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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 393699 FIU95 RS02535 WP 152451193.1 .MARGINKVILIGNLGNDPETKYMPSGGAVTNVSLATSESWKDKQTGQQQERTEWHRVVFFNRLAEIAGEYLRKGSKVYV   79
NTDB id 1166 A1552VC RS00795 WP 000168289.1 MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                     **!!!!**!*!!*!!****!!*!*!! ****!!!!*!*!* *!** !*!!!!********!!*!!*!!*!!* !!*

logo

NTDB id 1131 NGFG RS05740 WP 003695064.1     EGRIQSRKYQGK.DGIERTAYDIVAN....EMKMLGGRNENSGGAP.........................YDEGYGQSQ   126
NTDB id 1103 NMB RS07590 WP 002212976.1      EGRIQSRKYQGK.DGIERTAYDIVAN....EMKMLGGRNENSGGAP.........................YEEGYGQSQ   126
NTDB id 1390 A4U84 RS00055 WP 021115958.1    EGKLKTRKWQDQ.NGQDRYTTEIQGD....VLQMLDSRSSGGDFGGNQGSGWNQAPA......QTNYNQGGYSDNYA.QN   146
NTDB id 393699 FIU95 RS02535 WP 152451193.1 EGSLRTRKWQDKSSGQDRYTTEIVAS....EMQMLDGRGEQGGFGQGMGGAAMGAAGMGGQMGGHQGGQGGYEQQGGFQQ   155
NTDB id 1166 A1552VC RS00795 WP 000168289.1 EGQLQTRKWQDQ.SGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMPAQ...........................GGMNV   131
consensus                                   !!*****!!*!**  !**!*******    ***!!**! **** *                        *** ** **

logo

NTDB id 1131 NGFG RS05740 WP 003695064.1     EAYQRPAQQSRQPAPDAPS...HPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1103 NMB RS07590 WP 002212976.1      EAYQRPAQQSRQPASDAPS...HPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1    NNF....NGGNATRP.......QPA......QKPAAQAEPPMDNFDDDIPF   180
NTDB id 393699 FIU95 RS02535 WP 152451193.1 GGY....QQGNQGRP.APGNQQQPAQ.....QPSQGPAGGFDNSFDDDIPF   196
NTDB id 1166 A1552VC RS00795 WP 000168289.1 P.A....QQGSWGQPQQPAKQHQPMQQSAPQQYSQPQYNEPPMDFDDDIPF   177
consensus                                    **    *** *  * **    *!    *  **   ********!!!!!!
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X non conserved

X similar

X ≥ 50% conserved