```
logo
NTDB id 995011 AAVC22 RS13535 WP 020453117.1  .MIHIEHPASYSCELRSCLEQRHLLKSELSFPEPVIDWHIQEGLIKTEEGIKKTKRGFVCLRCGQHERFCFARYPCYRCN   79
NTDB id 108 BSU 35470 NP 391427.1             MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHSS..G   78
consensus                                     * * *!** !*!*!!  *!  !!!!**!!!!****!*!!!  ! !  !  !  !! * ! !!!!**  *!  ! * **

logo
NTDB id 995011 AAVC22 RS13535 WP 020453117.1  KCCVYCRACVMMGRVSECTSLLTWRGHGRHEWAPVYTEWKGVLSAGQEKAAKSIIDAIRRKEELLIWAVCGSGKTELLFQ   159
NTDB id 108 BSU 35470 NP 391427.1             KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP   158
consensus                                     !***!!! !!!!!!!!!!* *! *!* *  * ! **   ! ! !! !! !!!  *!*!! *!!!!!!!!!!! !!!!*!!*

logo
NTDB id 995011 AAVC22 RS13535 WP 020453117.1  GIEFALNNGLRVCIATPRTDVVLELEPRFRHAFPGMEIAALYGGSPDVGTLSPLVISTTHQLLRYKEAFDVIIIDEVDAF   239
NTDB id 108 BSU 35470 NP 391427.1             GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF   238
consensus                                     !!! !!!*!!!!!!!!!!!!!!!!!! !! **!!*! *! !!!!!!*! ! !!!!*!!!!!!!!!!!*! !!*!!!!!!!!

logo
NTDB id 995011 AAVC22 RS13535 WP 020453117.1  PYSIDNTLQYAVKKSAKRQSAHIYLTATPSRDMKKRAESGKLHTVRIPARFHRSPLPEPTLLWCGNWERGLKRRKVPLRL   319
NTDB id 108 BSU 35470 NP 391427.1             PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV   318
consensus                                     !!! !*!!!*!! !  !**! **!!*!!!****!**!  ! !!*!!!!!!*!! !!!!!  *!!!!! * ! ! !*!* *

logo
NTDB id 995011 AAVC22 RS13535 WP 020453117.1  KKWLFKHQELQHPVFLFVPSIPVLKTVVSLLKKETFRAEGVYAEDPERNEKVNRFRKSKLEVLVTTTILERGVTVKKAQV   399
NTDB id 108 BSU 35470 NP 391427.1             KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT   398
consensus                                     !*!*  !    *!!!!!!!!***!     * !  **!   !*!!!**! !!!* !!   !**!*!!!!!!!!!!!*! !

logo
NTDB id 995011 AAVC22 RS13535 WP 020453117.1  GVLGAESAVFSESALVQMAGRAGRHPEHTDGDVCFFHHGRTKSMNAARRHIQYMNKLSKKEMLID   464
NTDB id 108 BSU 35470 NP 391427.1             GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                                     !!!!!!! *!*!!!!!!*!!! !!!*!* !!!!**!!*!*!!!!  !!*!!  !! !  !  * !
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X non conserved

X similar

X ≥ 50% conserved