```
logo
NTDB id 1166 A1552VC RS00795 WP 000168289.1    MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
NTDB id 1390 A4U84 RS00055 WP 021115958.1      ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
NTDB id 1040016 ACDH70 RS19920 WP 228962857.1  .MARGINKVILVGNLGNDPDTKYTQAGMAITRVSLATTSVRKDR.DGNNQERTEWHRVVFFGKLGEIAGEYLRKGSQVYV   78
NTDB id 1103 NMB RS07590 WP 002212976.1        ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1131 NGFG RS05740 WP 003695064.1       ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
consensus                                         **!!!!**!*!!*!!*******!*!* ****!!*****!*  !** !*!!!!*********!*!!*!!*!!* !!*

logo
NTDB id 1166 A1552VC RS00795 WP 000168289.1    EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMPAQGG.M...NVPAQ........QGSWG...QPQQPA   145
NTDB id 1390 A4U84 RS00055 WP 021115958.1      EGKLKTRKWQDQNGQDRYTTEIQG....DVLQMLDSRSSGGDFGGNQG.SGWNQAPAQTNY....NQGGYS...DNYAQN   146
NTDB id 1040016 ACDH70 RS19920 WP 228962857.1  EGELRYDKYTGQDGVEKYSTDIVA....NEMQMLGGRGEGGSGGMGGDRPQRSQAPRQQQGGGGQGGGGYGGGGQDYAPR   154
NTDB id 1103 NMB RS07590 WP 002212976.1        EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYE....................EGYGQSQEAYQRP   132
NTDB id 1131 NGFG RS05740 WP 003695064.1       EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYD....................EGYGQSQEAYQRP   132
consensus                                      !!*****!*****!**********    ****!!**! ******         * * *         ****   * **

logo
NTDB id 1166 A1552VC RS00795 WP 000168289.1    KQHQ..PM........Q.QSAPQQYSQPQYNEPPMDFDDDIPF   177
NTDB id 1390 A4U84 RS00055 WP 021115958.1      NNFNGGNA........T.RPQPAQKPAAQAEPPMDNFDDDIPF   180
NTDB id 1040016 ACDH70 RS19920 WP 228962857.1  RQ........QPAQ............QQSAPPMDDFADDDIPF   177
NTDB id 1103 NMB RS07590 WP 002212976.1        AQQSRQPASDAPSHPQEAPAAPRRQPVPAAAPVE.DIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1       AQQSRQPAPDAPSHPQEAPAAPRRQPVPAAAPVE.DIDDDIPF   174
consensus                                       *    **   *         **   * * * *** * !!!!!!
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X non conserved
X similar
X $\geq$ 50% conserved