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logo

NTDB id 998118 ABDZ24 RS04645 WP 000879442.1  ..................MLAGKQLLLEELSSDLRRELSD.LKRKGEVVCVQGITKKASKYICQRCGNIEQRLFASFLCKR   62
NTDB id 108 BSU 35470 NP 391427.1             MNVPVEKNSSFSKELQQTLRSRHLLRTELSF..SDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHS..   76
consensus                                     ***************** !  **!!  !!! **  !* *** * ! * * * !*    *! !*!!!* *!! !  *****

logo

NTDB id 998118 ABDZ24 RS04645 WP 000879442.1  CSKVCTYCRKCITMGRVSECAVLVRGIAERTGEKSLNSLQWNGTLSTGQELAAQGVIEAIKQKESFFIWAVCGAGKTEML   142
NTDB id 108 BSU 35470 NP 391427.1             SGKNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEML   156
consensus                                     * ! * !!! !* !!!!!!* *!     !         ! ! ! !!*!!  !!* *!!!!  !!   !!!!!!!!!!!!!

logo

NTDB id 998118 ABDZ24 RS04645 WP 000879442.1  FYGIAKAIQKGERVCIATPRTDVVLELAPRLQEVFPHINVAALYGGSVDREKDAALVVATTHQLLRYYRAFHVMIVDEID   222
NTDB id 108 BSU 35470 NP 391427.1             FPGIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVD   236
consensus                                     !*!!  !** ! !!!!!!!!!!!!!!!!!!!   !**  * !!!!!! !* *  *!** !!!!!!!!  ! *!!!*!!*!

logo

NTDB id 998118 ABDZ24 RS04645 WP 000879442.1  AFPYHADQMLQYAVQQAMKEKAARIYLTATPDEKWKRNFRRGKQKGVIISGRYHRYPLPVPLFCWCGNWKKSLHHKKIPR   302
NTDB id 108 BSU 35470 NP 391427.1             AFPYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPP   316
consensus                                     !!!!*!!! !!*!!! ! !     *!!*!!!*   !!     !  * ! !**!*!! !!! ! !*!!!!!!! !** !!!*

logo

NTDB id 998118 ABDZ24 RS04645 WP 000879442.1  VLLQWLEMYVNKKHPIFLFVPHVRYIEEMSLLLKSLDNRVEGVHAEDPMRKEKVAAFRKGEIPLLVTTTILERGVTVKNL   382
NTDB id 108 BSU 35470 NP 391427.1             AVKRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKV   396
consensus                                      *  !*! *!   *!*!!!!!*!  *!    * ! ***!   !!!!!**!!!!!  !! ! **!!*!!!!!!!!!!!* *

logo

NTDB id 998118 ABDZ24 RS04645 WP 000879442.1  QVAVLGAEEEIFSESALVQIAGRAGRSFEEPYGEVVYFHCGKTEAMVRAKRHIQSMNKKAKEQGLID   449
NTDB id 108 BSU 35470 NP 391427.1             QTGVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                                     ! *!!!!!  !!*!!!!!!!!!! !!* ! * !*!*!!!*!!!  !* !**!!  !!  !    * !
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X non conserved

X similar

X ≥50% conserved