The benchmark dataset $\mathbb{S}$ contains 3224 RNA sequences, which are classified into subset $\mathbb{S}^{+}$ with 1612 human pre-miRNAs (positive samples) and subset $\mathbb{S}^{-}$ with 1612 false pre-miRNAs (negative samples).

(1) 1612 human pre-miRNAs

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