```
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 324700 EFP19 RS15930 WP 124836870.1 ..MASVNKVILVGNLGADPEVRYLPSGDAVANIRLATTDRYKDKASGDFKEMTEWHRVAFFGRLAEIVNEYLKKGSSVYI   78
NTDB id 1166 A1552VC RS00795 WP 000168289.1 MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                    **!!!!**!*!! !!**!**!*!*!!*****!!*****!* *!***!*!!!!********!!****!!*!!* !!*

logo
NTDB id 1131 NGFG RS05740 WP 003695064.1     EGRIQSRKYQGKDGIERTAYDIVAN....EMKMLGGRNENSGGAP....................YDEGYGQSQEAY....   129
NTDB id 1103 NMB RS07590 WP 002212976.1     EGRIQSRKYQGKDGIERTAYDIVAN....EMKMLGGRNENSGGAP....................YEEGYGQSQEAY....   129
NTDB id 1390 A4U84 RS00055 WP 021115958.1   EGKLKTRKWQDQNGQDRYTTEIQGD....VLQMLDSRSSGGDFGGNQGSGWNQAPAQTNYNQGGYSDNYA..........   144
NTDB id 324700 EFP19 RS15930 WP 124836870.1 EGRLRTRKWQGQDGQDRYSTEIVAD....QMQMLGGRGGSGGGGGGGGDDG.........YGGGGYGGGGGRGGDMERGGG   145
NTDB id 1166 A1552VC RS00795 WP 000168289.1 EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMPAQGGMN.......................V.......   131
consensus                                   !!*****!!*!***!**!********      **!!**!  ******                  * ****   *

logo
NTDB id 1131 NGFG RS05740 WP 003695064.1     QRPAQQSRQPAPDAPSH.....PQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1103 NMB RS07590 WP 002212976.1     QRPAQQSRQPASDAPSH.....PQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1   ..............QNNNFNGGNATRPQPAQKPAAQAEPPMDNFDDDIPF   180
NTDB id 324700 EFP19 RS15930 WP 124836870.1 GGRASGGGGGASRGGSG...GGGSSR..PSQPA....GGGFDEMDDDIPF   186
NTDB id 1166 A1552VC RS00795 WP 000168289.1 ..PAQQGSWGQPQQPAKQHQPMQQSA..PQQYSQPQYNEPPMDFDDDIPF   177
consensus                                     ****     *  ***        **** * **    ********!!!!!!
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X non conserved

X similar

X ≥ 50% conserved