```
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 1166 A1552VC RS00795 WP 000168289.1  MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
NTDB id 292209 DJ533 RS03630 WP 065993284.1 ..MRGVNKVILVGTLGRDPETKTFPNGGSLTQFSIATSESWTDKNTGERKEQTEWHRIVLHNRLGEIAQQYLRKGSKVYI   78
NTDB id 1390 A4U84 RS00055 WP 021115958.1   ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
consensus                                       **!!!!**! !!*!!*****!*!*** ****!!!!*!*!***!***!*!!!!**********!*!**!!*!!* !!*

logo
NTDB id 1103 NMB RS07590 WP 002212976.1      EGRIQSRKYQGKDGIERTAYDIVAN....EMKMLGGRNENSGGAPYEE....G..............YGQSQEAYQRPAQ   134
NTDB id 1131 NGFG RS05740 WP 003695064.1     EGRIQSRKYQGKDGIERTAYDIVAN....EMKMLGGRNENSGGAPYDE....G..............YGQSQEAYQRPAQ   134
NTDB id 1166 A1552VC RS00795 WP 000168289.1  EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQG...GM......................PAQGGMNVPAQ   134
NTDB id 292209 DJ533 RS03630 WP 065993284.1 EGSLRTRQWTDQNGQERYTTEIRGE....QMQMLDSRQQSEQGQGFGGDSG.GYAQPRFNNNNQQGGFNNNQGGYGNQSN   153
NTDB id 1390 A4U84 RS00055 WP 021115958.1   EGKLKTRKWQDQNGQDRYTTEIQGD....VLQMLDSRSSG...GDFGGNQGSGWNQAPAQTNY......NQGGYSDNYA   144
consensus                                   !!*****!***** !**!*******      **!!**!* *  ** *      *              * * !**** ***

logo
NTDB id 1103 NMB RS07590 WP 002212976.1      QSRQ.....PA.......SDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1     QSRQ.....PA.......PDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1166 A1552VC RS00795 WP 000168289.1  QGSWGQPQQPA.........KQHQPMQQSAPQQYSQPQYNEPPMDFDDDIPF   177
NTDB id 292209 DJ533 RS03630 WP 065993284.1 QGSYGNQGNSNQGNYGNAGNNVNQGFQSPKPAA.PAATPAQAPADLDDDLPF   204
NTDB id 1390 A4U84 RS00055 WP 021115958.1   QN.....NNFNG......G.....NATRPQPAQKPAAQAEPPMDNFDDDIPF   180
consensus                                   !       ***             *   ***  *    **  *****!!!*!!
```

X non conserved

X similar

X ≥ 50% conserved