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logo
NTDB id 1051001 O1Q82 RS06980 WP 386686472.1  MQRILELIRQLDIDEVAFCAILSVLSLYFLPERFLFCWQLCLLLFSLLLIMRLAIKKPQFIIKWINRILILLVFIGYAHF   80
NTDB id 1359 HI 0061 AAC21739.1               ........MKLNLITLVVLLIVADLTLLFLPQPLLLPWQVALVIALVLIFLFIFLR.RNF....LVSLAFFVASLGYFHY   67
consensus                                     ********  ! *  *  * !*  !*! !!! * !  !!**!**  *!* * * *****!*****  *   *  *!! !*

logo
NTDB id 1051001 O1Q82 RS06980 WP 386686472.1  IALNSLQQAQ.IFPQKIQTTFRIVEIHHQGDYQSLVLQ....TEQPNRRIYATWKVSQSPKLGELWQGELQLRPISSRLN  155
NTDB id 1359 HI 0061 AAC21739.1               SALSLSQQAQNITAQKQVVTFKIQEILHQQDYQTLIATATLENNLQEQRIFLNWKAKEVPQLSEIWQAEISLRSLSARLN  147
consensus                                      !!   !!!!*! *!!   !!*! !!*!! !!!*!*  ****   *  !!*  !!    ! ! !*!!*!* !!**! !!!

logo
NTDB id 1051001 O1Q82 RS06980 WP 386686472.1  ISGFDRQIWYFAKDIQAWGTVKSAVKITQDFSWREQRLADSLMQTQGLTQQGLLLALGFGERAWLNPDTWKIYQQTNTAH  235
NTDB id 1359 HI 0061 AAC21739.1               FGGFDRQQWYFSKGITAVGTVKSAVKIADVSSLRAEKLQQVKKQTEGLSLQGLLIALAFGERAWLDKTTWSIYQQTNTAH  227
consensus                                       !!!!! !!! ! ! ! !!!!!!!!!    ! !  *!     !! !!* !!!!*!!*!!!!!!! * !! !!!!!!!!!

logo
NTDB id 1051001 O1Q82 RS06980 WP 386686472.1  LIAISGLHIGLAMALGFCFGRVVQYMLPTPKITPIFPLCCGVVSALFYANLAGFAIPTLRASIALLILILLHFYRAYCTA  315
NTDB id 1359 HI 0061 AAC21739.1               LIAISGLHIGLAMGIGFCLARVVQVFFPTRFIHPYFPLVFGVLFALIYAYLAGFSVPTFRAISALVFVLFIQIMRRHYSP  307
consensus                                     !!!!!!!!!!!!!**!!! *!!!!   !!* !*! !!!**!!* !! !! !!!! *!! !!  !!* ** **  ! ****

logo
NTDB id 1051001 O1Q82 RS06980 WP 386686472.1  WQLYFRIVAVLLLYDPLMILSTSFWLSIGAVGCLILWYQLFPLHLLRWRGLPLSSKVRWILALFHLQLGLFCLFTPIQLA  395
NTDB id 1359 HI 0061 AAC21739.1               IQFFTLVVGFLLFCDPLMPLSVSFWLSCGAVGCLLLWYRYVPFSLFQWKNRPFSPKVRWIFSLFHLQFGLLLFFTPLQLF  387
consensus                                      ! *  *!* !! *!!!!*!! !!!!!*!!!!!!*!!!   ! *!  !*  ! *!!!!!  !!!!! !! * !!!*!!

logo
NTDB id 1051001 O1Q82 RS06980 WP 386686472.1  FFNGFSLQGFWANLLIVPLYSFLLVPVVLFAVFSNGSLYSWRLADFVADKITDLLSLFQHGWLSLSYLQSAYFNTL....  471
NTDB id 1359 HI 0061 AAC21739.1               LFNGLSLSGFLANFMAVPIYSFLLVPLILFAVFTNGTMFSWQLANKLAEGITGLISVFQGNWLTVSFNLALGLTALCAGI  467
consensus                                      !!! !! !! !! * !!*!!!!!!!**!!!!!*!!***!! !!  *!* !! !*!*!!* !!**!*        !****

logo
NTDB id 1051001 O1Q82 RS06980 WP 386686472.1  LAFLIWGMLYKIYTSNRKNISY..HKKPRCFSLKSDRSLSP...ILYARVQKGILLFILANGLQPLWHYFNQSDWQIDTL  546
NTDB id 1359 HI 0061 AAC21739.1               FMLIIWNI....YREPEISSSNWQIKRAKFFTLNLSKPLLKNERINVLRCSFGIILLC...FTILLFKQLSKPTWQVDTL  540
consensus                                        *!! *****!  *    ! ***!****!*!   **! ****!   !*  !!*! ****   *!**    * !!*!!!
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logo

NTDB id 1051001 O1Q82 RS06980 WP 386686472.1   DVGQGLATLIVKNQRGILYDTGASWQGGSMAELEIIPYLQRQGITLDYLIISHDDNDHAGGARAILQAFPQAMLVSPSQK   626
NTDB id 1359 HI 0061 AAC21739.1                DVGQGLATLIVKNGKGILYDTGSSWRGGSMAELEILPYLQREGIVLEKLILSHDDNDHAGGASTILKAYPNVELITPSRK   620
consensus                                      !!!!!!!!!!!!! *!!!!!!! !! !!!!!!!!!*!!!!! !! !* !!*!!!!!!!!!!!  !! !*!*  !**!! !

logo

NTDB id 1051001 O1Q82 RS06980 WP 386686472.1   NYSEKHRTFCQAEKQWLWQGIQIKVLSPKQIVERADNFHSCVLWLEKDKHSLLLTGDADIATERQILPLLNKVEVLQVGH   706
NTDB id 1359 HI 0061 AAC21739.1                NYGENYRTFCTAGRDWHWQGLHFQILSPHNVVTRADNSHSCVILVDDGKNSVLLTGDAEAKNEQIFARTLGKIDVLQVGH   700
consensus                                      !! ! *!!!! ! * !*!!!**  *!!!***! !!!! !!!!* **  !*!*!!!!!!*   !    * ! !**!!!!!!

logo

NTDB id 1051001 O1Q82 RS06980 WP 386686472.1   HGSKTSTGQGFVNKLQPDIALISSGRWNPWHFPNRSVMERLQQAQSAVYNTAISGQISVRFYAEQTKVVTARNAFSPWYQ   786
NTDB id 1359 HI 0061 AAC21739.1                HGSKTSTSEYLLSQVRPDVAIISSGRWNPWKFPHYSVMERLHRYKSAVENTAVSGQVRVNFFQDRLEIQQARTKFSPWYA   780
consensus                                      !!!!!!!    *  * !!*!*!!!!!!!!!*!!* !!!!!!*   !!! !!!*!!!* ! !* *   *  !!  !!!!!

logo

NTDB id 1051001 O1Q82 RS06980 WP 386686472.1   QIIDVQHSD   795
NTDB id 1359 HI 0061 AAC21739.1                RVIGLSKE.   788
consensus                                       *! * * *
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X non conserved

X similar

X $\geq$ 50% conserved