logo

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NTDB id 1103 NMB RS07590 WP 002212976.1          ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDRN.GQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1131 NGFG RS05740 WP 003695064.1         ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDRN.GQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1390 A4U84 RS00055 WP 021115958.1        ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
NTDB id 45682 CWS RS02755 WP 009874495.1         MASRGVNKVILIGHLGQDPEVRYMPNGNAVVNMTLATSENWKDKNTGENKEKTEWHRIVLFGKLAEIAGEYLRKGSQVYI   80
NTDB id 1166 A1552VC RS00795 WP 000168289.1      MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                            **!!!!**! !!*!!**!*!!*!*!! ****!!!!*!*!***!***!*!!!!********!!*!!*!!*!!* !!*
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NTDB id 1103 NMB RS07590 WP 002212976.1          EGRIQSRKYQGKDGIERTAYDIV....ANEMKMLGGRNENSGGAPYEEGYGQSQE.............AYQRPAQQSRQP   139
NTDB id 1131 NGFG RS05740 WP 003695064.1         EGRIQSRKYQGKDGIERTAYDIV....ANEMKMLGGRNENSGGAPYDEGYGQSQE.............AYQRPAQQSRQP   139
NTDB id 1390 A4U84 RS00055 WP 021115958.1        EGKLKTRKWQDQNGQDRYTTEIQ....GDVLQMLDSRSSGGDF.GGNQGSGWNQAPAQTNYNQGGYSDNYAQNNNFNGG.   152
NTDB id 45682 CWS RS02755 WP 009874495.1         EGSLQTRKWQDQNGLERYTTEIIVN.IGGTMQMLGNRNSNLQA.MTVNDKN...ST.......GIKIK.KTDAVEFDK..   145
NTDB id 1166 A1552VC RS00795 WP 000168289.1      EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGM.PAQGGMN...VPAQ....QGSWGQ.PQQPAKQHQ..   149
consensus                                        !!****!!*!** !**!******    *  **!!**!* * ** *   * *  *         *     ** **** *
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logo

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NTDB id 1103 NMB RS07590 WP 002212976.1          ASDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1         APDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1        .......NATRPQPAQKPAAQAEPPMDNFDDDIPF   180
NTDB id 45682 CWS RS02755 WP 009874495.1         .......KI..ETHESNKDLTHSPSEIDFDDEIPF   171
NTDB id 1166 A1552VC RS00795 WP 000168289.1      .......PMQQSAPQQYSQPQYNEPPMDFDDDIPF   177
consensus                                               *   **   *  * *  *****!!*!!!
```

X non conserved

X similar

X ≥ 50% conserved