAKWTTAPKPTMADELYNQDYPIHSVEDRHKLAAQKQFVTTTEFEPFCDAADFIRAGR
DIFAQRSQVTNYLGIEWMRRHLAPDYRVHISFKDPNPMHIDATFNIIGPVLVSNPDRPCHQIDLK
KAGWTIITPPTPIIPDDHPLWMSKWLMSMNVLMLEKRVMDANEVPIQKMFELGITTIKVNIRN
ANSLGGGFHCWTCVRRRGTLQSYLD

>d1bwda_ d.126.1.2 (A:) L-arginine: inosamine-phosphate amidinotransferase {Streptomyces griseus}

RSLSVHNEWDPLEEVIVGTAVGARVPTADRSVFAVEYAGDYESQEQIPSGAYPDRVLKETEEELHVL
AAELTKLGVTVRRPGRDHSALIKTPDWETDGFHDYCPDRGLLSVGQTIIETPMALRSRFLSLAYK
DLLLEYFASGSRWLSAPKPRLTDDSYAPQAPAGERLTDEEPVFDAANVLRFGTDLLYLVSDSGNELGA
KWLQSAVGDTYTVHPCRKLYASTHV DSTIVPLRPLVLTNPSRVNDENMPDFLRSWENITCPELVDI
GFTGDKPHCSVWIGMNLVVRPDLAVVDRRQTALIRLLEKHGMNVLPQLTHSRTLGGGFHCATLD
VRRTGALETYQF

>d1h70a_ d.126.1.3 (A:) Dimethylarginine dimethylaminohydrolase DDAH {Pseudomonas aeruginosa}

FMFKHIIARTPARSLVDGLTSSHLGKPDYAKALEQHNAYIRALQTCDVDITLLPPDERFPDSVFVEDP
VLCTSRCAITRPGAESRRGETEIIETVQRFYPGKVERIEAPGTVEAGDIMMVGDFHYIGESARTNAE
GARQMIAILEKHGLSGSVVRLEKVLHLKTGLAYLEHNNLLAAGEFVSKPEFQDFNIIPEEESYAANC
IWNERNVIMPAGYPRTREKIARLGYRVIEVDTSEYRKIDGGVSSMSLRF

>d1chma2 d.127.1.1 (A:157-402) Creatinase, catalytic (C-terminal) domain {Pseudomonas putida}

MIKSAEEHVMIRHGARIADIGGAAVVEALGDQVPEYEVALHATQAMVRAIADTFEDVELMDTWTW
FQSGINTDGAHNPVTRKVNKGDILSLNCFPMIAGYYTALERTLFLDHCSDHLRLWQVNVEVHEA
GLKLIKPGARCSDIARELNEIFLKHDLVLYRFTFGYGHSGFTLSHYYGREAGLELREDIDTVLEPGMVV
SMEPMIMLPEGLPGAGGYREHDILIVNENGAENITKFPYGPKEKNIIR

>d1c22a_d.127.1.1 (A:) Methionine aminopeptidase {Escherichia coli}
 AISIKTPEDIEKMRVAGRLAAEVLEMIPEYVKPGVSTGELDRICNDYIVNEQHAVSACLGYHGYPKSVC
 ISINEVVCHGIPDDAKLLKDGDIVNIDVTVIKDGFGHGDTSKMFIVGKPTIMGERLCRITQESLYLALRM
 VKPGINLREIGAAIQKFVEAEGFSVVREYCGHGIGQGFHEEPQVLHYDSRETNVVLKPGMTFTIEMP
 VNAGKKEIRTMKDGWTVKTKDRSLSAQYEHTIVVTDNGCEILTLRKDDTIPAIISHD

>d1xgsa2 d.127.1.1 (A:1-194,A:272-295) Methionine aminopeptidase {Archaeon Pyrococcus
 furiosus}
 MDTEKLMKAGEIAKKVREKAIKLARPGMLLELAESIEKMIMELGGKPAFPVNLISINEIAAHYTPYK
 GDTTVLKEGDYLIKIDVGVHIDGFIADTAVTVRVGMEDELMEAAKEALNAAISVARAGVEIKELGKAI
 ENEIRKRGFKPIVNLSGHKIERYKLHAGISIPNIYRPHDNYVLKEGDVFAIEPFATIGAXRNGIVAQFEH
 TIIVEKDSVIVTTE

>d1b6a_2 d.127.1.1 (110-374,449-478) Methionine aminopeptidase {Human (Homo
 sapiens)}
 KVQTDPPSPVICDLYPNGVFPKGQECEYPPTQDGRATAAWRTTSEEKKALDQASEEIWNDFREAAEA
 HRQVRKYVMSWIKPGMTMIEICEKLEDCSRKLIKENGLNAGLAFPTGCSLNNCAAHYTPNAGDTTV
 LQYDDICKIDFGTHISGRIIDCAFTVTFNPKYDTLLKAVKDATNTGIKCAGIDVRLCDVGEAIQEVMS
 YEVEIDGKTYQVKPIRNLNGHSIGQYRIHAGKTVPIVKGGEATRMEEGEVYAIETFGSTGKGVVXDIKG
 SYTAQFEHTILLRPTCKEVVSRGDDY

>d1az9_2 d.127.1.1 (177-440) Aminopeptidase P, C-terminal domain {Escherichia coli}
 SPEEIAVLRAGEITAMAHTAMEKCRPGMFEYHLEGEIHHEFNHRHGARYPSYNTIVGSGENGCILH
 YTENECEMRDGLDLIDAGCEYKGYAGDITRTFPVNGKFTQAQREIYDIVLESLETSLRLYRPGTSILE
 VTGEVVRIMVSGLVKLGILKGDVDELIAQNAHRPFFMHGLSHWLGLDVHDVGVYQDRSRILEPGM
 VLTVEPGLYIAPDAEVEPQYRIGIRIEDDIVITETGNENLTASVVKKPEEIEALMVAARKQ

>d1f52a2 d.128.1.1 (A:101-468) Glutamine synthetase, C-terminal domain {Salmonella
 typhimurium}
 DRDPRSIakraedyLRATGIADTVLFGPEPEFFLDDIRFGASISGSHVAIDDIEGAWNSSTKYEGGNK
 GHRPGVKGgyFPVPPVDSAQDIRSEMCLVMEQMGLVVEAHHHEVATAGQNEVATRFNTMTKKADE
 IQIYKYVHNVAHRFGKTATFMPKPMFGDNGSGMHCHMSLAKNGTNLFSGDKYAGLSEQALYYIGG
 VIKHAKAINALANPTTNSYKRLVPGYEAPVMLAYSARNRSASIRIPVVASPKARRIEVRFDPANPY
 LCFAALLMAGLDGIKNKIHPGEPMDKNLYDLPPEEAKEIPQVAGSLEEALNALDLDFLAKAGGVFT
 DEAIDAYIALRREEDDRVRMTPHPVEFELYYSV

>d1crka2 d.128.1.2 (A:99-380) Creatine kinase, C-terminal domain {Chicken (Gallus gallus),
 mitochondria}
 TMKHHTDLdaskithGQFDERYVLSSRVRTGRSIRGLSLPPACSRaerrevenVVVTALAGLKGdLS
 GKYYSLTNMSERDQQQLIDDHFLFDKPVSPLLTCAGMARDWPDARGIWHNNDKTFLVWINEEDHT
 RVISMEKGGNMKRVERFCRGLKEVERLIKERGWefmWNERLGYVLTCPNLGTGLRAGVHVKLPR
 LSKDPRFPKILENRLQKRGTGGVDTAADVYDISNLDRMGRSEVELVQIVIDGVNYLVDCEKKLEK
 GQDIKVPPLPQFGRK

>d1qh4a2 d.128.1.2 (A:103-381) Creatine kinase, C-terminal domain {Chicken (Gallus
 gallus), brain-type}
 TDEHKTDLNADNLQGGDDLDPNYVLSSRVRTGRSIRGFCLPPHCSRGERRAIEKLSVEALGSLGGDL
 KGKYYALRNMTDAEQQLIDDHFLFDKPVSPLLLASGMARDWPDARGIWHNNDKTFLVWINEED
 HLRVISMQKGGNMKEVFRFCTGLTQIETLFKSKNYEFMWNPHLGYILTCPNLGTGLRAGVHIKLP
 NLGKHEKFGEVLKRLRLQKRGTGGVDTAAVGGVFDVSNADRLGFSEVELVQMVVDGVKLLIEMEKR

LEKGSIDDLMPAQK

>d1qk1a2 d.128.1.2 (A:103-379) Creatine kinase, C-terminal domain {Human (Homo sapiens), mitochondria}

TTDLDASKIRSGYFDERYVLSRVRTGRSIRGLSLPPACTRAERREVERVVVDALSGLKGDLAGRYRRL
SEMTEAEQQQLIDDHFLFDKPVSPLLTAAGMARDWPDARGIWHNNEKSFLIWWNEEDHTRVISME
KGGNMKRVFERFCRGLKEVERLIQERGWEFMWNERLGYILTCPSNLGTGLRAGVHIKPLLSKDSRF
PKILENRLQKRGTGGVDTAATGGVDFDISNLDRLGKSEVELVQLVIDGVNYLIDCERRLERGQDIRIPT
PVIHTKH

>d2crka2 d.128.1.2 (A:103-381) Creatine kinase, C-terminal domain {Rabbit (Oryctolagus cuniculus)}

TDKHKTDLHNENLKGDDLDPHYVLSRVRTGRSIKGYTLPPHCSRGERRAVEKLSVEALNSLTGEF
KGGYYPKSMTEQEQQQLIDDHFLFDKPVSPLLLASGMARDWPDARGIWHNDNKSFLVWVNEED
HLRVISMEKGGNMKEVFRRCVGLQKIEEIFKAGHPFMWNEHLGYVLTCPNSLGTGLRGGVHVKL
AHLKHPKFEEILTRLRLQKRGTSVFDTAAVGSVDFDISNADRLGSSEVEVQVLVVDGVKLMVEMEKK
LEKGSIDDMIPAQK

>d1g0wa2 d.128.1.2 (A:103-381) Creatine kinase, C-terminal domain {Cow (Bos taurus), retinal isoform}

TDEHKTDLNPDLNQGDDLDPNYVLSRVRTGRSIRGFCLPPHCSRGERRAIEKLAVEALSSLDGDL
AGRYYALKSMTEAEQQQLIDDHFLFDKPVSPLLLASGMARDWPDARGIWHNDNKTFLVWVNEEDH
LRVISMQKGGNMKEVFRFCNGLTQIETLFKSKNYEFMWNPGLGYILTCPSNLGTGLRAGVHIKPLPH
LGKHEKFSEVLKRLRLQKRGTGGVDTAAVGSVDFVSNADRLGFSEVELVQMVVDGVKLLIEMEQL
EQGQAIDDLMPAQK

>d1bg0_2 d.128.1.2 (96-357) Arginine kinase {Horseshoe crab (Limulus polyphemus)}

TDKHPPKQWGDINTLVGLDPAGQFIISTRVRCGRSLQGYFPNCLTAEQYKEMEEKVSTLSSMEDEL
KGTYYPLTGMSKATQQQLIDDHFLFKEGDRFLQTANACRYWPTGRGIFHNDAKTFLVWVNEEDHL
RIISMQKGGDLKTVYKRLVTAVDNIESKLPFSHDDRFGLTFCPTNLGTTMRASVHIQLPKLAKDRKV
LEDIASFNLQVRGTRGEHTESEGGVYDISNKRRLGLTEYQAVREMQRDQILEMIKMEKAAA

>d1cdwa1 d.129.1.1 (A:155-252) TATA-box binding protein (TBP), C-terminal domain {Human (Homo sapiens)}

SGIVPQLQNIIVSTVNLGCKLDLKTIALRARNAEYNPKRFAAVIMRIREPRTTALIFSSGKMVCTGAKSE
ENSRLAARKYARVVQKLGFPKFLDFKI

>d1cdwa2 d.129.1.1 (A:253-333) TATA-box binding protein (TBP), C-terminal domain {Human (Homo sapiens)}

NMVGSCDVKFPIRLEGLVLTHQQFSSYEPELFPGLIYRMIKPRIVLLIFVSGKVLTGAKVRAEIYEAFE
NIYPILKGF

>d1qnaa1 d.129.1.1 (A:17-115) TATA-box binding protein (TBP), C-terminal domain {Arabidopsis thaliana}

HPSGIVPTLQNIIVSTVNLDCCKLDLKAIALQARNAEYNPKRFAAVIMRIREPKTTALIFASGKMVCTGA
KSEDFSKMAARKYARIVQKLGFPKFKDFKI

>d1qnaa2 d.129.1.1 (A:116-198) TATA-box binding protein (TBP), C-terminal domain {Arabidopsis thaliana}

QNIVGSCDVKFPIRLEGLAYSHAAFSSYEPELFPGLIYRMKVPKIVLLIFVSGKIVITGAKMRDETYKAF
ENIYPVLSEFRKI

>d1ytba1 d.129.1.1 (A:61-155) TATA-box binding protein (TBP), C-terminal domain {Baker's

yeast (*Saccharomyces cerevisiae*)
SGIVPTLQNIIVATVTLGCRLDLKTVALHARNAEYNPKRFAAVIMRIREPKTTALIFASGKMOVVTGAKS
EDDSKLASRKYARIIQKIGFAAKFTDF
>d1ytba2 d.129.1.1 (A:156-240) TATA-box binding protein (TBP), C-terminal domain
{*Baker's yeast (Saccharomyces cerevisiae)*}
KIQNIIVGSCDVKFPFIRLEGLAFSHGTFSSYEPELFPGLIYRMVVKPKIVLLIFVSGKIVLTGAKQREEIYQA
FEAIYPVLSEFRKM
>d1aisa1 d.129.1.1 (A:1-92) TATA-box binding protein (TBP), C-terminal domain {*Archaeon
Pyrococcus woesei*}
MVDMSKVKLRIENIVASVDLFAQLDLEKVLDLCPNSKYNPEEFPGIICHLDDPKVALLIFSSGKLVVTG
AKSVQDIERAVAKLAQKLKLSIGV
>d1aisa2 d.129.1.1 (A:93-181) TATA-box binding protein (TBP), C-terminal domain
{*Archaeon Pyrococcus woesei*}
KFKRAPQIDVQNMVFSGDIGREFNLDVVALTLPNCEYEPEQFPGVIYRVKEPKSVILLFSSGKIVCSGA
KSEADAWEA VRKLLRELDKY
>d1mpga2 d.129.1.2 (A:1-99) 3-Methyladenine DNA glycosylase II (gene *alkA* or *aidA*)
{*Escherichia coli*}
MYTLNWQPPYDWSWMLGFLAARAVSSVETVADSYARSLAVGEYRGVVT AIPDIARHTLHINLSAG
LEPVAAECLAKMSRFLDLQCNPQIVNGALGRLG
>d1ko9a2 d.129.1.2 (A:12-135) 8-oxoguanine glycosylase {*Human (Homo sapiens)*}
GHRTLASTPALWASIPCPRSELRLDLVLPSPGQSFWRREQSPAHWGVLADQVWTLTQTTEEQLHCTV
YRGDKSQASRPTPDELEAVRKYFQLDVTLAQLYHHWGSVDSHFQEVAKFKQGVRLLRQ
>d1f46a_d.129.4.1 (A:) Cell-division protein ZipA, C-terminal domain {*Escherichia coli*}
RKEAVIIMNVAHHGSELNGELLNSIQAGFIFGDMNIYHRHLSPDGSGPALFSLANMVKPGTFDP
EMKDFTTPGVTIFMQVPSYGDELQLFKLMLQSAQHIADEVGGVVLDDQRRMMTPQKLREYQDIIRE
VKDANA
>d3pmga4 d.129.2.1 (A:421-561) Phosphoglucomutase {*Rabbit (Oryctolagus cuniculus)*}
RNFFTRYDYEEVEAEGATKMMKDLEALMFDRSFGVKQFSANDKVYTVKADNFYHDPVDGGSVSK
NQGLRLIFADGSRIIFRLSGTGSAGATIRLYIDSYEKDNAKINQDPQVMLAPLISIALKVSQQLQERTGRT
APT VIT
>d1kfia4 d.129.2.1 (A:444-572) Exocytosis-sensitive phosphoprotein, pp63/parafusin
{*Paramecium tetraurelia*}
RNYYSRYDYEQVDSAGANKMMEHLKTKFYFEQLKQGNKADIYDYVDPVDQSVSKNQGVRFVFGD
GSRIIFRLSGTGSVGTIRIYFEQFEQQIQHETATALANIIKLGLEISDIAQFTGRNEPTVIT
>d1bv1_ d.129.3.1 (-) Major tree pollen allergen {*White birch (Betula verrucosa)*, Bet v 1}
GVFNYETETTSVIPAARLFKAFILDGDNLFKVPQAISSVENIEGNGGPGTIKKISFPEGLPFKYVKD
RVDEV DHTNFKNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNKYHTKGDHEVKAEQVKASKE
MGETLLRAVESYLLAHS DAYN
>d1e09a_d.129.3.1 (A:) Major tree pollen allergen {*Sweet cherry (Prunus avium)*, pru av 1}
GVFTYESEFTSEIPPRFLKAFVLDADNLVPKIAPQAIKHSEILEGDDGGPGTIKKITFGEGSQYGYVKH
KIDSIDKENYSYSYTLIEGDALGDTLEKISYETKLVASPSGGSIIKSTSHYHTKGNVEIKEEHVKAGKEK
ASNLFKLIETYLKGH PDAYN
>d1em2a_d.129.3.2 (A:) Lipid transport domain of Mln64 {*Human (Homo sapiens)*}
SFSAQEREYIRQGKEATAVVDQILAQEENWKFENNEYGDTVYTIIEVFPFHGKTFILKTF LPCPAELVY

QEVILQPERMVLWNKTVTACQILQRVEDNTLISYDVSAGAAGGVVSPRDFVNVRRIERRRDRYLSSGI
ATSHSAKPPTHKYVRGENGGPGGMIVLKSASNPRVCTFWWILNTDLKGRLPRYLHQSLAATMFEFAF
HLRQRISLGA

>d1fvza_d.129.3.4 (A:) Phosphatidylinositol transfer protein, PITP {Rat (Rattus norvegicus)}
VLLKEYRVILPVSVDYQVQGLYSVAEASKNETGGGEGVEVLVNEPYEKDDGEGKQYTHKIYHLQSKV
PTFVRMLAPEGALNIHEKAWNAYPYCRTVITNEYMKEDFLIKIETWHKPDLTQENVHKLPEAW
KHVEVIYIDIADRSQVLSKDYKAEEDPAKFKSITGRGPLGNWQELVNQKDCPYMCAYKLVTVKF
KWWGLQNKVENFIHKQEKRLFTNFHRQLFCWLDKWVDLTMDDIRMEETKRQLDEMQRKDPV
KGMTAD

>d1eg9a2 d.129.3.3 (A:155-447) Naphthalene 1,2-dioxygenase alpha subunit, C-domain
{Pseudomonas putida}

EAPPLMDYLGDAAWYLEPMPFKHSGGLELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRS
GESIFSSLAGNAALPPEGAGLQMTSKYSGMGVLWDGYSVHSADLPELMAFGGAKQERLNKEIG
DVRARIYRSHLNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRT
FGPAGFWESDDNDNMETASQNGKKYQSRSDLLSNLGFEDVYGDVYPGVVGKSAIGETSYRGFY
RAYQAHVSSSNWAEFEHASSTWHTELTKTT

>d1mxa_1 d.130.1.1 (1-102) S-adenosylmethionine synthetase {Escherichia coli}
AKHLFTSESVSEGHDPKIDQISDAVLDAILEQDPKARVACETYVKTGMVLVGGEITTSAWVDIEEIT
RNTVREIGYVHSDMGFDANSCAVLSAIGKQSPDI

>d1mxa_2 d.130.1.1 (108-231) S-adenosylmethionine synthetase {Escherichia coli}
RADPLEQGAGDQGLMFGYATNETDVLMPAPITYAHLRQVQAEVRKNGTLPWLRPDAKSQVTFQY
DDGKIVGIDAVVLSTQHSEEIDQKSLQEAVMEEIIPILPAEWLTSATKFFINPTGRFV

>d1mxa_3 d.130.1.1 (232-383) S-adenosylmethionine synthetase {Escherichia coli}
IGGPMGDCGLTGRKIIVDTYGGMARHGGGAFSGKDPKVDRAAAYAARYVAKNIVAAGLADRCEIQVS
YAIGVAEPTSIMVETFGTEKVPSEQLTLLVREFFDLRPYGLIQMLDLLHPIYKETAAYGHFGREHFPW
EKTDKAQLLRDAAGLK

>d1qm4a1 d.130.1.1 (A:17-116) S-adenosylmethionine synthetase {Rat (Rattus norvegicus)}
GAFMFTSESVGEGHPDKICDQISDAVLDAHLKQDPNAKVACETVCKTGMVLLCGEITSMAMIDYQRV
VRDTIKHIGYDDSAKGFDFKTCNVLVALEQQSP

>d1qm4a2 d.130.1.1 (A:129-252) S-adenosylmethionine synthetase {Rat (Rattus
norvegicus)}

EDVGAGDQGLMFGYATDETEECMPLTIVLAHKLNTRMADLRRSGVLPWLRPDSKTQVTVQYVQDN
GAVIPVRVHTIVISVQHNEEDITLEAMREALKEQVIKAVVPAKYLDEDTIYHLQPSGRFV

>d1qm4a3 d.130.1.1 (A:253-396) S-adenosylmethionine synthetase {Rat (Rattus
norvegicus)}

IGGPQGDAGVTGRKIIVDTYGGWGAHGGGAFSGKDYTKVDRSAAYAARWVAKSLVKAGLCRRVLVQV
SYAIGVAEPLSISIFTYGTSSKTERELLEVVNKNFDLRPGVIVRDLDLKKPIYQKTACYGHFGRSEFPW
EVPKKLVF

>d2pola1 d.131.1.1 (A:1-122) DNA polymerase III, beta subunit {Escherichia coli}
MKFTVEREHLKPLQVSGPLGGRPTLPILGNLLLQVADGTLSLTGTDLEMEMVARVALVQPHEPGA
TTVPARKFFDICRGLPEGAEIAVQLEGERMLVRSGRSRLSTLPAADFPNLDDW

>d2pola2 d.131.1.1 (A:123-244) DNA polymerase III, beta subunit {Escherichia coli}
QSEVEFTLPQATMKRLIEATQFSMAHQDVRYLNGMLFETEGEELRTVATDGHRLAVCSMPIGQSLP
SHSVIVPRKGVIELMRMLDGGDNPLRVQIGSNIRAHVGDFFITSKLVDGRFPDY

>d2pola3 d.131.1.1 (A:245-366) DNA polymerase III, beta subunit {Escherichia coli}
RRVLPKNPKHLEAGCDLLKQAFARAAILSNEKFRGVRLYVSENQLKITANNPEQEEAEIILDVITYSG
AEMEIGFNVSYVLDVLNALKCENVRMMLTDSVSSVQIEDAASQSAAYVVMMPRL

>d1b77a1 d.131.1.2 (A:1-110) gp45 sliding clamp {Bacteriophage RB69}
MKLSKDTIAILKNFASINSGILLSQKGFIMTRAVNGTTYAEANISDEIDFDVALYDLNSFLSILSLVSDDA
EISMHTDGNIKIADTRSTVYVWPAADKSTIVFPNKPIQFP

>d1b77a2 d.131.1.2 (A:111-228) gp45 sliding clamp {Bacteriophage RB69}
VASVITEIKAEDLQQLLRVSRGLQIDTIAITNKDGKIVINGYKVEDSGLTRPKYSLTLTDYDGSNNFNF
VINMANMKIQPGNYKVMLWGAGDKVAAKFESSQVSYVIAMEADSTHDF

>d1czda1 d.131.1.2 (A:1001-1110) gp45 sliding clamp {Bacteriophage T4}
MKLSKDTTALLKNFATINSGIMLKSGQFIMTRAVNGTTYAEANISDVIDFDVAIYDLNGFLGILSLVND
DAEISQSEDGNIKIADARSTIFWPAADPSTVVAPNKPIFPF

>d1czda2 d.131.1.2 (A:1111-1228) gp45 sliding clamp {Bacteriophage T4}
VASAVTEIKAEDLQQLLRVSRGLQIDTIAITVKEGKIVINGFNKVEDSALTRVKYSLTLGDYDAGENTFN
FIINMANMKMQPGNYKLLLWAKGKQGAAKFEGEHANYVVALEADSTHDF

>d1dmla1 d.131.1.2 (A:29-169) UL42 {Human herpes virus type 1}
APCQVVLQGAELNGILQAFAPLRTSLLDSLLVMGDRGILIHNTIFGEQVFLPLEHSQFSRYRWRGPTA
AFLSLVDQKRSLLSVFRANQYPLRRVELAITGQAPFRTLQRIWTTTSDGEAVELASETLMKRELTS
FVVLV

>d1dmla2 d.131.1.2 (A:170-319) UL42 {Human herpes virus type 1}
PQGTDPVQLRLTRPQLTKVLNATGADSATPTTFELGVNGKFSVFTTSTCVTFAAREEGVSSSTSTQVQ
ILSNALTKAGQAAANAKTVYGENTHRTFSVVVDDCSMRAVLRRLQVGGGTLKFFLTPVPSLCVTAT
GPNAVSAVFLKPKQK

>d1plq_1 d.131.1.2 (1-126) Prolifirating cell nuclear antigen (PCNA) {Baker's yeast
(Saccharomyces cerevisiae)}
MLEAKFEEASLFKRIIDGFKDCVQLVNFQCKEDGIIAQAVDDSRVLLVSLEIGVEAFQEYRCDHPVTLG
MDLTSLSKILRCGNNTDTLTLIADNTPDSIILLFEDTKKDRIAIEYSLKLMIDIDADFL

>d1plq_2 d.131.1.2 (127-258) Prolifirating cell nuclear antigen (PCNA) {Baker's yeast
(Saccharomyces cerevisiae)}
KIEELQYDSTLSLPSSEFSKIVRDLSQLSDSINIMITKETIKFVADGDIGSGSVIIPFVDMHEHPETSIKL
EMDQPVDLTFGAKYLLDIIKSSLSDRVGIRLSSEAPALFQFDLKSGLQFFLAPKFNDDEE

>d1axca1 d.131.1.2 (A:1-126) Prolifirating cell nuclear antigen (PCNA) {Human (Homo
sapiens)}
MFEARLVQGSILKKVLEALKDLINEACWDISSGVNLQSMDSHVSLVQLTLRSEGFDTYRCDRNLA
MGVNLTSMSKILKCAGNEDIITLRAEDNADTLALVFEAPNQEKVSDYEMKLMDL DVEQL

>d1axca2 d.131.1.2 (A:127-255) Prolifirating cell nuclear antigen (PCNA) {Human (Homo
sapiens)}
GIPEQEYSCVVKMPSGEFARICRDLSHIGDAVVISCAKDGVKFSASGELGNNGNIKLSQTSNVDKEEEAV
TIEMNEPVQLTFALRYLNFFTKATPLSSTVTLSMSADVPLVVEYKIADMGHLYLAPKI

>d1ge8a1 d.131.1.2 (A:2-117) Prolifirating cell nuclear antigen (PCNA) {Archaeon
Pyrococcus furiosus}
PFEIVFEGAKEFAQLIDTASKLIDEAAFKVTEGDGISM RAMDPSRVVLIDLNLPSIFSKYEVEPETIGV
NLDHLKKILKRKAKDTLILKKGEENFLEITIQTATRTFRVPLID

>d1ge8a2 d.131.1.2 (A:126-247) Prolifirating cell nuclear antigen (PCNA) {Archaeon

Pyrococcus furiosus}

PELPFTAQVVVLGKDAVKDASLVSDSIKFIARENEFIMKAEGETQEVEIKLTLEDEGLLDIEVQEE
TKSAYGVSYSLSMVKGLGKADEVTIKFGNEMPMQMEYYIRDEGRLLTFLAPRV

>d1h1ra4 d.133.1.1 (A:311-907) Aldehyde oxidoreductase {Desulfovibrio gigas}

MSGPAAAAEDAIEIHPGTPNVYFEQPIVKGEDTGPFIASADVTVEGDFYVGRQPHMPIEPDVAFAVMG
DDGKCYIHSKISGVHLHLYMIAPGVGLEPDQLVLVANPMGGTFGYKFSPTSEALVAAMATGRPVHL
RYNYQQQQYTGKRSPEMNVKFAAKKDGTLLAMESDWLVDHGPYSEFGDLLTLRGAQFIGAGYN
IPNIRGLGRTVATNHVWGSFRGYGAPQSMFASECLMDMLAEKLGMDPLELRYKNAYRPGDTNPTG
QEPEVFSPLDMIDQLRPKYQAALEKAQKESTATHKKGVGISIGVYGSGLDGPDAEAWAELNADGTIT
VHTAWEDHGQGADIGCVGTAHEALRPMGVAPEKIKFTWPNTATTPNSSGSGSREQVMTGNAIRVA
CENLLKACEKPGGGYYTYDELKAADKPTKITGNWTASGATHCDAVTGLGKPFVVMYGVFMAEVT
VDVATGQTTVDGMTLMADLGSCLNQLATDGGIYGGLAQIGLALSEDFEDIKKHATLVGAGFPFIKQI
PDKLDIVYVNHPRPDGPFASGVGELPLTSPHAAIINAISATGVRIYRLPAYPEKVLKALKA

>d1dgja4 d.133.1.1 (A:311-906) Aldehyde oxidoreductase {Desulfovibrio desulfuricans}

MSAPEAMAPDAIEIHPGTPNVYDQLEEKGEDTVPFFNDPANVVAEGSYTQRQPHLPIEPDVGYYG
INEQGQVVIHSKSVAIHLHALMIAPGLGLEFPKDLVLVQNTTGGTFGYKFSPTMEALVGVAVMATGRP
CHLRYNYEQQNYTGKRSPPFWTMMRYAADRQKILAMETDWSVDHGPYSEFGDLLTLRGAQYIGA
GYGIANIRGTGRTVATNHCWGAAFRGYGAPSEFPSEVLMDELAEKLGMDPFELRALNCYREGDTT
SSGQIPEVMSLPEMFDKMRPYYEESKKRVKERSTAEIKRGGVALGVYAGLDGPDSEAWVELND
DGSVTLGNSWEDHGQADAGSLGTAHEALRPLGITPENIHLVMNDTSKTPNSGPAGGSRSQVVTGN
AIRVACEMLIEGMRKPGGGFFTPAEMKAEGRPMRYDGKWTAPAKDCDAKGGSPFACMYGLFLTE
VAVEVATGKATVEKMVCVADIGKICNKLVDGQIYGGLAQGVGLALSEDYEDLKKHSTMGGAGIPSIK
MIPDDIEIVYVETPRKDGPFASGVGEMPLTAPHAAIINGIYNACGARVRHLPARPEKVLKALKA

>d1fo4a5 d.133.1.1 (A:695-1332) Xanthine oxidase, C-terminal domain {Cow (Bos taurus)}

IITIEDAIKNSFYGSELKIEKGLKKGFEADNVVSGELYIGGQDHFYLETHCTIAIPKGEEMELFV
STQNAMKTQSFVAKMLGVPVNRILVRVKRMGGGFGGKETRSTLVSAVALAAYKTGHPVRCMLDRN
EDMLITGGRHPFLARYKVGFMKTGTIVALEVDHYSNAGNSRDLSHSIMERALFHMDNCYKIPNIRGT
GRLCKTNLSSNTAFRFGGPPQALFIAENWMSEVAVTCGLPAEEVRWKNMYKEGDLTHFNQRLEGFS
VPRCWDECLKSSQYARKSEVDKFNKENCWKKRGLCIPTKFGISFTVPFLNQAGALIHVYTDGSVLV
SHGGTEMGQGLHTKMVQVASKALKIPISKIYISETSTNTVPNSSPTAASVSTDIYQAVYEACQTIKLR
LEPFKKNPDGSWEDWVMAAYQDRVSLSTTGFRTPNLGYSFETNSGNAFHYFTYGVACSEVEIDC
LTGDHKNLRTDIVMDVGSNLPAIDIGQVEGAFVQGLGLFTLEELHYSPEGLHTRGPSTYKIPAFGSI
PTEFRVSLLRDCPNKKAAYASKAVGEPPLFLGASVFFAIKDAIRAARAQHTNNNTKELFRLDSPATPE
KIRNACVDKFTTLCVTGAPGNCKPWSLRV

>d1jrob2 d.133.1.1 (B:124-777) Xanthine dehydrogenase chain B, C-terminal domain
{Rhodobacter capsulatus}

PAILTLDQALAADSRFEGGPVIWARGDVETALAGAAHLAEGCFEIGGQEHFYLEGQAALALPAEGGV
VIHCSSQHPSEIQHKVAHALGLAFHDVRVEMRRMGGGFGGKESQGNHLAIACAARATGRPCKMR
YDRDDDMVITGKRHDFRIRYRIGADASGKLLGADFVHLARCGWSADLSLPVCDRAMLHADGSYFVP
ALRIESHRLRTNTQSNTAFRFGGPPQALGMERAIEHLARGMGRDPAELRALNFYDPPERGGLSAP
PSPPEPIATKKTQTTHYGQEVADCVLGELVTRLQKSANFTTRRAEIAAWNSTNRTLARGIALSPVKF
GISFTLTHLNQAGALVQIYTDGSVALNHGGTEMGQGLHAKMVQVAAAVLGIDPVQVRITATDTSKVP
NTSATAASSGADMNGMAVKDACETLRGRLAGFVAAREGCAARDVIFDAGQVQASGKSWRFAEIVAA
AYMARISLSATGFYATPKLSWDRLRGQGRPFYFAYGAAITEVVIDRLTGENRILRTDILHDAGASLNP

ALDIGQIEGAYVQGAGWLTTEELVWDHCGRLMTHAPSTYKIPAFSDRPRIFNVALWDQPNREETIFR
SKAVGEPFFLLGISAFLLHDACAACGPHWPDQLQAPATPEAVLAAVRRRAEGRA

>d1qj2b2 d.133.1.1 (B:147-809) Carbon monoxide (CO) dehydrogenase molybdoprotein
{Pseudomonas carboxydovorans}

VDPFKAMEPDAPLLREDIKDKMTGAHGARKHHNHIFRWEIGDKEGTDATFAKAEVVSKDMFTYHR
VHPSPLETCQCVASMDKIKGELTLWGTFQAPHVIRTVVSLISGLPEHKIHIAPDIGGGFGNKVGGAYSG
YVCAVVASIVLGVVVKWVEDRMENLSTTSFARDYHMTTELAATKDGKILAMRCHVLADHGAFDAC
ADPSKWPAFGMNICGSYDMPVAHLAVDGVYTNKASGGVAYRXSFRVTEAVYAIERAIETLAQRLEM
DSADLRIKNFIQPEQFPYMAPLGWEYDSGNYPLAMKKAMDTVGYHQLRAEQKAKQEAFKRGETRE
IMGIGISFFTEIVGAGPSKNCILGVSMFDSAEIRIHPTGSVIARMGTKSQGGHETTYAQIIATELGIPA
DDIMIEEGNTDTAPYGLTYGSRSTPTAGAATAVAARKIKAKAQMIAAHMLEVHEGDLEWDVDRFR
VKGLPEKFKTMKELAWASYNPPNLEPGLEAVNYYDPPNMTYFPGAYFCIMDIDIDTGVAKTRRFY
ALDDCGTRINPMIIEGQVHGGLTEFAVAMGQEIYDEQGNVLGASFMDFLPTAVETPKWETDYTV
TPSPHHPIGAKGVGESPVGGVPCFSNAVNDAYAFNLNAGHIQMPHDAWRLWKVGEQLGLHV

>d1ffvb2 d.133.1.1 (B:147-803) Carbon monoxide (CO) dehydrogenase molybdoprotein
{Hydrogenophaga pseudoflava}

IDALKPDAPVLRREDLAGKTSGAHGPREHHNHIFTWGAGDKAATDAVFANAPVTVSQHMYYPVHP
CPLETCGCVASFDPIKGDLTYYITSQAPHVVRTVVSMLSGIPESKVRIVSPDIGGGFGNKVGIYPGYVCA
IVASIVLGRPVKWVEDRVENISTTAFARDYHMDGELAATPDGKILGLRVNVVADHGAFDACADPTKF
PAGLFHICSGSYDIPRAHCSVKGVTYTNKAPGGVAYRCSFRVTEAVYLIERMVDVLAQKLNMDKAEIRA
KNFIRKEQFPYTTQFGFEYDSGDYHTALKKVLDAVDYPALRAEQARRADPNSTLMGIGLVTFTEV
VGAGPSKMCILGVGMFDSCEIRIHPTGSAIARMGTITQGGHQTYYAQIIATELGIPSEVIQVEEGDT
STAPYGLTYGSRSTPVAGAAIALAARKIHAKARKIAAHMLEVNENDLDWEVDRFKVKGGDSKFKT
MADIAWQAYHQPPAGLEPGLEAVHYDPPNFTYFPGIYLCVVDIDRATGETKVVRRFYALDDCGTRIN
PMIIEGQIHGGLTEGYAVAMGQQMPFDAQGNLLGNTLMDYFLPTAVETPHWETDHTVTPSPHHPIG
AKGVAESPHVGSIPTFTAADVDAFAHVGVTHLDMPHTSYRVWVWKSLEHNLAL

>d1aop_3 d.134.1.1 (149-345) Sulfite reductase hemoprotein (SiRHP), domains 2 and 4
{Escherichia coli}

NDMNRNVLCTSNPYESQLHAEAYEWAKKISEHLLPRTRAYAEIWLDQEKVATTDEEPILGQTYLPR
KFKTTVVIPPQNDIDLHANDMNFVAIAENGKLVGFNLLVGGGLSIEHGKTKTYARTASEFGYLPLEHT
LAVAEAVVTTQRDWGNRTDRKNAKTKYTLERVGVETFKAEVERRAGIKFEPYRPFYFTGRGDR

>d1aop_4 d.134.1.1 (426-570) Sulfite reductase hemoprotein (SiRHP), domains 2 and 4
{Escherichia coli}

PQRENMACVSFPTCLAMAEAEERFLPSFIDNIDNLMAKHGVSDEHIVMRVTGCPNGCGRAMLAEV
GLVGKAPGRYNLHLGGNRIGTRIPRMYKENITEPEILASLDELIGRWAKEREAGEGFGDFTVRAGIIR
PVLDPARDLWD

>d1klqa_ d.135.1.1 (A:) The spindle assembly checkpoint protein mad2 {Human (Homo
sapiens)}

GSITLRGSAEIVAEFFSFGINSILYQRGIYPSETFTRVQKYGLTLLVTTDLELIKYLNNVVEQLKDWLYK
CSVQKLVVISNIESGEVLERWQFDIECDKTAKDDSAPREKSQKAIQDEIRSVIRQITATVTFPLLEVS
CSFDLLIYTDKDLVVPEKWEESGPQFITNSEEVRLRSFTTTIHKVNSMVAYKIPVND

>d1byra_ d.136.1.1 (A:) Nuclease Nuc {Salmonella typhimurium}

EPSVQVGYSPESARVLVLSAIDSAKTSIRMMAYSFTAPDIMKALVAAKRGVDVKIVIDERGNTGRAS
IAAMNYIANSIGPLRTDSNFPIQHDKVIIVDNTVETGSFNFTKAAETKNSENAVVIWNMPKLAESF

LEHWQDRWNQGRDYRS

>d1f0ia1 d.136.1.2 (A:6-263) Phospholipase D {*Streptomyces* sp.}

AATPHLDAVEQTLRQVSPGLEGDVWERTSGNKLDGSAADPSDWLLQTPGCWGDDKCADRVGTRK
LLAKMTENIGNATRTVDISTLAPFPNGAFQDAIVAGLKESAAGNSLKVRLVGAAPVYHMNGIPSKY
RDKLTAKLGKAAENITLNVASMTTSKTAFSWNHSKILVVDGQSALTGGINSWKDDYLDTTHPVSDV
DLALTGPAAGSAGRYLDTLWTWTCKNKSNIASVWFAASGNAGCMPTMHKDTNPKASPATG

>d1f0ia2 d.136.1.2 (A:264-514) Phospholipase D {*Streptomyces* sp.}

NVPVIAVGGGLGVGIKDVDPKSTFRPDLPTASDTKCVVGLHDNTNADRDYDTVNPEESALRALVASAK
GHIEISQQDLNATCPPLPRYDIRLYDALAAKMAAGVKVRIVVSDPANRGAVGSGGYSQIKSLSEISDTL
RNRLANITGGQQAAKTAMCSNLQLATFRSSPNGKWADGHPYAQHHKLVSVDSSTFYIGSKNLYPSW
LQDFGYIVESPEAAKQLDAKLLDPQWKYSQETATVDYARGICGA

>d1jy1a1 d.136.1.3 (A:145-350) Tyrosyl-DNA phosphodiesterase TDP1 {Human (*Homo sapiens*)}

LEDPGEGQDIWMLDKGNPFQFYLTRVSGVKPKYNSGALHIKDILSPLFGTLVSSAQFNCFDVDWL
VKQYPPEFRKKPILLVHGDKREAKAHLHAQAKPYENISLCQAKLDIAFGTHHTKMMLLLYEGLRVV
IHSTNLIHADWHQKTQGIWLSPLYPRIADGTHKSGESPETHKANLISYLTAYNAPSLKEWIDVIHKHD
LSET

>d1jy1a2 d.136.1.3 (A:351-608) Tyrosyl-DNA phosphodiesterase TDP1 {Human (*Homo sapiens*)}

NVYLIGSTPGRFQGSQKDNWGHFRLKLLKDHASSMPNAESWPVVGQFSSVGLGADESKWLCSEF
KESMLTLGKESKTPGKSSVPLYLIYPSVENVRTSLEGYPAGGSLPYSIQTAEKQNWLHSHYFHKWSAET
SGRSNAMPHIKTYMRPSPDFSKIAWFLVTSANLSKAAWGALEKNGTQLMIRSYELGVLFLPSALGLD
SFKVKQKFFAGSQEPMATFPVPYDLPELYGSKDRPWIIWNIPYVKAPDTHGNMWVPS

>d1ckv_ d.137.1.1 (-) Soluble methane monooxygenase regulatory protein B {*Escherichia coli*}

MSVNSNAYDAGIMGLKGGKDFADQFFADENQVVHESDVTVVLVLLKKSDEINTFIEILLTDYKKNVNPT
VNVEDRAGYWWIKANGKIEVDCDEISELLGRQFNVDYDFLVDVSSTIGRAYTLGNKFTITSELMGLDR
KLEDYHA

>d2moba_ d.137.1.1 (A:) Soluble methane monooxygenase regulatory protein B {*Methylosinus trichosporium*}

SNAVVLVLMKSDEIDAIIEDIVLKGKAKNPSIVVEDKAGFWWIKADGAIEIDAAEAGELLGKPFVSY
DLLINVSSTVGRAYTLGKFTITSEL

>d1g10a_ d.137.1.1 (A:) Toluene-4-monooxygenase catalytic effector protein {*Pseudomonas mendocina*}

STLADQALHNNNVGPIIRAGDLVEPVIAETAEIDNPGKEITVEDRRAYVRIAAEGELILTRKTLLEEQLGR
PFNMQELEINLASFAGQIQADEDQIRFYFDKTM

>d1hqi_ d.137.1.1 (-) Phenol hydroxylase P2 protein {*Pseudomonas* sp., CF600}

MSSLVYIAFQDNDNARYVVEAIIQDNPHAVVQHHPAMIRIEAEKRLEIRRETVEENLGRAWDVQEML
VDVITIGGNVDEDDDRFVLEWKN

>d1jjcb6 d.138.1.1 (B:191-399) B3/B4 domain of PheRS, PheT {*Thermus thermophilus* (*Thermus aquaticus*)}

LKAEALPLPFALKVEDPEGAPHFTLGAFGLRVAPSPLWMQRALFAAGMRPINNVVDVTNYVMLER
AQPMAHAFDLRFVGEIAVRRAREGERLKTLDGVERTLHPEDLVIAGWRGEESFPLGLAGVMGGAES
EVREDTEAIALEVACFPVSIRKTARRHGLRTEASHRFERGVDPGQVPAQRRLSLLQALAGARVAE

ALLEAGSPK

>d1clia2 d.139.1.1 (A:171-345) Aminoimidazole ribonucleotide synthetase (PurM) C-terminal domain {Escherichia coli}

DGSKVSDGDVLIALGSSGPHSNGYSLVRKILEVSGCDPQTTELDGKPLADHLLAPTRIIYVKSVELEIEK
VDVHAIHAHLTGGGFWENIPRVLPDNTQAVIDESSWQWPEVFNWLQTAGNVEHHEMYRTFNCGVG
MIIALPAPEVDKALALLNANGENAWKIGIHKASDSEQRVVIE

>d1hw7a_ d.193.1.1 (A:) Heat shock protein 33, Hsp33 {Escherichia coli}

HDQLHRYLFENFAVRGELVTVSETLQQILENHDPVQPVKNVLAELLVATSLLTATLKFDDITVQLQG
DGPMNLAVINGNNNQMRGVARVQGEIPENADLKTLVGNGYVVITITPSEGERYQGVVLEGDTLAA
CLEDYFMRSEQLPTRLFIRTGDVDGKPAAGGMLLQVMPAQNAQQDDFDHLATLTETIKTEELLTLPA
NEVLWRLYHEEEVTVYDPQDVEFKCTC

>d1jw3a_ d.208.1.1 (A:) Hypothetical protein MTH1598 {Archaeon Methanobacterium thermoautotrophicum}

MKGFEEFDVTADAGFWAYGHDLEEVFENAALAMFEVMTDTSLVEAAEERRVEITSEDRVSLLYDWL
DELLFIHDTEFILFSKFKV KIDEKDDGLHLTGAMGEEIKEGHERRDEVKAVTFHMMEILDEDGLIK
ARVILD

>d1dl5a2 d.197.1.1 (A:214-317) Protein-L-isoaspartyl O-methyltransferase, C-terminal domain {Thermotoga maritima}

NLLERNRKLLEFPFNREILLVRSIFVELVDLLTRRLTEIDGTFYYAGPNGVVEFLDDRMRIYGDPAE
IENLLTQWESCGYRSFEYLMHVGYNFASHISCSI

>d1seia_ d.140.1.1 (A:) Ribosomal protein S8 {Bacillus stearothermophilus}

VMTDPIADMLTAIRNANMVRHEKLEVPASKIKREIAEILKREGFIRDYIEYIEDNKQGILRIFLKYGPNE
RVITGLKRISKPLRVYVKAHEVPRVLNGLGAILSTSQVLTDKARQKGTGGEIAYVI

>d1an7a_ d.140.1.1 (A:) Ribosomal protein S8 {Thermus thermophilus}

TDPIADMLTRIRNATRVYKESTDVPASRFKEEILRILAREGFIKGYERVDVDGKPYLRVYLKYGPRRQ
GPDPRPEQVIHRRISKPGRRVYVGVKEIPVRRGLGAILSTSKGVLTREARKLGVGGELICEVW

>d1i94h_ d.140.1.1 (H:) Ribosomal protein S8 {Thermus thermophilus}

MLTDPIADMLTRIRNATRVYKESTEVPASRFKEEILKILAREGFIKGYERVEVDGKPYLRHLKYGPRR
QGPDRPEQVIKHRRISRPGRRVYVGVKEIPVRRGLGAILSTPKGVLTREARKLGVGGELICEVW

>d1i6ua_ d.140.1.1 (A:) Ribosomal protein S8 {Archaeon Methanococcus jannaschii}

SLMDPLANALNHISNCERVGKVVYIKPASKLIGRVLKVMQDNGYIGEFEFIEDGRAGIFKVELIGKIN
KCGAIKPRFPVKKFGYEFKRYLPARDFGILIVSTTQGVMSHEEAKKRGLGGRLAYVY

>d1rl6a1 d.141.1.1 (A:7-81) Ribosomal protein L6 {Bacillus stearothermophilus}

PIEIPAGVTVTVNGNTVTVKGPKGELTRTFHPDMTITVEGNVITVTRPSDEKHHRALHGTTTRSLAN
MVEGVSKG

>d1rl6a2 d.141.1.1 (A:82-170) Ribosomal protein L6 {Bacillus stearothermophilus}

YEKALELVGVGYRASKQGKLVLSVGYSHPVEIEPEEGLEIEVPSQTKIIVKGADKQRVGELAAANIRAV
RPPEPYKGGKIRYEGELVRL

>d1jj2e1 d.141.1.1 (E:1-79) Ribosomal protein L6 {Archaeon Haloarcula marismortui}

PRVELEIPEDVDAEQDHLDTVEGDNGSVTRRLWYPDIDVSDGDTVVIESDEDNAKTMSTIGTFQS
HIENMFHGVTEG

>d1jj2e2 d.141.1.1 (E:80-172) Ribosomal protein L6 {Archaeon Haloarcula marismortui}

WEYGMVEVFYSHFPMQVNVEGDEVVIENFLGEKAPRRRTTIHGDTDVEIDGEELTVSGPDIEAVGQTAA
DIEQLTRINDKDVRFVQDGVYITRKP

>d1gsa_2 d.142.1.1 (123-314) Glutathione synthetase {Escherichia coli}
 NEKLFTAWFSDLTPETLVTRNKAQLKAFWEKHSDIILKPLDGMGGASIFRVKEGDPNLGVIAETLTE
 HGTRYCMAQNYLPAIKDGDKRVLVVDGEPVYCLARIPQGGETRGNLAAGGRGEPRLTESDWKIA
 RQIGPTLKEKGLIFVGLDIIGDRLTEINVTSPTCIREIEAEFPVSITGMLMDAIEARLQ

>d1iow_2 d.142.1.1 (97-306) D-ala-D-ala ligase {Escherichia coli, gene ddIB}
 KLRSKLLWQGAGLPVAPWVALTRAEFKGLSDKQLAEISALGLPVIVKPSREGSSVGMKVVVAENAL
 QDALRLAFQHDEEVLEKWLSGPEFTVAILGEEILPSIRIQPSGTFYDYEAFLSDETQYFCPAGLEAS
 QEANLQALVLKAWTTLGCKGWGRIDVMLDSDGQFYLLANTSPGMTSHSLVPMARQAGMSFSQL
 VVRILELAD

>d1ehia2 d.142.1.1 (A:135-362) D-alanine:D-lactate ligase, VanA {Leuconostoc
 mesenteroides, Ddl2}
 DKALTKELLTVNGIRNTKYIVVDPESANNWSWDKIVAELGNIVFVKAANQGSSVGISRVTNAAEYTE
 ALSDSFYDYKVLIEEAVNGARELEVGVIGNDQPLVSEIGAHTVNPQSGDGWYDYNKFDNSAV
 HFQIPAQLSPEVTKEVKQMALDAYKVLNLRGEARMDFLLDENNVPYLGEPTLPGFTNMSLFKRL
 WDYSINNKLVDMLIDYGFEDFAQNKLS

>d1e4ea2 d.142.1.1 (A:132-342) D-alanine:D-lactate ligase, VanA {Enterococcus faecium}
 DKSLTYIVAKNAGIATPAFWVINKDDRPAATFTYFVFKPARSGSSFGVKKVNSADELDYAIESARQ
 YDSKILIEQAVSGCEVGC AVLGN SAALVGEVDQIRLQYGFRIHQEVEPEKGSNAVITVPADLSAEER
 GRIQETVKKIYKTLGCRGLARVDMFLQDNGRIVLNEVNTLPGFTSYSRYPRMMAAAGISLPELIDRLI
 VLALK

>d1dv1a3 d.142.1.2 (A:115-330) Biotin carboxylase subunit of acetyl-CoA carboxylase
 {Escherichia coli}
 DKVSAIAAMKKAGVPCVPGSDGPLGDDMDKNRAIAKRIGYPVIAKASGGGGGRGMRVVRGDAELAQ
 SISMTRAEAKAAFSNDMVYMEKYLENPRHVEIQVLADGQGNAIYLAERDCSMQRRHQKVVEEAPA
 PGITPELRRYIGERCAKACVDIGYRGAGTFEFLFENGEFYFIEMNTRIQVEHPVTEMITGVDLIKEQLR
 IAAGQPLSIKQEEVHV

>d1gsoa3 d.142.1.2 (A:104-327) Glycinamide ribonucleotide synthetase (GAR-syn)
 {Escherichia coli}
 SKAFTKDFLARHKIPTAEYQNFTEVEPALAYLREKGAPIVIVKADGLAAGKGVIVAMTLEEAEAAVHD
 MLAGNAFGDAGHRIVIEEFLDGEAEASFIVMVDGEHVLPMATSDHHRVGDKDTGPNTGGMGAYSPA
 PVVTTDDVHQRTERIHWPTVKGMAAEGNTYTGFLYAGLMIDKQGNPKVIEFNCRFGDLETQPIMLR
 MKSDLVELCLAACESKLDEKTSEWD

>d1b6ra3 d.142.1.2 (A:79-276) N5-carboxyaminoimidazole ribonucleotide synthetase, AIRC,
 PurK {Escherichia coli}
 DRLTQKQLFDKHLPTAPWQLLAERSEWPAVFDRLGELAIVKRRTGGYDGRGQWRRLRANETEQLP
 AECYGECEIVEQGINFSGEVSLVGARGFDGSTVFYPLTHNLHQDGILRTSVAFPPQANAQQARAEEMLS
 AIMQELGYVGMAMECFVTPQGLLINELAPRVHNSGHWTQNGASISQFELHLRAITDLPLPQPVV

>d1eyza3 d.142.1.2 (A:113-318) Glycinamide ribonucleotide transformylase PurT
 {Escherichia coli}
 NREGIRRLAAEELQLPTSTYRFADSESLFREAVADIGYPCIVKPVMSSSGKGQTFIRSAEQLAQAWKYA
 QQGGRAGAGRIVIEGVVDFEITLLTVSAVDGVHFCAPVGHREQEDGDYRESWQPQMSPLALERA
 QEIARKVVLALGGYGLFGVELFVCGDEVIFSEVSPRPHDTGMVTLISQDLSEFALHVRAFLGLPVGIR
 QY

>d1a9xa5 d.142.1.2 (A:128-402) Carbamoyl phosphate synthetase (CPS), large subunit

{Escherichia coli}

DRRRFDVAMKKIGLETARSGIAHTMEEALAVAADVGFPCIRPSFTMGGSGGGIAYNREEFEEICARG
LDLSPTKELLIDESLIGWKEYEMEVVRDKNDCIIVCSIENFDAMGIHTGDSITVAPAQTLTDKEYQI
MRNASMAVLREIGVETGGSNVQFAVNPKNRGLVIEMNPRVSRSSALASKATGFPIAKVAAKLAVGYT
LDELMNDITGG RTPASFEPSIDYVVTKIPRFNFEKFAGANDRLTTQMKS VGEVMAIGRTQQESLQKA
LRGL

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

RFQHAVERLKLKQPANATVTAIEMAVEKAKEIGYPLVVRAAMEIVYDEADLRRYFQTAVLLDHFLDD
AVEVDVDAICDGEMVLIGGIMEHIEQAGVHSGDSACSLPAYTLSQEIQDVMRQQVQKLAFELQVRGL
MNVQFAVKNNEVYLIEVNPRAARTVPFVSKATGVPLAKVAARVMAGKSLAEQGVTKVIPPYYSVKE
VVLPFNKFPDPLLGPEMRSTGEVMGVGRTFAEAFKAQLGS

>d1auva2 d.142.1.3 (A:214-417) Synapsin Ia, C-terminal domain {Cow (Bos taurus)}

NSLHSVYNFCDKPWVFAQMVRLHKKLGTEEFPLINQTFYPNHKEMLSSTTYPVVVKMGHAHSGMG
KVKVDNQHDQDIASVVALTPTYATTEPFIDAKYDVRIQKIGQNYKAYMRTSVSGNWKTNTGSAML
EQIAMS DRYKLWVDTCSEIFGGLDICAVEALHGKDGDRDHIEVVGSSMPLIGDHQDEDKQLIVELVVN
KMAQA

>d1jkjb2 d.142.1.4 (B:1-238) Succinyl-CoA synthetase, beta-chain, N-terminal domain
{Escherichia coli}

MNLHEYQAKQLFARYGLPAPVGYACTTPREAEAAASKIGAGPWVVKCQVHAGGRGKAGGVKVVNSK
EDIRAF AENWL GKRLVTYQTDANGQPVNQILVEAATDIAKELYLGAVVDRSSRRVVFMASTEGGVEI
EKVAEETPHLIHKVALDPLTGMPYQGRELAFKLGLEGKLVQQFTKIFMGLATIFLERDLALIEINPLV
ITKQGD LICLDGKLGADGNALFRQPD LREMRDQSQE

>d1eucb2 d.142.1.4 (B:0-245) Succinyl-CoA synthetase, beta-chain, N-terminal domain {Pig
(Sus scrofa)}

MVNLQEYQSKKLMSDNGVKVQRFFVADTANEALEAAKRLNAKEIVLKAQILAGGRGKGVFSSGLKG
GVHLTKDPEVVGQLAKQMIGYNLTKQTPKEGVKVNKVMVAEALDISRETYLAILMDRSCNGPVLV
GSPQGGVDIEVAASNPELIFKEQIDIIEGIKDSQAQRMAENLGLGPLQNQAADQIKKLYNLFLKIDA
TQVEVNPFGETPEGQVVCDAKINFDDNAEFRQKDIFAMDDKSEN

>d1kbla3 d.142.1.5 (A:2-376) Pyruvate phosphate dikinase, N-terminal domain {Clostridium
symbiosum}

AKWVYKFEEGNASMRNLLGGKGCNLAEMTILGMPPIQGFTVTTEACTEYYSNGKQITQEIQDQIFEA
ITWLEELNGKKFGDTEPLLVSVRSGARASMPGMMDTILNLGLNDVAVEGFAKKTGNPRFAYDSYR
RFIQMYS DVVMEVPKSHFEKIIDAMKEEKGVHFD TDLTADDLKELAEKFKAVYKEAMNGEEFPQEP
KDQLMGAVKAVFRSWDNPRAIVYRRMNDIPGDWGTAVNVQTMVFGNKGETSGTGVAFTRN PSTG
EKGIYGEYLINAQGEDVVAGVRTPQPITQLENDMPDCYKQFMDLAMKLEKHFRDMQDMEFTIEEG
KLYFLQTRNGKRTAPAALQIACDLVDEGMITEEEAVVRIEAKSLDQL

>d2hgsa2 d.142.1.6 (A:304-474) Eukaryotic glutathione synthetase {Human (Homo
sapiens)}

TKKVQQELSRPGMLEMLLPGQPEAVARLRATFAGLYSLDVGEEGDQAI AEA LAAPS RFVLKPQREGG
GNNLYGEEMVQALKQLKDSEERASYILMEKIEPEPFENCLLRPGSPARVVQCISELGIFGVYVRQEKT L
VMNKHVGHLLRRTKAIEHADGGVAAGVAVLDNPPYPV

>d2hgsa3 d.142.1.6 (A:3-201) Eukaryotic glutathione synthetase {Human (Homo sapiens)}

TNWGSLLDKQQL EELARQAVDRALAEVLLRTSQEPTSSEVVSYAPFTLFP SLVPSALLEQAYAVQ

MDFNLLVDAVSQNAAFLEQTLSSSTIKQDDFTARLFDIHKQVLKEGIAQTVFLGLNRSYMFQRSADG
SPALKQIEINTISASFGGLASRTPAVHRHVLSVLSKTKEAGKILSNNPSKGLALGIAKAWELYGS
>d1a0i_2 d.142.2.1 (2-240) ATP-dependent DNA ligase, N-terminal domain {Bacteriophage
T7}

VNIKTNPFKAVSFVESAIKKALDNAGYLIAEIKYDGVRGNICVDNTANSYWLSRVSKTIPALEHLNGF
DVRWKRLNDDRCFYKDFMLDGELMVKGVDFNTGSGLLRRTKWTDTKNQEFHEELFVEPIRKKD
KVPFKLHTGHLHIKLYAILPLHIVESGEDCDVMTLLMQEHVKNMLPLLQEYFPEIEWQAAESYEVYD
MVELQQLYEKRAEGHEGLIVKDPKCIYKRGKKSQGWKMK

>d1fvia2 d.142.2.1 (A:2-189) ATP-dependent DNA ligase, N-terminal domain {Chlorella virus,
PBCV-1}

AITKPLLAATLENIEDVQFPCLATPKIAGIRSVKQTQMLSRTFKPIRNSVMNRLLELLPEGSDEISIE
GATFQDTSVMTGHKMYNAKFSYYWFDYVTDPLKKYIDRVEDMKNYITVHPHILEHAQVKIPL
IPVEINNITELLQYERDVLSKGFEGVMIRKPDGKYKFRSTLKEGILLKMKQ

>d1b04a_ d.142.2.2 (A:) Adenylation domain of NAD⁺-dependent DNA ligase {Bacillus
stearothermophilus}

DRQQAERRAAELRELLNRYGYEYVLDLDRPSVPDAEYDRLMQELIAIEEQYPELKTSDSPTQRIGGPPL
EAFRQVAHRVPMMSLANAFGEGDLRDFDRRVRQEVGAAAYVCELAIDGLAVSVRYEDGYFVQGATR
GDGTTGEDITENLKTIRSLPLRLKEPVSLEARGEAFMPKASFLRLNEERKARGEELFANPRNAAAGS
LRQLDPKVAASRQLDLFVYGLADAEALGIASHSEALDYQLALGFKNPERRRCANIDEVIAFVSEWH
DKRPQLPYEIDGIVIKVDSFAQQRALGATAKSPRWAIAYKFPAE

>d1dgsa3 d.142.2.2 (A:1-314) Adenylation domain of NAD⁺-dependent DNA ligase
{Thermus filiformis}

MTRREEARRRINELRDLIRYHNYRYVVLADPEISDAEYDRLRELKELEERFPEFKSPDSPTEQVGARP
LEPTFRPVRHPTRMYSLDNAFTYEEVLAFEERLEREAEAPSLYTVHEHKVDGLSVLYEEGVWSTGSG
DGEVGEVETQNLITIPRRLKGVDPDRLEVRGEVYMPIEAFRLNNEELEERGEKVFKNPRNAAAGS
LRQKDPRTAKRGLRATFYALGLGLEESGLKSQYELLWLKEKGFVVEHCYKALGAEGVEEVYR
RGLAQRHALPFEADGVVLLKDDTLWLGELGYTARAPRFALAYKFP

>d1ckma2 d.142.2.3 (A:11-238) RNA guanylyltransferase (mRNA capping enzyme),
N-terminal domain {Chlorella virus, PBCV-1}

NITTERAVLTLNGLQIKLHKVVGESRDDIVAKMKDLAMDDHKFPRLPGPNPVSIERKDFEKLKQNK
YVSEKTDGIRFMMFFTRVFGFKVCTIIDRAMTVYLLPFKNIPRVLFQGSIFDGELCVDIVEKFFAFVL
FDAVVVSGVTVSQMDLASRFFAMKRSLKEFKNVPEDPAILRYKEWIPLEHPTIHKDHLKKANAIYHT
DGLIIMSVDEPVIYGRNFNLFKPKPG

>d1a48_ d.143.1.1 (-) SAICAR synthase {Baker's yeast (*Saccharomyces cerevisiae*)}

SITKTELDGILPLVARGKVRDIYEVDAGTLLFVATDRISAYDVIMENSIPEKGILLTKLSEFWFKLSND
VRNHLVDIAPGKTIFDYLPKLSPEPKYKTQLEDRLVHKKHKLIPLEVIVRGYITGSAWKEYVKTGTV
HGLKQPQLKESQEFPEPIFTPSTKAEQGEHDENISPAQAAELVGEDLSRRVAELAVKLYSKCKDYAK
EKGIIIADTKFEFGIDEKTNEIILVDEVLTDPSSRFWNGASYKVGESQDSYDKQFLRDWLTANKLNGV
NGVKMPQDIVDRTRAKYIEAYETLTGSKWSH

>d1bo1a_ d.143.1.2 (A:) Phosphatidylinositol phosphate kinase IIbeta, PIPK IIbeta {Human
(*Homo sapiens*)}

KLFRASEPILSVLMWGVNHTINELSNVPPVMLMPDDFKAYSKIKVDNHLFNKENLPSRFKFKKEYC
PMVFRNLRERFGIDDQDYQNSVTRSAPINSDSQGRCGTRFLTYYDRRFVIKTVSSEDVAEMHNILKK
YHQFIVECHGNTLLPQFLGMYRLTVDGVETYMVVTRNVFVSHRLTVHRKYDLKGSTVAREASDKEKA

KDLPTFKDNDNFLNEGQKLHVGEESKKNFLEKLRDVEFLAQLKIMDYSLLVGIHDVDRAEQEEMEV
EERAEDEECENDGVGGNLLCSYGTTPDSPGNLLSFPRFFGPGFEFDPVSVYAMKSHESPCKKEYVFM
AIIDILTPYDTKKKAAHAAKTVKHGAGAEISTVNPEQYSKRFNEFMSNILT

>d1blxa_ d.144.1.1 (A:) Cyclin-dependent PK (CDK, different isozymes) {Human (Homo sapiens)}

GLCRADQQYECVAEIGEGAYGKVKFARDLKNNGGRFVALKRVRVQTGEEGMPLSTIREVAVLRHLET
EHPNVVRLFDVCTVSRTDRETKLTLVFEHVDQDLTTYLDKVPEPGVPTETIKDMMFQLLRGLDFLH
SHRVVHRDLKPQNILVTSSGQIKLADFLARIYSFQMALTSVVVTLWYRAPEVLLQSSYATPVDLWSV
GCIFAEMFRRKPLFRGSSVDVQLGKILDVIGLPGEEDWPRDVALPRQAFHSKSAQPIEKFVTDIDELG
KDLLLLKCLTFNPAKRISAYSALSHPYFQDLERCKEN

>d1jvpp_ d.144.1.1 (P:) Cyclin-dependent PK (CDK, different isozymes) {Human (Homo sapiens)}

MENFQKVEKIGEGTYGVVYKARNKLTGEVVALKKIRLDTETEGVPSTAIRESLLKELNHPNIVKLLD
VIHTENKLYLVFEFLHQDLKKFMDASALTGIPLPLIKSYLFQLLQGLAFCHSHRVLHRDLKPQNLLIN
TEGAIKLADFLARAFGVPVPTYTHEVVTLWYRAPEILLGCKYYSTAVDIWSLGCIFAEMVTRRALFP
GDSEIDQLFRIFRTLGTDPDEVVWPGVTSMPDYKPSFPKWARQDFSKVVPPLDEDGRSLLSQMLHYD
PNKRISAKAALAHPPFQDVTKPVPHLRL

>d1apme_ d.144.1.1 (E:) cAMP-dependent PK, catalytic subunit {Mouse (Mus musculus)}

SEQESVKEFLAKAKEDFLKKWETPSQNTAQLDQFDRIKTLGTGSFGRVMLVKHKESGNHYAMKILD
KQKVVKLKQIEHTLNEKRILQAVNFPFLVKLEFSFKDNSLYMVMMEYVAGGEMFSLRRIGRFAEPH
ARFYAAQIVLTFEYLHSLDLIYRDLKPENLLIDQQGYIQVTDGFAKRVKGRWTWLCGTPEYLAPEIIL
SKGYNKAVDWWALGVLIYEMAAGYPPFFADQPIQIYKIVSGKVRFP SHFSSDLKDLLRNLLQVDLT
KRFGNLKNVNDIKNHKWFATTDWIAIYQRKVEAPFIPKFKGPGDTSNFDDYEEEEIRVSINEKCGK
EFTEF

>d1fota_ d.144.1.1 (A:) cAMP-dependent PK, catalytic subunit {Baker's yeast (Saccharomyces cerevisiae)}

YSLQDFQILRTLGTGSFGRVHLIRSRHNGRYAMKVLKKEIVVRLKQVEHTNDERLMLSIVTHPFIIR
MWGTFQDAQQIFMIMDYIEGGELFSLRKSQRFPNPVAKFYAAEVCLALEYLHSDIYRDLKPENIL
LDKNGHIKITDFGFAKYVPDVTYTLCGTPDYIAPEVVSTKPYNKSIDWWSFGILYEMLAGYTPFYDS
NTMKTYEKILNAELRFPFFNEDVKDLSRLITRDLSQLGNLQNGTEDVKNHPWFKEVVWEKLLS
RNIETPYEPPIQGQGDTSQFDKYPEEDINYGQGEDPYADLFRDF

>d1a06_ d.144.1.1 (-) Calmodulin-dependent protein kinase {Rat (Rattus norvegicus)}

WKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKKALEGKEGSMENEIAVLHKIKHPN
IVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQVLDAVKYLHDLGIVHRDLKPEN
LLYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAIYLLCGYP
PFYDENDAKLFEQILKAEYEFDSPYWDDISDAKDFIRHLMKDPKRFCEQALQHPWIAGDTAL
DKNIHQSVSEQIKKNFAKSKWKQAFNATAVVRHM

>d1ia8a_ d.144.1.1 (A:) Cell cycle checkpoint kinase chk1 {Human (Homo sapiens)}

AVPFVEDWDLVQTLGEGAYGEVQLAVNVRVTEEAVAVKIVDMKRAVDCPENIKKEICINKMLNHENV
VKFYGHRREGNIQYLFLEYCSGGELFDRIEPIGMPPEPDAQRFHQLMAGVVYLHGIGITHRDIKPEN
LLLDERDNLKISDFGLATVFRYNNRERLLNKMCGTLPYVAPELLKRREFHAEPVDVWSCGIVLTAML
AGELPWDQPSDSCQEYSWKEKKTLYLNPWKKIDSAPLALLHKILVENPSARITIPDIKKDRWYNKP
LKKGAKRP

>d1phk_ d.144.1.1 (-) gamma-subunit of glycogen phosphorylase kinase (Phk) {Rabbit

{Oryctolagus cuniculus}}

FYENYEPKEILGRGVSSVRRRCIHKPTCKEYAVKIIDVTGGGSFSAEEVQELREATLKEVDILRKVSGH
PNIIQLKDTYETNTFFFLVFDLMKKGELFDYLTEKVTLSEKETRKIMRALLEVICALHKLNIVHRDLK
PENILLDDDDMNIKLTDFGFSCQLDPGEKLEVCCTPSYLAPEIIECSMNDNHPGYGKEVDMWSTGVI
MYTLLAGSPPFWHRKQMLMLRMIMSGNYQFGSPEWDDYSDTVKDLVSRFLVVQPQKRYTAEELA
HPFFQQYV

>d1h8fa_d.144.1.1 (A:) Glycogen synthase kinase-3 beta (Gsk3b) {Human (Homo sapiens)}
SKVTTVVATPGQGPDRPQEVSYTDTKVINGSGFVVYQAKLCDSGELVAIKKVLQGKAFKNRELQIM
RKLHDCNIVRLRYFFYSSGEKKDEVYLNLDVYPETVYRVARHYSRAKQTLPIYVKLYMYQLFRSL
AYIHSFGICHARDIKPQNLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSID
VWSAGCVLAELLLGQPIFGDSGVDQLVEIKVLGTPTREQUIREMNPNYTEFAFPQIKAHPWTKVFR
PRTPEAIALCSRLLLEYTPARLTPLEACAHSSFFDELDPNVKLPNGRDTPALFNFTTQELSSNPPLA
TILIPPHARIQA

