```
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 1166 A1552VC RS00795 WP 000168289.1    MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
NTDB id 1097441 ACM000 RS00970 WP 016143745.1 ..MRGVNKVILVGTLGRDPETKTFPNGGSLTQFSIATSEAWTDKNTGERKEQTEWHRIVLHNRLGEIAQQFLRKGSKVYI   78
NTDB id 1390 A4U84 RS00055 WP 021115958.1     ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
consensus                                        **!!!!**! !!*!!*****!*!*** ****!!!!*!*!***!***!*!!!!*********!*!***!*!!* !!*

logo
NTDB id 1103 NMB RS07590 WP 002212976.1        EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYEEGYGQSQEAYQRPAQQS................   136
NTDB id 1131 NGFG RS05740 WP 003695064.1       EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYDEGYGQSQEAYQRPAQQS................   136
NTDB id 1166 A1552VC RS00795 WP 000168289.1    EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGG.MPAQGGMN..V................PAQQGSWGQP   141
NTDB id 1097441 ACM000 RS00970 WP 016143745.1 EGSLRTRQWTDQNGQERYTTEIRG....DQMQMLDARQQGEQ..GFAGGNDFNQPRFNAPQQGGNGYQNNNNQGGGYGQN   152
NTDB id 1390 A4U84 RS00055 WP 021115958.1     EGKLKTRKWQDQNGQDRYTTEIQG....DVLQMLDSRSSGGD.FGGNQGSGWNQAPAQ...........TNYNQGGYSDN   142
consensus                                     !!****!***** !**!******       **!!**!* * *  **  ! *  *  ** * *          * * *

logo
NTDB id 1103 NMB RS07590 WP 002212976.1        RQP.......ASDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1       RQP.......APDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1166 A1552VC RS00795 WP 000168289.1    QQP........AKQHQ.PMQQSAPQQYSQPQYNEPPMDFDDDIPF   177
NTDB id 1097441 ACM000 RS00970 WP 016143745.1 SGGGYGSQGGFGNGGS.NPQAGGFAPKAPQQPASAPADLDDDLPF   196
NTDB id 1390 A4U84 RS00055 WP 021115958.1      ....YAQNNNFNGGNA.TRPQP..AQKPAAQAEPPMDNFDDDIPF   180
consensus                                       **          * * *  ***   * * *** *****!!!*!!
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X non conserved

X similar

X ≥ 50% conserved