```
logo
NTDB id 995210 AAYR28 RS16290 WP 142925562.1  ......MNMDKAMELMGQLHSRHLLTVETKCPQSNLDWLEEKGLVNRSPAIERKANGFTCCRCGVSHKRYFAHSPCEVCQ   74
NTDB id 108 BSU 35470 NP 391427.1             MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYH..SSG   78
consensus                                     ****** !     !!   !*!!!!! !  **   **!*   ! *   * !      * !*!!! ** !!! *  ** *

logo
NTDB id 995210 AAYR28 RS16290 WP 142925562.1  KDCVYCRSCIMMGKAAECGFLYEWTGPQMVETGRAELTWQGELSKGQKRASERMIEAIKNKFDLLVWAVCGAGKTEVLFH   154
NTDB id 108 BSU 35470 NP 391427.1             KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP   158
consensus                                     ! **!!!!!*!!!*  !* *!! !  **       !!! ! !! !! *!   *!!!!  ! *!!*!!!!!!!!!!*!!

logo
NTDB id 995210 AAYR28 RS16290 WP 142925562.1  GIEYALNQGMSVCIATPRTDVVLELEPRLRKAFQGVIITVLYGGSSQRFQIAPLVITTTHQLMRYKNAFDVLIVDEVDAF   234
NTDB id 108 BSU 35470 NP 391427.1             GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF   238
consensus                                     !!! !!!!!* !!!!!!!!!!!!!! !!!* !!!!  !* !!!!!  *  * !!*!*!!!!!*!!! ! !!*!*!!!!!!

logo
NTDB id 995210 AAYR28 RS16290 WP 142925562.1  PYSMDERLQFAVLKAMRKNGGVRIYLSATPSKKMTREVSRGKLEAMKVPLRFHEHPLPVPTFHWIGHWKKKLKKNQLPPK   314
NTDB id 108 BSU 35470 NP 391427.1             PYSADQTLQFAVQKARKKN.STLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPA   317
consensus                                     !!! !  !!!!! !! *!!*   *!!!!!!*! * !    ! !* ***! !*! *!!! ! !*!*!*!!!!! *! *!!

logo
NTDB id 995210 AAYR28 RS16290 WP 142925562.1  VMNWMQRHIANKRRILLFVPSIAVMKKVTKILREQSLNVEGVSADDPDRKQKVQHFRDYVYDVLVTTTILERGVTIPNVQ   394
NTDB id 108 BSU 35470 NP 391427.1             VKRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQ   397
consensus                                     !  !*  !*   !** !!!!!* ** !   * *  **    !*!*!**!! !!!*!!!   !*!*!!!!!!!!!!*! !!

logo
NTDB id 995210 AAYR28 RS16290 WP 142925562.1  VGVLGSESTIFTESALVQISGRVGRHPDYCTGDVFLFHFGLTRSMKQAKKHIAKMNDTAAKEFSEKQCGFN   465
NTDB id 108 BSU 35470 NP 391427.1             TGVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD.....   463
consensus                                      !!!! !!*!!!!!!!!!! !! !!!**!* !!!   !!!! !*!!   !*!!!   !!*  !!!   *  *****
```

X non conserved

X similar

X ≥50% conserved