>d1tkia_d.144.1.1 (A:) Titin, kinase domain {Human (Homo sapiens)}
KELYEKYMAEDLGRGEFGIVHRCVETSSKTYMAKFKVVKGTDQVLVKEISILNIARHRNHLHLHE
SFESMEELVMIFEFISGLDIFERINTSAFELNEREIVSYVHQVCEALQFLHSHNIGHFDIRPENIYQTR
RSSTIKIIEFGQARQLKPGDNFRLFTAPEYYAPEVHQHDVVSTATDMWSLGLTVYVLLSGINPFLAE
TNQQIENIMNAEYTFDEEAFKEISIEAMDFVDRLLVKERKSRMTASEALQHPWLKQKIERVSTKVIR
TLKHRRYYHTLIKKDLNMVVSAAARISCGGAIRSQKGVSVAKVKVASI

>d1koba_d.144.1.1 (A:) Twitchin, kinase domain {California sea hare (Aplysia californica),
twk43}

INDYDKFYEDIWKYVQPVEVKQGSVYDYDILEELGSGAFGVVHRCVEKATGRVFAKFINTPYPL
DKYTVKNEISIMNQLHHPKLINLHDAFEDKYEMVLILEFLSGGELFDRIAAEDYKMSEAEVINYMRQ
ACEGLKHMHEHSIVHLDIKPENIMCETKKASSVKIIDFGLATKLNPEIVKVTTATAEFAAPEVDRE
PVGFYTDMWAIGVLGYVLLSGLSPFAGEDDLETLQNVKRCDWFEDEDAFSSVSPEAKDFIKNLLQKE
PRKRLTVHDALEHPWLKGDHSNLTSRIPSSRYNKIRQKIKEKYADWPAPQPAIGRIANFSSLRKHRP
QEYQIYDSYFDRKEAV

>d1koa_2 d.144.1.1 (5915-6264) Twitchin, kinase domain {Caenorhabditis elegans, pjk4}
YDNYVFDIWKQYYPQPVEIKHDHVLVDHYDIHEELGTGAFGVVHRVTERATGNNFAAKFVMTPHES
DKETVRKEIQTMSVLRHPTLVNLHDAFEDDNEMVMIYEFMSGGELFEKVADEHNKMSSEDAVEYEM
RQVCKGLCHMHENNYVHLDLKPENIMFTTKRSNELKLIDFGLTAHLDPKQSVKVTGTAEFAAPEV
AEGKPVGYTDMWSVGVLSYILLSGLSPFGGENDETLRNVKSCDWNMDDSAFSGISEDGKDFIRK
LLLADPNTRMTIHQALEHPWLTPGNAPGRDSQIPSSRYTKIRDSIKTKYDAWPEPLPPLGRISNYSSL
RKHRPQEYSIRDAFWDRSEA

>d1p38_d.144.1.1 (-) MAP kinase p38 {Mouse (Mus musculus)}
ERPTFYRQELNKTIWEVPERYQNLSPVGSGAYGSVCAAFDTKTGHRVAVKKLSRPFQSIHAKRTYRE
LRLKHKMHENVIGLLDVFTPARSLEEFNDVYLVTHLMGADLNNIVKCQKLTDDHVQFLIYQILRGL
KYIHSADIIHRDLKPSNLAVNEDCELKILDFGLARHTDDEMTGYVATRWRAPPEIMLNWMHYNQT
VDIWSVGCIMAELLTGRTLFPGTDHIDQLKLILRLVGTPGAELLKKISSESARNYIQSLAQMPKMNFA
NVFIGANPLAVDLLEKMLVLDSDKRITAAQALAHAYFAQYHDPDDEPVADPYDQSFESRDLLIDEWK
SLTYDEVISFVPPPLD

>d1cm8a_d.144.1.1 (A:) MAP kinase p38-gamma {Human (Homo sapiens)}
RSGFYRQEVTKTAWEVRAVYRDLQPVGSGAYGAVCSAVDGRGTGAKVAIKKLYRPFQSELFAKRAYRE
LRLKHKMRHENVIGLLDVFTPDDELDDFTDFYLVMPFMGTDLGKLMKHEKLGEDRIQFLVYQMLK

GLRYIHAAGIIHRDLKPGNLAVNEDCELKILDFGLARQADSEMTGYVVTRWYRAPEVILNWMRYTQ
TVDIWSVGCIMAEMITGKTLFKGSDHLDQLKEIMKVTGTPPAEFVQRLQSDEAKNYMKGLPELEKK
DFASILTNASPLAVNLEKMLVLDAEQRVTAGEALAHYPFESLHDTEDQVQKYDDSFDDVDRTLD
EWRKRVTYKEVLSFKP

>d1pme_ d.144.1.1 (-) MAP kinase Erk2 {Human (Homo sapiens)}

GQVFDVGPRTNLSYIGEGAYGMVCSAYDNVNKVRVAIKKISPFEHQTYCQRTLREIKILLRFRHENII
GINDIIRAPTIEQMKDVYLVTHLMGADLYKLLKTQHLSNDHICYFLYQILRGLKYIHSANVLRDLKP
SNLLLNTTCDLKICDFGLARVADPDHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAE
MLSNRPIFPKGKHYLDQLNHILGILGSPSQEDLNCIINLKARNYLLSLPHKNKVPWNRLFPNADSKAL
DLLDKMLTFNPHKRIEVEQALAHYPYEQYDPSDEPIAEAPFKFDMELDDLPEKELKELIFEETARF
QPGYRS

>d1jnk_ d.144.1.1 (-) c-jun N-terminal kinase (jnk3s) {Human (Homo sapiens)}

DNQFYSVEVDSTFTVLKRYQNLKPIGSGAQGIVCAAYDAVLDNRNVAIKKLSRPFQNTQTHAKRAYREL
VLMKCVNHKNIISLLNVFTPQKTLEEFQDVYLVMEMLMDANLCQVIQMELDHERMSYLLYQMLCGIK
HLHSAGIIHRDLKPSNIVVKSCTLKILDFGLARTAGTSFMMTPYVVTRYRAPEVILGMGYKENVDI
WSVGCIMGEMVRHKILFPGRDYIDQWNKVIEQLGTPCEPFMKKLQPTVRNYVENRPHYAGLTFPKL
FPDSLFPADSEHNKLKASQARDLLSKMLVIDPAKRISVDDALQHPYINWYDPAEVEAPPPQIYDKQ
LDEREHTIEEWKELIYKEVMN

>d1ckia_ d.144.1.1 (A:) Casein kinase-1, CK1 {Rat (Rattus norvegicus)}

MELRVGNRYRLGRKIGSGSFGDIYLGTDIAAGEEVAIKLECVTKHPQLHIESKIYKMMQGGVGIPTIR
WCGAEGDYNVMVMELLGPSLEDLNFNFCRSKFLKTVLLLADQMISRIEYIHSKNFIHRDVKPDNLF
MGLGKKNLVYIIDFGLAKKYRDARTHQHIPPYRENKNLTGTARYASINTHLGIEQSRRDDLESLGYVL
MYFNLSLWPQGLKAATKRQKYERISEKKMSTPIEVLCKGYPSEFATYLNFCRSLRFDDKPDYSYLR
QLFRNLFHRQGSYDYVFDWNMLKFGASR

>d1csn_ d.144.1.1 (-) Casein kinase-1, CK1 {Fission yeast (Schizosaccharomyces pombe)}

NVVGVHYKVGRRIGEGSFGVIFEGTNLLNNQVVAIKFEPRRSDAPQLRDEYRKYKLLAGCTGIPNVYY
FGQEGLHNVLVIDLLGPSLEDLLDLGCRKFSVKTVAMAAKQMLARVQSIHEKSLVYRDIKPDNLFGR
PNSKNANMIYVDFGMVKFYRDPVTKQHIPPYREKKNLSGTARYMSINTHLGREQSRRDDLEALGHV
FMYFLRGLPWQGLKAATNKQKYERIGEKKQSTPLRELCAGFPEEFYKYMHYARNLAFDATPDYDY
LQGLFSKVLRLNTTEDENFDWNL

>d1a6o_ d.144.1.1 (-) Protein kinase CK2, alpha subunit {Maize (Zea mays)}

SKARVYADVNVLRPKEYWDYEALTVQWGEQDDYEVVRKVGGRGKYSEVFEGINVNNNEKCIKILKP
VKKKKIKREIKILQNLCCGPNIVKLLDIVRDQHSKTPSLIFEYVNNNTDFKVLPTLTLDYDIRYYIYELLK
ALDYCHSQGIMHRDVKPHNVMIDHELRLRLIDWGLAEFYHPGKEYNVRVASRYFKGPELLVDLQD
YDYSLDMWSLGCMFAGMIFRKEPFFYGHNDHDQLVKIAKVLGTDGLNVYLNKYRIELDPQLEALVG
RHSRKPWLKFMNADNQHLSPEAIDFLDKLLRYDHQERLTALEAMTHPYFQQVRAAENS

>d1b6cb_ d.144.1.1 (B:) Type I TGF-beta receptor R4 {Human (Homo sapiens)}

TTLKDLIYDMTTSFGSGSGLPLLQRTIARTIVLQESIGKGRFGEVWRGKWRGEEVAVKIFSSREERSW
FREAEIYQTVMLRHENILGFIAADNKDNGTWTQLWLVSDYHEHGS�FDYLNRYTVTVEGMIKLALS
TASGLAHLHMEIVGTQGKPAIAHRDLKSKNILVKKNGTCCADLGLAVRHDSATDITIDIAPNHRVGTK
RYMAPEVLDDSSINMKHFESFKRADIYAMGLVFWIARRCSIGGIHEDYQLPYDLPSPDPSVEEMRK
VVCEQKLRPNIPNRWQSCEALRVMKIMRECWYANGAARLTALRIKKTLSQLSQEG

>d1f3mc_ d.144.1.1 (C:) pak1 {Human (Homo sapiens)}

SDEEILEKLSIVSVGDPKPKKYTRFEKIGQGASGTVYAMDVATGQEVAIRQMNLOQQPKELIINEIL

VMRENKPNIVNYLDSYLVGDELWVVMMEYLAGGSLTDVVTETCMDEGQIAAVCRECLQALEFLHSN
QVIHRDIKSDNILLGMDGSVKLTDFGCAQITPEQSKRSTMVGTPTYWMAPEVVTRKAYGPKVDIWSL
GIMAIEMIEGEPYLNENPLRALYLIATNGTPELQNP EKLSAIFRDFLNRCLDMDVEKRGSAKELLQH
QFLKIAKPLSSLPLIAAAKEATK

>d1howa_d.144.1.1 (A:) Sky1p {Baker's yeast (Saccharomyces cerevisiae)}

FHPAFKGEPIYKADARYILVRKLGWGHFSTVWLAKDMVNNTHVAMKIVRGDKVYTEAAEDEIKLLQR
VNDADNTKEDSMGANHILKLLDHFNHKGPNGVHVVMVFEVLGENLLALIKKYEHRGIPLIYVKQIS
KQLLLGLDYMHRRCGIIHTDIKPENVLMEIVDSPENLIQIKIADLGNACWYDEHYTNSIQTREYRSPE
VLLGAPWGGADIWSTACLIFELITGDFLFEPDEGHSYTKDDDHIAQIHELLGELPSYLLRNGKYTRTF
FNSRGLLRNISKLFKFWPLEDVLTEKYKFSKDEAKEISDFLSPMLQLDPRKRADAGLVNHPWLKDT
LGMEEIRVPDRELYGSGSDIPGWFEFVR

>d1qcfa3 d.144.1.2 (A:249-531) Haemopoetic cell kinase Hck {Human (Homo sapiens)}

KPQKPWEKDAWEIPRESLKLKLEKLGAGQFGEVWMATYKNHTKVAVKTMKPGSMSVEAFLAEANV
MKTLQHDKLVKLHAVVTKEPIYIITEFMAGSLLDFLKSDEGSKQPLPKLIDFSAQIAEGMAFIEQRN
YIHRDLRAANILVSASLVCKIADFGLARVIEDNEYTAREGAKFPIKWTAPEAINFGSFTIKSDVWSFGIL
LMEIVTYGRIPYPGMSNPEVIRALERGYRMPRENCPEELYNIMMRCWKNRPEERPTFEYIQSVLDD
FYTATESQYEEIP

>d1qpca_d.144.1.2 (A:) Lymphocyte kinase (lck) {Human (Homo sapiens)}

KPWWEDEWEVPRETLKLVRELKLGAGQFGEVWMGYNNGHTKVAVKSLKQGSMSPD AFLAEANLMK
QLQHQRVRLYAVVTQEPIYIITEYMENGLVDFLKTSPGIKLTINKLLDMAAQIAEGMAFIEERNYIH
RDLRAANILVSDTLCKIADFGLARLIEDNEYTAREGAKFPIKWTAPEAINYGTFTIKSDVWSFGILLT
EIVTHGRIPYPGMTNPEVIQNLERGYRMPRPDNCPEELYQLMRLCWKERPDRPTFDYLRVLEDF
FTATE

>d1fmk_3 d.144.1.2 (249-533) c-src tyrosine kinase {Human (Homo sapiens)}

KPQTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMGTWNGTTRVAIKTLKPGTMSPEAFLEQAQV
MKKLRHEKLVQLYAVVSEPIYIVTEYMSKGSLLDFLKGGETGKYLRLPQLVDMAAQIASGMAYVERM
NYVHRDLRAANILVGENLVCKVADFLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWS
FGILLTELTTKGRVPYPGMVNREVLQDQVERGYRMPPECPESLHDLMCQCWRKEPEERPTFEYLQ
AFLEDYFTSTEPQYQPGENL

>d1fgka_d.144.1.2 (A:) Fibroblast growth factor receptor 1 {Human (Homo sapiens)}

ELPEDPRWELPRDRLVLGKPLGEGAFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLIS
EMEMMKMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYSYNPSHNPEEQVSS
KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEEDNVMKIADFGLARDIHHIDYKKTNGRLPV
KWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELFKLLKEGHRMDKPSNCTNELY
MMMRDCWHAVPSQRPTFKQLVEDLDRIVALTS

>d1vr2a_d.144.1.2 (A:) Vascular endothelial growth factor receptor 2 (kdr) {Human (Homo sapiens)}

LPYDASKWEFPRDRLLKGLKPLGRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSE
LKILIHIGHHLNVNLLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVYPYKVPEDLYKDFLTLE
HLICYSFQVAKGMEFLASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLK
WMAPETIFDRVYTIQSDVWSFGVLLWEIFSLGASYPYGVKIDEEFCRRLKEGTRMRAPDYTTPEMY
QTMLDCWHGEPQRPTFSELVEHLGNLLQANA

>d1ir3a_d.144.1.2 (A:) Insulin receptor {Human (Homo sapiens)}

SSVFVPDEWEVSREKITLLRELGGSGFGMVYEGNARDIIEKGEATRVAVKTVNESASLRERIEFLNEA

SVMKGF TCHHVRL LGVVS KGQPTLV VMELMAHGDLKSYLRSLRPEAENNPGRPPPTLQEMIQMA
AEIADGMAYLNAKKFVHRDLAARNCMVAHDFTVKIGDFGMTRDIYETDYRKGKGLLPVRWVMAP
ESLKDGVFTTSSDMWSFGVVLWEITSLAEQPYQGLSNEQVLKFMVMDGGYLDQPDNCPERVTDLMR
MCWQFNPKMRPTFLEIVNLLKDDLHPSFPEVSFFHSEENK

>d1k3aa_d.144.1.2 (A:) Insulin-like growth factor 1 receptor {Human (Homo sapiens)}
VPDEWEVAREKITMSRELGGQSGFMVYEGVAKGVVKDEPETRVAIKTVNEAASMRERIEFLNEASV
MKEFNCHHVRL LGVVS QGQPTLVIMELMTRGDLKSYLRSLRPEMENNPVLAPPSLSKMIQMAGEI
ADGMAYLNANKFVHRDLAARNCMVAEDFTVKIGDFGMTRDIYETDYRKGKGLLPVRWVMSPEL
KDGVFTTYSVWSFGVVLWEIATLAEQPYQGLSNEQVLRVFMEGGLLDKPDNCPDMLLELMRMC
WQYNPKMRPSFLEIISSEEMEPGFREVSFYSEENK

>d1byga_d.144.1.2 (A:) C-terminal src kinase (csk) {Human (Homo sapiens)}
GVALNMKELKLLQTIGKGEFGDVMLGDYRGNKVAVKCIKNDATAQAFLEASVMTQLRHSNLVQLL
GVVIEEKGLYIVTEYMAKGLVDYLRSRGRSVLGGDCLLKFSLDVCEAMEYLEGNFVHRDLAARN
VLVSEDNVAKVSDFGLTKEASSTQDTGKLPVKWTAPEALREKKFSTKSDVWSFGILLWEIYSFGRVP
YPRIPLKDVVPRVEKGYKMDAPDGCPPAVYEVKNCWHLDAAMRPSFLQLEQLEHIKTHEL

>d1iepa_d.144.1.2 (A:) Abelson tyrosine kinase (abl) {Mouse (Mus musculus)}
MDPSSPNYDKWEMERTDITMKHKLGGGQYGEVYEGVWKKYSLTVAVKTLKEDTMEVEEFLKEAA
VMKEIKHPNLVQLLGVCTREPPFYIITEFMTYGNLLDYLRNCRQEVSAVLLYMATQISSAMEYLEK
KNFIHRDLAARNCLVGENHLVKVADFGLSRLMTGDTYTAHAGAKFPIKWTAPESLAYNKFSIKSDV
WAFGVLLWEIATYGMSPYPGIDLSQVYELLEKDYRMERPEGCPEKVYELMRACWQWNPSPDRPSFA
EIQAFETMFQ

>d1jpa_d.144.1.2 (A:) ephb2 receptor tyrosine kinase {Mouse (Mus musculus)}
KIFIDPFTFEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKQ
RRDFLSEASIMQFDHPNVHLEGVVTKSTPVMIIITEFMENGLSDSFLRQNDGQFTVIQLVGMRLGIA
AGMKYLADMNYVHRDLAARNILVNSNLVCKVSDFGLSRFLEDDTSDPTYTSALGGKIPIRWTAPEAI
QYRKFTSASDVWSYIVMWEVMSYGERPYWDMTNQDVINAIEQDYRLPPMDCPSALHQLMLDC
WQKDRNHRPKFGQIVNTLDKMIRNPNSLKA

>d1fvra_d.144.1.2 (A:) Tie2 kinase {Human (Homo sapiens)}
PTIYPVLDWNDIKFQDVIGEGNFGQVLKARIKKGDLRMDAAIKRMKEYASKDDHRDFAGELEVLCK
LGHHPNIIINLLGACEHRGYLYLAIEYAPHGNNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAAD
VARGMDYLSQKQFIHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYS
VYTTNSDVWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPGYRLEKPLNCDDEVYDLMRQCWREK
PYERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAE

>d1cjaa_d.144.1.3 (A:) Actin-fragmin kinase, catalytic domain {Slime mold (Physarum polycephalum)}

AGALWEIEKELFTKLPAPSSAINSHLQPAKPKVPQKKPSKWDPPAEFKVDLSTAVSYNDIGDINWKN
LQQFKGIERSEKGEGLFFVETESGVFIVKRSTNIESETFCSLLCMRLGLHAPKVRVSSNSEEETNML
ECLAAIDKSFVITLANQANILLMELVRGITLNKLTTSAPVLTSTMQQLGSLMALDVIVNNSDR
LPIAWTNEGNDNIMLSERGATVVPIDSKIPLDASHPHGERVRELLRTLIAHPGHESQFHSIRDIITL
YTGVDVGTGEGSISMQEGFLATVRECAFDFLDAFERELLSWQESLQKCHNLSISPQAIPFILRLRIFH

>d1ia9a_d.144.1.5 (A:) Trp Ca-channel kinase domain {Mouse (Mus musculus)}
YYSVAVERNLMRLSIPSFPVPPRGEPTVYRLEESSPSILNNSMSSWSQLGLCAKIEFLSKEEMG
GGLRAVKVLCWSEHDILKSGHLYIISFLPEVINTWSSYKEDTVLHLCLEIQQRAAQKLTFAFN
QMFKPSIPYSPRFLEVFLLYCHSAGQWFAVEECMTGFRKYNNGDEIIPNTTLEEIMLAFSHWTY

EYTRGELLVLDLQGVGENLTDPSPVIKAEKRSRCDMVFGPANLGEDAIKNFRAKHHCNSCCRKLKLPD
LKRNDYT

>d1e8xa4 d.144.1.4 (A:726-1092) Phosphoinositide 3-kinase (PI3K), catalytic domain {*Pig (Sus scrofa)*}

TAMLHDFTQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLPQSFVVPYDPGLK
AGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLQDMLILQILRIMESIWETESL
DLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNLTGAFKDEVLSHWLKEKCPIEEKFQAAVERFV
YSCAGYCVATFVLGIGDRHNDNIMISETGNIHFHIDFGHILGNYKSFLGINKERVFPVLTDFLVMGTS
GKKTSLHFQKFQDVCVKAYLALRHHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAK
KYFLDQIEVCRDKGWTQFNWFLHLVL

>d1j7la_ d.144.1.6 (A:) Type IIIa 3',5"-aminoglycoside phosphotransferase {*Enterococcus faecalis*}

AKMRISPELKKLIEKYRCVKDTEGMSPAKVYKLVGENENLYLKMTDSRYKGTTYDVEREKDMMMLW
LEGKLPVPKVLHFERHDGWSNLLMSEADGVLCEEYEDQSPKIIELYAECIRLFHSIDISDCPYTNS
LDSRLAELDYLLNNDLADVDCENWEEDTPFKDPRELYDFLKTEKPEEELVFSHGDLGDSNIFVKDG
KVS GFIDLGRSGRADKWYDIAFCVRSIREDIGEEQYVELFFDLLGIKPDWEKIKYYILLDEL

>d1e8ga2 d.145.1.1 (A:6-273) Vanillyl-alcohol oxidase {*Fungus (Penicillium simplicissimum)*}

EFRPLTLPKLSLSDFNFIQDIIRIVGSENEVEISSKDQIVDGSYMKPHTHTDPTHVMDQDYFLASAI
VAPRNADVQSIIVGLANKFSFPLWPISIGRNSGYGGAAPRVSGSVVLDMGKNMNRVLEVNVEGAYCV
VEPGVTYHDLHNYLEANNLRDKLWLDVPDLGGSVLGNNAVERGVGYTPYGDHMMHSGMEVVL
ANGELLRTGMGALPDPKRPETMGLKPEDQPWSKIAHLFPYGFPGPYIDGLFSQSNMGIVTKIGIWL
M PNP

>d1diqa2 d.145.1.1 (A:7-242) Flavoprotein subunit of p-cresol methylhydroxylase {*Pseudomonas putida*}

AVLPKGVVTQGEFNKAVQKFRALLGDDNVLVESDQLVPYNKIMMPVENAAHAPSAAVTATTVEQVQG
VVKICNEHKIPIWTISTGRNFGYGSAAVQVQVILDLLKMNKIIKIDPEMCYALVEPGVTFGQMYDY
IQENNLPMVLSFSAPSIAAGPVGNTMDRGVGYTPYGEHFMMQCGMEVVLANGDVYRTGMGGVPGS
NTWQIFKWGYGPTLDGMFTQANYGICTKMGFWLMPKP

>d1f0xa2 d.145.1.1 (A:9-273) D-lactate dehydrogenase {*Escherichia coli*}

NKAFLNELARLVGSSHLLTDPKARTARYRKGFRSGQDALAVVFPGSLELWRVLKACVTADKIILMQ
AANTGLTEGSTPNGNDYDRDVVIISTLRLDKLHVLGKGEQVLAYPGTTLYSLEKALKPLGREPHSVIG
SSCIGASVIGGICNNSGSLVQRGPAYTEMSLFARINEDGKLTLVNHLGIDLGETPEQILSKLDDDDRIKD
DDVRHDGRHAHDYDYVHRVRDIEADTPARYNADPDRLFESSGCAGKLAVFAVRLDTFEAE

>d1i19a2 d.145.1.1 (A:57-273) Cholesterol oxidase {*Brevibacterium sterolicum*}

VAPLPTPPNFPNDIALFQQAYQNSKEIMLDATWVCSPKTPQDVVRLANWAHEHDYKIRPRGAMH
GWTPLTVEKGANVEKVLADTMTHLNGITVNTGGPVATVTAGAGASIEAIVTELQKHDLGWANLPA
PGVLSIGGALAVNAHGAALPAVGQTTLPGHYGSLSNLVTELTAVVWNGTTTYALETYQRNDPRITPLL
TNLGRCLTSVTMQAGPN

>d1uxy_1 d.145.1.2 (3-200) Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain {*Escherichia coli*}

HSLKPWNTFGIDHNAQHIVCAEDEQQLLNAWQYATAEGQPVLILGEGSNVLFLEDYRGTVIINRIKGI
EIHDEPDWYLVHVGAGENWHRLVKYTLQEGMPGLENLALIPGCVGSSPIQNI GAYGVELQRVCAYVD
SVELATGKQVRLTAKECRFGYRDSIFKHEYQDRFAIVAVGLRPLKEWQPVLTYGDLTRLDPTT

>d1hska1 d.145.1.2 (A:15-208) Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain {Staphylococcus aureus}

NKDIYQALQQLIPNEKIKVDEPLKRYTYTKTGGNADFYITPTKNEEVQAVVKYAYQNEIPVTYLGNSS
NIIIREGGIRGIVISLLSLDHIEVSDDAIIAGSGAAIIDVSRVARDYALTGLEFACGIPGSIGGAVYMNAGAY
GGEVKDCIDYALCVNEQGSLLIKLTTKELELDYRNSIIQKEHLVVLEAAFTLAP

>d1qj2c2 d.145.1.3 (C:1-177) Carbon monoxide (CO) dehydrogenase flavoprotein, N-terminal domain {Pseudomonas carboxydovorans}

MIPGSFDYHRPKSIADAVALLTKLGEDARPLAGGHSLIPIMKTRLATPEHLVDLRDIGDLVIREEGTD
VVIGAMTTQHALIGSDFLAAKLPPIRETSLLIADPQIRYMGTTIGGNAANGDPGNDMPALMQCLGAAY
ELTGPEGARIVAARDYYQGAYFTAIEPGELLTAIRIPVPPT

>d1ffvc2 d.145.1.3 (C:1-177) Carbon monoxide (CO) dehydrogenase flavoprotein, N-terminal domain {Hydrogenophaga pseudoflava}

MIPPRFEYHAPKSVGEAVALLGLGSDAKLLAGGHSLPMMKLRFAQPEHLIDINRIPELRGIREEGS
TVVIGAMTVENDLISSPIVQARLPLLAEEAKLIADPQVRNRGTIGGDIAHGDPGNDHPALSIAVEAHF
VLEGPNGRRTPADGFFLGTMYMTLLEENEVMVEIRVPAFAQ

>d1fiqb2 d.145.1.3 (B:224-414) Xanthine oxidase, domain 3 (?) {Cow (Bos taurus)}

PKQLRFEGERVWQASTLKELLDLKAQHPEAKLVVGNTEIGIEMKFKNQLFPMIICPAWIPELNAVE
HGPEGISFGAALSSVEKTLLEAVAKLPTQKTEVFRGVLEQLRWFAGKQVKSVASLGGNIITASPISD
LNPVFMASGTKLTIVSRGTRRTPMDHTFFPSYRKTLLGPTEEILLSIEIPYSRE

>d1fo4a6 d.145.1.3 (A:192-414) Xanthine oxidase, domain 3 (?) {Cow (Bos taurus)}

SPSLFNPEEFMPLDPTQEPIFPPELLRLKDVPPKQLRFEGERVWQASTLKELLDLKAQHPEAKLVV
GNTEIGIEMKFKNQLFPMIICPAWIPELNAVEHGPEGISFGAALSSVEKTLLEAVAKLPTQKTEVFR
GVLEQLRWFAGKQVKSVASLGGNIITASPISDLNPVFMASGTKLTIVSRGTRRTPMDHTFFPSYRKT
LLGPTEEILLSIEIPYSRE

>d1jroa4 d.145.1.3 (A:179-345) Xanthine dehydrogenase chain A, domain 3 {Rhodobacter capsulatus}

PAFLPETS DALADWYLAHPEATLIAGGTDVSLWVTKALRDLPEVAFLSHCKDLAQIRETPDGYGIGA
GVTIAALRAFAEGPHALAGLLRRFASEQVRQVATIGGNIANGSPIGDGPPALIAMGASLTLRRGQERR
RMPLEDFLEYRKQDRRPGEFVESVTLPKSA

>d1uxy_2 d.146.1.1 (201-342) Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain {Escherichia coli}

VTPQQVFNAVCHMRTTKLPDPKVNGNAGAFFKNPVVSAETAKALLSQFPTAPNYPQADGSVKLAAG
WLIDQCQLKGMQIGGAHVHRQQALVLINEDNAKSEDDVQLAHHVRQKVGEKFNWLEPEVRFIGAS
GEVSAVETIS

>d1hska2 d.146.1.1 (A:209-317) Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain {Staphylococcus aureus}

GKMTEIQAKMDDLTERRESKQPLEYPCGSVVFQRPFGHFAGKLIQDSNLQHRIGGVEVSTKHAGF
MVNVDNGTATDYENLIHYVQKTVKEKFGIELNREVRRIIGHEHPK

>d1qlma_ d.147.1.1 (A:) Methenyltetrahydromethanopterin cyclohydrolase {Archaeon Methanopyrus kandleri}

MVSVNENALPLVERMIERAELLNVEVQLENGTTVIDCGVEAAGGFEAGLLFSEVCMGGLATVELTE
FEHDGLCLPAVQVTTDHPAVSTLAAQKAGWQVQVGDYFAMGSGPARALALKPKETYEEIDYEDDAD
VAILCLESSELPDEDAEHVADECGVDPENLYLLVAPTASIVGSVQVSARVVETGLYKLLVLEYDVTR
VKYATGTAPIAPVADDDGEAMGRTNDCILYGGTVYLYVEGDDELPEVVEELPSEASEDYGKPFMKIFE

EADYDFYKIDPGVFAPARVVNDLSTGKTYTAGEINVDVLKESFSL

>d1c4za_ d.148.1.1 (A:) Ubiquitin-protein ligase E3a, Hect catalytic domain (E6ap) {Human (Homo sapiens)}

NPYLRLKVRDDHIIDALVRLEMIAMENPADLKKQLYVEFEQGVDEGGVSKEFFQLVVEEIFNPDI
GMFTYDESTKLFWFNPSSFETEGQFTLIGIVLGLAIYNNCILDVHFPMVVYRKLGMGKGTFRDLGDS
HPVLYQSLKDLLEYEGNVEDMMITFQISQTDLFGNPMYDLKENGDKIPITNENRKEFVNLYSDYI
LNKSVEKQFKAFFRRGFHMVTNESPLKYLFRPEEIELLICGSRNLDFQALEETTEYDGGYTRDSVLIRE
FWEIVHSFTDEQKRLFLQFTTGTDRAPVGGGLGKLMIIAKNGPDTERLPTSHTCFNVLLLPEYSSKE
KLKERLLKAITYA

>d2ahja_ d.149.1.1 (A:) Nitrile hydratase alpha chain {Rhodococcus erythropolis}

IDHTTENAAPAQAPVSDRAWALFRALDGKGLVDPGYVEGWKKTFEEDFSPRGAELVARAWTDPE
FRQLLLTDGTAAVAQYGYLGPQGEYIVAVEDTPTLKNVIVCSLASCTAWPILGLPPTWYKSFEYRARV
VREPRKVLSEMGTEIASDIEIRVYDTTAETRYMVLQRPAGTEGWSQEQLQEIVTKDCLIGVAIPQV

>d1f7la_ d.150.1.2 (A:) Holo-(acyl carrier protein) synthase ACPS {Bacillus subtilis}

GIYGIGLDITELKRIASMAGRQKRFAERILTRSELDQYYELSEKRKNEFLAGRFAAKEAFSKAFGTGIG
RQLSFQDIEIRKDQNGKPYIICKLSPAAPHVHSITHKEYAAAQVVIER

>d1ftha_ d.150.1.2 (A:) Holo-(acyl carrier protein) synthase ACPS {Streptococcus pneumoniae}

MIVGHGIDIEELASIESAVTRHEGFARVLTALMERFTSLKGRRQIEYLAGRWSAKEAFSKAMGTGI
SKLGFQDLEVLNNERGAPYFSQAPFSGKIWLSISHTDQFVTASVILEEN

>d1qr0a1 d.150.1.1 (A:1-101) 4'-Phosphopantetheinyl transferase SFP {Bacillus subtilis}

MKIYGIYMDRPLSQEENERFMFTFISPEKREKRRFYHKEDAHRTLLGDVLRVSVISRQYQLDKSDIRF
STQEYKPCIPDLPAHFNISHSGRWVIGAFDS

>d1qr0a2 d.150.1.1 (A:102-228) 4'-Phosphopantetheinyl transferase SFP {Bacillus subtilis}

QPIGIDIEKTKPISLEIAKRFFSKTEYSDLLAKDKDEQTDYFYHLWSMKESFIKQEGKGLSLPLDSFSV
RLHQDQGVSIELPDSHSPCYIKTYEVDPGYKMAVCAAHPDFPEDITMVSYEELLRAAA

>d1ako_ d.151.1.1 (-) DNA-repair enzyme exonuclease III {Escherichia coli}

MKFVFSFNINGLRARPHQLEAIVEKHQPDVIGLQETKVHDDMFPLEEVAKLGYNVFYHGQKGHYGVA
LLTKETPIAVRRGFPGDDEEAQRRIIMAEIPSLGNVTVINGYFPQGESRDHPIKFPKAAQFYQNLQN
YLETTELKRDNPVLMGDMNISPTDLDIGIGEENRKRWLRTGKCSFLPEEREWMDRLMSWGLVDTF
RHANPQTADRFSWFDYRSKGFDDNRGLRIDLLLASQPLAECVETGIDYEIRSMKPSDHAPVWAT
FRR

>d1hd7a_ d.151.1.1 (A:) DNA repair endonuclease Hap1 {Human (Homo sapiens)}

LYEDPPDQKTSFSGKPATLKICSWNVDDLRAWIKKGLDWWKEEAPDILCLQETKCSENKLPALQE
LPGLSHQYWSAPSDKEGYSVGLLSRQCPLKVSYGIGDEEHDQEGRVIVAEFDSFVLVTAYVPNAGRG
LVRLEYRQRWDEAFRKFLLKGLASRKPLVLCGDLNVAHEEIDLRNPKGNKKNAGFTTPQERQGFCELL
QAVPLADSRHLYPNTPYAYTFWYMMNARSKNVGWRLDYFLLSHSLPALCDSKIRSKALGSDHC
PITLYLAL

>d2dnja_ d.151.1.1 (A:) Deoxyribonuclease I {Cow (Bos taurus)}

LKIAAFNIRTFGETKMSNATLASIYVIRVRRYDIVLIQEVRDLSHLVAVGKLLDYLNQDDPNTYHYVVSE
PLGRNSYKERYLFLFRPNKVSVDLTYQYDDGCESGNDSSFSREPAVVKFSSHSTKVKEFAIVALHSAP
SDAVAEINSLYDVYLDVQKQWHLNDVMLMGDFNADCSYVTSSQWSSIRLRTSSTFQWLIPDSADTT
ATSTNCAYDRIVVAGSLLQSSVVPGSAAPFDFQAAAYGLSNEMALAI SDHYPVEVTLT

>d1i9za_ d.151.1.2 (A:) Synaptojanin, IPP5C domain {Yeast (Schizosaccharomyces pombe)}

YDPIHEYVNHLELRKRENEFSEHKNVKIFVASYNLNGCSATTKLENWLFPEENTPLADIYVVGFEIVQ
LTPQQVISADPAKRREWESCVRLLNGKCTSGPGYVQLRSGQLVGTALMIFCKESCLPSIKNVEGTVK
KTGLGGVSGNKGAVAIRFDYEDTGLCFITSHLAAGYTNYDERDHDYRTIASGLRFRGRSIFNHDYV
WFGDFNYRISLTYEEVPCIAQGKLSYLFYDQLNKQMLTGKVFPPFSELPIFPPTYKFDIGTDIYDT
SDKHRVPAWTDRLYRGELVPHSYQSVPLYSDHRPIYATYEANIVKVDREKKKILFEELYNQRKQEV
RDASQ

>d1aora2 d.152.1.1 (A:1-210) Aldehyde ferredoxin oxidoreductase {Archaeon *Pyrococcus furiosus*}

MYGNWGRFIRVNLSTGDIKVEEYDEELAKKWLGSRGLAIYLLLKEMDPTVDPLSPENKLIIAAGPLT
GTSAPTGGRYNVVTKSPLTGFITMANSAGGYFGAELKFAGYDAIVVEGKAEKPVYIYIKDEHIEIRDASH
IWGKKVSETEATIRKEVGSEKVKIASIGPAGENLVKFAAIMNDGHRAAGRGGVGAVMGSKNLKAIIV
EGSKTVP

>d1b25a2 d.152.1.1 (A:1-210) Formaldehyde ferredoxin oxidoreductase {Archaeon *Pyrococcus furiosus*}

MYGWWGRILRVNLTTGEVKVQEYPEEVAKKFIGGRGLAAWILWNEARGVEPLSPENKLIFAAGPFN
GLPTPSGGKLVAAKSPLTGGYGDGNLGTMASVHLRRAGYDALVVEGKAKKPVYIYIEDDNVSILSAE
GLWGKTTTFETERELKEIHGKNVGVLTIGPAGENLVKYAVVISQEGRAAGRPGMGAVMGSKKLKAVVI
RGTKEIPVA

>d1gdoa_ d.153.1.1 (A:) Glucosamine 6-phosphate synthase, N-terminal domain {*Escherichia coli*}

CGIVGAIQRDVAEILLEGLRRLLEYRGYDSAGLAVVDAEGHMTRLRRLGKVQMLAQAAEEHPLHGGT
GIAHTRWATHGEPSEVNAHPHVSEHIVVVHNGIENHEPLREELKARGYTFVSETDTEVIAHLVNWE
LKQGGTLREAVLRAIPQLRGAYGTVMDSRHPDTLLAARSGSPLVIGLGMGENFIASDQLALLPVTRR
FIFLEEGDIAEITRRSVNIFDKTGAEVKRQDIESNL

>d1gph12 d.153.1.1 (1:1-234) Glutamine PRPP amidotransferase, N-terminal domain {*Bacillus subtilis*}

CGVFGIWGHEEAPQITYYGLHSLQHRGQEGAGIVATDGEKLTAKGQGLITEVFQNGELSKVKGKGA
GHVRYATAGGGGYENVQPLLFRSQNNGSLALAHNGNLVNATQLKQLENQGSIFQTSSTDEVLAHLI
KRSGHFTLKDQIKNSLSMLKGAYAFIMTETEMIVALDPNGLRPLSIGMMGDAYVVASETCAFDVVG
ATYLRVEVPGEMLIINDEGMKSERFSMNINRS

>d1ecfa2 d.153.1.1 (A:1-249) Glutamine PRPP amidotransferase, N-terminal domain {*Escherichia coli*}

CGIVGIAGVMPVNQSIYDALTVLQHRGQDAAGIITIDANNCFRRLRKANGLVSDVFEARHMQRLLQGNM
GIGHVRYPTAGSSSASEAQPFFVNSPYGITLAHNGNLNAHELKLFEEKRRHINTTSDSEILLNIFA
SELDNFRHYPLEADNIFAAIAATNRLIRGAYACVAMIIGHGMVAFRDPNGIRPLVLGKRDIDENRTEY
MVASESVALDTLGFDFLRDVAPGEAIYITEEGQLFTRQCADNPVS

>d1ct9a2 d.153.1.1 (A:1-192) Asparagine synthetase B, N-terminal domain {*Escherichia coli*}

ASIFGVFDIKTDAVELRKKALELSRLMRHRGPDWSGIYASDNAILAHERLSIVDVNAGAQPPLYNQKT
HVLAVNGEIYNHQUALRAEYGDYQFQTGSDCEVILALYQEKGPEFLDDLQGMFAFALYDSEKDAYLIG
RDHLGHIPLYMGYDEHGQLYVASEMKALVPVCRTIKEFPAGSYLWSQDGEIRSYH

>d1jgta2 d.153.1.1 (A:4-209) beta-Lactam synthetase {*Streptomyces clavuligerus*}

PVLPAAFGFLASARTGGGRAPGPVFATRGSHTDIDTPQGERSLAATLVHAPSVAPDRAVARSLTGAPT
TAVLAGEIYNRDELLSVLPAGPAPEGDAELVLRLLERYDLHAFRLVNGRFATVVRTGDRVLLATDHAG
SVPLYTCVAPGEVRASTEAKALAAHRDPKGFPLADARRVAGLTGVYQVPAGAVMDIDLGSQTAVTHR

TWT

>d1ea0a3 d.153.1.1 (A:1-422) Alpha subunit of glutamate synthase, N-terminal domain {Azospirillum brasilense}

CGVGFIAAIDGKPRRSVVEKGIKAVWHRGAVDADGKTGDGAGIHVAVPQKFFKDHVKVIGHRAP
DNKLAVGQVFLPRISLDAQEACRCIVETEILAFGYIYGWRQVPINVDIIGEKANATRPEIEQIIVGNK
GVSDEQFELDLYIIRRIEKAVKGEQINDFYICSLARSIIYKGMFLAEQLTTFYPDLLDERFESDFAIYH
QRYSTNTFPTWPLAQPFRLAHNGEINTVKGNNWMMKAHETRMHPAFGTHMQDLKPVIGVGLS
DSGSLDTVFEVMVRAGRTAPMVKMMLVLPQALTSSQTPDNHKALIQYCNSVMEPWGPAALAMT
DGRWVVGMDRNLRLPMRYTITTDGLIIGSETGMVKIDETQVIEKGRLLGPGEMIAVDLQSGKLYRD
RELKDHLATLKPWDKVVQN

>g1gk9.1 d.153.1.2 (A:,B:) Penicillin acylase {Escherichia coli}

QSSSEIKIVRDEYGMPHIYANDTWHLFYGYGYVAQDRLFQMEMARRSTQGTVAEVLGKDFVKFDK
DIRRNYWPDRAIRAQIAALSPEDMSILQGYADGMNAWIDKVNTPETLLPKQFNTFGFTPKRWEPFD
VAMIFVGTMANRFSSTSEIDNLALLTALKDKYGVSGMAVFNQLKWLNVNPSAPTTIAVQESNYPLK
FNQQNSQTAXSNMWVIGKSKAQDAKAIMVNGPQFGWYAPAYTYGIGLHGAGYDVTGNTPFAYPGLV
FGHNGVISWGSTAGFGDDVDIFAERLSAEKPGYLLHNGKWKMLSRREETITVKNQQAETFTVWRTV
HGNILQTDQTTQTAYAKSRAWGKEVASLLAWTHQMKAKNWQEWTTQAAKQALTNWYYADVN
GNIGYVHTGAYPDRQSGHDPRLPVPGTGKWDWKGLLPFEMNPKVYNPQSGYIANWNNSPQKDYP
ASDLFAFLWGGADRVTEIDRLLEQKPRLTADQAWDVIRQTSRQDLNLRFLPTLQAATSGLTQSDPR
RQLVETLTRWDGINLLNDDGKTWQQPGSAILNVWLTSMLKRTVVAAVPMPFDKWSASGYETTQD
GPTGSLNISVGAKILYEAVQGDKSPIQAVDLFAGKPPQEVVLALEDTWETLSKRYGNNVSNWKTP
AMALTFRANFFGVPPQAAAEEYTRHQAQYQNRGTENDMIVFSPTTSDRPVLAWDVVAPGQSGFIAP
DGTVDKHYEDQLKMYENFGRKSLWLTQDVEAHKESQEVLVHQR

>g1cp9.1 d.153.1.2 (A:,B:) Penicillin acylase {Providencia rettgeri}

ESTQIKIERDNYGVPHIYANDTYSLFYGYGYVAQDRLFQMEMAKRSTQGTVSEVFGKDYISFDKEIR
NNYWPDSIHKQINQLPSQEQLIRGYADGMNAWIKQINTKPDDLMPKQFIDYDFLPSQWTSFDVAM
IMVGTLANRFSDMNSEIDNLALLTALKDKYGEQLGVEFFNQINWLNPNAPTITISSEFTYSDXSNV
WLVGKTKASGAKAILLNGPQFGWFNPAYTYGIGLHGAGFNIVGNTPFAYPAILFGHNGHVSWGSTAG
FGDGDVIFAEQVSPEDPNSYLHQQQWKKMLSRQETLNVKGEQPITFEIYRTVHGNVVKRDKTTHTA
YSKARAWDGKELTSMAWVKQGAQNWQQWLDQAQNAQALTNWYYADKDGNGYVHTGHYPDR
QINHDPRLPVSGTGEWDWKGIPFANNPKVYNPKSGYIANWNNSPAKNYPASDLFAFLWGSADRV
KEIDNRIEAYDKLTADDMWAILQQTSRVDLNHRFLTPTLQATQGLPSNDNSVKLVSMQLQWWDGIN
QLSSDGKHYIHPGSAILDIWLKEMLKATLGQTPAPFDKWLASGYETTQEGPTGSLNISTGAKLLYE
SLEDKSPISQSIDLFSGQPQNDVIRKTLNTTYQKMIKYGDNPANWQTPATALTFRENNFFGIPQAL
PQENFHQNEYHNRGTENDLIVFTEEGVSAWDVVAPGQSGFISPQGGKPSPHYQDQLSLYQQFGKKPL
WLNSDEVAPYIESTETLIER

>g1fm2.1 d.153.1.2 (A:,B:) Cephalosporin acylase {Brevundimonas diminuta}

QAPIAAYKPRSNEILWDGYGVPHIYGVDPASAFYGYGWAQARSHGDNILRLYGEARGKGAEYWGPDY
EQTTVWLLTNGVPERAQQWYAQQSPDFRANLDAFAAGINAYAQQNPDDISPEVRQVLPVSGADVVA
HAHRLMNFYVAVSPGRTLXGNSWAVAPGKTANGNALLLQNPPLSWTTDYFTYEAHLVTPDFEYIY
GATQIGLPVIRFAFNQRMGITNTVNGMVGATNYRLTLQDGGYLYDGQVRPFERRQASYRLRQADGST
VDKPLEIRSSVHGPVFERADGTAVAVRVAGLDRPGMLEQYFDMITAHSFDDYEAAMARMQVPTFNI
VYADREGTINYSFNGVAPKRAEGDIAFWQGNVPGDSSRYLWTETHPLDDLPRVTNPPGGFVQNSND
PPWTPPTWPVTYCPANHPSYLAPQTPHSLRAQQSVRLMSENDLTLERFMALQFSHRVAMADRTLP

DLIPAALIDPDPEVQAAARLLAAWDRDFTSDSRAALLFEWARLFAGQNFAGQAAFATPWSLDKPV
STPYGVRDPKAAVDQLRTAIANTKRKYGAIDRPFGDASRMILNDVNVPGAAGYGNLGSFRVFTWSD
PDENGIRTPVHGETWVAMIEFSTPVRAYGLMSYGNRQPGTTHYSYDQIERVSRADFRELLLRREQVE
AAVQERTPFNF

>d2pvaa_ d.153.1.3 (A:) Penicillin V acylase {Bacillus sphaericus}

CSSLSIRTTDDKSLFARTMDFTEPDSKVIIVPRNYGIRLLEKENVVINNSYAFVGMGSTDITSPVLYD
GVNEKTYADEPKKGTGLMGAMLYATFATYADEPKKGTGINPVYVISQVLGNCVTVDDVIEKLTSYT
LLNEANIILGFAPPLHYTFTDASGESIVIEPKTGITIHRTIGVMTNSPGYEWHTNLRAYIGVTPNP
PQDIMMGDLTLPFGQGAGGLPLGDFTPSARFLRVAYWKKYTEKAKNETEGVTNLFHILSSVNIPK
GVVLTNEGKTDYTIYTSAMCAQSKNYYFKLYDNSRISAVSLMAENLNSQDLITFEWDRKQDIKQLNQ
VN

>d1pma1_ d.153.1.4 (1:) Proteasome beta subunit (catalytic) {Archaeon Thermoplasma acidophilum}

TTTVGITLKDVAIMATERVTMENFIMHKNKKLFQIDTYTGMTIAGLVGDAQVLVRYMKAELEYR
LQRRVNMPIEAVATLLSNMLNQVKYMPYMVQLLVGGIDTAPHVFSIDAAGGSVEDIYASTGSGSPFVY
GVLESQYSEKMTVDEGVLDVIRAISSAAKQRDSASGGMIDVAVITRKDGYYQLPTDQIESRIRKGLLIL

>d1ryp1_ d.153.1.4 (1:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

QFNPHYGDNGGTILGIAGEDFAVLGADTRNITDYSINSRYEPKVFDCGDNIVMSANGFAADGDALVKRF
KNSVKWYHFDHNDKLSINSAARNIQHLLYGKRFPPYVHTIIAGLDEDEGKGAIVSFDVPVGSYEREQ
CRAGGAAASLIMPFLDNQVNFKNQYEPGTNGKVKKPLKYLVSVEEVIKLVRDSFTSATERHIQVGDGL
EILIVTKDGVKRFYELKRD

>d1ryp2_ d.153.1.4 (2:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

TQQPIVTGTSVISMKYDNGVIAADNLGSYGSLRFNGVERLIPVGDNTVVGISGDISDMQHIERLLKD
LVTENAYDNPLADAEAELEPSYIFEYLATVMYQRRSKMNPLWNAIIVAGVQSNQDQFLRYVNLGGVT
YSSPTLATGFGAHMANPLLRKVVDRSDIPKTTVQVAEEAIVNAMRVLYYRDARSSRNFLAIIIDKNT
GLTFKKNLQVENMKWDFAKDIKGYGTQKI

>d1ryph_ d.153.1.4 (H:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

LKKGEVSLGASIMAVTFKDGVLGADSRTTTGAYIANRVTDKLRVHDKIWCCRSASAADTQAIADIV
QYHLELYTSQYGTPTETAASVFKELCYENKDNLTAGIIVAGYDDKNKGEVYTIPLGGSVHKLPHYAIAG
SGSTFIYGYCDKNFRENMSKEETVDFIKHSLSQAIKWGSSGGVIRMVVLTAAGVERLIFYPDEYEQL

>d1rypi_ d.153.1.4 (I:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

TTIVGVKFNNGVIAADTRSTQGPIVADKNCACLHRISPKIWCAGAGTAADTEAVTQLIGSNIELHSLY
TSREPRVVSALQMLKQHLFKYQGHIGAYLIVAGVDPTGSHLFSIHAHGSTDVGYYSLSGSLAAMAV
LESHWKQDLTKEEAIKLASDAIQAGIWNLDLGSNSVDVCVMEIGKDAEYLRNYLTPNVREEKQKSYK
FPRGTTAVLKESIVNICD

>d1rypj_ d.153.1.4 (J:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

SDPSSINGGIVVAMTGKDCVAIACDLRLGSQLGVSNNKFEKIFHYGHVFLGITGLATDVTTLNEMFRY
KTNLYKLKEERAIEPETFTQLVSSSLYERRFGPYFVGPVAVAGINSKSGKPFIAFGFDLIGCIDEAKDFIVSG
TASDQLFGMCESLYEPNLEPEDLFETISQALLNAADRDALSGWGAVVYIHKKDEVVKRYLKMQRD

>d1rypk_ d.153.1.4 (K:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

MDIILGIRVQDSVILASSKAVTRGISVLKDSDDKTRQLSPHTLMSFAGEAGDTVQFAEYIQANIQLYSIR
EDYELSPQAVSSFVRQELAKSIRSRPYQVNVLIGGYDKKKNKPELYQIDYLGTKVELPYGAHGYSGFY
TFSLLDHHYRPDMTTEEGDLLKLCVQELEKRMPMDFKGVIVKIVDKDGIRQVDDFQAQ

>d1rypl_ d.153.1.4 (L:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

TTTTLAFRFQGGIIVAVDSRATAGNWWASQTVKRVIEINPFLGTMAGGAADCQFWETWLGSQCRLH
ELREKERISVAAASKILSNLVYQYKAGLSMGTMICGYTRKEGPTIYYVDSGTRKGDIFCVGSGQTF
AYGVLDSDNYKWDLSVEDALYLGKRSILAAHRDAYSGGSVNLHYVTEDEGWYHGNHDVGELEFWKVK
EEEGSFNNVIG

>d1pmaa_ d.153.1.4 (A:) Proteasome alpha subunit (non-catalytic) {Archaeon Thermoplasma acidophilum}

TVFSPDGRLFQVEYAREAVKKGSTALGMKFANGVLLISDKKVRSLIEQNSIEKIQLIDDYVAAVTSGL
VADARVLVDFARISAQKEKVTYGLVNIENLVKRVADQMQQYTQYGGVVPYGVSLIFAGIDQIGPRLFD
CDPAGTINEYKATAIGSGKDAVVSFLEREYKENLPEKEAVTLGIKALKSSLEEGEELKAPEIASITVGN
KYRIYDQEEVKKFL

>d1rypa_ d.153.1.4 (A:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

AGYDRHITIFSPEGRLYQVEYAFKATNQTNINSLAVRGKDCVVISQKKVPDKLLDPTTVSYIFCISRTI
GMVVNGPIPDARNAALRAKAEAAEFYKYGYDMPCDVLAKRMANLSQIYTQRAYMRPLGVILTFVS
VDEELGPSIYKTDPAAGYVGYKATATGPKQQEITTNLENHFKKSKIDHINEESWEKVVFAITHMIDA
LGTEFSKNDLEVGVA TKDKFFTLAENIEERLVAIAEQD

>d1rypb_ d.153.1.4 (B:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

MTDRYSFSLTTFSPSGKLGQIDYALTAVKQGVTSLGIKATNGVVIATEKKSSSPLAMSETLSKVSLTPD
IGAVYSGMGPDYRVLVDKSRKVAHTSYKRIYGEYPPTKLLVSEVAKIMQEATQSGGVVPFVSVLLIAGH
DEFNGFSLYQVDPGSGYFPWKATAIGKGSVAAKTFLEKRWNDELELEDAIHIALLLTKESVEGEFNGD
TIELAIIGDENPDLLGYTGIPDKGPRFRKLTQSIEINDRLEAL

>d1rypc_ d.153.1.4 (C:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

GSRRYDSRTTIFSPEGRLYQVEYALESISHAGTAIGIMASDGIVLAAERKVTSTLLEQDTSTEKLYKLND
KIAVAVAGLTADAEILINTARIHAQNYLKYTNEDIPVEILVRRLSDIKQGYTQHGGLRPFVSVFIYAGYD
DRYGYQLYTSNPSGNYTGWKAISVGANTSAAQTLQMDYKDDMKVDDAIELALKTLKTTDSSALT
YDRLEFATIRKGANDGEVYQKIFKPQEIKDILVKTGIT

>d1rypd_ d.153.1.4 (D:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

GYDRALSIFSPDGHFQVEYALEAVKRGTCAVGKGNKCVVLCERRSTLKLQDTRITPSKVSKIDSHV
VLSFSGLNADSRILIEKARVEAQSHRLTLEDPVTVEYLTRYVAGVQQRYSQSGGVVPFVSVTLIAGFDP
RDDEPKLYQTEPSGIYSSWSAQITGRNSKTVREFLEKNYDRKEPPATVEECVKTIVRSLEVVQGTGAK
NIEITVVKPDSDIVALSSEEINQYVTQIEQEKQEQ

>d1rype_ d.153.1.4 (E:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

DRGVSTFSPEGRLFQVEYSLEAIKLGSTAIGIATKEGVVLGVEKRATSPLLESDSIEKIVEIDRHIGCAM

SGLTADARSMIEHARTAAVTHNLYYDEDINVESLTQSVCDLALRFEGEGASGEERLMSRPFVALLIAG
HDADDGYQLFHAEPSTFYRYNAKAIGSGSEGAQAE LLNEWHSSLTLKEAELLVLKILKQVMEEKLD
ENNAQLSCITKQDGFKIYDNEKTAELIKELKEKEAAE

>d1ryp_f_ d.153.1.4 (F:) Proteasome alpha subunit (non-catalytic) {Baker's yeast
(*Saccharomyces cerevisiae*)}

FRNNYDGDVTFTSPTGRLFQVEYALEAIKQGSVTVGLRSNTHAVLVALKRNADELSSYQKKIICDEH
MGLSLAGLAPDARVLSNYLRQQCNYSLVFNRLAVERAGHLLCDKAQKNTQSYGGRPYGVGLLIIG
YDKSGAHLLEFQPSGNVTELYGTAIGARSQGAKTYLERTLDTFIKIDGNPDELKAGVEAISQSLRDES
LTVDNLSIAIVGKDTPTFIYDGEAVAKYI

>d1rypg_ d.153.1.4 (G:) Proteasome alpha subunit (non-catalytic) {Baker's yeast
(*Saccharomyces cerevisiae*)}

GTGYDLSNSVDFSPDGRNFQVEYAVKAVENGTTSIGIKCNDGVVFAVEKLITSKLLVPQKNVKIQVDR
HIGCVYGLIPDGRHLVNRGEEAASFVKLYKTPPIPAFADRLGQYVQAHTLYNSVRPFGVSTIFGGV
DKNGAHLMLPEPSGSYWGKGAATGKGRQSAKAELEKLVDDHPEGLSAREAVKQAAKIIYLAHEDN
KEKDFELEISWCSLSETNGLHKFVKGDLLQE AIDFAQKEIN

>d1ht1a_ d.153.1.4 (A:) HslV (ClpQ) protease {*Escherichia coli*}

TTIVSVRRNGHVVIAGDGQATLGNVTVMKGNVKKVRRRLYNDKVIAGFAGGTADAFTLFELFERKLEM
HQGHVKA AVELAKDWRTDRMLRKLEALLAVADE TASLIITGNGDVVQPENDLIAIGSGGPYAQAAA
RALLENTELSAREIAEKALDIAGDICIYTNHFHTIEELSYK

>d1jjwa_ d.153.1.4 (A:) HslV (ClpQ) protease {*Haemophilus influenzae*}

TTIVSVRRNGQVVVGGDGQVSLGNVTVMKGNARKVRRRLYNGKVLGAFAGGTADAFTLFELFERKLEM
HQGHLLKSAVELAKDWRTDRALRKLEAMLIVADEKESLIITGIGDVVQPEEDQILAIGSGGNYSALSA
RALVENTELSAHEIVEKSLRIAGDICVFTNTNFTIEELP

>g1apy.1 d.153.1.5 (A;B:) Glycosylasparaginase (aspartylglucosaminidase, AGA) {Human
(*Homo sapiens*)}

SPLPLVVNTWPFKNATEAAWRALASGGSDAVESGCAMCEREQCDGSGVFGGSPDELGETTLDA
MIMDGTMDVGA VGLRRIKNAIGVARKVLEHTTHTLLVGESATTFAQSMGFINE DLSTSASQALHS
DWLARNCPNYWRNVIPDPSKYCGPYKPPXTIGMVVIHKTGHIAAGTSTNGIKFKIHGRVGDSPPIG
AGAYADDTAGAAAATGNGDILMRFLPSYQAVEYMRRGEDPTIACQKVISRIQKHFPEFFGAVICANVT
GSYGAACNKLSTFTQFSFMVYNSEKNQPTTEEKVDCI

>g2gac.1 d.153.1.5 (A;B:) Glycosylasparaginase (aspartylglucosaminidase, AGA)
{*Flavobacterium meningosepticum*}

NKPIVLSTWNFGLHANVEAWKVLKGGKALDAVEKGVRLVEDDPTERSVGYGGRPDRDGRVTLDAC
IMDENYNI GSVACMEHIKNPISVARAVMEKTPHVMLVGDGALEFALSQGFKKENLLTAESEKEWKE
WLKTXCIGMIALDAQGNLSGACTTSGMAYKMHGRVGDSPHIGAGLFDNEIGAATATGHGEEVIRTV
GTHLVVELMNQGRTPQQACKEAVERIVKIVNRRGKLNKDIQVGFIALNKKGEYGAYCIQDGFNFVAVH
DQKGNRLETP

>d1b65a_ d.154.1.1 (A:) L-aminopeptidase D-Ala-esterase/amidase {*Ochrobactrum
anthropi*}

KPRARDLGLPFTGVTGPYNAITDVDG VGVGFQTIENEP RPRGRKPARSGVTAILPHMQSETPVPVYA
GVHRFNNGEMTGTHWIEDGGYFLGPVVITNTHGIGMAHHATVRWMVDRYASTYQTD DDFLWIMP
VVAETYD GALNDINGFPVTEADVRKALDNVAGSPVQEGNCGGGTGMITYGFKGGTGTASRVVEFGGR
SFTIGALVQANHGQRDWLTIAGVPVQGHMRDGT PQSQLQERGSIIIVLATDLPLMPHQLKRLARRAS
IGIRNGTPGGNNSGDIFIAFSTANQRPMQHRSAFLD VEMVNDEPLD TVYLA AVDSVEEAVVNAMI

AAEDMGGTPFDRLLVQAIDHERLRAVLRQYGRLA

>g1pya.1 d.155.1.1 (A;B:) Histidine decarboxylase {*Lactobacillus* sp., strain 30a}
SELDAKLNKLGVDRIAISPYKQWTRGYMEPGNIGNGYVTGLKVDAGVRDKSDDVLDGIVSYDRAE
TKNAYIGQINMTTASXFTGVQGRVIGYDILRSPEVDKAKPLFTETQWDGSELPIYDAKPLQDALVEYF
GTEQDRRHYPAPGSFIVCANKGVTAERPKNADMKPGQGYGVWSAIAISFAKDPTKDSSMFVEDAG
VWETPNEDELLEYLEGRRKAMAKSIAECGQDAHASFESSWIGFAYTMMEPGQIGNAITVAPYVSLPI
DSIPGGSILTPDKDMEIMENLTMPEWLEKMGYKLSLANNALKY

>d1jl0a_d.156.1.1 (A:) S-adenosylmethionine decarboxylase {Human (*Homo sapiens*)}
HFFEGTEKLEEVWFSRQPDANQGGDLRTIPRSEWDILLKDVQCSIISVTKTDKQEAYVLESSMFV
SKRRFILKTCGTTLLKALVPLLKARDYSGFDSIQSFFYSRKNFMKPSHQGYPHRNFQEEIEFLNAIF
PNGAGYCMGRMNSDCWYLYTLDFPESRVISQPDQTLLEILMSELDPAVMDQFYMKGDVTAQDVRE
SGIRDLIPGSVIDATMFNPGYSMNGMKSDGTYWTIAITPEPEFSYVSFETNLSQTSYDDLIRKVVVEV
FKPGKFVTTLFVNQSSKCRVTLASPKIEGFKRLDCQSAMFNDYNFVFTSFACKQ

>d2bc2a_d.157.1.1 (A:) Zn metallo-beta-lactamase {*Bacillus cereus*}
TVIKNETGTISISQLNKNVWVHTELGSFNGEAVPSNGLVLNNTSKGLVLDSSWDDKLTKELIEMVEK
KFQKRVTDVIIITHAHADRIGGIKTLKERGIKAHSTALTAELAKKNGYEEPLGDLQTVTNLKFNGMKV
ETFYPGKGHTEDNIVVWLPQYNILVGGALVKSTSADLGNVADAYVNEWSTSIENVLKRYRNINAVV
PGHGEVGDKGLLLHTLDLLK

>d1a7ta_d.157.1.1 (A:) Zn metallo-beta-lactamase {*Bacteroides fragilis*}
SVKISDDISITQLSDKVYTYVSLAEIEGWGMVPSNGMIVINNHQAALLDTPINDAQTEMLVNWVTD
LHAKVTTFIPNHWHGDCIGGLGYLQRKGVQSYANQMTIDLAKKGLPVPEHGFTDSLTVSLDGMPL
QCYLLGGGHATDNIVVWLPTENILFGGCMKLDNQTTSIGNISDADVTAWPKTLDKVKAKFPSARYV
VPGHGNYGTELIEHTKQIVNQYIESTS

>d1smla_d.157.1.1 (A:) Zn metallo-beta-lactamase {*Xanthomonas maltophilia*}
EVPLPQLRAYTVDASWLQPMAPLQIADHTWQIGTEDLTALLVQTPDGAVLLDGGMPQMASHLLDN
MKARGVTPRDLRLLSHAHADHAGPVAELKRRTGAKVAANAESAVALARGGSDDLHFGDGITYPP
ANADRIVMDGEVITVGGIVFTAHFMAHGHTPGSTAWTWTDTNRNGKPVRIAYADSLAPGYQLQGNPR
YPHLIEDYRRSFATVRALPCDVLLTPHPGASNWDYAAGARAGAKALTCKAYADAAEQKFDGQLAKET
AG

>d1jjea_d.157.1.1 (A:) Zn metallo-beta-lactamase {*Pseudomonas aeruginosa*, IMP-1}
SLPDLKIEKLEDEGVYVHTSFEEVNGWGVVPKHGLVVLVNAEAYLIDTPFTAKDTEKLVTFVVERGYK
IKGSISSHFHSDSTGGIEWLNSRSIPTYASELTNELLKKDKGVQATNSFSGVNYWLKKNKIEVFYPPGPG
HTPDNVVWVWLPKILFGGCFIKPYGLGNLGDANIEAWPKSAKLLKSKYKAKLVVPSHSEVGDASL
LKLTLEQAVKGLNESKK

>d1qh5a_d.157.1.2 (A:) Glyoxalase II (hydroxyacylglutathione hydrolase) {Human (*Homo sapiens*)}
MKVEVLPALTDNYMYLVIDDETKEAAIVDPVQPQKVVDAAARKHGVKLTTVLTHHHWDHAGGNEK
LVKLESLKVGDDDRIGALTHKITHLSTLQVGLNVKCLATPCHTSGHICYFVSKPGGSEPPAVFTGD
TLFVAGCGKFYEGTADEMCKALLEVLGRLPPDTRVYCGHEYTINNLKFARHVEPGNAAIREKLAWA
KEKYSIGEPTVPSTLAEFTYNPFMRVREKTVQHQAGETDPVTTMRAVRREKQFKMPRD

>d1e5da2 d.157.1.3 (A:2-250) Rubredoxin oxygen:oxidoreductase (ROO), N-terminal domain {*Desulfovibrio gigas*}
QATKIIDGFHLVGAIDWNSRDFHGYTLSPMGTTYNAYLVEDEKTTLFDTVKAEYKGELLCGIASVIDP
KKIDYLVIIQHLELDHAGALPALIEACQPEKIF'TSSLGQKAMESHFHYKDWPVQVVKHGETLSLGRKRT

VTFYETRMLHWPDSMVSWFADEKVLISNDIFGQNIASERFSDQIPVHTLERAMREYYANIVNPYA
PQTLKAIETLVGAGVAPEFICPDHGVIFRGADQCTFAVQKYVEYAEQK

>d1a6q_ d.158.1.1 (-) Protein serine/threonine phosphatase 2C {Human (Homo sapiens)}
GAFLDKPKMEKHNAQQGNGRLRYGLSSMQGWRVEMEDAHTAVIGLPSGLESWSFFAVYDGHAGSQ
VAKYCCEHLLDHITNNQDFKGSAGAPSVENVKNGIRTGFLEIDEHMRVMSEKKHGADRSGSTAVGVL
ISPQHTYFINCGDSRGLLCRNRKVHFFTQDHKPSNPLEKERIQNAGGSVMIQRVNGSLAVSRALGDF
DYKCVHKGKPTQLVSPEPEVHDIERSEEDDQFILACDGIWDVMGNEELCDFVRSRLEVTDDLEKV
CNEVVDTCLYKGSRDNMSVILICFPNAPKVSPEAVKKEAELDKYLECRVEEIIKKQEGVDPDLVHVMR
TLASENIPSLPPGGELASKRNVIEAVYNRLNPY

>d4kbp2 d.159.1.1 (A:121-432) Plant purple acid phosphatase, catalytic domain {Kidney
bean (Phaseolus vulgaris)}

QTGLDVPYTFGLIGDLGQSFDSTTLSHYELSPKKGQTVLVFGDLSYADRYPNHDNVRWDTWGRFT
ERSVAYQPWIWTAGNHEIEFAPEINETEFPKPFYSRYHVPYEASQSTSPFWYSIKRASAHIIIVSSYSAY
GRGTPQYTWLKKELRKVKRSETPWLIVLMHSPLYNSYNHHFMEGEAMRTKFEAWFVKYKVDVVF
AGHVHAYERSERSVNIAYKITDGLCTPVKDQSAPVYITIGDAGNYVIDSNMIQPQPEYSAFREASFG
HGMFDIKNRTHAHFSWNRNQDGVAVEADSVWFFNRHWYPVDDST

>d1qhwa_ d.159.1.1 (A:) Mammalian purple acid phosphatase {Rat (Rattus norvegicus)}
STLRFVAVGDWGGVNPAPFHTAREMANAKEIARTVQIMGADFIMSLGDNFYFTGVHDANDKRFQE
TFEDVFSRDLRNIPWYVLAGNHDHLGNVSAQIAYSKISKRWNFPSYYRLRFKVPNSNITVAIFML
DTVMLCGNSDDFVSQQPEMPRDLGVARTQLSWLKKQLAAAKEDYVLVAGHYPIWSIAEHGPTRCLV
KNLRPLLAAYGVTAYLCGHDHNLQYLQDENGVGIVLSGAGNFMDPSVRHQKVPNGYLRFHGSED
SLGGFTYVEIGSKEMSITYVEASGKSLFKTSLPRRP

>d1utea_ d.159.1.1 (A:) Mammalian purple acid phosphatase {Pig (Sus scrofa)}
PTPILRFVAVGDWGGVNPAPFHTAREMANAKAIATTVKTLGADFILSLGDNFYFTGVHDAKDKRFQ
ETFEDVFSRDLRNIPWYVLAGNHDHLGNVSAQIAYSKISKRWNFPSYYRLRFKIPNSNVSVAIFM
LDTVTLGNSDDFVSQQPERPRNLALARTQLAWIKKQLAAAKEDYVLVAGHYVWWSIAEHGPTHCL
VKQLPLLTTHKVTAYLCGHDHNLQYLQDENGVLGVLGAGNFMDPSKHLRKPNGYLRFHFGAE
NSLGGFAYVEITPKEMSVTYIEASGKSLFKTKLPRRA

>d1ii7a_ d.159.1.4 (A:) Mre11 {Archaeon Pyrococcus furiosus}
MKFAHLADIHLGYEQFHQPQREEFQAEAFKNALEIAVQENVDFILIAGDLFHSSRSPGTLKKAIAL
QIPKEHSIPVFAIEGNHRTQRGPSVLNLLDFGLVYVIGMRKEKVENEYLTSERLNGEYLVKGVYK
DLEIHGMKYMSSAWFEANKEILKRLFRPTDNAILMLHQGVREVSEARGEDYFEIGLGDLPYLYYA
LGHYHRYETSYSVPGSLERWDFGDYEVRYEWDGIKFKERYGVNKGFYIVEDFKPRFVEIKV
RPFIDVKIKGSEEEIRKAIKRLIPLIPKNAYVRLNIGWRKPFDLTEIKELLNVEYLKIDTWRI

>d1ush_2 d.159.1.2 (26-362) 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal
domain {Escherichia coli}

YEQDKTYKITVLTNDHGHGFWRNEYGEYGLAAQKTLVDGIRKEVAEAGGSVLLSGGDINTGVPE
SDLQDAEPDFRGMNLVGYDAMAIGNHEFDNPLTVLRQKEKWKAFPLLSANIYQKSTGERLFPKVAL
FKRQDLKIAVIGLTTDDTAKIGNPEYFTDIEFRKPADEAKLVIQELQQTEKPDIIAATHMGHYDN
HGSNAPGDVEMARALPAGSLAMIVGGHSQDPVCMMAENKKQVDYVPGTPCKPDQNGIWIWQAHE
WGKYVGRADFERNEMKMVNYQLIPVNLKKKVTWEDGKSERVLYTPEIAENQQMISLLSPFQNK
GKAQLEV

