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logo
NTDB id 1118652 ELZ61 RS08255 WP 126372846.1  MKFSLKLDVILWLVIGAGLSLLYVPKALLLGVELMLCTVGIGILAVLTAYLFAYYKIAKGLVYGVIFVLSLGYFHHQALK   80
NTDB id 1359 HI 0061 AAC21739.1               ..MKLNLITLVVLLIVADLTLLFLPQPLLLPWQVALVI......ALVLIFLFIFLR.RNFLVSLAFFVASLGYFHYSALS   71
consensus                                     **  ! !  ** !*! ! !*!!**! *!!!*  * !* ******!**  *!! * **   !!    !! !!!!!!* !!

logo
NTDB id 1118652 ELZ61 RS08255 WP 126372846.1  ILSQAEQSASLNRISIPIKIEKILHQQDYQTVIATGKLAENLPSQRIYLQWQNSEKNLENKAAEQIKAGQIWQAELLLKP  160
NTDB id 1359 HI 0061 AAC21739.1               LSQQAQ.NITAQKQVVTFKIQEILHQQDYQTLIATATLENNLQEQRIFLNWKAKEV.........PQLSEIWQAEISLRS  141
consensus                                     *  !! *  * **  ** !!  !!!!!!!!!*!!!* !  !!* !!!*!*!   ! **********    !!!!!* !**

logo
NTDB id 1118652 ELZ61 RS08255 WP 126372846.1  LSGRLNQGGFDRQKWYFSQGITAYGRVKSAVQISQDFAWRERLLQASFQQTQGLPMQGLLLALGFGERAWLNTKHWQIYQ  240
NTDB id 1359 HI 0061 AAC21739.1               LSARLNFGGFDRQQWYFSKGITAVGTVKSAVKIADVSSLRAEKLQQVKKQTEGLSLQGLLIALAFGERAWLDKTTWSIYQ  221
consensus                                     !!*!!! !!!!!! !!!! !!!! ! !!!!! !       !   !!    !! !!**!!!!*!!*!!!!!!!   *! !!!

logo
NTDB id 1118652 ELZ61 RS08255 WP 126372846.1  KTNTAHLIAISGLHIGLAMLFGFALARGLQFFLPTHRIGAISPLLCSFFIASIYAQLAGFSIPTLRALLALGLVCLIRVL  320
NTDB id 1359 HI 0061 AAC21739.1               QTNTAHLIAISGLHIGLAMGIGFCLARVVQVFFPTRFIHPYFPLVFGVLFALIYAYLAGFSVPTFRAISALVFVLFIQIM  301
consensus                                      !!!!!!!!!!!!!!!!!!  !!*!!! *! ! !!* !**  !!**    ! !!! !!!!!*!! !!* !!  !* ! **

logo
NTDB id 1118652 ELZ61 RS08255 WP 126372846.1  RCYYTPWQYFQCVVALLILWDPLMLLSVSFWLSAGAVASLILWYQLVPLDLIQWQIYPIKNQWVKKILRWIFSLFHLQLG  400
NTDB id 1359 HI 0061 AAC21739.1               RRHYSPIQFFTLVVGFLLFCDPLMPLSVSFWLSCGAVGCLLLWYRYVPFSLFQWKNRPFS.....PKVRWIFSLFHLQFG  376
consensus                                     !**!*! !*! *!!* !* *!!!!*!!!!!!!!*!!!**!*!!!  !!  ! !!   !  ****** *!!!!!!!!!! !

logo
NTDB id 1118652 ELZ61 RS08255 WP 126372846.1  LLCLFTPIQLYFFHGTSLAGMVANLLAVPVFSLCLVPMVLFAVLSQGAFNSWQGANYLAEKITALLSQWQGNWMDLSENQ  480
NTDB id 1359 HI 0061 AAC21739.1               LLLFFTPLQLFLFNGLSLSGFLANFMAVPIYSFLLVPLILFAVFTNGTMFSWQLANKLAEGITGLISVFQGNWLTVSFNL  456
consensus                                     !!* !!!*!!* !*! !! ! *!! *!!!**! *!!!**!!!! **!   !!! !! !!! !!*!*! *!!!!* *! !

logo
NTDB id 1118652 ELZ61 RS08255 WP 126372846.1  SQWIVILLLILGLGYAFYLQKLPQKIAKKSILAGKKTISLNAEKLPSPLFLQRMKPIFAGLLGI...MLMNLAWQEINAP  557
NTDB id 1359 HI 0061 AAC21739.1               ALGLTALCAGIFMLIIWNIYREPEISSSNWQIKRAKFF...TLNLSKPLLKNERINVLRCSFGIILLCFTILLFKQLSKP  533
consensus                                        *  !*  * *   * * * !        *   !  ***   !* !!  *   **  *  !!****   ! *  *  !
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logo

NTDB id 1118652 ELZ61 RS08255 WP 126372846.1  KWRLETLDVGQGLATLLVKNQRGILYDTGAAWRGGSMATLEILPYLQRQGIVLDKLILSHDDNDHSGGASAILQAFPHAE   637
NTDB id 1359 HI 0061 AAC21739.1               TWQVDTLDVGQGLATLIVKNGKGILYDTGSSWRGGSMAELEILPYLQREGIVLEKLILSHDDNDHAGGASTILKAYPNVE   613
consensus                                      ! **!!!!!!!!!!!*!!! *!!!!!!!  !!!!!!! !!!!!!!!! !!!!*!!!!!!!!!!! !!!! !! !*!* !

logo

NTDB id 1118652 ELZ61 RS08255 WP 126372846.1  LITPSEKNHTKNHRTFCTQGQQWQWQGLHITALSPQKIRKRAENPDSCVLLIDDGNRKVLLTGDADSQTERQFADLAGKI   717
NTDB id 1359 HI 0061 AAC21739.1               LITPSRKNYGENYRTFCTAGRDWHWQGLHFQILSPHNVVTRADNSHSCVILVDDGKNSVLLTGDAEAKNEQIFARTLGKI   693
consensus                                     !!!!! !!*  !*!!!!! !  !*!!!!!   !!!* *  !!*!**!!!*!*!!!   !!!!!!!*   !  !!   !!!

logo

NTDB id 1118652 ELZ61 RS08255 WP 126372846.1  EILQVGHHGSKTSSSEYLLKTTQPKIALISSSRGNPWHFPHSVVLERLKAQQSAVYNTADFGQISLLFFPEQIKIYTARS   797
NTDB id 1359 HI 0061 AAC21739.1               DVLQVGHHGSKTSTSEYLLSQVRPDVAIISSGRWNPWKFPHYSVMERLHRYKSAVENTAVSGQVRVNFFQDRLEIQQART   773
consensus                                     **!!!!!!!!!!!!*!!!!!    ! *!*!!! ! !!!*!!!  !*!!!*   !!! !!!  !!* * !!** * !  !!*

logo

NTDB id 1118652 ELZ61 RS08255 WP 126372846.1  EFSPWYRGLSIGD..   810
NTDB id 1359 HI 0061 AAC21739.1               KFSPWYARVIGLSKE   788
consensus                                      !!!!!  *    **
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X non conserved

X similar

X ≥ 50% conserved