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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 413986 DXN09 RS21900 WP 033567096.1 MASRGINKVILVGNLGQDPEVRYMPNSNAVTTLSIATSESWRDKQTGEMKEQTEWHRVVLFGKLAEVASEYLRKGSQVYI   80
NTDB id 1166 A1552VC RS00795 WP 000168289.1 MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                       **!!!!**!*!!*!!**!*!!***!! ****!!!!*!*!* *!***!*!!!!********!!*!**!!*!!* !!*

logo

NTDB id 1103 NMB RS07590 WP 002212976.1      EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYEEGY..GQSQEAYQRPAQQSRQPA...SD.....   142
NTDB id 1131 NGFG RS05740 WP 003695064.1     EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYDEGY..GQSQEAYQRPAQQSRQPA...PD.....   142
NTDB id 1390 A4U84 RS00055 WP 021115958.1    EGKLKTRKWQDQNGQDRYTTEIQG....DVLQMLDSRSSGGD.F.......GGNQGSGWNQAPAQTNYNQGGYSDNYAQN   146
NTDB id 413986 DXN09 RS21900 WP 033567096.1 EGQLRTRKWQDQHGQDRYSTEVVV.NVNGSMQMLGSRQHSGS.PSSQ...HQGSQQQGWGQPQQPVS.............   142
NTDB id 1166 A1552VC RS00795 WP 000168289.1 EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGG.MPAQGGMNVPAQQGSWGQPQQPAK.............   146
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    NNFNGGNAT.RPQPAQKPAAQAEPPMDNFDDDIPF...............   180
NTDB id 413986 DXN09 RS21900 WP 033567096.1 ....GGQPSQVGPSS..TGSSAAGMPMDFDDDIPFIGCGYGVNRVTIHAI   186
NTDB id 1166 A1552VC RS00795 WP 000168289.1 ....QHQPMQQSAPQQYSQPQYNEPPMDFDDDIPF...............   177
consensus                                        **    **    *     ********!!!!!!
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X non conserved

X similar

X ≥ 50% conserved