```
logo
NTDB id 1099447 ACM67E RS03225 WP 416192185.1  MSDDKQREVLTGYEQLKRRNRRRLVMTSGLVVVAGILLASVLNMGGDDEEKASAQTAAVTRNNAQNAQNDVAALKPNVVQ   80
NTDB id 1129 NGFG RS01435 WP 003687618.1       MSENKQNEVLTGYEQLKRRNRRRLVTASSLVAASCILLAAALSSDPADSNPAPQAGET....GATESQTANTAQTPALKS   76
consensus                                      !!* !! !!!!!!!!!!!!!!!!!!  ! !!   *!!!!  !   * !  *!*     **** !   !    !  ! *

logo
NTDB id 1099447 ACM67E RS03225 WP 416192185.1  AQASAE.PARAPESVEPQQPVEVLKPAGASMPQDIGPPLVIINDKLVDSDIKGLEESEQVQQAEEEKQAGEEQKAEERRQ  159
NTDB id 1129 NGFG RS01435 WP 003687618.1       AAENGETAADKPQDLAGE.DKPSAADSEISEPENVGAPLVLINDRLEDSNIKGLEESEKLQQAETAKTEPKQAK.....Q  150
consensus                                      !   *!**!  !  * * ** *   *   ! !  *!*!!!*!!!*! !! !!!!!!!! *!!!!  !  *   !*****!

logo
NTDB id 1099447 ACM67E RS03225 WP 416192185.1  RLAEERAAKRAEERRVAAEKEAARKRAAAAKAEKAERNAEAERKRAEKAAAERKAKQAEERKAAAAKAKAQADKKAAAAQ  239
NTDB id 1129 NGFG RS01435 WP 003687618.1       RAAEKVSATADSTDTVAVEK...PKRSAEPKPQKAERTAEAKPKAKETKTAEKVA...DKPKTAAEKTKPDTAKS.....  219
consensus                                      ! !!   !        !! !!****!! ! *!* !!!! !!! *!  !   !!* !**** *! !! ! !*   ! *****

logo
NTDB id 1099447 ACM67E RS03225 WP 416192185.1  EAKVKQEAKAKEAEQKAAAK..KA.AAKKAEAAKAKTAEKNRPSEKTSAASAGRKASIQAGYAEKERAQSLQRKMKAAGI  316
NTDB id 1129 NGFG RS01435 WP 003687618.1       DSAVKEAKKADKAEGKKTAEKDRSDGKKHETAQKTDKADKTKTAEKEKSGKAGKKAAIQAGYAEKERALSLQRKMKAAGI  299
consensus                                      *  !!   !!  !! !  ! *** ** !*  ! !   !*! ** !!   * !!*!! !!!!!!!!!!! !!!!!!!!!!!

logo
NTDB id 1099447 ACM67E RS03225 WP 416192185.1  NATITEIKTDKGVVYRVKSGTYQNRQDAAKDLQKLRSKDGIAGQVVNE  364
NTDB id 1129 NGFG RS01435 WP 003687618.1       DSTITEIMTDNGKVYRVKSSNYKNARDAERDLNKLRV.HGIAGQVTNE  346
consensus                                        !!!!! !! ! !!!!!!  ! !  !! *!!*!!! **!!!!!! !!
```

X non conserved

X similar

X $\geq$ 50% conserved