```
logo
NTDB id 985888 MHI60 RS10080 WP 144483668.1  ......MNMDKAMELKRHLYSRHLLTVETRCAQSNLDWLEEKGLVNRTPAIERKADGFTCYRCGVSHKRYFAHSPCEECQ   74
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYH..SSG   78
consensus                                    ****** !     !!  *! !!!!!  !  *    **!*   ! *   * !      * ! !!! ** !!! *  ** *

logo
NTDB id 985888 MHI60 RS10080 WP 144483668.1  KDCVYCRSCIMMGKATECGFLYEWTGPKMVEAYRAELTWQGELSKGQKRASERMIEAIKNKFDLLVWAVCGAGKTEVLFH  154
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP  158
consensus                                    ! **!!!!!*!!!* *!* *!! !  *         !!! ! !! !! *!   *!!!!  ! *!!*!!!!!!!!!!*!!

logo
NTDB id 985888 MHI60 RS10080 WP 144483668.1  GIEYALNQGMSVCIATPRTDVVLELEPRLRKAFQGITIAVLYGGSSQRFQIAPLVIATTHQLMRYKNAFDVLIVDEVDAF  234
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF  238
consensus                                    !!! !!!!!* !!!!!!!!!!!!!! !!!* !!!!  !  !!!!!  *  * !!*! !!!!!*!!! ! !!*!*!!!!!!

logo
NTDB id 985888 MHI60 RS10080 WP 144483668.1  PYSMDERLQFAVLKAMRKNGGVRIYLSATPSKKMTIEVSRGKLEAIKIPLRFHQQPLPVPTFQWIGHWKKKLKKKQLPSK  314
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKN.STLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPA  317
consensus                                    !!! !  !!!!! !! *!!*   *!!!!!!*! *      ! !* **!! !*!  !!! ! ! !*!*!!!!! *  *!*

logo
NTDB id 985888 MHI60 RS10080 WP 144483668.1  VMNWMQRHIANKRRVLLFVPSIAVMKKATKILREHSLNVEGVSADDPDRKQKVQHFRDYAYDVLVTTTILERGVTIPNVQ  394
NTDB id 108 BSU 35470 NP 391427.1            VKRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQ  397
consensus                                    !  !*  !*   !*! !!!!!* ** !!  * * ***    !*!*!**!! !!!*!!!   !*!*!!!!!!!!!!*! !!

logo
NTDB id 985888 MHI60 RS10080 WP 144483668.1  VGVLGSESTIFTESALVQISGRVGRHPDYCTGDVFLFHFGLTRSMKQAKNHIVKMNDTAAKEFTEKQCGFN  465
NTDB id 108 BSU 35470 NP 391427.1            TGVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD.....  463
consensus                                     !!!! !!*!!!!!!!!!! !! !!!**!* !!!  !!!! !*!!  !* !!  !!* !!!  *  *****
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X non conserved

X similar

X ≥ 50% conserved