>d1jk7a_ d.159.1.3 (A:) Protein phosphatase-1 (PP-1) {Human (Homo sapiens)}
KLNIDSIIQRLLVVRGSKPGKNVQLQENEIRGLCLKSREIFLSQPILLELEAPLKICGDIHGQYYDLLRL

FEYGGFPPESNYLFLGDYVDRGKQSLETICLLLAYKIKYPENFFLLRGNHECASINRIYGFYDECKRRY
NIKLWKTFTDCFNCLPIAAIVDEKIFCCHGGLSPDLQSMEQIRIRMRPTDVPDQGLLCDLLWSDPK
DVLGWGENDRGVSFTFGAEVVAKFLHKHDLICRAHQVVEDGYEFFAKRQLVTLFSAPNYCGEFD
NAGAMMSVDETLMCSFQILKPA

>d1tcoa_ d.159.1.3 (A:) Protein phosphatase-2B (PP-2B, calcineurin A subunit) {Cow (Bos taurus)}

VPFPPSHRLTAKEVFDNDGKPRVDILKAHLMKEGRLEETVALRIITEGASILRQEKNLLDIDAPVTV
GDIHGQFFDLMKLFEVGGSPANTRYLFLGDYVDRGYFSIECVLYLWALKILYPKTLFLLRGNHECRHL
TEYFTFKQECKIKYSERVYDACMDAFDCLPLAALMNQQFLCVHGGLSPEINTLDDIRKLDRFKEPPA
YGPMDILWSDPLEDFGNEKTQEHFTHNTVTRGCSYFYSYPVAVCEFLQHNNLLSILRAHEAQDAGYR
MYRKSQTTGFPSLITIFSAPNYLDVYNNKAAVLKYENNVNIRQFNCSHPYWLPNFMDVFTWVSLP
FVGEKVTEMLVNLNIC

>d1aui_ d.159.1.3 (A:) Protein phosphatase-2B (PP-2B, calcineurin A subunit) {Human (Homo sapiens)}

TDRVVKAVPFPSSHRLTAKEVFDNDGKPRVDILKAHLMKEGRLEESVALRIITEGASILRQEKNLLDI
DAPVTVCGDIHGQFFDLMKLFEVGGSPANTRYLFLGDYVDRGYFSIECVLYLWALKILYPKTLFLLRG
NHECRHLTEYFTFKQECKIKYSERVYDACMDAFDCLPLAALMNQQFLCVHGGLSPEINTLDDIRKLD
RFKEPPAYGPMCDILWSDPLEDFGNEKTQEHFTHNTVTRGCSYFYSYPVAVCEFLQHNNLLSILRAHEA
QDAGYRMYRKSQTTGFPSLITIFSAPNYLDVYNNKAAVLKYENNVNIRQFNCSHPYWLPNFMDV
FTWVSLPFVGEKVTEMLVNLNICSDELGSEEDGFDGATAAARKEVIRNKIRAIGKMARVFSVLR
SESVLTLKGLTPTGMLPSGVLSSGKQTLQATVEAIEADEAIKGFSPQHKITSFEEAKGLDRINERMPP
R

>d1g5ba_ d.159.1.3 (A:) lambda ser/thr protein phosphatase {Bacteriophage lambda}

MRYYEKIDGSKYRNIWVVVDLHGCTNLNMLKLDITIGFDNKKDLLISVGDVDRGAENVECLELITFP
WFRVAVRGNHEQMMIDGLSERGNVNHVLLNGGGWFFNLDYDKEILAKALAHKADELPLIIELVSKD
KKYVICHADYPFDEYEFKGPVDHQVIVNRRERISNSQNGIVKEIKGADTFIFGHTPAVKPLKFNQM
YIDTGAVFCGNLTIQVQGA

>d1emsa2 d.160.1.1 (A:10-280) NIT-FHIT fusion protein, N-terminal domain {Nematode (Caenorhabditis elegans)}

MATGRHFIAVCQMTSDNDLEKNFQAAKNMIERAGEKKCEMVFLPECFDFIGLNKNEQIDLAMATD
CEYMEKYRELARKHNIWLSLGGGLHHKDPDAAHPWNTHLIIDSDGVTRAEYNKLHLFDLEIPGKVR
LMESEFSKAGTEMIPPVDTPIGRLGLSICYDVRFPESLWNRKGAQLLSFPSAFTLNTGLAHWETL
LRARAIENQCYVVAQAQTGAHNPKRQSYGHSMVVDPWGAVVAQCSERVDMCFAEIDLSYVDTLRE
MQPVFSHR

>d1f89a_ d.160.1.1 (A:) hypothetical protein y185 {Baker's yeast (Saccharomyces cerevisiae)}

SASKILSQKIKVALVQLSGSSPDKMANLQRAATFIERAMKEQPDTKLVVLPECFNSPYSTDQFRKYSE
VINPKEPSTSVQFLSNLANKFKIILVGGTIPELDPKTDKIYNTSIIFNEDGKLIDKHKRVHLFDVDIPNG
ISFHESETLSPGEKSTTIDTKYGFVGVGICYDMRPELAMLSARKGAFAMIYPSAFNTVTGPLHWHL
ARSAVDNQVYVMLCSPARNLQSSYHAYGHSIVVDPRGKIVAEAGEGEEIYAELDPEVIESFRQAVPL
TKQRRF

>d1erza_ d.160.1.2 (A:) N-carbamoyl-D-amino acid amidohydrolase {Agrobacterium sp.}

TRQMILAVGQQGPIARAETREQVVRLDMLTKAASRGANFIVFPELALTTFFPRWHFTDEAELDSF
YETEMPGPVVRPLFEKAAELGIGFNLGYAELVVEGGVKRRFNNTSILVDKSGKIVGKYRKIHLPGHKEY
EAYRPFQHLKRYFEPDGLGFPVYDVDAKMGMFICNDRRWPEAWRVMGLRGAEICGGYNTPTH

NPPVPQHDHLTSFHLLSMQAGSYQNGAWSAAAGKVGMEENCMLLGHSCIVAPTGEIVALTTTLED
EVITAAVDLDRCRELREHIFNFKQHRQPQHYGLIAEL
>d1hq0a_d.194.1.1 (A:) Type 1 cytotoxic necrotizing factor, catalytic domain {Escherichia coli}
SIESTSKSNFQKLSRGNIDVLKGRGSISSTRQRAIYPYFEANADEQQPLFFYIKKDRFDNHGYDQYFY
DNTVGPNGIPTLNTYTGEIPSDSSSLGSTYWKYKYNLTNETSIIRVSNARSARGANGIKIALEEVQEGKPVII
TSGNLSGCTTIVARKEGYIYKVHTGTTKSLAGFTSTTGKAVEVLELLTKEPIPRVEGIMSNDFLVDY
LSENFEDSLITYSSSEKKPDSQITIIRDNVSVFPYFLDNIPEHGFGTSATVLRVDGNVVVRSLSSESYSL
NADASEISVLKVFSSKF
>d1qdl_a_d.161.1.1 (A:) Anthranilate synthase aminodeoxyisochorismate synthase/lyase
subunit, TrpE {Archaeon Sulfolobus solfataricus}
AMEVHPISEFASPFVFKCIERDFKVGAGLLESIGGPQYKARYSVIAWSTNGYLKIHDDPVNINLNGYLD
LKLADIPGLFKGGMIGYISYDAVRFWEKIRDLKPAEDWPYAEFFTPDNIIYDHNEGKVYVNDLSS
VGGCGDIGEFKVSFYDESLNKNYSYERIVSESELEYIRSGYIFQVVLRSFYRYIFSGDPLRIYYNLRINPSP
YMFYLFDEKYLIGSSPELLFRVQDNIVETYPYIAGTRPRGADQEEDLKELELMNSEKDKAEHLMLV
DLARNDLGKVCVPGTVKPELMYVEKYSHVQHIVSKVIGTLKKKYNALNVLSTFPAGTVSGAPKP
MAMNIETLEEYKRGYPYAGAVGFISADGNAEFAIARTAFNLKELLRIHAGAGIVYDSNPESEYFETEH
KLKALKTAIGVR
>d1i1qa_d.161.1.1 (A:) Anthranilate synthase aminodeoxyisochorismate synthase/lyase
subunit, TrpE {Salmonella typhimurium}
KPTLELLTCDAAAYRENPTALFHQVCGDRPATLLESADIDSKDDLKSLLLVDSALRITALGDTVTIQUAL
SDNGASLLPLLDLTPAGVENDVLPAGRVLRFPPVSPLLDENARLCSLSVFDALRLLQGVVNIPTQER
EAMFFGGLFAYDLVAGFEALPHLEAGNCPDYCFYLAETLMVIDHQKSTRIQASLFTASDREKQRL
NARLAYLSQQLTQPAPLPVTPVPMRCECNQSDDAFGAVVRQLQKAIRAGEIFQVVPSSRRFSLPCPS
PLAAYYVLKKNPSPYMFFMQDNDFTLFGASPESSLKYDAASRQIEIYPIAGTRPRGRRADGTLDRDL
DSRIELDMRTDHKELSEHLMLVDLARNDLARICTPGSRYVADLTKVDRYSYVMHLVSRVVGELRHDL
DALHAYRACMNMGTLGAPKVRAMQLIADAEGQRRGSYGGAVGYFTAHDGLDTCIVIRSALVENGIA
TVQAGAGIVLDSVPQSEADETRNKARAVLRAIATAHHA
>d1i7qa_d.161.1.1 (A:) Anthranilate synthase aminodeoxyisochorismate synthase/lyase
subunit, TrpE {Serratia marcescens}
TKPQLTLLKQVQSYRGDPTTLFHQLCGARPATLLESAEINDKQNLQSLVIDSALRITALGHTVSVQA
LTANGPALLPLLDEALPPEVRNQARPNGRELTFFPAIDAVQDEDARLRSLSVFDALRILTILVDSPADER
EAVMLGGLFAYDLVAGFENLPALRQDQRCPDFCFYLAETLLVLDHQRGSRARLQASVFSEQASEAQL
QHRLEQLQAEQQPPPIPHQKLENMQLSCNQSDEEYGAVVSELQEAIRQGEIFQVVPSSRRFSLPCPA
PLGPYQTLKDNNSPYMFFMQDDFTLFGASPESSALKYDAGNRQIEIYPIAGTRPRGRRADGSLDLD
LDSRIELEMRTDHKELAEHLMLVDLARNDLARICQAGSRYVADLTKVDRYSFVMHLVSRVVGTLRA
DLVHAYQACMNMGTLGAPKVRAMQLIAALRSTRRGSYGGRVGYFTAVRNLDTCIVIRSAYVEDG
HRTVQAGAGVVQDSIPEREADETRNKARAVLRAIATAHHAKEVF
>d1k0ga_d.161.1.1 (A:) P-aminobenzoate synthase component I {Escherichia coli}
MKTLSPAVITLLWRQDAAEFYFSRLSHPWAMLLHSGYADHPYSRFDIVVAEPICTLTTFGKETVSE
SEKRTTTTDDPLQVLQVLDRADIRPTHNEDLPFQGGALGLFGYDLGRRFESLPEIAEQDIVLPDMA
VGIYDWALIVDHQRHTVSLSHNDVNARRAWLESQQFSPQEDFTLTSWQSNMTREQYGEKFRQV
QEYLHSGDCYQVNLQRFHATYSGDEWQAFQLNQNANRAPFSAFLRLEQGAILSLSPERFILCDNSEI
QTRPIKGTLPRLPDPQEDSKQAVKLANSAKDRAENLMIVDLMRNDIGRVAVAGSVKVPPELFFVVEFPF

AVHHLVSTITAQLPEQLHASDLLRAAFPGGSSITGAPKVRAMEIIDELEPQRRNAWCGSIGYLSFCGNM
DTSITIRTLTAINGQIFCSAGGGIVADSQEEAEYQETFDKVNRIKQLEK
>d1mla2 d.162.1.1 (A:145-313) Malate dehydrogenase {Pig (Sus scrofa)}
VTTLDIVRANAFVAELKGLDPAVSVVIGGHAGKTIIPISQCTPKVDFPQDQLSTLTGRIQEAGTEV
VKAKAGAGSATLSMAYAGARFVFSVLDAMNGKEGVVECSFVKSQETDCPYFSTPLLLGKKGIEKNLGI
GKISPFEEKMIAEAIPELKASIKKGEEFVKNM
>d5mdha2 d.162.1.1 (A:155-333) Malate dehydrogenase {Pig (Sus scrofa)}
TRLDHNRAKAQIALKLGVTSDVKNVHWNHSSSTQYPDVNHAKVKLQAKEVGVYEAVKDDSWLK
GEFITTVQQRGAAVIKARKLSSAMSAAKAICDHVRDIWFGTPEGEFVSMGIISDGNYSYVPPDLLYSF
PVTIKDKTWKIVEGLPINDFSREKMDLTAKELAEKETAFAFEFLSSA
>d7mdha2 d.162.1.1 (A:198-385) Malate dehydrogenase {Sorghum (Sorghum vulgare),
chloroplast}
TRLDENRAKQQLALKAGVFYDKVSNVTIWNHSTTQVPDFLNAKIDGRPVKEVIKRTKWLEEEFTI
TVQKRGGALIQKWGRSSAASTAVSIADAIAKSLVTPTEGDWDFSTGVYTTGNPYGIAEDIVFSMPCRSK
GDGDYELATDVSNDLFLWERIKKSEAELLAEKKCVAHLTGEGNAYCDVPEDTML
>d1civa2 d.162.1.1 (A:194-385) Malate dehydrogenase {Flaveria bidentis, chloroplast}
TRLDENRAKQQLALKAGVFYDKVSNVTIWNHSTTQVPDFLNAKIHGIPVTEVIRDRKWLEDEFTN
MVQTRGGVLIKKWGRSSAASTAVSIVDAIRSLVTPTEGDWDFSTGVYTTGNPYGIAEDIVFSMPCRSK
GDGDYEFVKDVIFDDYLSKKIKKSEDELLAEKKCVAHLTGEGIAVCDLPEDTMLPGEM
>d2cmd_2 d.162.1.1 (146-312) Malate dehydrogenase {Escherichia coli}
VTTLDIIRSNFVAELKKGQPEVEVPVIGGHSGVTILPLLSQVPGVSFTEQEVAADLTAKRIQNAAGTEVV
EAKAGGGSATLSMGQAAARFGLSLVRALQGEQGVVECAAYVEGDGQYARFFSQPLLLGKNGVEERKSI
GTLSAFEQNALEGMLDTLKKDIALGQEFVNK
>d1bdma2 d.162.1.1 (A:155-332) Malate dehydrogenase {Thermus flavus}
TRLDHNRAKAQLAKKTGTGVDRIIRMTVWGNHSSIMFPDLFHAEVDGRPALELVDMEWYKVFIP
TVAQRGAIIQARGASSAASAANAIEHIRDVALGTPEGDWVSMVPSQGEYGIPEGIVYSFPVTAKD
GAYRVVEGLEINEFARKRMEITAQELLEMEQVKALGLI
>d2h1pa2 d.162.1.1 (A:163-330) Malate dehydrogenase {Archaeon Haloarcula marismortui}
FGGRLDSARFRYVLSEEFDAPVQNVGVTILGEHGDAQVPVFSKVRVDGTDPEFSGDEKEQLLGDQLQE
SAMDVIERKGATEWGPARGVAHMVEAILHDTGRVLPASVKLEGEFGHEDTAFGVPVRLGNSNGVEEIV
EWDLDDYEQDLMADAAEKLSQYDKIS
>d1b8pa2 d.162.1.1 (A:159-329) Malate dehydrogenase {Aquaspirillum arcticum}
LRLDHNRALSQIAAKTGKPVSSIEKLFVWGNHSPMYADYRYAQIDGASVKDMINDDAWNDRDTFLP
TVGKRGAIIIDARGVSSAASAANAIDHIHDWVLGTAGKWTTMGIPSDGSYGIPEGVIFGFVPTTENG
EYKIVQGLSIDAFSQRINVTNLNELLQNGVQHLLG
>d1guya2 d.162.1.1 (A:144-306) Malate dehydrogenase {Chloroflexus aurantiacus}
AGVLDAARYRTFIAMEAGVSVEDVQAMLMGGHGDEMVPPLPRFSTISGIPVSEFIAPDRLAQIVERTR
KGGGEIVNLLKTSAYYAPAAATAQMVEAVLKDKKRVMVAAYLTGQYGLNDIYFGVPPVILGAGGVEK
ILELPLNEEEMALLNASAKAVRATLDTL
>d1gv0a2 d.162.1.1 (A:143-305) Malate dehydrogenase {Chlorobium tepidum}
AGVLDSARFRSFIAMELGVSMQDVTACVLGGHGDMVPPVVKYTTVAGIPVADLISAERIAELVERTRT
GGAEIVNHLKQGSFAFYSPATSVVEMVESIVLDRKRVLTCVSLDGQYIDGTFVGVPPVILGKNGVEHI
YEIKLDQSDLLQKSAKIVDENCKML
>d1guza2 d.162.1.1 (A:143-305) Malate dehydrogenase {Chlorobium vibrioforme}

AGVLDAARFRSFIAMELGVSMQDINACVLGGHGDAMVPVVKYTTVAGIPISDLLPAETIDKLVERTRN
GGAEIVEHLKQGSAPASSVEMVESIVLDRKRVLPCAVGLEGQYGDKTFVGVKLVGRNGVEQI
YEINLDQADLLQKSAKIVDENCML

>d1hya2 d.162.1.1 (A:167-329) L-2-hydroxyisocaproate dehydrogenase, L-HICDH
{Lactobacillus confusus}

GTLDDTARMQRAVGEAFDLDPRSVSGYNLGEHGNSQFVAWSTVRVMGQPIVTLADAGDIDLAAIEE
EARKGGFTVLNGKGYTSYGVATSAIRIAKAVMADAHAELVVSNNRRDDMGMYLSYPAIIGRDGVLAET
TLDLTTDEQEKLQSRDYIQRFDIVDTL

>d9lta2 d.162.1.1 (A:163-331) Lactate dehydrogenase {Pig (Sus scrofa)}

SGCNLDSARFRYLMGERLGVHPLSCHGWILGEHGDSSVPVWSGVNVAGVSLKLNHPGLTDADKEH
WKAVHKEVVD SAYEVIKLGKGYT SWAIGLSVADLAESIMKNLRRVHPVSTMIKGLYGIKENVFLSVPICL
GQNGISDVVKVTLTPPEEEAHLKKSADTLWGIQKELQF

>d1i0za2 d.162.1.1 (A:161-332) Lactate dehydrogenase {Human (Homo sapiens), heart
isoform (H chain)}

SGCNLDSARFRYLMAEKLGIHPSSCHGWILGEHGDSSVAVWSGVNVAGVSLQELNPEMGTDNSEN
WKEVHKMVVESAYEVIKLGKGYTNWAIGLSVADLIESMLKNLSRIHPVSTMVKGMYGIENEVFLSLPCI
LNARGLTSVINQKLKDDDEVAQLKKSADTLWDIQKDLKD

>d1i10a2 d.162.1.1 (A:160-331) Lactate dehydrogenase {Human (Homo sapiens), muscle
isoform (M chain)}

SGCNLDSARFRYLMGERLGVHPLSCHGWVWVLEHGDSSVPVWSGMNVAGVSLKTLHPDLGTDKDKKE
QWKEVHKQVVESAYEVIKLGKGYT SWAIGLSVADLAESIMKNLRRVHPVSTMVKGMYGIENEVFLSVPICL
ILGQNGISDLVKVTLTSEEEARLKKSADTLWGIQKELQF

>d2ldx_2 d.162.1.1 (160-331) Lactate dehydrogenase {Mouse (Mus musculus)}

SGCNLDSARFRYLIGEKLVNPTSCHGWVWVLEHGDSSVPIWSGVNVAGVTLKSLNPAIGTDKKNKQH
WKNVHKQVVEGGYEVLDKMGKGYT SWAIGLSVADLARSILKNLKRVPVTTLVKGFHGIKEEVFLSIPICL
VLGESGITDFVKVNMATAEEEGLLKKSADTLWNMQKNLEL

>d1ldm_2 d.162.1.1 (161-329) Lactate dehydrogenase {Dogfish (Squalus acanthias)}

SGCNLDSARFRYLMGERLGVHSCSCHGWVIGEHDSSVPSVWSGMNVASIKLHPLDGTNKDKQDWK
KLHKDVVD SAYEVIKLGKGYT SWAIGLSVADLAETIMKNLCRVHPVSTMVKDFYGIKDNVFLSLPCVL
NDHGISNIVKMKLKPNEEQQLQKSATTLWDIQKDLKF

>d1ceqa2 d.162.1.1 (A:164-329) Lactate dehydrogenase {Malaria parasite (Plasmodium
falciparum)}

GGVLDTSRLKYYISQKLVNCPDVDNAHIVGAHGKMKVLLKRYITVGGIPLQEFINNKLISDAELEAIFD
RTVNTALEIVNLHASPYPVAPAAAIIEMAESYLKDLKVKLICSTLLEGQYGHSDIFGGTPVVLGANGVEQ
VIELQLNSEEKAKFDEAIAETKRMKALA

>d1ldna2 d.162.1.1 (A:163-330) Lactate dehydrogenase {Bacillus stearothermophilus}

TILDARFRFLLEGEYFSVAPQNVHAYIIGEHDTELPVWSQAYIGVMPVIRKLVESKGEAAQKDLERIFV
NVRDAAYQIIEKKGATYYGIAMGLARVTRAILHNENAILTVSAYLDGLYGERDVYIGVPAVINRNGIRE
VIEIELNDDEKNRFHSAATLKSVLARAF

>d1llc_2 d.162.1.1 (165-334) Lactate dehydrogenase {Lactobacillus casei}

TSLDARFRQSIEMVNDARSVHAYIMGEHGDTEFPVWSHANIGGVTIAEWWKAHPEIKEDKLVK
MFEDVRDAAYEIIKLGATFYGIATALARISKAILNDENAVLPLSVYMDGQYGINLIGTPAVINRNGI
QNILEIPLTDHEEESMQKSASQLKKVLTDAFAKNDI

>d1ez4a2 d.162.1.1 (A:163-334) Lactate dehydrogenase {Lactobacillus pentosus}

TSLDSSRLRVALGKQFNVDPRSVDAYIMGEHGDSEFAAYSTATIGTRPVDRVAKQGVSDDDLAKLE
DGVRNKAYDIINLKGATFYGIGTALMRISKAILRDENAVLPVGAYMDGQYGLNDIYIGTPAIIGGTGLK
QIIESPLSADELKMQDSAATLKKVLDGLAELEN
>d1llda2 d.162.1.1 (A:150-319) Lactate dehydrogenase {Bifidobacterium longum, strain
am101-2}
TNLDSARLRFLIAQQTGVNVKNVHAYIAGEHGDSEVPLWESATIGGVPMSDWTPLPGHDPLDADKR
EEIHQEVKNAAYKIINGKATNYAIGMSGVDIIEAVLHDTNRILPVSSMLKDFHGISDICMSVPTLLNR
QGVNNTINTPVSDKELAALKRSAETLKETAQFGF
>d1a5z_2 d.162.1.1 (164-333) Lactate dehydrogenase {Thermotoga maritima}
GTVLDTARLRLIAQHCGFSPRSVHVYVIGEHDSEVPVWVGAMIGGIPLQNMCCQVCQKCDKILEN
FAEKTGRAAYEIIERKGATHYAIALAVADIVESIFFDEKRVLTLSVYLEDYLGVKDLCSVPVTLGKHGV
ERILELNLNEEELEAFRKSASILKNAINETAEN
>d1hyea2 d.162.1.1 (A:146-313) MJ0490, lactate/malate dehydrogenase {Archaeon
Methanococcus jannaschii}
LGTHLDSLRFKVAIAKFFGVHIDEVTRTRIIEGHGDSMVPLLSATSIGGIPIQKFERFKELPIDEIIEDVKT
KGEQIIRLKGGESEFGPAAAILNVVRCIVNNEKRLTL SAYVDGEFDGIRDVCIGVVPVKIGRDGIEEVVSI
LDKDEIIAFRKS AEIHKYCEEVKNL
>d1aiha_d.163.1.1 (A:) Integrase {Bacteriophage HP1}
ETELAFLYERDIYRLLAECDNSRNPDLGLIVRICLATGARWSEAETLTQSQVMPYKITFTNTKSKKNR
TVPISDELDFMLPKRGRFLFNDAYESFENAVLRAEIELPKGQLTHVLRHTFASHFMMNGGNILVLKEI
LGHSTIEMTMRYAHFAPSHLES AVKFNPLSNPAQ
>d1ae9a_d.163.1.1 (A:) Integrase (Int) {Bacteriophage lambda}
RSRLTADEYLKIYQAAESSPCWLRRLAMELAVVTGQRVGDLCMKWSDIVDGYLYVEQSKTGVKIAIP
TALHIDALGISMKETLDKCKEILGGETIIASTRREPLSSGTVSRYFMRARKASGLSFEQDPPTFHELRS
LSARLYEKQISDKFAQHLLGHKSDTMASQFRDDRGREWDKIEI
>d1f44a2 d.163.1.1 (A:130-343) Cre recombinase {Bacteriophage P1}
RAKQALAFERTDFDQVRSLMENS DRCQDIRNLAFLGIAYNTLLRIA E IARIRVKDISRTD GGRMLIHIG
RTKTLVSTAGVEKALSLGVTKLVERWISVSGVADDPNNYLF CRVRKNGVAAPSATSQ LSTRALEGIFE
ATHRLIYGAKDDSGQRYLAWSGHSARVGAARDMARAGVSIPEIMQAGGWTNVNIVMNFIRNL DSET
GAMVRLLEDGD
>d5cxb2 d.163.1.1 (B:130-314) Cre recombinase {Bacteriophage P1}
RAKQALAFERTDFDQVRSLMENS DRCQDIRNLAFLGIAYNTLLRIA E IARIRVKDISRTD GGRMLIHIG
RTKTLVSTAGVEKALSLGVTKLVERWISVSGVADDPNNYLF CRVRKNGVAAPSATSQ LSTRALEGIFE
ATHRLIYGAKDDSGQRYLAWSGHSARVGAARDMARAGVSIPEIMQAGG
>d1a0p_2 d.163.1.1 (111-292) Recombinase XerD {Escherichia coli}
KDLSEAQVERLLQAPLIDQPLELRDKAMLEVLYATGLRVSELVGLTMSDISLRQGVV RVIGKGNKERL
VPLGEEAVYWLETYLEHGRPWLLNGVSIDVLFPSQRAQMQMTRQTFWHRIKH YAVLAGIDSEKLSPH
VLRHAFATHLLNHGADLRVVQMLLGHSDLSTTQIYTHVATERLRQLHQ
>d1floa2 d.163.1.1 (A:135-423) F1p recombinase {Baker's yeast (Saccharomyces cerevisiae)}
KGNSSKMLKALLSEGESIWEITEKILNSFEYTSRFTKTKTLYQFLFLATFINCGRFS DIKNVDPKSF
KLVQNKYLGVIIQCLVTETKTSVSRHIYFFSARGRIDPLVYLDEF LRNSEPV LKRVNRTGNSSSNKQEY
QLLKDNLVRSYNKALKKNAPYSIFA IKNGPKSHIGRHLMTSFLSMKGLTELTNVVGNWSDKRASAVA
RTTYTHQITAIPDHYFALVSRYAYDPISKEMIALKDETNP IEEWQHIEQLKGS AEGSIRYPAWNGIISQ
EVL DYLSSYINRRI

>d1a31a1_d.163.1.2 (A:431-626,A:720-765) Eukaryotic DNA topoisomerase I, catalytic core {Human (Homo sapiens)}

PSSRIKGEKDWQKYETARRLKKCVDKIRNQYREDWKSSEMKVRQRAVALYFIDKLALRAGNEKEEG
ETADTVGCCSLRVEHINLHPELDGQEYVVEFDLGLKDSIRYYNKVPVEKRVFKNLQLFMENKQPEDD
LFDRLNTGILNKHLLQDLMEGLTAKVFRTYNASITLQQQLKELTAPDENIPAKILSYNRRANRAVXKLN
LDPRITVAWCKKWGWVPIEKIYNKTQREKFAWAIDMADEDYEF

>d1a41__d.163.1.2 (-) Eukaryotic DNA topoisomerase I, catalytic core {Vaccinia virus}

NAKRDRIFVRVYNVMKRINCFINKNIKSSSTDSNYQLAVFMLMETMFFIRFGKMKYLKENETVGLLT
LKNKHIEISPDEIVIKFVVGKDKVSHEFVVHKSRLYKPLLKLTDDSSPEEFLFNKLSERKVYECIKQFGI
RIKDLRTYGVNYTFLYNFWTNVKSISPLSPKLIALTIKQTAEVVGHTPSISKRAYMATTILEMVKDK
NFLDVVSKTTFDEFSLIVVDHVKS

>d1mhda_d.164.1.1 (A:) SMAD MH1 domain {Human (Homo sapiens)}

PIVKRLLGWKKGEQNGQEEKWCEKAVKSLVKKLKKTGQLDELEKAITTQNVNTKCITIPRSLDGRLLQ
VSHRKGPHVIYCRLLWRWPDLSHSHELRAMELCEFAFMKKDEVCVNPHYHYQRVET

>d1hufa_d.195.1.1 (A:) YopH tyrosine phosphatase N-terminal domain {Yersinia pestis}

LSDLHRQVSRVQVQESGDCGTGLRGNVAANKETTFQGLTIASGARESEKVFQAQTVLSHVANVVLTLQ
EDTAKLLQSTVKHNLNNYDLRSVGNNGSVLVSLSRSDQMTLQDAKVLLEAALRQES

>d1mrj__d.165.1.1 (-) alpha-Trichosanthin {Mongolian snake gourd (Trichosanthes kirilowii maxim)}

DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPQSRYALIHLYADETISVAIDVTNVYI
MGYRAGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAAGKIRENIPLGLPALDSAITT
LFYYNANSAASALMVLIQSTSEAARYKFIEQQIGKRVDKTFPLSLAISLENSWSALSQKIQIASTNNG
QFESPVVLINAQNQRVTITNVDAGVVTSNIALLLNRNMA

>d1bryy_d.165.1.1 (Y:) Bryodin {Red briony (Bryonia dioica)}

DVSFRLSGATTTSYGVFIKLNREALPYERKVYNIPLLRSSISGSGRYTLLHLYADETISVAVDVTNVY
IMGYLAGDVSYFFNEASATEAAKFVFKDAKKKVTLPYSGNYERLQTAAGKIRENIPLGLPALDSAITTL
YYYTASSAASALLVLIQSTAESARYKFIEQQIGKRVDKTFPLSLATISLENNWSALSQKIQIASTNNGQF
ESPVVLIDGNNQRVSITNASARVVTSNIALLLNRNNA

>d1mrg__d.165.1.1 (-) alpha-Momorcharin (momordin) {Bitter gourd (Momordica charantia)}

DVSFRLSGADPRSYGMFIKDLRNALPFREKVYNIPLLLPSVSGAGRYLLMHLFNDRDGKTITVAVDVTN
IYIMGYLADTTSYFFNEPAAELASQYVFRDARRKITLPYSGDYERLQIAAGKPREKIPIGLPALDSAIST
LLHYDSTAAAGALLVLIQTAAEARFKYIEQQIQERAYRDEVPSLATISLENSWSGLSKQIQLAQGNNG
IFRTPIVLVDNKGNRVQITNVTSKVVTSNIQLLLNRNI

>d1cf5a_d.165.1.1 (A:) Beta-momorcharin {Bitter gourd (Momordica charantia)}

DVNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLNLTSYAYETISVAIDVTNVYV
VAYRTRDVSYFFKESPEAYNILFKGTRKITLPYTGNYENLQTAHKIRENIDLGLPALSSAITTLFYNN
AQSAASALLVLIQTAAEARFKYIERHVAKYVATNFKPNLAISLENQWSALSQKIFLAQNQGGKFRN
PVDLIKPTGQRFQVTNVDSDVVKGNIKLLLNSRASTADEN

>d1ce7a_d.165.1.1 (A:) Mistletoe lectin I A-chain {European mistletoe (Viscum album)}

YERGLDVTAAQTGAGYFSFITLLRDYVSSGSFSNAIPLLSQSGGGGEAGRFVLVELTNSGGDGITVAID
VTNLYVVAYQAGSQSYFLSGPGRHGFTGTTRSSLPFNQSYDPLEQYGGQRKQIPLGIDQLIQSVTALK
FPGSTRTGARSILILIQMISEAARFNPIWRARQYINS GASFLPDVYMLELETSSWGGQSTQVQHSTDG
VFNNPIALADPGGGVTLTNVRDVIASLAIMLFVC

>d1abra_d.165.1.1 (A:) Abrin A-chain {Abrus precatorius}
EDRPIKFSTEGATSQSYKQFIEALRERLRGGLIHDPVLPDPTTLQERNRYITVELSNSDTESEIEVGIDV
TNAYVVAYRAGTQSYFLRDAPSSASDYLFRTGTDQHSLPFYGYGDLERWAHQSRQIPLGLQALTHGI
SFFRSGGNDNEEKARTLIVIIQMVAEAARFRYISNRVRSIQGTAFQPDAAAMISLENNWDNLSRGVQ
ESVQDTPFNQVTLTNRNEPVIVDSLSHPTVAVLALMLFVCNPPN

>d1apa_d.165.1.1 (-) Pokeweed antiviral protein alpha {Pokeweed (Phytolacca americana)}
INTITFDVGNATINKYATFMKSIHNQAKDPTLKYGIPMLPNTNLTPKYLLVTLQDSSLKTITLMLKR
NNLYVMGYADTYNGKCRYHIFKDISNTTERNDVMTTLCPNPSSRVGKNINYDSSYPALEKKVGRPRS
QVQLGIQILNSGIGKIYGVDSFTEKTEAEFLLVAIQMVSEAAARFKYIENQVKTNFNRAFYPNAKVLNLE
ESWKGKISTAIHNAKNGALTSPLELKNANGSKWIVLRVDDIEPDVGLLKVYVNGTCQAT

>d1d6aa_d.165.1.1 (A:) Pokeweed antiviral protein alpha {Pokeweed (Phytolacca americana)}
VNTIINYVGSTTISKYATFLNDRNEAKDPSLKYGIPMLPNTNLTNPKYVLVELQGSNKKTTITLMLRR
NNLYVMGYSDPFETNKCRYHIFNDISGTERQDVETTLCPNANSRVSKNINFDSTRYPTLESKAGVKSRS
QVQLGIQILDSNIGKISGVMSFTEKTEAEFLLVAIQMVSEAAARFKYIENQVKTNFNRAFNPKNKVLNLE
QETWGWKISTAIHDAKNGVLPKPLELVDASGAKWIVLRVDEIKPDVALLNYVGGSCQTT

>d1qi7a_d.165.1.1 (A:) Saporin So6 {Common soapwort (Saponaria officinalis)}
VTSITLDLVNPTAGQYSSFDKIRNNVKDPNLKYGGTDIAVIGPPSKEKFLRINFQSSRGTVSLGLKRD
NLYVVAYLAMDNNTNVNRAYYFKSEITSAELTALFPEATTANQKALEYTEDYQSIEKNAQITQGDKSRK
ELGLGIDLLTFMEAVNKKARVVKNEARFLIAIQMTAEVARFRYIQNLVTKNFPNKFDSDNKVIQFE
VSWRKISTAIYGDANGVFNKDYDFGFGKVRQVKDLQMGLLMLYLGPKK

>d1ift_d.165.1.1 (-) Ricin A-chain {Castor bean (Ricinus communis)}
YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALD
VTNAYVVGIRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYYTFAFGGNYDRLEQLAGNLRENIELGN
GPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITLENSW
GRLSTAIQESNQGAFASPIQLQRRNGSKFSVYDVSILIPIALMVYRCAPP

>d1hwma_d.165.1.1 (A:) Ebulin A-chain {Sambucus ebulus}
IDYPSVSNLAGAKSTTYRDFLKNLRDRVATGTYEVNGLPVLRRSEVQVKNRFVLVRLTNYNGDTV
TSAVDVTNLYLVAFSANGNSYFFKDATELQKSNLFLGTTQHTLSFTGNYDNLETAAGTRRESIELGPN
PLDGAITSLWYDGGVARSLVLIQMVPEAARFRYIEQEVRRSLQQLTSFTPNALMLSMENNWSSMSL
EVQLSGDNVSPFSGTVQLQNYDHTPRLVDNFEELYKITGIAILLFRCVA

>d1dm0a_d.165.1.2 (A:) Shiga toxin, A-chain {Shigella dysenteriae}
KEFTLDFSTAKTYVDSLNVIRSAIGTPLQTISSGGTSLLMIDSGTGDNLFAVDVRGIDPEEGRFNRLRI
VERNLYVTGFVNRTNNVFYRFADFSHVTFPGTTAVTLSGDSSYTTLQRVAGISRTGMQINRHSLTTS
YLDLMSHSGTSLTQSVARAMLRFVTVTAEALRFRQIQRGFRITLDDLGRSYVMTAEDVDLTLNWDG
RLSSVLPDYHGQDSVRVGRISFGSINAILGSVALILNCHHHASRVARMASDEFPSMCPADGRVGRITH
NKILWDSSTLGAILM

>g1lts.1 d.166.1.1 (A:,C:) Heat-labile toxin, A-chain {Escherichia coli, type IB}
RLYRADSRRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSLSLRSAH
LAGQSILSGYSTYYIYVIATAPNMFVNDVLDGVYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERL
HRNREYDRYRNLNIAPAEDGYRLAGFPDQAWREEPWIHHAPQCGXGDTCNEETQNLSTIY
LREYQSKVKRQIFSDYQSEVDIYNRI

>g1tii.1 d.166.1.1 (A:,C:) Heat-labile toxin, A-chain {Escherichia coli, type IIB}
NDYFRADSRTPDEVRRSGGLIPRGQDEAYERGTPININLYDHARGTATGNTRYNDGYVSTTTTLRQA

HLLGQNMLGGYNEYIYVVAAPNLFVNGVLGRYSPYSENEYAALGGIPLSQIIGWYRVSFGAIEG
GMHRNRDYRRDLFRGLSAAPNEDGYRIAGFPDGFPAWEEVPWREFAPNSCLPXTTCASLTNKLSQH
DLADFKKYIKRKFTLMTLLSINN

>d1f0la2 d.166.1.1 (A:1-187) Diphtheria toxin, N-terminal domain {Corynebacterium diphtheriae}

GADDVVDDSSKSFVMENFSSYHGTPGYVDSIQKGIQKPKSGTQGNYYDDDWKGFYSTDNKYDAAGYS
VDNENPLSGKAGGVVKTYPGLTKVLALKVDNAETIKKELGSLTEPLMEQVGTTEEFIKRFGDGASR
VVLSPFAEGSSSVEYINNWEQAKALSVELEINFETRGRKRGQDAMYEYMAQACA

>d1ikpa2 d.166.1.1 (A:395-606) Exotoxin A, C-terminal domain {Pseudomonas aeruginosa}

PTGAEFLGDGGDVSFSTRGTQNWTVRLLQHRQLEERGYVVFVGYHGTFLAAQSIVFGGVRARSQ
DLDAIWRGFYIAGDPALAYGYAQDQEPDARGRIRNGALLRVYVPRSSLPGFYRTSLTLAAPEAAAGEVE
RLIGHPLPLRLDAITGPEEEGGRLLETILGWPLAERTVVIPSAIPTDPRNVGGDLDPSSIPDKEQAISAL
PDYASQPGK

>d1prta_ d.166.1.1 (A:) Pertussis toxin, S1 subunit {Bordetella pertussis}

DPPATVYRYDSRPPEDVFQNGFTAWGNNDNVLEHLTGRSCQVGSNSAFVSTSSRRRYTEVYLEHR
MQEAVEAERAGRGTGHFIGIYEV RADNNFYGAASSYFEYVDTYGDNAGRILAGALATYQSEYLAHR
RIPPENIRRVTRVYHNGITGETTTTEYSNARYVSQQTRANPNPYTSRRSVASIVGLTVMRMAPVVGAC
MARQAESSEAMAASERAGEAMVLVYYESIAYSF

>g1xtc.1 d.166.1.1 (A;C:) Cholera toxin {Vibrio cholerae}

NDDKLYRADSRPPDEIKQSGGLMPRGQSEYFDRGTQMNNLYDHARGTQTFVRRHDDGYVSTSISLR
SAHLVGQTILSGHSTYYLYVLATAPNMFVNDVLAGYSPHPDEQEVSALGGIPYSQIYGWYRVHFGVL
DEQLHRNRGYRDRYNSNLDIAPAADGYGLAGFPPEHRAWREEPWIHHAPPGCGNAPRXSNTCDEK
TQSLGVKFLDEYQSKVKRQIFSGYQSDIDTHNRIKDEL

>d1qs1a1 d.166.1.1 (A:60-264) Vegetative insecticidal protein 2 (VIP2) {Bacillus cereus}

TDKVEDFKEDKEKAKEWKGKEKEWKL TATEKGMNNFLDNKNDIKTNYKEITFSMAGSFEDEIK
DLKEIDKMFDKTNLSNSIITYKNVEPTTIGFNKSLTEGNTINS DAMAQFKEQFLDRDIKFDSYLDTHL
TAQQVSSKERVILKVTVPSPGKSTTPTKAGVILNNSEYKMLIDNGYMHVVDKVS KVVKKGVECLQIE
GTLKK

>d1qs1a2 d.166.1.1 (A:265-461) Vegetative insecticidal protein 2 (VIP2) {Bacillus cereus}

SLDFKNDINAEASHWGMKNYEEWAKDLTDSQREALDGYARQDYKEINNYLRNQGGSGNEKLDAQI
KNISDALGKKPIPENITVYRWCGMPEFGYQISDPLPSLKDFEEQFLNTIKEDKGYMSTSLSSERLAAF
GSRKIILRLQVPKGSTGAYLSAIGGFASEKEILLDKDSKYHIDKVTEVIIKGVKRYVVDATLLT

>d1g24a_ d.166.1.1 (A:) Exoenzyme c3 {Clostridium botulinum}

AYSNTYQEFTNIDQAKAWGNAQYKKGSLKSEKEAIVSYTKSASEINGKLRQNKGVINGFSPNLIKQV
ELLDKSFNKMKT PENIMLFRGDDPAYLGTEFQNTLLNSNGTINKTAFEKAKAKFLNKDRLEYGYIST
SLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFAGQLEMLLPRHSTYHIDDMRLSSDGKQIITATMM
GTAINPK

>d1j7na3 d.166.1.1 (A:264-550) Anthrax toxin lethal factor, middle domain {Bacillus anthracis}

MLSRYEKWEKIKQHYQHWSDSLSEEGRLLKQLPIEPPKDDIIHLSLQEEKELLKRIQIDSSDFLST
EEKEFLKQLQIDIRDSLSEEEKELLNRIQVDSSNPLSEKEKEFLKLLKLDIQPYDINQRLQDTGGLIDS
PSINLDVRKQYKRDIQNI DALLHQSIGSTLYNKIYLYENMNINNL TATLGADLVDSTDN TKINRGIFNE
FKKNFKYSSNYMIVDINERPALDNERLKWRIQLSPDTRAGYLENGKLILQRNIGLEIKDVQIIKQSE
KEYIRIDAKVV

>d1a26_2 d.166.1.2 (797-1012) Poly(ADP-ribose) polymerase, C-terminal domain {Chicken (Gallus gallus)}

LRTDIKVVDDKDSEEAKIIKQYVKNTHAATHNAYDLKVVEIFRIEREGESQRYKPFKQLHNRQLLWHG
SRTTNFAGILSQGLRIAPPEAPVTGYMFGKGIYFADMVSKSANYCHTSQADPIGLILLGEVALGNMYE
LKNASHITKLPKGKHSVKGLGKTAPDPTATTTLDGVEVPLNGISTGINDTCLLYNEYIVYDVAQVNL
KYLLKLFNYKTS

>d1g2aa_ d.167.1.1 (A:) Peptide deformylase {Escherichia coli}

SVLQVLHIPDERLRKVAKPVEEVNAEIQRIVDDMFETMYAEEGIGLAATQVDIHQRIIVIDVSENDRDE
RLVLINPELLEKSGETGIEEGCLSIPEQRALVPRAEKVKIRALDRDGKPFLEADGLLAICIQHEMDHL
VGKLFMDYLSPLKQQRIRQKVEKLDRL

>d2def_ d.167.1.1 (-) Peptide deformylase {Escherichia coli}

VLQVLHIPDERLRKVAKPVEEVNAEIQRIVDDMFETMYAEEGIGLAATQVDIHQRIIVIDVSENDRDER
LVLINPELLEKSGETGIEEGCLSIPEQRALVPRAEKVKIRALDRDGKPFLEADGLLAICIQHEMDHLV
GKLFMDYLS

>d1jbia_ d.209.1.1 (A:) Cochlin {Human (Homo sapiens)}

TAPIAITCFTRGLDIRKEKADVLCPPGGCPLEEFVYGNIVYASVSSICGAAVHRGVISNSGGPVRVYSLP
GRENYSSVDANGIQSQMLSRWSASFTVTLE

>d1chua3 d.168.1.1 (A:238-353) L-aspartate oxidase {Escherichia coli}

LEFNQFHPTALYHPQARNFLLTEALRGEGAYLKRPDGTRFMPDFDERGELAPRDIRAIDHEMCR
LGADCMFLDISHKPADFIRQHFPMIYEKLLGLGIDLTQEPVPIVPAAHYT

>d1fuma3 d.168.1.1 (A:226-357) Fumarate reductase flavoprotein subunit {Escherichia coli}

MEFVQYHPTGLPGSGILMTEGCRGEGGILVNKNGYRYLQDYGMGPETPLGEPKNKYMELGPRDKVS
QAFWHEWRKNTISTPRGDVVYLDLRLHGEKKLHERLPFICELAKAYVGVDPVKEPIVVRPTAHYT

>d1qlaa3 d.168.1.1 (A:251-371) Fumarate reductase flavoprotein subunit {Wolinella succinogenes}

MEAVQFHPTPLFPGSILLTEGCRGDGGILRDVDGHRFMPDYEPEKELASRDVVSRRMIEHIRKGGK
VQSPYQHLWLDISILGRKHIEITNLRDVQEICEYFAGIDPAEKWAPVLPMPQHYS

>d1e39a3 d.168.1.1 (A:360-505) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella frigidimarina}

QYIQAAPTLVSVKGGVMVTEAVRGNNGAILVNREGKRFEITTRDKASAAILAQTGKSAYLIFDSDVRK
LSKIDKYIGLVAPTADSLVKGKMEGIDGKALTETVARYNSLVSSGKDTDFERPDLPRALNEGNYY
AIEVTPGVHH

>d1qo8a3 d.168.1.1 (A:360-505) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella frigidimarina}

HPTVKGDSRILISETVRGGVAVMVNKDGNRFISELTTRDKASDAILKQPGQFAWIIFDNQLYKKAKM
VRGYDHLEMLYKGDVTEQLAKSTGMKVADLAKTVSDYNGYVASGKDTAFGRADMPLNMTQSPYYA
VKVAPGIHHTMGGV

>d1d4ca3 d.168.1.1 (A:360-505) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella putrefaciens}

YIQAHPYSPAGGVMITEAVRGNNGAIVVNREGNRFMNEITTRDKASAAILQQKGESAYLVFDDSRKS
LKAIEGYVHLNIVKEGKTIEELAKQIDVPAEELAKTVTAYNGFVKSGKDAQFERPDLPRELVVAPFYA
LEIAPAVHHT

>d1jnra3 d.168.1.1 (A:257-401) Adenylylsulfate reductase A subunit {Archaeon Archaeoglobus fulgidus}

FEHRFIPFRFKDGYGPVGAWFLFFKCKAKNAYGEEYIKTRAAELEKYKPYGAAQPIPTPLRNHQVML
EIMDGNQPIYMHTTEALAELAGGDKKKLKHIEEAFEDFLDMTVSQALLWACQNIDPQEQPSEAAP
AEPYIMGSHSGE

>d1lit_ d.169.1.1 (-) Lithostathine, inhibitor of stone formation {Human (Homo sapiens)}
CPEGTNAYRSYCYFNEEDRETWVDADLYCQNMNSGNLVSVLTAEGAFVASLIKESGTDDFNVWIGL
HDPKKNRRWHWSSGSLVSYKSWGIGAPSSVNPGYCVSLTSSTGFQKWKDVPCEDKFSFVCKFKN

>d1qdda_ d.169.1.1 (A:) Lithostathine, inhibitor of stone formation {Human (Homo sapiens)}
QEAQTELPQARISCEGTNAYRSYCYFNEEDRETWVDADLYCQNMNSGNLVSVLTAEGAFVASLIK
ESGTDDFNVWIGLHDPKKNRAWHWSSGSLVSYKSWGIGAPSSVNPGYCVSLTSSTGFQKWKDVPCE
DKFSFVCKFKN

>d1b6e_ d.169.1.1 (-) CD94 {Human (Homo sapiens)}
CSCQEKWVGYRCNCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSSSQQFYWIGLSYSEEH
TAWLWENGSALESQYLFPSFETFNTKNCIAYNPNNGNALDESCEDKNRYICKQQLI

>d1e87a_ d.169.1.1 (A:) CD69 {Human (Homo sapiens)}
SSCEDWVGYQRKCYFISTVKRSWTSQAQACSEHGATLAVIDSEKDMNFKRYAGREEHWVGLKKE
PGHPWKWSNGKEFNNWFNVTGSDKCVFLKNTVSSMECEKNLYWICNKPYK

>d1hq8a_ d.169.1.1 (A:) NK cell-activating receptor nkg2d {Mouse (Mus musculus)}
GYCGPCPNWICHRNNCYQFFNEEKTWNQSQASCLSQNSSLLKIYSKEEQDFLKLKVSYHWMGLVQ
IPANGSWQWEDGSSLSYNQLTLVEIPKGSACAVYGSFKAYTEDCANLNTYICMKRAV

>d1hyra_ d.169.1.1 (A:) NK cell-activating receptor nkg2d {Human (Homo sapiens)}
ESYCGPCPNWICYKNNCYQFFDESKNWEYQASCSQNASLLKVYSKEDQDLLKLKVSYHWMGL
VHIPTNGSWQWEDGSILSPNLLTIEMQKGDALYASSFKGYIENCSTPNTYICMQRV

>d1egia_ d.169.1.1 (A:) Macrophage mannose receptor, CRD4 {Human (Homo sapiens)}
CPEDWGASSRTSLCFKLYAKGKHEKKTWFESRDFCRALGGDLASINNKEEQQTWRLITASGSYHKL
FWLGLTYGSPSEGFTWSDGSPVSYENWAYGEPNNYQNVEYCGELKGDPTMSWINDINCEHLNNWIC
QIQ

>d1bj3a_ d.169.1.1 (A:) Snake coagglutinin {Habu snake (Trimeresurus flavoviridis)}
DCPSGWSSYEGHCYKPFKLYKTWDDAERFCTEQAKGGHLVSISSAGEADFVAQLVTENIQNTKSYV
WIGLRVQGKEKQCSSEWSDGSSVSYENWIEAESKTCLEKETGFRKVVNIYCGQQNPFVCEA

>d1ixxa_ d.169.1.1 (A:) Snake coagglutinin {Habu snake (Trimeresurus flavoviridis)}
DCLSGWSSYEGHCYKAFKLYKTWEDAERVCTEQAKGAHLVSISSAGEADFVAQLVTQNMKRLDFYI
WIGLRVQGVKQCNSEWSDGSSVSYENWIEAESKTCLEKETDFRKVVNIYCGQQNPFVCEA

>d1ixxb_ d.169.1.1 (B:) Snake coagglutinin {Habu snake (Trimeresurus flavoviridis)}
DCPSDWSSYEGHCYKPFSEPKNWADAENFCTQQHAGGHLVFSQSSEADFVVKLAFQTFGHSIFW
MGLSNVWNQCNWQWSNAAMLRYKAWAEESYCVYFKSTNNKWRSRACRMMMAQFVCEFQA

>d1c3aa_ d.169.1.1 (A:) Snake coagglutinin {Habu snake (Trimeresurus flavoviridis),
flavocetin-A}

DFDCIPGWSAYDRYCYQAFSKPKNWEDAESFCEGVKTSHLVSISSGEGDFVAQLVAEKIKTSFQYV
WIGLRIQNKEQQCRSEWSDASSVNYENLVKQFSKCYALKKGTTELRTWVNVYCGTENPEVCKYTPE
C

>d1c3ab_ d.169.1.1 (B:) Snake coagglutinin {Habu snake (Trimeresurus flavoviridis),
flavocetin-A}

GFCCPLGWSSYDEHCYQVFQKMNWEDAEEKFCTQQHKGSHLVFSHSSEEVDFVTSKTFPILKYDFV
WIGLSNVWNECTKEWSDGTKLDYKAWSGSDCIVSKTTDNQWLSMDCSSKYVVKCFQA

>d1fvua_d.169.1.1 (A:) Snake coagglutinin {Snake (Bothrops jararaca), botrocetin}
DCPSGWSSYEGNCYKFFQQKMNWADAERFCSEQAKGGHLVSIKIYSKEKDFVGDVLTKNIQSSDLYA
WIGLRVENKEKQCSSEWSDGSSVSYENVVERTVKKCFALKEKDLGFLWINLYCAQKNPFVCKSPPP
>d1fvub_d.169.1.1 (B:) Snake coagglutinin {Snake (Bothrops jararaca), botrocetin}
DCPPDWSSYEGHCYRFFKEWMHWDDAEFCTEQQTGAHLVSFQSKEEADFVRSILTSEMLKGDVV
WIGLSDVWNKCRFEWTDGMEFDYDDYLLIAEYECVASKPTNKNWIIIPCTRFKNFVCEFQA
>d1ioda_d.169.1.1 (A:) Snake coagglutinin {Sharp-nosed viper (Deinagkistrodon acutus)}
DCSSGWSSYEGHCYKVFQKQKTWADAESFCTKQVNGGHLVSISSGEADFGQLIAQKIKSAKIHVWI
GLRAQNKEKQCSIEWSDGSSISYENWIEESKKCLGVHIETGFHKWENFYCEQQDPFVCEA
>d1iodb_d.169.1.1 (B:) Snake coagglutinin {Sharp-nosed viper (Deinagkistrodon acutus)}
DCPSDWSSYEGHCYKPFNEPKNWADAENFCTQQTGSHLVSFQSTEEADFFVVKLAFQTFDYGIFW
MGLSKIWNQCNWQWSNAAMLKYTDWAEESYCVYFKSTNNKWRSTCRMIANFVCEFQA
>d1jwia_d.169.1.1 (A:) Snake coagglutinin {Puff adder (Bitis arietans), bitiscetin}
CLPDWSSYKGHYKVFVKVGTWEDAEEKFCVENSGHLASIDSKEEADFVTKLASQTLTKFVYDAWIG
LRDESKTQQCSPQWTDGSSVYENVDEPTKCFGLDVHTEYRTWTDLPCGEKNPFICKS
>d1jwib_d.169.1.1 (B:) Snake coagglutinin {Puff adder (Bitis arietans), bitiscetin}
GCLPDWSSYKGHYKVFVEKTWADAEEKFCKELVNGGHLMSVNSREEGEFISKLALAKMRIVLVWI
GLSHFWRICPLRWTDGARLDYRALSDEPICFVAESFHNKWIQWTCNRKKS FVCKYRV
>d2afpa_d.169.1.1 (A:) Type II antifreeze protein {Sea raven (Hemitripterus americanus)}
QRAGPNC PAGWQPLGDRCIYYETTAMTWALAE TNCMKLGGHLASIHSQEEHSFIQTLNAGV VVWIGG
SACLQAGAWTWS DGTMPNFRSWCSTKPDDVLAACCMQMTAAADQCWDDLPCPASHKSVCAMTF
>d1h8ua_d.169.1.1 (A:) Eosinophil major basic protein {Human (Homo sapiens)}
RYLLVRS LQTF SQAWFTCRRCYRGNLVS IHNFNIN YRIQCSVSALNQQGVWIGGRITGSGRCRRFQW
VDGSRWNFAYWAAHQ PWSRGHCVALCTRGGYWRRAHCLRRLPFICSY
>d1qo3c_d.169.1.1 (C:) NK cell receptor ly49a {Mouse (Mus musculus)}
STVLD SLQHTGRGDKVYWF CYGMKCYFFVMDRKTWSGCKQTCQSSLSLLKIDDEDELKFLQLVVP
SDSCWVGLSYDNKKKDWAWIDNRPSKLALNTRKYNIRDGGCMLLSKTRLDNGNCDQVFICIGKRL
D
>d1qo3d_d.169.1.1 (D:) NK cell receptor ly49a {Mouse (Mus musculus)}
DKVYWF CYGMKCYFFVMDRKTWSGCKQTCQSSLSLLKIDDEDELKFLQLVVPDSCWVGLSYDNK
KKDWAWIDNRPSKLALNTRKYNIRDGGCMLLSKTRLDNGNCDQVFICIGKRLDK
>d1dv8a_d.169.1.1 (A:) H1 subunit of the asialoglycoprotein receptor {Human (Homo sapiens)}
CPVNWVEHERSCYWF SRSGKAWADADNYCRLEDAHLVVVTSWEEQKFVQHHIGPVNTWMGLHD
QNGPWKWVDGTDYETGFKNWRPEQPDDWYGHGLGGGEDCAHFTDDGRWNDDVCQRPYRWVC
ETEL
>d1k9ia_d.169.1.1 (A:) DC-SIGN (dendritic cell-specific ICAM-3 grabbing nonintegrin)
{Human (Homo sapiens)}
PCPWEWTF FQGCYFMSNSQRNWHDSITACKEVGAQLVVIKSAEEQNFLQLQSSRSNRFTWMGLS
DLNQEGTWQWVDGSP LPSFKQYWRGEPNNVGEEDCAEFSGNGWNDKCNLAKFWICKKSA
>d1k9ja_d.169.1.1 (A:) DC-SIGNR (DC-SIGN related receptor) {Human (Homo sapiens)}
CRHCPKDWTF FQGCYFMSNSQRNWHDSVTACQEVRAQLVVIKTAEEQNFLQLQTSRSNRFSWM
GLSDLNQEGTWQWVDGSP LPSFQRYWNSGEPNNSGNEEDCAEFSGSGWNDNRCDVDNYWICKKP
AA

>d1g1sa1 d.169.1.1 (A:1-118) E-selectin {Human (Homo sapiens)}
WTYHYSTKAYSWNISRKYCQNRYTDLVAIQNKNEIDYLNKVLPPYYSSYYWIGIRKNNKTWTWVGTK
KALTNEAENWADNEPNNKRNNEDCVEIYIKSPSAPGKWNDCLKKKHALCY

>d1g1ta1 d.169.1.1 (A:1-118) E-selectin {Human (Homo sapiens)}
WSYNTSTEAMTYDEASAYCQQRYPYTHLVAIQNKKEIEYLNLSILSYSPSYWIGIRKVNNVVWVWVGTQK
PLTEEAKNWAPGEPNNRQKDEDCVEIYIKREKDVGMWNDERCSKKKLALCY

>d1hup_1 d.169.1.1 (112-228) Mannose-binding protein A, lectin domain {Human (Homo sapiens)}
KQVGNKFFLTNGEIMTFEKVKALCVKFQASVATPRNAAENGAIQNLIKEEAFGLITDEKTEGQFVDLT
GNRLTYTNWNEGEPNNAGSDEDCVLLLKNGQWNDVPCSTSHLAVCEFP

>d1fifa1 d.169.1.1 (A:105-226) Mannose-binding protein A, lectin domain {Rat (Rattus norvegicus)}
KKSGKKFFVTNHERMPFSKVKALCSELRGTVAI PRNAAENKAIQEVAKTS AFLGITDEVTEGQFMVY
TGGRLTYSNWKKDQPDWYGHGLGGEDCVHIVDNLWND DSCQRPYTAVCEFP

>d1rdl1_ d.169.1.1 (1:) Mannose-binding protein A, lectin domain {Rat (Rattus norvegicus)}
KYFMSSVRRMPLNRAKALCSELQGT VATPRNAAENRAIQNVAKDVAFLGITDQRTE NVFEDLTGNR
VRYTNWNEGEPNNVSGENCVLLTNGKWNDVPCSDSFLVVCEFS

>d2msba_ d.169.1.1 (A:) Mannose-binding protein A, lectin domain {Rat (Rattus norvegicus)}
KKFFVTNHERMPFSKVKALCSELRGTVAI PRNAAENKAIQEVAKTS AFLGITDEVTEGQFMVVTGGR
LTYSNWKKDEPN DHGSGEDCVTIVDNLWNDIS CQASHTAVCEFP

>d1b08a1 d.169.1.1 (A:235-355) Surfactant protein, lectin domain {Human (Homo sapiens), SP-D}
PNGQSVGEKIFKTAGFVKPFTEAQLLCTQAGGQLASPRSAENAALQQLVVAKNEAAFLSMTDSKTE
GKFTYPTGESLVYSNWAPGEPND DGGSEDCVEIFTNGKWND RACGEKRLVVCEF

>d1byfa_ d.169.1.1 (A:) Lectin TC14 {Tunicate (Polyandrocarpa misakiensis)}
DYEILFSDETMNYADAGTYCQSRGMALVSSAMRDSTMVKAILAFTEVKGHDYVWGADNLQDGAYN
FLWNDGVSLPTSDSLWSPNEPSNPQSWQLCVQIWSKYNLLDDVGC GGARRVICEKELD

>d1tn3_ d.169.1.1 (-) Tetranectin {Human (Homo sapiens)}
ALQTVCLKGT KVHMKCFLAFTQTKTFHEASEDCISRGGTLSTPQTGSENDALYEYLRQSVGNEAEIW
LGLNDMAAEGTWVDMTGARIAYKNWETEITAQPDGGKTENCAVLSGAANGKWFDKRCRDQLPYI
CQFGIV

>d1prtb2 d.169.1.2 (B:4-89) Pertussis toxin, S2/S3 subunits, N-terminal domain {Bordetella pertussis}
GIVIPPQEITQHGPSYGRCA NKTRALTVAELRSGDLQEYLRHVTRGWSIFALYDGT YLGG EYGGVI
KDGTPGGAFDLKTTFCIM

>d1prtc2 d.169.1.2 (C:4-89) Pertussis toxin, S2/S3 subunits, N-terminal domain {Bordetella pertussis}
GIVIPPKALFTQGGAYGRCPNGTRALTVAELRGNAELQTYLRQITPGWSIYGLYDGT YLGGAYGGIHK
DAPPGAGFIYRETFCIT

>d1prea1 d.169.1.2 (A:2-84) Proaerolysin, N-terminal domain {Aeromonas hydrophila}
EPVYPDQLRLFSLGQGVCGDKYRPVNREEAQS VKSNIVGMMGQWQISGLANGWVIMGPGYNGEIKP
GTASNTWCYPTNPVTGE

>d1f00i3 d.169.1.3 (I:842-939) Intimin {Escherichia coli}

LIVPNMSKRVTYNDVNTCKNFGGKLPSSQNELENVFKAWGAANKYEYKSSQTIISWVQQAQDA
KSGVASTYDLVKQNPLNNIKASESNAYATCVK
>d1cwva5 d.169.1.3 (A:887-986) Invasin {Yersinia pseudotuberculosis}
NRWIYDGGRLSVSSLEASRQCQGSMDMSAVLESSRATNGTRAPDGLTWGEWGSALTAYSSDWQSGEYW
VKKTSTDFETMNMDTGALQPGPAYLAFPLCALSI
>d1tsg_ d.169.1.4 (-) TSG-6, Link module {Human (Homo sapiens)}
GVYHREARSGKYKLYAEAKAVCEFEFGHGLATYKQLEAARKIGFHVCAAGWMAKGRVGYPIVKPGP
NCGFGKTGIIDYGIRLNRSERWDAYCYNPHAK
>d1bnla_ d.169.1.5 (A:) Endostatin {Human (Homo sapiens)}
HSHRDFQPVLHLVALNAPLSGGMRGIRGADFQCFQQARAVGLAGTFRAFLSSRLQDLYSIVRRADRA
AVPIVNLKDELLFPSWEALFSGSEGPLKPGARIFSFQDGRDVLRHPTWPQKSVWHGSDPNRRLTESY
CETWRTEAPSATGQASSLLGGRLGQSAASCHHAYIVLCIENSF
>d1koe_ d.169.1.5 (-) Endostatin {Mouse (Mus musculus)}
QPVLHLVALNTPLSGGMRGIRGADFQCFQQARAVGLSGTFRAFLSSRLQDLYSIVRRADRGSPVIVNL
KDEVLSPSWDSLFGSQQLQPGARIFSFQDGRDVLRHPAWPQKSVWHGSDPSGRRLMESYCETWR
TETTGATGQASSLLSGRLLEQKAASCHNSYIVLCIENSF
>d1dy2a_ d.169.1.5 (A:) Endostatin domain of collagen alpha1(xv) {Mouse (Mus musculus)}
RPVLHLVALNTPVAGDIRADFQCFQQARAAGLLSTFRAFLSSHLQDLSTVVRKAERFGLPIVNLKGQV
LFNNWDSIFSGDGGQFNTHIPIYSFDGRDVMTPDPSWPQKVVWHGSPHGVRLVDKYCEAWRTTD
MAVTGFASPLSTGKILDQKAYSCANRLIVLCIENSF
>d1by2_ d.170.1.1 (-) M2BP {Human (Homo sapiens)}
AVNDGDMRLADGGATNQGRVEIFYRGQWGTVCNLDLTDASVVCRALGFENATQALGRAAFGQG
SGPIMLDEVQCTGTEASLADCKSLGWLKSNCRHERDAGVVCTNETRSTHTL
>d1mwp_ d.170.2.1 (A:) N-terminal domain of the amyloid precursor protein {Human
(Homo sapiens)}
LLAEPQIAMFCGRNLNMHMNVQNGKWSDPSGKTCTCIDTKEGILQYCQEVYPELQITNVVEANQPVT
IQNWCKRGRKQCKTHPHFVIPYRCLVGEFV
>d1fid_ d.171.1.1 (-) Fibrinogen C-terminal domains {Human (Homo sapiens), gamma}
QIHDTGKDCQDIANKGAKQSGLYFIKPLKANQQFLVYCEIDGSGNGWTVFQKRLDGSVDFKKNWIQ
YKEGFGHLSPTGTTEFWLGNKIHLLISTQSAIPYALRVELEDWNGRTSTADYAMFKVGPADKYRLT
YAYFAGGDAGDAFDGDFGDDPSDKFFTSNMGQFSTWDNDNDKFEKNCAEQDGSWWMNKCH
AGHLNGVYQGGTYSKASTPNGYDNGIHWATWKTRWYSMKKTMTMKIIPFNRLTIGEGQQHHL
>d1fzcb1 d.171.1.1 (B:200-458) Fibrinogen C-terminal domains {Human (Homo sapiens),
beta}
SCNIPVVSKECEEIIKGGGETSEMYLIQPDSSVKPYRVYCDMNTENGGWTVIQNRQDGSVDFGRKW
DPYKQGFNVATNTDGKNYCGLPGEYWLGNKISQLTRMGPTELLIEMEDWKGDKVKAHYGGFTV
QNEANKYQISVNKYRGTAGNALMDGASQLMGENRTMTIHNGMFFSTYDRDNDGWLTS DPRKQCS
KEDGGGWYNNRCHAANPNGRYYWGGQYTWDMAKHGTDDGVVWMNWKGSWYSMRKMSMKIR
PFF
>d1fzda_ d.171.1.1 (A:) Fibrinogen C-terminal domains {Human (Homo sapiens),
fibrinogen-420, alpha-E}
GGWLLIQRMDGSLNFRNTWQDYKRGFSLNDEGEFEFWLGNLYLHLLTQRGSVLRVELEDWAG
NEAYAEYHFRVGEAEQYALQVSSYEGTAGDALIEGSVEEGAETSHNNMQFSTFDRDADQWEENC
AEVYGGGWYNNRCHAANLNGIYYPGGSYDPRNNSPYEIEINGVVWVSFRGADYSLRAVRMKIRPLV

TQ

>d1jfec1 d.171.1.1 (C:142-393) Fibrinogen C-terminal domains {Chicken (*Gallus gallus*), gamma}

TAEIQETTGRDCQDIANKGARKSGLYFIKPQKAKQSFLVYCEIDTYGNGWTVLQRRLDGSEDFRRNW
VQYKEGFGHLSRDDTTEFWLGNKIHLLITQSTLPYALRIELEDWSGKKGTADYAVFKVGTTEEDKYR
LTYAYFIGGEAGDAFDGDFNFGDDPSDKSYTYHNGMRFSTFDNDNDNFEGNCAEQDGSWWMNRC
HAGHLNGPYYIGGVYSRDTGTNSYDNGIIWATWRDRWYSMKKTTMKIIPFNRLS

>d1jfeb1 d.171.1.1 (B:200-464) Fibrinogen C-terminal domains {Chicken (*Gallus gallus*), beta}

SPCVASCNIPVVS GRECEDIYRKGETSEMYIIQDPFPTTPYRVYCDMETDNGGWTLIQNRQDGSVN
FGRAWDEYKRGFNGIAKSGGKKYCDTPGEYWLGNKISQLTKIGPTKVLIEMEDWNGDKVSALYGG
FTIHNEGKYLQSVSNYKGNAGNALMEGASQLYGENRTMTIHNGMYFSTYDRDNDGWLTTPRQK
CSKEDGGWVYNRCHAANPNGRYYWGGTYSWDMAKHGTDDGIVWMNWKGSWYSMKKMSMKI
KPYFPD

>d1jc9a_ d.171.1.1 (A:) Tachylectin 5a {Japanese horseshoe crab (*Tachypleus tridentatus*)}

DPTDCADILLNGYRSSGGYRIWPKSWMTVGLTNVYCDMETDGGGWTVIQRNGNYGNPSDYFYKP
WKNYKLGFGNIEKDFWLGNDRIFALTNQRNYMIRFDLKDENDTRYAIYQDFWIENEDYLYCLHIG
NYSGDAGNSFGRHNGHNFSTIDKDHDTHETHCAQTYKGGWVYDRCHESNLNGLYLNGEHNSYAD
GIEWRAWKGYHYSPLQVEMKIRPVEF

>d1g9mg_ d.172.1.1 (G:) gp120 core {Human immunodeficiency virus type 1}

EVVLVNVTENFNMWKNMVEQMHEIISLWDQSLKPCVKLTPLCVAGSCNTSVITQACPKVSFEP
IPIHYCAPAGFAILKCNKTFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEEEVIRSVNFTDNA
KTIIVQLNTSVEINCTGAGHCNISRAKWNNLTKQIASKLREQFGNNTIIFKQSSGGDPEIVTHSFNCG
GEFFYCNSTQLFNSTWFNSTWSTEGSNTEGSDTITLPCRQIINMWQKVGKAMYAPPISGQIRCSS
NITGLLLTRDGGNSNNESEIFRPGGDMRDNRSELYKYKVVKIE

>d1g9ng_ d.172.1.1 (G:) gp120 core {Human immunodeficiency virus type 1}

LENVTENFNMWKNMVEQMHEIISLWDQSLKPCVKLTPLCVAGSCNTSVITQACPKVSFEP
YCAPAGFAILKCNKTFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEEEVIRSENFTNNAKTI
VQLNESVVINCTGAGHCNLSKTQWENTLEQIAIKLKEQFGNNTIIFNPSSGGDPEIVTHSFNCGGEF
FYCNSTQLFTWNDTRKLNNTGRNITLPCRQIINMWQEVGKAMYAPPPIRGQIRCSSNITGLLLTRD
GKDTNGTEIFRPGGDMRDNRSELYKYKVVKIE

>d1msk_ d.173.1.1 (-) Methionine synthase (activation domain) {*Escherichia coli*}

