```
logo
NTDB id 994323 AAG092 RS07585 WP 373389193.1  MTADALTLGELPGRRILRLYNLYRVTVGLALVLLISSQLDQELLQLAHVQLFRYGSWAYLIFNVLVAVFMQRPRHLAQVF   80
NTDB id 1472 PAKAF RS23995 WP 016253893.1     MRAERLRLSEEQGQRILRLYHLYRLTIGLVLVLLISSELEDQVLKLVHPELFHVGSWCYLVFNILVALFLPPSRQLLPIF   80
consensus                                     ! !* ! ! ! *! !!!!!!*!!!*!*!! !!!!!!! !*  *! ! !* !!* !!!*!!*!!*!!!*!****!*! **!

logo
NTDB id 994323 AAG092 RS07585 WP 373389193.1  GLALLDVLLLCALFYSAGGTPSGIGNLLVVAVAIANILLRGRIGLLIAAVAAIGMLSLTFYLSLTRSAATAQFVQAGALG  160
NTDB id 1472 PAKAF RS23995 WP 016253893.1     ILALTDVLMLCGLFYAGGGVPSGIGSLLVVAVAIANILLRGRIGLVIAAAASLGLLYLTFFLSLSSPDATNHYVQAGGLG  160
consensus                                      !!! !!!*!!*!!! *!! !!!!! !!!!!!!!!!!!!!!!!!!!*!!! ! *!*! !!!*!!!* * !! **!!!!*!!

logo
NTDB id 994323 AAG092 RS07585 WP 373389193.1  ALCFAAALFLQGLTRRLQQSESLAEQRAVDVASLEALNSLILQRMRTGILVLDKQHRVLLANQGALGMLGRGKLEGKVLA  240
NTDB id 1472 PAKAF RS23995 WP 016253893.1     TLCFAAALVIQALVRRQEQTETLAEERAETVANLEELNALILQRMRTGILVVDSRQAILLANQAALGLLRQDDVQGASLG  240
consensus                                      !!!!!!! *!*! !!  !*!*!!! !!  !! !! !! !!!!!!!!!!!!!*!  * *!!!!!*!!!*!    * !  !*

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NTDB id 994323 AAG092 RS07585 WP 373389193.1  PYCPELVRRLQQWQHNPTLRPQSLQAIPEGPVLQPSFIPLQRGEEQHTLVFLDDISQITQQAQQLKLASLGRLTAGIAHE  320
NTDB id 1472 PAKAF RS23995 WP 016253893.1     RHSPMLMHCMKQWRLNPSLRPPTLKVVPDGPTVQPSFISLNREDDQHVLIFLEDISQIAQQAQQMKLAGLGRLTAGIAHE  320
consensus                                     ***! !**** !! *!!*!!!**!  *!*!! *!!!!!*!*! **!! !*!!*!!!!! !!!!!*!!! !!!!!!!!!!!

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NTDB id 994323 AAG092 RS07585 WP 373389193.1  IRNPLGAISHAAQLLQESEALDDPDRRLAQIIQDHSRRMNMVIENVLQLSRRRQAEPQLLDLKYWLHRFASEFRNSARID  400
NTDB id 1472 PAKAF RS23995 WP 016253893.1     IRNPLGAISHAAQLLQESEELDAPDRRLTQIIQDQSKRMNLVIENVLQLSRRRQAEPQQLDLKEWLQRFVDEYPGRLRND  400
consensus                                     !!!!!!!!!!!!!!!!!!! !! !!!!! !!!!!*!*!!!*!!!!!!!!!!!!!!!! !!!! !!*!!  !**   ! !

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NTDB id 994323 AAG092 RS07585 WP 373389193.1  QTLHLETLGSGLQTRMDPHQLNQVLTNLVQNGLRYSAQKHQLGQVWLKLYRDSESDLPTLEVLDNGPGVPPDQVQHIFEP  480
NTDB id 1472 PAKAF RS23995 WP 016253893.1     SELHLQLGAGDIQTRMDPHQLNQVLSNLVQNGLRYSAQAHGRGQVWLSLARDPESDLPVLEIIDDGPGVPADKLNNLFEP  480
consensus                                      !!!    *  *!!!!!!!!!!!!!*!!!!!!!!!!!! !  !!!!! ! !!*!!!!! !!**! !!!!!*! ****!!!

logo
NTDB id 994323 AAG092 RS07585 WP 373389193.1  FYTTDNKGTGLGLYISRELCESNQARLDYKPREGGGSCFRITFAHPRKLS  530
NTDB id 1472 PAKAF RS23995 WP 016253893.1     FFTTESKGTGLGLYLSRELCESNQARIDYRNREEGGGCFRITFAHPRKLS  530
consensus                                     !*!!* !!!!!!!!*!!!!!!!!!!!!*!!**!! !! !!!!!!!!!!!!!
```

X non conserved
X similar
X $\geq$ 50% conserved