```
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 1390 A4U84 RS00055 WP 021115958.1        ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
NTDB id 1145356 DAQ1742 RS16960 WP 035344079.1  MASRGVNKVILIGNLGQDPEVRYMPNGGAVANLTLATSDSWRDKQTGEQKERTEWHRVALYGKLAEIAGEYLRKGSQVYI   80
NTDB id 1166 A1552VC RS00795 WP 000168289.1     MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                           **!!!!**!*!!*!!**!*!!*!*!!*****!!!**!*!* *!***!*!!!!********!!*!!*!!*!!* !!*

logo
NTDB id 1103 NMB RS07590 WP 002212976.1          EGRIQSRKYQGKDGIERTAYDIVAN....EMKMLGGRNENSGGAPYEE..GYGQSQ.........EAYQRPAQ..QSRQP   139
NTDB id 1131 NGFG RS05740 WP 003695064.1         EGRIQSRKYQGKDGIERTAYDIVAN....EMKMLGGRNENSGGAPYDE..GYGQSQ.........EAYQRPAQ..QSRQP   139
NTDB id 1390 A4U84 RS00055 WP 021115958.1        EGKLKTRKWQDQNGQDRYTTEIQGD....VLQMLDSRSSGGD.F..GGNQGSGWNQAPAQTNYNQGGYS..DNYAQNNNF   149
NTDB id 1145356 DAQ1742 RS16960 WP 035344079.1  EGQLRTRKWQDQSGQDRYTTEVVVD.VSGSMQMLGGRSGGG..APAGGNMGGGNMGNAMGGNAPQGGWGQPQQPQQANQF   157
NTDB id 1166 A1552VC RS00795 WP 000168289.1     EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQGGG.MPAQG.........GMNVPAQQGSWGQPQQPAKQHQP   150
consensus                                       !!****!!*!** !**!********     **!!**!  *** **  *  * ** *        ****  * *  *  **

logo
NTDB id 1103 NMB RS07590 WP 002212976.1          ASDAPSHPQEAPAAPRRQP.VPAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1         APDAPSHPQEAPAAPRRQP.VPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1        NGGNATRPQP.....AQKPAAQAEPPMDNFDDDIPF   180
NTDB id 1145356 DAQ1742 RS16960 WP 035344079.1  SGGAQSRPQQ.....SAPM.PGNEPP.MDFDDDIPF   186
NTDB id 1166 A1552VC RS00795 WP 000168289.1     ..MQQSAPQQ.....YSQP.QYNEPP.MDFDDDIPF   177
consensus                                          * * !!         **    ***!****!!!!!!
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X non conserved

X similar

X ≥ 50% conserved