```
logo
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 218436 B0D95 RS18120 WP 078045172.1 .MARGINKVILIGNIGQDPEVKYMPSGGAVTNVSVATSETWKDKNTGQPQERTEWHRVVFFNRLGEIAGEYLKKGSKVYI   79
NTDB id 1166 A1552VC RS00795 WP 000168289.1 MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                       **!!!!**!**!*!****!!*!*!! ***!!!!*!*!***!** !*!!!!*********!*!!*!!*!!* !!*

logo
NTDB id 1103 NMB RS07590 WP 002212976.1      EGRIQSRKYQGKDGIERTAYDIVANE....MKMLGGRNENSGGAPY.......EEGYGQSQEAYQRPAQQSR........   137
NTDB id 1131 NGFG RS05740 WP 003695064.1     EGRIQSRKYQGKDGIERTAYDIVANE....MKMLGGRNENSGGAPY.......DEGYGQSQEAYQRPAQQSR........   137
NTDB id 1390 A4U84 RS00055 WP 021115958.1    EGKLKTRKWQDQNGQDRYTTEIQGD....VLQMLDSRSSGGDFGGNQGS......G......WNQAPAQTNYNQGGYS..   140
NTDB id 218436 B0D95 RS18120 WP 078045172.1 EGSLRTRKWQAQDGSDRYTTEIVASE....MQMLDGRGDGSGMGNAMGGAAAMAGGFDQTPQYNNGPAQNAYNQAAPKPA   155
NTDB id 1166 A1552VC RS00795 WP 000168289.1 EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMPAQG........G........................   128
consensus                                   !!*****!!*!***! *!********     **!!**! **** *            !* **    * ****

logo
NTDB id 1103 NMB RS07590 WP 002212976.1      ............QPASDAPSH.PQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1     ............QPAPDAPSH.PQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1    ........DNYAQNNN..FNGGNATRPQPAQKPAAQAEPPMDNFDDDIPF   180
NTDB id 218436 B0D95 RS18120 WP 078045172.1 GNNQGGNQGGFGQPA.........NRPAPQQNVPP.QPAGFDSFDDDIPF   195
NTDB id 1166 A1552VC RS00795 WP 000168289.1 .MNVPAQQGSWGQPQQPAKQHQPMQQSAPQQYSQPQYNEPPMDFDDDIPF   177
consensus                                            **!**  *  * *   *** ** *  * ******!!!!!!
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X non conserved

X similar

X $\geq$ 50% conserved