```
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 289788 BTJ40 RS02875 WP 108731682.1 .MARGINKVILIGNLGNDPETKYMPSGGAVTNISLATSESWKDKQTGQQQERTEWHRVVFFNRLAEIAGEYLRKGAKVYV   79
NTDB id 1166 A1552VC RS00795 WP 000168289.1 MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                    **!!!!**!*!!*!!****!!*!*!! ****!!!!*!*!* *!** !*!!!!********!!*!!*!!*!!* !!*

logo
NTDB id 1131 NGFG RS05740 WP 003695064.1     EGRIQSRKYQGK.DGIERTAYDIVAN....EMKMLGGRNENSGGAPY.........................DEGYGQS   125
NTDB id 1103 NMB RS07590 WP 002212976.1     EGRIQSRKYQGK.DGIERTAYDIVAN....EMKMLGGRNENSGGAPY.........................EEGYGQS   125
NTDB id 1390 A4U84 RS00055 WP 021115958.1   EGKLKTRKWQDQ.NGQDRYTTEIQGD....VLQMLDSRSSGGDFGGNQGSGWNQA...............PAQTNYNQGGY   139
NTDB id 289788 BTJ40 RS02875 WP 108731682.1 EGSLRTRKWQDKNSGQDRYTTEIVAS....EMQMLDGRGEQGGFGQGMGGAGMGAAAGGQMGGGQPMGGPSGFDQQGGGF   155
NTDB id 1166 A1552VC RS00795 WP 000168289.1 EGQLQTRKWQDQ.SGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMPAQG.............................   127
consensus                                   !!*****!!*!**  !**!*******    ***!!**! **** *                          *   *

logo
NTDB id 1131 NGFG RS05740 WP 003695064.1     QEAYQRPAQQSRQPAP...DAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1103 NMB RS07590 WP 002212976.1     QEAYQRPAQQSRQPAS...DAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1   SDNYAQNNN...FNGG.NATR.......PQPAQKPAAQAEPPMDNFDDDIPF   180
NTDB id 289788 BTJ40 RS02875 WP 108731682.1 QGGYQQQGGQEAYGQGRTAPSPMAPANQQPQQQPNQGPAGGFDNSFDDDIPF   207
NTDB id 1166 A1552VC RS00795 WP 000168289.1 ..GMNVPAQQGSWGQPQQPAKQHQPMQQSAPQQYSQPQYNEPPMDFDDDIPF   177
consensus                                   ***** **** * * *  *  **  ***  *********!!!!!!
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X non conserved

X similar

X ≥ 50% conserved