```
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 155015 AK825 RS11245 WP 068037407.1 ..MRGVNKVIIIGNLGADPEARQFNNGGSVTNISVATSEQWTDKQSGEKREATEWHRIALFNRLGEIAAQYLRKGSKVYI   78
NTDB id 1390 A4U84 RS00055 WP 021115958.1   ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
consensus                                      **!!!!**!*!! !!**!****!**! ****!!!!*!*!* *!***!*!!!!*********!*!**!!*!!* !!*

logo
NTDB id 1103 NMB RS07590 WP 002212976.1      EGRIQSRKYQGKDGIERTAYDIVAN....EMKMLGGRNENSGGAPYEE.................................   120
NTDB id 1131 NGFG RS05740 WP 003695064.1     EGRIQSRKYQGKDGIERTAYDIVAN....EMKMLGGRNENSGGAPYDE.................................   120
NTDB id 1166 A1552VC RS00795 WP 000168289.1 EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMPAQGG...............................MNVP   132
NTDB id 155015 AK825 RS11245 WP 068037407.1 EGSLRTRKYQDQSGQDRYITEIRAE....QMQMLDGTSSGGQDSNNFGGQGSNQNQGGSYGNQGGQSNQNNFGQQANNQP   154
NTDB id 1390 A4U84 RS00055 WP 021115958.1   EGKLKTRKWQDQNGQDRYTTEIQGD....VLQMLDSRSSGGDFGGNQGS.GWNQAPAQ....................TN   133
consensus                                   !!*****!!*!** !**!* ******     **!!***  *** * * *

logo
NTDB id 1103 NMB RS07590 WP 002212976.1      ....GYGQSQEAYQRPAQQSRQPASDAP......SHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1     ....GYGQSQEAYQRPAQQSRQPAPDAP......SHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1166 A1552VC RS00795 WP 000168289.1 AQQGSWGQPQ................QPAKQ...HQPMQQSAPQQYSQPQYNEPPMDFDDDIPF   177
NTDB id 155015 AK825 RS11245 WP 068037407.1 AQQGGYNQAGGAAAQGSNQNSFNNQNAPAQQNQFNQPTQTP....AQSKPTAMPDGPVDDDIPF   214
NTDB id 1390 A4U84 RS00055 WP 021115958.1   YNQGGYSDN......YAQNNNFNGGNAT.....RPQPAQKP....AA..QAEPPMDNFDDDIPF   180
consensus                                    ******* * *    ***    *  **       *! * **    *  *** !****!!!!!!
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X non conserved

X similar

X ≥ 50% conserved