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logo

NTDB id 1131 NGFG RS05740 WP 003695064.1     ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYR.KLAEIAGQYLKKGGLVY    75
NTDB id 1103 NMB RS07590 WP 002212976.1      ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYR.KLAEIAGQYLKKGGLVY    75
NTDB id 1390 A4U84 RS00055 WP 021115958.1    ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFR.RQAEVAGQYLRKGSKVY    77
NTDB id 214857 BV511 RS22385 WP 076643847.1 .MAGSVNKVILVGNLGRDPETRRLSSGDPVVNLRIATSESWKDKASGERKEKTEWHSVVIYNDNLAKVAEQYLRKGSKVY    79
NTDB id 1166 A1552VC RS00795 WP 000168289.1 MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYG.KLAEVAGEYLRKGSQVY    79
consensus                                    **!!!!**!*!!*!!**!****!**! ****!!!!*!*!* *!***!*!!!! ***** **!**!**!!*!!* !!

logo

NTDB id 1131 NGFG RS05740 WP 003695064.1     LEGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYDEG..YGQ...........SQEAYQRPAQ....   134
NTDB id 1103 NMB RS07590 WP 002212976.1      LEGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYEEG..YGQ...........SQEAYQRPAQ....   134
NTDB id 1390 A4U84 RS00055 WP 021115958.1    VEGKLKTRKWQDQNGQDRYTTEIQG....DVLQMLDSRSSGGD..F................GGNQGSGWNQAPAQTNYN   135
NTDB id 214857 BV511 RS22385 WP 076643847.1 IEGQLQTRKWTDQSGAEKYTTEVVLQRFRGEMTILDGRGGGGGGDFAGEDEGGGQISRGGDRGGDRGGDRGGR.......   152
NTDB id 1166 A1552VC RS00795 WP 000168289.1 IEGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMPAQGGMNVP...........AQQGSWGQP.......   141
consensus                                   *!!****!!**** ! *********      ** *!**!  ****    *    **             *  *****

logo

NTDB id 1131 NGFG RS05740 WP 003695064.1     .........QSRQPAPDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1103 NMB RS07590 WP 002212976.1      .........QSRQPASDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1    QGGYSDNYAQNNNFNGGNA....TRPQPAQKPAAQAEPPMDNFDDDIPF   180
NTDB id 214857 BV511 RS22385 WP 076643847.1 .....DDYGSGRSGGGGG........GDRRPSSGGGAKPNYDLDDDIPF   188
NTDB id 1166 A1552VC RS00795 WP 000168289.1 .....QQPAKQHQPMQQS........APQQYSQPQYNEPPMDFDDDIPF   177
consensus                                          ** ****  *        **  **    ** !****!!!!!!
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X non conserved

X similar

X $\geq$ 50% conserved