logo

```
NTDB id 1131 NGFG RS05740 WP 003695064.1          ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDRN.GQRVERTEWHNITMYR.KLAEIAGQYLKK   70
NTDB id 1103 NMB RS07590 WP 002212976.1           ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDRN.GQRVERTEWHNITMYR.KLAEIAGQYLKK   70
NTDB id 1390 A4U84 RS00055 WP 021115958.1         ..MAGVNKVILVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFR.RQAEVAGQYLRK   72
NTDB id 1230703 LOKVESSMR4R RS06915 WP 087206951.1 .MAGSVNKVILIGNLGADPEIRSFQNGGKVANLRIATSETWKDKNSGERREKTEWHTVAIFQEGLVRVVEQYLKK   74
NTDB id 1166 A1552VC RS00795 WP 000168289.1       MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYG.KLAEVAGEYLRK   74
consensus                                                **!!!!**!*!! !!**!****!**!*****!!!!*!*!***!***!*!!!! ***** ********!!*!
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logo

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NTDB id 1131 NGFG RS05740 WP 003695064.1          GGLVYLEGRIQSRKYQGKDGIERTAYDIV....ANEMKMLGGRNENSGGAPYDEGYGQS..QEAYQRPAQQSRQP   139
NTDB id 1103 NMB RS07590 WP 002212976.1           GGLVYLEGRIQSRKYQGKDGIERTAYDIV....ANEMKMLGGRNENSGGAPYEEGYGQS..QEAYQRPAQQSRQP   139
NTDB id 1390 A4U84 RS00055 WP 021115958.1         GSKVYVEGKLKTRKWQDQNGQDRYTTEIQ....GDVLQMLDSRSSGGD.FGGNQ.......GSGWNQAPAQTNYN   135
NTDB id 1230703 LOKVESSMR4R RS06915 WP 087206951.1 GSKVYIEGKLQTRKWQDQSGADRYSTEVVLQGLGGTLTMLDGRGDGGG.NSGGGDYGAGSGGGGGGGG........   140
NTDB id 1166 A1552VC RS00795 WP 000168289.1       GSQVYIEGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGG.MPAQGGMNVPAQQGSWGQPQQPAKQH   148
consensus                                         !* !!*!!****!!*!** ! *!******    *  * !!**! **** **  ***    * *** * *****
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logo

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NTDB id 1131 NGFG RS05740 WP 003695064.1          A.........PDA..PSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1103 NMB RS07590 WP 002212976.1           A.........SDA..PSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1         QGGYSDNYAQNNNFNGGNATRPQPAQKPAAQAEPPMDNFDDDIPF   180
NTDB id 1230703 LOKVESSMR4R RS06915 WP 087206951.1 ......................RGSYNDGGYGGPSGGSDMDDEIPF   164
NTDB id 1166 A1552VC RS00795 WP 000168289.1       Q..............PMQQSAPQQYSQPQYNEP..PMDFDDDIPF   177
consensus                                                    * ***    *    *  *****!!*!!!
```

X non conserved

X similar

X ≥ 50% conserved