logo



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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 162432 WS71 RS25010 WP 066492547.1    ..MASVNKVILVGNLGADPEVRYLPSGDAVANVRLATTDRYKDKATGDYKEITEWHRISFFGRLAEIVSEYLKKGSSIYV   78
NTDB id 1166 A1552VC RS00795 WP 000168289.1   MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                         **!!!!**!*!! !!**!**!*!*!!*******!!*****!* *!***!*!!!!********!!****!!*!!* *!*
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NTDB id 1103 NMB RS07590 WP 002212976.1       EGRIQSRKYQGKDGIERTAYDIVANE....MKMLGGRNENSGGAPYEEGYGQSQEAYQRPAQQSRQ.....PA.......   140
NTDB id 1131 NGFG RS05740 WP 003695064.1      EGRIQSRKYQGKDGIERTAYDIVANE....MKMLGGRNENSGGAPYDEGYGQSQEAYQRPAQQSRQ.....PA.......   140
NTDB id 1390 A4U84 RS00055 WP 021115958.1     EGKLKTRKWQDQNGQDRYTTEIQGDV....LQMLDSRSSGGDFGG....N.QGSGWNQAPAQ.TNYNQGGYSDN.....Y   143
NTDB id 162432 WS71 RS25010 WP 066492547.1    EGKIRTRKWQGQDGQDRYSTEIVADQ....MQMLGGRNGGGRGEG..GGY.GGDGEF....EQGTRRQASPPAARPAPSQ   147
NTDB id 1166 A1552VC RS00795 WP 000168289.1   EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQG.......GM.PAQGGMNVPAQQGSWGQPQQPAKQHQPM.   151
consensus                                     !!****!!*!***!**!********    **!!**!*  **  **    **  *******  *****    *    **
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NTDB id 1103 NMB RS07590 WP 002212976.1       ...SDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF............   174
NTDB id 1131 NGFG RS05740 WP 003695064.1      ...PDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF............   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1     AQNNNFNGGNATRPQPAQKPAAQAEPPMDNFDDDIPF............   180
NTDB id 162432 WS71 RS25010 WP 066492547.1    APANTAARTQHSAPPPDQTRSYGGGGFADMDDDIPFLGWHTRAAWSVI   196
NTDB id 1166 A1552VC RS00795 WP 000168289.1   ...Q......QSAPQQYSQPQY..NEPPMDFDDDIPF............   177
consensus                                         *  *     ***!     *     ********!!!!!!
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X non conserved
X similar
X ≥ 50% conserved