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logo
NTDB id 1094763 ACLBKY RS16490 WP 138826871.1  ......MNLEKAMELSHKLQSRHLLPVECQCTQSELEWLENQGFIHRTPAVDRVASGLICCRCGVSNMRYFALSPCETCK   74
NTDB id 108 BSU 35470 NP 391427.1              MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYH..SSG   78
consensus                                      ****** !     !! * ! !!!!!* !* **   *!!*  *!*!*  * *        !*!!! *  !!!    ****

logo
NTDB id 1094763 ACLBKY RS16490 WP 138826871.1  KDCVYCRSCIMLGKVSECGFLYEWTGPQKKDTRQVELTWQGELSKGQKRASDRLVEAIQNKFDLLVWAVCGAGKTEVLFH   154
NTDB id 108 BSU 35470 NP 391427.1              KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP   158
consensus                                      ! **!!!!!*!*!*!!!* *!! !  **    * * !!! ! !! !! *!   !*!!!  ! *!!*!!!!!!!!!!*!!

logo
NTDB id 1094763 ACLBKY RS16490 WP 138826871.1  GIKYALNNGMSVCIATPRTDVVLELEPRMRKAFQGLNIAALYGGSSQRFQMAPLMIATTHQLMRYKNAFDVLIVDEVDAF   234
NTDB id 108 BSU 35470 NP 391427.1              GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF   238
consensus                                      !!   !!!*!* !!!!!!!!!!!!!! !!** !!!!  ! !!!!!!  *  * !!!! !!!!!*!!! ! !!*!*!!!!!!

logo
NTDB id 1094763 ACLBKY RS16490 WP 138826871.1  PYSIDERLQFAVLKSMKKTGVRIYLSATPSKKMQKDVARRQLEAIKIPLRFHQKPLPVPTFQWVGDWKKRLKRNRLPAST   314
NTDB id 108 BSU 35470 NP 391427.1              PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV   318
consensus                                      !!! !  !!!!! !  !!    *!!!!!!*! * *     !!* **!! !*! !!!! ! ! !*! !!!*! !!**!*

logo
NTDB id 1094763 ACLBKY RS16490 WP 138826871.1  MNWLHEHITKKKRVLLFVPSISTMKKVTHILQVQDVNVQGVSADDQERKQKVQHFRDHRYDVLVTTTILERGVTIQDVQV   394
NTDB id 108 BSU 35470 NP 391427.1              KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT   398
consensus                                        !** !*   **! !!!!!*! * !  **    **    !*!*! *!! !!!*!!!*  !*!*!!!!!!!!!!** !!

logo
NTDB id 1094763 ACLBKY RS16490 WP 138826871.1  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