```
logo
NTDB id 252994 CSE15 RS16950 WP 157774431.1  ......MNLEKAMELSHKLQSRHLLPVECQCTQSELEWLENQGFIHRTPAVDRVASGLICCRCGVSNKRYFALSPCETCK   74
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYH..SSG   78
consensus                                    ****** !     !! * ! !!!!!* !* **   *!!*  *!*!*  * *       !*!!! *  !!!    ****

logo
NTDB id 252994 CSE15 RS16950 WP 157774431.1  KDCVYCRSCIMLGKVSECGFLYEWTGPQKKETRQVELTWQGELSKGQKRASDRLVEAIQNKFDLLVWAVCGAGKTEVLFH   154
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP   158
consensus                                    ! **!!!!!*!*!*!!!* *!! !  **    * * !!! ! !! !! *!   !*!!!  ! *!!*!!!!!!!!!!*!!

logo
NTDB id 252994 CSE15 RS16950 WP 157774431.1  GIKYALNNGMSVCIATPRTDVVLELEPRMRKAFQGLNIAALYGGSSQRFQMAPLMIATTHQLMRYKNAFDVLIVDEVDAF   234
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF   238
consensus                                    !!  !!!*!* !!!!!!!!!!!!!! !!** !!!!  ! !!!!!!  *  * !!!! !!!!!*!!! ! !!*!*!!!!!!

logo
NTDB id 252994 CSE15 RS16950 WP 157774431.1  PYSIDERLQFAVLKSMKKTGVRIYLSATPSKKMQKDVARRQLEAIKIPLRFHQKPLPVPTFQWVGDWKKRLKRNRLPAST   314
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV   318
consensus                                    !!! !  !!!!! !  !!    *!!!!!!*! * *     !!* **!! !*! !!!! ! ! !*! !!!*! !!**!*

logo
NTDB id 252994 CSE15 RS16950 WP 157774431.1  MNWLHEHITKKKRVLLFVPSISTMKKVTHILQGQDVNVQGVSADDQERKQKVQHFRDHRYDVLVTTTILERGVTIQDVQV   394
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT   398
consensus                                      !** !*   **! !!!!!*! * !  **  ! **    !*!*! *!! !!!*!!!*  !*!*!!!!!!!!!!** !!

logo
NTDB id 252994 CSE15 RS16950 WP 157774431.1  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