```
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 87576 TOL5 RS01050 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 87576 TOL5 RS01050 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 87576 TOL5 RS01050 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