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logo

NTDB id 328358 EGH18 RS11530 WP 165865818.1  MNKTLKRQVFRHTALYAAILMFSHTGGGGGQAQARDYAIVMNGQNQPEVKSNV.PSSIRDKDRKREYTHHGYNTGGGSVS   79
NTDB id 1090 CAA90909.1 1..3114( )           MNKTLKRQVFRHTALYAAILMFSHTGGGGAMAQTHKYAIIMNERNQLEVKGNGQYSTIKDKDRERKFIYNKDRGGGGSVF   80
consensus                                    !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!* !! * !!!*!!  !!*!!! ! **!*!*!!!! ! * **    !!!!!

logo

NTDB id 328358 EGH18 RS11530 WP 165865818.1  FDNSDELVSQQSGTAVFGTATYLPPYGKVSGFDTDSLKGRANAAGWIRTTRIALAGYSYADVVCRDITGCPKLVYETKFA  159
NTDB id 1090 CAA90909.1 1..3114( )           FDNTDTLVSQQRGTAVFGTATYLPPYGKVSGFDADGLQKRNNAVDWIHTTQAGLAGYAYTDVICRS.NQCPQLVYETKFS  159
consensus                                    !!!*! !!!!! !!!!!!!!!!!!!!!!!!!!! ! !  ! !!  !!*!!  *!!!! ! !!*!! *  !! !!!!!!!

logo

NTDB id 328358 EGH18 RS11530 WP 165865818.1  FGQQGLQRKGSKLDIYEDKSRDNSPIYKLKDHPWLGVSFNLGSENTVKNSKSLNKLISSFSEGNNNQNIVSTTRDHPISL  239
NTDB id 1090 CAA90909.1 1..3114( )           FDGIGLAKNAGSLDRHPDPSRENSPIYKLKDHPWLGVSFNLGSENTVKDGKSFNKLISSFSEGNNNQTIVSTTRGHSISL  239
consensus                                    !    !! * *  !! **!*!!*!!!!!!!!!!!!!!!!!!!!!!!!!!  !! !!!!!!!!!!!!!! !!!!!! !*!!!

logo

NTDB id 328358 EGH18 RS11530 WP 165865818.1  GDSQREHTAVAYYLNAKLHLLDKKKIKDIT.GKTVQLGVLKPSIDVKTQNTGLAGLLNFWSKWDIKDNGQIPVKLGLPEV  318
NTDB id 1090 CAA90909.1 1..3114( )           SDWKREHTAMAYYLNAKLHLLDKKGIEDIAQGKTVDLGTLRPRVEATVR...RGELLNFWATWKIEDKGNITVRLGLPEV  316
consensus                                     !  !!!!!*!!!!!!!!!!!!!! ! !! *!!!! !! !*! **    *** * !!!!!  ! ! ! !*!*!*!!!!!!

logo

NTDB id 328358 EGH18 RS11530 WP 165865818.1  KAGRCTNKPNPNNNTKAPSPALTAPALWFGPVQNGKVQMYSASVSTYPDSSSSKIFLQNLSRNDDKNKPGRYSLKSLNDG  398
NTDB id 1090 CAA90909.1 1..3114( )           KAGRCVNKANPNPNAKAPSPALTAPALWFGPVKDGKAEMYSASVSTYPDSSSSRIYLQNLKRKTDPGKPGRHSLETLTEN  396
consensus                                    !!!!! !!*!!!*! !!!!!!!!!!!!!!!!  !!  !!!!!!!!!!!!!!!*!*!!!! !  !* !!!!*!! *! *

logo

NTDB id 328358 EGH18 RS11530 WP 165865818.1  EIQSRQPSFNGRQTIIRLDDGVHLIKLNGSKDEVAAFVNLNGNNTGKNDTFGIVKEANVNLDADEWKKVLLPWTVRGPGN  478
NTDB id 1090 CAA90909.1 1..3114( )           DIKSREPNFTGRQTIIRLNGGVREIKLDRNNTEVVNFNG....NDGNNDTFGIVKDLGVEPDTSEWKKVLLPWTVRGFAD  472
consensus                                    *! !! ! ! !!!!!!!!  !!* !!!     !!  !  ****! ! !!!!!!!!*  ! *!  !!!!!!!!!!!!!**

logo

NTDB id 328358 EGH18 RS11530 WP 165865818.1  DDKFKSINRES.....DKYSQRYRIRE..NGNRDLGDIVNSPIVAVGGYLATAANDGMVHIFKKNGGSDERSYNLKLSYI  551
NTDB id 1090 CAA90909.1 1..3114( )           DNKFKAFNKEENNDNKPKYSQKYRSRDNNKGERNLGDIVNSPIVAVGEYLATSANDGMVHIFKQSGG.DKRSYNLKLSYI  551
consensus                                    ! !!!  !*! ******!!!!*!! !*** ! ! !!!!!!!!!!!!!! !!!!! !!!!!!!!!!  !!*! !!!!!!!!!!
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logo

