```
logo
NTDB id 245389 CJ306 RS27005 WP 119684129.1  ...................MLAGKQLLLEELSSDLQRELND.LKKKGEVICVQGVKKKNSKYMCQRCGNVDRRLFASFLCKR   62
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSF..SDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHS..   76
consensus                                    ***************** !  **!!  !!! **  !* *** ! ! * * * *     *! !*!!!* ! ! !  *****

logo
NTDB id 245389 CJ306 RS27005 WP 119684129.1  CSKVCTYCRKCITMGRVSECAVLVRGIAERKREKNLNLLQWNGTLSAGQDLAAQGVIEAIRQKESFFIWAVCGAGKTEML  142
NTDB id 108 BSU 35470 NP 391427.1            SGKNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEML  156
consensus                                    * ! * !!! !* !!!!!!* *!     !         ! ! ! !! !!  !!* *!!!!  !!   !!!!!!!!!!!!!

logo
NTDB id 245389 CJ306 RS27005 WP 119684129.1  FYGINEALQKGERVCIATPRTDVVLELAPRLQEVFPYIKVAALYGGSVDKEKDAVLVVATTHQLLRYYRAFHVIVVDEID  222
NTDB id 108 BSU 35470 NP 391427.1            FPGIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVD  236
consensus                                    !*!!  !!* ! !!!!!!!!!!!!!!!!!!!   !*   * !!!!!! !! *  *!** !!!!!!!!  ! *!***!!*!

logo
NTDB id 245389 CJ306 RS27005 WP 119684129.1  AFPYCADQMLQYAVKQAMKEKAARIYLTATPDETWKRKFRKGEQKGVIVSGRYHRHPLPVPLFCWCGNWKKSLNRERIPR  302
NTDB id 108 BSU 35470 NP 391427.1            AFPYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPP  316
consensus                                    !!!!*!!! !!*!!  ! !     *!!*!!!*   !!!   !  * ! ***!*!!*!!! ! !*!!!!!!! !!! *!!*

logo
NTDB id 245389 CJ306 RS27005 WP 119684129.1  VLLQWLKMYLNKKYPVFLFVPHVRYIEEISSLLKSLHNKVEGIHAEDPMRKEKVAAFRKGEIPLLVTTTILERGVTVKNL  382
NTDB id 108 BSU 35470 NP 391427.1            AVKRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKV  396
consensus                                     *  !*  **     !!!!!!!*!  *!    * ! *!**   *!!!!**!!!!!  !! ! **!!*!!!!!!!!!!!* *

logo
NTDB id 245389 CJ306 RS27005 WP 119684129.1  QVAVLGAEEEIFSESALVQIAGRAGRSFEAPYGEVIYFHYGKTEAMVRAKKHIQGMNKNAKEQGLID   449
NTDB id 108 BSU 35470 NP 391427.1            QTGVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                                    ! *!!!!!  !!*!!!!!!!!!! !!* ! * !*!!!!!*!!!  !* !*!!!  !!  !    * !
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X non conserved

X similar

X ≥ 50% conserved