TPPVTLAAARDNDFAFDWQAYTPVAHRLGVQEVEASIELRNYIDWTPPFMTWSLAGKYPRIED
EVVGVEAQLFKDANDMLDKLSAEKTLNPRGVVGLFPANRVGDDIEIYRDETRTHVINVSHHLRQQ
TEKTGFANYCLADVFAPKLSGKADYIGAFVAVTGGLEEDALADAFEQAHDYDYNKIMVKALADRLAEAF
AEYLHERVRKVYWGYPNENLSNEELIRENYQGIRPAPGPACPEHTEKATIWELLEVEKHTGMKLT
ESFAMWPGASVSGWYFVSHPSKYVAQIQRDQVEDYARRKMSVTEVERWLAPNLGYDAD

>d1jwka_ d.174.1.1 (A:) Nitric oxide (NO) synthase oxygenase domain {Mouse (*Mus musculus*)}

QYVRIKNWGSGEILHDTLHHKATSCDFTCKSKSCLGSIMNPKSLTRGPRDKPTPLEELLPHAIEFINQ
YYGSFKEAKIEEHLARLEAVTKEIETTGTQYQLTDELIFATKMAWRNAPRCIGRIQWSNLQVFDARN
CSTAQEMFQHICRHILYATNNGNIRSAITVFPQRS DGKHDFRLWNSQLIRYAGYQMPDGTIRGDAATL
EFTQLCIDLGWKPARYGRFDVLPVLQADGQDPEVFEIPDLVLEVTMEHPKYEFWFQELGLKWYALP
AVANMLLEVGGLEFPACPFNGWYMGTEIGVRDFCDTQRYNILEEVGRRMGLEHTLASLWKDRAV

TEINVAVLHSFQKQNVTIMDHHTASESFMKHMQNEYRARGGCPADWIALVPPVSGSITPVFHQEML
NYVLSPFYYYYQIEPWKTHIWQN

>d1nos_ d.174.1.1 (-) Nitric oxide (NO) synthase oxygenase domain {Mouse (Mus musculus)}

NPKSLTRGPRDKPTPLEELLPHAIEFINQYYGSFKEAKIEEHLARLEAVTKEIETTGTYYQLTDELIFAT
KMAWRNAPRCIGRIQWSNLQVFDARNCSTAQEMFQHICRHILYATNNGNIRSAITVFPQRSDGKHD
FRLWNSQLIRYAGYQMPDGTIRGDAATLEFTQLCIDLGWKPRYGRFDVLPVLVQADGQDPEVFEIPP
DLVLEVTMEHPKYEWFQELGLKWYALPAVANMLLEVGGLFEPACPFNGWYMGTEIGVRDFCDTQR
YNILEEVGRRMGLETHTLASLWKDRAVTEINVAVLHSFQKQNVTIMDHHTASESFMKHMQNEYRA
RGGCPADWIWLVPPVSGSITPVFHQEMLNYVLSPFYYYYQIEPWKTHIWQNEHHHH

>d3nosa_ d.174.1.1 (A:) Nitric oxide (NO) synthase oxygenase domain {Human (Homo sapiens)}

KFPRVKNWEVGSITYDTLSAQAAQDGPCTPRRCLGSLVFPKRLQGRPSGPPAPEQLLSQARDFINQ
YYSSIKRSGSQAHEQRLQEVEAEVAATGTYYQLRESELVFGAKQAWRNAPRCVGRIQWGKLVFQDAR
DCRSAQEMFTYICNHIKYATNRGNLRSITVFPQRCPGRGDFRIWNSQLVRYAGYRQQDGSVRGDPA
NVEITELCIQHGWTGNGRFDVLPVLLQAPDEPELFLLPPELVLEVPLEHPTLEWFAALGLRWYAL
PAVSNMLLEIGGLEFPAAPFSGWYMSTEIGTRNLCDPHRYNILEDVAVCMDLDTTRTTSSLWKDKAAV
EINVAVLHSYQLAKVTIVDHHAATASFMKHLNEQKARGGCPADWAWIVPPISGSLTPVFNQEMVN
YFLSPAFRYQPDPW

>d4nosa_ d.174.1.1 (A:) Nitric oxide (NO) synthase oxygenase domain {Human (Homo sapiens)}

RHVRIKNWGSMTFQDTLHHKAKGILTCRSKSCLSIMTPKSLTRGPRDKPTPPDELLPQAIEFVNQ
YYGSFKEAKIEEHLARVEAVTKEIETTGTYYQLTDELIFATKQAWRNAPRCIGRIQWSNLQVFDARSC
STAREMFEHICRHVRYSTNNGNIRSAITVFPQRSDGKHDFRVWNAQLIRYAGYQMPDGSIRGDPANV
EFTQLCIDLGWKPKYGRFDVVPVLVQANGRDPPELFEIPDLVLEVAMEHPKYEWFRELELKWYALP
AVANMLLEVGGLFPGCFNGWYMGTEIGVRDFCDVQRYNILEEVGRRMGLETHKLASLWKDQAV
VEINIAVIHSFQKQNVTIMDHHSAAESFMKYMQNEYRSRGGCPADWIWLVPPMGSITPVFNQEML
NYVLSPFYYYYQVEAWKTHVWQD

>d1d0ca_ d.174.1.1 (A:) Nitric oxide (NO) synthase oxygenase domain {Cow (Bos taurus)}

GPKFPRVKNWELGSITYDTLCAQSQQDGPCTPRRCLGSLVLPKRLQTRPSPGPPPAEQLLSQARDFI
NQYYSSIKRSGSQAHEERLQEVEAEVASTGTYYHLRESELVFGAKQAWRNAPRCVGRIQWGKLVFQDAR
RDCSSAQEMFTYICNHIKYATNRGNLRSITVFPQRAPGRGDFRIWNSQLVRYAGYRQQDGSVRGDP
ANVEITELCIQHGWTGNGRFDVLPVLLQAPDEAPELFLVLPPELVLEVPLEHPTLEWFAALGLRWYA
LPVSNMLLEIGGLEFSAAPFSGWYMSTEIGTRNLCDPHRYNILEDVAVCMDLDTTRTTSSLWKDKAA
VEINLAVLHSFQLAKVTIVDHHAATVSFMKHLNEQKARGGCPADWAWIVPPISGSLTPVFNQEMV
NYLSPAFRYQPDPW

>d1k25a3 d.175.1.1 (A:67-263) Penicillin-binding protein 2x (pbp-2x), N-terminal domain {Streptococcus pneumoniae}

QITRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDKKYKSATGKILYVEDAQFNKVAEVFHKYLDMEE
SYVREQLSQPNLKQVSFGSKNGGITYANMMAIKKELETAEVKIDFTTSPNRSYPNGQFASSFIGLAQ
LHENEDEGSKSLLGTSGMESSLSILAGTDGITYEKDRVGNIVPGTELVSQQTVDGKDVYT

>d1qmea3 d.175.1.1 (A:71-263) Penicillin-binding protein 2x (pbp-2x), N-terminal domain {Streptococcus pneumoniae}

TVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVR

EQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKIDFTTSPNRSYPNGQFASSFIGLAQLHEN
EDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYT

>d1soxa3 d.176.1.1 (A:94-343) Sulfite oxidase, middle catalytic domain {Chicken (Gallus gallus)}

QDPFAGDPPRHPGLRVNSQKPFNAEPPAELLAERFLTPNELFFTRNHLVPVAVEPSSYRLRVDGPGG
GTLSSLAE LRSRFPKHEVTATLQCAGNRRSEMSRVRPVKGLPWDIGAISTARWGGARLRDVLHAG
FPEELQGEWHVCFEGLDADPGGAPYGASIPYGRALSPAADVLLAYEMNGTELPRDHGFPVRVVVPG
VVGARSVKWLRRVAVSPDESPSHWQQNDYKGFSPCVDWDTVDYRTAPAIQ

>d1hyoa2 d.177.1.1 (A:119-416) Fumarylacetoacetate hydrolase, FAH, C-terminal domain {Mouse (Mus musculus)}

ATIGDYTDFYSSRQHATNVGIMFRGKENALLPNWLHLPVGYHGRASSIVSGTPIRRPMGQMRPDN
SKPPVYGACRLDMELEMAFFVGPGRNRFGEPIPISKAHEHIFGMVLMNDWSARDIQQWEYVPLGPF
LGKSFGTISPWVPM DALMPFVVPNPKQDPKPLPYLCHSQPYTFDINLSVSLKGEQMSQAATICRS
NFKHMYWTMLQQLTHHSVNGCNLRPGDLLASGTISGSDPESFGSMLELSWKGTKAIDVGQGQTRT
FLLDGDEVIITGHCQGDGYRVGFGQCAGKVLPAL

>d1i7oa1 d.177.1.1 (A:1-213) 4-hydroxyphenylacetate degradation bifunctional isomerase/decarboxylase HpcE {Escherichia coli}

MKGTIFAVALNHRSQLDAWQEAFFQSPYKAPPKTAVWFIKPRNTVIGCGEPIFPQGEKVLSGATVA
LIVGKTATKVREEDAAEYIAGYALANDVSLPEESFYRPAIKAKCRDGFCEPIGETVALSNVDNLTITYEIN
GRPADHWNTADLQRNAAQLLSALSEFATLNPGDAILLGTTPQARVEIQPGDRVRVLAEGFPLENPVV
DEREVTTRK

>d1i7oa2 d.177.1.1 (A:214-429) 4-hydroxyphenylacetate degradation bifunctional isomerase/decarboxylase HpcE {Escherichia coli}

SFPTLPHPHGTLFALGLNYADHASELEFKPPEEPLVFLKAPNTLTGDNQTSVRPNNIEYMHYEALV
VVIGKQARNVSEADAMDYVAGYTVCNDYAIRDYLENYYRPNLRVKS RDGLTPMLSTIVPKEAIPDPH
NLTLRTFVNGELRQQGTTADLIFSVPFLIAYLSEFMTLNP GDMIATGTPKGLSDVVP GDEVVVEVEGV
GRLVNRIVSEETAK

>d1toh_ d.178.1.1 (-) Tyrosine hydroxylase {Rat (Rattus norvegicus)}

KVPWFPRKVELDKCHHLVTKFDPDLDDHPGFSDQVYRQRRKLAIEIAFYKHGEPIPHVEYTAEE
IATWKEVYVTLKGLYATHACREHLEGFQLLERYCGYREDSIPQLEDVSRFLKERTGFQLRPVAGLLSA
RDFLASLAFRVFQCTQYIRHASSPMHSPEPDCHELLGHVPM LADRTFAQFSQDIGLASLGASDEEIE
KLSTVYWFVTEVEFLCKQNGELKAYGAGLLSSYGELLHSLSEEPEVRAFDPDTAAVQPYQDQTYQPVY
FVSESFNDAKDKLRNYASRIQRPFSVKFDPYTLAIDVLDSPHTIQRSLEGVQDELHTLAHALSAIS

>d3pah_ d.178.1.1 (-) Phenylalanine hydroxylase {Human (Homo sapiens)}

TVPWFPRTIQELDRFANQILSYGAELDADHPGFKDPVYRARRKQFADIAYNYRHGQPIPRVEYMEEE
KKTWGTVFVKLTKSLYKTHACYEYNHIFLLEKYCGFHEDNIPQLEDVVSQFLQTCTGFRLRPVAGLLSS
RDFLGG LAFRVFHCTQYIRHGSKPMYTPEDICHELLGHVPLFSDRSFAQFSQEIGLASLGAPDEYIEK
LATIYWFVTEVEFLCKQGDSIKAYGAGLLSSFGELQYCLSEKPKLLPLELEKTAIQNYTVTEFQPLYVA
ESFNDAKEKVRNFAATIPRPFVRYDPYTQRIEVL

>d1pha2 d.178.1.1 (A:116-427) Phenylalanine hydroxylase {Rat (Rattus norvegicus)}

NTVPWFPRTIQELDRFANQILSYGAELDADHPGFKDPVYRARRKQFADIAYNYRHGQPIPRVEYTEE
EKQTWGTVFRTLKALYKTHACYEYHNHIFLLEKYCGFREDNIPQLEDVVSQFLQTCTGFRLRPVAGLL
SSRDFLGG LAFRVFHCTQYIRHGSKPMYTPEDICHELLGHVPLFSDRSFAQFSQEIGLASLGAPDEYI
EKLATIYWFVTEVEFLCKEGDSIKAYGAGLLSSFGELQYCLSDKPKLLPLELEKTACQEYSVTEFQPLYV

VAESFSDAKEKVRTFAATIPRPFVRYDPYTQRVEVLDNT

>d1dqaa4 d.179.1.1 (A:462-586,A:704-870) Substrate-binding domain of HMG-CoA reductase {Human (Homo sapiens)}

LSDAEIIQLVNAKHIPAYKLETLIETHERGVSIRRQLLSKKLSEPSLQYLPYRDYNYSLVMGACCENVI
GYMPIPVGVAGPLCLDEKEFQVPMATTEGCLVASTNRCRAIGLGGGASSRVLADXKSVVCEAVIPAK
VVREVLKTTTEAMIEVNINKNLVGSAMAGSIGGYNAHAANIVTAIYIACGQDAAQNVGSSNCITLMEA
SGPTNEDLYISCTMPSIEIGTVGGGTNLLPQQACLQMLGVQGACKDNPGENARQLARIVCGTVMAGE
LSLMAALAAGHLVKSHMIHN

>d1hw8a2 d.179.1.1 (A:441-586,A:704-861) Substrate-binding domain of HMG-CoA reductase {Human (Homo sapiens)}

EPRPNEECLQLGNAEKGAKFLSDAEIIQLVNAKHIPAYKLETLIETHERGVSIRRQLLSKKLSEPSLQ
YLPYRDYNYSLVMGACCENVIGYMPIPVGVAGPLCLDEKEFQVPMATTEGCLVASTNRCRAIGLGGG
ASSRVLADXKSVVCEAVIPAKVVREVLKTTTEAMIEVNINKNLVGSAMAGSIGGYNAHAANIVTAIYIA
CGQDAAQNVGSSNCITLMEASGPTNEDLYISCTMPSIEIGTVGGGTNLLPQQACLQMLGVQGACKDN
PGENARQLARIVCGTVMAGELSLMAALAAGH

>d1hw8c2 d.179.1.1 (C:488-586,C:704-860) Substrate-binding domain of HMG-CoA reductase {Human (Homo sapiens)}

HERGVSIRRQLLSKKLSEPSLQYLPYRDYNYSLVMGACCENVIGYMPIPVGVAGPLCLDEKEFQVPM
ATTEGCLVASTNRCRAIGLGGGASSRVLADXKSVVCEAVIPAKVVREVLKTTTEAMIEVNINKNLVGS
AMAGSIGGYNAHAANIVTAIYIACGQDAAQNVGSSNCITLMEASGPTNEDLYISCTMPSIEIGTVGGGT
NLLPQQACLQMLGVQGACKDNPGENARQLARIVCGTVMAGELSLMAALAAG

>d1qaxa2 d.179.1.1 (A:4-110,A:221-428) Substrate-binding domain of HMG-CoA reductase {Pseudomonas mevalonii}

DSRLPAFRNLSPAARLDHIGQLLGLSHDDVSLANAGALPMDIANGMIENVIGTFELPYAVASNFQIN
GRDVLVPLVVEEPSIVAAASYMAKLARANGGFTTSSSAPXRLARAQVRITPQQLETAEFSGEAVIEGIL
DAYAFAAVDPYRAATHNKGIMNGIDPLIVATGNDWRAVEAGAHAYACRSGHYGLTTWEKDNNHGL
VGTLEMPMPVGLVGGATKTHPLAQLSLRILGVKTAQALAEIYAVAVGLAQNLGAMRALATEGIQRGHM
ALHARNIAVVAGARGDEVDWVARQLVEYHDVRADRAVALLKQKRGQ

>d1qaxb2 d.179.1.1 (B:504-610,B:721-875) Substrate-binding domain of HMG-CoA reductase {Pseudomonas mevalonii}

DSRLPAFRNLSPAARLDHIGQLLGLSHDDVSLANAGALPMDIANGMIENVIGTFELPYAVASNFQIN
GRDVLVPLVVEEPSIVAAASYMAKLARANGGFTTSSSAPXRLARAQVRITPQQLETAEFSGEAVIEGIL
DAYAFAAVDPYRAATHNKGIMNGIDPLIVATGNDWRAVEAGAHAYACRSGHYGLTTWEKDNNHGL
VGTLEMPMPVGLVGGATKTHPLAQLSLRILGVKTAQALAEIYAVAVGLAQNLGAMRALATE

>d1k92a2 d.210.1.1 (A:189-444) Argininosuccinate synthetase, C-terminal domain {Escherichia coli}

AYSTDSNMLGATHEAKDLEYLNSSVKIVNPIMGVKFWDESVKIPAEVTVRFEQGHVPVALNGKTFSD
DVEMMLEANRIGGRHGLGMSDQIENRIEAKSRGIYEAPGMALLHIAYERLLTGIHNEDTIEQYHAH
GRQLGRLLYQGRWFDSQALMLRDSLQRWVASQITGEVTLELRRGNDYSILNTVSENLTYPKPERLTME
KGDVSVFPDDRIGQLTMRNLDITDTREKLFYAKTGLLSSSAASGVPQVENLENK

>d16vpa_ d.180.1.1 (A:) Conserved core of transcriptional regulatory protein vp16 {Herpes simplex virus type 1}

SRMPSPMPVPPAALFNRLDDLGFSAGPALCTMLDTWNEDLFSALPTNADLYRECKFLSTLPSDV
VEWGDAYVPERTQIDIRAHGDVAFPTLPATRDGLGLYEEALSRRFFHAELRAREESYRTVLANFCSALY

RYLRASVRQLHRQAAMRGRDRDLGEMLRATIADRYRETARLARVFLHLYLFLTREILWAAAYAEQ
MMRPDLFDCLCCDLESWRQLAGLFQPFMFVNGALTVRGVPIEARRLRELNHIREHLNPLVRSAAAT
EEPAPLTPPTLHGNQARASGYFMVLIRAKLDSYSSFTTSPSEAVMREHAYSRAPTKNNYGSTIEGL
LDLPDDDAPEEAGLAAPRLSFL

>d1bdfa2 d.181.1.1 (A:53-178) RNA polymerase alpha subunit {Escherichia coli}
GCAVTEVEIDGVLHEYSTKEGVQEDILEILLNLKGLAVRVQKDEVILTNLKSGIGPVTAADITHDGDV
EIVKPKQHVICHLTDENASISMRIKVRGRGVPASTRIHSEEDERPIGRLLVDACYS

>d1i6va2 d.181.1.1 (A:50-172) RNA polymerase alpha subunit {Thermus aquaticus}
GTAVTSVYIEDVLHEFSTIPGVKEDVVEIILNLKELVVRFLDPKMASTTLILRAEGPKEVRAVDFTPSA
DVEIMNPDHLIATLEEGGKLYMEVRVDRGVGYVPAERHGIKDRINAIPVDAIFS

>d1i50c2 d.181.1.1 (C:42-172) RPB3 {Baker's yeast (Saccharomyces cerevisiae)}
PTLAIDSVEVETNTTVLADEFIAHRLGLIPLQSMIDIEQLEYSRDCFCEDHCDKCSVVLTLQAFGESEST
TNVYSKDLVIVSNLMGRNIGHPIIQDKEGNGVLICKLRKGQELKLTCAVAKKIAKEHAKWGP

>d1e16a_ d.182.1.1 (A:) Baseplate structural protein gp11 {Bacteriophage T4}
SRLADFLGFRPKTGDIDVMNRQSVGSVTISQLAKGFYEPNIESAINDVHNFSIKDVGTIITNKTGVSPE
GVSQTDYWAFSGTVDLSPGSPITVLFGLPVSATTGMTAIEFVAKVRVALQEAIASFTAINSYKDH
PTDGSKLEVTYLDNQKHLVSTYSTYGITISQEIISESKPGYGTWNLLGAQTVTLDNQQTPTVYHFER
TA

>d1fh6a_ d.183.1.1 (A:) Major capsid protein gp5 {Bacteriophage HK97}
SLGSDADSAGSLIQPMQIPGIIMPGLRRLTIRDLLAQGRTSSNALEYVREEVFTNNADVVAEKALKPES
DITFSKQTANVKTIAHWVQASRQVMDDAPMLQSYINNRLMYGLALKEEGQLLNGDGTGDNLEGLN
KVATAYDTSLNATGDTRADIIAHAIYQVTESEFSASGIVLNPRDWHNIALKDNENGRYIFGGPQAFTS
NIMWGLPVVPTKAQAAGTFTVGGFDMASQVWDRMDATVEVSREDRDNFVKNMLTILCEERLALA
HYRPTAIHKGFSS

>d1fn9a_ d.196.1.1 (A:) Outer capsid protein sigma 3 {Reovirus}
MEVCLPNGHQVVDLINNAFEGRVSIIYSAQEGWDKTISAQPDMMVCGGAVVCMHCLGVVGSQRKL
KHLPHHRCNQQRHQDYVDVQFADRVTAHWKRGMLSFVAQMHEMMNDVSPDDLDRVRTEGGSLV
ELNWLQVDPNSMFRSIHSSWTDPLQVDDLDTKLDQYWTALNLMIDSSDLIPNFMRRDPSHAFN
GVKLGGDARQTQFSRTFDSRSSLEWGMVYDYSELEHDPKGRAYRKELVTPARDFGHFGLSHYSR
ATTPILGKMPAVFSGMLTGNCMKMYPFIKGTAKLKTVRKLVEAVNHAWGVKIRYALGPGGMTGWYN
RTMQQAPIVLTAAALTMFPDTIKFGDLNYPVMIGDPMILG

>d1qgwa_ d.184.1.1 (A:) Phycoerythrin 545 alpha-subunits {Cryptophyte (Rhodomonas sp.),
cs24}
AMDKSAKAPQITIFDHRGCSRAPKESTGGKAGGQDDEMMVKVASTKVTVSESDAAKKLQEFITFEK
GIDGPFTSKN

>d1qgwb_ d.184.1.1 (B:) Phycoerythrin 545 alpha-subunits {Cryptophyte (Rhodomonas sp.),
cs24}
AMDKSAKAPVITIFDHRGCSRAPKEYTGAKAGGKDDEMMVKAQSVKIEVSTGTAEGVLATSLAKMT
K

>d1jyoe_ d.184.1.2 (E:) Virulence effector SptP domain {Salmonella typhimurium}
DKAYVAPEKFSSKVLTLWLGKMPFKNTEVVQKHTENIRVQDQKILQTFLHALTEKYGETAVNDALL
MSRINMNKPLTQRLAVQITECVKAADEGFNLIKSK

>g1hle.1 e.1.1.1 (A;B:) Elastase inhibitor {Horse (Equus caballus)}
MEQLSTANTHFAVDLFRALNESDPTGNIFISPLSISSALAMIFLGTGRNTAAQVSKALYFDTVEDIHSR

FQSLNADINKPGAPYILKLANRLYGEKTYNFLADFLASTQKMYGAELASVDFQQAPEDARKEINEWV
KGQTEGKIPELLVKGMVDNMTKLVLVNAIYFKGNWQQKFMKEATRDAPFRLNKKDKTKTKVMMYQ
KKKFPYNYIEDLKCRVLELPYQKGKELSMILLPDDIEDESTGLEKIEKQLTLDKLEWTKPENLYLAEV
NVHLPRFKLEESYDLTSHLARLVQDLFNRGKADLSGMSGARDLFSKIIHKSFDLNEEGTEAAAA
TAGTILLAXEENFNADHPFIFIRHNPSANILFLGRFSSP

>d1ovaa_ e.1.1.1 (A:) Ovalbumin {Hen (Gallus gallus)}

GSIGAASMEFCFDVFKELKVHHANENIFYCPIAIMSALAMVYLGAKDSTRTQINKVVRFDKLPFGD
SIEAQCGTSVNVHSSLRDILNQITKPNVVSFSLASRLYAEERYPILPEYLQCVKELYRGGLEPINFQTA
ADQARELINSWVESQTNGIIRNVLQPSSVDSQTAMVLVNAIVFKGLWEKAFKDEDTQAMPFRVTEQ
ESKPVQMMYQIGLFRVASMASEKMKILELPFASGTMSMLVLLPDEVSGLEQLESIINFEKLTETWSSN
VMEERKIKVYLPRMKMEEKYNLTVLMAMGITDVFSSSANLSGSSAESLKISQAVHAAHAEINEAG
REVVGSAEAGVDAASVSEEFRADHPFLFCIKHIATNAVLFFGRCVSP

>g1as4.1 e.1.1.1 (A;B:) Antichymotrypsin, alpha-1 {Human (Homo sapiens)}

GLASANVDFAFSLYKQLVLKAPDKNVIFSPSISTALAFSLGAHNTTLTEILKGLKFNLTETSEAEIHQ
SFQHLLRTLNLQSSDELQLSMGNAMFVKEQLSLLDRFTEDAKRLYGSEAFATDFQDSAAAKKLINDYV
KNGTRGKITDLIKDLSQTMMVLVNYIFFKAKWEMPFDQDTHQSRFYLSKKKVVMPMMSLHH
LTIPYFRDEELSCTVVELKYTGNASALFILPDQDKMEEVEAMLLPETLKRWRDSLEFREIGELYLPKF
SISRDNLNLDILLQLGIEEAFTSKADLSGITGARNLAVSQVVHKAVLDVFEEGTEASRATAVKITLLXG
TIVRFNRPFMIIVPTDTQNIFFMSKVTNPKQ

>d1qlpa_ e.1.1.1 (A:) Antitrypsin, alpha-1 {Human (Homo sapiens)}

FNKITPNLAEFAFSLYRQLAHQSNSTNIFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTETPEAQI
HEGFQELLRTLNLQPSQLQLTTGNGLFLSEGLKLVDFLEDVKKLYHSEAFVNFVGDTEEAKKQIND
YVEKGTQGKIVDLVKELDRDVFALVNYIFFKWKWERPFVVDTEEDFHVDQVTTVKVPMMKRLG
MFNIQHCKKSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLNEDRRSASLHLPKLSI
TGTYDLKSVLGQLGITKVFVNGADLSGVTEEAPLKLKAVHKAVLTIDEKGTEAAGAMFLEAIPMSIP
PEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK

>d1atta_ e.1.1.1 (A:) Antithrombin {Cow (Bos taurus)}

VEDVCTAKPRDIPVNPNCIYRATEGQGSEQKIPGATNRRVWELSKANSHFATAFYQHLADSKNNND
NIFLSPLSISTAFAMTKLGACNNTLTQLMEVFKFDTISEKTSQIHFFFKLNCRLYRKANKSSELVSA
NRLFGDKSITFNETYQDISEVVYGAQLQPLDFKGNAEQSRLTINQWISNKTEGRITDVIPPQAINFTV
LVLVNTIYFKGLWKSFKSPENTRRELKELFYKADGESCSVLMYQESKFRYRRVAESTQVLELPFKGDDIT
MVLILPKLEKTLAKVEQELTPDMLQEWLDELTTLLVHMPRFRIEDSFSVKEQLQDMGLEDLDFSP
EKSRLPGIVAEGRSPLYVSDAFHKAFLEVNEEGSEAAASTVISIAGRSLRVTFKANRPFLVLIREVALN
TIIFMGRVANPCVD

>d1e05i_ e.1.1.1 (I:) Antithrombin {Human (Homo sapiens)}

SPVDICTAKPRDIPMNPNCIYRSPEKKATEDEGSEQKIPEATNRRVWELSKANSRFATTFYQHLADS
KNDNDNIFLSPLSISTAFAMTKLGACNDTLQQLMEVFKFDTISEKTSQIHFFFKLNCRLYRKANKS
SKLVSANRLFGDKSLTFNETYQDISELVYGAQLQPLDFKENAEQSRAAINKWVSNKTEGRITDVIPSE
AINELTVLVLVNTIYFKGLWKSFKSPENTRRELKELFYKADGESCSASMMYQEGKFRYRRVAESTQVLELP
FKGDDITMVLILPKPEKSLAKVEKELTPEVLQEWLDELEEMMLLVHMPRFRIEDGFSLEQLQDMG
LVDLFSPEKSKLPGIVAEGRDDLYVSDAFHKAFLEVNEEGSEAAASTAVVIAGRSLNPNRVTFKANRP
FLVFIREVPLNTIIFMGRVANPCV

>d1a7ca_ e.1.1.1 (A:) Plasminogen activator inhibitor-1 {Human (Homo sapiens)}

HHPPSYVAHLASDFGVRVFFQVAQASKDRNVVFSYGVASVLAMLQLTTGGETQQQIQAAAMGFKID

DKGMAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFMPPHFFRLFRSTVKQVDFSEVERAR
FIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNGQWKT PFPDSSTHRRLFHKSDGSTVSV
MMAQTNKFNYTEFTTPDGHYYDILELPYHGD TLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNM
TRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQVKKIEVNESGT
VESSTAVIVSARMAPEEIIIMDRPFLFVVRHNPTGTVLFGQVMEP

>d1by7a_e.1.1.1 (A:) Plasminogen activator inhibitor-2 {Human (Homo sapiens)}

EDLCVANTL FALNLFKHLAKASPTQNLFLSPWSISSTMAMVYMGSRGSTEDQMAKVLQFNEVGAA
ADKIHSSFRSLSSAINASTGNYLLESVNKLFGEKSASFREYIRLCQKYSSSEPQAVDFLECAEEARKKI
NSWVKTQTKGKIPNLLPEGSVDG DTRMVLVNAVYFKGKWKTPFEKKLNGLYPFRVNSAQRTPVQM
MYLREKLNIGYIEDLKAQILELPYAGDVSMFLLLPDEIADVSTGLELLESEITYDKLNKWT SKDKMAE
DEVEVYIPQFKLEEHYELRSILRSMGMEDAFNKGRANFSGMSERNDLFLSEVFHQAMVDVNEEGTE
AAAGTGGVMTGRTGHGGPQFVADHPFLFLIMHKITNCILFFGRFSSP

>g1jjo.1 e.1.1.1 (A:,C:,E:) Neuroserpin {Mouse (Mus musculus)}

TITEWSVNMVYHNRGTGEDENILFSPSLIALAMGMELGAXENQYVMKLANSLFVQNGFHVNEEF
LQMLKMYFNAEVNHVDFSQNVAVANSINKWVENYTNLLKDLVSPEDFDGVTNLALINAVYFKGN
WKSQFRPENTRTFSFTKDDSEVQIPMMYQQGEFYGFSDGSNEAGGIYQVLEIPYEGDEISMMLA
LSRQEVPLATLEPLLKAQLIEEWANSVKKQKVEVYLPRFTVEQEIDLKDKALGVTEIFIKDANLTA
MSDKKELFLSKAVHKSCIEVNEEGSEAAAASGMIAISXYPQVIVDHPFLYLIRNRKSGIILFMGRVMNP
HH

>d1sek__e.1.1.1 (-) Serpin K {Tobacco hawkmoth (Manduca sexta)}

GETDLQKILRESNDQFTAQMFSEVVKANPGQNVVLSAFSVLPPLGQLALASVGESHDELLRALALPN
DNVTKDVFADLNRGVRVAVKGVLDKMASKIYVAKGLELND DFAAVSRDVFGEVQNVDFVKSVEAAG
AINKWVEDQTNRIKLNLDALDETTRSVLVNAIYFKGSWKDKFNKERTMDRDFHVSKDKTIKV
PTMIGKKDVRVADVPELDAMIEMSYEGDQASMIILPNQVDGITALEQKLKDPKALSRAEERLYNTE
VEIYLPKFKIETTTDLKEVLSNMNIKKLFTPGAARLENLLKT KESLYVDAAIQKAFIEVNEEGAEAAA
ANAFKITTYSFHFVPKVEINKPFFFSLKYNRNSMFSGVCVQP

>d1k9oi_e.1.1.1 (I:) Alaserpin (serpin 1) {Tobacco hornworm (Manduca sexta)}

GETDLQKILRESNDQFTAQMFSEVVKANPGQNVVLSAFSVLPPLGQLALASVGESHDELLRALALPN
DNVTKDVFADLNRGVRVAVKGVLDKMASKIYVAKGLELND DFAAVSRDVFGEVQNVDFVKSVEAAG
AINKWVEDQTNRIKLNLDALDETTRSVLVNAIYFKGSWKDKFKERTMDRDFHVSKDKTIKV
PTMIGKKDVRVADVPELDAMIEMSYEGDQASMIILPNQVDGITALEQKLKDPKALSRAEERLYNTE
VEITLPKFKIETTTDLKEVLSNMNIKKLFTPGAARLENLLKT KESLTVDAAIQKAFIEVNEEGAEAAA
ANAFGIVPKSLILYPEVHIDRPFYFELKIDGIPMFNGKVIEP

>g1f0c.1 e.1.1.1 (A:,B:) Viral serpin crmA (cytokine response modifier protein) {Cowpox virus}

MDIFREIASSMKGENVFISPPSISSVLTILYGGANGSTAEQLSKYVEKEADKNKDDISFKSMNKVYGRY
SAVFKDSFLRKIGDNFQTVDFDTCRTVDAINKVDIFTEGKINPLLEPLSPDTCLLAISAVYFKAKW
LMPFEKEFTSDYPFYVSPTEMVDVSMMSMYGEAFNHASVKESFGNFSIHELPHYVGD TSMVVILPDNI
DGLSIEQNLDTNFKKWCDSMDAMFIDVHIPKFKVTGSYNLVDALVKLGLTEVFGSTGDYSNMCNS
DVSVDAMIHKTYIDVNEEYTEAAAATCALVADCA XSTVTNEFCADHPFIYVIRHVDGKILFVGRYCSP
TTN

>d1imva_e.1.1.1 (A:) Rignent epithelium-derived factor, PEDF {Human (Homo sapiens)}

TGALVEEEDPFFKVPVNKLAAAVSNFGYDLYRVRSSMSPTTNVLLSPLSVATALSALS LGADERTESII
HRALYYDLISSPDHGTYKELLDVTAPQKNLKSASRIVFEKKLRIKSSFVAPLEKSYGTRPRVLTGNP

RLDLQEINNWWVQAQMKGKLARSTKEIPDEISILLGVAHFQGWVTKFDSRKTSLDFYLDEERTVR
VPMMSDPKAVLRYGLSDLSCKIAQLPLTGSMSIIFLPLKVTQNLTLIEESLTSEFIHDDRELKTVQA
VLTVPKLLKLSYEGEVTKSLQEMKLSLDFSPDFSKITGKPIKLTQVEHRAGFEWNEGAGTTPSPGL
QPAHLTFPLDYHLNQPFIFVLRD TDTGALLFIGKILDPRGP

>d1ecra_e.2.1.1 (A:) Replication terminator protein (Tus) {Escherichia coli}

DLVDRLNNTFRQMEQELAIFAHAHLEQHKLVARVFSLPEVKKEDEHNPLNRIEVKQHLGNDAQSLA
LRHFRHLFIQQQSENRSKAAVRLPGVLCYQVDNLSQAALVSHIQHINKLKTTFEHIVTVESELPTAA
RFEWVHRHLPGLITLNAYRTLTVLHDPATLRFWGWANKHIIKNLHRDEVLAQLEKSLKSPRSVAPWT
REEWQRKLEREYQDIAALPQNAKLIKRPVKVQPIARVWYKGDQKQVQHACPTPLIALINRDNGAG
VPDVGELLYNDADNVQHRYKPAQPLRLIIPRLHLYVAD

>d1es5a_e.3.1.1 (A:) D-ala carboxypeptidase/transpeptidase {Streptomyces sp., K15}

KPTIAAVGGYAMNNGTGTTLYTKAADTRRSTGSTTKIMTAKVVLAQSNLNLDAKVTIQKAYS DYVVA
NNASQAHLVGDKVTVRQLLYGLMLPSGCDAAYALADKYSGSGSTRAARVKSFIGKMNTAATNLGLHN
THFDSFDGIGNGANYSTPRDLTKIASSAMKNSTFRVVKTKAYTAKTVTKTGSIRTMDTWKNTNGL
LSSYSGAIGVKTGAGPEAKYCLVFAATRGGKTVIGTVLASTSIPARESDATKIMNYGFAL

>d1hvba_e.3.1.1 (A:) D-ala carboxypeptidase/transpeptidase {Streptomyces sp., R61}

DLPAPDDTGLQAVLHTALSQGAPGAMVRVDDNGTIHQSEGADRATGRAITTTDRFRVGSVTKSFS
AVVLLQLVDEGKLDLDASVNTYLPGLLPDDRITVRQVM SHRSGLYDYTNMFAQTVPGFESVRNKV
FSYQDLITLSLKHGVTNAPGAAYSNTNFVAGMLIEKLTGHSVATEYQNRIFTPLNLDTFYVHPD
TVIPGTHANGYLTPDEAGGALVDSTEQTVSWAQSAGAVISSTQDLDTFFSALMSGQLMSAAQLAQM
QQWTTVNSTQGYGLLRRDLSCGISVYGHGTGVQGYTYAFASKDGKRSVTALANTSNNVNLNT
MARTLES AFCGKP

>d1ci9a_e.3.1.1 (A:) Esterase EstB {Burkholderia gladioli}

AASLAARLDAVFDQALRERRLVGAVAIVARHGEILYRRAQGLADREAGRPMREDTLFRLASVTKPIVA
LAVLRLVARGELALDAPVTRWLPEFRPRLADGSEPLVTIHHLLTHTSGLGYWLLEGAGSVYDRLGISD
GIDLRDFDLDENLRRLASAPLSFAPGSGWQYSLALDVLGAVVERATGQPLAAAVDALVAQPLGMRDC
GFVSAEPPERFAVPYHDGQPEPVRMRDGEVPLPEGHGAAVRFAPSRVFEPGAYPSGGAGMYGSADDV
LRALAIRANPGFLPETLADAARRDQAGVGAETRPGWGFYLSAVLDDPAAAGTPQHAGTLQWG
GVYGHSWFVDRALGLSVLLLTNTAYEGMSGPLTIALRDAVYA

>d1bt1_e.3.1.1 (-) beta-Lactamase, class A {Escherichia coli, TEM-1}

HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMSTFKVLLCGAVLSRIDAGQEQLGR
RIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTIGGPKELTAFLHNMGDHVT
RLDRWEPELNEAIPNDERDTTMPVAMATTLRKLTLGELLTLASRQQLIDWMEADKVAGPLLRSLP
AGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIAEIGASLIKHW

>d1bza_e.3.1.1 (-) beta-Lactamase, class A {Escherichia coli, TOHO-1}

SVQQQLEALEKSSGRLGVALINTADNSQILYRADERFAMCSTSKVMAAAAVLKQSESKHLLNQRV
EIKKSDLVNYNPIAEKHVNGTMTLAE LGAAALQYSDNTAMNKLIAHLGGPKVTAFAARSLGDETFR
LDRAPTNTAIPGDPDRDTTTP LAMAQTLKNLTGKALAETQRAQLVTWLKGNNTGSASIRAGLPKS
WVVGDKTGS GDYGTNDIAVIWPENHAPLVLVTYFTQPEKAEERRRDILAAA AKIVT

>d1g56a_e.3.1.1 (A:) beta-Lactamase, class A {Klebsiella pneumoniae, SHV-1}

SPQPLEQIKLSESLSGRVGMIEMDLASGRTLTAWRADERFPMSTFKVLLCGAVLARVDAGDEQL
ERKIHRYRQDLVDYSPVSEKHLADGMTV GELCAAITMSDNSAANLLLATVGGPAGLTAFLRQIGDN
VTRLDRWETELNEALPGDARDTTTPASMAATLRKLTSQRLSARSQRQLLQWVDDR VAGPLIRSV
LPAGWFIADKTGAGERGARGIVALLGPNNKAERIVVIYLRDTPASMAERNQIAGIGAALIEHWQR

>d1g6aa_ e.3.1.1 (A:) beta-Lactamase, class A {Pseudomonas aeruginosa, PSE-4 carbenicillinase}

SKFQQVEQDVKAIEVSL SARIGVSVLDTQNGEYWDYNGNQRFLPTSTFKTIACAKLLYDAEQGKVNPNSTVEIKKADLVITYSPVIEKQVGVQAITLDDACFATMTSDNTAANIILSAVGGPKGVDFLRQIGDKETRLDRIEPLDNEGKLGDLRDTTPKAIASSTLNKFLFGSALSEMNNQKKLESWMVNNQVTGNLLRSVLPAGWNIADKSGAGGFGARSITAVVWSEHQAPIIVSIYLAQTQASMEERNDIVKIGHSIFDVYTS

>d1alq_ e.3.1.1 (-) beta-Lactamase, class A {Staphylococcus aureus}

SEPIVLVIFTNKDNKSDKPNDKLISETAKSVMKEFAAGSKNAAKELNDLEKKYNAHIGVYALDTKSGKEVKFNSDKRFAYASTSKAINSAILLEQVPYNKLNKKVHINKDDIVAYSPILEKYVGGKDLTKALIEASMTYSNTANNKIIKEIGGIKVKQRLKELGDKVTNPVRYEIELNYSPKSKKDTSTPAAFGKTLNKLIANGLSKENKKFLLDLMLNNSGDTLIKDGVPKDYKVADKSGQAITYASRNDVAFVYPK

>d1ghpa_ e.3.1.1 (A:) beta-Lactamase, class A {Staphylococcus aureus}

KELNDLEKKYNAHIGVYALDTKSGKEVKFNSDKRFAYASTSKAINSAILLEQVPYNKLNKKVHINKDDIVAYSPILEKYVGGKDLTKALIEASMTYSNTANNKIIKEIGGIKVKQRLKELGDKVTNPVRYDIELQYSPKSKKDTSTPAAFGKTLNKLIANGLSKENKKFLLDLMLNNSGDTLIKDGVPKDYKVADKSGQAITYASRNDVAFVYPKGQSEPIVLVIFTNKDNKSDKPNDKLISETAKSVMKEF

>d4blma_ e.3.1.1 (A:) beta-Lactamase, class A {Bacillus licheniformis}

DDFAKLEEQFADAKLGFALDTGTNRTVAYRPERFAFASTIKALTVGVLLQKSIDLNQRITYTRDDL VNYNPITEKHVDTGMTLRELADASLRYSNAAQNLILKQIGGPESLKKELRKIGDEVNTNPERFEPELNEVNPGETQDTSTARALVTSLRAFALEDKLPSEKRELLIDWMKRNTTGDALIRAGVPDGEVADKTGAASYGTRNDIAIHWPPKGDVAVLSSRDKKDAKYDDKLI AEATKVVMKALN

>d1buea_ e.3.1.1 (A:) beta-Lactamase, class A {Enterobacter cloacae, NMC-A carbapenemase}

NTKGIDEIKNLETDFNGRIGVYALDTGSGKSFSYRANERFPLCSSFKGFLAAAVLKGSDNRLNLNQI VNYNTRSLEFHSPITTKYKDNMGSLGDMAAAALQYSDNGATNIIERYIGGPEGMTKFMRSIGDEDFRLDRWELDLNTAIPGDERDTSTPAAVAKSLKTLALGNILSEHEKETYQTWLKGNNTGAARIRASVPSDWVVVGDKTGSCGAYGTANDYAVVWPKNRAPLIISVYTTKNEKEAKHEDKVIAEASRIAIDNLK

>d1bsg_ e.3.1.1 (-) beta-Lactamase, class A {Streptomyces albus G}

SDAERRLAGLERASGARLVYAYDTGSGRTVAYRADELFPMSVFKTLSSAAVLRDLDRNGEFLSRRI LYTQDDVEQADGAPETGKPQNLANGMTVEELCEVSITASDNCAANMLRELGGPAAVTRFVRS LGDRVTRLDRWEPELNSAEPGRVTDTTSPRAITRTYGRVLGDALNPRDRRLTSWLLANTTS GDRFRA GLPDDWTLGDKTGAGRYGTNNDAGVTWPPGRAPIVLTVLTAKTEQDAARDGLVADAARVLAETL G

>d1mfoa_ e.3.1.1 (A:) beta-Lactamase, class A {Mycobacterium fortuitum}

APIDDQLAELERRDNVLI GLYAANLQSGRRITHRPDEMFCSTFKGYVAARVLQMAEHGEISLDNR VFDADALVPNSPVTEARAGAEMTLAELCQAALQRSDNTAANLLLKTIGGPAAVTAFARVSGDERTR LDRWEVELNSAIPGDPRDTSTPAALAVGYRAILAGDALSPQRLLEDWMRANQTSSMRAGLPEG WTTADKTGSGDYGSTNDAGIAFGPDGQRLLVMMTRSQAHDPKAENLRPLIGELTALVLPSSL

>d1e25a_ e.3.1.1 (A:) beta-Lactamase, class A {Pseudomonas aeruginosa, PER-1}

SPLLKEQIESIVIGKKATVGVAVWGPDDLEPLLINPFKFPMSVFKLHLAMLVLHQVDQGLDLNQ TVIVNRAKVLQNTWAPIMKAYQGDEFSPVQQLQYSVSHSDNVACDLLFELVGGPAALHDIYQSMG IKETAVVANEAMHADDQVYQNWTS MKGAAEILKKFEKQTLSETSQALLWKWMVETTTGPER LKGLLPAGTVVAHKTGTSQIKAGKTAATNDLGIILLPDGRPLLVAVFVKDSAESSRTNEAIIAQAQTAY QFELKKLSAL

>d1dy6a_ e.3.1.1 (A:) beta-Lactamase, class A {Serratia marcescens, Sme-1}

NKSDAAAKQIKKLEEDFDGRIGVFAIDTGSNTFGYRSDEFPLCSSFKGFLAAVLERVQKKLNDIN
QKVKYESRDLEYHSPITTKYKSGMTLGDMSAALQYSDNGATNIIMERFLGGPEGMTKFMRSIGD
NEFRLDRWELELNTAIPGDKRDTSTPKAVANSLNKLALGNVNLAKVKAIYQNWLKGNNTGDARIRA
SVPADWVVGDKTSGCGAYGTANDYAVIWPKNRAPLIVSIYTTTRKSKDDKHSDKTIAEASRIAIQAID

>d1fr1a_e.3.1.1 (A:) AMPC beta-Lactamase, class C {*Citrobacter freundii*}

AAKTEQQIADIVNRTITPLMQEQAIIPGMAVAIIYQGKPYFTWKGADIANNRPVTQQTFLFELGSVSK
TFNGVLGGDAIARGEIKLSDPVVTQYWPELTGKQWQGISLLHLATYTAGGLPLQVPDDVTDKAALLRF
YQNWQPQWAPGAKRLYANSSIGLFGALAVKPSGMSYEEAMSKRVLHPLKLAHTWITVPQSEKDYA
WGYREGKPVHVSPGQLDAEAYGVKSSVIDMTRWVQANMDASQVQEKTLQGGIELAQSRWRIGDM
YQGLGWEMLNWPVKADSIISGSDSKVALAALPAVEVNPAPAVKASWVHKTGSTGGFGSYVAFVPE
KNLGIVMLANKSYPNPVRVEAAWRILEKLQ

>d1ga0a_e.3.1.1 (A:) AMPC beta-Lactamase, class C {*Enterobacter cloacae*, P99,
cephalosporinase}

PVSEKQLAEVVANTVTPLMKAQSVPGMAVAVIYQGKPHYFTFGKADIAANKPVTQQTFLFELGSISKT
FTGVLGGDAIARGEISLDDPVTRYWPQLTGKQWQGIIRMLDLATYTAGGLPLQVPDEVTDNASLLRFY
QNWQPQWKPGRTRYANASIGLFGALAVKPSGMPYEQAMTTRVLKPLKLDHTWINVPKAEAAHYA
WGYRDGKAVRAVRVSPGMLDAQAYGVKTNVQDMANWVMANMAPENVADASLKQGIALAQSRYW
RIGSMYQGLGWEMLNWPVEANTVVEGSDSKVALAPLVAEVNPPAPPVKASWVHKTGSTGGFGSY
VAFIPEKQIGIVMLANTSYPNPARVEAAHYHILEALQ

>d1i5qa_e.3.1.1 (A:) AMPC beta-Lactamase, class C {*Escherichia coli*, cephalosporinase}

APQQINDIVHRTITPLIEQQKIPGMAVAVIYQGKPYFTWGYADIKKQPVTQQTFLFELGSVSKTFTG
VLGGDAIARGEIKLSDPTTKYWPELTAKQWNGITLLHLATYTAGGLPLQVPDEVKSSDLLRFYQNW
QPAWAPGTQRLYAASSIGLFGALAVKPSGLSFEQAMQTRVFQPLKLNHTWINVPPAEKKNYAWGYR
EGKAVHVSPGALDAEAYGVKSTIEDMARWVQSNLKLPLDINEKTLQGGIQLAQSRYWQTDGMYQGLG
WEMLDWPVNPDSIINGSDNKIALAARPVKAITPPTPAVRASWVHKTGATGGFGSYVAFIPEKELGIV
MLANKNYPNPARVDAAWQILNALQ

>d1k55a_e.3.1.1 (A:) Class D beta-lactamase {*Pseudomonas aeruginosa*, OXA-10}

SITENTSWNKEFSAEAVNGVFVLCSSKSCATNDLARASKEYLPASTFKIPNAIIGLETGVKNEHQV
FKWDGKPRAMKQWERDLTLRGAIQVSAVPVFQIAREVGEVRMQLKFKFSYGNQNISGGIDKFW
LEGQLRISAVNQVEFLESYLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSVGTESNPGVAWW
VGWVEKETEVYFFAFNMDIDNESKLPLRKSIPTKIMESEGIIG

>d1k25a4_e.3.1.1 (A:264-631) Penicillin-binding protein 2x (pbp-2x), transpeptidase domain
{*Streptococcus pneumoniae*}

TLSSPLQSFMETQMDAFLEKVKGKYMATLVSAKTGEILATTQRPTFNADTKEGITEDFVWRDILYQ
SNYEPGSAMKVMTLASSIDNNTFPGGEVFNSELKIADATTRDWDVNEGLTTGGMMTFLQGFHSS
NVGMSLLEQKMGDATWLDYLRKFKGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLR
AFTAIANDGVMLEPKFISAIYDTNNSVRKSQKEIVGNPVSKEAASTTRNHMILVGTDPYGTMYNH
YTGKPIITVPGQNVAVKSGTAQIADEKNGGYLVGSTNYIFSAVTMNPAENPDFILYVTVQQPEHYSGIQ
LGEFATPILERASAMKESLNLQSPAKNLDKVT

>d1qmea4_e.3.1.1 (A:264-620) Penicillin-binding protein 2x (pbp-2x), transpeptidase
domain {*Streptococcus pneumoniae*}

TISSPLQSFMETQMDAFQEKVKGKYMATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQ
SNYEPGSTMKVMMLAAAIDNNTFPGGEVFNSELKIADATIRDWDVNEGLTTGGRMMTFSQGFHSS
SNVGMTLLEQKMGDATWLDYLRKFKGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMI

RAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKDAAASLRTNMVLVGTDPVYGTMYN
HSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGI
QLGEFANPILERASAMKDSLNL

>d1hd8a2 e.3.1.1 (A:3-262) Penicillin-binding protein 5, N-terminal domain {Escherichia coli}

LNIKTMIPGVPPQIDAESYILIDYNSGKVLAEQNADVRRDPASLTKMMTSYVIGQAMKAGKFKETDLV
TIGNDAWATGNPVFKGSSLMFLKPGMQVPVSQLIRDINLQSGNDACVAMADFAAGSQDAFVGLMNS
YVNALGLKNTHFQTVHGLDADGQYSSARDMALIGQALIRDVPNEYSIYKEKEFTFNGIRQLNRNGLL
WDNSLNVDDGIKTGHTDKAGYNLVASATEGQMLISAVMGGRTFKGREAESKLLTWGFRF

>d1ei5a3 e.3.1.1 (A:3-335) D-aminopeptidase, N-terminal domain {Ochrobactrum anthropi}

KFDTSALEAFVRHIPQNYKGGVAVVKDGEVVLQHAWGFADLRTRTPMTLDRMPICSVSKQFT
CAVLLDAVGEPELLDDALEAYLDFEDERPAVRDLCNNQSGLRDYWALSVLGADPEGVFLPAQAQS
LLRRLKTTTHFEPGSHYSYCNNGNFRILADLIEAHTGRTLVDILSERIFAPAGMKRAELISDTALFDECTG
YEGDTRVGRFLPATNRIQWMDAGICASLNDMIAWEQFIDATRDESGLYRRLSGPQTFKDGVAAPY
GFGLNLHETGGKRLTGHHGALRGWRCQRWHCADERLSTIAMFNFEGGASEVAFKLMNIALGVSSS

>d1lbea_ e.4.1.1 (A:) ADP ribosyl cyclase {Sea hare (Aplysia californica)}

IVPTRELENVFLGRCKDYETRYLDILPRVRSDCSALWKDFFKAFSFKNPCDLLDLSYKDFFTSAQQQ
LPKNKVMFWSGVYDEAHDYANTGRKYITLEDLPGYMLNSLVWCGQRANPGFNEKVCDFKTCPV
QARESFWMASSSYAHSAEGEVTYMVDGSNPKVPAYRPSFFGKYELPNLTNKVTRVKVIVLHRLG
EKIEKCGAGSLLDLEKLVKAKHFADFDCVENPRAVLFLLCSDNPNARECRL

>d4blca_ e.5.1.1 (A:) Catalase I {Cow (Bos taurus)}

NRDPASDQMKHWKEQRAAQKPDVLTGGGNPVGDKLNSLTVGPRGPLLVDVVFTDEMAHFDRE
RIPERVVHAKGAGAFGYFEVTHDITRYSKAKVFEHIGKRTPIAVRFSTVAGESGSADTVRDRPGRFAVK
FYTEDGNWDLVGNNTPIFFIRDALLFPSFIHSQKRNPQTHLKDPMVWDFWLSRPESLHQVSFLFS
DRGIPDGHRHMDGYGSHTFKLVNADGEAVYCKFHYKTDQGIKNSVEDAARLAHEDPDYGLRDLFN
AIATGNYPSTWLYIQVMTFSEAEIFPFNPFDLTKVWPHGDYPLIPVGKLVNLRNPVNYFAEVEQLAF
DPSNMPPGIEPSPDKMLQGRLFAYPDTHRHRLGPNYLQIPVNCYPYRARVANYQRDGPMMMDNQG
GAPNYYPNSFSAPEHQPSALEHRTHFSGDVQRFNSANDDNVTQVRTFYLKVLNEEQRKRLCENIAG
HLKDAQIFIQKAVKNFSDVHPEYGSRIQALLDKYNE

>d1dgfa_ e.5.1.1 (A:) Catalase I {Human (Homo sapiens)}

RDPASDQMHWKEQRAAQKADVLTGAGNPVGDKNLVITVGPGRGPLLVDVVFTDEMAHFDRE
PERVVHAKGAGAFGYFEVTHDITKYSKAKVFEHIGKKTPIAVRFSTVAGESGSADTVRDRPGRFAVKFY
TEDGNWDLVGNNTPIFFIRDPIPFPSFIHSQKRNPQTHLKDPMVWDFWLSRPESLHQVSFLFS
GIPDGHRHMNGYGSHTFKLVNANGEAVYCKFHYKTDQGIKNSVEDAARLSQEDPDYGIRDLFNAIA
TGKYPSTWTFYIQVMTFNQAETFFPNPFDLTKVWPHKDYPLIPVGKLVNLRNPVNYFAEVEQIAFDP
SNMPPGIEASPDKMLQGRLFAYPDTHRHRLGPNYLHIPVNCYPYRARVANYQRDGPMMQDNQGGGA
PNYYPNSFGAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFVNVNLNEEQRKRLCENIAGHL
KDAQIFIQKAVKNFTEVHPDYGSHIQALLDKYN

>d1a4ea_ e.5.1.1 (A:) Catalase I {Baker's yeast (Saccharomyces cerevisiae)}

DVREDRVVTNSTGNPINEPFVTQRIGEHGPLLQDYNLIDSLAHFNRENIPQRNPHAHGSGAFGYFE
VTDDITDICGSAMFSKIGKRTKCLTRFSTVGGDKGSADTVRDRPGRFATKFYTEEGNLDWVYNNTPVF
FIRDPSKFPFIHTQKRNPQTNLRDADMFWDFLTTPENQVAIHQVMILFSDRGTPANYRSMHGYSG
HTYKWSNKNGDWHYVQVHIKTDQGIKNLTIEEATKIAGSNPDYCCQDLFEAIQNGNYPSWTVYIQT
MTERDAKKLPFSVFDLTKVWPQGFPLRRVKGIVLNENPLNFFAQVEQAAFAPSTTVPYQEASADP

VLQARLFSYADAHRYRLGPNFHQIPVNCYPYASKFFNPAIRDGPMNVNGNFGSEPTYLANDKSYTYIQ
QDRPIQQHQEVWNGPAIPYHWATSPGDVDFVQARNLYRVLGKQPGQQKNLAYNIGIHVEGACPQIQ
QRVYDMFARVDKGLSEAIKKVAE

>d1e93a_e.5.1.1 (A:) Catalase I {*Proteus mirabilis*}

KKLTTAAGAPVVDNNNVITAGPRGPMMLQDVWFLEKLAHFDREVIPERRMHAKGSGAFGTFVTH
DITKYTRAKIFSEVGKKTEMFARFSTVAGERGAADAERDIRGFALKFYTEEGNWDVMGNNTPVFYL
RDPLKFPDLNHIVKRDPRTNMRNMAYKWDFFSHLPESLHQLTIDMSDRGLPLSYRFVHGFSGHTYS
FINKDNERFWVKFHFRCQQGIKNLMDDEAEALVGKDRESSQRDLFEAIKRGDYPRWKLQIQIMPEK
EASTVPYNPFDLTKVWPHADYPLMDVGYFELNRNPDNYFSDVEQAAFSANIVPGISFSPDKMLQG
RLFSYGDAHRYRLGVNHHQIPVNAPKCPFHNYHRDGAMRVDGNSGNGITYEPNSGGVFQEOPDFK
EPPLSIEGAADHWNHREDEDYFSQPRALYELLSDDHQRMFARIAGELSQASKETQQRQIDLFTKV
HPEYGAGVEKAIKVLE

>d1hbza_e.5.1.1 (A:) Catalase I {*Micrococcus lysodeikticus*}

TTPHATGSTRQNGAPAVSDRQSLTVGSEGPVLDHDLHLETHQHFNRMNIPERRPHAKGSGAFGEFE
VTEDVSKYTKALVFQPGTKTETLLRFSTVAGELGSPDTWRDVRGFALRFYTEEGNYDLVGNNTPIFF
LRDPMKFTHFIRSQRKLPDSGLRDATMQWDFWTNNPESAHQVTYLMGPRGLPRTWREMNGYGS
HTYLWVNAQGEKHVVKYHFISQQGVHNSNDEATKIAGENADFHRQDLFESIAKGDHPKWDLYIQ
AIPYEEGKTYRFNPFDLTKTISQKDYPRIKVGTLLNRNPKNHFAQIESAAFPSNTVPGIGLSPDRML
LGRAFYHDAQLYRVGAHVNLQPVNRPKNAVHNYAFEGQMWDHTGDRSTYVPNSNGDSWSDDET
GPVDDGWEADGTLTREAQALRADDGDFGQAGTLVREVFSDQERDDFVETVAGALKGVRQDVQARA
FEYWKVNDATIGQRIEDEVKRHEGDGIPGVEAGGEARI

>d1cf9a2_e.5.1.1 (A:27-597) Catalase II {*Escherichia coli*, HPII}

DSLAPEDGSHRPAAEPTPPGAQPTAPGSLKAPDTRNEKLSLEDVRKGSNEYALTTNQGVIADDQ
NSLRAGSRGPTLLEDFILREKITHFDHERIPERIVHARGSAAHGYFQPYKLSLSDITKADFLSDPNKITP
VFVRFSTCQGGAGSADTVRDIRGFATKFYTEEGIFDLVGNNTPIFFIQDAHKFPDFVHAVKPEPHWAI
PQQQSAHDTFWDYVSLQPETLHNVMWAMSDRGIPRSYRTMEGFGIHTFRLINAEGKATFVRFHWK
PLAGKASLVWDEAQKLTGRDPDFHRRELWEAIEAGDFPEYELGFQLIPEEDEFKDFDLLDPTKLIP
EELVPVQRVGMVLNRNPDNFFAENEQAAFHPGHVPLDFTNDPLLQGRFYSYTDQISRLGGPNF
HEIPINRPTCPYHNFQRDGMHRMGIDTNPANYEPNSINDNWPRETPPGPKRGGFESYQERVEGNK
VRERSPSFGYSSHPRFLWLSQTPFEQRHIVDGFSELSKVVRPYIRERVVDQLAHIDLTLAQAVAKN
LGIELTDDQLNITPPPVDVNLKDKDPSLSLYAIPDGD

>d1buca2_e.6.1.1 (A:1-232) Butyryl-CoA dehydrogenase {*Megasphaera elsdenii*}

MDFNLTDIQQDFLKLADHDFGEKLLAPTPTERDHHKGIYDKELIDELLSLGITGAYFEEKYGGSGDDGG
DVLSYILAVEELAKYDAGVAITLSATVSLCANPIWQFGTEAQKEKFLVPLVEGTLKGAFGLTEPNAGTD
ASGQQTIAATKNDDGTYTLNGSKIFITNGGAADIYVIFAMTDKSKGNHGITAFILEDGTPGFYTKKED
KMGIHSTQTMELVFQDVKVPANMLGEE

>d1jqia2_e.6.1.1 (A:4-234) Butyryl-CoA dehydrogenase {Rat (*Rattus norvegicus*)}

VYQSVELPETHQMLRQTCRDFAEKELVPIAAQLDKEHLFPTSQVKKMGELGLLAMDVPEELSGAGL
DYLAYSIALEEISRGCASTGVIMSVNNSLYLGPILKFGSSQQKQWITPFTNGDKIGCFALSEPENGSD
AGAASTTAREEGDSWVLNGTKAWITNSWEASATVFASTDRSRQNKGISAFVPMPTPGLTLGKKE
DKLGIRASSTANLIFEDCRIPKENLLGEPG

>d3mda2_e.6.1.1 (A:11-241) Medium chain acyl-CoA dehydrogenase {Pig (*Sus scrofa*)}

GFSFELTEQQKEFQATARKFAREEIIPVAAEYDRTGEYPVLLKRAWELGLMNTHIPESFGGLGLGIID
SCLITEELAYGCTGVQTAIEANTLGQVPLIIGGNYQQKYLGRMTEEPLMCAYCVTEPGAGSDVAGI

KTKAEKKGDEYIINGQKMWITNGGKANWYFLLARSDPDPKAPASKAFTGFIVEADTPGVQIGRKEI
NMGQRCS DTRGIVFEDVVRVPKENVLTGE

>d1egda2_e.6.1.1 (A:10-241) Medium chain acyl-CoA dehydrogenase {Human (Homo sapiens)}

LGFSFEFTEQKQEFQATARKFAREEIIPVAAEYDKTGEYPVPLIRRAWELGLMNTHIPENCGGLGLGT
FDACLISEELAYGCTGVQTAIEGNSLGQMPIIIAGNDQQKKYLGRMTEEPLMCAYCVTEPGAGSDVA
GIKTKAEKKGDEYIINGQKMWITNGGKANWYFLLARSDPDPKAPANKAFTGFIVEADTPGIQIGRKE
LNMGQRCS DTRGIVFEDVKVPKENVLIGD

>d1ivha2_e.6.1.1 (A:6-241) Isovaleryl-coa dehydrogenase {Human (Homo sapiens)}

VDDAINGLSEEQRQLRQTMAKFLQEHLAPKAQEIDRSNEFKNLREFWKQLGNLGVLGITAPVQYGG
SGLGYLEHVLVMEEISRASGAVGLSYGAHNSLNCINQLVRNGNEAQKEKYLPKLISGEYIGALAMSEPN
AGSDVVSMKLKAEKKNHYILNGNKFWITNGPDADVLIVYAKTDLAAVPASRGITAFIVEKGMPPGFS
TSKKLDKLGMRGSNTCELIFEDCKIPAANILGHEN

>d1frpa_e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Pig (Sus scrofa)}

NIVTLTRFVMEQGRKARGTGEMTQLLNSLCTAVKAISTAVRKAGIAHLYGIAGATNVTGDQVKKLDV
LSNDLVINVLKSSFATCVLVTEEDKNAIIVEPEKRGKYVVCDFDPLDGSSNIDCLVSIGTIFGIYRKNSTDE
PSEKDALQPGRNLVAAGYALYGSATMLVLAMVNGVNCFMLDPAIGEFILVDRNVKIKKKGSIYSINEGY
AKEFDPAITEYIQRKKFPPDNSAPYGARYVGSMAVHVHRTLTVYGGIFMYPANKKSPKGLRLLLYECNP
MAYVMEKAGGLATTGKEAVLDIVPTDIHQRAPILGSPEDVTELEIYQKHA

>d1ftaa_e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Human (Homo sapiens)}

DVVTLTRFVMEGRKARGTGELTQLLNSLCTAVKAISSAVRKAGIAHLYGIAGSTNVTGDQVKKLDVL
SNDLVMNMLKSSFATCVLVSEEDKHAIIVEPEKRGKYVVCDFDPLDGSSNIDCLVSVGTIFGIYRKKSTD
EPSEKDALQPGRNLVAAGYALYGSATMLVLAMDCGVNCFMLDPAIGEFILVDKDKVKKKKGKIYSLNE
AYAKDFDPAVTEYIQRKKFPPDNSAPYGARYVGSMAVHVHRTLTVYGGIFLYPANKKSPNGKLRLLLYEC
NPMAYVMEKAGGMATTGKEAVLDVIPTDIHQRAPILGSPDDVLEFLKVYEKHS

>d1bk4a_e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Rabbit (Oryctolagus cuniculus)}

FDTDISTMTRFVMEGRKAGGTGEMTQLLNSLCTAVKAISTAVRKAGIAHLYGIAGSTNVTGDQVKK
LDVLSNDLVMNMLKSSFATCVLVSEEDKNAIIVEPEKRGKYVVCDFDPLDGSSNIDCLVSIGTIFGIYRKK
STDEPSTKDALQPGRNLVAAGYALYGSATMLVLAGGSGVNSFMLDPAIGEFILVDKNVKIKKKGNIYSL
NEGYAKDFDPAVTEYIQRKKFPPDNSSPYGARYVGSMAVHVHRTLTVYGGIFLYPANKKSPDGKLRLLLY
ECNPMFIMEKAGGMATTGKEAILDIVPTDIHQRAPVILGSPDDVQEFLEIYKHKHAVK

>d1spia_e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Spinach (Spinacia oleracea)}

AATQTKARTRSKYEIETLTGWLLKQPMAGVIDAELTIVLSSISLACKQIASLVQRAGISNLTGIQGAVNI
QGEDQKKLDVVSNEVFSSCLRSSGRTGIIASEEEDVPVAVEESYSGNYIVVFDPLDGSSNIDAAVSTGSI
FGIYSPNDECIVDSHDHDESQLSAEEQRCVVNVCQPGDNLLAAGYCMYSSSVIFVLTIGKGVYAFTLDP
MYGEFVLTSEKIQIPKAGKIYSFNEGNYKMWDPDKLKKYMDLKEPGESQKPYSSRYIGSLVGFHRT
LLYGGIYGYPRDAKSKNGKLRLLLYECAPMSFIVEQAGGKSGDGHQRILDIQPTTEIHQRVPLYIGSVEEV
EKLEKYLA

>d1dcua_e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Garden pea (Pisum sativum)}

KRSGYEIITLTSWLLQEQKGIIDAELTIVLSSISMACKQIASLVQRANISNLTGTQGAVNIQGEDQKKL
DVISNEVFSNCLRSSGRTGIIASEEEDVPVAVEESYSGNYIVVFDPLDGSSNLDAAVSTGSI
CLPDFGDDSDNTLGTTEEQRIVNVCQPGSNLLAAGYCMYSSSVIFVLTIGKGVVFTLDPLYGEFVLT
QENLQIPKSGKIYSFNEGNYKLW DENLKKYIDDLKEPGSGPKPYSARYIGSLVGFHRTLLYGGIYGY
RDKKSKNGKLRLLLYECAPMSFIVEQAGGKSGDGHQRVLDIQPTTEIHQRVPLYIGSTEEVEKVEKYLA

>d2hhma_e.7.1.1 (A:) Inositol monophosphatase {Human (Homo sapiens)}
WQECMDYAVTLARQAGEVVCEAIKNEMNVMLKSSPVDLVTATDQKVEKMLISSIKEKYPSSHSFIGEE
SVAAGEKSILTDNPTWIIDPIDGTTNFVHRFPFVAVSIGFAVNKKIEFGVVYSCVEGKMYTARKGKGAF
CNGQKLQVSQQEDITKSLVTELGSSRTPETVRMVLNMEKLCIPVHGIRSVGTAAVNMCLVATGGA
DAYYEMGIHCWDVAGAGIIVTEAGGVLMVDTGGPFDLMSRRVIAANNRILAERIAKEIQVIPLQRDD
E

>d1g0ha_e.7.1.1 (A:) Archaeal inositol monophosphatase/fructose-1,6-bisphosphatase
{Archaeon Methanococcus jannaschii, MJ0109}
MKWDEIGKNIAKEIEKEILPYFGRKDKSYVVGTSVSGDETEIFDKISEDIALKYLKSLNVNIVSEELGVI
DNSSEWTVVIDPIDGSGFNFININGIPFFAFCFGVFKNNEPYYGLTYEFLTCSFYEAYKGGKAYLNGRKIKV
KDFNPNNIVISYYPSSKIDLEKLRNKVKVRVIFGAFGLEMCYVAKGTLDVDFVVRPKVRAVDIASSYII
CKEAGALITDENGDELKFDLNATDRLNIIIVANSKEMLDIILDLL

>d1inp_e.7.1.1 (-) Inositol polyphosphate 1-phosphatase {Cow (Bos taurus), brain}
MSDILQELLRVSEKAANIARACRQETLQLLIEEKKEGEKNKFAVDFKTLADVLVQEVIKENMEN
KFPGLGKKIFGEESNELTNDLGEKIIMRLGPTEETVALLSKVLNGNKLASEALAKVVHQDVFFSDPA
LDSVEINIPQDILGIWVDPIDSTYQYIKGSADITPNQGIFPSGLQCVTVLIGVYDIQTGVPLMGVINQPF
VSQDLHTRRWKGQCYWGLSYLGTNIHSLPPVSTRNSEAQSQGTQNPSSGSCRFSVVISSTSEKETI
KGALSHVCGERIFRAAGAGYKSLCVILGLADIYIFSEDITTFKWDSCAAHAILRAMGGGMVDLKECLER
NPDTGLDLPQLVYHVGNEGAAGVDQWANKGGLIAYRSEKQLETFLSRLQLHLAPVATHT

>d1ka1a_e.7.1.1 (A:) 3';5'-adenosine bisphosphatase, PAP phosphatase {Baker's yeast
{Saccharomyces cerevisiae}}
ALERELLVATQAVRKASLLTKRIQSEVISHKDDSTTITKNDNSPVTTGDYAAQTHIINAIKSNFPDDKVVG
EESSGLSDAFVSGILNEIKANDEVYNKNYKDDFLFTNDQFPLKSLEDVRQIIDFGNYEGGRKGRF
WCLDPIDGTKGFLRGEQFAVCLALIVDGVVQLGCIGCPNLVSSYGAQDLKGHESFGYIFRAVRGLGAF
YSPSSDAESWTKIHVRHLKDTKDMITLEGVEKGHSSHDEQTAIKNKLNISKSLHLDLSDQAKYCLLALG
LADVYLRLPIKLSYQEKIWDHAAGNVIVHEAGGIHTDAMEDVPLDFGNGRTLATKGVIASSGPRELH
DLVVSTSCDVIQSR

