```
logo
NTDB id 316805 D6022 RS00645 WP 003185720.1  .MIHIEQPAFYTRELRSCLEQRHLLKSELPFRESVVDWHIQEGLIKTEEGIKKTKKGFICLRCGQHERSFFARYPCYRCS   79
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHS..SG   78
consensus                                    * * *! *  ***!!  *!  !!!!**!!*! * ***!!!  ! !  !  !   !* * ! !!!!**  *!  ! ****

logo
NTDB id 316805 D6022 RS00645 WP 003185720.1  KCCVYCRSCVMMGRVSDCTPLLTWHMHVSHKWAPVHTEWKGALSAGQEKAAKSIINAIRRKEELLVWAVCGSGKTELLFQ  159
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP  158
consensus                                    !***!!!!!!!!!!!!** !! *!* *  * ! ***  ! ! !! !! !!!  *! !! *!!!!!*!!!!! !!!!*!!*

logo
NTDB id 316805 D6022 RS00645 WP 003185720.1  GIEFALNNGLTVCIATPRTDVVLELAPRFRQAFPGVEIAALYGGSSDVGNLSPLIISTTHQLLRYKEAFDVIIIDEVDAF  239
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF  238
consensus                                    !!! !!!*!! !!!!!!!!!!!!!!!!! * !!*! *! !!!!!! ! ! !!!!*!!!!!!!!!!!!*! !!*!!!!!!!!

logo
NTDB id 316805 D6022 RS00645 WP 003185720.1  PYSIDNTLQYAVKKSAKRQSAHIYLTATPSADMKKRAESGKLDTVRIPARFHRSPLPEPTLIWCGNWKKSLKRRKVPFRL  319
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV  318
consensus                                    !!! !*!!!*!! !  !**! **!!*!!!* **!**!  ! !**!!!!!!*!! !!!!!  *!!!!!!! ! ! !*!* *

logo
NTDB id 316805 D6022 RS00645 WP 003185720.1  KKWLFKHQELQQPVFLFVPSVPVLKSVVSVLKKETFRAEGVYADDPDRNEKVNRFRESKLEVLVTTTILERGVTVKKAQV  399
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT  398
consensus                                    !*!*  !      !!!!!!!!!**!     * !  **!   !*!*!**! !!!* !!*  !**!*!!!!!!!!!!!*! !

logo
NTDB id 316805 D6022 RS00645 WP 003185720.1  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