```
logo
NTDB id 968751 MHH68 RS16120 WP 339164086.1  ......MNMDKAMELGQHLQSRHLLTAETRCSQSDLNWLEEKGLVMRTPAIERKANGLICCRCGVSKNWYFAHSPCDKCQ   74
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYH..SSG   78
consensus                                    ****** !     !! !*! !!!!!  !  *!   * !*   ! *   * !        !*!!! * * !! *  ** *

logo
NTDB id 968751 MHH68 RS16120 WP 339164086.1  KDCVYCRSCIMMGKTKECGFLYEWTGPQREEPCHTELTWQGNLSKGQKRASEKLIKAIKSKSDLLIWAVCGAGKTEVLFH  154
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP  158
consensus                                    ! **!!!!!*!!!*  !* *!! !  **   ***  !!! ! !! !! *!   !! !!  ! *!!!!!!!!!!!!!*!!

logo
NTDB id 968751 MHH68 RS16120 WP 339164086.1  GIEYALHQGMSVCIATPRTDVVLELEPRLKKAFQGLNIAVLYGGSPQRFQIAPLVIATTHQLMRYKHAFDVLIIDEVDAF  234
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF  238
consensus                                    !!! !!*!!* !!!!!!!!!!!!!! !!!! !!!!  !  !!!!!* *  * !!*! !!!!!*!!!*! !!*!!!!!!!!

logo
NTDB id 968751 MHH68 RS16120 WP 339164086.1  PYSIDERLQFAVLKAMRKKGVRVYLSATPSKKMIKDVFRGQLEAIKIPLRFHQQPLPVPSFHWVGNWKKKLKKNQLPSKV  314
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV  318
consensus                                    !!! !  !!!!! !! *!    !!!!!!!*! * *    !!!* **!! !*!  !!! ! !*!*!!!!!!! *! *!* !

logo
NTDB id 968751 MHH68 RS16120 WP 339164086.1  MNWMQNHITKKRRTLFFVPSISTMKKVTKVLRKHHLNVEGVSAEDPDRKQKVQQFRDDKYDVLVTTTILERGVTIPNVQV  394
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT  398
consensus                                      !*  !*   !*   !!!!*! * !   * * *!*    !*!!!**!! !!!!!!!   !*!*!!!!!!!!!!*! !!

logo
NTDB id 968751 MHH68 RS16120 WP 339164086.1  GVLGAESTIFTESALVQISGRAGRHPDFFKGDVFFFHFGLTRNMKQAKKHIVKMNDTAEKEFSEK   459
NTDB id 108 BSU 35470 NP 391427.1            GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                                    !!!!!!!*!!!!!!!!!!! !! !!!***  !!! *!!!! !* !  !*!!!  !!* ! !  *
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X non conserved

X similar

X ≥ 50% conserved