```
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 1146679 VCBK1071 RS12370 WP 000168287.1  MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI    80
NTDB id 1166 A1552VC RS00795 WP 000168289.1      MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI    80
NTDB id 1390 A4U84 RS00055 WP 021115958.1        ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV    78
consensus                                            **!!!!**!*!!*!!**!*!!*!*!!*****!!!!*!*!* *!***!*!!!!*********!!*!!*!!*!!* !!*

logo

NTDB id 1103 NMB RS07590 WP 002212976.1          EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYEEGYGQSQ.........EAYQRPAQQSRQPASDA   143
NTDB id 1131 NGFG RS05740 WP 003695064.1         EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYDEGYGQSQ.........EAYQRPAQQSRQPAPDA   143
NTDB id 1146679 VCBK1071 RS12370 WP 000168287.1  EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQG.GMPAQGG...MNAPAQ....QGSWGQPQQPAK....QH   148
NTDB id 1166 A1552VC RS00795 WP 000168289.1      EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQG.GMPAQGG...MNVPAQ....QGSWGQPQQPAK....QH   148
NTDB id 1390 A4U84 RS00055 WP 021115958.1        EGKLKTRKWQDQNGQDRYTTEIQG....DVLQMLDSRSSGG.DFGGNQGSGWNQAPAQTNYNQGGYSDNYAQNN....NF   149
consensus                                        !!*****!!*!** !**!*******     ***!!**!  ** * *** ! *  * ***    ****  * ** *    *

logo

NTDB id 1103 NMB RS07590 WP 002212976.1          PSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1         PSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1146679 VCBK1071 RS12370 WP 000168287.1  Q..PMQQSAPQQYSQPQYNEPPMDFDDDIPF   177
NTDB id 1166 A1552VC RS00795 WP 000168289.1      Q..PMQQSAPQQYSQPQYNEPPMDFDDDIPF   177
NTDB id 1390 A4U84 RS00055 WP 021115958.1        NGGNATRPQPAQKPAAQAEPPMDNFDDDIPF   180
consensus                                        *  *   *** **   **  !****!!!!!!
```

X non conserved

X similar

X ≥ 50% conserved