```
logo
NTDB id 1131 NGFG RS05740 WP 003695064.1      ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1103 NMB RS07590 WP 002212976.1       ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1166 A1552VC RS00795 WP 000168289.1   MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
NTDB id 976077 AADH33 RS02760 WP 348549484.1 ..MRGVNKVIIIGNLGADPEARQFNNGGSVTNISVATSEQWTDKQSGEKREATEWHRISLFNRLGEIAAQYLRKGSKVYI   78
NTDB id 1390 A4U84 RS00055 WP 021115958.1    ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
consensus                                        **!!!!**!*!! !!**!****!**! ****!!!!*!*!* *!****!*!!!!*********!*!**!!*!!* !!*

logo
NTDB id 1131 NGFG RS05740 WP 003695064.1      EGRIQSRKYQGKDGIERTAYDIVAN....EMKMLGGRNENS..GGAPYD...........EGYGQSQEAY..........   129
NTDB id 1103 NMB RS07590 WP 002212976.1       EGRIQSRKYQGKDGIERTAYDIVAN....EMKMLGGRNENS..GGAPYE...........EGYGQSQEAY..........   129
NTDB id 1166 A1552VC RS00795 WP 000168289.1   EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQ.....GGMPAQGGMNVPAQQGSWGQPQQPA..........   145
NTDB id 976077 AADH33 RS02760 WP 348549484.1 EGSLRTRKYQDQNGQDRYITEIRAE....QMQMLDGASGGGQSQGGSYGSQGGQNSFGQQGGYNQAGGVAAQGMAQGGNQ   154
NTDB id 1390 A4U84 RS00055 WP 021115958.1    EGKLKTRKWQDQNGQDRYTTEIQGD....VLQMLDSRSSGGDFGGNQ.G...........SGWNQAP..AQTNYNQGGYS   140
consensus                                    !!****!!*!** !**!* ******      **!!***  *   *** *            ***! *  *

logo
NTDB id 1131 NGFG RS05740 WP 003695064.1      ...QRPAQQSRQPAPDAPSHPQEAPA.APRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1103 NMB RS07590 WP 002212976.1       ...QRPAQQSRQPASDAPSHPQEAPA.APRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1166 A1552VC RS00795 WP 000168289.1   ................KQHQPMQQSAPQQYSQPQYNEP.PMDFDDDIPF   177
NTDB id 976077 AADH33 RS02760 WP 348549484.1 GGYNNQNAYNNQSN..PQQNPFNQPA.QNASQPKPTAMPDGPVDDDIPF   200
NTDB id 1390 A4U84 RS00055 WP 021115958.1    DNYAQNNNNFNGGNA..TRPQPAQKPA.AQ......AEPPMDNFDDDIPF   180
consensus                                       *   *   * *     *! * *! **  ** *** *****!!!!!!
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X non conserved

X similar

X ≥ 50% conserved