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logo
NTDB id 1064913 ACHV18 RS04910 WP 162869652.1  MKNALLSMSVVTVFSACSLLWLPEHFLLHWHITLLVFALLLVSIIICVLCGKNHWISPLIFVMSSVGILGYIHDQARQTL   80
NTDB id 1359 HI 0061 AAC21739.1                MKLNLITLVVLLIVADLTLLFLPQPLLLPWQVALVIALVLIF...LFI.FLRRNFLVSLAFFVASLGYFHY...SALSLS   73
consensus                                      !!  !*** !* *  **!!*!!  !! !** !**  *!* ******** * *** *! ! * !*!  *!*** !

logo
NTDB id 1064913 ACHV18 RS04910 WP 162869652.1  LQADLVAQLPRKIETEFKIIEVLQQKNYQTFVVSAQLSPQQAKQKMILQWHAQEKAQIGEIWKGELRLRPISSRLNMGGF  160
NTDB id 1359 HI 0061 AAC21739.1                QQAQ..NITAQKQVVTFKIQEILHQQDYQTLIATATLENNLQEQRIFLNWKAKEVPQLSEIWQAEISLRSLSARLNFGGF  151
consensus                                       !! **   * !   !!! !*!*!  !!! * *! ! **   !** !*!*! ! *!* !!! *!* !!**! !!! !!!

logo
NTDB id 1064913 ACHV18 RS04910 WP 162869652.1  DKQQWYFAKGITAYATVKSAVKISEQLSWREKWLREGVKQTMQLEYQGLLLALAFGERAWLPTDIWQTYQKTNTAHVIAI  240
NTDB id 1359 HI 0061 AAC21739.1                DRQQWYFSKGITAVGTVKSAVKIADVSSLRAEKLQQVKKQTEGLSLQGLLIALAFGERAWLDKTTWSIYQQTNTAHLIAI  231
consensus                                      !*!!!!! !!!!! *!!!!!!!! *  ! !   !   !!!  !  !!!!*!!!!!!!!!!*   !  !! !!!!!*!!!

logo
NTDB id 1064913 ACHV18 RS04910 WP 162869652.1  SGLHIGLAMGIGYFFIRLIQFLLPLKWVTPTLPIIVGLLFAWFYAELAGFSIPTSRAFFALTVVSWVKLWRRSYSVWQFF  320
NTDB id 1359 HI 0061 AAC21739.1                SGLHIGLAMGIGFCLARVVQVFFPTRFIHPYFPLVFGVLFALIYAYLAGFSVPTFRAISALVFVLFIQIMRRHYSPIQFF  311
consensus                                      !!!!!!!!!!!!**  !**!   ! ****!  !** !*!!!  !! !!!!!*!! !!  !!  ! ** * !!*!!* !!!

logo
NTDB id 1064913 ACHV18 RS04910 WP 162869652.1  LLVVALLLLGEPCMILSSSFWLSVGAVSVLMLWYQIFPLSLLHWRGKKITESPWRNCRWLFSLLHLQLGLLWLFTPVQLL  400
NTDB id 1359 HI 0061 AAC21739.1                TLVVGFLLFCDPLMPLSVSFWLSCGAVGCLLLWYRYVPFSLFQWKNRPFS....PKVRWIFSLFHLQFGLLLFFTPLQLF  387
consensus                                       !!!* !! **!*!*!! !!!!!*!!! *!*!!!   ! !! *!* ** ****** *!!*!!! !!! !!!  !!!*!!

logo
NTDB id 1064913 ACHV18 RS04910 WP 162869652.1  LFQGIALTSFMANVLVVPIYSVILIPLILLAVITQGAFSFWSIANTIAKYVTMLLTPLQSHWVVFSQQEILCLIAILALT  480
NTDB id 1359 HI 0061 AAC21739.1                LFNGLSLSGFLANFMAVPIYSFLLVPLILFAVFTNGTMFSWQLANKLAEGITGLISVFQGNWLTVSFNLALGLTALCAGI  467
consensus                                      !!*!* !* !*!! * !!!!! *!*!!!! !! !*!    ! *!! *!  *! !*** ! *!*  ! *  !*! !**!

logo
NTDB id 1064913 ACHV18 RS04910 WP 162869652.1  FILLIWYLYDLKKESLKC.YAKVPRFFHLNQMRLLNPSLKWKTYLLAVGISLYCFLQILYKEISQPLWRLDTLDVGQGLA  559
NTDB id 1359 HI 0061 AAC21739.1                FMLIIWNIYREPEISSSNWQIKRAKFFTLNLSKPLLKNERINVLRCSFGIILLCFTILLFKQLSKPTWQVDTLDVGQGLA  547
consensus                                      !***!! *!  *  !  **  ! **!!*!!  **! *  *     *  !! ! !!  *!*! *! ! ! *!!!!!!!!!!
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logo

NTDB id 1064913 ACHV18 RS04910 WP 162869652.1  NLIVVNGKGVLYDTGASWAGGSMAELEILPYLQREGIELEQVILSHDDNDHVGGAETILKHYPQAKLMTASAQNYGKTDR   639
NTDB id 1359 HI 0061 AAC21739.1                TLIVKNGKGILYDTGSSWRGGSMAELEILPYLQREGIVLEKLILSHDDNDHAGGASTILKAYPNVELITPSRKNYGENYR   627
consensus                                       !!! !!!!*!!!!! !! !!!!!!!!!*!!!!!!!! !! *!!!!!!!!! !!! !!!!*!!*  !*!*!  !!!    !

logo

NTDB id 1064913 ACHV18 RS04910 WP 162869652.1  TFCEAGKTWTWQHLTFKALSPTKIVKRAKNTDSCVLLISDGSHHLLLTGDADIAAEKQFVNQLSQLDVLQVGHHGSKTST   719
NTDB id 1359 HI 0061 AAC21739.1                TFCTAGRDWHWQGLHFQILSPHNVVTRADNSHSCVILVDDGKNSVLLTGDAEAKNEQIFARTLGKIDVLQVGHHGSKTST   707
consensus                                      !!! !!* !*!!*!*!  !!!* *! !! !**!!!*!* !! ***!!!!!!*   !  !   !  *!!!!!!!!!!!!!!

logo

NTDB id 1064913 ACHV18 RS04910 WP 162869652.1  GYELLYQTRPKIALISSGRWNPWQFPHVQVVQRLKRYQTAVYNTGELGQISLLFHAKHIEIQTARTDFSPWYRRLIGL..   797
NTDB id 1359 HI 0061 AAC21739.1                SEYLLSQVRPDVAIISSGRWNPWKFPHYSVMERLHRYKSAVENTAVSGQVRVNFFQDRLEIQQARTKFSPWYARVIGLSK   787
consensus                                        !! ! !! *!*!!!!!!!!!! !!!  !* !!*!! *!! !!*  !!* * !*  **!!! !!! !!!!! !*!!!**

logo

NTDB id 1064913 ACHV18 RS04910 WP 162869652.1  .   797
NTDB id 1359 HI 0061 AAC21739.1                E   788
consensus                                      *
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X non conserved

X similar

X ≥ 50% conserved