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logo
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NTDB id 1103 NMB RS07590 WP 002212976.1          ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1131 NGFG RS05740 WP 003695064.1         ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1390 A4U84 RS00055 WP 021115958.1        ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
NTDB id 1111958 SMDB11 RS18320 WP 025304438.1    MASRGVNKVILVGNLGQDPEVRYMPNGGAVANITLATSESWRDKATGEQKEKTEWHRVVLFGKLAEVAGEYLRKGSQVYI   80
NTDB id 1166 A1552VC RS00795 WP 000168289.1      MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                           **!!!!**!*!!*!!**!*!!*!*!!*****!!!!*!*!* *!***!*!!!!*********!!*!!*!!*!!* !!*
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logo
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NTDB id 1103 NMB RS07590 WP 002212976.1          EGRIQSRKYQGKDGIERTAYDIV....ANEMKMLGGRNENSGGAPY.........EEGYGQSQEA.......YQRPAQQS   136
NTDB id 1131 NGFG RS05740 WP 003695064.1         EGRIQSRKYQGKDGIERTAYDIV....ANEMKMLGGRNENSGGAPY.........DEGYGQSQEA.......YQRPAQQS   136
NTDB id 1390 A4U84 RS00055 WP 021115958.1        EGKLKTRKWQDQNGQDRYTTEIQ....GDVLQMLDSRSSGGD.FGGNQ.......GSGWNQAPAQTNYNQGGYSDNYAQN   146
NTDB id 1111958 SMDB11 RS18320 WP 025304438.1    EGSLQTRKWTDQSGVEKYTTEVVVN.VGGTMQMLGGRQGGGA..PAG...QSAGGQGGWGQPQQP............QGG   142
NTDB id 1166 A1552VC RS00795 WP 000168289.1      EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGG.MPAQGGMNVPAQQGSWGQPQQP............AKQ   147
consensus                                        !!*****!!**** !********** *  **!!**!* ***  **          ***! *       *    **
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logo
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NTDB id 1103 NMB RS07590 WP 002212976.1          RQPASDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1         RQPAPDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1        NNFNG....GNATRPQPAQKPAAQAEPPMDNFDDDIPF   180
NTDB id 1111958 SMDB11 RS18320 WP 025304438.1    NQFSG...GQQQSRPAQSSAPAASSNEPPMDFDDDIPF   177
NTDB id 1166 A1552VC RS00795 WP 000168289.1      HQP......MQQSAPQQYS..QPQYNEPPMDFDDDIPF   177
consensus                                         **        ****!*    *     *   !****!!!!!!
```

X non conserved
X similar
X ≥ 50% conserved