>d1jp4a_e.7.1.1 (A:) PIPase {Rat (Rattus norvegicus)}
HNVLMRLVASAYSIAQKAGTIVRCVIAEGDLGIVQKTSATDLQTKADRMVQMSICSSLSRKFPKLTIIIG
EEDLPPGEVDQELIEDGQSEEILKQPCPSQYSAIKEEDLVVWVDPVDGTKEYTEGLLDNVTVLIGIAY
EGKAIAGIINQPYNYQAGPDAVLGRTIWGVLGLGAFGFQLKEAPAGKHIIITTRSHSNKLVTDICIAA
MNPDNVLRVGGAGNKIIQLIEGKASAYVFASPGCKKWDTCAPVILHAVGGKLTDIHGNPLQYDKEV
KHMNSAGVLAALRNYEYASRPESVKSALIP

>d1kfsa2_e.8.1.1 (A:519-928) DNA polymerase I (Klenow fragment) {Escherichia coli}
HKGPLNVFENIEMPLVPVLSRIERNGVKIDPKVLHNHSEELTLRLAELEKKAHEIAGEEFNLSSTKQL
QTILFEKQGIKPLKKTGGAPSTSEEVLEELALDYPLPKVILEYRGLAKLKSTYTDKLPKMINPKTGRV
HTSYHQAVTATGRLSSTDPNLQNIQVVRNEEGRRIRQAFIAPEDYVIVSADYSQIELRIMAHLSRDKGLL
TAFEAGKDIHRATAAEVFGVPLETVTSEQRSAKAINFGLIYGMSAFGLARQLNIPRKEAQKYMPLYF
ERYPGVLEYMERTRAQAKEQGYVETLDGRRLYLPDIKSSNGARRAAAERAAINAPMQGTAADIHKRA
MIAVDAWLQAEQPRVRMIMQVHDELVFEVHKDDVDVAVAKQIHQLMENCTRLDVPLLEVEVSGEN
WDQAH

>d1qtma2_e.8.1.1 (A:423-831) DNA polymerase I (Klenow fragment) {Thermus aquaticus}
EERLLWLYREVERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLSRDQ
LERVLFDELGLPAIGKTEKTGKRSTSAVLEALREAHPIVEKILQYRELTCLKSTYIDPLPLIHPRTGR

LHTRFNQTATATGRLSSSDPNLQNIPTVPLGQRIRRAFIAEEGWLLVALDYSQIELRVLAHLSGDEN
LIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPYEEAQAFIE
RYFQSFQKPVRAWIEKTLEEGRRRGYVETLFGRRRYVPDLEARVKSVREAAERMAFNMPVQGTAADL
MKLAMVKLFPRLEEMGARMLLQVHDELVLEAPKERAEAVARLAKEVMEGVYPLAVPLEVEVGIGE
DWLSAK

>d1xwl_2 e.8.1.1 (469-876) DNA polymerase I (Klenow fragment) {Bacillus
stearothermophilus, newly identified strain as yet unnamed}

EQDRLLVELEQPLSSILAEMEFAGVKVDTKRLEQMGKELAEQLGTVEQRIYELAGQEFNINSPKQLG
VILFEKLQPLVKKTKTGYSTSADVLEKLAPYHEIVENILHYRQLGKLQSTYIEGLLKVVPRPDTKKVH
TIFNQALTQTGRSSSTEPNLQNIPIRLEEGRKIRQAFVPSSEDLIFAADYSQIELRVLAHIAEDDNLN
EAFRRDLIHTKTAMDIFQVSEDEVTNMRQAKAVNFGIVYGISDYGLAQLNLNISRKEAAEFIERF
ESFPGVKRYMENIVQEAQKQGYVTLLHRRRYLPDITSRNFNRSFAERMAMNTPIQGSAAIHKKA
MIDLNARLKEERLQAHLLQVHDELILEAPKEEMERLCRLVPEVMEQAVTLRVPLKVDYHYGSTWY
DAK

>d1t7pa2 e.8.1.1 (A:211-704) T7 phage DNA polymerase {Bacteriophage T7}

LEAVDIEHRAAWLLAKQERNGFDFDKAIEELYVELAARRSELLRKLTTETFGSWYQPKGGTEMFCHP
RTGKPLPKYPRIKTPKVGIFKKPKNKAQREGREPCELDTREYVAGAPYTPVEHVFNPSRDHIQK
KLQEAGWVPTKYTDKGAPVVDDEVLEGVVDDPEKQAAIDLIKEYLMIQKRIGQSAEGDKAWLRYV
AEDGKIHGVSNNPNAVAVTGRATHAFPNAQIPGVRSPYGEQCRAAFGAEHHLDGITGKPWVQAGIDA
SGLELRCLAHFMARFDNGEYAHEILNGDIHTKNQIAAELPTRDNAKTFFIYGFYAGDEKIGQIVGAG
KERGKELKKKFLNTPAIAALRESIQQLVLESSQWVAGEQVQVWKRWRWIKGLDGRKVHVRSPHAAL
NTLLQSAGALICKLWIIKTEEMLVEKGLKHGWDGDFAYMAVHDEIQVGCRTTEEIAQVVIETAQEA
MRVWGDHWNFRCLLDTEGKMGNWAICH

>d1ih7a2 e.8.1.1 (A:376-903) T4-like DNA polymerase {Bacteriophage RB69}

QNKVIPQGRSHVPQYPGAFVKEPIPNRYKYVMSFDLTSLYPSIIRQVNIISPETIAGTFKVAPLHDYINA
VAERPSDVYSCSPNGMMYYKDRDGVVPTTEITKVFNRKEHKGYMLAAQRNGEIIKEALHNPNSVD
EPLDVDYRDFDSDEIKEKIKKLSAKSLNEMLFRAQRTEVAGMTAQINRKLINSLYGALGNVWFRYY
DLRNATAITTFQMALQWIERKVNEYLNEVCGETEAEFVLYGDTDSIYVSADKIIDKVGESKFRDTN
HWVDFLDKFAFERMEPAIDRGFREMCEYMNNKQHLMFMDREAIAGPPLGSKGIGGFWTGKKRYA
LNVWDMEGTRYAEPKLIKIMLETQKSSTPKAVQKALKECIRRMQLQEGEESLQYEFKEFEKEFRQLN
YISIASVSSANNIAKYDVGGFPGKCPFHIRGILTYNRAIKGNIDAPQVVEGEKVYVPLPREGNPFGDK
CIAWPSGTEITDLIKDDVLHWMDYTVLLEKTFIKPLEGFTSAAKLDYEKKASLDFDMFDF

>d1tgoa2 e.8.1.1 (A:348-773) T4-like DNA polymerase {Archaeon Thermococcus
gorgonarius}

STGNLVEWFLLRKAYERNELAPNKPDERELARRRESYAGGYVKEPERGLWENIVYLDFRSLYPSIIIT
HNVSPDTLNREGCEEYDVAPQVGHKFKDFPGFIPSLLDLLEERQKVKKMKATIDPIEKLLDYR
QRAIKILANSFYGYGYAKARWYCKEAEVTAWGRQYIETTIREIEEKFGFKVLYADTDGFFATIPGA
DAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWSEIA
KETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPEKLVIIYEQITRDLKDYKATGPHVAVAKRLA
ARGIKIRPGTVISYIVLKGSGRIGDRAIPDFDFPAKHKYDAEYIENQVLPAYERILRAFGYRKEDLRY
QKTRQVGLGAWLKPKT

>d1qhta2 e.8.1.1 (A:348-750) T4-like DNA polymerase {Archaeon Thermococcus sp., 9on-7}

STGNLVEWFLLRKAYKRNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIIT
HNVSPDTLNREGCKEYDVAPEVGHKFKDFPGFIPSLLDLLEERQKIKRKMATVDPLEKLLDYR

QRAIKILANSFYGYGYAKARWYCKECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHATIPG
ADAETVKKKAKEFLKYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEI
AKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIEHQITRDLRDYKATGPHVAVAKRL
AARGVKIRPGTVISYIVLKGSGRIGDRAIPAEFDPTKHRYDAEYYIENQVLP AVERILKAFGY
>d1d5aa2 e.8.1.1 (A:348-756) T4-like DNA polymerase {Archaeon Desulfurococcus tok}
STGNLVEWFLLRKAYERNDVAPNKPDERELARRTESYAGGYVKEPEKGLWENIVYLDYKSLYPSIIIT
HNVSPDTLNREGCREYDVAPQVGHFRCKDFPGFIPSLLDLLEERQKVKKMKATVDPIERKLLDYR
QRAIKILANSYGYAYANARWYCRECAESVTAWGRQYIETTMREIEEKFGFKVLYADTDGFFATIPG
ADAETVKNKAKEFLNYINPRLPGLLELEYEGFYRRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWSEI
AKETQARVLEAILKHGDVEEAVRIVKEVTEKLSRHEVPPEKLVIEAGPHVAAAATVISYIVLKGPRV
GDRAIPFDEFDPKHYDAEYYIENQVLP AVERILRAFGYRKEDLR
>d1gcxa2 e.8.1.1 (A:348-758) T4-like DNA polymerase {Archaeon Pyrococcus
kodakaraensis}
STGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYEGGYVKEPERGLWENIVYLDFRSLYPSIIIT
HNVSPDTLNREGCKEYDVAPQVGHFRCKDFPGFIPSLLDLLEERQKIKKKMKATIDPIERKLLDYR
QRAIKILANSYGYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYSDTDGFFATIPGA
DAETVKKKAMEFLKYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIA
KETQARVLEALLKGDVEKAVRIVKEVTEKLSKYEVPPEKLVIEHQITRDLKDYKATGPHVAVAKRL
AARGVKIRPGTVISYIVLKGSGRIGDRAIPFDEFDPKHKYDAEYYIENQVLP AVERILRAFGYRKEDL
RYQ
>d1jx4a_ e.8.1.5 (A:) DinB homolog (DBH) {Archaeon Sulfolobus solfataricus, DNA
polymerase IV}
MIVLFDYDFYFAQVEEVLNPSLKGKPVVVCVFSGRFEDSGAVATANYEARFKGVKAGIPIVEAKKILP
NAVYLP MRKEVYQVSSRIMNLLREYSEKIEIASIDEAYLDISDKVRDYREAYNLGLEIKNKILEKEKI
TVTVGISKNKVFAKIAADMAKPNGIKVIDDEEVKRLIRELDIADVPGIGNITAELKLLGINKLVDTLS
IEFDKLGKMGIEAKAKYLISLARDEYNEPIRTRVRKSIGRIVTMKRNSRNLEEIKPYLFRAIEESYYKL
DKRIPKAIHVAVTEDLDIVSRGRTFPHGISKETAYSESVKLLQKILEEDERKIRRIGVRFKFI
>d1im4a_ e.8.1.5 (A:) DinB homolog (DBH) {Archaeon Sulfolobus solfataricus}
HHHHHIVFDYFFAQQVEEVLNPQYKKGKPLVVCVYSGRTKTS GAVATANYEARGLGVKAGMPIIKA
MQIAPSAIYVPMRKPIYEA FSNRIMNLLNKHADKIEVASIDEAYLDVTNKVEGNFENGIELARKIKQEI
LEKEKITVTVGVAPNKILAKIIADKSKPNGLGVIRPTEVQDFLNELDIDEIPGIGSVLARRLNELGIQKL
RD
>d1k1sa_ e.8.1.5 (A:) DinB homolog (DBH) {Archaeon Sulfolobus solfataricus}
MIVIFVDFDYFFAQQVEEVLNPQYKKGKPLVSVYSGRTKTS GAVATANYEARGLGVKAGMPIIKAMQIA
PSAIYVPMRKPIYEA FSNRIMNLLNKHADKIEVASIDEAYLDVTNKVEGNFENGIELARKIKQEILEKE
KITVTVGVAPNKILAKIIADKSKPNGLGVIRPTEVQDFLNELDIDEIPGIGSVLARRLNELGIQKLRDIL
SKNYNELEKITGKAKALYLLKLAQNKYSEPVENKSKIPHGRYLTL PYNTRDVKLVILPYLKKAIN EAYN
KVNGIPMRITVIAIMEDLDILSKGKFKHGISIDNAYKVAEDLLRELLVRDKRRNRRRIGVKLDNIIIN
>d1jiha_ e.8.1.5 (A:) DNA polymerase eta {Baker's yeast (Saccharomyces cerevisiae)}
MSKFTWKELIQLGSPSKAYESSLACIAHIDMNAFFAQQVEQMRCGLSKEDPVVVCVQWNSIIAVSYAAR
KYGISRMDTIQEALKKCSNLIPIHTAVFKKGEDFWQYHDGCGSWVQDPAKQISVEDHKVSLEPYRRE
SRKALKIFKSACDLVERASIDEVFLDLGRICFNMLMFDNEYELTGDLKLDALSNIREFIGGN YDINS
HLPLIPEKIKSLKFEGDFVNPEGRDLITDWDVILALGSQVCKGIRDSIKDILGYTTSCGLSSTKNVCK
LASNYKKPDAQTIVKNDCLLDLDCGKFEITSFWTLGGVVGKELIDVLDLPHENSIXHIRETWP DNA

GQLKEFLDAKVKQSDYDRSTSNIIDPLKTADLAEKLFKLSRGRYGLPLSSRPVVKSMMSNKNLRGKSC
NSIVDCISWLEVFCAELTSRIQDLEQEYNKIVIPRTVVISLKTksyeVYRKSGPVAYKGINFQSHELLKV
GIKFVTDLDIKGNKSYPLTKLSMTITNFDII

>d1mml_ e.8.1.2 (-) MMLV reverse transcriptase {Moloney murine leukemia virus}
TWLSDFPQAWAETGGMGLAVRQAPLIIPKATSTPVSISIKQYPMSQEARLGIKPHIQRLLDQGILVPCQ
SPWNTPLLVPKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPSSHQWYTVLDLKDADF
CLRLHPTSQPLFAFEWRDPEMIGSQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYV
DDLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLK

>d1c9ra2 e.8.1.2 (A:1-429) HIV-1 reverse transcriptase {Human immunodeficiency virus
type 1}
PISPIETVPVKLAPGMDGPKVKQWPLTAEIAALVAICTAMEAEGKISKIGPENPYNTPVFAIKKAAAA
AAAALVDFRELNKRTQDFWEVQLGIPHPAGLKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIPSIA
NATPGIRYQYNVLPQGKWSAIFQSSMTKILEPFKQNPDIYQYIDDLYVGSDEIGQHATKIAEL
RQHLLAWGLTTPDKKHAAEPPFLWMGYELHPDAWTVAPAALAAAASAANDIQKLVGKLNWASQI
YPGIAVRALSAAAAGTKAAAEAAAATAAAALALAAAREALAAPVHGVYDPSKDLIAEIQAQGGQ
WTYQIYQEPFKNLKTGKYARMRGAHTNDVKQLTEAVQKITTESIVIWGKTPKFKLPIQKETWETW
WTEYWQATWIPEWEFVNTPLVWLYQL

>d1c9rb1 e.8.1.2 (B:) HIV-1 reverse transcriptase {Human immunodeficiency virus type 1}
PISPIETVPVKLAPGMDGPKVKQWPLTEEKIKALVEICTEMEKEGKISKIGPENPYNTPVFAIKKDDST
KWRKLVDFRELNKRTQDFWEAALGIPHPAGLKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIPSIN
NETPGIRYQYNVLPQGKWSAIFQSSMTKILEPFKAQNPDIYQYIDDLYVGSDEIGQHRTKIEEL
RQHLLRWGLTTPDKKHQKEPPFLWMGYELHPDKWAAAAAAAAAAAAAAAAATVNDIQKLVGKLNWAA
QIYPGIAAALSALAGTKALTAAPLTAATALELANRAAAAAAAAAAGVYDPSKDLIAEIQAQGGQ
WTYQIYQEPFKNLKTGKYARMRGAHTNDVKQLTEAVQKITTESIVIWGKTPKFKLPIQKETWETW
WTEYWQATWIPEWEFVNTPLVALWYALE

>d1har_ e.8.1.2 (-) HIV-1 reverse transcriptase {Human immunodeficiency virus type 1}
PISPIETVPVKLAPGMDGPKVAQWPLTAAKIAALVAICTEMEKEGKISKIGPENPYNTPVFAIKKDDST
KWAKLVDFRELNKRTQDFWEVQLGIPHPAGLKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIPSIN
NETPGIRYQYNVLPQGKWSAIFQSSMTKILAPFKAANPDIVYQYMDDLYVGSDLAIGAHRTKIEE
LRQHLLRWGLTT

>d1vrta2 e.8.1.2 (A:4-429) HIV-1 reverse transcriptase {Human immunodeficiency virus
type 1}
PIETVPVKLAPGMDGPKVKQWPLTEEKIKALVEICTEMEKEGKISKIGPENPYNTPVFAIKKDDSTK
WRKLVDFRELNKRTQDFWEVQLGIPHPAGLKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIPSINN
ETPGIRYQYNVLPQGKWSAIFQSSMTKILEPFKQNPDIYQYIDDLYVGSDEIGQHRTKIEELR
QHLLRWGLTTPDKKHQKEPPFLWMGYELHPDKWTVQPIVLEKDSWTVNDIQKLVGKLNWASQI
YPGIKVRQLCKLLRGTKALTEVIPLTEEALELAENREILKEPVHGVYDPSKDLIAEIQAQGGQWT
YQIYQEPFKNLKTGKYARMRGAHTNDVKQLTEAVQKITTESIVIWGKTPKFKLPIQKETWETWWTE
YWQATWIPEWEFVNTPLVWLYQL

>d1ceza_ e.8.1.3 (A:) T7 RNA polymerase {Bacteriophage T7}
IAKNDFSDIELAAIPFNTLADHYGERLAREQLALEHESYEMGEARFRKMFERQLKAGEVADNAAK
PLITLLPKMIARINDWFEEVKAKRGKRPTAFQFLQEIKPEAVAYITIKTTLACLTSADNTTVQAVASA
IGRAIEDEARFGRIRDLEAKHFKNVEEQLNKRVGHVYKAFMQVVEADMLSKGLLGGEAWSSWH
KEDSIHVGVRCIEMLIESTGMVSLHRQNAGVVGQDSEITIELAPEYAEIATRAGALAGISPMFQPCVV

PPKPWTGITGGGYWANGRRPLALVRTHSKKALMRYEDVYMPEVYKAINIAQNTAWKINKKVLAVA
NVITKWKHCPVEDIPAIEREELPMKPEDIDMNPEALTAWKRAAAAVYRKDKARKSRRISLEFMLEQ
ANKFANHKAIWFPYNMDWRGRVYAVSMFNPQGNDMTKGLLTLAKGKPIGKEGYWLKIHGANCA
GVDKVPFPERIKFIEENHENIMACAKSPLNTWWAEQDSPFCFLAFCFEYAGVQHHGLSYNCSLPLA
FDGSCSGIQHFSAMLRDEVGGRAVNLLPSETVQDIYGIVAKKVNEILQADAINGTDNEVVTVTDENT
GEISEKVKLGTKALAGQWLAYGVTRSVTKRSVMTLAYGSKEFGFRQQVLEDTIQPAIDSGKGLMFTQ
PNQAAGYMAKLIWESVSVTVVAAVEAMNWLKSAKLLAAEVKDKKTGEILRKRCVHWVTPDGF
VWQEYKPIQTRLNLMFLGQFRLQPTINTNKDSEIDAHKQESGIAPNFVHSQDGSHLRKTVVWAHE
KYGIESFALIHDSFGTIPADAANLFKAVRETMVDTYESCDVLADFYDQFADQLHESQLDKMPALPAK
GNLNLRDILESDFafa

>d1rdr_ e.8.1.4 (-) Viral RNA-dependent RNA-polymerase {Poliovirus type 1, strain Mahoney}

VGYPIINAPSKTKLEPSAFHYVFEGVKEPAVLTKNPRLKTDFFEEAIFSKYVGNKITEVDEYMKEAVD
HYAGQLMSLDINTEQMCLDAMYGTDGLEALDLSTSAGYPYVAMGKKKRDLNKQTRDTKEMQKL
LDTYGINLPLVTVKDELRSKTKVEQGSRLIEASSLNDVAMRMAFGNLYAAFHKNPGVITGSAVGC
DPDLFWSKIPVLMEEKLFAFDYTGIDASLSPAWEALKMVLEKIGFGDRVDYIDYLNHSHHLYKNKT
YCVKGGMPSCSGTSIFNSMINNLIIRTLKTYKIDLDHLKMIAYGDDVIASYPHEVDASLLAQSGK
DYGLTMTPADKSATFETVTWENVTFKRRFRADKYPFLIHPVMPMKEIHESIRWTKDPRNTQDH
VRSLCLLAWHNGEEYKFLAKIRSVPIGRALLPEYSTLYRRWLDSF

>d1c2pa_ e.8.1.4 (A:) Viral RNA-dependent RNA-polymerase {Hepatitis C virus}

HHSYTWGTALITPCAAEESKLPINALSNSLLRHHNMVYATTSRSAGLRQKKVTFDRLQVLDDHYRD
VLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRNLSSKAVNHIHSVWKDLLEDVT
PIDTTIMAKNEVFCVQPEKGGKPARLIVFPDLGVRVCEKMALYDVVSTLPQVVMGSSYGFQYSPGQ
RVEFLVNTWKSCKNPMGFSYDTRCFDSTVTENDIRVEESYQCCDLAPPEARQAIKSLTERLYIGGPLT
NSKGQNCGYRRCRASGVLTTSCGNTLTCYLKASAACRAAKLQDCTMLVNGDDLVICESAGVQEDAA
SLRAFTEAMTRYSAAPPDPPQPEYDLELITSCSSNVSAHDASGKRVYLRDPTTPLARAAWETAR
HTPVNSWLGNIIYAPTLWARMILMTHFFSILLAQEQLKALDCQIYGACYSIEPLDLPQIIRLHGLS
AFSLHSYSPGEINRVASCLRKLGVPPLRVWRHRARSVRARLLSQGGRAATCGKYLFNWAVKTKLKL
PIPAASQLDLSGWVAVAGYSGGDIYHS

>d1khva_ e.8.1.4 (A:) Viral RNA-dependent RNA-polymerase {Rabbit hemorrhagic disease virus}

FCGEPIDYRGITAHRLVGAEPVPPVSGTRYAKVPGVPDEYKTGYRANLGRSDPDSKSLMNIAVKNL
QVYQEQPKLDKVDEFIERAAADVLGYLRFLTGERQANLNFKAANTLDLSTSCGPFVPGKKIDHVK
DGVMDQVLAKHLYKCWSVANSKALHHIYACGLKDELRLDKVKEGKRLWGCVDVAVCAA
FHNICYKLMVARFGPIAVGVDMSRVDVVIINLTSKASDFLCLDYKWDSTMSPCVVRLAIDLAD
CCEQTELTKSIVLTLKSHPMTILDAMIVQTKRGLPSGMPFTSVINSICHWLLWSAAVYKSCAEIGLHC
SNLYEDAPFYTYGDDGVYAMTPMMVSLPAIENLRDYGLSPTAADKTEFIDVCPNLIKISFLKRTFELT
DIGWVSKLDKSSILRQLEWSKTTSRHMVIEETYDLAKEERGVQLEELQVAAAAAHGQEFFNFVCRELE
RQQAYTQFSVYSYDAARKILADRKR

>d1hhsa_ e.8.1.6 (A:) dsRNA phage RNA-dependent RNA-polymerase {Bacteriophage PHI-6}

PRRAPAFPLSDIKAQMLFANNIKAQASKRSFKEGAIETYEGLLSVDPRFLSFKNELSRYLTDHFPAN
VDEYGRVYNGVVRTNFFGMRHMNGFPMIPATWPLASNLKCRADADLADGPVSRDNLFRAAVRL
MFSDLPLKIRKGSSTCIPYFSNDMGTKIEIAERALEKAEEAGNMLQKGFDDAYQLHQMGGAYY
VYVRAQSTDAITLDPKTGKVFVKDRMVADEFYAVTGGEQGSLFAASKDASRLKEQYIDVDPDGFCE

RRRTAMGGPFALNAPIMAVAQPVRNKIYSKYAYTFHHTTRLNKEEKVKEWSLCVATDVSDHDTFWP
GWLRLDICDELLNMGYAPWWVKLFETSLKLPVYVVGAPAPEQGHTLLGDPSNPDLVGLSSGQGATD
LMGTLMSITYLVMQLDHTAPHLNSRIKDMPSACRFLDSYWQGHEEIRQISKSDDAMLGWTKGRAL
VGGHRLFEMLKEGKVNPSPYMKISYEHGGAFLGDILLYDSRREP GSAIFVGNINSMLNMQFSPEYGV
QSGVRDRSKRKRPFPG LAWASMKDTYGACPIYSVLEAIERCWWNAFGESYRAYREDMLKRDTLEL
SRYVASMARQAGLAELTPIDLEVLADPNKLQYKWTEADVSANIHEVLMHGVSVKTERFLRSVMR
>d1i50a_e.29.1.1 (A:) RBP1 {Baker's yeast (*Saccharomyces cerevisiae*)}
VGQYSSAPLRTVKEVQFGLFSPEEVRAISVAKIRFPETMDETQTRAKIGGLNDPRLGSDRNLCQQT
CQEGMNECPGHFGHIDLAKPVFHVGFIAKIKKVCCEVCMHCGKLLLEHNELMRQALAIKDSKKRF
AAIWTLCCKTKMVCETDVPSEDDPTQLVSRGGCGNTQPTIRKDGKLVGSKKDRATGDAPELVR
LSTEEILNIFKHISVKDFTSLGFNEVFSRPEWMILTCLPVPVPPVPSISFNESQRGEDDLTKLADILK
ANISLETLEHNGAPHHAIEEAESLLQFHVATYMDNDIAGQPQALQKSGRPVKSIRARLKGKEGRIRG
NLMGKRVD FSARTVISGDPNLELDQVGVPKSIAKTLTYPEVVTYPYNIDRLTQLVRNGPNEHPGAKYVI
RDSGDRIDLRYSKRAGDIQLQYGWKVERHIMDNDPVLFNRPQSLHKMSMMAHRVKVIPYSTFRLN
LSVTSPYNADFDGDEMNLHVPQSEETRAELSQLCAVPLQIVSPQSNKPCM GIVQDTLCGIRKLTLRD
TFIELDQVLNMLYWVPDWDGVIPTPAIKPKPLWSGKQILSVAIPNGIHLQRFDEGTTLLSPKDNMGL
IIDGQIIFGVVEKKT VGSNGLIHVV TREKGPQVCAKLF GNIQKVVNFWLLHNGFSTGIGDTIADGPT
MREITETIAEAKKVL DVTKEAQANLLTAKHGMTLRESFEDNVVRF LNEARDKAGRLAEVNLKDLN
NVKQMMV MAGSKGSFINIAQMSACVGGQSV EKGRIAFGFVDRTLPHFSKDDYSPESKGFVENSYL RGL
TPQEFFFHAMGGREGLIDTAVKTAETGYIQRRLVKALEDIMVHYDNTTRNSLGNVIQFIYGEDGMDA
AHIEKQSLDTIGGSDAAFEKRYRVDLLNTDHTLDPSLLESGSEILGDLKLQVLLDEEYKQLVKDRKFL
REVFVDGEANWPLPVNIRRIIQAQQT FHDHTKPSDLTIKDIVLGVKDLQENLLVLRGKNEIIQNAQ
RDAVTLFCCLLRSLATRRVLQEYRLTKAFDWWLSNIEAQFLRSVHPGEMVGVLAQAQSIGEPATQ
MTLNTFH FAGVASKKVTSGVPRLKEILNVAKNMKTPSLTVYLEPGAADQEQA KLIRSAIEHTTLKS
VTIASEIYYDPDRSTVIPED EIIQLHFSLLEDEAEQSFQQSPWLLRLELDRAAMNDKDLTMGQV
GERIKQTFKNDL FVIWSEDNDEKLIIRCVRVRPKSLDAETEA EEDHMLKKIENTMLENITLRGVENIE
RVVMMKYDRKVPSP TGEYVKEPEWVLET DGVNLSEVMTVP GIDPTRIYTNSFIDIMEVLGIEAGRA
ALYKEYVNVIASDGSYVNYRHMALLVDVMTTQGGLTSVTRHGFNRSNTGALMRC SFEEVVEILFEAG
ASAELDDCRGVSENVILGQMAPIGTGAFDVMIDEESL

>d1i6vc_e.29.1.1 (C:) RNA-polymerase beta {*Thermus aquaticus*}
KIKRFGRIREVIPLPLTEIQVESYKKALQADVPPEKRENVGIQA AFKETFPIEEGDKGKGGVLDFLE
YRIGDPPFSQDECREKDLTYQAPLYARLQLIHKDTGLIKEDEVFLGHLPLMTEDGSFIINGADRIVVSQ
IHRSPGVYFTPD PARPGRYIASIPLPKRGPWIDLEVEASGVVTMKNRKRKFP LVLRLVLYDQETLV
RELSAYGDLVQGLLDEAVLAMRPEEAMVRLFTLLRPGDPPKDKALAYLFGLLADPKRYDLGEAGR
YKAEKLGVLGSGRTLVR FEDGEFKDEVFLPTLRYLFALTAGVPGHEVDDIDHLGNRRIRTVGELMA
DQFRVGLARLARGVRERMVMGSPDTLTPAKLVNSRPLEAALREFFSRSQLSQFKDETNP LSSLRHKR
RISALGPGLTRERAGFDVRDVHRTHYGRICPVETPEGANIGLITSLAAYARVDALGFIRTPYRRVKN
VVTEEVVYMTASEEDRYTIAQANTPLEGDRIATDRVVARRRGEPVIVAPEEVEFMDVSPKQVFLSNT
NLIPFLEHDDANRALMGSNMQTQAVPLIRAQAPVVM TGLEERVVRDSLAAALYAEEDGEVVKVDGTR
IAVRYEDGRLVHPLRRYARSNQTAFDQRPRVRVQQRVKKGDLLADGPASEEGFLALGQNVLVAIMP
FDGYNFEDAIVISEELLKRDFYTSIHIERYEIEARDTKLGP ERITRDIPHLSEAALRDLEEGIVRIGAE
VKPGDILVGRTSFKGEQEPSPEERLLRSIFGEKARDVKDTS LRVPPEGEGIVVGRRLRRLRGPVVELK
PGVREVVRVFAQKRKLQVGDKLANRHGNKGVVAKILPVEDMPHL PDGTPVDVILNPLGVPSRMNL
GQILETHLGLAGYFLGQRYISPVFDGATEPEIKELLA EAFNLYFGKRQGEFGVDKREKEVLARA EKL

GLVSPGKSPEEQKELFDLKGKVVLYDGRTGEPFEGPIVVGQMFIMKLYHMVEDKMHARSTGPYSLIT
QQPLGGKAQFGGQRFGEVWALEAYGAAHTLQEMLTIKSDDIEGRNAAYQAIKGEDVPEPSVPES
FRVLVKELQALALDVQTLDEKDNPVDFEGL

>d1i50b_e.29.1.2 (B:) RBP2 {Baker's yeast (*Saccharomyces cerevisiae*)}

FEDESAPITAEDSWAVISAFFREKGLVSQQLDSFNQFVDYTLQDIICEDSTLILEQLAQHTTESDNISR
KYEISFGKIYVTKPMVNESDGVTHALYPQEARLRNLTYSGLFVDVKKRTYEVIDVPGRELKYELIAE
ESEDDESSEKGVFIGRLPIMLRSKNCYLSEATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIV
QVFKKAAPSPISHVAEIRSALEKGSRFISTLQVKLYGREGSSARTIKATLPYIKQDIPVIFRALGIIPDG
EILEHICYDVNDWQMLEMLKPCVEDGFVIQDRETALDFIGRRGTALGIKKEKRIQYAKDILQKEFLPH
ITQLEGFESRKAFFLGYMINRLLCALDRKDQDDRDHFGKRLDLAGPLLAQLFKTLFKKLTKDIFR
YMQRTVEEAHDFNMKLAINAKTITSGLYALATGNWGEQKKAMSSRAGVSQVLNRYTYSSTLSHLR
RTNTPIGRDGKLAQPRQLHNTHWGLVCPAETPEGQACGLVKNLSLMSCISVGTDPMPITFLSEWGM
EPLDYVPHQSPDATRVFVNGVWHGVHRNPARLMETLRTLRRKGDINPEVSMIRDIREKELKIFTD
AGRVYRPLFIVEDDESLGHKELKVRKGGHIAKLMATEYQDIEGGFEDVEEYTWSSLLNEGLVEYIDAE
EESILIAMQPEDLEPAEANEENDLDVDPKRIRVSHHATTFTTHCEIHPSMILGVAASIIPFDHNQSPR
NTYQSAMGKQAMGVFLTYNVRMDTMANILYYPQKPLGTTAMEYLKFRRELPAQNAIVAIAACYSG
YNQEDSMIMNQSSIDRGLFRSLFFRSYMDQEKYKMSITETFEKPQRTNTLRMKHGTYDKLDDDG
IAPGVRVSGEDVIIKTTPISPDEEELGQRTAYHSCRDASTPLRSTENGIVDQVLVTTNQDGLKFKVVR
VRTTKIPQIGDKFASRHGQKGTIGITYRREDMPFTAEGIVPDLINPHAIPSRMTVAHLIECLLSKVAAL
SGNEGDASPFDTITVEGISKLLREHGYQSRGFEVYNGHTGKKLMAQIFFGPTYQRLRHMVDDKI
HARARGPMQVLRQPVEGRSRDGLRFGEEMERDCMIAHGAASFLKERLMEASDAFRVHICGICGLM
TVIAKLNHNQFECKGCDNKIDYQIHIPYAAKLLFQELMAMNITPRLYTDRSRDF

>d1i6vd_e.29.1.2 (D:) RNA-polymerase beta-prime {*Thermus aquaticus*}

KEVRKVRIALASPEKIRSWSYGEVEKPETINYRTLKPERDGLFDERIFGPIKDYEACAGKYKRQRFEA
KVCERCAVEVTRSIVRRYRMAHIELATPAAHWFVKDVPSKIATLLDLSATELEQVLYFNKYIVLDPK
AAVLDAVPVEKRQLLTDXX
ELDLEKLERELLEEMKHPSRARRAKARKRLEVVRVAFVLDVSGNRPEWVILEAVPVLPPDLRPMVQVD
GGRFATSDLNDLYRRLINRNRLLKLLAQGAPEIIRNEKRMLQEAVDAVIDNGRRGSPVTNPGSERP
LRSITDILSGKQGRFRQNLGKRVDSGRSVIVVGPQLKLHQGLPKRMALELFPKFLKMEEKAF
APNVKAARRMLERQRDIKDEVWDALEEVHIGKVVLLNRAPTLHRLGIQAFQPVVLEGGQSIQLHPLV
CEAFNADFDGDMVHVPLSSFAQAEARIQMLSANLLSPASGEPLAKPSRDIIILGLYITQVRKEKK
GAGMAFATPEEALAAAYERGEVALNAPIVVAGRETSVGRKLVFANPDEALLAVAHGLLDLQDVTVTR
YLGRRLETSPGRILFARIVGEAVGDEKVAQELIQMDVPQEKNSLKDLYQAFLRLGMEKTARLLDALK
YYGFTLSTTSGITIGIDDAVIPEEKQRYLEEADRKLQIEQAYEMGFLTDREYDQVIQLWTETTEKVT
QAVFNNFEENYPFNPLYVMAQSGARGNPQQRQLCGMRGLMQKPSGETFEVPRSSFREGLTVLEY
FISSHGARKGGADTALRTADSGYLTRKLVDAHEIVVREADCGTTNYISVPLFQMDEVTRTLRLRKR
DIESGLYGRVLAREVEALGRRLEEGRYLSLEDVHFLIKAAEAGEVREVPVRSPLTCQTRYGVCQKCYG
DLSMARPVSIGEAVGVAAESIGEPGTQTMRTFHTGGVAVGTDITQGLPRVIELFEARRPKAKAVISE
IDGVVRIEEDRLSVFVESEGFKEYKLPKDARLLVKDGDYVEAGQPLTRGAIDPHQLLEAKGPEAV
ERYLVDEIQKVYRAQGVKLHDKHIEIVVRQMLKYVEVTDPGDSRLLEGQVLEKWDVEALNERLIAE
GKVPVAWKPLLMGVTKSALSTKSWSAASFQNTTHVLTEAAIAGKKDELIGLKENVILGRLIPAGTGS
DFVRFTQVVDQRTLKAI

>d1bpya2_e.9.1.1 (A:92-335) DNA polymerase beta, catalytic (31 kD) fragment {Human
(*Homo sapiens*)}

DTSSINFLTRVSGIGPSAARKFVDEGIKTLEDLRKNEDKLNHHQRIGLKYFGDFEKRIPREEMLQMQ
DIVLNEVKKVDSEYIATVCGSFRRGAESSGDMVLLTHPSFTSESTKQPKLLHQVVEQLQKVHFITDT
LSKGETKFMGVCQLPSKNDEKEYPHRRIDIRLIPKDQYYCGVLYFTGSDIFNKNMRAHALEKGFINE
YTIRPLGVTGVAGEPLPVDSEKDIFDYIQWKYREPKDRSE

>d1jn3a_ e.9.1.1 (A:) DNA polymerase beta, catalytic (31 kD) fragment {Rat (*Rattus norvegicus*)}

DDTSSINFLTRVTGIGPSAARKLVDEGIKTLEDLRKNEDKLNHHQRIGLKYFEDFEKRIPREEMLQMQ
QDIVLNEVKKLDPEYIATVCGSFRRGAESSGDMVLLTHPNFTSESSKQPKLLHRVVEQLQKVRFITD
TLKGETKFMGVCQLPSENDENEYPHRRIDIRLIPKDQYYCGVLYFTGSDIFNKNLRAHALEKGFINE
EYTIRPLGVTGVAGEPLPVDSEQDIFDYIQWRYREPKDRSE

>d1jmsa2 e.9.1.1 (A:243-510) Terminal deoxynucleotidyl transferase {Mouse (*Mus musculus*)}

DERYKSFKLFTSVFGVGLKTAEKWFRMGFRTLSKIQSDKSLRFTQMOKAGFLYEDLVSCVNRPEAE
AVSMLVKEAVVTFPLDALVTMTGGFRRGKMTGHDVDFLITSPEATEDEEQQLLHKVTDVFWKQQL
LLYCDILESTFEKFKQPSRKVDALDHFQKCFILKLDHGRVHSEKSGQEGKGWKAIRVDLVMCPYD
RRAFALLGWTGSRQFERDLRRYATHERKMMLDNHALYDRTKRVFLEAESEEEIFAHGLGLDYIEPWE
RNA

>d1jaja_ e.9.1.1 (A:) DNA polymerase X {African swine fever virus}

MLTLIQGKKIVNHLRSRLAFEYNGQLIKILSKNIVAVGSLRREEKMLNDVDLLIIVPEKLLKHVLPNI
RIKGLSFSVKVCGERKCVLFIEWEKKTYQLDLFTALAEKPYAIFHFTGPVSYLIRIRAALKKKNYKLN
QYGLFKNQTLVPLKITTEKELIKELGFTYRIPKKRL

>d1fa0a2 e.9.1.2 (A:3-351) Poly(A) polymerase, catalytic domain {Baker's yeast (*Saccharomyces cerevisiae*)}

SQKVFGITGPVSTVGATAAENKLNDSLIQELKKEGSFETEQETANRVQVLKILQELAQRFVYEVSKKK
NMSDGMARDAGGKIFTYGSYRLGVHGPSIDITLVVVPKHVTREDFFTVFDSELLRERKELDEIAPVP
DAFVPIIKIKFSGISIDLICARLDQPQVPLSLTSDKNLLRNLDKDLRALNGTRVTDIILELVPKPNVF
RIALRAIKLWAQRRAVYANIFGFPGGVAVAMLVARICQLYPNACSAVILNRFIILSEWNWPQPVILKP
IEDGPLQVRVWNPKIYAQDRSHRMPVITPAYPSMCATHNITESTKKVILQEFVRGVQITNDIFSNNKKS
WANLFEK

>d1f5aa2 e.9.1.2 (A:20-364) Poly(A) polymerase, catalytic domain {Cow (*Bos taurus*)}

YGITSPISLAAPKETDCLLTQKLVE TLKPFVFE EEEELQRRILILGKLNVLKWEWIREISESKNLPQSV
IENVGGKIFTFGSYRLGVHTKGADIDALCVAPRHVDRSDFFTSFYDKLKLQEEVKDLRAVEEAFVPI
KLCFDGIEIDILFARLALQTIPEDLDRDSSLKLNLDIRCIRSLNGCRVTDEILHLVFNIDNFRLLTRAI
KLWAKRHNINYSNILGFLGGVSWAMLVARTCQLYPNAIASTLVHKFFLVFSKWEWPNPVLKQPEECN
LNLPVWDPRVNPSPDRYHLMPIITPAYPQQNSTYNVSVSTRMVMVEEFKQGLAITDEILLSKAEWSKL
FEA

>d1knya_ e.9.1.3 (A:) Kanamycin nucleotidyltransferase (KNTase) {*Staphylococcus aureus*}

MNGPIIMTREERMKIVHEIKERILDKYGDDVKAIGVYGLGRQTDGPYSDIEMMCMSTEEAEFSHE
WTTGEWKVEVNFYSEEILLDYASQVESDWPLTHGQFFSILPIYDSGGYLEKVYQTAKSVEAQTFFHDAI
CALIVEELFEYAGKWRNIRVQGPTTFLPSLTVQVAMAGAMLIGLHHRICYTTSASVLTEAVKQSDLPS
GYDHLQCQFVMSGQLSDSEKLLSLENFWNGIQEWTERHGYIVDVSKRIPF

>d1k8ta_ e.9.1.4 (A:) Adenylyl cyclase toxin (the edema factor) {*Bacillus anthracis*}

DRIDVLKGEKALKASGLVPEHADAFKKIARELNTYILFRPVNKLATNLIKSGVATKGLNVHKGSSDW
GPVAGYIPFDQDLSKKHGGQLAVEKGNLENKKSITEHEGEIGKIPLKLDHLRIEELKENGHILKGGKEI

DNGKKYYLLESNNQVVEFRISDENNEVQYKTKEGKITVLGEKFNWRNIEVMAKNVEGVKPLTADY
DLFALAPSLTEIKKQIPQKEWDKVVNTPNSLEKQKGVTNLLIKYGIERKPDSTKGTLSNWQKQMLDR
LNEAVKYTGTYGGDVVNHGTEQDNEEFPEKDNEIFIINPEGEFILTKNWEMTGRFIEKNITGKDLYL
YFNRSYNKIAPGNKAYIEWTDPITKAKINTIPTSAEFIKNLSSIRSSNVGVYKDSGDKDEFAKKESVK
KIAGYLSDYNSANHIFSQEKKRKISIFRGIQAYNEIENVLKSQIAPEYKKNYFQYLKERITNQVQLLLT
HQKSNIEFKLLYKQLNFTENETDNFEVFKIIDE

>d1cy9a_ e.10.1.1 (A:) DNA topoisomerase I, 67K N-terminal domain {Escherichia coli}

FVPEEFWEVDASTTTTSGEALALQVTHQNDKPFPRVNKEQTQAASVLEKARYSVLEREDKPTTSK
PGAPFITSTLQQAASRLGFGVKKTMMAQRLYEAGYITYMRTDSTNLSQDAVNMVRGYISDNFGK
KYLPEPNQYASKENSQEAHEAIRPSDVNVMAESLKDMEADAQKLYQLIWRQFVACQMTPAKYDST
TLTVGAGDFRLKARGRILRFDGWTKVMPALRKGDEDRILPAVNKGDALTLVELTPAQHFTKP

>d1ecl_ e.10.1.1 (-) DNA topoisomerase I, 67K N-terminal domain {Escherichia coli}

GKALVIVESPAKAKTINKYLGSDYVVKSSVGHIRDLTSGSAAKKSADSTSTKTAKPKPDERGALVN
RMGVPDWHNWEAHYEVLPGEKVVSELKQLAEKADHIYLATDLREGEAIAWHLREVIGDDARY
SRVVFNEITKNAIRQAFNKPGEINIDRVNAQQARRFMDRVVGYMVSPLLWKKIARGLSAGRVQSVAV
RLVVEREREIKAFVPEEFWEVDASTTTTSGEALALQVTHQNDKPFPRVNKEQTQAASVLEKARYSV
LEREDKPTTSKPGAPFITSTLQQAASRLGFGVKKTMMAQRLYEAGYITYMRTDSTNLSQDAVNM
VRGYISDNFGKKYLPEPNQYASKNSQEAHEAIRPSDVNVMAESLKDMEADAQKLYQLIWRQFVAC
QMTPAKYDSTTLTVGAGDFRLKARGRILRFDGWTKVMPALRKGDEDRILPAVNKGDALTLVELTPAQ
HFTKPPARFSEASLVKELEKRGIGRPSTYASIISTIQRGYVRVENRRFYAEKMGEIVTDRLEENFREL
MNYDFTAQMENSLDQVANHEAEWKAVALDHFFSDFTQQLDKAEKDPEEGGMRPN

>d1i7da_ e.10.1.1 (A:) DNA topoisomerase III {Escherichia coli}

MRLFIAEKPSLARAIAADVLPKPHRKGDFIECGNGQVVTWCIGHLLEQAQPDAYSRYARWNLADL
PIVPEKWQLQPRPSVTKQLNVIKRFLHEASEIVHAGDPDREGQLLVDEVLDYLLQLAPEKRQQVQRCL
INDLNPQAVERAIDRLRSNSEFVPLCVSALARARADWLYGINMTRAYTILGRNAGYQGVLSVGRVQT
PVLGLVRRDEEIEFVAKDFFEVKAHIVTPADERFTAIWQPSEACEPYQDEEGRLLHRPLAEHVVN
RISGQPAIVTSYNDKRESESAPLPSLSALQIEAAKRFGLSAQNVLDICQKLYETHKLITFPRSDCRYLP
EEHFAGRHAVMNAISVHAPDLLPQPVDPDIRNRCWDDKKVDAHHAIIPTARSSAINLTENEAKVY
NLIARQYLMQFCPDAVFRKCVIELDIAGKGFVAKARFLAEAGWRTLLGSKERDEENDGTPLPVVAKG
DELLCEKGEVVERQTQPPRHFTDATLLSAMTGIAFRVQDKDLKILRATDGLGTEATRAGIHELLFKR
GFLTCKGRYIHSTDAGKALFHSLPEMATRPDMTAHWESVLTQISEKQCRYQDFMQPLVGTLYQLIDQ
AKRTPVRQFRGIVAP

>d1gkub3 e.10.1.1 (B:499-1054) Topoisomerase "domain" of reverse gyrase {Archaeon
Archaeoglobus fulgidus}

QEFDLIKPALFIVESPTKARQISRFFGKPSVKVLDGAVVYEIPMQKYVLMVTASIGHVVDLITNRGFHG
VLVNGRFVPVYASIKRCRDCGYQFTEDRESCPKCGSENVDNSRSRIEALRKLADAEFVIVGTDPDTE
GEKIAWDLKNLLSGCGAVKRAEFHEVTRRAILEALESRLDVENLVKAQVRRIEDRWIGFVLSQKL
WERFNRRNLSAGRAQTLVLGWIIDRFQESRERRKIAIVRDFDLVLEHDEEFDLTIKLVEEREELRTP
LPPYTTETMLSDANRILKFSVKQTMQIAQELFENGLITYHRTDSTRVSDVGQRIAKEYLGDDFVGRE
WGESGAHECIRPTRPLTRDDVQRLIQEGVLVVEGLRWEHFALYDLIFRRFMASQCRPFKVVVKKYSI
EFDGKTAEEERIVRAEGRAYELYRAVWVKNELPTGTFRVKAEVKSVKVLPTQSEIIQMMKERGIG
RPSTYATIVDRLFMRNYVVEKYGRMIPTKLGIDVFRFLVRRYAKFVSEDRTDRDLESRMDAIERGELDY
LKALEDMYAEIKSID

>d1bjt_ e.11.1.1 (-) DNA topoisomerase II, C-terminal fragment (residues 410-1202)

{Baker's yeast (*Saccharomyces cerevisiae*)}

RKSRITNYPKLEDANKAGTKEGYKCTLVLTEGDSALS LAVAGLAVVGRDYYGCYPLRGKMLNVREAS
ADQILKNAEIQAIAKKIMGLQHRKKYEDTKSLRYGHLMMIMTDQDHDGSHIKGLIINFLESSFLGLLDIQ
GFLLEFITPIIKVSITKPTKNTIAFYNMPDYEKWREEESHKFTWKQKYYKGLGTS LAQEVREYFSNLD
RHLKIFHSLQGNDKDYIDLAFSKKKADDRKEWLRQYEPGTVLDPTLKEIPISDFINKELILFSLADNI
RSIPNVLDGFKPGQRKVLYGCFKKNLKSELKVAQLAPYVSECTAYHHGEQSLAQTIIGLAQNFVGSNN
IYLLLPNGAFGTRATGGKDAARYYITELNKLTRKIFHPADDPLYKYIQEDEKTVEPEWYLPILPMIL
VNGAEGIGTWSTYIPFPNPLEIKNIRHLMNDEELEQMHPWFRGWTGTIEEIEPLRYRMYGRIEQI
GDNVLEITELPARTWTSTIKEYLLLGLSGNDKIKPWIKDMEEQHDDNIKFIITLSPEEMAKTRKIGFY
ERFKLISPISLMNMVAFDPHGKIKKYNVNEILSEFYVRYEYYQKRKDHMSERLQWEVEKYSFQVK
FIKMIIEKELTVTNKPRNAIQELENLGFPRFNKEGKPYGSPNDEIAEQINDVKGATSDEEDEESSHE
DTENVINGPEELYGTYEYLLGMRIWSLTKERYQKLLKQKQEKETELENLLKLSAKDIWNTDLKAFEV
GYQEFQRDAEARG

>d1ab4_ e.11.1.1 (-) DNA Gyrase A {*Escherichia coli*}

VGRALPDVRDGLKPVHRRVLYAMNVLGNDWNKAYKKSARVVGDVIGKYHPHGDSAVYDTIVRMAQ
PFSLRYMLVDGQGNFGSIDGDSAAAMRYTEIRLAKIAHELMADLEKETVDFVDNYDGTEKIPDVMP
TKIPNLLVNGSSGIAVGMATNIPPHNLTEVINGCLAYIDDEDISIEGLMEHIPGPDFPTAAIINGRRGIEE
AYRTGRGKVYIRARAEVEVETIIVHEIPYQVNKARLIEKIAELVKEKRVEGISALRDESDDKGMRIVIE
GEVVLNNLYSQTQLQVSFGINMVALHHGQPKIMNLKDIIAAFVRHRREVVTTRTIFELRKARDRAHI
LEALAVANIDPIELRHAPTPAEAKTALVANPWQLGNVAAMLEDAARPEWLEPEFGVRDGLYYL
TEQQAQAILDLRLQKLTGLEHEKLLDEYKELLDQIAELLRILGSADRLMEVIREELELVREQFGDKRR
TEIT

>d1d3ya_ e.12.1.1 (A:) DNA topoisomerase IV, alpha subunit {Archaeon *Methanococcus jannaschii*}

QAKIFAQTTKMLEFAKQLETTDDFSTLREAYYVSKNWGEARFDDQQASNNVIEDLEAALGVLREHL
GFIPEEDGSSVVGPLKIIIEETPEGELVVDCTKLTGTAYNIPNDVTKLNLETDAFILAIETSGMFARLN
AERFWDKHNLCILVSLKGVPARATRRFIKRLHEEHDLPLVLFVTDGDPYGLNIYRTLKVGSGKAIHLA
DKLSIPAARLIGVTPQDIIDYDLPTHPLKEQDIKRIKDGKNDDFVRSFPEWQKALKQMLDMGVRAE
QQSLAKYGLKYVVNTYLPEKIKDESTWLP

>d1dd9a_ e.13.1.1 (A:) DNA primase DnaG catalytic core {*Escherichia coli*}

TLYQLMDGLNTFYQQSLQQPVATSARQYLEKRGLSHEVIARFAIGFAPPGWDNVLKRFGGNPENRQS
LIDAGMLVTNDQGRSYDRFRERVMFPIRDKRGRVIGFGGRVLGNDTPKYLNSPETDIFHKGRQLYGL
YEAQQDNAEPNRLLVVEGYMDVVALAQYGINAVASLGTSTTADHIQLLFRATNNVICCYDGDRAGR
DAAWRALETALPYMTDGRQLRFMFLPDGEDPDTLVRKEGKEAFEARMEQAMPLSAFLFNSLMPQ
VDLSTPDGRARLSTLALPLISQVPGETLRIYLRQELGNKLGILDDSQL

>d1ee8a_ e.14.1.1 (A:) DNA repair protein MutM (Fpg) {*Thermus thermophilus*}

PELPEVETTRRRRLRPLVLGQTLRQVVHRDPARYRNTALAEGRRILEVDRRGKFLLEGGVELVAH
LGMTGGFRLEPTPHTRAALVLEGRTLYFHDPRRFGRLFGVRRGDYREIPLLLRLGPEPLSEAFAPPGF
FRGLKESARPLKALLDQRLAAGVGNIADEALFRARLSPFRPARSLTEEEARRLYRALREVLAEAVE
LGGSTLSDQSYRQPDGLPGGFQTRHAVYGREGLPCPACGRPVERRVVAGRGTHFCPTCQGGEP

>d1i3ja_ e.30.1.1 (A:) DNA-binding domain of intron endonuclease I-TevI {Bacteriophage T4}

KFCKCGVRIQTSAYTCSKCRNRSGENNSFFNHKHSITKSKISEKMKGKKPSNIKKISCDGVIFDCAAD
AARHFKISSGLVTYRVKSDKWNWFYIN

>d1a31a2 e.15.1.1 (A:215-430) Eukaryotic DNA topoisomerase I, N-terminal DNA-binding

fragment {Human (Homo sapiens)}

IKWKFLKHKGPVFAPPYEPLPENVKFYDYGKVMKLSPKAAEEVATFFAKMLDHEYTTKEIFRKNFFK
DWRKEMTNEEKNIITNLSKCDFTQMSQYFKAQTEARKQMSKEEKLKIKEENEKLLKEYGFCIMDN
HKERIANFKIEPPGLFRGRGNHPKMGMLKRRIMPEDIHNSKDAKVPSPPPGHKWKEVRHDNKVT
WLVSWTENIQGSIKYIMLN

>d1ois_ e.15.1.1 (-) Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment
{Baker's yeast (Saccharomyces cerevisiae)}

DTIKWVTLKHNGVIFPPPYQPLPSHIKLYYDGKPVLDLPPQAEVAGFFAALLESDHAKNPVFQKNFF
NDFLQVLKESGGPLNGIEIKEFSRCDFTKMFDFYQLQKEQKKQLTSQEKKQIRLEREKFEEDYKFCEL
DGRREQVGNFKVEPPDLFRGRGAHPKTGKLKRRVNPEDIVLNLSKADAPVPPAPEGHKWGEIRHDN
TVQWLAMWRENIFNSFKYVRLAA

>d1g71a_ e.16.1.1 (A:) DNA primase {Archaeon Pyrococcus furiosus}

MLMREVTKEERSEFYSKEWSAKKIPKFIVDTLESREFGFDHNGEGPSDRKNQYSDIRDLEDYIRATS
PYAVYSSVAFYENPREMEGWARGAELVFDIDAKDLPLKRCNHEPGTVCPICLEDAKELAKDTLILREE
LGFENIHVVYSGRGYHIRILDEWALQLDSKSRERILAFISASEIENVEEFRFLLEKRGWVFLKHGYPR
VFRLRLGYFILRVNPHLLSIGIRRNIAKKILDHKEEIEYEGFVRKAILASFPEGVGIEMAKLFALSTRFS
KAYFDGRVTVDIKRILRLPSTLHSHKGLIATYVGTKEREVMKFNPFRRHAVPKFRKKEVREAYKLWRE
SL

>d1jeya_ e.31.1.1 (A:) Ku70 subunit {Human (Homo sapiens)}

GRDSLIFLVDASKAMFESQSEDELTPFDMSIQCIQSVYISKIISDRDLLAVVFGTEKDKNSVNFKNY
VLQELDNPGAKRILELDQFKGQGGQKRFQDMMGHGSDYSLSEVLWVCANLFSVQFKMSHKRIML
FTNEDNPHGNDSAKASRARTKAGDLRDTGIFLDMHLKPKGGFDISLFYRDIISIAEDEDLRVHFEE
SKLEDLLRKVRACKETRKRALSRLKLNKDIVISVGIYNLVQKALKPPPIKLYRETNEPVKTKTRTFN
TSTGGLLLPSDTKRSQIYGSRQIILEKEETEELKRFDDPGLMLMGFKPLVLLKHHYLRPSLFVYPEE
SLVIGSSTLFSALLIKCLEKEVAALCRYTPRRNIPPYFVALVPQEEELDDQKIQVTPPGFQLVFLPFADD
KRKMPFTEKIMATPEQVGKMKAIVEKLRFTYRSDSFENPVLQQHFRNLEALALDLMEPEQAVDLTL
PKVEAMNKRLGSLVDEFKELVYPPDY

>d1jeyb_ e.31.1.2 (B:) Ku80 subunit {Human (Homo sapiens)}

NKAAVLCMDVGFTMSNSIPGIESPFQAKKVITMFVQRQVFAENKDEIALVLFGTGTDNPLSGGD
QYQNITVHRHMLPDFDLLEDIESKIQPGSQADFLDALIVSMDVIQHETIGKKFEKRHIEIFTDLSSR
FSKSQLDIIIHSLKCDISLQFFLPFSLGKEDGSGDRGDGPFRLGGHGSPFLKIGITEQQKEGLEIVKM
VMISLEGEDGLDEIYSFSESLRKLKCVFKKIERHSIHWPCRLTIGSNLSIRIAAYKSILQERVKKTWTVVD
AKTLKKEDIQKETVYCLNDDDETEVLKEDIQGFYRGSDIVPFSKVDEEQMKYKSEGKCFVSLGFKS
SQVQRRFFMGNQVLKVFAARDDEAAVALSSLIHALDDLDMVAIVRYAYDKRANPQVGVAFPHIKH
NYECLVYVQLPFMEDLRQYMFSSKNSKYPTEAQLNAVDALIDSMSLAKKDEKTDLTLEDLFPTT
KIPNPRFQRLFQCLLHRALHPREPLPIQQHIWNMLNPPAEVTTKSQIPLSKIKTLFPLIEAKK

>d1daaa_ e.17.1.1 (A:) D-amino acid aminotransferase {Bacillus sp., strain YM-1}

GYTLWNDQIVKDEEVKIDKEDRGYQFGDGVYEVVKVYNGEMFTVNEHIDRLYASAEKIRITIPYTKD
KFHQLLHELVEKNELNTGHIYFQVTRGTSPRAHQFPENTVKPVIIGYTKENPRPLENLEKGVKATFV
EDIRWLRCDIKSLNLLGAVLAKQEAHEKGCYEAILHRNNTVTEGSSSNVFGIKDGILYTHPANNMILK
GITRDVVIACANEINMPVKEIPFTTHEALKMDELFTSTTSEITPVIEIDGKLIRDGKVGWTRKQLQ
QFETKIP

>d1i1ka_ e.17.1.1 (A:) Branched-chain amino acid aminotransferase {Escherichia coli}

KADYIWFNGEMVRWEDAKVHVMSHALHYGTSVFEGIRCYDSSHKGPVFRHREHMQRLLHDSAKIY

RFPVQSIDELMEACRDVIRKNNLTSAYIRPLIFVGDVGMGVNPPAGYSTDVIIAAFPWGAYLGAEALE
QGIDAMVSSWNRAAPNTIPTAAKAGGNLSSLLVGSEARRHGYQEGIALDVNGYISEGAGENLFEVK
DGVLFPTFPPTSSALPGITRDAIKLAKELGIEVREQVLSRESLYLADEVFMSGTAAEITPVRSVDGIQVG
EGRCGPVTKRIQQAFFGLFTGETEDKWGWLDQVNQ

>d1ekfa_e.17.1.1 (A:) Branched-chain amino acid aminotransferase {Human (Homo sapiens),
mitochondrial}

ASSSFKAADLQLEMTQKPHKKPGPEPLVFGKTFDTHMLMVEWNDKGGWQPRIQPFQNLTLHPAS
SSLHYSLQLFEGMKAFKGDQVRLFRPWLNMDRMLRSAMRLCLPSFDKLELLECIRRLIEVDKD
WVPDAAGTSLYVRPVLIGNEPSLGVSQPRRALLFVILCPVGAYFPGGSVTPVSLPADPAFIRAWVGGV
GNYKLGNGYGPVTLVQEQEALKRGCEQVLWLYGPDHQLTEVGTMNIFVYWTHEDGVLELVTPPLNGV
ILPGVVRQSLDMAQTWGEFRVVERTITMKQLLRAL EEGRVREVFSGGTACQVCPVHRILYKDRNLH
IPTMENGP ELILRFQKELKEIQYGIRAH EWMFPV

>d1et0a_e.17.1.1 (A:) Aminodeoxychorismate lyase {Escherichia coli}

MFLINGHKQESLAVSDRATQFGDGCFTTARVIDGKVSLLSAHIQRLQDACQRLMISCDFWPQLEQEM
KTLAAEQQNGVLKVVISRGSGGRGYSTLNSGPATRILSVTAYPAHYDRLRNEGITLALSPVRLGRNPH
LAGIKHLNRLEQVLIRSHLEQTNADALVLDSEGWVTECCAANLFWRKGNVVYTPRLDQAGVNGIM
RQFCIRLLAQSSYQLVEVQASLEESLQADEMVICNALMPVMPVCACGDVSFSSATLYEYLAPLCE

>d2frvb_e.18.1.1 (B:) Nickel-iron hydrogenase, large subunit {Desulfovibrio gigas}

NKIVVDPITRIEHLRIEVEVEGGKIKNAWSMSTLFRGLEMILKGRDPRDAQHFTQRACGVCTYVHA
LASVRAVDNCGVKIPENATLMRNLTMGAYMHDHLVHFYHLHALDWVNVANALNADPAKAARL
ANDLSPKKT'TTESLKAVQAKVKALVESGQLGIFTNAYFLGGHPAYVLP AEVDLIATAHYLEALRVQVK
AARAMAIFGAKNPHTQFTVVGCTNYDSLPERIAEFRKLYKEVREFIEQVYITDLLAVAGFYKNWA
GIGKTSNFLTCGEFPTDEYDLNSRYTPQGVWGNLSDKVDNFNPD LIEEHVKYSWYEGAGAHHPYK
GVTKPKWTEFHGEDRYSWMKAPRYKGEAFEVGPLASVLVAYAKKHEPTVKAVDLV LKTLG VGP EAL
FSTLGRTAARGIQCLTAAQEVEVWLDKLEANVKAGKDDLYTDWQYPTESQGVGFVNAPRGMLSHW
IVQRGGKIENFQLVVPSTWNLGPRCAEGKLSAVEQALIGTPIADPKRPVEILRTVHSYDPCIAACGVH

>d1h2rl_e.18.1.1 (L:) Nickel-iron hydrogenase, large subunit {Desulfovibrio vulgaris}

SSYSGPIVDPVTRIEGHLRIEVEVENGVKNAYSSSTLFRGLEIILKGRDPRDAQHFTQRTCGVCTYT
HALASTRCVDNAVGVHIPKNATYIRNLV LGAQYLHDHIVHFYHLHALDFVDVTAALKADPAKAAKV
ASSISPRKTTAADLKAVQDKLKTFFVETGQLGPFTNAYFLGGHPAYYLDPETNLIATAHYLEALRLQVK
AARAMAVFGAKNPHTQFTVVGVT CYDALTPQRIAEFEALWKETKAFVDEVYIPDLLVAAAYKDW
TQYGGTDNFITFGFEPKDEYDLNSRFFKPGVVFKRDFKNIKPFDKMQIEEHVRHSWYEGAEARHP
WKGQTQPKYTDLHGDDRYSWMKAPRYMGPEMETGPLAQVLIAYSQGHPKVAVTDAVLAKLGVG
PEALFSTLGRTAARGIETAVIAEYVGVMLQEYKDNIAKGDNVICAPWEMPKQAEGVGFVNAPRGGLS
HWIRIEDGKIGNFQLVVPSTWTLGPRCDKNNVSPVEASLIGTPVADAKRPVEILRTVHSFDPCIAACGV
H

>d1frfl_e.18.1.1 (L:) Nickel-iron hydrogenase, large subunit {Desulfovibrio fructosovorans}

TPQSTFTGPIVDPITRIEHLRIMVEVENGVKDAWSSSQLFRGLEIILKGRDPRDAQHFTQRACGV
CTYVHALASSRCVDDAVKVSIPANARMNRNLV MASQYLHDHLVHFYHLHALDWVDVTAALKADP
NKA AKLAASIDTARTGNSEKALKAVQDKL KAFVESGQLGIFTNAYFLGGHKAYYLPPEVNL IATAHYL
EALHMVKAASAMAILGGKNPHTQFTVVGCSNYQGLTKDPLANYLALSKEVCQFVNECYIPDLLAV
AGFYKDWGGIGGTSNYLAFGEFATDDSSPEKHLATSQFPSGVITGRDLGKVDNVDLGA IYEDVKYSW
YAPGGDGKHPYDGVTDPKYTKLDDKDHYSWMKAPRYK GKAMEVGPLARTFIAYAKQPDFKKVVD
MVLGKLSVPATALHSTLGRTAARGIETAIVCANMEKWIKEMADSGAKDNTLCAK WEMPEESKGVGL

ADAPRGSLSHWIRIKGKKIDNFQLVVPSTWNLGPRGPQGDKSPVEEALIGTPIADPKRPVEILRTVHA
FDPCIACGVH

>d1cc1l_e.18.1.1 (L:) Nickel-iron hydrogenase, large subunit {Desulfomicrobium baculatum}
VKISIDPLTRVEGHLKIEVEVKDGVVDAKCSGGMFRGFEQILRGRDPRDSSQIVQRICGVCPTAHCTA
SVMAQDDAFGVKVTNNGRITRNLIFGANYLQSHILHFYHLAALDYVKGPDVSPFVPRYANADLLTDR
IKDGAKADATNTYGLNQYLKALEIRRICHEMVAMFGGRMPHVQGMVVGGATEIPTADKVAEYAARF
KEVQKFVIEEYLPLIYTLGSVYTDLFETGIGWKNVIAFGVFPEDDDYKTFLKPGVYIDGKDEEFDSKL
VKEYVGHSHFFDHSAPGGLHYSVGETNPNPKPGAYSFVKAPRYKDKPCEVGPLARMWVQNPESPV
GQKLLKELYGIEAKKFRDLGDKAFSIMGRHVLRAEETWLTAVAVEKWLKQVQPGAETYVKSEIPDAA
EGTGFTEAPRGALLHYLKIKDKKIENYQIVSATLWLNANPRDDMGQRGPIEEALIGVPPDIKNPVNV
GRLVRSYDPXLGCAVH

>d1e3db_e.18.1.1 (B:) Nickel-iron hydrogenase, large subunit {Desulfovibrio desulfuricans}
TPRSNYTGPIVVDPLTRIEGHLRIEVEVEGGVIKEARSCATLFRGIETILKGRDPRDAQHFTQRTCGVC
TYTHALASTRCLIEDAINKPIANATYIRNLVLGNQFMHDHLVHFYHLHALDFVDVTSALLADPAKAA
KLANSISPRKATTEEFAAVQAKLKTFFVASGQLGPFTNAYFLGGHEGYMDPEANLVCTAHYLQALRA
QVEVAKGMAVFGAKNPHTQFTVAGGVTCYEALTPERIKQFRELYVKARAFIEEVYIPDLLLVASYK
WGKIGGTNNFMAFGEFPAPGGERDLNSRWYKPGVIYDRKVGSVQPFDPKIEEHVRHSWYEGKAR
APFEGETNPHFTFMGDTDKYSWNKAPRYDGHAVETGPLAQMLVAYGHNHKTIKPTIDAVLGKLN
GPEALFSTLGRTAARGIQLVIAQQMENWLNEYENNIVKDKQIVEDYAVPTSARGVGFADVSRGGLS
HWMTIEDGKIDNFQLVVPSTWNLGPRDDKGVPSAAEAALVGTVPADPKRPVEILRTIHSFDPCIAC
TH

>d2frva_e.19.1.1 (A:) Nickel-iron hydrogenase, small subunit {Desulfovibrio gigas}
KKRPSVYVYLHNAECTGCSESVLRTVDPYVDELILDVISM DYHETLMAGAGHAVEEALHEAIKGFVC
VIEGGIPMGDGGYWGKVGGRNMYDICA EVAPKAKAVIAIGTCATYGGVQAAKPNPTGTVGVNEALG
KLGVKAINIAGCPPNPMNFVGTVVHLLTKGMPELDKQGRPVMFFGETVHDNCPRLKHFEAGEFATS
FGSPEAKKGYCLYELGCKGPDYNNCPKQLFNQVNWVPVQAGHPCACSEPNFWDLYSPFYSA

>d1h2rs_e.19.1.1 (S:) Nickel-iron hydrogenase, small subunit {Desulfovibrio vulgaris}
LMGPRRPSVYVYLHNAECTGCSESVLRAFEPYIDTLILD TSLDYHETIMAAAGDAAEALEQAVNSP
HGFIAVVEGGIPTAANGIYGKVANHTMLDICSRLPKAQAVIAYGTCATFGGVQAAKPNPTGAKGVND
ALKHLGVKAINIAGCPPNPNVLTIVYYLKNKAPELDSLNRPTMFFGQTVHEQCPRLPHFDAGEF
APSEFESEARKGWCLYELGCKGPVTMNNCPKIKFNQTNWVPVDAGHPCIGCSEPDFWDAMTPFYQN

>d1frfs_e.19.1.1 (S:) Nickel-iron hydrogenase, small subunit {Desulfovibrio fructosovorans}
KHRPSVWVYLHNAECTGCTEAAIRTIKPYIDALILD TISLDYQETIMAAAGETSEALHEALEGKDGYY
LVVEGGLPTIDGGQWGMVAGHPMIETCKKAAAKAKGIICIGTCSPYGGVQKAKPNPSQAKGVSEALG
VKTINIPGCPPNPFVAVVHVLTKGIPDLDENGRPKLFYGELVHDNCPRLPHFEASEFAPSF DSEEA
KKGFLYELGCKGPVTYNNCPKVLFNQVNWVPVQAGHPCLGCSEPDFWDTMTPFYEQG

>d1cc1s_e.19.1.1 (S:) Nickel-iron hydrogenase, small subunit {Desulfomicrobium
baculatum}

KKAPVIWVQGGCTGCSVSLNAVHPRIKEILLDVISLEFHPTVMASEGEMALAHMYEIAEKFNNGF
FLLVEGAIPTAKEGRYCVGETLDAKAHHHEVTMMELIRD LAPKSLATVAVGTCSAYGGIPAAEGNVT
GSKSVRDFFADEKIEKLLVNPVGCPPHPDWMVGT LVAASHVLPTEHPLPELDDDGRPLLFFGDN
IHENCPYLDKYDNSEFAETFTKPGCKAELGCKGPSTYADCAKRRWNNGINWCVENAVCIGCV EPDF
PDGKSPFYVAE

>d1e3da_e.19.1.1 (A:) Nickel-iron hydrogenase, small subunit {Desulfovibrio desulfuricans}

SRPSVVYLHAAECTGCSEALLRTPYQPFIDTLILDITISLDYHETIMAAAGEAAEEALQAAVNGPDGFICL
VEGAIPTGMDNKYGYIAGHTMYDICKNILPKAKAVVSIGTCACYGGIQAAPNPNTAAKGINDCYADLG
VKAINVPGCPPNPLNMVGTLVAFKLGQKIELDEVGRPVMFFGQSVHDLCCERRKHFDFAGEFAPSFNSE
EARKGWCLYDVGCKGPETYNNCPKVLNETNWPVAAGHPCIGCSEPNFWDDMTPFYQN

