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logo

NTDB id 1131 NGFG RS05740 WP 003695064.1     ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDRN.GQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL    76
NTDB id 1103 NMB RS07590 WP 002212976.1     ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDRN.GQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL    76
NTDB id 1166 A1552VC RS00795 WP 000168289.1 MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI    80
NTDB id 302001 DS737 RS00875 WP 113996553.1 ..MRGVNKVILVGTLGKDPETKTFPNGGSLTQFSIATSESWTDKNTGERKEQTEWHRIVLHNRLGEIAQQYLRKGSKVYI    78
NTDB id 1390 A4U84 RS00055 WP 021115958.1   ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV    78
consensus                                      **!!!!**! !!*!!*****!*!*** ****!!!!*!*!***!***!*!!!!**********!*!**!!*!!* !!*

logo

NTDB id 1131 NGFG RS05740 WP 003695064.1     EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYDEGYGQS......QEAYQRPAQQSR.........   137
NTDB id 1103 NMB RS07590 WP 002212976.1     EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYEEGYGQS......QEAYQRPAQQSR.........   137
NTDB id 1166 A1552VC RS00795 WP 000168289.1 EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMP.AQGGMNVP....AQQGSWGQPQQPAK.........   146
NTDB id 302001 DS737 RS00875 WP 113996553.1 EGSLRTRQWTDQNGQERYSTEIRG....DQMQMLDSRQQSEQSG...GDFNQPRFNNNQGGGYQNTGHSNN......QNG   145
NTDB id 1390 A4U84 RS00055 WP 021115958.1   EGKLKTRKWQDQNGQDRYTTEIQG....DVLQMLDSRSSGGDFG...G.........NQGSGWNQAPAQTNYNQGGYSDN   142
consensus                                   !!****!***** !**!******      **!!**!* * * *   *** *       ** *********

logo

NTDB id 1131 NGFG RS05740 WP 003695064.1     .........QPAPDAP.....SHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1103 NMB RS07590 WP 002212976.1     .........QPASDAP.....SHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1166 A1552VC RS00795 WP 000168289.1 ......................QHQPMQQSAPQQYSQPQYNEPPMDFDDDIPF   177
NTDB id 302001 DS737 RS00875 WP 113996553.1 YGQGGGFNGGNQGNYAGNPQAGNGFNTPKSAPQPAA...TAPADLDDDLPF   193
NTDB id 1390 A4U84 RS00055 WP 021115958.1   YAQNNNFNGGNAT.............RPQPAQKPAAQAEPPMDNFDDDIPF   180
consensus                                              *           *   **    *     *  *****!!!*!!
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X non conserved

X similar

X $\geq$ 50% conserved