```
logo
NTDB id 985052 MKY83 RS16960 WP 142671660.1  ......MNMDKAMELGQHLQSRHLLTAETRCSQSDLDWLEEKGLVIRTPAIERKANGLICCRCGVSKNRYFAHSPCDKCQ   74
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYH..SSG   78
consensus                                    ****** !     !! !*! !!!!!  !  *!   **!*   ! *   * !        !*!!! * *!!! *  ** *

logo
NTDB id 985052 MKY83 RS16960 WP 142671660.1  KDCVYCRSCIMMGKTTECGFLYEWTGPQMEEACHSELTWQGDLSKGQKRASEKLIEAIKHKSDLLIWAVCGAGKTEVLFH   154
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP   158
consensus                                    ! **!!!!!*!!!* *!* *!! !  **    **  !!! ! !! !! *!   !!!!! *! *!!!!!!!!!!!!!*!!

logo
NTDB id 985052 MKY83 RS16960 WP 142671660.1  GIEYALHQGMSVCIATPRTDVVLELEPRLKKAFQGMKIAVLYGGSPQRFQIAPLVIATTHQLMRYKHAFDVLIIDEVDAF   234
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF   238
consensus                                    !!! !!*!!* !!!!!!!!!!!!!! !!!! !!!!  !  !!!!!* *  * !!*! !!!!!*!!!*! !!*!!!!!!!!

logo
NTDB id 985052 MKY83 RS16960 WP 142671660.1  PYSIDERLQFAVLKAMRKKGVRVYLSATPSKKMIRDVSRGQLEAVKIPLRFHQQPLPVPSFQWIGHWKKKLKKNQLPPKV   314
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV   318
consensus                                    !!! !  !!!!! !! *!    !!!!!!!*! * !    !!!* !*!! !*!  !!! ! ! !*!*!!!!! *! *!! !

logo
NTDB id 985052 MKY83 RS16960 WP 142671660.1  MNWMQKHITKKRRVLLFVPSISTMKKVTKVLRKHHLNVEGVSADDPDRKQKVQQFRDYKYDVLVTTTILERGVTIPNVQV   394
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT   398
consensus                                      !*  !*   !*! !!!!!*! * !   * * *!*    !*!*!**!! !!!!!!!   !*!*!!!!!!!!!!*! !!

logo
NTDB id 985052 MKY83 RS16960 WP 142671660.1  GVLGAESTIFTESALVQISGRAGRHPDFFKGDVFFFHFGLTRSMKQAKKHIVKMNDTAEKEFSEK   459
NTDB id 108 BSU 35470 NP 391427.1            GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                                    !!!!!!!*!!!!!!!!!!! !! !!!***  !!! *!!!! !*!!  !*!!!  !!* ! !  *
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X non conserved

X similar

X ≥ 50% conserved