>d1dg4a_e.20.1.1 (A:) DnaK {Escherichia coli}

LSLGIETMGGVMTTLIAKNTTIPTKHSQVFSTAEDNQSAVTIHVLQGERKRAADNKSLGQFNLDGIN
PAPRGMPQIEVTFDIDADGILHVSADKNSGKEQKITIKASSGL

>d1dkza_e.20.1.1 (A:) DnaK {Escherichia coli}

VLLLDVTPSLGIETMGGVMTTLIAKNTTIPTKHSQVFSTAEDNQSASVIHVLQGERKRAADNKSLG
QFNLDGINPAPRGMPQIEVTFDIDADGILHVSADKNSGKEQKITIKASSGLNEDEIQMVRDAEAN
AEADRKFEELVQTRNQGDHLLHSTRKQVEEAGDKLPADDKTAIESALTALETALKGEDKAAIEAKM
QELAQVSQKLMEIAQ

>d2bpr_e.20.1.1 (-) DnaK {Escherichia coli}

SIEGRVKDVLDDVTPSLGIETMGGVMTTLIAKNTTIPTKHSQVFSTAEDNQSAVTIHVLQGERKRA
ADNKSLGQFNLDGINPAPRGMPQIEVTFDIDADGILHVSADKNSGKEQKITIKASSGLNEDEIQM
VRDAEANA AEADRKFEELVQTRNQGDHLLHSTRKQVEEA

>d1ckra_e.20.1.1 (A:) DnaK {Rat (Rattus norvegicus)}

SENVQDLLLLDVTPSLGIETAGGVMTVLIKRNTTIPTKQTQTFTTYSDNQPGVLIQVYEGGERAMTK
DNNLLGKFELTGIPPAPRGVPQIEVTFDIDANGILNVSAVDKSTGKENKITITNDKGRLSKEDIERMVQ
EAEKYKADEKQRDKVSSKNSLE

>d1dqsa_e.22.1.1 (A:) Dehydroquinase synthase, DHQS {Aspergillus nidulans}

PTKISILGRESIADFGWLWRNYVAKDLISDCSSTTYVLVTDNIGSIYTPSFEEAFKRRAAEITPSPRLLI
YNRPPGEVSKSRQTKADIEDWMLSQNPPCGRDTVVIALGGGVIGDLTGFASTYMRGVRYVQVPTTL
LAMVDSSIGGKTAIDTPLGKNLIGAIWQPTKIYIDLEFLETLPVREFINGMAEVIKTA AISSEEEFTALE
ENAETILKAVRREVTPEHRFEGTEEILKARILASARHKAYVVSADEREGGLRNLLNWGHSIGHAIE
AILTPQILHGECVAIGMVKEAELARHLGILKGVAVSRIVKCLAAAYGLPTSLKDARIRKLTAGKHCSVDQL
MFNMALDKKNDGPKKKIVLLSAIGTPYETRASVVANEDIRVVL

>d1jq5a_e.22.1.2 (A:) Glycerol dehydrogenase {Bacillus stearothermophilus}

AAERVFISPAKYVQGKNVITKIANYLEGIGNKTVVIADIVWKIAGHTIVNELKKGNIAAEEVVSFGEA
SRNEVERIANIARKAEAAIVIGVGGGKTLDTAKAVADELDAIVIVPTAASTDAPTSALSVIYSDDGVE
SYRFYKKNPDLVLDTKIIANAPRLLASGIADALATWVEARSVIKSGGKTMAGGIPTIAEAIAEKCE
QTLFKYGLAYESVKAKVVTPALEAVVEANTLLSGLGFESGGLAAAHAIHNGFTALEGEIHHLTHGEK
VAFGTLVQLALEEHSQEIERYIELYCLDLPVTLEDIKLKDASREDILKVAKAATAEGETIHNAFNVT
ADDVADAIFAADQYAKAYKEK

>d1kq3a_e.22.1.2 (A:) Glycerol dehydrogenase {Thermotoga maritima, TM0423}

HMITTTIFPGRYVQGAGAINILEEELSRFGERAFVVIDDFVDKNVLGENFFSSFTKVRVKNQIFGGES
DEEIERLSGLVEEETDVVVVIGGGKTLDTAKAVAYKPKPVVIVPTIASTDAPCSALSVIYTPNGEFKRY
LFLPRNPDVLDTEIVAKAPARFLVAGMGDALATWFEAESCKQKYAPNMTGRLGSMTAYALARLCY
ETLLEYGVLAKRSVEEKSVTPALEKIVEANTLLSGLGFESGGLAAAHAIHNGLTVLENTHKYLHGEKV
AIGVLASLFLTDKPRKMIEEVYSFCEEVGLPTTLAEIGLDGVSDEDLMKVAEKACDKNETIHNEPQP
TSKDVFFALKAADRYGRMRKNL

>d1lci_e.23.1.1 (-) Luciferase {Firefly (Photinus pyralis)}

AKNIKKGPAPFYPLEDGTAGEQLHKAMKRYALVPGTIAFTDAHIEVNITYAEYFEMSVRLAEAMKRY
GLNTNHRIVVCSENSLQFFMPVLGALFIGVAVAPANDIYNERELLSMNSIQPTVVVFSKKGLOKILN

VQKKLPPIQKIIIMDSKTDYQGFQSMYTFVTSHLPPGFNEYDFVPESFDRDKTIALIMNSSGSTGLPKG
VALPHRTACVRFSHARDPIFGNQIIPDTAILSVPFHHGFGMFTTLGYLICGFRVVLMYRFEEELFLRS
LQDYKIQSALLVPTLFSFFAKSTLIDKYDLNLHEIASGGAPLSKEVGEAVAKRFHLPGIRQGYGLTETT
SAILITPEGDDKPGAVGKVVPPFEAKVVDLDTGKTLGVNQRGELCVRGPMIMSGYVNNPEATNALID
KDGWLHSGDIAYWDEDEHFFIVDRLKSLIKYKGYQVAPAELESILLQHPNIFDAGVAGLPDDDAGELP
AAVVVLEHGKTMTEKEIVDYVASQVTTAKKLRGGVVFVDEVPKGLTGKLDARKIREILIKAKK

>d1amua_ e.23.1.1 (A:) Phenylalanine activating domain of gramicidin synthetase 1 {*Bacillus brevis*}

GTHEEEQYLFAVNNTKAEYPRDKTIHQLFEEQVSKRPNNVAIVCENEQLTYHELNVKANQLARIFIE
KGIGKDTLVGIMMEKSIDLFIGILAVLKAGGAYVPIDIEYPKERIQYILDDSQARMLLTQKHLVHLIHN
QFNGQVEIFEEDTIKIREGTLNHVPSKSTDLAYVIYTSGTTGNPKGTMLEHKGISNLKVVFFENSLNVT
EKDRIGQFASISFDASVWEMFMALLTGASLYIILKDTINDFVKFEQYINQKEITVITLPPTYVVHLDPE
RILSIQTLITAGSATSPSLVNKWKKEKVTYINAYGPTETTICATTWVATKETIGHSPVIGAPIQNTQIYIV
DENLQLKSVGEAGELCIGGEGGLARGYWKRPELTSQKFVDNPFVPGKLYKTGDQARWLSGDNIEYLG
RIDNQVKIRGHRVELEEESILLKHMYSIETAVSVHKDHQEQPYLCAYFVSEKHIPLEQLRQFSSEELP
TYMIPSYFIQLDKMPLTSNGKIDRKQLPEPDLTF

>d1ad2_ e.24.1.1 (-) Ribosomal protein L1 {*Thermus thermophilus*}

KRYRALLEKVDPNKIYTIIDAAHLVKELATAKFDVETVEVHAKLGLIDPRRSDQNVRGTVSLPHGLGKQ
VRVLAIAKGEKIKEAEEAGADYVGGEEIIQKILDGWMDFDAVVATPDVMGAVGSKLGRILGPRGLLPN
PKAGTVGFNIGIEIREIKAGRIEFRNDKTGAIHAPVGKACFPPEKLADNIRAFIRALEAHKPEGAKGTF
LRSVYVTTTTMGPSVRINPHS

>d1cjsa_ e.24.1.1 (A:) Ribosomal protein L1 {Archaeon *Methanococcus jannaschii*}

MDREALLQAVKEARELAKPRNFTQSFEFIATLKEIDMRKPENRIKTEVVLPHPGRGKEAKIAVIGTGD
LAKQAEELGLTVIRKEEIEELGKNKRKLRKIAKAHDFFIAQADLMPLIGRYMGVILGPRGKMPKPVPA
NANIKPLVERLKKTVVINTRDKPYFQVLVGNEKMTDEQIVDNIEAVLNVVAKKYEKGLYHIKDAYVKL
TMGPAVKVKK

>d1dwua_ e.24.1.1 (A:) Ribosomal protein L1 {Archaeon *Methanococcus thermolithotrophicus*}

MDRENILKAVKEARSLAKPRNFTQSLDLIINLKELDLSRPENRLKEQVVLPNGRGKEPKIAVIAKGD
AAQAEEMGLTVIRQDELEELGKNKKMAKKIANEHDFFIAQADMPLVGKTLGPVLGPRGKMPQPV
PANANLTPVERLKKTVLINTRDKPLFHVVLVGNEKMSDEELAENIEAILNTVSRKYEKGLYHVKSAYT
KLTMGPPAQIEK

>d1dn1a_ e.25.1.1 (A:) Neuronal Sec1, NSec1 {Rat (*Rattus norvegicus*)}

IGLKAVVGEKIMHDVIKKVKKKGEWKVLVVDQLSMRMLSSCCKMTDIMTEGITIVEDINKRREPLPS
LEAVYLITPSEKSVHSLISDFKDPPTAKYRAAHVFFTDSCPDALFNELVKSRAAKVIKTLTEINIAFLPY
ESQVYSLDSADSFQSFYSPHKAQMKNPILERLAEQIATLCATLKEYPAVRYRGEYKDNALLAQLIQDK
LDAYKADDPTMGEGPDKARSQLLILDRGFDPSSPVLHELTFQAMSYDLLPIENDVYKYETSGIGEAR
VKEVLLDEDDDLWIALRHKHIAEVSQEVTRSLKDFSSSKRMNTGEKTTMRDLSQMLKMPQYQKE
LSKYSTHLHLAEDCMKHYQGTVDKLCRVEQDLAMGTDAEGEKIKDPMRAIVPILLDANVSTYDKIRI
ILLYIFLKNNGITEENLNKLIQHAQIPPEDSEIITNMAHLGVPIVTDSTLRRRSKPERKERISEQTYQLSR
WTPHDKDIMEDTIEDKLDTKHYPYISTRSSASFSTTAVSARYGHWKKNKAPGEYRSGPRLIIFILGGVS
LNEMRCAYEVTQANGKWEVLIGSTHILTPQKLLDTLKKNKTDEEI

>d1epua_ e.25.1.1 (A:) Neuronal Sec1, NSec1 {Longfin inshore squid (*Loligo pealei*)}

ALKTAVHEKIMNDVVLAVKKNAEWKVLIVDQLSMRMVSACCKMHEIMSEGITLVEDINRRREPLPL

LEAVYLITPTEESVKCLMADFQNPDPQYRGAIFFTEACPEELFKELCKSTTARFIKTLKEINIAFLP
YESQIFSLDSPDTFQVYYNPSRAQGGIPNKERCAEQIATLCATLGEYPSVRYRSDFDENASFAQLVQQK
LDAYRADDPTMGEQPQKDRSOLLILDRGFDPISSLHELTFQAMAYDLLPIENDVYKYVNTGGNEVP
EKEVLLDEKDDLWVEMRQHIAVVSQNVTKLQKQFADEKRMGTAADKAGIKDLSQMLKMPQYQ
KELSKYSTHLHLAEDCMKQYQHVVDKLCVQDLAMGTDADGEKIRDHMRNIVPILLDQKISAYDK
IRILLYIIHKGGISEENLAKLVQHAHIPAEKWIINDMQNLGVPIIQDGGRRKIPQPYHTHNRKERQA
DHTYQMSRWTPYMKDIMEAAVEDKLDTRHYPFLNGGGPRPSCQQPVSVRYGHWKDKGQASYKS
GPRLIIFVVGISYSEMRSAYEVTQTAKNNWEVILGSTHILTPEGLLRDLRKISNP

>d1e2ua_e.26.1.1 (A:) Hybrid cluster protein (prismane protein) {Desulfovibrio vulgaris}
MFCFQCQETAKNTGCTVKGMCGKPEETANLQDLLIFVLRGIAIYGEKLELQGPDRSNDDFVLQGLF
ATITNANWDDARFEAMISEGLARRDKLRNAFLAVYKAKNGKDFSEPLPEAATWTGDSTAFAEKAKS
VGILATENEDVRSRELLIIGLKGVAAYAEHA AVLGRKTEIDEFMLEALASTTKDLSVDEMVALVMK
AGGMAVTTMALLDEANTTTYGNPEITQVNIGVGNPILISGHDLKDMAELLKQTEGTGVDVYTHG
EMLPANYYPAFKKYPHFVGNYGGSWWQNPFEFESFNGPILLTNTCLVPLKENTYLDRLYTTGVVG
YEGAKHIADRPAGGAKDFSALIAQAKKCPPVEIETGSIVGGFAHHQVLALADKVVEAVKSGAIKRFV
VMAGCDGRQKRSRYTEVAENLPKDTVILTACAKYRYNKLNLGDIGGIPRVLADAGQCNDSSYLAVIA
LKLKEVFGDLDINDLPVSYDIAWYEQKAVAVLLALLFLGVKGIRLGP TLP AFLSPNVAKVLVENFNKIP
IGTVQDDIAAMMAGK

>d1jya_e.26.1.2 (A:) Ni-containing carbon monoxide dehydrogenase {Carboxydotherrhus
hydrogenoformans}
QNLKSTDRAVQMLDKAKREGIQTVWDRYEAMKPCGFGETGLCCRHLQGPCRINPFGDEPKVGI
CGATAEVIVARGLDRSIAAGAAGHSGHAKHLAHTLKKAVQGAASYMIKDRTKLHSAKRLGIPTEG
QKDEDIALEVAKAALADFHEKDPVLWVTTVLPSPRVKLSAHLIPAGIDHEIAEIMHRTSMGCDA
DAQNLLGLRCSLADLAGCYMGTDLADILFGTPAPVVTESNLGVLKADAVNVAVHGHNPVLSDIIVS
VSKEMENEARAAGATGINVVGICCTGNEVLMRHGIPACTHSVSQEMAMITGALDAMILDYQCIQPSV
ATIAECTGTTVITMEMSKITGATHVNFAEEAAVENAKQILRLAIDTFKRRKGPVEIPNIKTKVVAG
FSTEAIINALSKLNANDPLKPLIDNVVNGNIRGVCLFAGCANNVKVPQDQNF TTIARKLLKQNVLVAT
GCGAGALMRHGFMDPANVDELCDGLKAVLTAIGEANGLGGPLPPVLHMGSCVDNSRSVALVAALA
NRLGVDMDRLPVVASAAQAMHEKAVAIGTWAVTIGLPTHIGVFPPITGSLPVTQILTSSVKDITGGYFI
VELDPQVAADKLLAAINERRAGLGLPR

>d1jqka_e.26.1.2 (A:) Ni-containing carbon monoxide dehydrogenase {Rhodospirillum
rubrum}
ETAWHRYEKQPQCGFGSAGLCCRICKGPCRIDPFGEKPKYVCGADRDTIVARHLVIRMIAAGTAA
HSEHGRHIALAMQHISQGELHDYSIRDEAKLYAIAKTLGVATEGRGLLAIVGDLAAITLGDFQNDYD
KPCAWLAASLTPRRVKRLGDLGLLPHNIDASVAQTMSTRTHVGCADPTNLILGGLRVAMADLDGSM
LATELSDALFGTPQPVVSAANLGMKRGAVNIAVNGHNPMLSDIICDVAADLRDEAIAAGAAEGINII
GICCTGHEVMMRHGVPLATNYLSQELPILTGAEAMVVDVQCIMPSPRIAECFHTQIITTDKHNKIS
GATHVPFDEHKAVETAKTIIRMAIAAFGRDPNRVAIPAFKQKSIVGFSAEAVVAALAKVNADDPLKP
LVDNVVNGNIQIVLFGVGNNTTKVQQDSAYVDLAKSLAKRNVLVATGCAAGAFKAGLMTSEATTQ
YAGEGLKGVLSAIGTAAGLGGPLPLVMHMGSCVDNSRAVALATALANKLGVLDLPLVASAPECMSE
KALAIQSWAVTIGLPTHVGSVPPVIGSQIVTKLVETETAKDLVGGYFIVDTPKSAGDKLYAAIQERRAG
L

>d1h5wa_e.27.1.1 (A:) Upper collar protein gp10 (connector protein) {Bacteriophage
PHI29}

RQKRNRWFIHYLNYLQSLAYQLFEWENLPPTINPSFLEKSIHQFGYVGFYKDPVISYIACNGALSGQR
DVYNQATVFRAASPVYQKEFKLYNYRDMKEEDMGVVIYNNDMAFPTTPTLELFAAEELAEELKEIISVN
QNAQKTPVLIRANDNNQLSLKQVYNQYEGNAPVIFAHEALSDSIEVFKTDAPYVVDKLNQKNAV
WNEMMTFLGIKNANLEKKERMVTDEVSSNDEQIESSGTVFLKSREEACEKINELYGLNVKVKFRYDI
>d1io1a_e.32.1.1 (A:) F41 fragment of flagellin {Salmonella typhimurium}

NIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELAVQSANSTNSQSDLDISQAEITQRLNEIDR
VSGQTQFNGVKVLAQDNTLTIQVGANDGETIDIDLKQINSQTLGLDNLVQQKYKVSATAATVTGYA
DTTIALDNSTFKASATGLGGTDQKIDGDLKFDTTGKYAKVTVTGGTGKDGYYEVSVDKTNGEVTL
AGGATSPLTGGLPATATEDVKNVQVANADLTEAKAALTAAGVTGTASVVKMSYTDNNGKTIDGGLAV
KVGDDYYSATQNKDGSISINTTKYTADDGTSKTALNKLGGADGKTEVVSIGGKTYAASKAEGHNFKA
QPDLAEEAAATTTENPLQKIDAALAQVDTLRSDLAAVQNRFNSAITNLGNTVNNLTSAR

>d1htya_e.33.1.1 (A:) Golgi alpha-mannosidase II {Fruit fly (Drosophila melanogaster)}
CQDVVQDVPNVVDVQMLELYDRMSFKDIDGGVWVKQGWNIKYDPLKYNAHKKLVFVPHSHNDPG
WIQTFEYYQHDTKHILSNALRHLHDNPEMKFIWAEISYFARFYHDLGENKKLQMSIVKNGQLEF
VTGGWVMPDEANSHWRNVLLQLTEGQTWLQFMNVTPTASWAIDPFGHSPTMPYILQKSGFKNM
LIQRTHYSVKKELAQQRQLEFLWRQIWDNKGDTALFTHMMPFYSYDIPHTCGPDPKVCQFDFKR
MGSFGLSCPWKVPPRTISDQNVAAARSDDLVDQWKKKAELYRTNVLLIPLGDDFRFKQTEWDVQR
VNYERLFEHINSQAHFNVQAQFGTLQEYFQDAVHQAERAGQAEFPTLSGDFFTYADRSDNYWSGYT
SRPYHKRMDRVLMHYVRAAEMLSAWHSWDGMARIEERLEQARRELSLFQHHDGITGTAKTHVVV
DYEQRMQEALKACQMVMQQSVYRLLTKPSIYSPDFSFYSYFTLDDSRWPGSGVEDSRTTIILGEDILPS
KHVVMHNTLPHWREQLVDFYVSSPFVSVTDLANNPVEAQVSPVWSWHHDTLTKTIHPQGSTTKY
RIIFKARVPPMGLATYVLTISDSKPEHTSYASNLLLRKNPTSLPLGQYPEDVKFGDPREISLRVNGPT
LAFSEQGLLKSILQTDSPHVPVHFKFLKYGVRSHGDRSGAYLFLPNGPASPVELGQPVVLTGKLE
SSVSVGLPSVVHQTIMRGGAPEIRNLVDIGSLDNTEIVMRLETHIDSGDIFYTDLNLQFIKRRRLDKL
PLQANYYPISGMFIEDANTRTLTGTQPLGGSSLASGELEIMQDRRLASDDERGLGQGVLDNKPVL
HIYRLVLEKVNNCVRPSKLPAGYLTSAAHKASQSLDPLDKFIFAENEWIGAQQGFGGDHPSARED
LDVSVMRRLTKSSAKTQRVGYVLHRTNLMQCGTPEEHTQKLDVCHLLPNVARCERTTLTFLQNLEH
LDGMVAPEVCPMETAAYVSSH

>d1knza_e.34.1.1 (A:) NSP3 homodimer {Simian 11 rotavirus}
TQQMAVSIINSSFEAAVVAATSALENMGIEYDYQDIYSRVKNKFDVMDDSGVKNNPIGKAITIDQAL
NNKFGSAIRNRNLADTSRPAKLEDEVNKLRLMMLSSKGIDQKMRVLNACFSVKRIPGKSSSIKCTK
LMRDKLERGEVEVDDSFVDEKM

>g1jmu.1 e.35.1.1 (A:,B:) Membrane penetration protein mu1 {Reovirus}
TINVTGDGNVFKPSAETSSTAVPSLSLSPGMLNXPGGVPWIAIGDETSVTPGALRRMTSKDIPETAI
NTDNSSGAVPSESALVPYNDEPLVVVTEHAIANFTKAEMALEFNREFLDKLRVLSVSPKYSDLLTYV
DCYVGVSARQALNNFQKQVPVITPTRQTMVDSIQAAALKALEKWEIDLRVAQTLLPTNVPIGEVSCP
MQSVVLLDDQLPDDSLIRRYPKAAVALAKRNGGIQWMDVSEGTVMNEAVNAVAASALAPSASAP
PLEEKSKLTEQAMDVTAPEEIIASLVPVPAPVFAIPPKPADYNVRTLKIDEATWLRMIPKTMGTLF
QIQVTDNTGTNWHFNLGGTRVVNLDQIAPMRFVLDLGGKSYKETSWDPNGKKGVFVQSKIPFE
LWTAASQIGQATVVNYVQLYAEDSSFTAQSIATTSLAYNYEPEQLNKTDPEMNYLLATFIDSAAITP
TNMTQPDVWDALLTMSPLSAGEVTVKGAVVSEVPAELIGSYTPESLNASLPNDAARCMIDRASKIA
EAIKIDDDAGPDEYSPNSVPIQQLAISQLETGYGVRIFNPKGILSKIASRAMQAFIGDPSTIITQAAPVL
SDKNNWIALAQGVKTSRTRKSLSAGVKTAVSKLSSSESIQNWTTQGFLLDKVSTHFPAP

>d2btva_e.28.1.1 (A:) BTV inner layer core protein vp3 {Bluetongue virus, strain 1}

VDFTVPDVQQILDDIKALAAEQVYKIVKVPSTSRHIVTQSRDRVLRVDTYEEMSQVGDVITEDEPE
KFYSTIHKVRFIRGKGSFILHDIPARDHRGMEVAEPEVLGVEFKNVLPVLTAEHRAMIQNALDGSIE
NGNVATRDVDFIGACSEPIYRIYNRLQGYIEAVQLQELRNSIGWLERLGQRKRITYSQEVLTDFFRRQ
DMIWVLALQLPVNPQVWVDVPRSSIANLIMNIATCLPTGEYIAPNPRISSITLTQRITTTGPFALTGST
PTAQQLNDRKIYALMFPGQIILDLKIDPGERMDPAVRMVAGVVGHLLFTAGGRFTNLTQNMARQ
LDIALNDYLLMYNTRVQVNYGPTGEPLDFQIGRNQYDCNVFRADFATGTGYNGWATIDVEYRDP
PYVHAQRYIRYCGIDSRELINPTTYGIGMTHCYNEMLRMLVAAGKDSEAAAYFRSMLPFHMVRFARI
NQIINEDLHSVFLPDDMFNALLPDLIAGAHQNAADPVLDVSWISLWFAFNRSFEPHTRNEMLEIAP
LIESVYASELSVMKVDMRHLSLMQRRFPDVLIQARPSHFVKAVLNDSPKAVMNLSSHNFNINIR
DMMRWVLLPSLQPSLKLVEEEAWAAANDFEDLMLTDQVYMRDMLPEPRDDIERFRQEGFY
TNMLEAPPEIDRVVQYTYEIARLQANMGQFRAALRRIMDDDDWVRFGGVLRVTVRVKFFDARPPDD
ILQGLPFSYDTNEKGGLSYATIKYATETTFIYLIYNVEFSNTPDSLVLINPTYTMTKVFINKRIVERVRV
GQILAVLNRRFVAYKGMKMRIMDITQSLKMGTKLAAPT

>d1cola_f.1.1.1 (A:) Colicin A {Escherichia coli}

AKDERELLEKTSELIAGMGDKIGEHLGDKYKAIKDIADNIKNFQKTIRSFDDAMASLNKITANPA
MKINKADRDALVNAWKHVDAQDMANKLGNLSKAFKVADVVMKVEKREKSIEGYETGNWGPML
LEVESWVLSGIASSVALGIFSATLGAYALSGVPAIAGVGIAGILLAAVVGALIDDKFADALNNEIR

>d1a87_f.1.1.1 (-) Colicin N {Escherichia coli}

SAKVGIEITITPDNSKPGRYISSNPEYSLAKLIDAESIKGTEVYTFHTRKGGYVKTVPDSNIDKMRVD
YVNWKGPKYNNKLVKRFVSQFLFRKEEKEKNEKEALLKASELVSGMGDKLGEYLVGKYKNVAKEV
ANDIKNFHGRNIRSYNEAMASLNKVLANPKMKVNSDKDAIVNAWKQVNAKDMANKIGNLGKAF
KVADLAIKVEKIREKSIEGYNTGNWGPMLLEVESWIIGGVVAGVAISLFGAVLSFLPISGLAVTALGVIGI
MTISYLSFFIDANRVSNINNISSVIR

>d1cii_1 f.1.1.1 (451-624) Colicin Ia {Escherichia coli}

DAINFTEFLKSVSEKYGAKAEQLAREMAGQAKGKKIRNVEEALKTYEKYRADINKKINAKDRAAIA
AALESVKLSDISSNLNRFSRGLGYAGKFTSLADWITEFGKAVRTENWRPLFVKTTETIAGNAATALVA
LVFSILTGSALGIIGYLLMAVTGALIDESLVEKANKFW

>d1f0la3 f.1.2.1 (A:201-380) Diphtheria toxin, middle domain {Corynebacterium diphtheriae}

CINLDWDVIRDKTKTKIESLKEHGPIKNKMSSEPNKTVSEEKAKQYLEEFHQTALEHPELSELKTVT
GTNPVFAGANYAAWAVNVAQVIDSETADNLEKTTAALSILPGIGSVMGIADGAVHHNTEEIVAQSIAL
SSLMVAQAIPLVGELVDIGFAAYNFVESIINLFQVVHNSYNRPAY

>d1dlc_3 f.1.3.1 (61-289) delta-Endotoxin (insecticide), N-terminal domain {Bacillus thuringiensis tenebrionis, CRYIIIA (BT13)}

TTKDVIQKGISVVDLLGVVGFPPFGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQKIADYAK
NKALAEQLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNSMPSFAISGYEVLV
LTTYAQAANTHLFLLKDAQIYGEWGYEKEDIAEFYKRQLKLTQEYTDHCVKWYNVGLDKLRGSSY
ESWVNFNRYRREMTLTVLDLIALFPLYDVR

>d1ji6a3 f.1.3.1 (A:64-290) delta-Endotoxin (insecticide), N-terminal domain {Bacillus thuringiensis, CRY3bb1}

DAVGTGISVVGQILGVVGVFAGALTSFYQSFLNTIWPSPADPWKAFMAQVEVLIDKKIEEYAKSKAL
AELQGLQNNFEDYVNALNSWKKTPLSLRKRSQDRIRELFSQAESHFRNSMPSFAVSKFEVLFLPTY
AQAANTHLLLLKDAQVFGEEWGYSSDVAEFYHRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAW
VKFNRRREMTLTVLDLIVLFPFYDIR

>d1ciy_3 f.1.3.1 (33-255) delta-Endotoxin (insectocide), N-terminal domain {Bacillus thuringiensis, CRYIA (A)}

YTPIDISLSLTQFLLSEFVPGAGFVLGLVDIHWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGL
SNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLS
VLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRE
LTLTVLDIVALFSNYDSRRY

>d1i5pa3 f.1.3.1 (A:1-263) delta-Endotoxin (insectocide), N-terminal domain {Bacillus thuringiensis subsp. kurstaki, CRY2AA}

MNNVLNSGRTTICDAYNVVAHDPFSFEHKSLDTIQKEWMEWKRTDHSLYVAPVVGTVSSFLKKVVG
SLIGKRILSELWGIIFPSGSTNLMQDILRETEQFLNQLRLNTDTLARVNAELIGLQANIREFNQQVDNF
LNPTQNPVPLSITSSVNTMQQLFLNRLPQFQIQGYQLLLLPLFAQAANMHLSFIRDVILNADEWGISA
ATLRTYRDYLRNYTRDYSNYCINTYQTAFRGLNTRLHDMLEFRTYMFLNVFEYVSIWLSLFK

>d1g5ma_ f.1.4.1 (A:) Bcl-2 {Human (Homo sapiens)}

HAGRTGYDNREIVMKYIHYKLSQRGYEWDAGDDVEENRTEAPEGTESEVHHLALRQAGDDFSRRY
RGDFAEMSSQLHLTPFTARGRFATVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIAL
WMTEYLNRLHHTWIQDNGGWDAFVELYGPSMR

>d1bxa_ f.1.4.1 (A:) Apoptosis regulator Bcl-xL {Human (Homo sapiens)}

MSMAMSQSNRELVDFLSYKLSQKGYWSQFSDVEENRTEAPEGTESEAVKQALREAGDEFELRYR
RAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIA
AWMATYLNHLEPWIQENGGWDTFVELYGNNAEAESRKGQERLEHHHHHH

>d1xl_ f.1.4.1 (-) Apoptosis regulator Bcl-xL {Human (Homo sapiens)}

MSMAMSQSNRELVDFLSYKLSQKGYWSQFSDVEENRTEAPEGTESEMTPSAINGNPSWHLAD
SPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNE
LFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAMATYLNHLEPWIQENGGWDTFVEL
YGNNAEAESRKGQERLEHHHHHH

>d1maz_ f.1.4.1 (-) Apoptosis regulator Bcl-xL {Human (Homo sapiens)}

MSQSNRELVDFLSYKLSQKGYWSQFSDVEENRTEAPEGTESEMTPSAINGNPSWHLADSPAVN
GATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRD
GVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAMATYLNHLEPWIQENGGWDTFVELY

>d2bida_ f.1.4.1 (A:) Proapoptotic molecule Bid {Human (Homo sapiens)}

GSMDCEVNNSSLRDECITNLLVFGFLQSCSDNSFRRELDALGHELPLVAPQWEGYDELQTDGNRSS
HSRLGRIEADSESQEDIIRNIARHLAQVGDSDMSRIPPGLVNGLALQLRNTSRSEEDRNRDLATALEQ
LLQAYPRDMEKEKTMLVLALLLAKKVASHTPSLLRDVFHTTVNFINQNLRTYVRSRSLARNGMD

>d1ddba_ f.1.4.1 (A:) Proapoptotic molecule Bid {Mouse (Mus musculus)}

MDSEVNSGSLGAKHITDLLVFGFLQSSGCTRQELEVLRGRELVPQAYWEADLEDELQTDGSQASRSF
NQGRIEPPDESQEEIHNIAARHLAQIGDEMHNIPQTLVRQLAAQFMNGSLSEEDKRNCLAKALDEV
KTAFPRDMENDKAMLIMTMLLAKKVASHAPSLLRDVFHTTVNFINQNLFSYVRNLVRNEMD

>d1f16a_ f.1.4.1 (A:) Proapoptotic molecule Bax {Human (Homo sapiens)}

MDGSGEQPRGGGPTSSEQIMKTGALLLQGFIQDRAGRMGGEAPELALDPVPQDASTKKLSECLKRIG
DELDSNMELQRMIAAVDTPSPREVFVRVAADMFSDDGNFNWGRVVALFYFASKLVKALCTKVPPELI
RTIMGWTLDFLRERLLGWIQDQGGWDGLLSYFGTPTWQTVTIFVAGVLTASLIWKKMG

>d1ikpa3 f.1.5.1 (A:252-394) Exotoxin A, middle domain {Pseudomonas aeruginosa}

EGGSLAALTAHQACHLPLETFTRHRQPRGAEQLEQCQYPVQRLVALYLAARLSWNQVDQVIRNALAS
PGSGGDLGEAIREQPEQARLALTLAAAESERFVRQGTGNDEAGAANADVSLTCPVAAGECAGPADS

GDALLERNY

>d1c3wa_f.2.1.1 (A:) Bacteriorhodopsin {Halobacterium salinarum}

TGRPEWIWLALGTALMGLGTYFLVKMGVSDPDAKKFYAITTLVPAIAFTMYLSMLLGYGLTMVVPF
GGEQNPIYWARYADWLFTTPLLLLDLALLVDADQGTILALVGADGIMIGTGLVGALTKVYSYRFVWWW
AISTAAMLYILYVLFVFGFSMRPEVASTFKVLRNVTVVLWSAYPVVWVWLGSEGAGIVPLNIETLLFMVLD
VSAKVGFGLILLRSRAIFG

>d1c8sa_f.2.1.1 (A:) Bacteriorhodopsin {Halobacterium salinarum}

TGRPEWIWLALGTALMGLGTYFLVKMGVSDPDAKKFYAITTLVPAIAFTMYLSMLLGYGLTMVVPF
GGEQNPIYWARYADWLFTTPLLLLNALLVDADQGTILALVGADGIMIGTGLVGALTKVYSYRFVWWW
AISTAAMLYILYVLFNVTVVLWSAYPVVWVWLGSEGAGIVPLNIETLLFMVLDVSAKVGFGLI

>d1e12a_f.2.1.1 (A:) Halorhodopsin {Halobacterium salinarum}

RENALLSSSLWVNVALAGIAILVFVYMGRITRPGRPRLIWGATLMIPLVSISSYLGLLSGLTVGMIEMPA
GHALAGEMVRSQWGRYLTWALSTPMILLALGLLADVDLGSFLTVAADIGMCVTGLAAAMTTSALL
FRWAFYAISCAFFVVVLSALVTDWAASASSAGTAEIFDTRLRVLTVVWLWLGYPVWVAVGVEGLALVQSV
GATSWAYSVLDVFAKYVFVAFILLRWVANNERTVAV

>d1h68a_f.2.1.1 (A:) Sensory rhodopsin II {Natronobacterium pharaonis}

VGLTTLFWLGAIGMLVGTLAFWAGRDAGSGERRYVTVLGVISGIAAVAYVVMALGVGWVPAERTV
FAPRYIDWILTTPILIVYFLGGLLAGLDSREFGIVITLNTVVMVLAGFAGAMVPGIERYALFGMGAVAFGLL
VYYLVGPMTESASQRSSGIKSLYVRLRNLTIVILWAIYPIFWLLGPPGVALTPTVDVALIVYLDLVTKVG
FGFIALDAAATL

>d1hzxa_f.2.1.1 (A:) Rhodopsin {Cow (Bos taurus)}

MNGTEGPNFYVPFSNKTGVVRSPEAPQYYLAEPWQFSMLAAYMFLIMLGFIPINFLTYVTVQHK
KLRTPLNYILLNLAVADLFMVFGGFTTTLTYTSLHGYFVFGPTGCNLEGFFATLGGEIALWVSLVLAIER
YVVVCKPMSNFRFGENHAIMGVAFTWVMALACAAPPLVGWSRYIPEGMQCSCGIDYYTPHEETNN
ESFVIYMFVVHFIPLIVIFFCYGQLVFTVKEAAAQQQESATTQKAEKEVTRMVIIMVIAFLICWLPYAG
VAFYIFTHQGSDFGPIFMTIPAFFAKTSAVYNPVIYIMMNKQFRNCMVTTLCCGKNPLGDDEASTTVS
KTETSQVAPA

>d1jfp_a_f.2.1.1 (A:) Rhodopsin {Cow (Bos taurus)}

LAAYMFLIMLGFIPINFLTYVTVQHKKLRTPLNYILLNLAVADLFMVFGGFTTTLTYTSLHGYFVFGPT
GCNLEGFFATLGGEIALWVSLVLAIERVYVVVCKPMSNFRFGENHAIMGVAFTWVMALACAAPPLVG
WSRYIPEGMQCSCGIDYYTPHEETNNESFVIYMFVVHFIPLIVIFFCYGQLVFTVKEAAAQQQESATT
QKAEKEVTRMVIIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAVYNPVIYIMMNKQ
FRNCMVTTLCCGKNPLGDDEASTTVSKTETSQVAPA

>d1dxrh2 f.2.1.2 (H:1-36) Photosynthetic reaction centre, L-, M- and H-chains
{Rhodospseudomonas viridis}

MYHGALAQHLDIAQLVWYAQWLVIWTVVLLYLRRD

>d1dxrl1 f.2.1.2 (L:) Photosynthetic reaction centre, L-, M- and H-chains
{Rhodospseudomonas viridis}

ALLSFERKYRVRGGTLIGGDLDFWVGPYFVGFVSAIFFIFLGVSLIGYAASQGPTWDPFAISINPPD
LKYGLGAAPLLEGGFWQAITVCALGAFISWMLREVEISRKLGIGWHVPLAFCVPIFMFCVLQVFRPLL
LGSWGHAFFPYGILSHLDWVNNFGYQYLNWFYNPGHMSSVSFLVFNAMALGLHGGLILSVANPGDG
DKVKTAEHENQYFRDVVGYSIGALSIIHRLGLFLASNIFLTGAFGTIASGPFWTRGWPEWGWWDI
PFWS

>d1dxrm1 f.2.1.2 (M:) Photosynthetic reaction centre, L-, M- and H-chains

{Rhodopseudomonas viridis}

ADYQTIYTQIQARGPHITVSGEWDNDRVGKPFYSYWLKIGDAQIGPIYLGASGIAAFAGSTAILIL
FNMAAEVHFDPLQFFRQFFWLGLYPPKAQYGMGIPPLHDGGWWLMAGLFMTLSLGSWWIRVYSR
ARALGLGTHIAWNFAAAIFFVLCIGCIHPTLVGSWSEGVVPGIWPIDWLTAFSIRYGNFYPCWHGF
SIGFAYGCGLLFAAHGATILAVARFGGDREIEQITDRGTAVERAALFWRWTIGFNATIESVHRWGWFF
SLMVMVSASVGILLTGTFVDNWYLWCVKHGAAPDYPAYLPATPDPASLPGAPK

>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}

ALLSFERKYRVPGGTLVGGNLFDFWVGPFFYVGGFVATFFFAALGILIAWSAVLQGTWNPQLISVYP
PALEYGLGGAPLAKGGLWQIITICATGAFVSWALREVEICRKLIGYHIPFAFAFAILAYLTLVLFVRPVM
MGAWGYAFPYGIWTHLDWVSNVTGYTYGNFHYNPAHMIAISFFFTNALALALHGALVLSAANPEKKG
EMRTPDHEDTFFRDLVGSIGTLGIHRLGLLLSLAVFFSALCMIITGTIWFQVVDWWQWWVKLP
WWANIPGGING

>d1qovm1 f.2.1.2 (M:) Photosynthetic reaction centre, L-, M- and H-chains {Rhodobacter
sphaeroides}

AEYQNIFSQVQVRGPADLGMTEDVNLANRSGVGPFFSTLLGWFGNAQLGPIYLGSLGVLSLFSGLMWF
FTIGIWFYQAGWNPVFLRDLFFFSLEPPAPEYGLSFAAPLKEGGLWLIASFFMFVAVWSWWGRT
YLRAQALGMGKHTAWAFLSAIWLWMVLGFIRPILMGSWSEAVPYGIFSHLDWTNNFSLVHGNLFY
NPFHGLSIAFLYGSALLFAMHGATILAVSRFGGERELEQIADRGTAAERAALFWRWTMGFNWTMEG
IHRWAIWMAVLVTLTGGIGILLSGTVVNDNWYVWQNHG

>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}

HYIDAAQITIWAFFWLFFFGLIYYLRREDKREGYPLDS

>d1eysl1 f.2.1.2 (L:) Photosynthetic reaction centre, L-, M- and H-chains
{Thermochromatium tepidum}

AMLSFEKKYRVRGGTLIGDLDLDFWVGPFFYVGGFVGFCTLLGVLLIVWGATIGPTGPTSDLQTY
NLWRISIAPPDLSYGLRMAPLTEGGLWQIITICAAGAFISWALREVEICRKLIGIFHVPFAFSFAIGAYL
VLVFRPLLMGAWGHGFPYGILSHLDWVSNVGYQFLHFHYNPAHMLAISFFFTNCLALSMHGSLILS
VTNPQRGEPVKTSEHENTFFRDIVGYSIGALAIHRLGLFLALSAAFWSAVCILISGPFWTRGWPEWW
NWWLELPLW

>d1eysm1 f.2.1.2 (M:) Photosynthetic reaction centre, L-, M- and H-chains
{Thermochromatium tepidum}

PEYQNIFTAVQVRAPAYPGVPLPKGNLPRIGRPIFSYWLKIGDAQIGPIYLGTLTGLSIFGLVAISHIGF
NMLASVHWDVDFQLKHFVWLGLEPPPPQYGLRIPPLSEGGWWLIAGLFLTLISILLWVVRTYKRAEA
LGMSQHLWAFAAAIFFYLVLFIRPVMMSWAKAVPFGIFPHLDWTAAFSIRYGNLYNPFHMLSI
AFYGSALLFAMHGATILSVSRFGGDREIDQITHRGTAEEGAALFWRWTMGFNATMESIHRWAWW
CAVLTIVITAGIGILLSGTVVNDNWYLWAVKHGMAYPEVVTAVNPYET

>d1ocra1 f.2.1.3 (A:) Cytochrome c oxidase {Cow (Bos taurus)}

MFINRWLFSTNHKDIGTLYLLFGAWAGMVGTALESLLIRAELGQPGTLLGDDQIYNVVVTAHAFVMIF
FMVMPIMIGGFNGWLVPLMIGAPDMAFPRMNNMSFWLLPPSFLLLASSMVEAGAGTGWTVYPP
LAGNLAHAGASVDLTFSLHLAGVSSILGAINFITTIINMKPPAMSQYQTPLFVWSVMITAVLLLLSLPV
LAAGITMLLTDRNLNTFFDPAGGGDPILYQHLFWFFGHPEVYILILPGFGMISHIVTYYSQKKEPFGY
MGMVWAMMSIGFLGFIVWAHMHMFTVGMVDVTRAYFTSATMIIAIPITGVKVFWSLATLHGNIKWS
PAMMWALGFIFLFTVGGTGLVLANSSLDIVLHDTYYVVAHFHYVLSMGAVFAIMGGFVHWFPFLFSG
YTLNDTWAKIHFAIMFVGVNMTFFPQHFLGLSGMPRRYSYDPDAYTMWNTISSMGSFISLTAVMLM
VFIIWEAFASKREVLTVDLTTNLEWLNGCPPPYHTFEPTYVNLK

>d1ocrb2 f.2.1.3 (B:1-90) Cytochrome c oxidase {Cow (Bos taurus)}

MAYPMQLGFQDATSPIMEELLHFHDHTLMIVFLISSLVLYIISLMLTTKLHTSTMDAQEVETIWTILP
AIIILIALPSLRILYMMDEI

>d1ocr1 f.2.1.3 (C:) Cytochrome c oxidase {Cow (Bos taurus)}

MTHQTHAYHMVNPSPWPLTGALSALLMTSGLTMWFHNSMTLLMIGLTTNMLTMYQWWRDVIR
ESTFQGHHTPAVQKGLRYGMILFISEVLFFTGFFWAFYHSSLAPTPELGGCWPPTGIHPLNPLEVPL
LNTSVLLASGVSITWAHHSLEMEGDRKHMLQALFITITLGVYFTLLQASEYYEAPFTISDGVYGSTFFVA
TGFHGLHVIIGSTFLIVCFRQLKFHFTSNHHFGFEAGAWYWHFVDVVWLFVLYVSIYWWGS

>d1ocrd1 f.2.1.3 (D:) Cytochrome c oxidase {Cow (Bos taurus)}

SVVKSEDYALPSYVDRRDYPLPDVAHVKNLSASQKALKEKEKASWSSLSIDEKVELYRLKFESFAE
MNRSTNEWKTVVGAAMFFIGFTALLLIWEKHVYVYGPPIHTFEEEWVAKQTKRMLDMKVAPIQGFS
AKWDYDKNEWKK

>d1ocrg1 f.2.1.3 (G:) Cytochrome c oxidase {Cow (Bos taurus)}

ASAAKGDHGGTGARTWRFLTFGLALPSVALCTLNSWLHSGHRERPAFIPYHHLRIRTKPFSWGDGN
HTFFHNPRVNPLPTGYEK

>d1ocri1 f.2.1.3 (I:) Cytochrome c oxidase {Cow (Bos taurus)}

STALAKPQMRGLLARRLFHIVGAFMVSLGFATFYKFAVAEKRRKAYADFYRNYDSMKDFEEMRKA
GIFQSAK

>d1ocrj1 f.2.1.3 (J:) Cytochrome c oxidase {Cow (Bos taurus)}

FENRVAEKQKLFQEDNGLPVHLKGGATDNILYRVMTLCLGGTLYSLYCLGWASFPHK

>d1ocrk1 f.2.1.3 (K:) Cytochrome c oxidase {Cow (Bos taurus)}

APDFHDKYGNVAVLASGATFCVAVVYMATQIGIEWNPSVGRVTPKEWR

>d1ocr11 f.2.1.3 (L:) Cytochrome c oxidase {Cow (Bos taurus)}

SHYEEGPGKNIPFSVENKWRLAMMTLFFGSGFAAPFFIVRHQLLKK

>d1ocrm1 f.2.1.3 (M:) Cytochrome c oxidase {Cow (Bos taurus)}

ITAKPAKTPTSPKEQAIGLSVTFLSFLLPAGWVLYHLDNYKKS

>d1ar1a1 f.2.1.3 (A:) Cytochrome c oxidase {Paracoccus denitrificans}

GFFTRWFMSTNHKDIGILYLFYTAGIVGLISVCFTVYMRMELQHPGVQYMCLEGARLIADASAECTPN
GHLWNVMITYHGVLMMFFVVPALFGGFGNYFMPLHIGAPDMAFPRLNLSYWYVCGVALGVAS
LLAPGGNDQMGSGVWVLYPPLSTTEAGYSMDLAIFAVHVSASSILGAINIITFLNMRAPGMTLFK
VPLFAWSVFITAWLILLSPLVLAGAITMLMDRNFQTFFDPAGGGDPVLYQHILWFFGHPEVYIILP
GFGIISHVISTFAKKPIFYGLPMVLAAMAAIGLGFVVWAHMHMYTAGMSLTQQAYFMLATMTIAVPTGI
KVFWSWIATMWGGSIEFKTPMLWAFGFLFTVGGVTGVVLSQAPLDRVYHDTYYVVAHFHYVMSLG
AVFGIFAGVYVWIGKMSGRQYPEWAGQLHFWMMFIGSNLIFFPQHFLGRQGMPPRYIDYPVEFAYW
NNISSIGAYISFASLFFIGIVFYTLFAGKRVNVPNYWNEHADTLEWTLPSPPPEHTFET

>d1ar1b2 f.2.1.3 (B:1-107) Cytochrome c oxidase {Paracoccus denitrificans}

QDVLGDLPVIGKPVNGGMNFQPASSPLAHDQQWLDHFVLYIITAVTIFVCLLLLICIVRFNRRANPVP
ARFTHNTPIEVIWTLVPLVILVAIGAFSLPILFRSQEMP

>d1qlec1 f.2.1.3 (C:) Cytochrome c oxidase {Paracoccus denitrificans}

AHVKNHDYQILPPSIWPFPGAIGAFVMLTGAVAWMKGITFFGLPVEGPWMFLIGLVGVLYVMFGWW
ADVNEGETGEHTPVVVRIGLQYGFILFIMSEVMFFVAWFVAFIKNALYPMGPDSPKDGVPPEGIV
TFDPWHLPLINTLILLSSGVAVTWAHHAFAVLEGRKTTINGLIVAVILGVCFTGLQAYEYSHAFLA
DTVYAGAFYMATGFHGAHVIIIGTIFLFLVCLIRLLKQMTQKQHVGFEEAAWYWHFVDVVWVWLFV
YIWGR

>d1qled1 f.2.1.3 (D:) Cytochrome c oxidase {Paracoccus denitrificans}

TDHKGEMDIRHQATFAGFIKATWVSILSIAVLVFLALANS

>d1ehka1 f.2.1.3 (A:) Cytochrome c oxidase {Thermus thermophilus, ba3 type}

AYPEKKATLYFLVLGFLALIVGSLFGPFQALNYGNVDAYPLLKRLLPFVQSYQGLTLHGVLNAIVFTQ
LFAQAIMVYLPARELNMRPNMGLMWLSWWMFIGLVVAALPLANEATVLYTFYPPLKGHWFYFL
GASVFLSTWVSIYVLDLWRRWKAANPGKVTPLVTYMAVVFWMWFLASLGLVLEAVLFLLPWS
FGLVEGVDPLVARTLFWWTGHPVYFWLLPAYAIIYTLPKQAGGKLVSDPMARLAFLFLLLSTPVG
HHQFADPGIDPTWKMHSVTLFVAVPSLMTAFTVAASLEFAGRLRGGRLFGWIRALPWNPAFV
APVLGGLGFIPGGAGGIVNASFTLDYVVHNTAWVPGHFHLQVASLTLTAMGSYVLLPNLTGKPID
AQRRLGLAVVWVWFLGMMIMAVGLHWAGLLNVP RRAYIAQVPDAYPHAAPMVFNVLGIVLLVA
LLLFIYGLFSVLLSRERKPELAEAPLPFAEVISGPEDRRLVLAMDRIGFWFAVAAILVVLAYGPTLVQLF
GHLNPVPGWRLW

>d1ehkb2 f.2.1.3 (B:3-40) Cytochrome c oxidase {Thermus thermophilus, ba3 type}

DEHKAHKAILAYEKGWLAFLSLAMLFVFIALIAATLATH

>d1ehkc1 f.2.1.3 (C:) Cytochrome c oxidase {Thermus thermophilus, ba3 type}

EKPKGALAVILVLTILTILVFWLGVYAVFFARG

>d1ffta1 f.2.1.3 (A:) Ubiquinol oxidase {Escherichia coli}

VDHKRLGIMYIIVAVMLLRGFADAIMMRSQQALASAGEAGFLPPHHYDQIFTAHGVMIFFVAMPFV
IGLMNLVPLQIGARDVAFPLNLSFWFTVVGIVLVNLSLGVGEFAQTGWLAYPPLSGIEYSPGVGV
DYWIWSLQLSGIGTTLTGINFFVTILKMRAPGMTMFKMPVFTWASLCANVLIASFILTVTVALLTL
DRYLGTHFFTNMGGNMMYINLIWAWGHPEVYILILPVFGVFSEIAATFSRKRLFYTSLVWATVC
ITVLSFIVWLHFFTMGAGANVNAFFGITTMIIAIP TGVKIFNWLFTMYQGRIVFHSAMLWTIGFIVT
FSVGGMTGVLLAVPGADFLHNSLFLIAHFHNVIIGGVVFGCFAGMTYWWPKAFGKLNWTKR
AFWFWIIGFFVAFMPYALGFMGMTRRLSQIDPQFHTMLMIAASGAVLIALGILCLVIQMYVSIRDR
DQNRDLTGDPWGGRTLEWATSSPPPFYNF

>d1fftb2 f.2.1.3 (B:27-117) Ubiquinol oxidase {Escherichia coli}

SALLDPKGQIGLEQRSLILTAFLMLIVVIPAILMAVGFVWYKIRASNKDAKYSNWSHSNKVEAVVW
TVPIIIIFLAVLTWKTTHALEPS

>d1fftc1 f.2.1.3 (C:) Ubiquinol oxidase {Escherichia coli}

HDAGGTKIFGFWIYLMSCILFSILFATYAVLVNGTAGGPTGKDIFELPFVLVETFLLLFSSITYGMAAI
AMYKNNKSQVISWLALTWLFAGAGFIGMEIYEFHHLIVNGMGPDRSGFLSAFFALVGTHGLHVTSGLI
WMAVLMVQIARRGLTSTNRTRIMCLSLFWHFLDVVVICVFTVVYLMGA

>d1c0va_ f.2.1.4 (A:) Subunit C {Escherichia coli}

MENLNMDLLYMAAAVMMGLAAIGAAIGIGILGGKFLEGAARQPDLIPLLR TQFFIVMGLVDAIPMIAV
GLGLYVMFAVA

>d1c17m_ f.2.1.4 (M:) Subunit A {Escherichia coli}

HGKSKLIAPLALTIFVWVFLMNLMDLLPIDLLPYIAEHLVGLPALRVVPSADVNVTLMSALGVFILILF
YSIKMKGIGGFTKELTLQPFNHWAFIPVNLILEGVSLLSKPVSLGLRFLFGNMYAGELIFILIAGLLPWW
SQWILNVPWAIFHILITLQAFIFMVLTIYVLS

>d1h6ia_f.2.1.5 (A:) Aquaporin-1 {Human (Homo sapiens)}

LFWRAVVAEFLATTLFVVISIGSALGFKYPVGNNTAVQDNVKSLSLAFGLSIATLAQSVGHISGAHLNP
AVTLGLLLSCQISIFRALMYIIAQCVGAIVATAILSGITSSLTGNSLGRNDLADGVNSGQGLGIEIIGTLQL
VLCVLATTDRRRRDLGGSAPLAIGLSVALGHLLAIDYTGCGINPARSFGSAVITHNFSNHWIFWVGPF
GGALAVLIYDFILAP

>d1fx8a_f.2.1.5 (A:) Glycerol uptake facilitator protein GlpF {Escherichia coli}

TLKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLTAGVSGAHLNPAVTIA
LWLFACFDKRKVIPFIVSQVAGAFCAAALVYGLYNNLFFDFEQTHHIVRGSVESVDLAGTFSTYPNPHI
NFVQAFVEMVITAILMGLLALTDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKV
FAWLAGWGNVAFTGGRDIPYFLVPLFGPIVGAIVGAFAYRKLIGRHL

>d1kpk_a_f.2.1.13 (A:) Clc chloride channel {Escherichia coli}

QAARLRRRQLIRQLLERDKTPLAILFMAAVVGTLVGLAAVAFDKGVAWLQNQRMGALVHTADNYPL
LLTVAF LCSAVLAMFGYFLVRKYAPEAGGSGIPEIEGALEDQRPVRRWVRVLPVKFFGGGLTGGGMV
LGREGPTVQIGGNIGRMVLDIFRLKGDEARHTLLATGAAAGLAAAFNAPLAGILFIIEMRPQFRYTLI
SIKAVFIGVIMSTIMYRIFNHEVALIDVGKLSDAPLNTLWLYLILGIIFGIFGPIFNKWVLMQDLLHRV
HGGNITKWVLMGGAIGGLCGLLGFVAPATSGGGFNLIPIATAGNFSMGMLVFIFVARVITLLCFSSGA
PGGIFAPMLALGTVLGTAFGMVAVELFPQYHLEAGTFAIAGMGALLAASIRAPLTGILVLEMTDNYQL
ILPMIITGLGATLLAQFTGGKPLYSAILARTLAKQEAEQL

>d1kpl_a_f.2.1.13 (A:) Clc chloride channel {Salmonella typhimurium}

TPLAILFMAAVVGTTLGLVGVAFKAVSWVQNMRIAGLVQVADHAFLLWPLAFILSALLAMVGYFLV
RKFAPAEAGGSGIPEIEGALEELRPVRRWVRVLPVKFIGGMGTGAGMVLGREGPTVQIGGNLGRMV
DVFRMRSAEARHTLLATGAAAGLSAAFNAPLAGILFIIEMRPQFRYNLISIKAVFTGVIMSSIVFRIFN
GEAPIIEVGLSDAPVNTLWLYLILGIIFGVVGPVFNLSVLRQDMFQRFHGGGEIKKWVLMGGAIGGL
CGILGLIEPAAAGGFFNLPIAAAGNFSVGLLLFIFITRVVTTLLCFSSGAPGGIFAPMLALGTLGTA
FGMAAAVLPQYHLEAGTFAIAGMGALMAASVRAPLTGIVLVLEMTDNYQLILPMIITCLGATLLAQFLG
GKPLYSTILARTLAKQDAEQ

>d1f6ga_f.2.1.11 (A:) Potassium channel protein {Streptomyces lividans}

MPPMLSGLLARLVKLLGRHGSALHWAAAGAATVLLVIVLLAGSYLAVLAERGAPGAQLITYPAALW
WSVETATTVGYGDLYPVTWGRCAVVMVAGITSFGLVTAALATWVFGREQERRGHFVRHSEKAA
EEAYTRTRALHERFDRLERMLDDNRR

>d1jq2a_f.2.1.11 (A:) Potassium channel protein {Streptomyces lividans}

LWGRCAVVMVAGITSFGLVTAALATWVFGREQ

>d1k4cc_f.2.1.11 (C:) Potassium channel protein {Streptomyces lividans}

SALHWRAAGAATVLLVIVLLAGSYLAVLAERGAPGAQLITYPRALWWSVETATTVGYGDLYPVTW
GRCAVVMVAGITSFGLVTAALATWVFGREQERRGH

>d1g4yb_f.2.1.11 (B:) Small conductance potassium channel {Rat (Rattus norvegicus)}

DTQLTKRVKNAAANVLRETWLIYKNTKLVKKIDHAKVRKHQRKFLQAIHQLSVKMEQRKLNDAQ
NTLVDLAKTQLEHHHHH

>d1kkda_f.2.1.11 (A:) Small conductance potassium channel {Rat (Rattus norvegicus)}

RKLELTKAEKHVHNFMMDTQLTKRVKNAAANVLRETWLIYKNTKLVKKIDHAKVRKHQRKFLQAI
HQLSVKMEQRKLNDAQNTLVDLAKTQ

>d1msla_ f.2.1.11 (A:) Gated mechanosensitive channel {Mycobacterium tuberculosis}
ARGNIVDLAVAVVIGTAFTALVTKFTDSIITPLINRIGVNAQSDVIGILRIGIGGGQTIDLNVLLSAAINF
LIAFAVYFLVLPYNTLRKKGEVEQPGDTQVLLTEIR

>d1be3c1 f.2.1.8 (C:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}
MTNIRKSHPLMKIVNNAFIDLPAFISNISSWWNFGSLLGICLILQILTGLFLAMHYTSDTTTAFSSVTHI
CRDVNYGWIIRYMHANGASMFICLYMHVGRGLYGSYTFLETWNIGVILLTVMATAFMGYVLPW
GQMSFWGATVITNLLSAIPYIGTNLVEWIWGGFSVDKATLTRFFAFHFILPFIIMAIAMVHLLFLHET
GSNNPTGISSDVKIPFHPYITIKDILGALLLILALMLLVLFAPDLLGDPDNYTPANPLNTPPHIKPEW
YFLFAYAILRSIPNKLGGVLALAFSILILALIPLLHTSKQRSMMFRPLSQCLFWALVADLLTLTWIGGQP
VEHPYITIGQLASVLYFLLILVLMPTAGTIENKLLKW

>d1be3e2 f.2.1.8 (E:1-69) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}
SHTDIKVPDFSDYRRPEVLDSTKSSKESSEARKGFSYLVATTTTVGVAYAAKNVVSQFVSSMSASADV
L

>d1be3f1 f.2.1.8 (F:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}
AVSASSRWLEGIRKWYYNAAGFNKLGMRDDTIHENDDVKEAIRRLPENLYDDRFRKRALDLISM
RQQILPKEQWTKYEEDKSYLEPYLKEVIRERKEREEWAKK

>d1be3g1 f.2.1.8 (G:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}
GRQFGHLTRVRHVITYSLSPFEQRAFPHYFSKGIPNVLRRTACILRVAPPFVAFYLVYTWGTQEFEEKS
KRKNPAAAYENDR

>d1be3k1 f.2.1.8 (K:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}
RNWVPTAQLWGAVGAVGLVSAT

>d1qcr1 f.2.1.8 (G:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}
GRQFGHLTRVRHVITYSLSPFEQRAFPHYFSKGIPNVLRRTACILRVAPPFVAFYLVYTWGTQEFEEKS
K

>d1qcrh1 f.2.1.8 (H:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}
TTVREQCEQLEKCVKARERLELCDERVSSRSQTEEDCTEELDLHARDHCVAHKLFNSL

>d1qcrk1 f.2.1.8 (K:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}
MLTRFLGPRYRLARNWVPTAQLWGAVGAVGLVSATDSRLILDWV

>d1bcc1 f.2.1.8 (C:) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}
APNIRKSHPLLKMINNSLIDLPAFISNISAWWNFGSLLAVCLMTQILTGLLLAMHYTADTSLAFSSVAH
TCRNVQYGLIRNLHANGASFFIFLHIGRGLYGSYLYKETWNTGVILLTLMATAFVGYVLPWG
QMSFWGATVITNLFSAIPYIGHTLVEWAWGGFSVDNPTLTRFFALHFLLPFAIAGITIIHLTFLHESGS
NNPLGISSDSDKIPFHPYYSFKDILGLTLMLTPFLTLALFSPNLLGDPENFTPANPLVTPPHIKPEWYF
LFAYAILRSIPNKLGGVLALAAASVLILFLIPFLHKSQRMTFRPLSQTLFWLLVANLLILTWIGSQPVE
HPFIIHGQMASLSYFTILLILFPTIGTLENKMLNY

>d1bccd3 f.2.1.8 (D:196-241) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}
PEHHRKRMGLKMLLMGLLVPLVYYMKRHKWSVLKSRKLAYRPPK

>d1bcce2 f.2.1.8 (E:1-69) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}
SHTDIKVPNFSYRRPPDDYSTKSSRES DPSRKGFSYLVAVTTLVGVAYAAKNVVTQFVSSMSASADV
L

>d1bccf1 f.2.1.8 (F:) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}
SRWLEGIRKWYYNAAGFNKYGLMRDDTIYENDDVKEAIRRLPENLYDDRFRKRALDLNMRQQI

LPKEQWTKYEEDVPYLEPYLKEVIRERKEREEWDK
 >d1bccg1 f.2.1.8 (G:) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}
 RQFGHLTRVRHLITYSLSPFEQRPFPHYFSKGVPNVWRRRLRACILRVAPPFLAFYLLYTWGTQEFEEKS
 KRKNPAAAYVN
 >d1bcch1 f.2.1.8 (H:) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}
 LVDPLTTVREQCEQLEKCVKARERLELCDERVSSRSQTEEDCTEELDFDLHARDHCVAHKLFNSLK
 >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)}
 MAFRKSINVYLSLVNSYIIDSPQPSSINYWWNMGSLLGLCLVIQIVTGIFMAMHYSSNIELAFSSVEHIM
 RDVHNGYILRYLHANGASFFFMVMFMHMAKGLYYSYRSPRVTLWNVGVIIFTLTIATAFLGYCCVYG
 QMSHWGATVITNLFSAIPFVGNDIVSWLWGGFSVSNPTIQRFFALHYLVPFIIAAMVIMHLMALHIH
 GSSNPLGITGNLDRIPMHSYFIFKDLVTVFLMFLILALFVFYSPNTLGHPDNYIPGNPLVTPASIVPEW
 YLLPFYAILRSIPDKLLGVITMFAAILVLLVLPFTDRSVVRGNTFKVLSKFFFFIFVFNFVLLGQIGACHV
 EVPYVLMGQIATFIYFAYFLIIVPVISTIENVLFYIGRVNK
 >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)}
 QSFTSIARIGDYILKSPVLSKLCVPVANQFINLAGYKKLGLKFDDLIAEENPIMQTALRRLPEDESYARA
 YRIIRAHQTELTTHLLPRNEWIKAQEDVPYLLPYILEAEAAAKEKDELNDNIEVSK
 >d1ezvg1 f.2.1.8 (G:) Cytochrome bc1 transmembrane subunits {Baker's yeast
 (Saccharomyces cerevisiae)}
 GPPSGKTYMGWWGHMGGPKQKGITSYAVSPYAQKPLQGIFHNAVFNFSFRRFKSQFLYVLIPAGIYWY
 WWKNGNEYNEFLYSKAGREELERVNV
 >d1ezvh1 f.2.1.8 (H:) Cytochrome bc1 transmembrane subunits {Baker's yeast
 (Saccharomyces cerevisiae)}
 VTDQLEDLREHFKNTEEGKALVHHYEECAERVKIQQQQPGYADLEHKEDCVVEEFFHLQHYLDTATA
 PRLFDKLLK
 >d1ezvi1 f.2.1.8 (I:) Cytochrome bc1 transmembrane subunits {Baker's yeast
 (Saccharomyces cerevisiae)}
 SSLYKTFKRNNAVFGTIFAGAFVFTVFDTAITSWYENHNKGKLWKDVKARIAA
 >d1fumc_ f.2.1.9 (C:) Fumarate reductase respiratory complex transmembrane subunits
 {Escherichia coli}
 TTKRKPYPVPMSTSTWWKKLPFYRFYMLREGTAVPAVWFSIELIFGLFALKNGPEAWAGFVDFLQNP
 VIVIINLITLAAALLHTKTWFELAPKAANIIVKDEKMGPEPIIKSLWAVTVVATIVILFVALYW
 >d1fumd_ f.2.1.9 (D:) Fumarate reductase respiratory complex transmembrane subunits
 {Escherichia coli}
 INPNPKRSDEPVFWGLFGAGGMWSAIIAPVMILLVGILLPLGLFPGDALSYERVLAFQAQSFGRVFLFL

MIVLPLWCGLHRMHAMHDLKIHVPAGKWVFGYGLAAILTVVTLIGVVTI

>d1qlac_ f.2.1.9 (C:) Fumarate reductase respiratory complex transmembrane subunits {Wolinella succinogenes}

MTNESILESYSVTPERKKSMPAKLDWWQSATGLFLGLFMIGHMFFVSTILLGDNVMLWVTKKFE
LDFIFEGGKPIVVSFLAAFVFAVIAHAFLAMRKFPINRQYLTFKTHKDLMRHGDTTLWWIQAMTG
FAMFFLGSVHLYIMMTQPQTIGPVSSFRMVSEWMWPLYLVLLFAVELHGVSGLYRLAVKWGWFDG
ETPDKTRANLKKLKTLMMSAFLIVLGLLTFGAYVKKGLEQTPNIDYKYFDYKRTH

>d1jb0a_ f.2.1.12 (A:) Photosystem I {Synechococcus elongatus}

RVVVDNDPVPTSFEKWAKPGHFDRTLARGPQTTTWIWNLHALAHDFDTHTSDELEDISRKIFSAHF
GHLAVVFIWLSGMYFHGAKFSNYEAWLADPTGIKPSAQVWVPIVGGILNGDVGGGFHGIQITSGLF
QLWRASGITNEFQLYCTAIGGLVMAGLMLFAGWFHYHKRAPKLEWFQNVESMLNHHLAGLLGLGS
LAWAGHQIHVSLPINKLLDAGVAAKDIPLPHEFILNPSLMAELYPKVDWGGFFSGVIPFFTFNWAAYS
DLTNGGLNPVTGGLWLSDTAHHHLAIAVLFIIAGHMYRTNWGIGHSLKEILEAHKGPFTGAGHKGL
YEVLTTSWAHQLAINLAMMGSLSIHAQHMYPYPYLAATDYPTQLSLFTHHMWIGGFLVGGAA
HGAIFMVRDYDPAMNQNNVLDRLRHRDAIISHLNWVCIFLGFHSFGLYVHNDTMRAFGRPQDMF
SDTGIQLQPVAQWVQNLHTLAPGGTAPNAAATASVAFGGDVAVGGKVAMMPIVLGTADFVHHI
HAFTIHVTVLILLKGVLFARSSRLIPDKANLGRFPCDGPGRGGTCQVSGWDHVFLGLFWMYNCISV
VIFHFSWKMQSDVWGTVPDGTVSHITGGNFAQSAITINGWLRDFLWAQASQVIGSYGSALSAYGLL
FLGAHFIWAFSLMFLFSGRGYWQELIESIVWAHNKLVAPAIQPRALSIIQGRAVGAHYLLGGIATT
WAFFLARIISVG

>d1jb0b_ f.2.1.12 (B:) Photosystem I {Synechococcus elongatus}

ATKFPKFSQDLAQDPTTRRIWYAIAMAHD FESHGDMTEENLYQKIFASHFGHLAIIFLWVSGSLFHV
AWQGNFEQWVQDPVNTRPIAHAIWDPQFGKAAVDAFTQAGASNPVDIAYSGVYHWWYTIGMRTN
GDLYQGAIFLLILASLALFAGWLHLQPKFRPSLSWFKNAESRLNHHLAGLFGVSSLAWAGHLIHAIP
ESRGQHVGWDNFLSTMPHPAGLAPFFTGNWGVYAQNPD TASHVFGTAQGAGTAILTFLGGFHPQTE
SLWLTDMAHHHLAIAVLFIVAGHMYRTQFGIGHSIKEMMDAKDFFGTKVEGPFNMHPHQGIYETYN
SLHFQLGWHLACLGVITSLVAQHMYSLPPYAFIAQDHTTMAALYTHHQYIAGFLMVGAFAGHAIPLV
RDYDPAQNKGNVLDRLVQHQEAIISHLWSVSLFLGFHTLGLYVHNDVVVAFGTPEKQILIEPVFAQFI
QAAHGKLLYGFDTLLSNPDSIASTAWPNYGNVWLPGWLDAINS GTNSLFLTIGPGDFLVHHAIALGL
HTTTLILVKGALDARGSKLMPDKKDFGYAFPCDGPGRGGTCDISAWDAFYLAMFWMLNTIGWVTF
YWHWKHLGVWEGNVAQFNESSTYLMGWLRDYLWLNSSQLINGYNPFGTNNLSVWAWMFLFGHL
VWATGFMFLISWRGYWQELIETLVWAHERTPLANLVRWKDKPVALSIVQARLVGLAHFSVGYILTYA
AFLIASTAAKF

>d1jb0f_ f.2.1.12 (F:) Photosystem I {Synechococcus elongatus}

DVAGLVPCKDSPAFAQKRAAAVNNTTADPASGQKRFERYSQALCGEDGLPHLVVDGRLSRAGDFLIPS
VLFLYIAGWIGWVGRAYLIAVRNSGEANEKEIIIDVPLAIKMLTGFAWPLAALKELASGELTAKDNEI
TVSPR

>d1jb0i_ f.2.1.12 (I:) Photosystem I {Synechococcus elongatus}

MMGSYAASFLPWIFPVVCWLMPTVVMGLLFLYIEGEA

>d1jb0j_ f.2.1.12 (J:) Photosystem I {Synechococcus elongatus}

MKHFLTYLSTAPVLAIIWMTITAGILIEFNRFYDILLFHPL

>d1jb0k_ f.2.1.12 (K:) Photosystem I {Synechococcus elongatus}

ILCNLFAIALGRYAIQSRGKGPLIALPALFEGFGLPELLATTSFGHLLAAGVVSGL

>d1jb0l_ f.2.1.12 (L:) Photosystem I {Synechococcus elongatus}

LVKPYNGDPFVGHSTPISDSGLVKTFIGNLPAYRQGLSPILRGLEVGMAHG YFLIGPWVKLGPLRDS
DVANLGG LISGIALILVATACLAAYGLVSFQKGGSSDPLKTSEGWSQFTAGFFVGAMGSAFVAFFLLE
NFLVVDGIMTGLFN

