```
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 1153708 LQ142 RS05955 WP 071687500.1 MTVRGINKVIIVGNLGQDPEVRYMPNGGAVANLSLATSESWRDKQTGEMRENTEWHRVVLFGKLAEVACEYLRKGAQVYV   80
NTDB id 1166 A1552VC RS00795 WP 000168289.1  MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                        **!!!!**!*!!*!!**!*!!*!*!!*****!!!!*!*!* *!***!*!!!!********!!*!**!!*!!* !!*
```

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logo
NTDB id 1131 NGFG RS05740 WP 003695064.1      EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYDEG.........YGQSQEAYQRPAQQSRQPA...   140
NTDB id 1103 NMB RS07590 WP 002212976.1       EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYEEG.........YGQSQEAYQRPAQQSRQPA...   140
NTDB id 1390 A4U84 RS00055 WP 021115958.1     EGKLKTRKWQDQNGQDRYTTEIQG....DVLQMLDSRSSGGDFG.GNQGS.......GWNQA......PAQTNYNQGGYS   140
NTDB id 1153708 LQ142 RS05955 WP 071687500.1 EGQLRTRNWQDDSGVTRYVTEIVV.GQNGTMQMLGGRRDGGQSQ.STAPQQ......QSAQPQ....TPATPSQPAGTP.   147
NTDB id 1166 A1552VC RS00795 WP 000168289.1  EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMP.AQGGMNVPAQQGSWGQPQ....QPAKQHQPMQ...   152
consensus                                    !!****!**!*  !**!* *****      **!!**! **** *     *          **! *     !!*** * *
```

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logo
NTDB id 1131 NGFG RS05740 WP 003695064.1      ..........PDAPSHPQEAPAAPRRQPVP.AAAPVEDIDDDIPF   174
NTDB id 1103 NMB RS07590 WP 002212976.1       ..........SDAPSHPQEAPAAPRRQPVP.AAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1     DNYAQNNNFNGGNATRPQ...PA..QKPAAQAEPPMDNFDDDIPF   180
NTDB id 1153708 LQ142 RS05955 WP 071687500.1 ...EKSPKAKGGRKGRQSAAPSQ..QVPQPL.PDDYPPMDDDAPF   186
NTDB id 1166 A1552VC RS00795 WP 000168289.1  ................QSAPQ...QYSQPQYNEPPMDFDDDIPF   177
consensus                                                 * ** ** *  * * * *  *****!!!*!!
```

X non conserved

X similar

X $\geq$ 50% conserved