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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 146161 IMCC21906 RS04625 WP 047011190.1   .MARGVNKVIIVGNLGQDPETRYMPSGGAVTNVTVATSENWKDKQTGQPQERTEWHRVVFFNRLAEIAGEYLKKGSKVYV    79
NTDB id 1166 A1552VC RS00795 WP 000168289.1       MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI    80
consensus                                             **!!!!**!*!!*!!**!*!!*!*!! ****!!!!*!*!* *!** !*!!!!********!!*!!*!!*!!* !!*

logo

NTDB id 1131 NGFG RS05740 WP 003695064.1          EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYDEGYGQ....SQEAYQRPAQQSRQP.....APDA   143
NTDB id 1103 NMB RS07590 WP 002212976.1           EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYEEGYGQ....SQEAYQRPAQQSRQP.....ASDA   143
NTDB id 1390 A4U84 RS00055 WP 021115958.1         EGKLKTRKWQDQNGQDRYTTEIQG....DVLQMLDSRSSGGD.FGGNQGSGWNQAPAQTNYNQGGYSDNYAQNNNFNGGN   153
NTDB id 146161 IMCC21906 RS04625 WP 047011190.1   EGSLRTRKWQGQDGQDRYTTEIVA....GEMQMLDSRGGGGG.SGSGGYDDYAA..PQQQ.RAPQQS..........RPA   141
NTDB id 1166 A1552VC RS00795 WP 000168289.1       EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGG.MPAQGGMNVPA..QQGSWGQPQQP...........AK   146
consensus                                         !!*****!!*!***!**!*******     ***!!**!  ***  *   * *      !  ** ***            *

logo

NTDB id 1131 NGFG RS05740 WP 003695064.1          PSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1103 NMB RS07590 WP 002212976.1           PSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1         ATRPQ....PAQKPAAQAEPPMDNFDDDIPF   180
NTDB id 146161 IMCC21906 RS04625 WP 047011190.1   APRPQSNNTPPPANDPPSSGGFDDFDDDIPF   172
NTDB id 1166 A1552VC RS00795 WP 000168289.1       QHQPMQQSAPQQYSQPQYNEPPMDFDDDIPF   177
consensus                                          * !*   *** **  ** ******!!!!!!
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X non conserved

X similar

X $\geq$ 50% conserved