```
logo                                              [sequence logo]
NTDB id 79993 L6497 RS06070 WP 236793314.1   MSEQNTAKTLPDRNEIEESSTWRLEDIFQTDTEWEKFQAIKELLPKLTEFKGKLGDSANNLLEALQYEDEISMRLGKLYTYAHM   85
NTDB id 480 HSISS4 RS02090 WP 002890133.1     ........MSDNRTHLEEKYTWDLTTIFATDADWETEYESTVQDLKKASAYAGHLLDSAKNLLGATELYMSLMRRLEKIYVYASM   77
consensus                                     *******  *  !  **!!  !! !    **  *  * !*  !!! !!!       *   !!  !*!  !!*!

logo                                              [sequence logo]
NTDB id 79993 L6497 RS06070 WP 236793314.1   RYDQDTTNSVYQALNDRATNLYSQVSSSTAYIVPEILSISEDTLQTFLKENRDLSVYEHALEEITRQRPHVLSEAEEALLAEASE   170
NTDB id 480 HSISS4 RS02090 WP 002890133.1    KNDQDTTVGLYQEYQAKASNLYSQLSEAFAYFEPEFMALDKKLAEFKEQEPGLGLYDHYFERLLANKDHVLSQEAEELLAAAGD   162
consensus                                     *****!!   *! **!**!! !! ! **     **  * *   !! !   !   * ! *  ***!!!!  ! !!!!*

logo                                              [sequence logo]
NTDB id 79993 L6497 RS06070 WP 236793314.1   VMSASSNTFGMLNNADLKFPSIKGEDGEEVEITHGRYIQFLESDDRRVREDAFKAVYETYGKYKNTHASTLSGAVKRNNFNARVR   255
NTDB id 480 HSISS4 RS02090 WP 002890133.1    IFNGPTDTFNVLDNADILFPWVSDGQGDVVELTHGNFITLMESKDRDIRKGAYEAMYGTYEQFQHTYAQTLQGVVKVHNYQAKVR   247
consensus                                     *  *** !! !  ** !! *  *   **!! !!*! ** **! ** !*! !! !**! !! !  !! *!**!*!!

logo                                              [sequence logo]
NTDB id 79993 L6497 RS06070 WP 236793314.1   KYDSARQAALSNNNIPEAVYDQLIESVNDNLHLLHRYIDIRKRALGLDELHMYDLYTPLVPEVKMNVKYEEAQDMLLKSLHVLGD   340
NTDB id 480 HSISS4 RS02090 WP 002890133.1    HYNSARHAALAANFIPESVYDSLLESVNKHLPLLHRYLDLRKKVLGLDELKMYDVYTPLSET.ETALTYEESLKKAEEVLAIFGE   331
consensus                                     *! !!!!**!  !!  !** !!*!! !****! ! ! !  ! !* !!*!!*!!!   *   * !***!!!! *  !** !!**

logo                                              [sequence logo]
NTDB id 79993 L6497 RS06070 WP 236793314.1   EYVDILKEAYENRWVDVYENKGKRSGAYSSGAYGTNPYILMNWHDNVNNLFTLAHEFGHSVHSYYTRKTQPHVYGDYSIFVAEVA   425
NTDB id 480 HSISS4 RS02090 WP 002890133.1    EYSKGVHAAFTERWIDVHPNKGKRSGAYSGGAYDTNAFMLLNWQDTLDNLFTLVHETGHSLHSTFTRQTQPYVYGDYPIFLAEIA   416
consensus                                     !!  **  !!   *! !!**! *!!!!!!!*!!!   *! ! !! !! !!!!!* !*!!! !!! !*! !!!!!*!!!*!!*

logo                                              [sequence logo]
NTDB id 79993 L6497 RS06070 WP 236793314.1   STCNEALLNDYLLKTTEDKKERLYLLNHYLEGFRGTVFRQTMFAEFEHIIYKKVQEGHAVTPDMLTELYYDLNKKYFGDALVIDE   510
NTDB id 480 HSISS4 RS02090 WP 002890133.1    STTNENILTETLLKEVKDDKTRFAILNHYLDGFKGTVFRQTQFAEFEHAIHEADASGQILTADFMNKLYADLNEKYFNLKAEDNY   501
consensus                                     !!  *! *! !!!   *!   !  !!*!!!!*!!*!!!!!!*!* *!!*!!! !  !*!! *  *! !! *! !*! !!*

logo                                              [sequence logo]
NTDB id 79993 L6497 RS06070 WP 236793314.1   EIGLEWSRIPHFYYNYYVYQYATGFSAATALSKQILEEGQPAVERYINEFLKAGSSDYPLEVLKKAGVDMASPEPVKEALQVFEE   595
NTDB id 480 HSISS4 RS02090 WP 002890133.1    EIQFEWERIPHFYMNYYVYQYATGFAAASYLAEKIVHGTEEDKEAY.LTTYLKAGSSDYPLEVIKKAGVDMTNTDYLDAAFKVFED   585
consensus                                     !!  !! !!!!**!!*!!!!!!!!!!*   !  !!  !** *       * !!!!!!!!!!!*!!*!!!!!!! ****  !  !!!*
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logo

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                                          RLVELEALVEKGV
                                          KLNELEALLEEEKHLS
NTDB id 79993 L6497 RS06070 WP 236793314.1  KLNELEALLFEEK...   608
NTDB id 480 HSISS4 RS02090 WP 002890133.1   RLVELEALVEKGVHLS   601
consensus                                   *! !!!!!*   ***
```

X   non conserved
X   similar
X   ≥ 50% conserved