```
logo
NTDB id 245137 CK945 RS20490 WP 096748475.1  .MIHIEHPASYSCELRSCLEQRHLLKSELSFPEPVIDWHIQEGLIKTEEGIKKTKRGFVCLRCGQHERFCFARYPCYRCN   79
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHSS..G   78
consensus                                    * * *!** !*!*!!   *!  !!!!**!!!!****!*!!!  ! !  !  !   !! * ! !!!!**  *!   ! * **

logo

NTDB id 245137 CK945 RS20490 WP 096748475.1  KCCVYCRACVMMGRVSECTSLLTWRGHGRHEWAPVYTEWKGVLSAGQEKAAKSIIDAIRRKEELLIWAVCGSGKTELLFQ   159
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP   158
consensus                                    !***!!! !!!!!!!!!* *! *!* *  * ! **   ! ! !! !! !!!  *!*!! *!!!!!!!!!!! !!!!*!!*

logo

NTDB id 245137 CK945 RS20490 WP 096748475.1  GIEFALNNGLRVCIATPRTDVVLELEPRFRHAFPGMEIAALYGGSPDVGTLSPLVISTTHQLLRYKEAFDVIIIDEVDAF   239
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF   238
consensus                                    !!! !!!*!!!!!!!!!!!!!!!!!! !! **!!*! *! !!!!!!*! ! !!!!*!!!!!!!!!!!!*! !!*!!!!!!!!

logo

NTDB id 245137 CK945 RS20490 WP 096748475.1  PYSIDNTLQYAVKKSAKRQSAHIYLTATPSRDMKKRAESGKLDTVRIPARFHRSPLPEPTLIWCGNWKKSLKRRKVPFHL   319
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV   318
consensus                                    !!! !*!!!*!! !   !**! **!!*!!!****!**!   ! !**!!!!!!*!! !!!!!   *!!!!!!! ! ! !*!***

logo

NTDB id 245137 CK945 RS20490 WP 096748475.1  KKWLFKHQELQQPVFLFVPSVPVLKSVVSVLKKETFRAEGVYADDPDRNEKVNRFRESKLEVLVTTTILERGVTVKKAQV   399
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT   398
consensus                                    !*!*  !      !!!!!!!!!**!     * !   **!    !*!*!**! !!!* !!*   !**!*!!!!!!!!!!!*! !

logo

NTDB id 245137 CK945 RS20490 WP 096748475.1  GVLGAESAVFTESALVQMAGRAGRHPEHTDGDVCFFHYGRTKSMNAARRHIQNMNKMSKKEMLID   464
NTDB id 108 BSU 35470 NP 391427.1            GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                                    !!!!!!! *!!!!!!!!*!!! !!!*!* !!!!**!!*!*!!!!   !!*!!   !! *   !   * !
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X non conserved

X similar

X $\geq$ 50% conserved