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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 1115038 BTSPAZIEG RS01895 WP 075472919.1 MASRGINKVILIGNLGQDPEIRYMPNGGAVLNMTLATSDTWKDKKTGEAKEKTEWHRLVVFGKLAEIAAQYLHKGSQIYI   80
NTDB id 1166 A1552VC RS00795 WP 000168289.1      MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                            **!!!!**!*!!*!!**!*!!*!*!! ****!!!**!*!* *!***!*!!!!*********!!*!**!!*!!* *!*

logo

NTDB id 1131 NGFG RS05740 WP 003695064.1          EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYDEGYGQSQEA....YQRPAQQSRQPAPDA...PS   145
NTDB id 1103 NMB RS07590 WP 002212976.1           EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYEEGYGQSQEA....YQRPAQQSRQPASDA...PS   145
NTDB id 1390 A4U84 RS00055 WP 021115958.1         EGKLKTRKWQDQNGQDRYTTEIQG....DVLQMLDSRSSGGDF.GGNQGSGWNQAPAQTNYNQGGYSDN..YAQNNNFNG   151
NTDB id 1115038 BTSPAZIEG RS01895 WP 075472919.1 EGSLQTRKWQDQNGIDRYITEVIVN.ITGTMQMLGNRNSNQNI.SRDSLG.TKYSS........SISEKKNKIQDENYSL   149
NTDB id 1166 A1552VC RS00795 WP 000168289.1      EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGM.PAQGG..MNVPA.....QQGSWGQPQQ.PAKQHQPM   151
consensus                                        !!*****!!*!** !**!* *****      **!!**!* * *  * * * *  * *    **  *   **        *

logo

NTDB id 1131 NGFG RS05740 WP 003695064.1          HPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1103 NMB RS07590 WP 002212976.1           HPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1         GNATRPQPAQKPAAQAEPPMDNFDDDIPF   180
NTDB id 1115038 BTSPAZIEG RS01895 WP 075472919.1  KN.SDEELKKQDNLINSTTKLDFEDEIPF   177
NTDB id 1166 A1552VC RS00795 WP 000168289.1       QQ.SAP..QQYSQPQYNEPPMDFDDDIPF   177
consensus                                          * ***   **  * *  ******!*!!!
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X non conserved

X similar

X ≥ 50% conserved