```
logo
NTDB id 1103 NMB RS07590 WP 002212976.1        ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDRN.GQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1131 NGFG RS05740 WP 003695064.1       ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDRN.GQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1390 A4U84 RS00055 WP 021115958.1      ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
NTDB id 1041831 ACD631 RS01040 WP 039217393.1 MATKGVNKVILVGNLGNDPEVRYMPNGNAVANLSLATSESWKDQQ.GQVQERTEWHRLTMYRRLAEIAGEYLKKGSQIYV   79
NTDB id 1166 A1552VC RS00795 WP 000168289.1   MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                         **!!!!**!*!!*!!**!*!!*!*!!*****!!!!*!*!** !** !*!!!!********!!*!!*!!*!!* *!*

logo
NTDB id 1103 NMB RS07590 WP 002212976.1        EGRIQSRKYQGKDGIERTAYDIVAN....EMKMLGGRNENSGGAP.................YEEGYGQSQE..AYQRPA   133
NTDB id 1131 NGFG RS05740 WP 003695064.1       EGRIQSRKYQGKDGIERTAYDIVAN....EMKMLGGRNENSGGAP.................YDEGYGQSQE..AYQRPA   133
NTDB id 1390 A4U84 RS00055 WP 021115958.1      EGKLKTRKWQDQNGQDRYTTEIQGD....VLQMLDSRSSGGDFGG................NQGSGWNQAPAQTNYNQGG   138
NTDB id 1041831 ACD631 RS01040 WP 039217393.1 EGKLQTRKWQDQQGQDRYTTEIIVD....QMQMLGGRGGEGGGGNGGYQRPQNNQGGYNQAPAQGGYNQAPQQGGGQQGG   155
NTDB id 1166 A1552VC RS00795 WP 000168289.1   EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMPA.........QGGMNVPAQQGSWGQPQ.QPAKQ...   147
consensus                                     !!****!!*!** !**!********     **!!**!  *****                    ***! * * ***   *

logo
NTDB id 1103 NMB RS07590 WP 002212976.1        QQSRQPA.SDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1       QQSRQPA.PDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1      YSDNYAQNNNFNGGNATRPQPAQKPAAQAEPPMDNFDDDIPF   180
NTDB id 1041831 ACD631 RS01040 WP 039217393.1 YNSNQGGGYNQAPQGG...NQGQPKNPPMAEPDFDFDDDIPF   194
NTDB id 1166 A1552VC RS00795 WP 000168289.1   .........HQPMQQS...APQQYSQPQYNEPPMDFDDDIPF   177
consensus                                      ** * *    *      **  **   *** !****!!!!!!
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X non conserved

X similar

X ≥ 50% conserved