```
logo
NTDB id 1131 NGFG RS05740 WP 003695064.1        ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1103 NMB RS07590 WP 002212976.1         ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1390 A4U84 RS00055 WP 021115958.1       ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
NTDB id 1008365 ABNF92 RS07230 WP 069185089.1  .MARGVNKVILIGNLGQDPDTRYTPNGNAVVNLNLATDESYKDRQTGQLVPKTEWHRVVMFGKIAEVAGQYLRKGSKVYI   79
NTDB id 1166 A1552VC RS00795 WP 000168289.1    MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                          **!!!!**!*!!*!!**!**!*!*!! ****!!*!***!* *!*****!!!!********!!*!!*!!*!!* !!*

logo
EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYDEGYGQ.........SQEAYQRPAQQSRQPAPDA   143
EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYEEGYGQ.........SQEAYQRPAQQSRQPASDA   143
EGKLKTRKWQDQNGQDRYTTEIQG....DVLQMLDSRSSGG.DFGGNQGSGWNQAPAQTNYNQGGYSDNYAQNNNFNGGN   153
EGKLQTRKWQNKEGQDVYTTEVVV.DINGQMQMLDSRGGEG.GMNQGAPAG..RPQ.....QSG.YNAPAGQQNNPPP..   147
EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQG.GMPAQGGMN..VPA.....QQGSWGQPQQPAKQHQP..   150
consensus                !!****!!*! **!**********      **!!**!  **  * *   * *          ****** **** *** *

logo
PSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
PSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
ATRPQ....PAQKPAAQAEPPMDNFDDDIPF   180
QSGGY....SNQPSQGSMPEPVDDFDDDIPF   174
MQQSA....PQQYSQPQYNEPPMDFDDDIPF   177
consensus                * **       **     *  !****!!!!!!
```

X non conserved

X similar

X $\geq$ 50% conserved