NTDB id 328358 EGH18 RS11530 WP 165865818.1  PGTMPRQYFDNDTSALKGSTLAQELRTFAEKGYVGDRYGVDGGFVLRQVE.....DRVFMFGAMGFGGRGAYALDLSKIN   626
NTDB id 1090 CAA90909.1 1..3114( )           PGTMPRKDIQNTE.....STLAKDVRTFAEKGYVGDRYGVDGGFVLRKVDNLNGQNRVFMFGAMGFGGRGAYALDLTKAD   626
consensus                                    !!!!!!     !  *****!!!! **!!!!!!!!!!!!!!!!!!!!!! !****** !!!!!!!!!!!!!!!!!!!!*!

logo

NTDB id 328358 EGH18 RS11530 WP 165865818.1  GNYPAAAPLFDVKDGDNNGKNRVKVKLGYTVGTPQIGKTQNGKYAAFLASGYAAKDIVS.SDNTTALYVYDLKDTL.GTP   704
NTDB id 1090 CAA90909.1 1..3114( )           GSDPTAVSLFDVKDNGNNGNNR..VELGYTVGTPQIGKTHDGKYAAFLASGYATKEIITSGDNKTALYVYDLEGNGTNNL   704
consensus                                    !  ! ! *!!!!!!  !!! !!**! !!!!!!!!!!!!!* !!!!!!!!!!!! !*!*** !! !!!!!!!!    *  *

logo

NTDB id 328358 EGH18 RS11530 WP 165865818.1  IAKIEVQGGKGGLSSPTLVDKDLDGTVDIAYAGDRGGNMYRFDLSNSDPNKWSAKAIFEGTKPITSAPAVSRLADKRVVI   784
NTDB id 1090 CAA90909.1 1..3114( )           IKKIEVPGGKGGLSSPTLVDKDLDGTVDIAYAGDRGGNMYRFDLSSQDPQQWSVRTIFEGTKPITSAPAISQLKDKRVVI   784
consensus                                    ! !!!!*!!!!!!!!!!!!!!!!!! !!!!!!!!!!!!!!!!!!!  !!* !! * !!!!!!!!!!!!!*! ! !!!!!!

logo

NTDB id 328358 EGH18 RS11530 WP 165865818.1  FGTGSDLSEQDVVGTDQQYIYGIFDDDKPTVNVKVTNGTGGGLLEQVLSE..ENKILFLINNKASGGSADKGWVVKLREG   862
NTDB id 1090 CAA90909.1 1..3114( )           FGTGSDLSEEDVDNMEEQYIYGIFDDDTATTGTVNFSDSGGGLLEQVLRRDNDNKTLFLTDYKRSDGSGNKGWVVKLKDG   864
consensus                                    !!!!!!!!! !!   * !!!!!!!!!! *!        *!!!!!!!!!  ***!! !!!   ! ! !!* !!!!!!!**!

logo

NTDB id 328358 EGH18 RS11530 WP 165865818.1  ERVTVKPTVVLRTAFVTIRKYND.GGCGAETAILGINTADGGALTPRSARPIVPDHD.SVAQYSGHKKTAGGKSVPIGCM   940
NTDB id 1090 CAA90909.1 1..3114( )           QRVTVKPTVVLRTAFVTIHKYTGTDKCGAETAILGINTADGGKLTKKSARPIVPEANTAVAQYSGHKKGTNGKSIPIGCM   944
consensus                                     !!!!!!!!!!!!!!!!!!*!!  *  !!!!!!!!!!!!!!!! !!**!!!!!!!** * !!!!!!!!!   !!!*!!!!!

logo

NTDB id 328358 EGH18 RS11530 WP 165865818.1  WKNGKTVCPNGYVYDKPVNVRYLDEKKTDDFPVTADGDAGGSGTFKEGKKPARNNRCFSGKGVRTLLMNDLDSLDITGPM  1020
NTDB id 1090 CAA90909.1 1..3114( )           QKSNEIVCPNGYVYDKPVNVRYLDEKKTDGFSTTADGDAGGSGIDPAGKRSGKNNRCFSQKGVRTLLMNDLDSLDITGPT  1024
consensus                                     !    !!!!!!!!!!!!!!!!!!!!!!!! !* !!!!!!!!!!  * !!****!!!!!! !!!!!!!!!!!!!!!!!!!

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logo

NTDB id 328358 EGH18 RS11530 WP 165865818.1  CGIKRLSWREVFF.  1033
NTDB id 1090 CAA90909.1 1..3114( )           CGMKRISWREVFY*  1037
consensus                                    !!*!!*!!!!!!!*
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X non conserved
X similar
X $\geq$ 50% conserved