```
logo
NTDB id 37648 HPB8 RS02595 WP 000814183.1  MKQSLLKKIGLGVGGFVVLMALGLLANKG..SNNNNKEEIFQVSESKFPLSDYFFEEVKEEPKEKAKETPEVTTQEPTTQTSPNP   83
NTDB id 1218 CAA10657.1 2413..3543( )      .MNKWLKGVIVFIGGFATITTISLVYHQKPKAPLNNQPSLLNDDEVKYPLQDYTFTQNPQPTNTESSKDATIKALQEQLKAA...   81
consensus                                  * *  !! * * *!!!  *  * !* *  ** * !! * * *  ! !*!! !! !   * **       * *    *     ***

logo
NTDB id 37648 HPB8 RS02595 WP 000814183.1  SVSANPNIKDYSHLNNNLNQQNNTITHLQQVLQSPSKIKPKPKHTKEQLEFLNTRLKPLEPTKPA......TKPDTEYGVDSFTN  162
NTDB id 1218 CAA10657.1 2413..3543( )      LKALNSKEMNYSK...........EETFKSPPIDPNTTPPKKDFSLKQLDLLAARITPFKQSPKNYEENLIFPVDNPKGIDGFTN  155
consensus                                     !*     !!************  *    **   !    *!!* **   !!* !  !* !   **** ****** **! * !*! !!!

logo
NTDB id 37648 HPB8 RS02595 WP 000814183.1  LKYKDIGTNEHKLLRTITADRMIPAFLITPISSQIAGKVTAQVESDIFASMGRAVLIPKGSKVIGYYNNNNQIGQYRLNIAWTRI  247
NTDB id 1218 CAA10657.1 2413..3543( )      LKEKDIATNENKLLRTITADKMIPAFLITPISSQIAGKVIAQVESDIFAHMGKAVLIPKGSKVIGYYSNNNKMGEYRLDIVWSRI  240
consensus                                  !! !!!*!!!*!!!!!!!!!*!!!!!!!!!!!!!!!!!! !!!!!!!!!*!!*!!!!!!!!!!!!!! !!! *! !!! ! !*!!

logo
NTDB id 37648 HPB8 RS02595 WP 000814183.1  ITPQGINIMLTNARGADVKGYNGLVGKYISRNFQRYGIPLLTNTLSNGLLIGITSALANRQNRKGDGNPFFGDYLLMQLTRNTGM  332
NTDB id 1218 CAA10657.1 2413..3543( )      ITPHGINIMLTNAKGADIKGYNGLVGELIERNFQRYGVPLLLSTLTNGLLIGITSALNNRGNKEGA.TNFFGDYLLMQLMRQSGM  324
consensus                                  !!!*!!!!!!!!!!*!!!*!!!!!!!!  ! !!!!!!!*!!!  !!*!!!!!!!!!!!! !! !* ! * *!!!!!!!!!! !**!!

logo
NTDB id 37648 HPB8 RS02595 WP 000814183.1  GINQVINQMLRQYGAQNPIIIREGSRVFISPNLDIFIPKPKDGEILAEFFKEKKPPIKTKEEINNEEEI   402
NTDB id 1218 CAA10657.1 2413..3543( )      GINQVVNQILRDKSKIAPIVVIREGSRVFISPNTDIFFPIPRENEVIAEFLK ................   376
consensus                                  !!!!!*!!*!!       !!**!!!!!!!!!!!! !!! ! !** !**!!! !*****************
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X non conserved

X similar

X $\geq$ 50% conserved