```
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 393887 FIU83 RS16205 WP 152485000.1 .MARGVNKVILIGNLGQDPEVRFTPSGTAVANLNLATTDTWMDRQSGQRQERTEWHRVVMFNKLAEIAQQYLKKGSKLYV    79
NTDB id 1166 A1552VC RS00795 WP 000168289.1 MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI    80
consensus                                       **!!!!**!*!!*!!**!**!*!*!!******!!***!*!* *!** !*!!!!********!!*!**!!*!!* *!*
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logo
NTDB id 1103 NMB RS07590 WP 002212976.1      EGRIQSRKYQGKDGIERTAYDIVANEM....KMLGGRNENSGGA....PYEEGYGQSQEAYQRPAQQS............    136
NTDB id 1131 NGFG RS05740 WP 003695064.1     EGRIQSRKYQGKDGIERTAYDIVANEM....KMLGGRNENSGGA....PYDEGYGQSQEAYQRPAQQS............    136
NTDB id 1390 A4U84 RS00055 WP 021115958.1    EGKLKTRKWQDQNGQDRYTTEIQGD....VLQMLDSRSSG...GDFGGNQGSGWNQAPAQTNY.............NQGG    138
NTDB id 393887 FIU83 RS16205 WP 152485000.1 EGRLQTRKWQDQNGQDKYSTEIVANDM....QMLDGRGDGGQGGGFGGPQGGGYGGGGQQGGGRPPQGGQYGGQPPQQGGG    155
NTDB id 1166 A1552VC RS00795 WP 000168289.1 EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQ....................QGGMPAQGGM...........    129
consensus                                   !!****!!*!** !************     *!!**! *    **     *    **** * * *****
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logo
NTDB id 1103 NMB RS07590 WP 002212976.1      ..........RQPASDAPSHPQEAPAAP........RRQPVPAAAPVEDIDDDIPF    174
NTDB id 1131 NGFG RS05740 WP 003695064.1     ..........RQPAPDAPSHPQEAPAAP........RRQPVPAAAPVEDIDDDIPF    174
NTDB id 1390 A4U84 RS00055 WP 021115958.1    YS..DNYAQNNNFNGGNATRPQPAQKPAAQ............AEPPMDNFDDDIPF    180
NTDB id 393887 FIU83 RS16205 WP 152485000.1 FGGQQPPQQGGQYGGGQPQRPAPQPAPPQQGGQQGGNYGAPD.PGSFDDFDDEIPF    210
NTDB id 1166 A1552VC RS00795 WP 000168289.1 ....NVPAQQGSW..GQPQQPAKQHQPMQQSAPQ..QYSQPQYNEPPMDFDDDIPF    177
consensus                                          *  *** **** !* ***** *             * ******!!*!!!
```

X non conserved

X similar

X ≥ 50% conserved