```
logo
NTDB id 1066533 ACH2FV RS16680 WP 395894762.1  ......MNMDKAMELMRQLHSRHLLTVETKCPQSNLDWLEEKGLVNRSPAIERKANGFTCCRCGVSHKRYFAHSPCEVCQ   74
NTDB id 108 BSU 35470 NP 391427.1              MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYH..SSG   78
consensus                                       ****** !     !!   !*!!!!!  !  **   **!*   ! *   * !      * !*!!! ** !!! *  ** *

logo
NTDB id 1066533 ACH2FV RS16680 WP 395894762.1  KDCVYCRSCIMMGKAAECGFLYEWTGPQMEETCRAELTWQGELSKGQKRASERIIEAIKNKFDLLVWAVCGAGKTEVLFH   154
NTDB id 108 BSU 35470 NP 391427.1              KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP   158
consensus                                       ! **!!!!!*!!!*  !* *!! !  **    *   !!! ! !! !! *!   *!!!!  ! *!!*!!!!!!!!!!*!!

logo
NTDB id 1066533 ACH2FV RS16680 WP 395894762.1  GIEYALNQGMSVCIATPRTDVVLELEPRLRKAFQGVTITVLYGGSSQRFQITPLVITTTHQLMRYKNAFDVLIVDEVDAF   234
NTDB id 108 BSU 35470 NP 391427.1              GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF   238
consensus                                       !!! !!!!!* !!!!!!!!!!!!!! !!!* !!!!  !* !!!!!  *  **!!*!*!!!!!*!!! ! !!*!*!!!!!!

logo
NTDB id 1066533 ACH2FV RS16680 WP 395894762.1  PYSMDERLQFAVLKAMRNNKGVRIYLSATPSKKMTREVSRGKLEAIKIPLRFHEQPLPVPTFHWIGHWKKKLKKKQLPPK   314
NTDB id 108 BSU 35470 NP 391427.1              PYSADQTLQFAVQKARKKN.STLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPA   317
consensus                                       !!! !  !!!!! !! * !*   *!!!!!!*! * !    ! !* **!! !*!  !!! ! !*!*!*!!!!! *  *!!

logo
NTDB id 1066533 ACH2FV RS16680 WP 395894762.1  VMNWMQRHIANKRRILLFVPSIAVMKKVTKILREQSLNVEGVSADDPDRKQKVQHFRDYVYNVLVTTTILERGVTIPNVQ   394
NTDB id 108 BSU 35470 NP 391427.1              VKRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQ   397
consensus                                       !  !*  !*   !** !!!!!* ** !   * *  **    !*!*!**!! !!!*!!!    *!*!!!!!!!!!!*! !!

logo
NTDB id 1066533 ACH2FV RS16680 WP 395894762.1  VGVLGSESTIFTESALVQISGRVGRHPDYCTGDVFLFHFGLTRSMKQAKKHIAKMNETAAKEFSEKQCGFN   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