```
logo
NTDB id 1103 NMB RS07590 WP 002212976.1      ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1131 NGFG RS05740 WP 003695064.1     ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1166 A1552VC RS00795 WP 000168289.1  MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
NTDB id 213397 BVG18 RS14995 WP 004281391.1 ..MRGVNKVILVGTLGKDPETKTFANGGSLTQFSIATSDSWTDKSTGERKEQTEWHRIVLHNRLGEIAQQYLRKGSKVYI   78
NTDB id 1390 A4U84 RS00055 WP 021115958.1   ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
consensus                                       **!!!!**! !!*!!*******!*** ****!!!**!*!* *!***!*!!!!**********!*!**!!*!!* !!*

logo

NTDB id 1103 NMB RS07590 WP 002212976.1      EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGA.......................PYEEGYGQ..SQ   126
NTDB id 1131 NGFG RS05740 WP 003695064.1     EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGA.......................PYDEGYGQ..SQ   126
NTDB id 1166 A1552VC RS00795 WP 000168289.1  EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGM.................................PAQ   126
NTDB id 213397 BVG18 RS14995 WP 004281391.1 EGSLRTRQWTDQNGQERYTTEIRG....EQMQMLDSSRPQNDQGESSFNQPRFNNNNQANNNQGGYGNNPQSGYGSAPQQ   154
NTDB id 1390 A4U84 RS00055 WP 021115958.1   EGKLKTRKWQDQNGQDRYTTEIQG....DVLQMLDSRSSGGDFG.......................GNQGSGWNQAPAQ   131
consensus                                   !!*****!***** !**!*******      **!!***  * * *                          **** * !

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NTDB id 1103 NMB RS07590 WP 002212976.1      EAYQRPAQQSRQPASDAP..SHPQEAPAAPRRQP.VPAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1     EAYQRPAQQSRQPAPDAP..SHPQEAPAAPRRQP.VPAAAPVEDIDDDIPF   174
NTDB id 1166 A1552VC RS00795 WP 000168289.1  GGMNVPAQQGSWGQPQQPAKQHQPMQQSAPQQYSQPQYNEPPMDFDDDIPF   177
NTDB id 213397 BVG18 RS14995 WP 004281391.1 GGFNN.....NQG..GG..YGNNNPSGFAPKSAPA.PTAAPAADLDDDLPF   195
NTDB id 1390 A4U84 RS00055 WP 021115958.1   TNYNQGGYSDNYAQNNN..FNGGNATRPQPAQKPAAQAEPPMDNFDDDIPF   180
consensus                                    *** ****  **   **   * *    *!*  *  ****!****!!!*!!
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X non conserved

X similar

X ≥ 50% conserved