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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 207808 BSR55 RS20190 WP 004826134.1   ..MRGVNKVILVGTLGRDPETKTFPNGGSLTQFSIATSESWTDKNSGERKEQTEWHRIVLHNRLGEIAQQYLRKGSKVYI   78
NTDB id 1390 A4U84 RS00055 WP 021115958.1     ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
consensus                                        **!!!!**! !!*!!*****!*!*** ****!!!!*!*!***!***!*!!!!*********!*!**!!*!!* !!*

logo

NTDB id 1131 NGFG RS05740 WP 003695064.1      EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYDEGYGQSQE.......................   127
NTDB id 1103 NMB RS07590 WP 002212976.1       EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYEEGYGQSQE.......................   127
NTDB id 1166 A1552VC RS00795 WP 000168289.1   EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQ.GGMPAQGGMNV...P.....................AQQG   136
NTDB id 207808 BSR55 RS20190 WP 004826134.1   EGSLRTRQWTDQNGQERYTTEIRG....EQMQMLDNNRQQ.GEAGENGGY..NQ.PRFNNNQQGGFNNNQGGGYNQGNQG   150
NTDB id 1390 A4U84 RS00055 WP 021115958.1     EGKLKTRKWQDQNGQDRYTTEIQG....DVLQMLDSRSSG.GDFGGNQGSGWNQAPAQTN................YNQG   137
consensus                                     !!*****!***** !**!*******       **!!***  * !*** * !**  * *                    ***

logo

NTDB id 1131 NGFG RS05740 WP 003695064.1      AYQRPAQQSRQP.APDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1103 NMB RS07590 WP 002212976.1       AYQRPAQQSRQP.ASDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1166 A1552VC RS00795 WP 000168289.1   SWGQPQQ.......PAKQHQPMQQSAPQQYSQPQYNEPPMDFDDDIPF   177
NTDB id 207808 BSR55 RS20190 WP 004826134.1   GYGNAAPQGGYGNGGNNVNQGFQSPKPQQAP....ATAPADLDDDLPF   194
NTDB id 1390 A4U84 RS00055 WP 021115958.1     GYSDNYAQNNNFNGGNA.....TRPQPAQKPAAQAEPPMDNFDDDIPF   180
consensus                                     **  ****  *  *  *   *   *** **    ** *****!!!*!!
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X non conserved

X similar

X $\geq$ 50% conserved