```
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 357616 E5677 RS02515 WP 062845291.1  ..MRGVNKVIIIGNLGADPEARQFSNGGSVTNISVATSEQWTDKQSGEKREATEWHRISLFNRLGEIAAQYLRKGSKVYI   78
NTDB id 1390 A4U84 RS00055 WP 021115958.1    ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
NTDB id 1166 A1552VC RS00795 WP 000168289.1 MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                       **!!!!**!*!! !!**!****!**! ****!!!!*!*!* *!***!*!!!!*********!*!**!!*!!* !!*

logo
NTDB id 1103 NMB RS07590 WP 002212976.1      EGRIQSRKYQGKDGIERTAYDIVAN....EMKMLGGRNENSGGAPY......EEGYGQS................QEAYQ   130
NTDB id 1131 NGFG RS05740 WP 003695064.1     EGRIQSRKYQGKDGIERTAYDIVAN....EMKMLGGRNENSGGAPY......DEGYGQS................QEAYQ   130
NTDB id 357616 E5677 RS02515 WP 062845291.1  EGSLRTRKYQDPNGQDRYITEIRAE....QMQMLDGQSGGQDSSNFGGQNQGQGGYGNQGGQSNQNNFGQQANNQQGGYN   154
NTDB id 1390 A4U84 RS00055 WP 021115958.1    EGKLKTRKWQDQNGQDRYTTEIQGD....VLQMLDSFSSGGDF...GGNQ.GS.GWN.........QAPAQTNYNQGGYS   140
NTDB id 1166 A1552VC RS00795 WP 000168289.1 EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAAQQGGMPAQGGMNV.....................PAQQGSWG   139
consensus                                   !!*****!!*!*  !**!* ******     **!!***  * *   *** *    ****               *!****

logo
NTDB id 1103 NMB RS07590 WP 002212976.1      RPAQQS..........RQPASDA..PSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1     RPAQQS..........RQPAPDA..PSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 357616 E5677 RS02515 WP 062845291.1  QAVGASQGGQNSFNNQNAPAQQNQFNQPTQQR....PAQSKPTAMPDGPVDDDIPF   206
NTDB id 1390 A4U84 RS00055 WP 021115958.1    DNYAQ....NNNFNGGNATR.....PQPAQKP....AAQ...AEPPMDNFDDDIPF   180
NTDB id 1166 A1552VC RS00795 WP 000168289.1 QP..............QQPAKQ...HQPMQQSAPQQYSQPQ.YNEPPMDFDDDIPF   177
consensus                                    *  **          ****     *** !        !* *** !****!!!!!!
```

X non conserved

X similar

X ≥ 50% conserved