>d1jb0m_ f.2.1.12 (M:) Photosystem I {Synechococcus elongatus}
MALTDTQVYVALVIALLPVLAFLRSTELYK

>d1jb0x_ f.2.1.12 (X:) Photosystem I {Synechococcus elongatus}
PTYAFRTFWAVLLLAINFLVAAYYFAAAA

>d1eula_ f.2.1.10 (A:) Calcium ATPase {Rabbit (Oryctolagus cuniculus)}
MEAAHSKSTEECLAYFGVSETTGLTPDQVKRHLEKYGHNELPAEEGKSLWELVIEQFEDLLVRILLLA
ACISFVLAWFEEGEETITAFVEPFVILLILIANAVGVWQERNAENAIEALKEYEPEMGKVYRADRS
VQRIKARDIVPGDIVEVAVGDKVPADIRILSIKSTTLRVDQSILTGESVSVIKHTEPVPDPRAVNQDKKN
MLFSGTNIAAGKALGIVATTGVSTEIGKIRDQMAATEQDKTPLQQLDEFGEQLSKVISLICVAVWLI
NIGHFNDPVHGGSWIRGAIYFKIAVALAVAAIPEGLPAVITTCALGTRRMAKKNIVRSLPSVETLG
CTSVICSDKTGTLTQMSVCKMFHDKVDGDFCSLNEFSITGSTYAPEGEVLKNDKPIRSGQFDGLVE
LATICALCNDSLDFNETKGVYEKVG EATETALTTLVEKMNVFNTEVRNLSKVERANACNSVIRQLM
KKEFTLEFSRDRKSM SVYCSPAKSSRAAVGNKMFVKGAPEGVIDRCNYVRVGTTRVPM TGVPVKEKIL
SVIKEWGTGRDTRLCLALATRDTPPKREEMVLDDSSRFMEYETDLTFVGVVGM LDPPRKEVMGSIQ
LCRDAGIRVIMITGDNKGTAIAICRRIGIFGENEEVADRAYTGREFDDLPLAEQREACRRACCFARVEP
SHKSKIVEYLQSYDEITAMTGDGVNDAPALKKAEIGIAMSGTAVAKTASEMVLADDFSTIVA AVEE
GRAIYNNMKQFIRYLISNVGEVVCIFLTAALGLPEALIPVQLLWVNLVTDGLPATALGFNPPDLDIMD
RPPRSPKEPLISGWLFFRYMAIGGYVGAATVGAAAWWFMYAEDGPGV TYHQLTHFMQCTEDHPHF
EGLDCEIFEAPEPMTMALSVLVTIEMCNALNSLSENQSLMRMPPWVNIWLLGSICLSMSLHFLILYV
DPLPMIFKALKALDLTQWLMVLKISLPVIGLDEILKFIARNYLEG

>d1kzua_ f.3.1.1 (A:) Light-harvesting complex subunits {Purple bacterium
(Rhodopseudomonas acidophila)}

MNQGKIWTVVNP AIGIPALLGSVTVIAILVHLAILSHTTWFPAYWQGGV

>d1kzub_ f.3.1.1 (B:) Light-harvesting complex subunits {Purple bacterium
(Rhodopseudomonas acidophila)}

ATLTAEQSEELHKYVIDGTRVFLGLALVAHFLAFS ATPWLH

>d1lgha_ f.3.1.1 (A:) Light-harvesting complex subunits {Rhodospirillum molischianum}
SNPKDDYKIWLVINPSTWLPVIWIVATVVAIAVHA AVLAAPGFNWIALGAAKSAK

>d1lghb_ f.3.1.1 (B:) Light-harvesting complex subunits {Rhodospirillum molischianum}
RSLSGLT EEEAIAVHDQFKTTFSAFIILAAVAHVLVVWVWKPWF

>d1jo5a_ f.3.1.1 (A:) Light-harvesting complex subunits {Rhodobacter sphaeroides}
ADKSDLGYTGLTDEQAQELHSVYMSGWLWFSAVAIVAHLAVYIWRPWF

>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}
AEVLTSEQA EELHKHVIDGTRVFLVIAAIAHFLAFTLTPW

>d1g90a_ f.4.1.1 (A:) Outer membrane protein A (OMPA) transmembrane domain
{Escherichia coli}

APKDNTWYTGAKLGF SQYHDTGFINNNGP THENQLGAGAFGGYQVNPYVGFEMGYDFLGRMPYKG
SVENGAYKAQGVQLTAKLGY PITDDLDIYTRLGGMVFRADTKSNVYGNHDTGVSPVFAGGVEYAIT
PEIATRLEYQFTN NIGDAHTIGTRPDNGMLSLGVS YRFGQGEAA

>d1qjpa_ f.4.1.1 (A:) Outer membrane protein A (OMPA) transmembrane domain {Escherichia coli}

APKDN TWYTGAKL GWSQYHDTGLIN NNGP THENKLGAGAFGGYQVNPYVGFEMGYDWLGRMPY
KGSVEN GAYKAQGVQLTAKLGY PITDDLDIYTRLGGMVWRADTYSNVY GKNHDTGVSPVFAGGVEY
AITPEIATRLEYQWTNNIGDAHTIGTRPDNGM LSLGVSYRFG

>d1qj8a_ f.4.1.1 (A:) Outer membrane protein X (OMPX) {Escherichia coli}

ATSTVTGGYAQSDAQGQMNMKGGFNLKYRYEEDNSPLGVIGSFTYTEKSRTASSGDYKNKNQYYGITA
GPAYRINDWASIYGVVGVGYGKFQTTEYPTYKNDTSDYGF SYGAGLQFNPMENVALDFSYEQSRIRSV
DVGTW IAGVGYRF

>d1i78a_ f.4.4.1 (A:) Outer membrane protease OMPT {Escherichia coli}

STETLSFTPDNINADISLGTLSGKTKERVYLAEEGG RKVSQLDWKFNNAIIKGA INWDLMPQISIGA
AGWTTLGSRRGNMVDQDWMDSSNPGTWTDEARHPDTQLNYANEFDLNIKGWLLNEPNYRLGLM
AGYQESRYSFTARGGSYIYSSEEGFRDDIGSFPNGERAIGYKQRFKMPYIGLTGSYRYEDFELGGTFKYS
GWVESSDNDEHYDPKGRITYRSKVKDQNYYSVAVNAGYYVTPNAKVYVEGAWNRVTNKKGNTSLY
DHNNNTSDYSKNGAGIENYFITTAGLK YTF

>g1qd6.1 f.4.2.1 (A;C:) Outer membrane phospholipase A (OMPLA) {Escherichia coli}

AVRGSIIANMLQEXFTLYPYDTNYLIYTQTS DLNKEAIASYDWAENARKDEVKFQLSLAFPLWRGILG
PNSVLGASYTQKSWWQLSNSEESSPFRETN YEPQLFLGFATDYRFAGWTLRDVEMGYNHDSNGRS
DPTSRSWNRLYTRLMAENGNWLVEVKPWYVVGNTDDNPDITKYM GYYQLKIGYHLGDAVLSAKGQ
YNWNTGYGGAELGLSYPITKHVRLYTQVYSGYGESLIDYNFNQTRVGVGVMLNDLF

>d1hxxa_ f.4.3.1 (A:) Porin {Escherichia coli, different sequences}

AEIYNKDG NKVDLYGKAVGLHYFSKNGENSYGGNGDMTYARLGFKGETQINSDLTGYGQWEYNFQ
GNNSEGADAQTGNKTR LAFAGLKYADVGSFDYGRNYGVVFDALGYTDMLPEFGGDTAYSDDFFVGR
VGGVATYRNSNFFGLVDGLNFAVQYL GKNERDTARRSNGDGVGGSISYEYEGFGIVGAYGAADR TNLQ
EAQPLGNGKKA EQWATGLKYDANNIYLAANYGETRNATPITNKFTNTSGFANKTQDVLVAQYQFD
FGLRPSIAYTKSKAKDVEGIGD VDLVNYFEVGATYYFNKNMSTYVDYIINQIDSDNKLGVGSDDTVAV
GIVYQF

>d1pho_ f.4.3.1 (-) Porin {Escherichia coli, different sequences}

AEIYNKDG NKLDVYGKVKAMHYMSDNASKDGDQSYIRFGFKGETQINDQLTGYGRWEAEFAGNKA
ESDTAQKQTRLAFAGLKYKDLGSFDYGRNLGALYDVEAWTDMFPEFGGDS SAQTDNFMTKRASGLA
TYRNTDFFGVIDGLNLT LQYQGKNENRDVKKQNGDGFGTSLTYDFGGSDFAISGAYTNSDR TNEQNL
QSRGTGKRAEAWATGLKYDANNIYLATFYSETRKMT PITGGFANKTQNF EAVAQYQFD FGLRPSLGY
VLSKGDIEGIGDEDLVN YIDVGATYYFNKNMSAFVDYKINQLDSDNKL NINND DIVAVGMTYQF

>d2por_ f.4.3.1 (-) Porin {Rhodobacter capsulatus}

EVKLSGDARMGVMYNGDDWNFSSRSRVLFTMSGTTDSGLEFGASFKAHESVGAETGEDGTVFLSGA
FGKIEMGDALGASEALFGDLYEVGYTDLDDRGGNDIPYLTGDERLTAEDNPVLLYTY SAGAFSVAASM
SDGKVGETSEDDAQEMAVAAAYTFGNYTVGLGYEKIDSPD TALMADMEQLELAAIAKFGATNVKAY
YADGELDRDFARAVFDLTPVAAAATAVDHKAYGLSVDSTFGATTVGGYVQVLDIDITDDV TYYYGLGAS
YDLGGGASIVGGIADNDLPNSDMVADLGVKFKF

>d3prn_ f.4.3.1 (-) Porin {Rhodopseudomonas blastica, strain DSM2131}

MISLNGYGRFGLQYVEDR GVGLEDTHISSRLRINIVGTTETDQGVTFGAKLRMQWDDGDAFAGTAGN
AAQFWTSYNGVTVSVGNVD TAFDSVALTYDSEMGEWSSFGDAQSSFFAYNSKYDASGALDNYNGIA
VTYSISGVNLYLSYVDPDQTV DSSLVTEEFGIAADWSNDMISLAAAYTTDAGGIVDNDIAFVGAAYKF
NDAGTVGLN WYDNLSTAGDQVTLYGN YAFGATTVRAYVSDIDRAGADTAYGIGADYQFAEGVKVSG

SVQSGFANETVADVGVRFDF

>d1osma_f.4.3.1 (A:) Porin {Klebsiella pneumoniae}

AEIYNKDGKLDLYGKIDGLHYFSDDKDVKDQTYMRLGVKGETQINDQLTGYGQWEYNVQANNT
ESSSDQAWTRLAFAGLKFGDAGSFDYGRNYGVVYDVTSWTDVLPFEGGDTYGSDFLQSRANGVAT
YRNSDFFGLVDGLNFALQYQGNKSVSGEGATNNGRGALKQNGDGFSTVYDIFDGISAGFAYANS
KRTDDQNQLLLGEGDHAETYTGGLKYDANNIYLATQYTQTYNATRAGSLGFANKAQNFVAAQYQF
DFGLRPSVAYLQSKGKDLNGYGDQDILKYVDVGATYYFNKNMSTYVDYKINLLDDNSFTRSAGISTD
DVVALGLVYQF

>d1e54a_f.4.3.1 (A:) Porin {Comamonas acidovorans}

ESSVTLFGIVDTNVAYVNKDAAGDSRYGLTSGASTSRLGLRGTEDLGGGLKAGFWLEGEIFGDDGN
ASGFNFKRRSTVLSGNFGEVRLGRDLVPTSQKLTSYDLFSATGIGPFMGFRNWAAGQGADDNGIRA
NNLISYYTPNFGGFNAGFGYAFDEKQTIGTADSVGRYIGGYVAYDNGPLSASLGLAQKTAVGGGLTD
RDEITLGASYNFVAKLSGLLQQTQKFKRDIGDIIKTSNYMLGASAPVGGVGEVKLQYALYDQKAIDSK
AHQITLGYVHNSKRTALYGNLAFLNKDASTLGLQAKGVYAGGVQAGESQTVGVQVIRHAF

>d1af6a_f.4.3.2 (A:) Maltoporin (also LamB protein) {Escherichia coli}

VDFHGYARSGIGWTGSGGEQQCFQTTGAQSKYRLGNECETYAELKLGQEVWKEGDKSFYFDTNVAY
SVAQQNDWEATDPAFREANVQGNLIEWLPGSTIWAGKRFYQRHVDVHMIDFYWDISGPGAGLEN
IDVGFGLSLAATRSSEAGSSSFASNNIYDYTNETANDVFDVRLAQMEINPGGTLELGVYGRANLR
DNYRLVDGASKDGWLFTEHTQSVLKGFNKFVVQYATDSMTSQGKLSQSGVAFDNEKFAYNINN
NGHMLRILDHGAISMGDNDMMYVGMQDINWDNDNGTKWWTVGIRPMYKWTPI MSTVMEIG
YDNVESQRTGDKNNQYKITLAQQWQAGDSIWSRPAIRVFATYAKWDEKWGYDYTGADNANNANFG
KAVPADFNNGSFGRGDSDEWTFGAQMEIWW

>d2mpa_f.4.3.2 (A:) Maltoporin (also LamB protein) {Salmonella typhimurium}

VDFHGYARSGIGWTGSGGEQQCFQATGAQSKYRLGNECETYAELKLGQEVWKEGDKSFYFDTNVAY
SVNQQNDWESTDPAFREANVQGNLIEWLPGSTIWAGKRFYQRHVDVHMIDFYWDISGPGAGIENI
DLGFGKLSLAATRSTEAGGSYTFSSQNIYDEVKDTANDVFDVRLAGLQTNPDGVLELGVYGRANTT
DGYKLADGASKDGWMFTAHTQSMKGYNKFVVQYATDAMTTQGGKQARGSDGSSSFTEKINYAN
KVINNNGMWRILDHGAISLGDKWDLMYVGMQDINWDNDNLGTEWWTVGVRPMYKWTPI MST
LLEVGYDNVKSQQTGDRNNQYKITLAQQWQAGDSIWSRPAIRIFATYAKWDEKWGYIKDGDNISRY
AAATNSGISTNSRGDSDEWTFGAQMEIWW

>d1a0tp_f.4.3.2 (P:) Sucrose-specific porin {Enterobacterium (Salmonella typhimurium)}

SGFEFHGYARSGVIMNDSGASTKSGAYITPAGETGGAIGRLGNQADTYVEMNLEHKQTLDNQATTRF
KVMVADGQTSYNDWTASTSDLNVRQAFVELGNLPTFAGPFKSTLWAGKRFDRDNFDIHWIDSDV
VFLAGTGGGIYDVKWNGLRSNFSLYGRNFGDIDSSNSVQNYILTMNHFAGPLQMMVSGLRKDN
DERKDSNGLAKGDAANTGVHALLGLHNSFYGLRDGSSKTALLYGHGLGAEVKIGSDGALRPGA
DTWRIASYGTTPLSENWSVAPAMLAQRSKDRYADGDSYQWATFNLRLIQAINQNFALAYEGSYQYM
DLKPEGYNDRQAVNGSFYKLTFAPTFKVGSIGDFFSRPEIRFYTSWMDWSKLNLYASDDALGSDGF
NSGGEWSFGVQMETWF

>d1by5a_f.4.3.3 (A:) Ferric hydroxamate uptake receptor FhuA {Escherichia coli}

QESAWGPAATIAARQSATGKTDTPIQKVPQSISVVTAEEMALHQPKSVKEALSYTPGVSVGTRGAS
NTYDHLIIRGFAAEGQSQNNYLNLKLGQNFYNDVIDPYMLERAEIMRGPVSVLYGKSSPGGLLNM
VSKRPTTEPLKEVQFKAGTDSLFTGDFSDSLDDDGVYSYRLTGLARSANAQQKGSEEQRYAIAPAF
TWRPDDKTNFTFLSYFQNEPETGYYGWLKPEGTVEPLNGKRLPTDFNEGAKNNTYSRNEKMGVY
SFDHEFNDFTVRQNLRAENKTSQNSVYGYVCSDPANAYSQKCAALAPADKGYLARKYVVDDE

KLQNFSDVTQLQSKFATGDIDHTLLTGVD FMRMRNDINAWFGYDDSVPLLNLYNPVNTDFDFNAK
DPANSGPYRILNKQKQTGVYVQDQAQWDKVLVTLGGRYDWADQESLNRVAGTTDKRDDKQFTWR
GGVNYLFDNGVTPYFYSSESFEPSQVKGDNIFAPSKGKQYEVGVKYPEDRPIVVTGAVYNLTKTN
NLMADPEGSFFSVEGGEIRARGVEIEAKRPLSASVNVVGSYTYTDAEYTTDTTYKGNTPAQVPKHMA
SLWADYTFFDGPLSGLTLGTGGRYTGSSYGPANSFKVGSYTVVDALVRYDLARVGMAGSNVALHVN
NLFDREYVASCFTYGCFWGAERQVVATATFRF

>d1fepa_f.4.3.3 (A:) Ferric enterobactin receptor FepA {Escherichia coli}

DDTIVVTAEEQLQAPGVSTITADEIRKNPVARVDSKIIRTMPGVNLTGNSTSGQRGNRQIDIRGMG
PENTLILIDGKPVSSRNSVRQGWGERDTRGDTSWVPPEMIERIEVLRGPAAARYGNGAAGGVNII
TKKSGSEWHGSDAYFNAPEHKEEGATKRTNFSLTGPLGDEF SFRLYGNLDKTQADAWDINQGHQ
SARAGTYATTLPAGREGVINKDINGVVRWDFAPLQSLLEAGYSRQGNLYAGDTQNTNSDSYTRSKY
GDETNRLYRQNYALTWNGGWDNGVTTSNWVQYEHTRNSRIPEGLAGGTEGKFNEKATQDFVDIDL
DDVMLHSEVNLPIDFLVNQTLTLGTEWNQQRMKDLSNTQALTGTNTGGAIDGVSTTDRSPYSKAE
IFSLFAENMELTDSTIVTPGLRFDHHSIVGNNWSPALNISQGLGDDFTLKMGIARAYKAPSLYQTNP
NYILYKGGQCYASAGGCYLQGNDDLKAETSINKEIGLEFKRDGWLAVTWFNRNDYRNKIEAGYVAV
GQNAVGTDLQWQDNVPAKAVVEGLEGLSLNVPVSETVMWTNNITYMLKSENKTTGDRLSIIPEYTLNS
TLWQAREDLQMOTTFWYWGKQPKKYNKYKQPAVGPETKEISPYIVGLSATWDVTKNVSLTGGV
DNLFDKRLWRAGNAQTTGDLAGANYIAGAGAYTYNEPGRTWYMSVNTHF

>d1ek9a_f.5.1.1 (A:) Integral outer membrane protein TolC, efflux pump component
{Escherichia coli}

ENLMQVYQARLSNPELRKSAADRDAAFEKINEARSPLLPQLGLGADYTSNGYRDANGINSNATSA
SLQLTQSIFDMSKWRALTLQEKAAGIQDVTYQTDQQTLLINTATAYFNVLNAIDVLSYTAQKEAIYR
QLDQTTQRFNVGLVAITDVQNARAQYD TVLANELTARNLNDNAVEQLRQITGNYPPELAALNVENF
KTDKQPVNALLKEAEKRNL SLLQARLSQDLAREQIRQAQDGHLPTLDLTA STGISDTSYSGSKTRGA
AGTQYDDSNMGQNKVGLSFLPIYQGGMVNSQVKQAQYNFVGASEQLESAHRSVVQTVRSSFNNIN
ASISSINAYKQAVVSAQSSLDAMEAGYSVGTTRTIVDVL DATTTLYNAKQELANARYNYLINQLNIKSAL
GTLNEQDLLALNNALS KPVSTNPE

>d7ahla_f.6.1.1 (A:) Alpha-hemolysin {Staphylococcus aureus}

ADSDINIKTGTTDIGSNTTVKTDGLVTDYDKENGMHKKVFYSFIDDKNHNKLLVIRTKGTIAGQYRV
YSEEGANKSGLAWPSAFKVQLQLPDNEVAQISDYPRNSIDTKEYMSTLT YGFNGNVTGDDTGKIGG
LIGANVSIGHTLKYVQPDFK TILESPTDKKVGWVKVIFNNMVNQNWGPYDRDSWNPVYGNQLFMKT
RNGSMKAADNFLDPNKASSLLSSGFSPDFATVITMDRKASKQQT NIDVIYERVRDDYQLHWTSTNW
KGTNTKDKWTD RSSERYKIDWEKEEMTN

>d1pvl_f.6.1.1 (-) Leucocidin K component LukF-PV {Staphylococcus aureus}

AQHITPVSEKKVDDKITLYKTTATSDSKL KISQILTFNFIKDKSYDKDTLILKAAGNIYSGYTKPNPK
DTISSQFYWGSKY NISINSDSNDSVNVVDYAPKNQNEEFQVQQT VGYSGGDINISNGLSGGGNGSKS
FSETINYKQESYRTSLDKRTNFKKIGWDVEAHKIMNNGWGPYGRDSYHSTYGNEMFLGSRQSNLNA
GQNFLEYHKMPVLSRGNFNF EFIGVLSRKQNAAKKSKITV TYQREMDRYTNFWNQLHWIGNNYKD
ENRATHTSIYEVDWENHTV KLIDTQSKEKNPMS

>d3lkfa_f.6.1.1 (A:) Leucocidin F (HlgB) {Staphylococcus aureus}

EGKITPVSVKVDKVTLYKTTATADSKFKISQILTFNFIKDKSYDKDTLVLKATGNINS GFVKPNPN
DYDFSKLYWGAKYNVSISSQSNDSVNVVDYAPKNQNEEFQVQNTLGYTFGGDISISNGLSGGLNGNT
AFSETINYKQESYRTLSRNTNYKNVGVGVEAHKIMNNGWGPYGRDSFHPTYGNELFLAGRQSSAY
AGQNFIAQHQMPLLSRSNFNPEFLSVLSHRQDGAKKSKITV TYQREMDLYQIRWNGFYWAGANYKN

FKTRTFKSTYEIDWENHKVLLDTKETENNK

>d1prea2 f.8.1.1 (A:85-470) (Pro)aerolysin, pore-forming lobe {*Aeromonas hydrophila*}
IPTLSALDIPDGDEVDVQWRLVHDSANFIKPTSYLAHYLGAWVGGNHSQYVGEDMDVTRDGDGW
VIRGNNDGGCDGYRCGDKTAIKVSNFAYNLDPDSFKHGDVTQSDRQLVKTVVGWAVNDSPTQSGY
DVTLRYDTATNWSKTNTYGLSEKVTTKNKFKWPLVGETELSIIEAANQSWASQNGGSTTTLSQSVR
PTVPARSKIPVKIELYKADISYPYEFKADVSYDLTSLGFLRWGGNAWYTHPDNRPNWNHTFVIGPYK
DKASSIRYQWDKRYIPGEVKWWDWNWTIQQNGLSTMQNNLARVLRPVFRAGITGDFSAESQFAGNI
EIGAPVPLAADSKVRRARSVDGAGQGLRLEIPLDAQELSGLGFNNVSLSVTPAANQ

>d1pfo_ f.9.1.1 (-) Perfringolysin {*Clostridium perfringens*}
DITDKNQSIDSGISSLSYNRNEVLASNGDKIESFVPKEGKAGNKFIVVERQKRSLTSPVDISIIDSVN
DRYTPGALQLADKALVENRPTILMVKRKPININIDLPLKGENSIKVDPTYGKVSQAIDELVSKWNE
KYSSTHTLTPARTQYSESMVYSKQISSALNVNAKVLNSLGVDFNAVANNEKKVMILAYKQIFYTVSA
DLPKNPSDLFDDSVTFNDLKQKGVSNAPPLMVSNAVAYGRTIYVKLETTSSSKDVQAFAKALIKNTDI
KNSQQYKDIYENSSTAVVLGGDAQEHNKVVTKDFDEIRKVIKDNATFSTKNPAYPISYTSVFLKDNS
VAAVHNKTDYIETTSTEYSKGINLDHSGAYVAQFEVAWDEVSYDKEGNEVLTHKTWDGNYQDKTA
HYSTVIPLEANARNIRIKARECTGLAWEWWRDWISEYDVPLTNNINVISIWGTTLYPGSSITYN

>d1svb_2 f.10.1.1 (1-302) Envelope glycoprotein, central and dimerisation domains
{Tick-borne encephalitis virus}
SRCTHLENRDFVTGTQGTTRVTLVLELGGCVTITAEGKPSMDVWLDIAIQENPAKTREYCLHAKLSD
TKVAARCPTMGPATLAEHQGGTVCKRDQSDRGWGNHCGLFGKGSIVACVKAACEAKKATGHVY
DANKIVYTVKVEPHTGDYVAANETHSGRKTASFTISSEKTILTMGEYGDVSLLCRVASGVDLAQTVIL
ELDKTVEHLPTAWQVHRDWFNDLALPWKHEGAQNWNNNAERLVEFGAPHAVKMDVYNLGDQTG
VLLKALAGVPVAHIEGTYHLKSGHVTCEVGLEKLMKGL

>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}
DGRPLAAAGIVVTGDKAVNIYTSSQTGSIIKLLXQITSPALTQLTIQALYNLAGGNMDYLLTKLGVGNN
QLSSLISSGLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRATYLETLSVSTTKGFASALVPKVVTQVGS
VIEELDTSYCIETDLDLYCTRIVTFPMSPGIYSLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMT
TCRCADPPGIISQNYGEAVSLIDRQSCNLSLDGITLRLSGEFDATYQKNISIQDSQ

>d1acc_ f.11.1.1 (-) Anthrax protective antigen {*Anthrax bacillus* (*Bacillus anthracis*)}
SSSQGLLGYFSDLNQAPMVVTSSTTGDLSPSSELENIPSENQYFQSAIWSGFIKVKKSDEYTFATS
ADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQRENPTKGLDFKLYWTDSONKKEVISS
DNLQLPELKQKSSNSRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKG
LTKYKSSPEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENILSKNEDQSTQNTD
SETRTISKNTSTSRHTSEVHGNAEVHASFFDIGGSVSAGFNSNSSTVAIDHSLSLAGERTWAETMG
LNTADTARLNANIRYVNTGTAPIYNVLPSTSLVLGKNQTLATIKAKENQLSQILAPNNYPSKNLAPI
ALNAQDDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIAATYNFENGRVVRVDTGSNWSEVLPQIQ
ETTARIIFNGKDLNLVERRIA AVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNLQYQGDITEFDNF
FDQQT SQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDRNNIAVGADES VVKEAHREVI
NSSTEGLLL NIDKDIRKILSGYIVEIEDTEGLKEVINDRYDMLNISSLRQDGKTFIDFKKYNDKLPYIS
NPNYKVVVYAVTKENTIINPSENGDTSTNGIKKILIFS 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)}
FVNQHLCGSHLVEALYLVCGERGFFYTPKTRRYPGDVVRGIVEQCCTSICSLYQLENYCN
>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)}
EVNQHLCSSELVEALELVCGERGFFYEPKXGIVEQCCTSICSLYQLENYCN
>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)}
NQHLCSHSLVEALYLVCGERGFFXGIVEQCCTSICSLYQLENYCN
>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)}
GPETLCGAELVDALQFVCGDRGFYFNKPGIVDECCFRSCDLRRLRLEMYCAPLPAKSA
>d1igl_g.1.1.1 (-) Insulin-like growth factor {Human (Homo sapiens)}
AYRPSSETLCGGELVDTLQFVCGDRGFYFSRPASRVSRRSRGIVEECCFRSCDLALLETYCATPAKSE
>d1imxa_g.1.1.1 (A:) Insulin-like growth factor {Human (Homo sapiens)}
ETLCGAELVDALQFVCGDRGFYFNKPTGYGSSRRAPQTGIVDECCFRSCDLRRLRLEMYCAPL
>d2gf1_g.1.1.1 (-) Insulin-like growth factor {Human (Homo sapiens)}
GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSRRAPQTGIVDECCFRSCDLRRLRLEMYCAPLPAK
SA
>d3lria_g.1.1.1 (A:) Insulin-like growth factor {Human (Homo sapiens)}
MFPAMPLSSLFVNGPRTLGAELVDALQFVCGDRGFYFNKPTGYGSSRRACQTGIVDECCFRSCDLR
RLEMYCAPLPAKSA
>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}
STQSNKKDLCEHYRQIAKESCKKGFVLDGTDGACFGAQIMVAAKGC
>d1vib_g.2.2.1 (-) Neurotoxin B-IV {Milky ribbon worm (Cerebratulus lacteus)}
ASATWGAAYPACENNCRRKDYDLRCQGWAGKRGKCAAHCHIQKNNCKGKCKKE
>d1wgta3 g.3.1.1 (A:87-129) Wheat germ agglutinin (WGA) {Wheat (Triticum vulgaris)}
IKCGSQAGGKLCNNLCCSQWGYCGLGSEFCGEGCQNGACSTD
>d2cwga2 g.3.1.1 (A:53-86) Wheat germ agglutinin (WGA) {Wheat (Triticum vulgaris)}

ATCTNNQCCSQYGYCGFGAEYCGAGCQGGPCRAD
 >d9wga1 g.3.1.1 (A:1-52) Wheat germ agglutinin (WGA) {Wheat (Triticum vulgaris)}
 ERGEGQSNMECPNNLCCSQYGYCGMGGDYCGKGCQNGACWTSKRCSQAGG
 >d9wga2 g.3.1.1 (A:53-86) Wheat germ agglutinin (WGA) {Wheat (Triticum vulgaris)}
 ATCPNNHCCSQYGHCGFGAEYCGAGCQGGPCRAD
 >d9wga3 g.3.1.1 (A:87-129) Wheat germ agglutinin (WGA) {Wheat (Triticum vulgaris)}
 IKCGSQSGGKLCPNLCCSQWGFCLGSEFCGGGCQSGACSTD
 >d9wga4 g.3.1.1 (A:130-171) Wheat germ agglutinin (WGA) {Wheat (Triticum vulgaris)}
 KPCGKDAGGRVCTNNYCCSKWGS CGIGPYCGAGCQSGGCDA
 >d1ehda1 g.3.1.1 (A:1-45) Isolectin VI {Stinging nettle (Urtica dioica), UDA}
 ERGCSQGGGATCPGLRCCSIWGWCGDSEPYCGRTCENKCWSGERS
 >d1ehda2 g.3.1.1 (A:46-89) Isolectin VI {Stinging nettle (Urtica dioica), UDA}
 DHRCGA AVGNPPCGQDRCCSVHGWCGGGNDYCSGGKCYRCS
 >d1en2a1 g.3.1.1 (A:1-45) Isolectin VI {Stinging nettle (Urtica dioica), UDA}
 ERGCSQGGGTC PALWCCSIWGWCGDSEPYCGRTCENKCWSGERS
 >d1en2a2 g.3.1.1 (A:46-86) Isolectin VI {Stinging nettle (Urtica dioica), UDA}
 DHRCGA AVGNPPCGQDRCCSVHGWCGGGNDYCSGSKCYR
 >d1hev_ g.3.1.1 (-) Hevein {Hevea brasiliensis}
 EQCGRQAGGKLCPNLCCSQWGWCGSTDEYCS PDHNCQSNCKD
 >d1mmc_ g.3.1.2 (-) Antimicrobial peptide 2, AC-AMP2 {Tassel (Amaranthus caudatus)}
 VGECVRGRCPSGMCCSQFGYCGKGPKYCGR
 >d1f2si_ g.3.2.1 (I:) Trypsin inhibitor {Bitter melon (Momordica charantia), linn.
 Cucurbitaceae, seed}
 RICPRIWMECKRSDCMAECICVMGHCG
 >d1mcti_ g.3.2.1 (I:) Trypsin inhibitor {Bitter melon (Momordica charantia), linn.
 Cucurbitaceae, seed}
 RICPRIWMECTRSDCMAKICVAGHCG
 >d2stai_ g.3.2.1 (I:) Trypsin inhibitor {Squash (Cucurbita maxima)}
 RVCPRILMECKKSDCLAECVLEHGYCG
 >d1ha9a_ g.3.2.1 (A:) Trypsin inhibitor {Spiny bitter melon (Momordica cochinchinensis),
 MCOTI-II}
 SGSDDGGVCPKILKCRSDCPGACICRGNGYCG
 >d2btci_ g.3.2.1 (I:) Trypsin inhibitor {Vegetable marrow (Cucurbita pepo)}
 RVC PKILMECKKSDCLAECVLEHGYCG
 >d2let_ g.3.2.1 (-) Trypsin inhibitor {Jumping cucumber (Ecballium elaterium)}
 GCPRLLMRCKQSDCLAGCVCGPNGFCG
 >d4cpai_ g.3.2.1 (I:) Carboxypeptidase A inhibitor {Potato}
 ZHADPICNKPKTHDDCSGAWFCQACWNSARTCGPYV
 >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)}
 SWPVCTRNLPCVGETCVGGTCNTPGCTC
 >d1df6a_ g.3.3.2 (A:) Cycloviolacin O1 {Plant (Viola odorata)}

SCVYIPCTVTALLGCSCSNRVCYNGIPCAE
>d1bh4_ g.3.3.3 (-) Circulin A {Chassalia parviflora}
CGESCWVWIPICISAALGCSCKNKVCYRNGIP

>d1c4ea_ g.3.4.1 (A:) Gurmarin, a sweet taste-suppressing polypeptide {Gymnema sylvestre}
EQCVKKDELCPYYLDCCEPLECKKVNWWDHKCIQ

>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}
CVRLHESCLGQQVPCCDPCATCYCRFFNAFCYCRKLG TAMNPCSRT

>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}
ACSGRGRCPPQCCMGLRCGRGNPQKCI GAHEDV

>d1cnna_ g.3.6.1 (A:) Conotoxin {Sea snail (Conus magus), M VIIc}
CKGKGAPCRKTM YDCCSGSCGRRGKC

>d1omg_ g.3.6.1 (-) Conotoxin {Sea snail (Conus magus), M VIIa}
CKGKGAKCSRLMYDCCTGSCRS GKC

>d1mvj_ g.3.6.1 (-) Conotoxin {Conus striatus, S VIb}
CKLKGQSCRKTSYDCCSGSCGRSGKC

>d1fyga_ g.3.6.1 (A:) Conotoxin {Conus striatus, SO3}
CKAAGKPCSRIAYNCCTGSCRS GKC

>d1kcp_ g.3.6.1 (-) Conotoxin {Conus purpurascens, kappa-pVIIa}
CRIPNQKCFQHLDCCSRKCNRFNKCV

>d1eyoa_ g.3.6.1 (A:) Conotoxin {Conus tulipa, T VIIa}
SCSGRDSRCP PVCCMGLMCSR GKCVSIYGE

>d1g1za_ g.3.6.1 (A:) Conotoxin {Conus ermineus, E VIa}
DDCIKPYGFCSLPILKNGLCCSGACVGCADL

>d1f3ka_ g.3.6.1 (A:) Conotoxin {Conus textile, Tx VII}
CKQADEPCDV FSLDCCTGICLGVC MW

>d1agg_ g.3.6.2 (-) omega-Agatoxin IV, IVa, IVb {Funnel web spider (Agelenopsis aperta)}
EDNCIAEDYGKCTWGGTKCCRGRPCRC SMIGTNCECTPRLIMEGLSFA

>d1oav_ g.3.6.2 (-) omega-Agatoxin IV, IVa, IVb {Funnel web spider (Agelenopsis aperta)}
KKKCIADYGRCKWGGTPCCRGRGCICSIMGTNCECKPRLIMEGLGLA

>d1omb_ g.3.6.2 (-) omega-Agatoxin IV, IVa, IVb {Funnel web spider (Agelenopsis aperta)}
CIAEDYGKCTWGGTKCCRGRPCRC SMIGTNCECTP

>d1eit_ g.3.6.2 (-) mu-Agatoxin-I {Funnel web spider (Agelenopsis aperta)}
ECVPENHCRD WYDECCEGFYCSQRPPKICRNNN

>d1kqha_ g.3.6.2 (A:) ACTX-HI:OB4219 {Funnel-web spider (Hadronyche infensa)}
KCLAEAADCS PWSGDSCCKPYLCSCIFFYPCSRPKG W

>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)}

CIPSGQPCYPNENCCSQSCTGGRC

>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)}

CAKKRNWCGKNEDECCCPMKCIYAWYNQQGSCQTTITGLFKKC

>d1qk6a_ g.3.6.2 (A:) Huwentoxin-I {Chinese bird spider (Selenocosmia huwena)}

ACKGVFDACPTPGKNECCPNRVCSDKHKWCKWKL

>d1i25a_ g.3.6.2 (A:) Huwentoxin-II {Chinese bird spider (Selenocosmia huwena)}

LFECFSCEIEKEGDKPCKKKKCKGGWKCKFNMCVKV

>d1qk7a_ g.3.6.2 (A:) Lectin SHL-I {Chinese bird spider (Selenocosmia huwena)}

GCLGDKDYNNGCCSGYVCSRTWKWCVLGPW

>d1d1ha_ g.3.6.2 (A:) Hanatoxin 1 {Tarantula (Grammostola spatulata)}

ECRYLFGGCKTTSDCCKHLGCKFRDKYCAWDFTFS

>d1emxa_ g.3.6.2 (A:) Heteropdatoxin 2, hptx2 {Spider (Heteropodidae venatoria)}

DDCGKLFSGCDTNADCCGYVCRLWCKLDW

>d1c6wa_ g.3.6.2 (A:) Maurocalcin {Scorpio maurus}

GDCLPHLKLCKENKDCCKKRRGTNIEKRRCR

>d1i26a_ g.3.6.3 (A:) PTU-1 {Assassin bug (Peirates turpis)}

AEKDCIAPGAPCFGTDPCCNPRAWCSSYANKCL

>d1jzaa_ g.3.7.1 (A:) Scorpion toxin {Centruroides sculpturatus ewing, variant 2}

KEGYLVNKSTGCKYGLKLGGENEGCDKECKAKNQGGSYGYCYAFACWCEGLPESTPTYPLPNKSCS

>d2sn3_ g.3.7.1 (-) Scorpion toxin {Centruroides sculpturatus ewing, variant 3}

KEGYLVKKSDBGCKYGLKLGGENEGCDTECKAKNQGGSYGYCYAFACWCEGLPESTPTYPLPNKSC

>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}

KEGYLVKKSDBGCKYDCFWLGKNEHCNTECKAKNQGGSYGYCYAFACWCEGLPESTPTYPLPNKSC

>d1nr_ g.3.7.1 (-) Scorpion toxin {Centruroides sculpturatus ewing, variant V}

KKDGYPVDSGNCKYECLKDDYCNDLCLERKADKGYCYWGVKVCYCYGLPDNSPTKTSKGCNPA

>d1aho_ g.3.7.1 (-) Scorpion toxin {Scorpion (Androctonus australis hector), Toxin II}

VKDGYIVDDVNCTYFCGRNAYCNEECTKLKGESGYCQWASPYGNACYCYKLPDHRVTKGPRCH

>d1cn2_ g.3.7.1 (-) Scorpion toxin {Mexican scorpion (Centruroides noxius hoffmann), toxin II}

KEGYLVDKNTGCKYECLKLGDNDYCLRECKQYQYKGGAGGYCYAFACWCTHLYEQAIWVPLPNKRCS

>d1bcg_ g.3.7.1 (-) Scorpion toxin {Scorpion (Buthotus judaicus), BJXTR-IT}

MKKNGYPLDRNGKTTECSGVNAIAPHYCNSECTKVYYAESGYCCWGACYCFGLEDDKPIGPMKIDIT

KKYCDVQI

>d1snb_ g.3.7.1 (-) Scorpion toxin {Scorpion (Buthus martensii), toxin m8}

GRDAYIADSENCTYFCGSPNYCNDVCTENGAKSGYCWAGRYGNACYCIDLPASERIKEGGRCG
>d1dja_ g.3.7.1 (A:) Scorpion toxin {Chinese scorpion (Buthus martensii), toxin m1}
VRDAYIAKPHNCVYECARNEYCNDLCTKNGAKSGYCWVWGKYNGCWCIELPDNVPIRVPKCH
>d1sn4a_ g.3.7.1 (A:) Scorpion toxin {Chinese scorpion (Buthus martensii), toxin m4}
VRDAYIAKPENCVYHCAGNEGCNKLCTDNGAESGYCWGGRYGNACWCIKLPDDVPIRVPKCH
>d1dq7a_ g.3.7.1 (A:) Scorpion toxin {Indian red scorpion (Buthus tamulus), neurotoxin}
GEDGYIADGDNCTYICTFNNYCHALCTDKKGDGACDWWVPYGVVCWCELDLPTVPPIRSGSKCR
>d1b7da_ g.3.7.1 (A:) Scorpion toxin {Scorpion (Tityus serrulatus)}
KEGYLMDHEGCKLSCFIRPSGYCGRECGIKKSSGYCAWPACYCYGLPNWVKVWDRATNKC
>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}
VRDAYIAKNYNCVYECFRDSYCNLCTKNGASSGYCWAGKYGNACWCYALPDNVPIRVPKCH
>d1lqi_ g.3.7.1 (-) alpha toxin {Scorpion (Leiurus quinquestriatus hebraeus)}
MVRDAYIAKNYNCVYECFRDAYCNELCTKNGASSGYCWAGKYGNACWCYALPDNVPIRVPKCR
>d1bmr_ g.3.7.1 (-) LQH III alpha-like toxin, LQH {Hebraei scorpion (Leiurus
quinquestriatus hebraeus)}
VRDGYIAQPENCVYHCFPGSSGCDTLCKEKGSTSGHCGFKVGHGLACWCNALPDNVGIIVEGKCHS
>d1big_ g.3.7.2 (-) Bmtx1 {Buthus martensii}
EFTDVKCTGSKQCWPVCKQMFQKPNGKCMNGKCRYS
>d1bkt_ g.3.7.2 (-) Bmktx {Buthus martensii}
VGINVKCKHSGQCLKPCKDAGMRFGKINGKCDCTPK
>d2bmt_ g.3.7.2 (-) Bmtx2 {Buthus martensii}
EFTNVSCSASSQCWPVCKKLFQTYRGKCMNSKCRYS
>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)}
TIINVKCTSPKQCSKPKELYGSSAGAKCMNGKCKCYNN
>d1txm_ g.3.7.2 (-) Maurotoxin {Scorpion (Scorpio maurus)}
VSCTGSKDCYAPCRKQTGCPNAKINKSCKCYGC
>d1cmr_ g.3.7.2 (-) Charybdotoxin {Scorpion (Leiurus quinquestriatus hebraeus)}
CTTSKECWSVCQRLHNTSKGWCDHRGICICES
>d2crd_ g.3.7.2 (-) Charybdotoxin {Scorpion (Leiurus quinquestriatus hebraeus)}
EFTNVSCCTTSKECWSVCQRLHNTSRGKCMNKKCRYS
>d1scy_ g.3.7.2 (-) Scyllatoxin {Scorpion (Leiurus quinquestriatus hebraeus)}
AFCNLRMCQLSCRSLGLLGKIGDKCECVKH
>d1agt_ g.3.7.2 (-) Agitoxin {Scorpion (Leiurus quinquestriatus hebraeus)}

GVPINVSTGSPQCIKPKDAGMRFKCMNRKCHCTPK
 >d1chl_ g.3.7.2 (-) Chlorotoxin {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)}
 VVIGQRRCYRSPDCYSACKKLVGKATGKCTNGRDCD
 >d1sis_ g.3.7.2 (-) Toxin I5a {Scorpion (Buthus eupeus)}
 MCMPCFTTDPNMAKKCRDCCGGNGKCFGPQCLCNR
 >d1pnh_ g.3.7.2 (-) Toxin analog {Scorpion (Androctonus mauretanicus mauretanicus)}
 TVCNLRRQCQLSCRSLGKIGVKCECVKH
 >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)}
 GVIINVKCKISRQCLEPCKKAGMRFKCMNGKCHCTPK
 >d2ktx_ g.3.7.2 (-) Kaliotoxin (KTX) {Scorpion (Androctonus mauretanicus mauretanicus)}
 GVEINVKCSGSPQCLKPKDAGMRFKCMNRKCHCTPK
 >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}
 TISCTNEKQCYPHCKKETGYPNACKMNRKCKCFGR
 >d1qky_ g.3.7.2 (A:) PI7 {Scorpion (Pandinus imperator)}
 DEAIRCTGKDCYIPCRYITGCFNSRCINKSCKCYGCT
 >d1fjna_ g.3.7.3 (A:) Defensin MGD-1 {Mediterranean mussel (Mytilus galloprovincialis)}
 GFGCPNNYQCHRHCKSIPGRCCGGYCGGWHRLRCTCYRCG
 >d1i2ua_ g.3.7.4 (A:) Heliomicin {Tobacco budworm (Heliothis virescens)}
 DKLIGSCVWGAVNYTSDCNGECKRRGYKGGHCGSFANVNCWCET
 >d1myn_ g.3.7.4 (-) Drosomycin {Fruit fly (Drosophila melanogaster)}
 DCLSGRYKGPACVWDNETCRRVCKEEGRSSGHCSPLKWCCEGC
 >d1ica_ g.3.7.4 (-) Defensin A {Flesh fly (Phormia terranova), larva}
 ATCDLLSGTGINSACAAHCLLRGNRGGYCNGKGVVCRN
 >d1gpt_ g.3.7.5 (-) gamma-Thionin {Barley (Hordeum vulgare)}
 RICRRRSAGFKGPCVSNKNCAQVCMQEGWGGNCDGPLRRCKCMRRC
 >d1gps_ g.3.7.5 (-) gamma-Thionin {Wheat (Triticum turgidum)}
 KICRRRSAGFKGPCMSNKNCAQVCQEGWGGNCDGPFRRCKCIRQC
 >d1ayj_ g.3.7.5 (-) Antifungal protein 1 (RS-AFP1) {Radish (Raphanus sativus)}
 EKLCERPSGTWSGVCNNACKNQCINLEKARHGSCNYVFAHKCICYFPC
 >d1bk8_ g.3.7.5 (-) Antimicrobial protein 1 (AH-AMP1) {Horse chestnut (Aesculus hippocastanum)}
 LCNERPSQTSWNGCNTAHCDKQCQDWEKASHGACHKRENHWKCFYFNC
 >d1jkza_ g.3.7.5 (A:) Defensin 1 (PSD1) {Pea (Pisum sativum)}
 KTCEHLADTYRGVCFNASCDDHCKNKAHLISGTCHNWKCFCTQNC
 >d1brz_ g.3.7.5 (-) Brazzein {J'oublie (Pentadiplandra brazzeana)}
 EDKCKKVYENYPVSKCQLANQCNYDCKLDKHARGECFYDEKRNLQCICDYCEY

>d2cbh_g.3.8.1 (-) Cellobiohydrolase I {Trichoderma reesei, ct-cbh I}
TQSHYGQCGGIGYSGPTVCASGTTTCQVLNPYYSQCL

>d1boea_g.3.9.1 (A:) Insulin-like growth factor-binding protein-5 (IGFBP-5) {Human (Homo sapiens)}
ALAEQSCGVYTERCAQGLRCLPRQDEEKPLHALLHGRGVCLNEKS

>d1igra3_g.3.9.1 (A:150-299) Cys-rich domain of the type 1 insulin-like growth factor receptor {Human (Homo sapiens)}
DLCPGTMEEKPMCEKTTINNEYNYRCWTTNRCQKMCPCSTCGKRACTENNECCHPECLGSCSAPDN
DTACVACRHHYYAGVCPACPPNTYRFEGWRCVDRDFCANILSAESSDSEGFVIHDGECMQECPSGFI
RNGSQSMYCIPCEGPCP

>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)}
ENSECSAFTLYGVYYKPCERGLTCEGDKSLVGSITNTNFGICHNV

>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)}
AVITGACERDLQCGKGTCCAVSLWIKSVRVTTPVGT

>d1imt_2_g.3.10.1 (37-80) Intestinal toxin 1 {Black mamba (Dendroaspis polylepis polylepis)}
SGEDCHPASHKIPFSGQRMHHTPCAPNLACVQTSPKFKKLSK

>d1edmb_g.3.11.1 (B:) Factor IX (IXa) {Human (Homo sapiens)}
VDGDQCESNPCLNGGSKDDINSYECWCPFGFEGKNCEL

>d1rfnb_g.3.11.1 (B:) Factor IX (IXa) {Human (Homo sapiens)}
MTCNIKNGRCEQFCKNSADNKVVCSTEGYRLAENQKSCEPAVPFPCGRVSVSQTSK

>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)}
TCNIKNGRCKQFCKTGADSKVLCSTTG YRLAPDQKSKPAVPFPCGRVSVSHSPTTLTR

>d1danl1_g.3.11.1 (L:49-86) Coagulation factor VIIa {Human (Homo sapiens)}
QCASSPCQNGGSKDQLQSYICFCLPAFEGRNCETHKD

>d1danl2_g.3.11.1 (L:87-142) Coagulation factor VIIa {Human (Homo sapiens)}
DQLICVNENGGCEQYCS DHTGTRSCRHEGYLLADGVSTPTVEYPCGKIPILE

>d1dval1_g.3.11.1 (L:42-86) Coagulation factor VIIa {Human (Homo sapiens)}
ISYSDGDQCASSPCQNGGSKDQLQSYICFCLPAFEGRNCETHKD

>d1f7ea_g.3.11.1 (A:) Coagulation factor VIIa {Human (Homo sapiens)}
SDGDQCASSPCQNGGSKDQLQSYICFCLPAFEGRNCETHKDDGSA

>d1g1sa2_g.3.11.1 (A:119-158) E-selectin, EGF-domain {Human (Homo sapiens)}
TASCQDMSCSKQGELETIGNYTCSCYPGFYGPCEYVRD

>d1g1ta2_g.3.11.1 (A:119-157) E-selectin, EGF-domain {Human (Homo sapiens)}
TAACTNTSCSGHGECVETINNYTCKCDPGFSGLKCEQIV

>d1fjls_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)}

DQCETSPCQNGKCKDGLGEYTCTCLEGFEGKNCELFTR
>d1apo_ g.3.11.1 (-) Factor X, N-terminal module {Cow (Bos taurus)}
KGDQCEGHPCLNQGHCKDGIGDYTCTCAEGFEGKNCEFSTR
>d1kigl_ g.3.11.1 (L:) Factor X, N-terminal module {Cow (Bos taurus)}
CSLDNNGCDQFCREERSEVRCSCAHGYVLGDDSKSCVSTERFPCGKFTQGR
>d1autl1 g.3.11.1 (L:49-96) Activated protein c (autoprothrombin IIa) {Human (Homo sapiens)}
QCLVLPLEHPCASLCCGHGTCIDGIGSFSCDCRSWEGRFCQREVSFL
>d1autl2 g.3.11.1 (L:97-146) Activated protein c (autoprothrombin IIa) {Human (Homo sapiens)}
NCSLDNNGCTHYCLEEVGWRRCSAPGYKLGDDLLQCHPAVKFPCGRPWK
>d1eqga2 g.3.11.1 (A:33-73) Prostaglandin H2 synthase-1, EGF-like module {Sheep (Ovis aries)}
VNPCCYYPQHQGICVRFGLDRYQCDCTRTGYSGPNCTIPE
>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 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)}
QVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCEIDKSKT
>d1hae_ g.3.11.1 (-) Heregulin-alpha, EGF-like domain {Human (Homo sapiens)}
SHLVKCAEKEKTFVNGGECFMVKDLSNPSRYLCKCQPGFTGARCTENVPMKVQNQEKAEEELY
>d1adx_ g.3.11.1 (-) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}
QMFCNQACPADCDPNTQASCECEGYILDDGFICTDIDE
>d1dx5i1 g.3.11.1 (I:345-387) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}
VEPVDPCFRANCEYQCQLDQTSYLCVCAEGFAPIPEPHRCQ
>d1dx5i2 g.3.11.1 (I:388-422) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}
MFCNQACPADCDPNTQASCECEGYILDDGFICT
>d1dx5i3 g.3.11.1 (I:423-462) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}
DIDECENGGFCSGVCHNLPGTFCICGPDSALAGQIGTDC
>d1zaq_ g.3.11.1 (-) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}

EPVDPFRANCEYQCQPLNQTSYLCVCAEGFAIPHEPHRCQMF
>d1emo_1 g.3.11.1 (2124-2166) Fibrillin-1 fragment (residues 2124-2205) {Human (Homo sapiens)}
SAVDMDECKEPPDVCKHGCINTDGSYRCECPFGYILAGNECVD
>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 {Human (Homo sapiens)}
CSEPRCFNNGGTCQQALYFSDFVCQCEGFAGKSCEIDTRAT
>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)}
IDECQDPDTCSQLCVNLEGGYKQCCEEGFQLDPHTKACKAV
>d1ijqa2 g.3.11.1 (A:643-692) Low density lipoprotein (LDL) receptor, different EGF domains {Human (Homo sapiens)}
VNWCERTTSLNNGGCQYLCLPAPQINPHSPKFTCACPDGMLLARDMRSCLT
>d1jv2b4 g.3.11.6 (B:532-562) Integrin beta EGF-like domains {Human (Homo sapiens)}
KGEMCSGHGQCSCGDCLCSDWTGYCNCTT
>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)}
CPCPGSSCAIVPKTKEVVCTHCPTGTAGKRCELDDGYFGDPLGSNGPVRLCRP
>d1klo_2 g.3.11.2 (66-121) Laminin gamma1 chain {Mouse (Mus musculus)}
CQCNDNIDPNAVGNCRNLTGCECLKCIYNTAGFYCDRCKEGFFGNPLAPNPADKCKA
>d1klo_3 g.3.11.2 (122-172) Laminin gamma1 chain {Mouse (Mus musculus)}
CACNPYGTVQQSSCNPVGTGQCQLPHVSGRDCGTCDPGYYNLQSGQGGER
>d1nuba2 g.3.11.3 (A:53-77) Domain of BM-40/SPARC/osteonectin {Human (Homo sapiens)}
APCQNHHCCKHGKVCELDENNTPMCV
>d1b9wa1 g.3.11.4 (A:1-45) Merozoite surface protein 1 (MSP-1) {Plasmodium cynomolgi}
MSSEHRCIDTNVPENAAACYRYLDGTEEWRLLYFKEDAGKCVAP
>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}
NISQHQCVKKQCPQNSGCFRHLDEREACKLLNYKQEGDKCVENP

>d1ceja2 g.3.11.4 (A:46-96) Merozoite surface protein 1 (MSP-1) {Plasmodium falciparum}
NPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSN

>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)}
TACSECVCPLRXEYKCYCXDLISPND CVK

>d1pi2_ g.3.13.1 (-) Bowman-Birk inhibitor, BBI {Soybean (Glycine max), PI-II}
YSKPCCDLCMCTRSMPPQCSCEDRINSCHSDCKSCMCTRSQPGQCRCLDTNDFCYKPKCSR

>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)}
DDESKPCCDQCACTKSNPPQCRCSDMRLNSCHSACKSCICALSYPAQCFCVDITDFCYEPCKPSEDD
KEN

>d1pbia_ g.3.13.1 (A:) Bowman-Birk inhibitor, BBI {Winter pea (Pisum sativum)}
KSACCDTCLCTKSNPPTCRCVDVGETCHSACLSCICAYSNPPKQCFTDQKFCYKQCHNSELEEVIKN

>d1df9c_ g.3.13.1 (C:) Bowman-Birk inhibitor, BBI {Mung bean (Vigna radiata)}
SHDEPSESSEPCDSCDCTKSIPPQCHCANIRLNSCHSACKSCICTRSMGKCRCLDTDDFCYKPCES
MDKD

>d1c2aa1 g.3.13.1 (A:4-64) Bowman-Birk inhibitor, BBI {Barley (Hordeum vulgare)}
KRPWKCCDEAVCTRSIPPICTCMDEVFECPKTCKSCGSPMGDPSRRICQDQYVGDGPGICR

>d1c2aa2 g.3.13.1 (A:65-123) Bowman-Birk inhibitor, BBI {Barley (Hordeum vulgare)}
PWECCKAICTRSNPPTCRCVDEVKKAAPTCKTCLPSRSPRRVCIDSYFGVPPRCT

>d1tabi_ g.3.13.1 (I:) Bowman-Birk inhibitor, BBI {Adzuki bean (Phaseolus angularis)}
SESSKPCCDQCSCTKSMPPKCRCSDIRLNSCHSACKSCACTYSIPAKCFCTDINDFCYEPCK

>d1flel_ g.3.14.1 (I:) Elafin, elastase-specific inhibitor {Human (Homo sapiens)}
TKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCEGSCGMACFVPQ

>d2rel_ g.3.14.1 (-) Elafin, elastase-specific inhibitor {Human (Homo sapiens)}
AQEPVKGVPSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCEGSCGMACFVPQ

>d1bx7_ g.3.15.1 (-) Hirustasin {Medicinal leech (Hirudo medicinalis)}
GNTCGGETCSAAQVCLKGKVCNEVHCRIRCKYGLKKDENGCEYPCSCAKA

>d1ejab_ g.3.15.1 (B:) Bdellastasin {Medicinal leech (Hirudo medicinalis)}
TTPCGPVTCGAQMCEVDKCVGSDLHCKVKCEHGFKKDDNGCEYACICADAPQ

>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)}
VVYTDCTESGQNLCLCEGSNVCGQGKNCILGSDGEKNQCVTGEGTPKPQSH

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

>d4htci_g.3.15.2 (I:) Hirudin {Leech (Hirudo medicinalis)}
ITYTDCTESGQNLCLCEGSNVCGKGNKCILGSNGKGNQCVTGEGTPKPESHNNNGDFEEIPEEYLQ

>d1dec_g.3.15.2 (-) Decorsin {North american leech (Macrobdella decora)}
APRLPQCQGDDQEKCLCNKDECPPGQCRFPRGDADPYCE

>d1e0fi_g.3.15.2 (I:) Haemadin {Indian leech (Haemadipsa sylvestris)}
IRFGMGKVPKPDGEVGYTCDCEGKICLYGQSCNDGQCSGDPKPSSEFEFEFEIDEEEEK

>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)}
DHVCCDDNFSPAGSTCSSAFGFRNLSLVWGCSPVE

>d1hy9a_g.3.17.1 (A:) Satiety factor CART (cocaine and amphetamine regulated transcript)
{Human (Homo sapiens)}
YGQVPMCDAGEQCAVRKRGARIGKLCDCPRGTSCNSFLLKCL

>d1gl1i_g.4.1.1 (I:) Protease inhibitor PMP-C {Migratory locust (Locusta migratoria)}
ISCEPGKTFKDKCNTCRGADGKSAACTLKACP

>d1gl0i_g.4.1.1 (I:) Protease inhibitor PMP-D2V {Migratory locust (Locusta migratoria)}
KCTPGQVKQDCNTCTCTPTGVWGCTLMGCQP

>d1kgma_g.4.1.1 (A:) Protease inhibitor SGCI {Desert locust (Schistocerca gregaria)}
EVTCEPGTTFKDKCNTCRGSDGKSAACTLKACPQ

>d1kioa_g.4.1.1 (A:) Protease inhibitor SGCI {Desert locust (Schistocerca gregaria)}
EVTCEPGTTFKDKCNTCRGSDGKSAACTRMACPQ

>d1kj0a_g.4.1.1 (A:) Protease inhibitor SGTI {Desert locust (Schistocerca gregaria)}
EQECTPGQTKKQDCNTCNCTPTGVWACTRKGCP

>d1mkna_g.5.1.1 (A:) Midkine, a heparin-binding growth factor, N-terminal domain
{Synthetic}
KKKDKVKKGGPGSECAEAWWGPCTPSSKDCGVGFREGTCGAQTQRIRCRVPCNWKKEFG

>d1mkca_g.5.1.2 (A:) Midkine, a heparin-binding growth factor, C-terminal domain
{Synthetic}
CKYKFENWGACDGGTGTKVRQGLKARYNAQCQETIRVTKPC

>d2bbg_g.6.1.1 (-) Amb V allergen {Giant ragweed (Ambrosia trifida), pollen}
DDGLCYEGTNCGKVGKYCCSPIGKYVCYDSKAICNKNCT

>d3ebx_g.7.1.1 (-) Erabutoxin B (also neurotoxin B) {Sea snake (Laticauda semifasciata)}
RICFNHQSSQPQTTKTCSPESSCYHKQWSDFRGTIHERGCGCPTVKPGIKLSCCESEVCNN

>d1tgxa_g.7.1.1 (A:) gamma-Cardiotoxin {Snake (Naja nigricollis)}
LKNQQLIPPFWKTCPKGNLCYKMTMRAAPMVPVKRGCIDVCPKSSLLIKYMCNTDKCN

>d1fas_g.7.1.1 (-) Fasciculin {Green mamba (Dendroaspis angusticeps)}
TMCYSHTTTSRAILTNCGENSCYRKSRRHPPKMVLGRGCGCPPDDYLEVKCCTSPDKCNY

>d1qm7a_g.7.1.1 (A:) Fasciculin {Green mamba (Dendroaspis angusticeps)}
TMCYSHTTTSRAILTNCGETNCYKKSRRHPPKMVLGRGCGCPTVAPGIKLNCTTDKCN

>d1ntn_g.7.1.1 (-) Neurotoxin I {Snake (Naja naja oxiana)}
ITCYKTPHITSETCAPGQNLCTYTKTWCDAWCGSRGKVIELGCAATCPTVESYQDIKCCSTDNCNPHPK
QKRP

>d1cdta_g.7.1.1 (A:) Cardiotoxin V4II (Toxin III) {Naja mossambica mossambica}
LKCNKLIPIAYKTCPEGKNLCYKMMLASKKMVPVKRGCINVC PKNSALVKYVCCSTDRCN

>d1kxia_g.7.1.1 (A:) Cardiotoxin V {Taiwan cobra (Naja naja atra)}
LKCHNTQLPFIYKTCPEGKNLCFKATLKKFPLKFPVKRGCADNCPKNSALLKYVCCSTDKCN

>d2ctx_g.7.1.1 (-) alpha-Cobrotoxin {Cobra (Naja naja siamensis)}
IRCFITPDITSKDCPNGHVCTKTWCDAFCSIRGKRVDLGCAATCPTVKTGVDIQCSTDN CNPFPTR
KRP

>d1lsi_g.7.1.1 (-) Long neurotoxin 1 (component LSIII) {Sea snake (Laticauda semifasciata)}
RECYLNPHDTQTCPSGQEICYVKS WCNAWCSSRGKVLEFGCAATCPSVNTGTEIKCCSADKCNTYP

>d1tfs_g.7.1.1 (-) FS2 toxin {Black mamba (Dendroaspis polylepis polylepis)}
RICYSHKASLPRA TKTCVENTCYKMFIRTHREYISERGC GCPTAMWPYQTECCKGDR CNK

>d1hc9a_g.7.1.1 (A:) Bungarotoxin {Many-banded krait (Bungarus multicinctus),
Alpha-bungarotoxin}
IVCHTTATSPISAVT CPPGENLCYRKMWCDFVFCSSRGKVVELGCAATCPSKKPYEEVTCSTDKCNPH
PKQRPG

>d2abxa_g.7.1.1 (A:) Bungarotoxin {Many-banded krait (Bungarus multicinctus),
Alpha-bungarotoxin}
IVCHTTATIPSSAVT CPPGENLCYRKMWCDAFCSRGKVVELGCAATCPSKKPYEEVTCSTDKCNHP
PKRQPG

>d1kbaa_g.7.1.1 (A:) Bungarotoxin {Many-banded krait (Bungarus multicinctus),
kappa-bungarotoxin}
RTCLISPSSTPQTC PNGQDICFLKAQCDKFCSIRGPVIEQGC VATCPQFRSNYRSLLCCTTDNCNH

>d1f94a_g.7.1.1 (A:) Bucandin {Malayan krait (Bungarus candidus)}
MECYRCGVSGCHLKITCSAEETFCYKWL NKISNERWLGC AKTCTEIDTWNVYNKCC TTNLCNT

>d2cdx_g.7.1.1 (-) Cardiotoxin CTXI {Taiwan cobra (Naja naja atra)}
LKCNKLIPIASKTCPAGKNLCYKMFMSDLTIPVKRGCIDVCPKNSLLVKYVCCNTDR CN

>d1chvs_g.7.1.1 (S:) Cardiotoxin II {Taiwan cobra (Naja naja atra)}
LKCNKLVPLFYKTC PAGKNLCYKMFMVSNKMVPVKRGCIDVCPKSSLLVKYVCCNTDR CN

>d1cb9a_g.7.1.1 (A:) Cardiotoxin II {Central asian cobra (Naja naja oxiana)}
LKCKKLVPLFSKTC PAGKNLCYKMFMAAPHVPVKRGCIDVCPKSSLLVKYVCCNTDKCN

>d1i02a_g.7.1.1 (A:) Cardiotoxin III {Taiwan cobra (Naja naja atra)}
LKCNKLVPLFYKTC PAGKNLCYKMFMVATPKVPVKRGCIDVCPKSSLLVKYVCCNTDR CN

>d1kbs_g.7.1.1 (-) Cardiotoxin IV {Taiwan cobra (Naja naja atra)}
RKC NKLVPLFYKTC PAGKNLCYKMFVSNLTPVKRGCIDVCPKNSALVKYVCCNTDR CN

>d1cod_g.7.1.1 (-) Cobrotoxin II (ct2) {Taiwan cobra (Naja naja atra)}
LECHNQSSQTPTTTGCSGGETN CYKKRWRDHRGYRTERGCGCPSVKNGIEINCCTTDR CNN

>d1g6ma_g.7.1.1 (A:) Cobrotoxin II (ct2) {Monocled cobra (Naja kaouthia)}
LECHNQSSQTPTTTGCSGGENN CYKKEWRDNRGYRTERGCGCPSVKKGIGINCCTTDR CNN

>d1nea_g.7.1.1 (-) alpha-Toxin {Snake (Naja nigricollis)}
LECHNQSSQPPTTKTC PGETN CYKKVWRDHRGTI IERGCGCPTVKPGIKLNCCTTDR CNN

>d1ntx_g.7.1.1 (-) alpha-Toxin {Black mamba (Dendroaspis polylepis polylepis)}
RICYNHQSTTRATTKSCEENSCYK KYWRDHRGTI IERGCGCPKVKPGVGIHCCQSDKCN Y

>d1nor_g.7.1.1 (-) Neurotoxin II (Nt2) {Central asian cobra (Naja naja oxiana)}
LECHNQSSQPPTTKTC SGETN CYKKWWSDRGTI IERGCGCPKVKPGVNLNCCRTDR CNN

>d1txb_g.7.1.1 (-) Toxin B (long neurotoxin) {King cobra (Ophiophagus hannah)}
TKCYVTPDATSQTCPDGDICYTKTWCDGFCSSRGKRIDLGCAATCPKVKPGVDIKCCSTDNCNPFPTWKRKH

>d1jgka_g.7.1.1 (A:) Codoxin {Malayan krait (Bungarus candidus)}
MKCKICNFDTCRAGELKVCASGEKYCFKESWREARGTRIERGCAATCPKGSVYGLYVLCCTTDDCN

>d1drs_g.7.1.2 (-) Dendroaspis {Dendroaspis jamesoni kaimosae}
RICYNHLGKTPPTTETCQEDSCYKNIWTFDNIIRRGCGFTPRGDMPGPYCCESDKCNL

>d1erh_g.7.1.3 (-) CD59 {Human (Homo sapiens)}
LQCYNCNPNTADCKTAVNCSSDFDACLITKAGLQVYNKWCWKFHCNFDVTTTLRENELTYCYCKKDLCN

>d1btea_g.7.1.3 (A:) Type II activin receptor {Mouse (Mus musculus)}
ETQECLFFNANWERDRTNQTGVEPCYGDKDKRRHCFATWKNISGSIEIVKQGCWLDDINCYDRDTCIEKKDSPEVYFCCCEGNMCNEKFSYFPEME

>d1es7b_g.7.1.3 (B:) BMP receptor Ia ectodomain {Human (Homo sapiens)}
TLPFLKCYCSGHCPDDAINNTCITNGHCFAIIEEDDQGETTLASGCMKYEGSDFQCKDSPKAQLRRTIECCRTNLCNQYLQPTLPP

>d1ktzb_g.7.1.3 (B:) TGF-beta type II receptor extracellular domain {Human (Homo sapiens)}
PQLCKFCDVRFSTCDNQKSCMSNCSITSICEKPQEVCAVWRKNDENITLETVCHDPKLPYHDFILEDAASPKCIMKEKKKPGETFFMCSSSDECNDNIIFSEYY

>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)}
RPDFCLEPPYTGPCRLRIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTC GGA

>d1faki_g.8.1.1 (I:) Pancreatic trypsin inhibitor, BPTI {Cow (Bos taurus)}
APDFCLEPPYDGPCRALHLRYFYNAKAGLCQTFYGGCLAKRNNFESAEDCMRTC

>d1g6xa_g.8.1.1 (A:) Pancreatic trypsin inhibitor, BPTI {Cow (Bos taurus)}
RPDFCLEPPYAGACRARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTC GGA

>d3bthi_g.8.1.1 (I:) Pancreatic trypsin inhibitor, BPTI {Cow (Bos taurus)}
DFCLEPPYTGPCHARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTC GGA

>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)}
DYKDDDDKLPDFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNICEDG PNGF

>d1irha_g.8.1.1 (A:) Tissue factor pathway inhibitor {Human (Homo sapiens)}
EFHGSPWCLTPADRGLCRANENRFYNSVIGKCRPFKYSGCCGNENNFTSKQECLRACKKG

>d1tfxc_g.8.1.1 (C:) Tissue factor pathway inhibitor {Human (Homo sapiens)}
KPDFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNICEDG

>d1aapa_g.8.1.1 (A:) Alzheimer's amyloid B-protein precursor, A β 1 {Human (Homo sapiens)}

VREVCSEAETGPCRAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVAVCG
>d1bik_1 g.8.1.1 (25-78) Bikunin from inter-alpha-inhibitor complex {Human (Homo sapiens)}
SCQLGYSAGPCMGMTSRYFYNGTSMACETFQYGGCMGNGNMFVTEKECLQTCRT
>d1bik_2 g.8.1.1 (79-134) Bikunin from inter-alpha-inhibitor complex {Human (Homo sapiens)}
VAACNLPIVRGPCRAFIQLWAFDAVKGKCVLFPYGGCQNGNKFYSEKECREYCGV
>d1dtx_ g.8.1.1 (-) alpha-Dendrotoxin {Green mamba (Dendroaspis angusticeps)}
EPRRKLCILHRNPGRCYDKIPAFYFNQKKKQCERFDWSGCGGNSNRFKTIEECRRTCIG
>d1bunb_ g.8.1.1 (B:) beta2-bungarotoxin, neurotoxin chain {Many-banded krait (elapid) (Bungarus multicinctus)}
RKRHPDCDKPPDTKICQTVVRAFYYKPSAKRCVQFRYGGCNGNGNHFKSDHLRCECLEYR
>d1shp_ g.8.1.1 (-) Trypsin inhibitor {Sea anemone (Stichodactyla helianthus)}
SICSEPKKVGRCGYFPRFYFDSETGKCTPFYGGCGGNGNMFETLHQCRAICRA
>d1dtk_ g.8.1.1 (-) Dendrotoxin K {Black mamba (Dendroaspis polylepis polylepis)}
AAKYCKLPLRIGPCKRKIPSFYKWKAKQCLPFDYSGCGGNANRFKTIIEECRRTCIG
>d1den_ g.8.1.1 (-) Dendrotoxin I {African elapid snake (Dendroaspis polylepis polylepis)}
QPLRKLCILHRNPGRCYQKIPAFYFNQKKKQCEGFTWSGCGGNSNRFKTIEECRRTCIRK
>d1bf0_ g.8.1.1 (-) Calcicludine (cac) {Green mamba (Dendroaspis angusticeps)}
WQPPWYCKEPVRIGSCKKQFSSFYFKWTAKKCLPFLFSGCGGNANRFQTIGECRKKCLGK
>d1toct1 g.8.1.2 (R:1A-56) Ornithodorin {Soft tick (Ornithodoros moubata)}
SLNVLCCNNPHTADCNNDAQVDYRFREGTTCLMSPACTSEGYASQHECQQACFVGGED
>d1toct2 g.8.1.2 (R:57-119) Ornithodorin {Soft tick (Ornithodoros moubata)}
HSSEMHSCLGDPPTSCAEGTDITYYDSKTCCKVLAASCPSGENTFESEVECQVACGAPIEG
>d1d0da_ g.8.1.2 (A:) Anticoagulant protein, factor Xa inhibitor {Soft tick (Ornithodoros moubata)}
YNRLCIKPRDWIDECDSENEGGERAYFRNGKGGCDSFWICPEDHTGADYSSYRDCFNACI
>d1dfna_ g.9.1.1 (A:) Defensin HNP-3 {Human (Homo sapiens)}
DCYCRIPACIAGERRYGTICIQGRLWAFCC
>d1ijva_ g.9.1.1 (A:) Beta-defensin, BD {Human (Homo sapiens), HBD1}
DHYNVSSGGQCLYSACPIFTKIQTICYRGKAKCKK
>d1e4qa_ g.9.1.1 (A:) Beta-defensin, BD {Human (Homo sapiens), HBD2}
PVTCLKSGAICHVPVFCPRRYKQIGTCGLPGTKCCKKP
>d1fd3a_ g.9.1.1 (A:) Beta-defensin, BD {Human (Homo sapiens), HBD2}
GIGDPVTCLKSGAICHVPVFCPRRYKQIGTCGLPGTKCCKKP
>d1e4ta_ g.9.1.1 (A:) Beta-defensin, BD {Mouse (Mus musculus), MBD5}
NSKRACYREGGECLQRCIGLRFHKIGTCNFRFKCCKFQ
>d1e4ra_ g.9.1.1 (A:) Beta-defensin, BD {Mouse (Mus musculus), MBD6}
NEPVCIRNGGICQYRCIGLRHKIGTCGSPFKCKK
>d1bnb_ g.9.1.1 (-) Beta-defensin, BD {Cow (Bos taurus), BD12}
APLSCGRNGGVCIPRCPVPMRQIGTCFGRPVKCCRSW
>d1ewsa_ g.9.1.1 (A:) Alpha-defensin rk-1 {Rabbit (Oryctolagus cuniculus)}
MPCSCKKYCDPWEVIDGSCGLFNISKYICCREK
>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}
IMFFEMQACWSHSGVCRDKSERNCKPMAWTYCENRNQKCEY
>d2bds_ g.9.1.1 (-) BDs-I defensin {Sea anemone (Anemonia sulcata)}
AAPCFCSGKPGRGDLWILRGTCPPGGYGYTSNICYKWPNICCYPH
>d1sh1_ g.9.1.1 (-) Sea anemone neurotoxin-1 {Sea anemone (Stichodactyla helianthus)}
AACKCDEGPDIRTAPLTGTVDLGSCNAGWEKCASYYTHIADCCRKKK
>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)}
GVSCLCSDGSPVRGNTLSGTLWLYPGCPGWHNCKAHGPTIGWCKKQ
>d1apf_ g.9.1.1 (-) Anthopleurin-B {Giant green sea anemone (Anthopleura xanthogrammica)}
GVPCLCSDGPRPRGNTLSGILWFYPSGCPGWHNCKAHGPNIGWCKK
>d1bhta1 g.10.1.1 (A:35-126) Hepatocyte growth factor {Human (Homo sapiens)}
RRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPP
NSMSSGVKKEFGHEFDLYENKDYIR
>d1gmb1 g.10.1.1 (B:42-125) Hepatocyte growth factor {Human (Homo sapiens)}
FKKSAKTTLIKIDPALKIKTKKVNTADQCADRCTRNKGLPFTCKAFVFDKARKQCLWFPPNSMSSGV
KKEFGHEFDLYENKDYI
>d1i8na_ g.10.1.2 (A:) Anti-platelet protein {Leech (Haementeria officinalis)}
ETITAGNEDCWSKRPGWKLPDNLTKTEFTSVDECRKMCEESAVEPSCYILQINTETNECYRNNEG
DVTWSSLQYDQPNVQWHLHACS
>d1ans_ g.11.1.1 (-) Neurotoxin III (ATX III) {Sea anemone (Anemonia sulcata)}
RSCPCYWGGCPWGQNCYPEGCSGPKV
>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)}
PGGCHTDEFQCRLDGLCIPLRWRCGDGTD CMDSSDEKSCEGV
>d1d2la_ g.12.1.1 (A:) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}
GSPPQCQPGEFACANSRCIQERWKCDGNDCLDNSDEAPALCHQH
>d1f5ya1 g.12.1.1 (A:1-44) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}
GSAVGDR CERNEFQCQDGK CISYKWVCDGSAECQDGSDESQETC
>d1f5ya2 g.12.1.1 (A:45-85) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}
LSVTCKSGDFSCGGRVNRICIPQFWRCDGQVDCDNGSDEQGC
>d1f8za_ g.12.1.1 (A:) Ligand-binding domain of low-density lipoprotein receptor {Human

(Homo sapiens)}
ATCRPDEFQCSGNCIHGSRQCDREYDCKDMSDEVGCVN
>d1j8ea_g.12.1.1 (A:) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}
GSHSCSTQFKCNSGRCIPEHWTCGDNDGCDYSEETHANCTNQ
>d1ldl_g.12.1.1 (-) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}
AVGDRCERNEFQCQDGKICISYKWVCDGSAECQDGSDESQETCLSVT
>d1k7ba_g.12.1.1 (A:) soluble Tva ectodomain, sTva47 {Quail (Coturnix coturnix)}
SCPPGQFRCSEPPGAHGECYPQDWLDCGHPDCDDGRDEWGCG
>d1ejga_g.13.1.1 (A:) Crambin {Abyssinian cabbage (Crambe abyssinica)}
TTCCPSIVARSNFNVCRLPGTPEALCATYTGCIHPGATCPGDYAN
>d1bhp_g.13.1.1 (-) beta-Purothionin {Wheat (Triticum aestivum)}
KSCCKSTLGRNCYNLCRARGAQKLCANVCRCKLTSGLSCPDKDFPK
>d2plh_g.13.1.1 (-) alpha-1-Purothionin {Wheat (Triticum aestivum)}
KSCCRSTLGRNCYNLCRARGAQKLCAGVCRCKISSGLSCPDKDFPK
>d1ed0a_g.13.1.1 (A:) Viscotoxin a3 {European mistletoe (Viscum album)}
KSCCPNTTGRNIYNACRLTGAPRPTCAKLSGCKIISGSTCPSDYPK
>d1i5ka_g.14.1.1 (A:) Plasminogen kringles {Human (Homo sapiens)}
ECMHGSGENYDGKISKTMGLECQAWDSQSPHAHGYIPSKFPNKNLKNYCRNPDRDLRPWCFTT
DPNKRWEYCDIPRC
>d1krn_g.14.1.1 (-) Plasminogen kringles {Human (Homo sapiens)}
DCYHGDGQSYRGTSTTTTTGKKCQSWSSMTPHRHQKTPENYPNAGLTMNYCRNPADAKGPWCFT
TDPSVRWEYCNLKKC
>d1pmla_g.14.1.1 (A:) Plasminogen kringles {Human (Homo sapiens)}
SDCYFNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQUALGLGKHNYCRNPDGDAKPWC
HVLKNRRLTWEYCDVPSCST
>d1ceaa_g.14.1.1 (A:) Plasminogen kringle domains {Human (Homo sapiens)}
ECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDNDPQGPWCYT
TDPEKRYDYCDILEC
>d5hpga_g.14.1.1 (A:) Plasminogen kringle domains {Human (Homo sapiens)}
DCMFGNGKGYRGKRVTTVTGTPCQDWAAQEPHRHSIFTPETNPRAGLEKNYCRNPDGDVGGPWC
YTTNPRKLYDYCDVPQCAAP
>d2pf1_1 g.14.1.1 (66-156) Prothrombin kringle domain {Cow (Bos taurus)}
CAEGVGMNYRGNVSVTRSGIEQLWRSRYPHKPEINSTTHPGADLRENFCRNPDGSITGPWCYTTS
PTLRREECVPPVCGQDRVTVEVIPR
>d2pf2_1 g.14.1.1 (66-146) Prothrombin kringle domain {Cow (Bos taurus)}
CAEGVGMNYRGNVSVTRSGIEQLWRSRYPHKPEINSTTHPGADLRENFCRNPDGSITGPWCYTTS
PTLRREECVPPVCGQ
>d1a0ha1 g.14.1.1 (A:164-270) Meizothrombin kringle domain {Cow (Bos taurus)}
SPLLETCPDRGREYRGLAVTTHGSRCLAWSSEQAKALSKDQDFNPAVPLAENFCRNPDGDEEGA
WCYVADQPGDFEYCDLNYCEEPVDGDLGDRLGEDPDPDAAIEG
>d2hppp_g.14.1.1 (P:) Meizothrombin kringle domain {Cow (Bos taurus)}
CVPDRGREYRGLAVTTSRCLAWSSEQAKALSKDQDFNPAVPLAENFCRNPDGDEEGAWCYVAD

QPGDFEYCNLNYC
>d2hqpq_ g.14.1.1 (P:) Meizothrombin kringle domain {Human (Homo sapiens)}
CVPDRGQQYQGR LAVTTHGLPCLAWASQA KALSKHQDFNSAVQLVENFCRNP DGDDEEGVWCYVA
GKPGDFGYCDLNYC
>d1kdu_ g.14.1.1 (-) Urokinase-type plasminogen activator kringle domain {Human (Homo sapiens)}
TCYEGNGHFYRGKASTDTMGRPCLPWN SATVLQQTYHAHRSDALQLGLGKHNYCRNP DNRRRPW
CYVQVGLKPLVQECMVHDCAD
>d3kiv_ g.14.1.1 (-) Apolipoprotein A kringle domain {Human (Homo sapiens), IV-10/M66 variant}
QCYHGNGQSYRGTFSTTVTGRT CQSWSSMTPHRHQRT PENYPNDGLTMNYCRNP DADTGPWCFT
TDPSIRWEYCNLTRC
>d1i71a_ g.14.1.1 (A:) Apolipoprotein A kringle domain {Human (Homo sapiens), IV-7 variant}
DCYHGDGQSYRGSFSTTVTGRT CQSWSSMTPHWHQRTTEYYPNGGLTRNYCRNP DAEIRPWCYTM
DPSVRWEYCNLTQCPVME
>d1bhta2 g.14.1.1 (A:127-210) NK1 fragment of hepatocyte growth factor {Human (Homo sapiens)}
NCIIGKGRSYKGTVSITKSGIKQPWSSMIPHEHSFLPSSYRGKDLQENYCRNP RGEEGPWCFTSNP
EVRYEVC DIPCSEVE
>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)}
AVTQTYGGNSNGEPCVLPFTYNGRTFYSC TTEGRQDGHLCSTTSNYEQDQKYSFCTDHT
>d1e88a2 g.14.1.2 (A:102-160) Fibronectin {Human (Homo sapiens)}
VLVQTRGGNSGALCHFPFLYNNHNYTDCTSEGR RDNMKWCGTTQNYDADQKFGFCPMA
>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)}
ALFTMGGNAEQPCKFPFRFQGTSYDSCTTEGRTDGYRWCGTTEDYDRDKKYGFCPET
>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:) Ovomuroid III domain {Turkey (Meleagris gallopavo)}
VDCSEYKPKACTAEYRPLCGSDNKTYGNKCNFCNAVVESNGTLTL SHFGKC
>d3ovo_ g.15.1.1 (-) Ovomuroid III domain {Japanese quail (Coturnix coturnix japonica)}
LAAVSVDCEYKPKACPKDYRPVCGSDNKTYSNKCNFCNAVVESNGTLTLNHFGKC
>d2ovo_ g.15.1.1 (-) Ovomuroid III domain {Silver pheasant (Lophura nycthemera)}

LAAVSVCSEYPPKACTMEYRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
>d1hpt_ g.15.1.1 (-) Secretory trypsin inhibitor {Human (Homo sapiens)}
DSLGREAKCYNELNGCTYEYRPVCGTDGDTYPNECVLCFENRKRQTSILIQKSGPC
>d1tgsi_ g.15.1.1 (I:) Secretory trypsin inhibitor {Pig (Sus scrofa)}
TSPQREATCTSEVSGCPKIYNPVC GTDGITYSNECVLCS ENKKRQTPVLIQKSGPC
>d1tbrr1 g.15.1.1 (R:1-51) Rhodniin {Bug (Rhodnius prolixus)}
EGGEPACPHALHRVCGSDGETYSNPCTLNCAKFNGKPELVKVHDGPCEPD
>d1tbrr2 g.15.1.1 (R:52-103) Rhodniin {Bug (Rhodnius prolixus)}
EDEDVCQECDGDEYKPVCGSDDITYDNNCRLECASISSPGVELKHGEGPCRT
>d1nuba3 g.15.1.1 (A:78-135) Domain of BM-40/SPARC/osteonectin {Human (Homo sapiens)}
CQDPTSCPAPIGEFEKVCSDNKTFDSSCHFFATKCTLEGTKKGHKLHLDYIGPCKYI
>d2bus_ g.15.1.1 (-) Seminal plasma inhibitor IIa {Cow (Bos taurus)}
EGAQVDCAEFKDPKVYCTRESNPHCGSNGETYGNKCAFCKAVMKSGGKINLKHGKGC
>d1pce_ g.15.1.1 (-) PEC-60 peptide {Pig (Sus scrofa)}
EKQVFSRMPICEHMTESPDCSRIYDPVCGTDGVTYESECKLCLARIENKQDIQIVKDGECE
>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)}
PICTNCCAGYKGCNYYSANGAFICEGQSDPKPKACPLNCDPHIAYSKCPR
>d1ce3a_ g.15.1.2 (A:) Multidomain proteinase inhibitor {Winged tobacco (Nicotiana glauca)}
MKACTLNCDPRIAYGVCPRSEEKKNDRICTNCCAGTKGCKYFSDDGTFVCEGES
>d1fyba1 g.15.1.2 (A:1-55) Multidomain proteinase inhibitor {Winged tobacco (Nicotiana glauca)}
DRICTNCCAGTKGCKYFSDDGTFVCEGESDPRNPKACTLNCDPRIAYGVCPRSEE
>d1tih_ g.15.1.2 (-) Multidomain proteinase inhibitor {Winged tobacco (Nicotiana glauca)}
DRICTNCCAGTKGCKYFSDDGTFVCEGESDPRNPKACPRNCDPRIAYGICPLA
>g1qh2.1 g.15.1.2 (B;A:) Multidomain proteinase inhibitor {Winged tobacco (Nicotiana glauca)}
RICTNCCAGKKGCKYFSDDGTFICEGESXKACTLNCDPRIAYGVCPR
>d2pspa1 g.16.1.1 (A:1-53) Pancreatic spasmolytic polypeptide {Pig (Sus scrofa)}
EKPAACRCRQDPKNRVNCGFPGITSDQCFTSGCCFDSQVPGVPWCFKPLPAQ
>d2pspa2 g.16.1.1 (A:54-106) Pancreatic spasmolytic polypeptide {Pig (Sus scrofa)}
ESEECVMQVSARKNCGYPGISPEDCAARNCCFSDTIPEVPWCFPPMSVEDCHY
>d1hi7a_ g.16.1.1 (A:) PNR-2/PS2, TFF1 {Human (Homo sapiens)}
EAQTETCTVAPRERQNCGFPGVTPSQCANKGCCFDDTVRGVPWCFYPNTIDVPPPEEECEF
>d1e9ta_ g.16.1.1 (A:) Intestinal trefoil factor {Human (Homo sapiens)}
EEYVGLSANQCAVPAKDRVDCGYPHVTPKECNRGCFDSRIPGVPWCFKPLQEAECTF
>d1pdga_ g.17.1.1 (A:) Platelet-derived growth factor BB {Human (Homo sapiens)}
EPAMIAECKTRTEVFEISRRLIDRTNANFLVWPPCVEVQRCSGCCNNRNVQCRPTQVQLRPVQVRKI

EIVRKKPIFKKATVTLEDHLACKCETVAA

>d1flt_v.g.17.1.1 (V:) Vascular endothelial growth factor, VEGF {Human (Homo sapiens)}

EVVKFMDVYQRSYCHPIETLVDIFQEYPDEIEYIFKPCVPLMRCGGCCNDEGLECVPTTEESNITMQI
MRIKPHQGQHIGEMSFLQHNKCECRPK

>d1fzva_g.17.1.1 (A:) Placenta growth factor-1, PLGF-1 {Human (Homo sapiens)}

SSEVEVVPFQEVWGRSYCRALERLVDVVSEYPSEVEHMFSPSCVSLLRCTGCCGDENLHCVPVETAN
VTMQLLKIRSGDRPSYVELTFSQHVRCECRPLR

>d1ktza_g.17.1.2 (A:) TGF-beta3 {Human (Homo sapiens)}

ENCCVRPLYIDFRQDLGWKVVHEPKGYANFCSGPCPYLRSADTTHTSTVLGLYNTLNPEASAPCCV
PQDLEPLTILYVGRTPKVEQLSNMVVKSCCKS

>d1tgi_g.17.1.2 (-) TGF-beta3 {Human (Homo sapiens)}

ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKVVHEPKGYANFCSGPCPYLRSADTTHTSTVLGLYN
TLNPEASAPCCVPPQDLEPLTILYVGRTPKVEQLSNMVVKSCCKS

>d2tgi_g.17.1.2 (-) TGF-beta2 {Human (Homo sapiens)}

ALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKVIHEPKGYANFCAGACPYLWSSDTQHSRVLSLYN
TINPEASAPCCVSDLEPLTILYIYIGKTPKIEQLSNMIVKSCCKS

>d1klaa_g.17.1.2 (A:) TGF-beta1 {Human (Homo sapiens)}

ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKVIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQ
HNPGASAAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCCKS

>d1bmp_g.17.1.2 (-) Bone morphogenetic protein-7 (BMP-7) {Human (Homo sapiens)}

QACKKHELYVSFRDLGWQDWIIAPEGYAAYCEGECAFLNSYMNATNHAIVQTLVHFINPETVPPK
CCAPTQLNAISVLYFDDSSNVILKKYRNMVVRACGCH

>d1es7a_g.17.1.2 (A:) Bone morphogenetic protein-2 (BMP-2) {Human (Homo sapiens)}

KSSCKRHPLYVDFSDVGWWDWIVAPPGYHAFYCHGECFPPLADHLNSTNHAIVQTLVNSVNSKIPKA
CCVPTELSAISMLYLDENEKVVLLKNYQDMVVEGCGCR

>d1agqa_g.17.1.2 (A:) Glial cell-derived neurotrophic factor, GDNF {Rat (Rattus norvegicus)}

NRGCVLTAIHLNVTDLGLGYETKEELIFRYCSGSCAAETMYDKILKNLSRRLTSKVGQACCRPV
AFDDDLFLDDSLVYHILRKHSKRCGCI

>d1bnda_g.17.1.3 (A:) Brain-derived neurotrophic factor/neurotrophin 3 heterodimer,
BDNF/NT3 {Human (Homo sapiens)}

GQLSVCDSISEWVTAADKKTAVDMSGGTVTVLEKVPVSKGQLKQYFYETKCNPMGYTKEGCRGIDK
RHWNSQCRTTQSYVRALTMDSKKRIGWRWFIRIDTSCVCTLTIK

>d1bnda_g.17.1.3 (B:) Brain-derived neurotrophic factor/neurotrophin 3 heterodimer,
BDNF/NT3 {Human (Homo sapiens)}

RGEVSVCDSESLWVTDKSSAIDIRGHQVTVLGEIKTQNSPVKQYFYETRCKEARPVKNGCRGIDDKH
WNSQCKTSQTYVRALTSENNKLVGWRWIRIDTSCVCALSRLK

>d1b8mb_g.17.1.3 (B:) Neurotrophin 4 {Human (Homo sapiens)}

GELAVCDAVSGWVTDRTAVDLRGREVEVLGEVPAAGGSPLRQYFFETRCKADNAEEGGPGAGGGG
CRGVDRRHVVSECKAKQSYVRALTADAQGRVGVWRWIRIDTACVCTLLSRTGRA

>d1hcfa_g.17.1.3 (A:) Neurotrophin 4 {Human (Homo sapiens)}

GVSETAPASRRGELAVCDAVSGWVTDRTAVDLRGREVEVLGEVPAAGGSPLRQYFFETRCKADNAE
EGGPGAGGGGCRGVDRRHVVSECKAKQSYVRALTADAQGRVGVWRWIRIDTACVCTLLSRT

>d1bet_g.17.1.3 (-) beta-Nerve growth factor {Mouse (Mus musculus)}

GEFSVCDSVSVVVGDKTTATDIKKEVTVLAEVNINNSVFRQYFFETKCRASNPVESGCRGIDSKHW

NSYCTTHTFVKALTTDEKQAAWRFIRIDTACVCVLSRKA
>d1wwwv_g.17.1.3 (V:) beta-Nerve growth factor {Human (Homo sapiens)}
SSHPIFHRGEFSVCDSSVSVWVGDKTTATDIKGKEVMVLGEVNINNSVFKQYFFETKCRDPNPVDSGC
RGIDSKHWNYSYCTTHTFVKALTMGDKQAAWRFIRIDTACVCVLSRK
>d1hcna_g.17.1.4 (A:) Glycoprotein hormones alpha chain (Gonadotropin A, Follitropin
alpha) {Human (Homo sapiens)}
QDCPECTLQENPFPSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYNRVTVM
GGFKVENHTACHCSTCY
>d1hcnb_g.17.1.4 (B:) Gonadotropin B chain {Human (Homo sapiens)}
KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFESIRL
PGCPRGVNPVVSVAVALSCQCALCRRSTTDCGGPKDHPLTCD
>d1fl7b_g.17.1.4 (B:) Follicle stimulating hormone, follitropin, beta chain {Human (Homo
sapiens)}
CELTNITIAIEKEECRFCISINTAWCAGYCYTRDLVYKDPARPQIKTCTFKELVYETVRVPGCAHHD
SLYTPVATQCHCGKCDSDSTDCTVRGLGPSYCSFGEM
>d1jpya_g.17.1.6 (A:) Interleukin 17F, IL-17F {Human (Homo sapiens)}
HTFFQKPESCPPVPGGSMKLDIGIINENQRVSMRNIERSRSTSPWNYTVTWDPNRYPSEVVQAQCR
NLGCINAQKEDISMNSVPIQQETLVVRRKHQGCSVSFQLEKVLVTVGCTCVTPV
>d1aoca_g.17.1.5 (A:) Coagulogen {Japanese horseshoe crab (Tachypleus tridentatus)}
ADTNAPICLCEDEPGVLGRTQIVTTEIKDKIEKAVEAVAQESGVSGRGSIFSHPVFRECGKYECRTVR
PEHSRCYNFPFTHFKSECPVSTRDCEPVFGYTVAGEFRVIVQAPRAGFRQCVWQHKKRFGSNSCGY
NGRCTQQRSVRLVTYNLEKDGFLCESFRTCCGCPCRSF
>d1hcc_g.18.1.1 (-) Factor H, 15th and 16th modules {Human (Homo sapiens)}
EGLPCKSPPEISHGVVAHMSDSYQYGEVYKCFEGFGIDGPAIAKCLGEKWSHPSCI
>d1hfi_g.18.1.1 (-) Factor H, 15th and 16th modules {Human (Homo sapiens)}
EKIPCSQPPQIEHGTINSSRSSQESYAHGTKLSYTCGGFRISEENETTCYMGKWSSPPQCE
>d1g40a1 g.18.1.1 (A:1-64) Complement control protein {Vaccinia virus}
CCTIPSRPINMKFKNVETDANANYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGWTLFNQCIK
>d1g40a2 g.18.1.1 (A:65-126) Complement control protein {Vaccinia virus}
RRCPSPRDIDNGQLDIGVDFGSSITYSCNSGYHLIGESKSYCELGSTGSMVWNPEAPICES
>d1g40a3 g.18.1.1 (A:127-184) Complement control protein {Vaccinia virus}
VKCQSPPSISNGRHNGYEDFYTDGSVVYSCNSGYSLIGNSGVLCSSGGEWSDPPTCQI
>d1g40a4 g.18.1.1 (A:185-243) Complement control protein {Vaccinia virus}
VKCPHTISNGYLSSGFKRSYSYNDNVDKCKYGYKLSGSSSTCSPGNTWKPELPCV
>d1ckla1 g.18.1.1 (A:1-62) CD46 (membrane cofactor protein, MCP) {Human (Homo
sapiens)}
CEEPPTFEAMELIGKPKPYEIGERVDYKCKKGYFYIPPLATHITICDRNHTWLPVSDDACYR
>d1ckla2 g.18.1.1 (A:63-126) CD46 (membrane cofactor protein, MCP) {Human (Homo
sapiens)}
ETCPYIRDPLNGQAVPANGTYEFGYQMHFICNEGYLLIGEEILYCELKGSVAIWSGKPPICEKV
>d1c1za5 g.18.1.1 (A:244-326) beta2-glycoprotein I {Human (Homo sapiens)}
SCKLPVKKATVVYQGERVKIQEKFKNGMLHGDKVSFFCKNKEKKCSYTEDAQCIDGTIEVPKCFKEH
SSLAFWKTDASDVKPC
>d1quba1 g.18.1.1 (A:1-62) beta2-glycoprotein I {Human (Homo sapiens)}

GRTCPKPDDLPFSTVPLKTFYEPGEEITYSCKPGYVSRGGMRKFICPLTGLWPINTLKCTP
>d1quba2 g.18.1.1 (A:63-120) beta2-glycoprotein I {Human (Homo sapiens)}
RVC PFAGILENGAVRYTTFEYPNTISFSCNTGFYLN GADSAKCTEEGKWSPELPVCAP
>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)}
VKCPFPSRPDNGFVNYPKPTLYYKDKATFGCHDGYSLDGPEEIECTKLG NWSAMPSCKA
>d1quba5 g.18.1.1 (A:244-326) beta2-glycoprotein I {Human (Homo sapiens)}
SCKVPVKKATVVYQGERVKIQEKFKNGMLHGDKVSFFCKNKEKKCSYTEDAQCIDGTIEVPKCFKEH
TDASDVKPC
>d1ghqb1 g.18.1.1 (B:1-66) Complement receptor 2, cr2 {Human (Homo sapiens)}
AISC GSPPPILNGRISYYSTPIAVGTVIRYSCSGTFRLIGEKSLLCITKDKVDGTW DKPAPKCEYF
>d1ghqb2 g.18.1.1 (B:67-129) Complement receptor 2, cr2 {Human (Homo sapiens)}
NKYSSCEPIVPGGYKIRGSTPYRHGDSVTFACKTNFSMNGNKS VWCQANNMWGPTRLPTCVS
>d1elva2 g.18.1.1 (A:342-409) Complement C1S protease domain {Human (Homo sapiens)}
LDCGIPES IENKVEDPESTLFGSVIRYTCEEPYYMENG GGGGEYHCAGNGSWVNEVLGPELPKCV
V
>d1bgk_ g.19.1.1 (-) Sea anemone toxin k {Sea anemone (Bunodosoma granulifera), BGK}
VCRDWFKETACRHA KSLGNCRTS QKYRANCAKTCELC
>d1c2ua_ g.19.1.1 (A:) Sea anemone toxin k {Sun anemone (Stichodactyla helianthus), SHK}
RSXIDTIPKSRCTAFQCKHSAKYRLSFCRKT CGTX
>d1roo_ g.19.1.1 (-) Sea anemone toxin k {Sun anemone (Stichodactyla helianthus), SHK}
RSCIDTIPKSRCTAFQCKHSMKYRLSFCRKT CGTC
>d2ech_ g.20.1.1 (-) Echistatin {Echis carinatus}
ECESG PCCR NCKFLKEGTICKRARGDDMDDYCN GKTCD CPRNPHKGPAT
>d1fvl_ g.20.1.1 (-) Flavoridin {Snake (Trimeresurus flavoviridis)}
GEECDGSPSNPCCDAATCKLRPGAQCADGLCCDQCRFKKRTICRIARGDFPDDRCTGLSND CPR
WNDL
>d1kst_ g.20.1.1 (-) Kistrin {Agkistrodon rhodostoma}
GKECDSSPENPCCDAATCKLRPGAQCGEGLCCEQCKFSRAGKICRIPRGDMPDDRCTGQSAD CPR
H
>d1mdal_ g.21.1.1 (L:) Methylamine dehydrogenase {Paracoccus denitrificans}
VDPRAKWQPQDN DIQACDYWRHCSIAGNICDCSAGSLTSCPPGTLVASGSWVGSCYNPPDPNKYITA
YRDCCGYNVSGRCACL NTEGELPVYNKDANDI IWCFGGEDGMTYHCSISPVSGA
>d2bbkl_ g.21.1.1 (L:) Methylamine dehydrogenase {Paracoccus denitrificans}
TDPRAKWVPQDN DIQACDYWRHCSIDGNICDCSGSLTNCPPGTKLATASWVASCYNPTDGQSYLIA
YRDCCGYNVSGRCPLNTEGELPVYRPEFANDI IWCFGAEDDAMTYHCTISPIV GKAS
>d1atb_ g.22.1.1 (-) Ascaris trypsin inhibitor, ATI {Pig roundworm (Ascaris Lumbricoides),
variant suum}
EA EKCTKPNEQWTKCGGCEGTCAQKIVPCTRECKPPRCECIASAGFVRDAQGN CIKFEDCPK
>d1eaic_ g.22.1.1 (C:) Ascaris elastase inhibitor {Pig roundworm (Ascaris suum)}
GQESCGPNEVWTECTGCEMKCGPDENTPCPLMCRRPSCECSPGRGMRRRTNDGKCIPASQCP
>d1coua_ g.22.1.1 (A:) Anticoagulant protein {Dog hookworm (Ancylostoma caninum)}
KATMQCGENEKYDCSGSKECDKKCKYDGV EEDDEEPNVPCLVRVCHQDCVCEE GFYRNKDDKCVS

AEDCELDNMDFIYPGTRNP

>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*)}

NFVCPGQTFQTCASSCPKTCETRNLVLCDDKKNQRCGCISGTVLKSDDSSECVHPSKC

>d1apj_ g.23.1.1 (-) Fibrillin {Human (*Homo sapiens*)}

SAQDLRMSYCYAKFEGGKCSSPKSRNHSKQECCALKGEGWGDPCELCPTPEDEAFRQICPYGSGIIV
GPDDSA

>d1exta1 g.24.1.1 (A:13-71) Tumor necrosis factor (TNF) receptor {Human (*Homo sapiens*)}

SVCPQGGKYIHPQNSICCTKCHKGTLYNDPCPGQDTDCRECESGSFTASENHLRHCL

>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*)}

NCSLCLNGTVHLSCQEKGQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIEN

>d1ncfa3 g.24.1.1 (A:116-150) Tumor necrosis factor (TNF) receptor {Human (*Homo sapiens*)}

NCSLCLNGTVHLSCQEKGQNTVCTCHAGFFLRENECVSCSN

>d1ncfb3 g.24.1.1 (B:116-155) Tumor necrosis factor (TNF) receptor {Human (*Homo sapiens*)}

NCSLCLNGTVHLSCQEKGQNTVCTCHAGFFLRENECVSCSN

>d1d0gr1 g.24.1.1 (R:21-61) Death receptor-5 (dr5) fragment {Human (*Homo sapiens*)}

SSPSEGLCPPGHHISEDGRDCISCKYQDYSTHWNDLLFCL

>d1d0gr3 g.24.1.1 (R:102-128) Death receptor-5 (dr5) fragment {Human (*Homo sapiens*)}

KCRTGCPGPMVKVGDCTPWSDIECVHK

>d1d4va1 g.24.1.1 (A:69-114) Death receptor-5 (dr5) fragment {Human (*Homo sapiens*)}

PQQRSSPSEGLCPPGHHISEDGRDCISCKYQDYSTHWNDLLFCL

>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*)}

KCRTGCPGPMVKVGDCTPWSDIECVHKESGD

>d1du3a3 g.24.1.1 (A:102-123) Death receptor-5 (dr5) fragment {Human (*Homo sapiens*)}

KCRTGCPGPMVKVGDCTPWSDI

>d1jmab1 g.24.1.1 (B:4-59) Cellular receptor HveA {Human (*Homo sapiens*)}

CKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTIAHLNGLSKCLQCQ

>d1jmab2 g.24.1.1 (B:60-105) Cellular receptor HveA {Human (*Homo sapiens*)}

MCDPAMGLRASRNSRTENAVCGCSPGHFCIVQGDHCAACRAYAT

>d1vgh_ g.25.1.1 (-) Heparin-binding domain from vascular endothelial growth factor {Human (*Homo sapiens*)}

ARQENPCGPCSERRKHLFVQDPQTCKCCKNTDSRCKARQLELNERTCRCDKPRR

>d1afp_ g.26.1.1 (-) Antifungal protein (AGAFP) {Mold (*Aspergillus giganteus*)}

ATYNGKCYKKDNICKYKAQSGKTAICKCYVKKCPRDGAKCEFDSYKKGKCYC

>d1e88a3 g.27.1.1 (A:1-41) Fibronectin {Human (*Homo sapiens*)}

YGHCVTDSGVVYSVGMQWLKTQGKQMLCTCLGNGVSCQET
>d1fbr_1 g.27.1.1 (1-46) Fibronectin {Human (Homo sapiens)}
AEKCFDHAAGTSYVVGGETWEKPYQGWMMVDCTCLGEGSGRITCTSR
>d1fbr_2 g.27.1.1 (47-93) Fibronectin {Human (Homo sapiens)}
NRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNRGEWK CERHTS
>d1qgba1 g.27.1.1 (A:17-60) Fibronectin {Human (Homo sapiens)}
SKPGCYDNGKH YQINQQWERTYLGNALVCTCYGGSRGFN CESKP
>d1qgba2 g.27.1.1 (A:61-109) Fibronectin {Human (Homo sapiens)}
EAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANR
>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)}
LTKQEEVSHIPAVHPGSFRPKCDENGNLPLQCYGSIGYCWCVFPNGTEVPNTRSRGHHNCSES
>d1e8ra_ g.29.1.1 (A:) Endo-1;4-beta-xylanase A CBDX {Pseudomonas fluorescens, subsp. cellulosa}
MGNQQCNWYGTLYPLCVTTTNGWGWEDQRSCIA RSTCAAQPAPFGIVGSG
>d1e8qa_ g.55.1.1 (A:) Cellulose docking domain, docking {Piromyces equi}
ASCWAQSQGYNCCNNPSSTKVEYTDASGQWGVQNGQWCGIDYSYGQ
>d1dtdb_ g.30.1.1 (B:) Carboxypeptidase inhibitor {Medicinal leech (Hirudo medicinalis)}
DESFLCYQPDQVCCFICRGAAPLPSEGE CNPHPTAPWCREGAVEWVPYSTGQCRTTCIPYV
>d1hdla_ g.57.1.1 (A:) Serine proteinase inhibitor lekti, domain one {Human (Homo sapiens)}
KNEDQEMCHEFQAFMKNKGLFCPQDKKFFQSLDGIMFINKCATCKMILEKEAKSQ
>d1dqca_ g.31.1.1 (A:) Tachycitin {Horseshoe crab (Tachypleus tridentatus)}
YLAFRCGRYSPCLDDGPNVNL YSCCSFYNCHKCLARLENC PKGLHYNAYLKVCDWPSKAGCTSVNKE
CHLWKT
>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)}
ANKGFLEEVVRKGNLREECLEEPSREEAFEALLESLSATDAFWAKYTACESARNPREKLNECLEGN
>d1cfi_ g.32.1.1 (-) Coagulation factor IX (IXa) {Human (Homo sapiens)}
YNSGKLEEFVQGNLERECMEEEKCSFEEAREVFENTERTTEFWKQYVD
>d1pfxl3 g.32.1.1 (L:1-46) Coagulation factor IX (IXa) {Pig (Sus scrofa)}
YNSGKLEEFVRGNLERECIEEEKCSFEEAREVFENTEKTNEFWKQYV
>d1iodg_ g.32.1.1 (G:) Coagulation factor X {Cow (Bos taurus)}
ANSFLEEVKQGNLERECLEEACSL EEAAREVFEDAEQTDEFWSKY
>d1d6ga_ g.33.1.1 (A:) Cholecystokinin A receptor, N-domain {Human (Homo sapiens)}
MDVVDSLLVNGSNITPPCELGLENETLFC LDQPRPSKEWQPAQVILL
>d1vpu_ g.34.1.1 (-) HIV-1 VPU cytoplasmic domain {Human immunodeficiency virus type

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LQIDRLIDRITERAEDSGNESEGDQEELSALVERGHLAPWDVDDL

>d1isua_g.35.1.1 (A:) HIPIP (high potential iron protein) {Rhodocyclus tenuis}
GTNAAMRKAFFNYQDTAKNGKKCSGCAQFVPGASPTAAGGCKVIPGDNQIAPGGYCDAFIVKK

>d1b0ya_g.35.1.1 (A:) HIPIP (high potential iron protein) {Allochrochromatium vinosum,
(formerly Chromatium vinosum)}
SAPANAVAADNATAIALKYNQDATKSERVAARPLPPEEQQCANCQFMQADAAGATDEWKGCQL
FPGKLINVNGWCASWTLKAG

>d1js2a_g.35.1.1 (A:) HIPIP (high potential iron protein) {Allochrochromatium vinosum,
(formerly Chromatium vinosum)}
MEFMSAPANAVAADDATAIALKYNQDATKSERVAARPLPPEEQHCANCQFMQADAAGATDEWK
GCQLFPGKLINVNGWSASWTLKAG

>d3hipa_g.35.1.1 (A:) HIPIP (high potential iron protein) {Chromatium purpuratum}
VPAVAVTESDPAAVALKYHRDAASSERVAARPLPPEEQHCENCQFMNPDSAAADWKGCQLFPG
KLINLSGWCASWTLRAG

>d2hipa_g.35.1.1 (A:) HIPIP (high potential iron protein) {Ectothiorhodospira halophila}
EPRAEDGHAHDYVNEAADASGHPRYQEGQLCENCAFWGEAVQDQGWGRCTHPDFDEVLVKAEGWC
SVYAPAS

>d1hpi_g.35.1.1 (-) HIPIP (high potential iron protein) {Ectothiorhodospira vacuolata}
MERLESEDDPAAQALEYRHDASSVQHPAYEEGQTCLNCLLYTDASAQDWGPCSVFPGKLVANGWCT
AWVAR

>d1eyta_g.35.1.1 (A:) HIPIP (high potential iron protein) {Thermochromatium tepidum}
AAPANAVTADDPTAIALKYNQDATKSERVAARPLPPEEQHCANCQFMQANVGEQDWKGCQLFP
GKLINVNGWCASWTLKAG

>d1dj7a_g.36.1.1 (A:) Ferredoxin thioredoxin reductase (FTR), catalytic beta chain
{Synechocystis sp.}
NNKTLAAMKNFAEQYAKRTDTYFCSDLVAVVIEGLARHKEELGSPCLPCRHYEDKEAEVKNTFW
NCPCVPMRERKECHCMLFLTPDNDFAGDAQDIPMETLEEVKAS

>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)}
QKPFQCRICMRNFSDHLTTHIRHTG

>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)}
RPYACPVESCDRRFSRDELTRHIRIHTG

>d1f2ig1_g.37.1.1 (G:1093-1131) ZIF268 {Mouse (Mus musculus)}
NLLNYVVPKMRPYACPVESCDRRFSRDELTRHIRIHTG

>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}
 FTKEGEHTYRCKVCSRVTTHISNFCRHYVTSHKRNVK
 >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}
 KAYACGLCNRAFTRRDLLIRHAQKIHSGL
 >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}
 PYPCLCNRAFTRRDLLIRHAQKIHSGLGE
 >d1znf_ g.37.1.1 (-) XFIN, third domain {Xenopus laevis}
 YKGLCERSFVEKSALSRRHQRVHKN
 >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)}
 TLPGRSIDKYVKEMDPKTFECLFPGCTKTFKRRYNIRSHIQTHLEDR
 >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)}
 KEFVCHWGGCSRELRFKAQYMLVVHMRRHTGE
 >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)}
 KYICEEGIRXKKPSMLKKHIRTHTDVR
 >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)}
 RPFMCTWSYCGKRFTRSDQLRHKRTHHTGK
 >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)}
TIACPHKGCTKMFRDNSAMRKHLHTHG
>d1ubdc2 g.37.1.1 (C:323-350) Ying-yang 1 (yy1, zinc finger domain) {Human (Homo sapiens)}
RVHVCAECGKAFVLESSKLRHQLVHTGE
>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}
KNFTCDSGCDLRFTTKANMKKHFNRFHNIK
>d1tf6a1 g.37.1.1 (A:10-40) Transcription factor IIIA, TFIIIA {Xenopus laevis}
YKRYICSFADCGAAYNKNWKLQAHLCCKHTGE
>d1tf6a4 g.37.1.1 (A:101-131) Transcription factor IIIA, TFIIIA {Xenopus laevis}
KICVYVCHFENCGKAFKHNQLKVHQFSHTQ
>d1tf6a5 g.37.1.1 (A:132-160) Transcription factor IIIA, TFIIIA {Xenopus laevis}
QLPYECPHEGCDKRFSRLKRHEKVHA
>d1tf6a6 g.37.1.1 (A:161-188) Transcription factor IIIA, TFIIIA {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)}
GSAAEVMKKYCSTCDISFNKYVKTLYLAHKQFYCKNKP
>d1fv5a_ g.37.1.2 (A:) U-shaped transcription factor, different fingers {Fruit fly (Drosophila melanogaster)}
GSLKPARFMCLPCGIAFSSPSTLEAHQAYYCSHRI
>d1aw6_ g.38.1.1 (-) Gal4 {Baker's yeast (Saccharomyces cerevisiae)}
MKLLSSIEQACDICRLKCLKSKEKPKCAKCLKNNWECRYSPK
>d1d66a1 g.38.1.1 (A:8-48) Gal4 {Baker's yeast (Saccharomyces cerevisiae)}
EQACDICRLKCLKSKEKPKCAKCLKNNWECRYSPKTKRSP
>d1pyia1 g.38.1.1 (A:30-71) PPR1 {Baker's yeast (Saccharomyces cerevisiae)}
SRTACKRCRLKIKCDQEFPSCKRCAKLEVPCVSLDPATGKD
>d1zmecl 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
 >d2hpc1_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}
 GSMADTRRRQNHSCDPCRKGKRRCDAPENRNEANENGWVSCSNCKRWNKDCTFNWLSSQRSKN
 SS
 >d3gata_g.39.1.1 (A:) Erythroid transcription factor GATA-1 {Chicken (Gallus gallus)}
 KRAGTVCSNCQTSTTTLWRRSPMGDPVCNACGLYYKLHQVNRPLTMRKDGITRNRKVSSKGGKR
 R
 >d7gata_g.39.1.1 (A:) Erythroid transcription factor GATA-1 {Chicken (Gallus gallus)}
 MKNGEQNGPTTCTNCFQTTPVWRRNPEGQPLCNACGLFLKLHGVRPLSLKTDVIKRRNRNSAN
 S
 >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 domain {Human (Homo
 sapiens)}
 GSFTKHICAICGDRSSGKHYGVYSCEGCKGFFKRTVRKDLTYTCRDNKDCLIDKRQRNRCQYCRYQKC
 LAMGMKREAVQEERQR
 >d2nlla_g.39.1.2 (A:) Retinoid X receptor (RXR-alpha) DNA-binding domain {Human (Homo
 sapiens)}
 CAICGDRSSGKHYGVYSCEGCKGFFKRTVRKDLTYTCRDNKDCLIDKRQRNRCQYCRYQKCLAMGM
 >d2nllb_g.39.1.2 (B:) Thyroid hormone receptor (TR-beta) DNA-binding domain {Human
 (Homo sapiens)}
 DELCVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLHPSYSCKYEGKCVIDKVTRNQCQECRFKCCIY
 VGMATDLVLDLDDSKRLAKRKLIEENREKRRREELEK
 >d1cita_g.39.1.2 (A:) Orphan nuclear receptor NGFI-B {Rat (Rattus norvegicus)}
 GRCAVCGDNASCQHYGVRTCEGCKGFFKRTVQKSAKYICLANKDCPVDKRRRNRCQFCRFQKCLAV
 GMVKEVVRTDSLKGRRGRLPSKP
 >d1hcqa_g.39.1.2 (A:) Estrogen receptor DNA-binding domain {Human and chicken (Homo
 sapiens) and (Gallus gallus)}
 MKETRYCAVCNDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCPATNQCTIDKNRRKSCQACRLRK
 CYEVGMMK
 >d1glua_g.39.1.2 (A:) Glucocorticoid receptor DNA-binding domain {Rat (Rattus
 norvegicus)}
 MKPARPCLVCSDEASGCHYGVLTCGSKVFFKRAVEGQHNYLCAGRNDCIIDKIRRNKCPACRYRKCL
 QAGMNLEARKTKK
 >d1lata_g.39.1.2 (A:) Glucocorticoid receptor DNA-binding domain {Rat (Rattus
 norvegicus)}
 RPCLVCSDEASGCHYGVLTCGCKAFFKRAVEGQHNYLCKYEGKCIIDKIRRNKCPACRYRKCLQAGM
 NLE
 >d2gda_g.39.1.2 (-) Glucocorticoid receptor DNA-binding domain {Rat (Rattus norvegicus)}

LCLVCSDEASGCHYGVLTGCGSCKVFFKRAVEGQHNYLCAGRNDICIIDKIRRKNCPCACRYRKCLQAGMNL
LEAR
>d1dsza_g.39.1.2 (A:) Retinoic acid receptor DNA-binding domain {Human (Homo sapiens)}
PCFVCQDKSSGYHYGVSAEGCKGFFRRSIQKNMVTCHRDKNCIINKVTRNRCQYCRLLQKCFEVM
SKESVRND
>d1hra_g.39.1.2 (-) Retinoic acid receptor DNA-binding domain {Human (Homo sapiens)}
PPRVYKPCFVCQDKSSGYHYGVSAEGCKGFFRRSIQKNMIYTCHRDKNCVINKVTRNRCQYCRLLQK
CFEVMGMSKESVRN
>d1a6ya_g.39.1.2 (A:) Orphan nuclear receptor reverb {Human (Homo sapiens)}
LLCKVCGDVASGFHYGVHACEGCKGFFRRSIQQNIQYKRLKNENCSIVRINRNRCQQCRFKKCLSVG
MSRDAVRFGR
>d1b8ta1_g.39.1.3 (A:1-35) Cysteine-rich (intestinal) protein, CRP, CRIP {Chicken (Gallus
gallus)}
MPNWGGGKCGVCQKAVYFAEEVQCEGSSFHKSCF
>d1b8ta2_g.39.1.3 (A:36-100) Cysteine-rich (intestinal) protein, CRP, CRIP {Chicken (Gallus
gallus)}
LCMVCKKNLDSTTVAVHGDEIYCKSCYGGKYGPKGKGMGAGTLSTDKGESLGIKYEEGQSHRP
>d1b8ta3_g.39.1.3 (A:101-143) Cysteine-rich (intestinal) protein, CRP, CRIP {Chicken (Gallus
gallus)}
TNPNASRMAQKVGSDGCPRCGQAVYAAEKVIGAGKSWHKSCF
>d1b8ta4_g.39.1.3 (A:144-192) Cysteine-rich (intestinal) protein, CRP, CRIP {Chicken (Gallus
gallus)}
RCAKCGKSLESTTLADKDGGEIYCKGCYAKNFGPKGFGFGGAGALIHSQ
>d1ctl_1_g.39.1.3 (1-35) Cysteine-rich (intestinal) protein, CRP, CRIP {Chicken (Gallus
gallus)}
MAQKVGSDGCPRCGQAVYAAEKVIGAGKSWHKSC
>d1a7i_1_g.39.1.3 (8-35) Cysteine-rich (intestinal) protein, CRP, CRIP {Japanese quail
(Coturnix coturnix japonica), CRP2}
NKCGACGRTVYHAEVQCDGRSFHRCCF
>d1a7i_2_g.39.1.3 (36-67) Cysteine-rich (intestinal) protein, CRP, CRIP {Japanese quail
(Coturnix coturnix japonica), CRP2}
LCMVCRKNLDSTTVAIHDAEVYCKSCYGGKYG
>d1ibia1_g.39.1.3 (A:117-144) Cysteine-rich (intestinal) protein, CRP, CRIP {Japanese quail
(Coturnix coturnix japonica), CRP2}
AEKCSRCDGSVYAAEKVIGAGKPWHKNC
>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)}
KCEKCGKTLTSGGHAEHEGKPYCNHPCYSAMFGPKGFGGGAESHTFK
>d1g47a1_g.39.1.3 (A:1-35) Pinch (particularly interesting new Cys-His) protein {Human
(Homo sapiens)}

MANALASATCERCKGGFAPAEEKIVNSNGELYHEQC
>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)}
MEFDYVICEEGKKEFMDSYLMDFDLPTCDDCRDAD
>d1xpa_2 g.39.1.5 (98-133) DNA repair factor XPA DNA- and RPA-binding domain, N-terminal subdomain {Human (Homo sapiens)}
MEFDYVICEEGKKEFMDSYLMNHDFDLPTCDNCRDAD
>d1jj2t_ g.39.1.6 (T:) Ribosomal protein L24e {Archaeon Haloarcula marismortui}
RECDYCGTDIEPGTGTMFVHKDGATTHFCSSKCNNADLGREARNLEWTD TAR
>d1fjgn_ g.39.1.7 (N:) Ribosomal protein S14 {Thermus thermophilus}
ARKALIEKAKRTPKFKV RAYTRCVRRCGRARSVYRFFGLCRICLRELAHKGQLPGVRKASW
>d1aaf_ g.40.1.1 (-) HIV nucleocapsid {Human immunodeficiency virus type 1, different isolates}
MQRGNFRNQRKIIKCFNCGKEGHI AKNCRAPRKRGCWKC GKEGHQMKDCTERQAN
>d1eska_ g.40.1.1 (A:) HIV nucleocapsid {Human immunodeficiency virus type 1, different isolates}
NVKCFNCGKEGHTARNCRAPRKKGCWKC GKEGHQMKDCTERQ
>d1f6ua_ g.40.1.1 (A:) HIV nucleocapsid {Human immunodeficiency virus type 1, different isolates}
MQKGNFRNQRKTVKCFNCGKEGHI AKNCRAPRKKGCWKC GKEGHQMKDCTERQAN
>d1nc8_ g.40.1.1 (-) HIV nucleocapsid {Human immunodeficiency virus type 2}
AQRKVICWNCGKEGHSARQC RARRRQG
>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}
PPGLCPRCKKGYHWKSECKSKFDK DGNPLPP
>d1f4la3 g.41.1.1 (A:141-175) Methionyl-tRNA synthetase (MetRS), Zn-domain {Escherichia coli}
VKGTC PKCKSPDQYGDNCEVCGATYSPT ELIEPKS
>d1mea_ g.41.1.1 (-) Methionyl-tRNA synthetase (MetRS), Zn-domain {Escherichia coli}
GSDRFVKGTC PKCKSPDQYGDNCEVCGA
>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 "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)}
KTGGTQTDLFTCGKCKKKNCTYTQVQTRSADPMTTFVVCNECGNRWKFC

>d1pft_ g.41.3.1 (-) Transcription initiation factor TFIIIB, N-terminal domain {Archaeon Pyrococcus furiosus}
MVNKQKVCACESAELIYDPERGEIVCAKCGYVIEENIIDMGPEWRAFDA

>d1dl6a_ g.41.3.1 (A:) Transcription initiation factor TFIIIB, N-terminal domain {Human (Homo sapiens)}
ASTSRDLALPRVTCPNHPDAILVEDYRAGDMICPECGLVVGDRVIDVGSEWRTFSNDK

>d1d0qa_ g.41.3.2 (A:) Zinc-binding domain of DNA primase {Bacillus stearothermophilus}
GHRIPETIEAIRRGVDIVDVIGEYVQLKRQGRNYFGLCPFHGEKTPSFSVSPEKQIFHCFCGAGGNA
FTFLMDIEGIPFVEAAKRLAAKAGVDLSVYELD

>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}
EKLRYLADAPQQDPEGNKTMRFRSRKTKQYVSSEKDGKATGWSAFYVDGKWVEGKK

>d1qf8a_ g.41.4.1 (A:) Casein kinase II beta subunit {Human (Homo sapiens)}
VSWISWFCGLRGNEFFCEVEDEDIQDKFNLTGLNEQVPHYRQALDMILDLEPDEELEDNPNQSDLIE
QAAEMLYGLIHARYILTNRGIAQMLEKYQQGDFGYCPRVYCNQPMPLPIGLSDIPGEAMVKLYCPKCM
DVYTPKSSRHHHTDGAYFGTGFPHMLFMVHPEYRPKRP

>d1rb9_ g.41.5.1 (-) Rubredoxin {Desulfovibrio vulgaris}
MKKYVCTVCGYEYDPAEGDPDNGVKPGTSFDDLPAWVCPVCGAPKSEFEAA

>d2rdva_ g.41.5.1 (A:) Rubredoxin {Desulfovibrio vulgaris}
MKKYVCTVCGYEYDPAEGDPDNGVKPGTAFEDVPADWVCPICGAPKSEFEPA

>d1rdg_ g.41.5.1 (-) Rubredoxin {Desulfovibrio gigas}
MDIYVCTVCGYEYDPAKGDPSGIKPGTKFEDLPDDWACPVCGASKDAFEKQ

>d6rxn_ g.41.5.1 (-) Rubredoxin {Desulfovibrio desulfuricans, strain 27774}
MQKYVCNVCGYEYDPAEHDNVPFDQLPDDWCCPVCGVSKDQFSPA

>d1iro_ g.41.5.1 (-) Rubredoxin {Clostridium pasteurianum}
MKKYTCTVCGYIYNPEDGDPDNGVNPSTDFKIPDDWVCPLCGVGKDQFEEVE

>d5rxn_ g.41.5.1 (-) Rubredoxin {Clostridium pasteurianum}
MKKYTCTVCGYIYDPEDGDPDDGVNPGTDFKIPDDWVCPLCGVGKDEFEEVEE

>d1brfa_ g.41.5.1 (A:) Rubredoxin {Archaeon Pyrococcus furiosus}
AKWVCKICGYIYDEDEDAGDPDNGISPGTKFEELPDDWVCPICGAPKSEFEKLED

>d1qcva_ g.41.5.1 (A:) Rubredoxin {Archaeon Pyrococcus furiosus}
AKWVLKITGYIYDEDEDAGDPDNGISPGTKFEELPDDWVAPITGAPKSEFEKLED

>d1dx8a_ g.41.5.1 (A:) Rubredoxin {Guillardia theta}
MEIDEGKYECEACGYIYEPEKGDKFAGIPPGTDFVLDLSDSFMCPACRSPKNQFKSIKKVIAGFAENQKY
G

>d1h7va_ g.41.5.1 (A:) Rubredoxin {Guillardia theta}
MEIDEGKYECEACGYIYEPEKGDKFAGIPPGTDFVLDLSDSFMCPACRSPKNQFKSIKKVI

>d1dvba2 g.41.5.1 (A:148-191) Rubrerythrin, C-terminal domain {Desulfovibrio vulgaris}
FLREQATKWRCRNCGYVHEGTGAPELCPACAHPKAHFELLGINW

>d1dxga_ g.41.5.2 (A:) Desulfoferredoxin {Desulfovibrio gigas}
ANEGDVYKCELCGQVVKVLEEGGGTLVCCGEDMVKQ

>d1dfx_2 g.41.5.2 (1-36) Desulfoferredoxin N-terminal domain {Desulfovibrio desulfuricans}
PKHLEVYKCTHCGNIVEVLHGGGAELVCCGEPMKHM

>d1ocrf_ g.41.5.3 (F:) Cytochrome c oxidase Subunit F {Cow (Bos taurus)}
ASGGGVPTDEEQATGLEREVMLAARKGQDPYINILAPKATSGTKEDPNLVPSITNKRIVGCICEEDNST
VIWFWLHKGEAQRCPSCGTHYKLVPHQLAH

>d1gh9a_ g.41.6.1 (A:) Hypothetical protein MTH1184 {Archaeon Methanobacterium
thermoautotrophicum}
MYIIFRCDCGRALYSREGAKTRKCVCGRTVNVKDRRIFGRADDFEEASELVRKLQEEKYGSCHFTNPS
KRE

>d1d09b2 g.41.7.1 (B:101-153) Aspartate carbamoyltransferase, Regulatory-chain,
C-terminal domain {Escherichia coli}
ERIDNVLVCPNSNCISHAEPVSSFAVRKRANDIALKCKYCEKEFSHNVLAN

>d2atcb2 g.41.7.1 (B:101-152) Aspartate carbamoyltransferase, Regulatory-chain,
C-terminal domain {Escherichia coli}
ERNIDVLVCPDSCNSNCISHAEPVSSFAVRRADDIALKCKYCEKEFSHNVLAN

>d1ffkw_ g.41.8.1 (W:) Ribosomal protein L37ae {Archaeon Haloarcula marismortui}
PTGRFGPRYGLKIRVRVRDVEIKHKKKYPVCGFPLKRASTSIWVCGHCGYKIAGGAYTPETVAGK
AVMKA

>d1jj2y_ g.41.8.1 (Y:) Ribosomal protein L37ae {Archaeon Haloarcula marismortui}
RTGRFGPRYGLKIRVRVADVEIKHKKKHKPCVCGFKLKRAGTGIWMCGHCGYKIAGGCYQPETVAG
KAVMKA

>d1jj2z_ g.41.8.2 (Z:) Ribosomal protein L37e {Archaeon Haloarcula marismortui}
TGAGTPSQGKKNNTTHTKCRRCGEKSYHTKKKVCSSCGFGKSAKRRDYEWQSKAGE

>d1jj22_ g.41.8.3 (2:) Ribosomal protein L44e {Archaeon Haloarcula marismortui}
MQMPRRFNTYCPHCNEHQEHEVEKVRSGRQTGMKWIDRQRERNSGIGNDGKFSKVPGGDKPTTK
TDLKYRCGECGKAHLREGWRAGRLEFQE

>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)}
MTTFRFCRDCNNMLYPREDKENRLLFECRTCSYVEEAGSPLVYRHELI
>d1i50i2 g.41.9.1 (I:50-122) RBP9 subunit of RNA polymerase II {Baker's yeast (Saccharomyces cerevisiae)}
TNIGETAGVVQDIGSDPTLPRSDRECPKCHSRENVFFQSQQRRKDTSMVLFFVCLSCSHIFTSDQKNK
RTQFS
>d1i50l_ g.41.9.2 (L:) RBP12 subunit of RNA polymerase II {Baker's yeast (Saccharomyces cerevisiae)}
ATLKYICAECSSKLSLRTDAVRCKDCGHRILLKARTKRLVQFEAR
>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)}
EKCEHDERLKLYCKDDGTLSCVICRDSLKHASHNFLPI
>d1fbva4 g.44.1.1 (A:356-434) CBL {Human (Homo sapiens)}
TPQDHIKVTQEYELYCEMGSTFQLCKICAENDKDVKIEPCGHLMCTSCLTSWQESEGQGPCFCRCEI
KGTEPIVVDPF
>d1rmd_2 g.44.1.1 (1-86) V(D)J recombination activating protein 1 (RAG1), dimerization domain {Mouse (Mus musculus)}
NCSKIHLSTKLLAVDFPAHFVKSISQCICEHILADPVETSCKHLFCRICILRCLKVMGSYCPSCRYPCFP
TDLESPVKSFLNILNS
>d1chc_ g.44.1.1 (-) Immediate early protein, IEEHV {Equine herpes virus type 1}
MATVAERCPICLEDPSNYSMALPCLHAFCYVCITRWIRQNPTCPLCKVPVESVHTIESDSEFGDQLI
>d1bor_ g.44.1.1 (-) Acute promyelocytic leukaemia proto-oncoprotein PML {Human (Homo sapiens)}
EEEEQFLRCQQCAEAKCPKLLPCLHTLCSGCLEASGMQCPCQAPWPLGADTPAL
>d1g25a_ g.44.1.1 (A:) TFIIH Mat1 subunit {Human (Homo sapiens)}
MDDQGCPRCKTTKYRNPSLKLMVNVCGHTLCECVDLLFVRGAGNCPECGTPLRKS NFRVQLFED
>d1e4ua_ g.44.1.1 (A:) Not-4 N-terminal RING finger domain {Human (Homo sapiens)}
MSRSPDAKEDPVECPLCMEPLEIDDINFFPCTCGYQICRFCWHRI RTDENGLCPACRKPYPEDPAVY
KPLSQEELQRI
>d1jm7a_ g.44.1.1 (A:) brca1 RING domain {Human (Homo sapiens)}
MDLSALRVEEVQNVINAMQKILECPICLELIKEPVSTKCDHIFCKFCMLKLLNQQKGPSQCPLCKNDI
TKRSLQESTRFSQLVEELLKIICAFQLDTGLEAYN
>d1jm7b_ g.44.1.1 (B:) bard1 RING domain {Human (Homo sapiens)}
MEPDGRGAWAHSRAALDRLEKLLRCSRCTNILREPVLGGCEHIFCSNVCSDCIGTGCPVCYTPAWI
QDLKINRQLDSMIQLCSKLRNLLHDNELSD
>d1dcqa2 g.45.1.1 (A:247-368) Pyk2-associated protein beta ARF-GAP domain {Mouse (Mus musculus)}
LTKEIISEVQRMTGNDVCCDCGAPDPTWLSTNLGILTCIECSGIHRELGVHYSRMQSLTLDVLGTSELL
LAKNIGNAGFNEIMECCLPSEDPVKPNPGSDMIARKDYITAKYMERRYARKKH
>d1mhu_ g.46.1.1 (-) Metallothionein {Human (Homo sapiens)}
KSCCSCPVGCAKCAQGCICKGASDKCSCCA

>d2mhu_ g.46.1.1 (-) Metallothionein {Human (Homo sapiens)}
MDPNCSAAGDSCTCAGSCKCKECKCTSCK

>d2mrb_ g.46.1.1 (-) Metallothionein {Rabbit (Oryctolagus cuniculus)}
MDPNCSAAAGDSCTCANSCTCKACKCTSCK

>d1mrt_ g.46.1.1 (-) Metallothionein {Rat (Rattus rattus)}
KSCCSCPVGCAKCSQGCICKEASDKSCCA

>d2mrt_ g.46.1.1 (-) Metallothionein {Rat (Rattus rattus)}
MDPNCSCATDGCSCAGSCKCKQCKCTSCK

>d4mt2_ g.46.1.1 (-) Metallothionein {Rat (Rattus rattus)}
MDPNCSCATDGCSCAGSCKCKQCKCTSCKKSCCSCPVGCAKCSQGCICKEASDKSCCA

>d1dfsa_ g.46.1.1 (A:) Metallothionein {Mouse (Mus musculus)}
KSCCSCPVGCSKCAQGCVCKGAADKCTCCA

>d1dfta_ g.46.1.1 (A:) Metallothionein {Mouse (Mus musculus)}
MDPNCSSTGGCTCTSSACKNCKCTSCK

>d1ji9a_ g.46.1.1 (A:) Metallothionein {Mouse (Mus musculus)}
KSCCSCPAGCEKCAKDCVCKGEEGAKAEAEKSCCQ

>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)}
QNEGHECQCQCGSCKNNEQCQKSCSPTGCNSDDKPCPGN

>d1qjka_ g.46.1.1 (A:) Metallothionein {Purple sea urchin (Strongylocentrotus purpuratus)}
PDVKVCCTEGKECACFGQDCCVTGECCKDGTCCGI

>d1qjla_ g.46.1.1 (A:) Metallothionein {Purple sea urchin (Strongylocentrotus purpuratus)}
ICTNAACKCANGCKCGSGCSTEGNCAC

>d1jjda_ g.46.1.1 (A:) Cyanobacterial metallothionein SmtA {Synechococcus sp., PCC 7942}
TLVKACCEPCLCNVDPSKAIDRNGLYYCSEACADGHTGGSKGCGHTGCNCHG

>d1co4a_ g.47.1.1 (A:) Zinc domain conserved in yeast copper-regulated transcription factors {Synthetic}
MIVINGVKYACDSCIKSHKAAQCEHNRPLKILKPRGRPPPT

>d1adn_ g.48.1.1 (-) Ada DNA repair protein, N-terminal domain (N-Ada 10) {Escherichia coli}
MKKATCLTDDQRWQSVLARDPNADGEFVFAVRTTGIFCRPSCRARHALRENVSFYANASEALAAGF
RPFCKRCQPDKANPRQHRLDKITHACR

>d1ptq_ g.49.1.1 (-) Protein kinase C-delta (PKCdelta) {Mouse (Mus musculus)}
HRFKVYNYMSPTFCDHCGSLLWGLVKQGLKCEDCGMNVHVKREKVANLC

>d1faq_ g.49.1.1 (-) RAF-1 {Human (Homo sapiens)}
LTTHNFARKTFLKLAFCDICQKFLNGFRCQTCGYKFHEHCSTKVPTMCVDW

>d1tbo_ g.49.1.1 (-) Protein kinase c-gamma {Rat (Rattus rattus)}
QTDDPRNKHKFRLLHSYSSPTFCDHCGSLLYGLVHQGMKSCCEMNVRRCVRSVPSLCGVDHTERR

>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)}
DWIDSDACMICKKFSLLNRKHHCRSCGGVFCQEHSNSIPLPDLGIYEPVRVCDSCFEDYEFIVTD
>d1joca1_g.50.1.1 (A:1348-1411) Eea1 {Human (Homo sapiens)}
KWAEDNEVQNCMACGKGFVTVRRHHCRQCIGNIFCAECSAKNALTSSKPKVVRVCDACFNDLQG
>d1dvpa2_g.50.1.1 (A:149-220) Hrs {Fruit fly (Drosophila melanogaster)}
MFTADTAPNWADGRVCHRCRVEFTFTNRKHHCRNCGQVFCGQCTAKQCPLPKYGIEKEVRVCDGCF
AALQRG
>d1zbdb_g.50.1.1 (B:) Effector domain of rabphilin-3a {Rat (Rattus norvegicus)}
EELTDEEKEIINRVIARAEMETMEQERIGRLVDRLETMRKNVAGDGVNRCILCGEQLGMLGSASVV
CEDCKKNVCTKCGVETSNNRPHPVWLCKICLEQREVWKRSGAWFFKGFQVLPQPM
>d1f62a_g.50.1.2 (A:) Williams-Beuren syndrome transcription factor, WSTF {Human
(Homo sapiens)}
ARCKVCRKKGEDDKLILCDECNKAFHLFCLRPALYEVDPDGEWQCPACQPAT
>d1fp0a1_g.50.1.2 (A:19-88) Nuclear corepressor KAP-1 (TIF-1beta) {Human (Homo
sapiens)}
GTLDDSATICRVCQKPGDLVMCNQCEFCFHLDDCHLPALQDVPGEWWSLCHVLPDLKEEDVDLQA
CKLN
>d1adt_2_g.51.1.1 (266-385) First Zn-domain of early E2A DNA-binding protein, ADDBP
{Human adenovirus type 5}
TGCALWLHRCAEIEGELKCLHGSIMINKEHVIEDVTSSENGQALKEQSSKAKIVKNRWGRNVVQIS
NTDARCCVHDAACPANQFSGKSCGMFFSEGAKAQVAFKQIKAFMQALYPNAQT
>d1adt_3_g.51.1.1 (386-529) Second Zn-domain of early E2A DNA-binding protein, ADDBP
{Human adenovirus type 5}
GHGHELLMPLRCECNSKPGHAPFLGRQLPKLTPFALSNAEDLDADLISDKSVLASVHHPALIVFQCCN
PVYRNSRAQGGPNCDFKISAPDLLNALVMVRSLSWSENFTELPRMVVPQFKWSTKHQYRNVSLPV
AHSARQNPFD
>d1qbha_g.52.1.1 (A:) 2MIHB/C-IAP-1 {Human (Homo sapiens)}
GSHMQTHAARMRTFMYPSSVPVQPEQLASAGFYVGRNDDVKCFCCDGLRCWESGDDPWVE
HAKWFPRCEFLIRMGQEFVDEIQGRYPHLLQLLSTS
>d1f9xa_g.52.1.1 (A:) BIR domains of XIAP {Human (Homo sapiens)}
MSDAVSSDRNFPNSTNLPRNPSMADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGG
GLTDWKPSEDPWEQHAKWYPGCKYLLEQKQYINNIHLTHSLEECLVRTT
>d1g73c_g.52.1.1 (C:) BIR domains of XIAP {Human (Homo sapiens)}
LPRNPSMADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQH
AKWYPGCKYLLEQKQYINNIHL
>d1g73d_g.52.1.1 (D:) BIR domains of XIAP {Human (Homo sapiens)}
LPRNPSMADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQH
AKWYPGCKYLLEQKQYINNIHLTHSLEECLVRTTE
>d1i3oe_g.52.1.1 (E:) BIR domains of XIAP {Human (Homo sapiens)}
FALDRPSETHADYLLRTGQVVDISDTIYPRNPAMYSEEARLKSFNWPDYAHLPRELASAGLYYTG
GDQVQCFACGGKLNWEPGDRAWSEHRRHFPNCFFVLGRNLNI
>d1jd5a_g.52.1.1 (A:) BIR2 domain of DIAP1 {Fruit fly (Drosophila melanogaster)}
GNYFPQYPEYAIETARLRTFEAWPRNLKQKPHQLAEAGFFYTGVDVRVRCFSCGGGLMDWVNDNDE

PWEQHALWLSQCRFVKLMKGQLYIDTVAAKPVLAEEKEES

>d1e31a_g.52.1.1 (A:) Anti-apoptotic protein survivin {Human (Homo sapiens)}

TLPPAWQPFLKDHRISTFKNWPFLEGCCTPERMAEAGFIHCPTENEPDLAQCFKCFKELEGWEPD
DDPIEEHKKHSSGCAFLSVKKQFEELTLGEFLKDRERAKNKIAKETNNKKKEFEETAKKVRRAIEQ
LAA

>d1f81a_g.53.1.1 (A:) CREB-binding transcriptional adaptor protein CBP {Mouse (Mus musculus)}

SPQESRRLSIQRCIQSLVHACQCRNANCSLPSCQMKRQVHTKGGCKRKTNGGCPVCKQLIALCCYH
AKHCQENKCPVPFCLNIKHK

>d1hc7a3_g.56.1.1 (A:404-477) C-terminal domain of ProRS {Thermus thermophilus}

TRKVDTYEAFKEAVQEGFALAFHCGDKACERLIQEETTATTRCVPFEAEPPEGFCVRCGRPSAYGKR
VVFAKAY

>d1exka_g.54.1.1 (A:) Cysteine-rich domain of the chaperone protein DnaJ. {Escherichia coli}

GVTKEIRIPTLEECDVCHGSGAKPGTQPQTCTCHGSGVQMRQGFFAVQQTCPHCQGRGTLIKDPC
NKCHGHGRVERS