```
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 141843 KO116 RS20905 WP 035563958.1 .MARGINKVILIGNLGQDPEVRFTPSGTAVANLNLATTDTWMDRQSGQRQERTEWHRVVMFNKTAEIAQQYLKKGSKVYI   79
NTDB id 1166 A1552VC RS00795 WP 000168289.1 MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                       **!!!!**!*!!*!!**!**!*!*!!*****!!***!*!* *!** !*!!!!********!!*!**!!*!!* !!*

logo
NTDB id 1103 NMB RS07590 WP 002212976.1      EGRIQSRKYQGKDGIERTAYDIVANEM....KMLGGRNENS.............................GGAPYEEGY   122
NTDB id 1131 NGFG RS05740 WP 003695064.1     EGRIQSRKYQGKDGIERTAYDIVANEM....KMLGGRNENS.............................GGAPYDEGY   122
NTDB id 1390 A4U84 RS00055 WP 021115958.1    EGKLKTRKWQDQNGQDRYTTEIQGDV....LQMLDSRSSGGDFGGNQGSGWNQAPA...........QTNYNQGGYSDNY   143
NTDB id 141843 KO116 RS20905 WP 035563958.1 EGRLQTRKWQDQNGQDRYSTEIVANDM....QMLDGRSG..DFQGAG.AGQNSYPQNAPQNAPQNAPAPNSQGGGYPQQG   152
NTDB id 1166 A1552VC RS00795 WP 000168289.1 EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRA..............................QQGGMPAQG   127
consensus                                   !!****!!*!** !**!********     *!!**!                                  ***** ***

logo
NTDB id 1103 NMB RS07590 WP 002212976.1      GQSQEAYQRPAQQSRQPA..SDAPSHPQEAPAAP...RRQPVPAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1     GQSQEAYQRPAQQSRQPA..PDAPSHPQEAPAAP...RRQPVPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1    AQNN..NF.NGGNATRPQPAQKP................AAQAEPPMDNFDDDIPF   180
NTDB id 141843 KO116 RS20905 WP 035563958.1 GAPQGGNYPDGQSPQQPRPAKPAPQQGNQAPPPNQQNSSYGAPDPGNFDDFDDEIPF   209
NTDB id 1166 A1552VC RS00795 WP 000168289.1 GMNVPAQQGSWGQPQQPAKQHQP...MQQSAPQQYSQPQYNE....PPMDFDDDIPF   177
consensus                                   ** * ***  ***  *!*    **   * **           ** ******!!*!!!
```

X non conserved

X similar

X $\geq$ 50% conserved