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logo

NTDB id 113 BSU 40900 NP 391970.1          ....MLNRVVLVGRLTKDPELRYTPNGAAVATFTLAVNRTFTNQS.GE..READFINCVTWRRQAENVANFLKKGSLAGV   73
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  ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFRRQAEVAGQYLRKGSKVYV   78
NTDB id 989590 AAHB66 RS01365 WP 039031947.1 MASRGVNKVILVGNLGQDPEVRYMPSGGAVANITLATSESWRDKATGEMKEQTEWHRVVLFGKLAEVAGEYLRKGSQVYI   80
NTDB id 1166 A1552VC RS00795 WP 000168289.1 MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                     *!*!***! !* !!**!**!*! !!** **!***** **  !*  * **** * *****!!*****!*!!* ***

logo

NTDB id 113 BSU 40900 NP 391970.1          DGRLQTRNYENQQGQRVFVTEVQ....AESVQFLEPKNGGGSGSG...GYNEGNSGGGQ........YFGGGQNDNPFGG   138
NTDB id 1103 NMB RS07590 WP 002212976.1    EGRIQSRKYQGKDGIERTAYDIV....ANEMKMLGGRNENSGGAPYE.........EGYGQSQ.......EAYQRPAQQS   136
NTDB id 1131 NGFG RS05740 WP 003695064.1   EGRIQSRKYQGKDGIERTAYDIV....ANEMKMLGGRNENSGGAPYD.........EGYGQSQ.......EAYQRPAQQS   136
NTDB id 1390 A4U84 RS00055 WP 021115958.1  EGKLKTRKWQDQNGQDRYTTEIQ....GDVLQMLDSRSSGGD.FGG.......NQGSGWNQAPAQTNYNQGGYSDNYAQN   146
NTDB id 989590 AAHB66 RS01365 WP 039031947.1 EGQLRTRKWTDQSGAEKYTTEVVVN.VGGTMQMLGGRQG.GG.APAGGGQ...QQQGGWGQP............QQPQGG   142
NTDB id 1166 A1552VC RS00795 WP 000168289.1 EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGG.MPAQGGMNVPAQQGSWGQP............QQPAKQ   147
consensus                                   *!****!*** * ! *** ****    *  ***!****  **  *            ****          *   *

logo

NQNNQRR....NQGNSFNDDPFANDGKPIDISDDDLPF   172
RQPASDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
RQPAPDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NNFNGGN....ATRPQPAQKPAAQAEPPMDNFDDDIPF   180
NQFSGGA....QSRPQQPSAPAQSNEPPM.DFDDDIPF   175
HQPM..Q....QSAPQQY.SQPQYNEPPM.DFDDDIPF   177
consensus  *          * **            !*** !!!*!!
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X non conserved

X similar

X ≥ 50% conserved