logo

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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 1351223 AHTJR RS00875 WP 004641476.1 ..MRGVNKVILVGTLGKDPETKTFPNGGSLTQFSIATSESWTDKNTGERKEQTEWHRIVLHNRLGEIAQQYLRKGSKVYI   78
NTDB id 1390 A4U84 RS00055 WP 021115958.1    ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
consensus                                       **!!!!**! !!*!!*****!*!*** ****!!!!*!*!***!***!*!!!!**********!*!**!!*!!* !!*
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NTDB id 1103 NMB RS07590 WP 002212976.1      EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYEEGYGQS......QEAYQRPAQQSR.........   137
NTDB id 1131 NGFG RS05740 WP 003695064.1     EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYDEGYGQS......QEAYQRPAQQSR.........   137
NTDB id 1166 A1552VC RS00795 WP 000168289.1  EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMP.AQGGMNVP....AQQGSWGQPQQPA..........   145
NTDB id 1351223 AHTJR RS00875 WP 004641476.1 EGSLRTRQWTDQNGQERYSTEIRG....DQMQMLDSRQQSEQSG...GDFNQPRFNNNQGGGYQNTGHNN..NQ....NG   145
NTDB id 1390 A4U84 RS00055 WP 021115958.1    EGKLKTRKWQDQNGQDRYTTEIQG....DVLQMLDSRSSGGDFG...G.........NQGSGWNQAPAQTNYNQGGYSDN   142
consensus                                    !!*****!***** !**!*******      **!!**!* * * *   *** *       ** *********
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NTDB id 1103 NMB RS07590 WP 002212976.1      .........QPASDAPS.....HPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1     .........QPAPDAPS.....HPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1166 A1552VC RS00795 WP 000168289.1  ....................KQHQPMQQSAPQQYSQPQYNEPPMDFDDDIPF   177
NTDB id 1351223 AHTJR RS00875 WP 004641476.1 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 ≥ 50% conserved