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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 189685 BB934 RS23860 WP 099511917.1 .MAGSVNKVILVGNLGRDPEVRRLSNGEPVVNLRIATSETWKDKGTGERKEKTEWHSVVIFNENLGRVAEQYLKKGSKVY    79
NTDB id 1166 A1552VC RS00795 WP 000168289.1 MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYG.KLAEVAGEYLRKGSQVY    79
consensus                                     **!!!!**!*!!*!!**!****!**! *****!!!!*!*!* *!***!*!!!! ****** *****!**!!*!!* !!

logo

NTDB id 1131 NGFG RS05740 WP 003695064.1     LEGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYDEGYGQS....QEAYQRPAQQS...........   136
NTDB id 1103 NMB RS07590 WP 002212976.1      LEGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYEEGYGQS....QEAYQRPAQQS...........   136
NTDB id 1390 A4U84 RS00055 WP 021115958.1    VEGKLKTRKWQDQNGQDRYTTEIQG....DVLQMLDSRSSGGDFGGN.QG.........SGWNQAPAQTNYNQGGYSDNY   143
NTDB id 189685 BB934 RS23860 WP 099511917.1 IEGQLQTRKWQDQSGVEKYSTEVVLQRFRGELTILDSRGGGGGASEY.GDEEQGQIARGGDFGRSPSQD...........   147
NTDB id 1166 A1552VC RS00795 WP 000168289.1 IEGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMPAQ.GGMNV..PAQQGSWGQPQQPA...........   145
consensus                                   *!!****!!*!** !*********      ** *!**!  ***** *  *  *      * ***** ***

logo

NTDB id 1131 NGFG RS05740 WP 003695064.1     ...........RQPAPDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1103 NMB RS07590 WP 002212976.1      ...........RQPASDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1    AQNNNFNGGNATRPQPAQ......KP......AAQAEPPMDNFDDDIPF   180
NTDB id 189685 BB934 RS23860 WP 099511917.1 ...........RRPAPSSGGGNSAGG......NSGGGSRYSDIDDDIPF   179
NTDB id 1166 A1552VC RS00795 WP 000168289.1 ...........KQHQPMQQSAPQQYS......QPQYNEPPMDFDDDIPF   177
consensus                                              *****   * ** **         ** *****!!!!!!
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X non conserved

X similar

X $\geq$ 50% conserved