```
logo
NTDB id 1103 NMB RS07590 WP 002212976.1      ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDRN.GQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1131 NGFG RS05740 WP 003695064.1     ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDRN.GQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1390 A4U84 RS00055 WP 021115958.1    ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
NTDB id 31116 CJA RS03555 WP 041551011.1     .MARGINKVILIGNIGQDPEVKYMPSGGAVTNISVATSETWKDKNTGQAQERTEWHRVVLFNRLGEIAGEYLRKGSKVYI   79
NTDB id 1166 A1552VC RS00795 WP 000168289.1 MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                     **!!!!**!**!*!****!!*!*!! ****!!!!*!*!***!** !*!!!!*********!*!!*!!*!!* !!*
```

```
logo
NTDB id 1103 NMB RS07590 WP 002212976.1      EGRIQSRKYQGKDGIERTAYDIVANE....MKMLGGRNENSGGAPYE...........EGYGQ.................   124
NTDB id 1131 NGFG RS05740 WP 003695064.1     EGRIQSRKYQGKDGIERTAYDIVANE....MKMLGGRNENSGGAPYD...........EGYGQ.................   124
NTDB id 1390 A4U84 RS00055 WP 021115958.1    EGKLKTRKWQDQNGQDRYTTEIQGD....VLQMLDSRSSGGDFGGNQ.......G...SGWNQAPAQ...........TN   133
NTDB id 31116 CJA RS03555 WP 041551011.1     EGSLRTRKWQGQDGSDRYTTEIVASE....MQMLDGRGDNAGAGMGGGAAAGAMGAGMGGYDQSPQYNSAPQGGFNQGGG   155
NTDB id 1166 A1552VC RS00795 WP 000168289.1 EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMPAQGGMNVPAQ.........................   134
consensus                                    !!*****!!*!***! *!********     **!!**! ******              ** *
```

```
logo
NTDB id 1103 NMB RS07590 WP 002212976.1      .SQEAYQRPAQQSRQPASDAPSHPQEAPAAPRRQPV..PAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1     .SQEAYQRPAQQSRQPAPDAPSHPQEAPAAPRRQPV..PAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1    YNQGGYSDNYAQNNNNFNGGNATRP.....QPAQKPAAQAEP.PMDNFDDDIPF   180
NTDB id 31116 CJA RS03555 WP 041551011.1     YNQGGYNPQQQPNRGF.......N.....QPAQNPAPNNPPSGFDSFDDDIPF   196
NTDB id 1166 A1552VC RS00795 WP 000168289.1 ..QGSWGQPQQPAKQHQPMQQSAP.....QQYSQPQYNEPPM...DFDDDIPF   177
consensus                                     !**** * ** **       * *      **   *!   *   * *****!!!!!!
```

X non conserved

X similar

X ≥ 50% conserved