```
logo

NTDB id 1103 NMB RS07590 WP 002212976.1      ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1131 NGFG RS05740 WP 003695064.1     ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1166 A1552VC RS00795 WP 000168289.1 MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
NTDB id 72638 PKHYL RS03315 WP 071002203.1  ..MRGVNKVIIIGNLGADPEARQFNNGGSVTNISVATSEQWTDKQSGEKREATEWHRISLFNRLGEIAAQYLRKGSKVYI   78
NTDB id 1390 A4U84 RS00055 WP 021115958.1   ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
consensus                                      **!!!!**!*!! !!**!****!**! ****!!!!*!*!* *!***!*!!!!*********!*!**!!*!!* !!*

logo

NTDB id 1103 NMB RS07590 WP 002212976.1      EGRIQSRKYQGKDGIERTAYDIVANEMKMLGGRNE...NSGGAPYEEGYGQ..SQEAYQRPAQQSRQPA...........   140
NTDB id 1131 NGFG RS05740 WP 003695064.1     EGRIQSRKYQGKDGIERTAYDIVANEMKMLGGRNE...NSGGAPYDEGYGQ..SQEAYQRPAQQSRQPA...........   140
NTDB id 1166 A1552VC RS00795 WP 000168289.1 EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMPAQGGMNVPAQQGSWGQPQQPAKQHQP..........   150
NTDB id 72638 PKHYL RS03315 WP 071002203.1  EGSLRTRKYQDQNGQDRYITEIRAEQMQMLDGMSGGQSDNGGFSNNQGGQ...NSNSYGNQGGQSNQNNFGQQAGGQPAQ   155
NTDB id 1390 A4U84 RS00055 WP 021115958.1   EGKLKTRKWQDQNGQDRYTTEIQGDVLQMLDSRSSGGD....FGGNQGSG.......WNQA............PAQTNYN   135
consensus                                   !!*****!!*!** !**!* ****** **** **  *  * ** * * ! *    *  **********

logo

NTDB id 1103 NMB RS07590 WP 002212976.1      .........S.......DAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1     .........P.......DAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1166 A1552VC RS00795 WP 000168289.1 ..................MQQSAPQ..QYSQPQY....NEPPMDFDDDIPF   177
NTDB id 72638 PKHYL RS03315 WP 071002203.1  RGGYNNQPSGGQNSFNNQNAPAPQN.QFNQPAQSKPTAMSDGPVDDDIPF   204
NTDB id 1390 A4U84 RS00055 WP 021115958.1   QGGYSDNY.AQNNNFNGGNATRPQP.AQKPAAQAEP...PMDNFDDDIPF   180
consensus                                                 * * !!     *  *  * * *****!!!!!!
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X non conserved

X similar

X ≥ 50% conserved