logo

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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 1060143 ACF3OJ RS09920 WP 392405629.1    ..MAGVNKVILIGNLGNDPDMRYMPNGEPVANISIATSETWNDKNTGEKREKTEWHRVVAYRRTAEIIGQYTRKGSKLYV   78
NTDB id 1390 A4U84 RS00055 WP 021115958.1        ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
consensus                                           **!!!!**!*!!*!!**!*!!*!**!*****!!!!*!*!***!***!*!!!!***********!!**!*!**!!* *!*
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NTDB id 1103 NMB RS07590 WP 002212976.1          EGRIQSRKYQGKDGIERTAYDIVANEMKMLGGRNENS...GGA.........PYEEGYGQSQEAYQRPAQQSRQPASDAP   144
NTDB id 1131 NGFG RS05740 WP 003695064.1         EGRIQSRKYQGKDGIERTAYDIVANEMKMLGGRNENS...GGA.........PYDEGYGQSQEAYQRPAQQSRQPAPDAP   144
NTDB id 1166 A1552VC RS00795 WP 000168289.1      EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMPAQGGMNVPAQQGSWGQPQQ.................P   144
NTDB id 1060143 ACF3OJ RS09920 WP 392405629.1    EGRLQTRKWTDQSGQQRYTTEIVADNIQMLDSRGGGEGSFGGNGGGNYPGNRSNSGGYGQQGGGYDQDYGGSYDQDYDAP   158
NTDB id 1390 A4U84 RS00055 WP 021115958.1        EGKLKTRKWQDQNGQDRYTTEIQGDVLQMLDSRSSG.GDFGGNQQSGWNQAPAQ...TNYNQGGYSDNYAQ....NN.NF   149
consensus                                        !!****!!**** !**!******** **** * * * !! * * **** * ** ** ***
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NTDB id 1103 NMB RS07590 WP 002212976.1          SHPQEAPAAPRRQPV.........PAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1         SHPQEAPAAPRRQPV.........PAAAPVEDIDDDIPF   174
NTDB id 1166 A1552VC RS00795 WP 000168289.1      A....KQHQPMQQSAPQQYSQ...PQYNEPPMDFDDDIPF   177
NTDB id 1060143 ACF3OJ RS09920 WP 392405629.1    SGGNRPQPPTPNKPVPPQNNTGGLGGPTLDQDNFDDDIPF   198
NTDB id 1390 A4U84 RS00055 WP 021115958.1        NGGNATRPQPAQKPAA.........QAEPPMDNFDDDIPF   180
consensus                                        *  *      * **** *          *  *****!!!!!!!
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X non conserved
X similar
X ≥ 50% conserved