logo

```
NTDB id 1131 NGFG RS05740 WP 003695064.1          ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYR.KLAEIAGQYLKKGGLVY   75
NTDB id 1103 NMB RS07590 WP 002212976.1           ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYR.KLAEIAGQYLKKGGLVY   75
NTDB id 1390 A4U84 RS00055 WP 021115958.1         ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFR.RQAEVAGQYLRKGSKVY   77
NTDB id 240532 ANTHELSMS3 RS17865 WP 094036060.1  .MAGSVNKVILVGNLGRDPEVRTFQNGGKVCNLRIATSENWKDRSTGERRERTEWHSVAIFQEGLVRVAEQYLRKGSKVY   79
NTDB id 1166 A1552VC RS00795 WP 000168289.1       MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYG.KLAEVAGEYLRKGSQVY   79
consensus                                              **!!!!**!*!!*!!**!****!**!*****!!!!*!*!* *!***!*!!!! ***** *****!**!!*!!* !!
```

logo

```
NTDB id 1131 NGFG RS05740 WP 003695064.1          LEGRIQSRKYQGKDGIERTAYDIV....ANEMKMLGGRNENSGGAPY.....DEGYG.QSQEAYQRPAQQSRQPAPDAPS   145
NTDB id 1103 NMB RS07590 WP 002212976.1           LEGRIQSRKYQGKDGIERTAYDIV....ANEMKMLGGRNENSGGAPY.....EEGYG.QSQEAYQRPAQQSRQPASDAPS   145
NTDB id 1390 A4U84 RS00055 WP 021115958.1         VEGKLKTRKWQDQNGQDRYTTEIQ....GDVLQMLDSRSSGGDFGGNQGSGWNQA...PAQTNYNQGGYSDNYAQNNNFN   150
NTDB id 240532 ANTHELSMS3 RS17865 WP 094036060.1  IEGQLQTRKWQDQSGQDRYSTEVVLQGFGGTLVMLDGRSEGGGGGGGGFSGGGSDYGGGGGGGYDDPGYGGGS.......   152
NTDB id 1166 A1552VC RS00795 WP 000168289.1       IEGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMPAQGG....MNVP.AQQGSWGQPQQPAKQHQPM...   151
consensus                                         *!!****!!*!** !**!******    *  * !!***! *******        ***   * *** ***  **
```

logo

```
NTDB id 1131 NGFG RS05740 WP 003695064.1          HP.QEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1103 NMB RS07590 WP 002212976.1           HP.QEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1         GGNATRPQPAQKPAAQAEPPMDNFDDDIPF   180
NTDB id 240532 ANTHELSMS3 RS17865 WP 094036060.1  ......SGGSGGGSGPSRAPSRDIDDEIPF   176
NTDB id 1166 A1552VC RS00795 WP 000168289.1       ....QQSAPQQYSQPQYNEPPMDFDDDIPF   177
consensus                                              ***  *   ** *!****!!*!!!
```

X non conserved

X similar

X ≥ 50% conserved