```
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 1166 A1552VC RS00795 WP 000168289.1    MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
NTDB id 1060355 ACFN7Z RS00870 WP 058951561.1 ..MRGVNKVILVGTLGRDPETKTFPNGGSLTQFSIATSDSWTDKSTGERKEQTEWHRIVLHNRLGEIAQQYLRKGSKVYI   78
NTDB id 1390 A4U84 RS00055 WP 021115958.1      ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
consensus                                          **!!!!**! !!*!!*****!*!*** ****!!!**!*!* *!***!*!!!!**********!*!**!!*!!* !!*

logo
NTDB id 1103 NMB RS07590 WP 002212976.1        EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYE...............EGYGQSQE.......AYQ   130
NTDB id 1131 NGFG RS05740 WP 003695064.1       EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYD...............EGYGQSQE.......AYQ   130
NTDB id 1166 A1552VC RS00795 WP 000168289.1    EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGG.MPAQGGM..NVP....AQQGSWGQPQ...........   142
NTDB id 1060355 ACFN7Z RS00870 WP 058951561.1 EGSLRTRQWTDQNGQERYTTEIRG....EQMQMLDNNRQQGE.QMQGGNDGYAQPRFNNNQGGGYNNN.....NNQGGYG   148
NTDB id 1390 A4U84 RS00055 WP 021115958.1      EGKLKTRKWQDQNGQDRYTTEIQG....DVLQMLDSRSSGGD.FG.............GNQGSGWNQAPAQTNYNQGGYS   140
consensus                                      !!****!***** !**!******       **!!***  ***  *              *  **** *        **

logo
NTDB id 1103 NMB RS07590 WP 002212976.1        .RPAQQSRQPASDAPSHPQEAPAAPRRQP.VPAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1       .RPAQQSRQPAPDAPSHPQEAPAAPRRQP.VPAAAPVEDIDDDIPF   174
NTDB id 1166 A1552VC RS00795 WP 000168289.1    .QPAKQ..........HQPMQQSAPQQYSQPQYNEPPMDFDDDIPF   177
NTDB id 1060355 ACFN7Z RS00870 WP 058951561.1 ANPAAGNSNNQQSGYANNNPSGFAPKAAPQSAPAAAPADMDDDLPF   194
NTDB id 1390 A4U84 RS00055 WP 021115958.1      DNYAQNNN......FNGGNATRPQPAQKPAAQAEPPMDNFDDDIPF   180
consensus                                       **!**  *    *  * *    *!*  *   ********!!!*!!
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X non conserved

X similar

X $\geq$ 50% conserved