```
logo
NTDB id 423229 G4D59 RS16460 WP 026050154.1  ......MNLEKAMELSHKLQSRHLLPVECQCTQSELEWLENQGFIHRTPAVDRVASGLICCRCGVSNKRYFALSSCETCK   74
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYH..SSG   78
consensus                                    ****** !     !! * ! !!!!!* !* **   *!!*  *!*!*  * *       !*!!! *  !!!   *****

logo
NTDB id 423229 G4D59 RS16460 WP 026050154.1  KDCVYCRSCIMLGKVSECGFLYEWTGPQKKETRQVELTWQGELSKGQKRASDRLVEAIQNKFDLLVWAVCGAGKTEVLFH  154
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP  158
consensus                                    ! **!!!!!*!*!*!!!* *!! !  **    * * !!! ! !! !! *!   !*!!!  ! *!!*!!!!!!!!!!!*!!

logo
NTDB id 423229 G4D59 RS16460 WP 026050154.1  GIKYALNNGMSVCIATPRTDVVLELEPRMRKAFQGLNIAALYGGSSQRFQMAPLMIATTHQLMRYKNAFDVLIVDEVDAF  234
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF  238
consensus                                    !!  !!!*!* !!!!!!!!!!!!!! !!** !!!!  ! !!!!!!  *  * !!!! !!!!!*!!! ! !!*!*!!!!!!

logo
NTDB id 423229 G4D59 RS16460 WP 026050154.1  PYSMDERLQFAVLKSMKKTGVRIYLSATPSKKMQKDVARRQLEAIKIPLRFHQKPLPVPTFQWVGDWKKRLKRNRLPAST  314
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV  318
consensus                                    !!! !  !!!!! !  !!    *!!!!!!*! * *     !!* **!! !*! !!!! ! ! !*! !!!*! !!**!*

logo
NTDB id 423229 G4D59 RS16460 WP 026050154.1  MNWLHEHITKKKRVLLFVPSISTMKKVTHILQGQDVNVQGVSADDQERKQKVQHFRDHRYDVLVTTTILERGVTIQDVQV  394
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT  398
consensus                                      !** !*   **! !!!!!*! * !  **  ! **    !*!*! *!! !!!*!!!*  !*!*!!!!!!!!!!** !!

logo
NTDB id 423229 G4D59 RS16460 WP 026050154.1  GVLGAESPIFTESALVQISGRAGRHPDFFNGDVYFFHFGLTRSMKQAKKHIVKMNNTAEKEFSEK   459
NTDB id 108 BSU 35470 NP 391427.1            GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                                    !!!!!!!*!!!!!!!!!!! !! !!!***  !!! *!!!! !*!!  !*!!!  !!  ! !  *
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X non conserved

X similar

X $\geq$ 50% conserved