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logo
NTDB id 1141696 DQN58 RS06505 WP 006717932.1  MGVSLDKFAGSLIVSGITLVFLPDRFLVSWQTALYLSLLLCPLILLARGLSCHKTKYSLLWLLLFTLNLAYVHQPAIQLL   80
NTDB id 1359 HI 0061 AAC21739.1               MKLNLITLVVLLIVADLTLLFLPQPLLLPWQVALVIALVLIFLFIFLRR.......NFLVSLAFFVASLGYFHYSALSLS   73
consensus                                     ! * !       !!!   *!!*!!! * !**!! !! * !*!**! *   ! *******  !* !   !    !*! ! *!* !

logo
NTDB id 1141696 DQN58 RS06505 WP 006717932.1  NQADNIAHLPKTIHTEFIVEEILHQQQYQTLILRAKLADNRPEQRLYANWKLKQNVNIGERYVGDLRLRPISSRLNKDGF  160
NTDB id 1359 HI 0061 AAC21739.1               QQAQNITAQKQ..VVTFKIQEILHQQDYQTLIATATLENNLQEQRIFLNWKAKEVPQLSEIWQAEISLRSLSARLNFGGF  151
consensus                                     *!! !! * * ***   ! * !!!!!! !!!!!   !  !   ! *!!!** !!! !   *** ! * *** !!**! !!!   !!

logo
NTDB id 1141696 DQN58 RS06505 WP 006717932.1  DRQQWYFSKRITAWAEVKSAVKIEQFFSWRQTALHQARQQIENLSQQGLLLALGFGERAWLENATWQIYQKTNTAHLIAI  240
NTDB id 1359 HI 0061 AAC21739.1               DRQQWYFSKGITAVGTVKSAVKIADVSSLRAEKLQQVKKQTEGLSLQGLLIALAFGERAWLDKTTWSIYQQTNTAHLIAI  231
consensus                                     !!!!!!!!! !!! * !!!!!!!    ! !   !*! * ! ! !! !!!!*!!*!!!!!!!*  !! !!! !!!!!!!!!

logo
NTDB id 1141696 DQN58 RS06505 WP 006717932.1  SGLHIGLAMMLGFALARLLQFTFPTHYITPTFPIFCGMILALLYSQLAGLAIPTLRAIIALALLYAIQHLRLHWTVWQLL  320
NTDB id 1359 HI 0061 AAC21739.1               SGLHIGLAMGIGFGLARVVQVFFPTRFIHPYFPLVFGVLFALIYAYLAGFSVPTFRAISALVFVLFIQIMRRHYSPIQFF  311
consensus                                     !!!!!!!!! *!!*!!!**!   !!!**!*! !!* *!** !!*!   !!!   *!! !!! !!   *   !!**! !*** !

logo
NTDB id 1141696 DQN58 RS06505 WP 006717932.1  LRVVALLIFIDPLILLSTSFWLSVGAVTCLIVWYQCFPLSLLHWRGKPLTHTHWRKVRYVFGLFHLQLGLLWLFTPIQLF  400
NTDB id 1359 HI 0061 AAC21739.1               TLVVGFLLFCDPLMPLSVSFWLSCGAVGCLLLWYRYVPFSLFQWKNRPFS....PKVRWIFSLFHLQFGLLLFFTPLQLF  387
consensus                                       !!* !*!*!!!**!! !!!!!*!!! !!**!! * ! !! *!* *! ******!!!**! !!!!! !!!   !!!*!!!

logo
NTDB id 1141696 DQN58 RS06505 WP 006717932.1  FFNGISLNSFITNLIAVPLYSFILVPLVLFAVLTQGSWNTWWLANDLAEKITALLAPLQDHWLAISIPHSLWITLVLTCL  480
NTDB id 1359 HI 0061 AAC21739.1               LFNGLSLSGFLANFMAVPIYSFLLVPLILFAVFTNGTMFSWQLANKLAEGITGLISVFQGNWLTVSFNLALGLTALCAGI  467
consensus                                      !!!*!!   !* ! *!!!*!!!*!!!!*!!!! !*!*   *! !!! !!! !!*!* * ! *!! *! ** ! *! ** **

logo
NTDB id 1141696 DQN58 RS06505 WP 006717932.1  FLGLLYYVYKPQKPLSSTLELAKLTRLKGFHLAAERTLSFPLQKTIYGLGCGLIVFCNTTLAHHYLSRPNWQLDTLDVGQ  560
NTDB id 1359 HI 0061 AAC21739.1               FMLIIWNIYREPEISSSNWQIK...RAKFFTLNLSKPLLKNERINVLRCSFGIILLCFTILLFKQLSKPTWQVDTLDVGQ  544
consensus                                     !* *** *!*** * !!   * ***! ! !*!   **!  *    *  * *!*!* ! ! ! ** !!*! !!*!!!!!!!
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logo

NTDB id 1141696 DQN58 RS06505 WP 006717932.1  GLATLIVKDGKGVLYDTGSSWEGGSMAQLEILPYLQRQGIQLEWLILSHDDNDHSGGARAMLAAYPDIQLTTASQKRYGE   640
NTDB id 1359 HI 0061 AAC21739.1               GLATLIVKNGKGILYDTGSSWRGGSMAELEILPYLQREGIVLEKLILSHDDNDHAGGASTILKAYPNVELITPSRKNYGE   624
consensus                                     !!!!!!!! !!!*!!!!!!!! !!!!! !!!!!!!!! !! !! !!!!!!!!!! !!!  *! !!! * ! !*! ! !!!

logo

NTDB id 1141696 DQN58 RS06505 WP 006717932.1  KNTEENDRTFCLANKQWTWQGLHFTVLSPNNIVSRAENPDSCTLLLTDGKYNILLTGDADLSVEYKILPKLDKIHVLQVG   720
NTDB id 1359 HI 0061 AAC21739.1               .....NYRTFCTAGRDWHWQGLHFQILSPHNVVTRADNSHSCVILVDDGKNSVLLTGDAEAKNEQIFARTLGKIDVLQVG   699
consensus                                     *****! !!!! ! * !*!!!!!! *!!!*!*!*!!*!**!! *!* !!!  *!!!!!!*   !    * ! !!*!!!!!

logo

NTDB id 1141696 DQN58 RS06505 WP 006717932.1  HHGSKTSTGEALVRHTQPDIALISSGRWNPWHFPNGDVMARLKQQGTQSYNTAETGQITLLFHENKIEIQTARAEFSPWY   800
NTDB id 1359 HI 0061 AAC21739.1               HHGSKTSTSEYLLSQVRPDVAIISSGRWNPWKFPHYSVMERLHRYKSAVENTAVSGQVRVNFFQDRLEIQQARTKFSPWY   779
consensus                                     !!!!!!!! ! !* *  !!*!*!!!!!!!!!*!!*  !! !!*   *   !!! *!!* * !*  **!!! !!  !!!!!

logo

NTDB id 1141696 DQN58 RS06505 WP 006717932.1  RRLIGLKGK   809
NTDB id 1359 HI 0061 AAC21739.1               ARVIGLSKE   788
consensus                                      !*!!!
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X non conserved

X similar

X $\geq$ 50% conserved