```
logo
NTDB id 249117 CP942 RS14755 WP 105980589.1  .MIHIEHPASYSCELRSCLEQRHLLKSELPFPEPVIDWHIQEGLIKTEEGIKKTKRGFVCLRCGQHERFCFARYPCYRCN   79
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHSS..G   78
consensus                                    * * *!** !*!*!!   *!  !!!!**!!*!****!*!!!  ! !  !  !  !! * ! !!!!**  *!  ! * **

logo

NTDB id 249117 CP942 RS14755 WP 105980589.1  KCCVYCRACFMMGRVSECTSLLTWRGHGRHEWAPVYTEWKGVLSAGQEKAAKSIIDAIRRKEELLIWAVCGSGKTELLFQ  159
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP  158
consensus                                    !***!!! ! !!!!!!!* *! *!* *  * ! **   ! ! !! !! !!!  *!*!! *!!!!!!!!!!! !!!!*!!*

logo

NTDB id 249117 CP942 RS14755 WP 105980589.1  GIEFALNNGLRVCIATPRTDVVLELEPRFRHAFPGVEIAALYGGSPDVGTLSPLVISTTHQLLRYKEAFDVIILDEVDAF  239
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF  238
consensus                                    !!! !!!*!!!!!!!!!!!!!!!!!! !! **!!*! *! !!!!!!*! ! !!!!*!!!!!!!!!!!!*! !!*!*!!!!!!

logo

NTDB id 249117 CP942 RS14755 WP 105980589.1  PYSIDNTLQYAVKKSAKRQSAHIYLTATPSRDMKKRAESGKLHTVRIPARFHRSPLPEPTLIWCGNWERGLKRRKVPFRL  319
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV  318
consensus                                    !!! !*!!!*!! !  !**! **!!*!!!****!**!  ! !!*!!!!!!*!! !!!!!  *!!!!! * ! ! !*!* *

logo

NTDB id 249117 CP942 RS14755 WP 105980589.1  KKWLFKHQELQHPVFLFVPSIPVLKTVVSLLKKETFRAEGVYAEDPERNEKVNRFRKSKLEVLVTTTILERGVTVKKAQV  399
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT  398
consensus                                    !*!*  !    *!!!!!!!!***!    * !  **!   !*!!!**! !!!* !!   !**!*!!!!!!!!!!!*! !

logo

NTDB id 249117 CP942 RS14755 WP 105980589.1  GVLGAESAVFSESALVQMAGRAGRHPEYTVGDVCFFHHGRTKSMNAARRHIQYMNKLSKKEMLID   464
NTDB id 108 BSU 35470 NP 391427.1            GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                                    !!!!!!! *!*!!!!!!*!!! !!!*!!  !!!**!!*!*!!!!  !!*!!  !! !  !  * !
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X non conserved

X similar

X ≥ 50% conserved