```
logo

NTDB id 1103 NMB RS07590 WP 002212976.1      ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1131 NGFG RS05740 WP 003695064.1     ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1390 A4U84 RS00055 WP 021115958.1    ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
NTDB id 52309 MRBBS RS03005 WP 041635449.1  .MARGINKVILIGNLGQDPDTRYTPNGNAVVNLSIATDESYKDRQTGQMVPKTEWHKIVMFGKVAEVAGQYLRKGSKIYV   79
NTDB id 1166 A1552VC RS00795 WP 000168289.1 MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                     **!!!!**!*!!*!!**!**!*!*!! ****!!*!***!* *!*****!!!!********!!*!!*!!*!!* *!*

logo

NTDB id 1103 NMB RS07590 WP 002212976.1      EGRIQSRKYQGKDGIERTAYDIVAN....EMKMLGGRNENSGGAPYEE........GYGQSQEAYQRPAQQSRQPASD..   142
NTDB id 1131 NGFG RS05740 WP 003695064.1     EGRIQSRKYQGKDGIERTAYDIVAN....EMKMLGGRNENSGGAPYDE........GYGQSQEAYQRPAQQSRQPAPD..   142
NTDB id 1390 A4U84 RS00055 WP 021115958.1    EGKLKTRKWQDQNGQDRYTTEIQGD....VLQMLDSRSSGGDFGGNQG.......SGWNQAPA................Q   131
NTDB id 52309 MRBBS RS03005 WP 041635449.1  EGKLQTRKWQNKDGQDVYTTEVVVD.ISGQMQMLDSRNSDGGGMNQGQ.....GQGQQGQGQP.QNRPQQQAPARPQNANQ   152
NTDB id 1166 A1552VC RS00795 WP 000168289.1 EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMPAQGGMNVPAQQGSWG..QP.Q........QPAKQHQ   149
consensus                                   !!*****!!*! **!***********     **!!**!* ***** *          **** *    *** *    ***    *

logo

NTDB id 1103 NMB RS07590 WP 002212976.1      ................APSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1     ................APSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1    TNYNQGGYSDNYAQNNNFNGGNATRPQPAQKPAAQAEPPMDNFDDDIPF   180
NTDB id 52309 MRBBS RS03005 WP 041635449.1  PPQDDGGYNQG.SQNENYNQQPVNAPS..SPQKNTMPDPVDDFDDDIPF   198
NTDB id 1166 A1552VC RS00795 WP 000168289.1 PMQQ...................SAPQ..QYSQPQYNEPPMDFDDDIPF   177
consensus                                                     *  *!    **   *  !****!!!!!!
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X non conserved

X similar

X ≥ 50% conserved