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logo

NTDB id 304987 DV114 RS05875 WP 101755101.1  MSDNKQKETPNGYDLDGYEQLKRRNRRRLVLASGLVVASGMLFGLALTSGLDKNSPFKEAP.VGQSQVKTADEPSNAVVL   79
NTDB id 1129 NGFG RS01435 WP 003687618.1     MSENKQ.....NEVLTGYEQLKRRNRRRLVTASSLVAASCILLAAALSSDPADSNPAPQAGETGATESQTANTAQ.....   70
consensus                                    !!*!!!*****   ! !!!!!!!!!!!!!! !! !! !!**! * !!*! *    ! * !** ! *   !!   * *****

logo

NTDB id 304987 DV114 RS05875 WP 101755101.1  EPNKEDVAMAEEAARHADAEAQSKPQNAGDEEDNAPVEVLKPNRESAPEDVGEPLVLINDTLDDGNIKGLEESERIQRAE  159
NTDB id 1129 NGFG RS01435 WP 003687618.1     TPALK......SAAE.NGETAADKPQDLAGEDK....PSAADSEISEPENVGAPLVLINDRLEDSNIKGLEESEKLQQAE  139
consensus                                     !   ****** !! *    !  !!!  * !* *****   *   ! !! !! !!!!!!! !*! !!!!!!!!!**! !!

logo

NTDB id 304987 DV114 RS05875 WP 101755101.1  AAKREAAERRAEERRQRQAEQRAAAARKTQAQQEAAEKENALAAKKRALQARAEKAEREAAAERNKLAQLEKAEKA....  235
NTDB id 1129 NGFG RS01435 WP 003687618.1     TAKTEPKQAKQ.....RAAEKVSATADSTDT........VAVEKPKRSAEPKPQKAERTAEAKP.KAKETKTAEKVADKP  205
consensus                                     !! !*   * *****! !!   ! !  !  ******** !*  *!!   *** !!!! ! ! **!      !!! ****

logo

NTDB id 304987 DV114 RS05875 WP 101755101.1  ..IAERKS.AKNSKDSVKDKAEPAKKAEAKVEKPKNEKAKPETAKAEKADKVKTAEKPSEKAKPKAEKETAEAKPAKKAA  312
NTDB id 1129 NGFG RS01435 WP 003687618.1     KTAAEKTKPDTAKSDSAVKEAKKADKAEGKK...TAEKDRSDGK......KHETAQKTDKADKTKTAEKEKSGKAGKKAA  276
consensus                                    ** !!*  *     !!    ! *! !!!*! ***  !! ***  ******!* !! !*    !*!       *!**!!!!

logo

NTDB id 304987 DV114 RS05875 WP 101755101.1  IQAGYAEKERAQSLQRKMKAAGIDSTITEVMTDKGKVYRVKSASYKNARDAERDLNKLRVHGIAGQVTSE   382
NTDB id 1129 NGFG RS01435 WP 003687618.1     IQAGYAEKERALSLQRKMKAAGIDSTITEIMTDNGKVYRVKSSNYKNARDAERDLNKLRVHGIAGQVTNE   346
consensus                                    !!!!!!!!!!! !!!!!!!!!!!!!!!!!!*!!! !!!!!!!!  !!!!!!!!!!!!!!!!!!!!!!!!! !
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X non conserved

X similar

X $\geq$ 50% conserved