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logo

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 66349 AS4 RS00990 WP 096732634.1     ..MRGVNKVILVGTLGRDPETKTFPNGGSLTQFSIATSESWTDKNSGERKEQTEWHRIVLHNRLGEIAQQYLRKGSKVYI   78
NTDB id 1390 A4U84 RS00055 WP 021115958.1    ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
consensus                                       **!!!!**! !!*!!*****!*!*** ****!!!!*!*!***!***!*!!!!**********!*!**!!*!!* !!*

logo

NTDB id 1103 NMB RS07590 WP 002212976.1      EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYE.EGYGQSQE.......A.................   128
NTDB id 1131 NGFG RS05740 WP 003695064.1     EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYD.EGYGQSQE.......A.................   128
NTDB id 1166 A1552VC RS00795 WP 000168289.1  EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMPA..QGGMNVPAQ.....QGSWGQ..............   140
NTDB id 66349 AS4 RS00990 WP 096732634.1     EGSLRTRQWTDQNGQERYTTEIRG....EQMQMLDNNRQQGEGAAADNGGYNQPRF.NNNQQGGFNNNQGGGGYANQGNQ   153
NTDB id 1390 A4U84 RS00055 WP 021115958.1    EGKLKTRKWQDQNGQDRYTTEIQG....DVLQMLDSRSSGGDFGGNQGSGWNQAPAQTNYNQGGYSD.............   141
consensus                                    !!*****!***** !**!*******       **!!***  ****** *  !***         ****

logo

NTDB id 1103 NMB RS07590 WP 002212976.1      ...YQRPAQQSRQPA.SDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1     ...YQRPAQQSRQPA.PDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1166 A1552VC RS00795 WP 000168289.1  ......PQQ.......PAKQHQPMQQSAPQQYSQPQYNEPPMDFDDDIPF   177
NTDB id 66349 AS4 RS00990 WP 096732634.1     GGGYGNANPQGGYGNGGNNVNQGFQSPKPAVAPSAPTAAP.ADLDDDLPF   202
NTDB id 1390 A4U84 RS00055 WP 021115958.1    ......NYAQNNNFNGGN.....ATRPQPAQKPAAQAEPPMDNFDDDIPF   180
consensus                                       *  * **  *          *   ***  *   ****!****!!!*!!
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X non conserved

X similar

X ≥ 50% conserved