```
logo
NTDB id 328367 EGH17 RS00335 WP 071236973.1  MNKTLKRRVFRHTALYTAILMFSHTGGGGAMAQTHQYAIIMNERKQPEVKWKDQYNQSALKDKSRERTFSHTSQKNGLGI   80
NTDB id 1090 CAA90909.1 1..3114( )           MNKTLKRQVFRHTALYAAILMFSHTGGGGAMAQTHKYAIIMNERNQLEVKGNGQYST..IKDKDRERKFIYNKDRGGGG.   77
consensus                                    !!!!!!! !!!!!!!! !!!!!!!!!!!!!!!!!! !!!!!!!! !*!!!   !!  ***!!! !!! ! *   * ! !*

logo
NTDB id 328367 EGH17 RS00335 WP 071236973.1  TSNFISFNNNDELVSQQSGTAVFGTATYLPPYGKVSGFDTAELNKRGNAVNWIHTTRPGLAGYGYTGIRCGSTKDCPKLT  160
NTDB id 1090 CAA90909.1 1..3114( )           ...SVFFDNTDTLVSQQRGTAVFGTATYLPPYGKVSGFDADGLQKRNNAVDWIHTTQAGLAGYAYTDVICRS.NQCPQLV  153
consensus                                    *** * ! ! ! !!!!! !!!!!!!!!!!!!!!!!!!!   !*!! !!! !!!!! *!!!!!*!! * ! !*  !! !

logo
NTDB id 328367 EGH17 RS00335 WP 071236973.1  YKTRFSFDNPDLLKTRGGLDRHTEPSRENSPIYKLKDYPWLGVSFNLGGEGTAKDGRSSSKLVSSFDENNSNSNQNLVYT  240
NTDB id 1090 CAA90909.1 1..3114( )           YETKFSFDGIGLAKNAGSLDRHPDPSRENSPIYKLKDHPWLGVSFNLGSENTVKDGKSFNKLISSFSEGN..NNQTIVST  231
consensus                                    ! !*!!!! * ! !  ! !!!!**!!!!!!!!!!!!!*!!!!!!!!!! ! ! !!!*!  !!*!!! ! !** !! *! !

logo
NTDB id 328367 EGH17 RS00335 WP 071236973.1  TEDHRISLSNWQQETTAMAYYLNAKLHLLDKKGIKDIT.GKTVRLGVLKPSIDVKTQNTGLSGILNFWSKWDIKDNGQIP  319
NTDB id 1090 CAA90909.1 1..3114( )           TRGHSISLSDWKREHTAMAYYLNAKLHLLDKKGIEDIAQGKTVDLGTLRPRVEATVR...RGELLNFWATWKIEDKGNIT  308
consensus                                    !  ! !!!! !  !*!!!!!!!!!!!!!!!!!!! !! *!!!! !! !*! **    ***   *!!!!  ! ! ! !*!*

logo
NTDB id 328367 EGH17 RS00335 WP 071236973.1  VKLGLPEVKAGRCINEPNPNKNTQAPSPALTAPALWFGPGQNGKVQMYSASVSTYPGSSSSRIFLQELKTQTDPARPGRH  399
NTDB id 1090 CAA90909.1 1..3114( )           VRLGLPEVKAGRCVNKANPNPNAKAPSPALTAPALWFGPVKDGKAEMYSASVSTYPDSSSSRIYLQNLKRKTDPGKPGRH  388
consensus                                    !*!!!!!!!!!!!*! *!!!*!  !!!!!!!!!!!!!!!  !!  !!!!!!!!!! !!!!!!*!! !!  !!!**!!!!

logo
NTDB id 328367 EGH17 RS00335 WP 071236973.1  SLAALNARDIKSREPNFNSRQTVIRLPGGVYRIGPTR..NGIVGLNGNDGKNDTFGIYKDRLVTPEVDEWAKVLLPWTVR  477
NTDB id 1090 CAA90909.1 1..3114( )           SLETLTENDIKSREPNFTGRQTIIRLNGGVREIKLDRNNTEVVNFNGNDGNNDTFGIVKDLGVEPDTSEWKKVLLPWTVR  468
consensus                                    !!  !   !!!!!!!!!  !!!*!!!*!!!  ! * !**  *!  !!!!! !!!!!! !!  ! !*  !! !!!!!!!!

logo
NTDB id 328367 EGH17 RS00335 WP 071236973.1  YYGNDDIFKTFNQPNNKKQSDKKQYSQKYRIRTKEDDNDKPRDLGDIVNSPIVAVGGYLATSANDGMVHLFKRNGTNQRG  557
NTDB id 1090 CAA90909.1 1..3114( )           GFADDNKFKAFNKEENN..DNKPKYSQKYRSR...DNNKGERNLGDIVNSPIVAVGEYLATSANDGMVHIFKQSGGDKRS  543
consensus                                     ** !  !! !! * ! **  !* !!!!!! !***! !  *! !!!!!!!!!!!!! !!!!!!!!!!!!*!!  !   !
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logo
NTDB id 328367 EGH17 RS00335 WP 071236973.1  YELKLSYIPGTMERKDIENQDSTLAKELRAFAEKGYVGDRYGVDGGFVLRRITDDQDREKHFFMFGAMGLGGRGAYALDL   637
NTDB id 1090 CAA90909.1 1..3114( )           YNLKLSYIPGTMPRKDIQNTESTLAKDVRTFAEKGYVGDRYGVDGGFVLRKVDN.LNGQNRVFMFGAMGFGGRGAYALDL   622
consensus                                    ! !!!!!!!!!!*!!!! ! *!!!!!**! !!!!!!!!!!!!!!!!!!!!!** *     * !!!!!!! !!!!!!!!!!

logo
NTDB id 328367 EGH17 RS00335 WP 071236973.1  TKIDSSNNLTGVSMFDVQNDKNNNNNDSNRVKLGYTVGTPQIGKTQNGKYAAFLASGYAAKDIVS.SDNTTALYVYDLKDT   716
NTDB id 1090 CAA90909.1 1..3114( )           TKADGSDPTAVSLFDVKDNG...NNGNNRVELGYTVGTPQIGKTHDGKYAAFLASGYATKEIITSGDNKTALYVYDLEGN   699
consensus                                    !! !   *!*!!*!!!    ***!! !!! !!!!!!!!!!!!* !!!!!!!!!!!! !*!*** !! !!!!!!!!

logo
NTDB id 328367 EGH17 RS00335 WP 071236973.1  L.GTPIAKIEAPGGKGGLSSPTLVDKDLDGTVDIAYAGDRGGNMYRFDLSSDKPSEWAVRTIFEGTKPITSAPAVSRLAD   795
NTDB id 1090 CAA90909.1 1..3114( )           GTNNLIKKIEVPGGKGGLSSPTLVDKDLDGTVDIAYAGDRGGNMYRFDLSSQDPQQWSVRTIFEGTKPITSAPAISQLKD   779
consensus                                     *  *! !!! !!!!!!!!!!!!!!!!!!!!
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X non conserved
X similar
X $\geq$ 50% conserved