```
logo
NTDB id 1142602 DQL22 RS06930 WP 111300117.1  MNISLDKFAGTLIFSGLTLLFLPDKWLLSWQVALYIFLPLLFITLLCYCLKLTKLLTLLTYLLLLLALLVYVHFPALSML   80
NTDB id 1359 HI 0061 AAC21739.1               MKLNLITLVVLLIVADLTLLFLPQPLLLPWQVALVIALVLIFLFIFLRR.......NFLVSLAFFVASLGYFHYSALSLS   73
consensus                                     ! * !       !!   !!!!!!! * !!*!!!!! ! !*!*!* * * ********  !  !   *! ! ! !**!!!*

logo
NTDB id 1142602 DQL22 RS06930 WP 111300117.1  KQADNIANLPKILHTEFTVQEVLNQQDFQTVVIAAKLAEDLPEQRIYAQWKTPQIVQIGERYKGDLRLRPISSRLNFNGF  160
NTDB id 1359 HI 0061 AAC21739.1               QQAQNITAQKQV..VTFKIQEILHQQDYQTLIATATLENNLQEQRIFLNWKAKEVPQLSEIWQAEISLRSLSARLNFGGF  151
consensus                                      !! !!   * ***  ! *!!*!*!!!*!!**  ! !   !*!!!!* *!! * **!* ! * *** !!**! !!!! !!

logo
NTDB id 1142602 DQL22 RS06930 WP 111300117.1  DRQQWYFGKHISAWASVQSAVKIENVFSWRQTALNNALKQTENLSQQGLLLALSFGERAWLDNETWQIYQKTNTAHLIAI  240
NTDB id 1359 HI 0061 AAC21739.1               DRQQWYFSKGITAVGTVKSAVKIADVSSLRAEKLQQVKKQTEGLSLQGLLIALAFGERAWLDKTTWSIYQQTNTAHLIAI  231
consensus                                     !!!!!!! !*!*! **! !!!!!  ! ! !   !**  !!!! !! !!!!*!! !!!!!!!!  !! !!! !!!!!!!!!

logo
NTDB id 1142602 DQL22 RS06930 WP 111300117.1  SGLHIGLAMLLGYGLARLLQFFLPTRYLTPTLPILCGLLCALLYSQLAGMAIPTLRAMVALAILYAIQGLRLYWTPWRLL  320
NTDB id 1359 HI 0061 AAC21739.1               SGLHIGLAMGIGFCLARVVQVFFPTRFIHPYFPLVFGVLFALIYAYLAGFSVPTFRAISALVFVLFIQIMRRHYSPIQFF  311
consensus                                     !!!!!!!!! *!**!!!**! ! !!!***!  !***!*!*!!*!  !!!  *!! !!* !!  *  !! *! ***!

logo
NTDB id 1142602 DQL22 RS06930 WP 111300117.1  WRVLALLILIDPLMLLSTSFWLSVSAVISLMLWYRYVPLSLLQWRQSSLTHSPWHKVRWIFSLFHLQLGLLWLFTPIQLF  400
NTDB id 1359 HI 0061 AAC21739.1               TLVVGFLLFCDPLMPLSVSFWLSCGAVGCLLLWYRYVPFSLFQWKNRPFS....PKVRWIFSLFHLQFGLLLFFTPLQLF  387
consensus                                       !** !* *!!!!*!! !!!!!* !! *!**!! * ! !! !!** * ***** !!!!!!!!!!!! !!!  !!!*!!!

logo
NTDB id 1142602 DQL22 RS06930 WP 111300117.1  FFNGLSLNGFIANLIAVPIYSFLLVPLVLFAVFTQGTLYSWQAANNLSEKITALLAYGQDGWLAVSLQQSLWLTLLLTIA  480
NTDB id 1359 HI 0061 AAC21739.1               LFNGLSLSGFLANFMAVPIYSFLLVPLILFAVFTNGTMFSWQLANKLAEGITGLISVFQGNWLTVSFNLALGLTALCAGI  467
consensus                                      !!!!!! !!*!! *!!!!!!!!!!!!!*!!!!!!*!!**!!! !! ! ! !!*!*   !  !! !! *  ! !! !*

logo
NTDB id 1142602 DQL22 RS06930 WP 111300117.1  FLSVLHFVYKAPKPIVSPIELAKQSRNKGFHLNPARKLDLGLPIKAYAIGGGLVVFCITSLIYLSISRPHWQLETLDVGQ  560
NTDB id 1359 HI 0061 AAC21739.1               FMLIIWNIYREPEISSSNWQI...KRAKFFTLNLSKPLLKNERINVLRCSFGIILLCFTILLFKQLSKPTWQVDTLDVGQ  544
consensus                                     !* *** *!* ! *  !*  **** ! ! !*!!* **!    *!    *  !*** ! ! !**  *!*!*!!**!!!!!!
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logo

NTDB id 1142602 DQL22 RS06930 WP 111300117.1  GLATLIVKNGKGVLYDTGPSWNNGSMARLEILPYLQREGIELDWLILSHDDNDHAGGAKDILAAYPTVKFISPSDKIYGE   640
NTDB id 1359 HI 0061 AAC21739.1               GLATLIVKNGKGILYDTGSSWRGGSMAELEILPYLQREGIVLEKLILSHDDNDHAGGASTILKAYPNVELITPSRKNYGE   624
consensus                                     !!!!!!!!!!!!!*!!!!!*!!  !!!! !!!!!!!!!!!! !* !!*!!!!!!!!!!!  !! !!! !  !*!! ! !!!

logo

NTDB id 1142602 DQL22 RS06930 WP 111300117.1  KNDRKIDRTLCQTGEKWHWQGLSFSVLSPDNIVPRAENKDSCTLLLSDGQHQILLTGDADLGVEYKILPKLGKIDVLQVG   720
NTDB id 1359 HI 0061 AAC21739.1               N.....YRTFCTAGRDWHWQGLHFQILSPHNVVTRADNSHSCVILVDDGKNSVLLTGDAEAKNEQIFARTLGKIDVLQVG   699
consensus                                      ***** !! !  !  !!!!!!*! *!!!*!*!*!!*! *!! *!* !! * *!!!!!!*   !    * !!!!!!!!!!

logo

NTDB id 1142602 DQL22 RS06930 WP 111300117.1  HHGSKTSTGEALVQQTEPKIALISSGRWNPWHFPHKDVVARLRRQNTQIYNTAEHGQIRLLFQDNKIKIQTARAEFSPWY   800
NTDB id 1359 HI 0061 AAC21739.1               HHGSKTSTSEYLLSQVRPDVAIISSGRWNPWKFPHYSVMERLHRYKSAVENTAVSGQVRVNFFQDRLEIQQARTKFSPWY   779
consensus                                     !!!!!!!! ! !* !   ! *!*!!!!!!!!!*!!!  !* !!*!  * * !!! *!!*!* !   ** !! !!  !!!!!

logo

NTDB id 1142602 DQL22 RS06930 WP 111300117.1  RRLIGLQTK   809
NTDB id 1359 HI 0061 AAC21739.1               ARVIGLSKE   788
consensus                                      !*!!!
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X non conserved

X similar

X $\geq$ 50% conserved