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 1178649 A6F57 RS11215 WP 057794667.1 MATKGVNKVILVGNLGNDPEVRYMPNGNAVANLSLATSESWKDP.QGQMQERTEWHRLTMYRRLAEIAGEYLKKGSQIYV   79
NTDB id 1166 A1552VC RS00795 WP 000168289.1 MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                    **!!!!**!*!!*!!**!*!!*!*!!*****!!!!*!*!* *!** !*!!!!*********!!*!!*!!*!!* *!*
```

logo

```
NTDB id 1103 NMB RS07590 WP 002212976.1     EGRIQSRKYQGKDGIERTAYDIVANE....MKMLGGRNENSGGAPY.....................EEGYGQSQEAYQRPA   133
NTDB id 1131 NGFG RS05740 WP 003695064.1    EGRIQSRKYQGKDGIERTAYDIVANE....MKMLGGRNENSGGAPY.....................DEGYGQSQEAYQRPA   133
NTDB id 1390 A4U84 RS00055 WP 021115958.1   EGKLKTRKWQDQNGQDRYTTEIQGDV....LQMLDSRSSGGDFGGNQGSGWNQAPAQTNYNQGGYSDNY.......AQNN   147
NTDB id 1178649 A6F57 RS11215 WP 057794667.1 EGKLQTRKWQDQSGQDRYTTEIIVDQ....MQMLGGRGGEGGG.GNAGGGYQRPQN...NQQGGYQQQGGQSQGGYQQQG   151
NTDB id 1166 A1552VC RS00795 WP 000168289.1 EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGM.PAQGG.MNVPAQ.....QGS.............   137
consensus                                    !!****!!*!** !**!********      **!!**!  ******  *   *          **   * ***** ***  *
```

logo

```
NTDB id 1103 NMB RS07590 WP 002212976.1     QQSRQPASDA...PSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1    QQSRQPAPDA...PSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1   .NFNGGNAT....RPQP......AQKPAAQAEPPMDNFDDDIPF   180
NTDB id 1178649 A6F57 RS11215 WP 057794667.1 GQSQGGQNQGGYQQQAPNQGGGQSQPKQPPMAEPDFDFDDDIPF   195
NTDB id 1166 A1552VC RS00795 WP 000168289.1 ....WGQPQQPAKQHQPMQQSAPQQYSQPQYNEPPMDFDDDIPF   177
consensus                                    **  **  *      !* * *  **   *** !****!!!!!!
```

X non conserved

X similar

X ≥ 50% conserved