```
logo
NTDB id 1131 NGFG RS05740 WP 003695064.1     ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1103 NMB RS07590 WP 002212976.1     ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1390 A4U84 RS00055 WP 021115958.1   ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
NTDB id 324646 EFO25 RS29495 WP 015877024.1 ..MASVNKVILVGNLGADPEVRYLPSGDAVANIRLATTDRYKDKASGDFKEMTEWHRVAFFGRLAEIVNEYLKKGSSVYI   78
NTDB id 1166 A1552VC RS00795 WP 000168289.1 MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                     **!!!!**!*!! !!**!**!*!*!!*****!!*****!* *!***!*!!!!********!!****!!*!!* !!*

logo
NTDB id 1131 NGFG RS05740 WP 003695064.1     EGRIQSRKYQGKDGIERTAYDIVAN....EMKMLGGRNENSGGA....................PYDEGYGQSQEAYQ...   130
NTDB id 1103 NMB RS07590 WP 002212976.1     EGRIQSRKYQGKDGIERTAYDIVAN....EMKMLGGRNENSGGA....................PYEEGYGQSQEAYQ...   130
NTDB id 1390 A4U84 RS00055 WP 021115958.1   EGKLKTRKWQDQNGQDRYTTEIQGD....VLQMLDSRSSGGDFGGNQGSGWNQAPAQTNYNQGGYSDNYAQNN.......   147
NTDB id 324646 EFO25 RS29495 WP 015877024.1 EGRLRTRKWQGQDGQDRYSTEIVAD....QMQMLGGRGGSGGGGGGGGDDG.........YGGGGYGGGGGRGGDMERGGG   145
NTDB id 1166 A1552VC RS00795 WP 000168289.1 EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMPAQGGMN.......................V.......   131
consensus                                   !!****!!*!***!**!********      **!!**!  ******                  * ***** **

logo
NTDB id 1131 NGFG RS05740 WP 003695064.1     .RPAQQSRQPAPDAPSH.....PQEAPAAPRRQP.VPAAAPVEDIDDDIPF   174
NTDB id 1103 NMB RS07590 WP 002212976.1     .RPAQQSRQPASDAPSH.....PQEAPAAPRRQP.VPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1   ................NFNGGNATRP.QPAQKPAAQAEPPMDNFDDDIPF   180
NTDB id 324646 EFO25 RS29495 WP 015877024.1 GGRASGGGGGASRGGSGG...GGSSR...P...SQP.AGGGLDEMDDDIPF   186
NTDB id 1166 A1552VC RS00795 WP 000168289.1 ..PAQQGSWGQPQQPAKQHQPMQQSA...PQQYSQPQYNEPPMDFDDDIPF   177
consensus                                     ****    *  ***       ****  !   *   ********!!!!!!
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X non conserved

X similar

X ≥ 50% conserved