```
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 1170788 ACOFKY RS15490 WP 105713882.1 ..MRGVNKVILVGTLGRDPETKTFPNGGSLTQFSIATSESWTDKNSGERKEQTEWHRIVLHNRLGEIAQQYLRKGSKVYI   78
NTDB id 1390 A4U84 RS00055 WP 021115958.1      ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
consensus                                         **!!!!**! !!*!!*****!*!*** ****!!!!*!*!***!***!*!!!!*********!*!**!!*!!* !!*

logo
NTDB id 1103 NMB RS07590 WP 002212976.1        EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYE.EGYGQSQE.......A................   128
NTDB id 1131 NGFG RS05740 WP 003695064.1       EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYD.EGYGQSQE.......A................   128
NTDB id 1166 A1552VC RS00795 WP 000168289.1    EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMPA..QGGMNVPAQ.....QGSWG...............   139
NTDB id 1170788 ACOFKY RS15490 WP 105713882.1 EGSLRTRQWTDQNGQERYTTEIRG....EQMQMLDNNRQQGEGAAADNGGYNQPRF.NNNQQGGFNNNQGGGGYANQGNQ   153
NTDB id 1390 A4U84 RS00055 WP 021115958.1      EGKLKTRKWQDQNGQDRYTTEIQG....DVLQMLDSRSSGGDFGGNQGSGWNQAPAQTNYNQGGYS..............   140
consensus                                      !!****!***** !**!*******       **!!***  ****** *  !***        ****

logo
NTDB id 1103 NMB RS07590 WP 002212976.1        ...YQRPAQQSRQP.ASDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1       ...YQRPAQQSRQP.APDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1166 A1552VC RS00795 WP 000168289.1    .....QPQQ.......PAKQHQPMQQSAPQQYSQPQYNEPPMDFDDDIPF   177
NTDB id 1170788 ACOFKY RS15490 WP 105713882.1 GGGYGNANPQGGYGNGGNNVNQGFQSPKPAATPSAPTAAP.ADLDDDLPF   202
NTDB id 1390 A4U84 RS00055 WP 021115958.1      .....DNYAQNNNNFNGGN.....ATRPQPAQKPAAQAEPPMDNFDDDIPF   180
consensus                                         *  * **  *  *      *   ***  *   ****!****!!!*!!
```

X non conserved

X similar

X $\geq$ 50% conserved