```
logo
NTDB id 983455 NSQ34 RS16165 WP 342500965.1  ......MNMDKAMELMGQLHSRHLLTVETKCPQSNLDWLEEKGLVNRSPAIERKANGFTCCRCGVSHKRYFAHSPCEVCQ   74
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYH..SSG   78
consensus                                    ****** !     !!   !*!!!!!  !  **   **!*   ! *   * !      * !*!!! ** !!! *  ** *

logo
NTDB id 983455 NSQ34 RS16165 WP 342500965.1  KDCVYCRSCIMMGKAAECGFLYEWTGPQMVETGRAELTWQGELSKGQKRASERMIEAIKNKFDLLVWAVCGAGKTEVLFH  154
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP  158
consensus                                    ! **!!!!!*!!!*  !* *!! !  **        !!! ! !! !! *!   *!!!!  ! *!!*!!!!!!!!!!*!!

logo
NTDB id 983455 NSQ34 RS16165 WP 342500965.1  GIEYALNQGMSVCIATPRTDVVLELEPRLRKAFQGVIITVLYGGSSQRFQIAPLVITTTHQLMRYKNAFDVLIVDEVDAF  234
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF  238
consensus                                    !!! !!!!!* !!!!!!!!!!!!!! !!!* !!!!  !* !!!!!  *  * !!*!*!!!!!*!!! ! !!*!*!!!!!!

logo
NTDB id 983455 NSQ34 RS16165 WP 342500965.1  PYSMDERLQFAVLKAMRKNGGVRIYLSATPSKKMTREVSRGKLEAMKVPLRFHEHPLPVPTFHWIGHWKKKLKKNQLPPK  314
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKN.STLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPA  317
consensus                                    !!! !  !!!!! !! *!!*   *!!!!!!*! * !    ! !* ***! !*! *!!! ! !*!*!*!!!!! *! *!!

logo
NTDB id 983455 NSQ34 RS16165 WP 342500965.1  VMNWMQRHIANKRRILLFVPSIAVMKKVTKILREQSLNVEGVSADDPDRKQKVQHFRDYVYDVLVTTTILERGVTIPNVQ  394
NTDB id 108 BSU 35470 NP 391427.1            VKRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQ  397
consensus                                    !  !*  !*   !** !!!!!* ** !   * *  **    !*!*!**!! !!!*!!!   !*!*!!!!!!!!!!*! !!

logo
NTDB id 983455 NSQ34 RS16165 WP 342500965.1  VGVLGSESTIFTESALVQISGRVGRHLDYCTGDVFLFHFGLTRSMKQAKKHIAKMNDTAAKEFSEKQCGFN  465
NTDB id 108 BSU 35470 NP 391427.1            TGVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD.....  463
consensus                                     !!!! !!*!!!!!!!!!! !! !!! *!* !!!  !!!! !*!!  !*!!!  !!* !!!  *  *****
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X non conserved

X similar

X $\geq$ 50% conserved