```
logo
NTDB id 1092875 ACK25W RS15925 WP 142393300.1  ......MNMDKAMELRQQLQSRHLLTAETRCSQSDLDWLVEKGLVIRTPAIERKANGLTCCRCGVSKKRYFAHTPCDMCQ   74
NTDB id 108 BSU 35470 NP 391427.1              MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYH..SSG   78
consensus                                      ****** !     !! ! ! !!!!!  !  *!   **!**  ! *   * !        !*!!! *  !!! *  ** *

logo
NTDB id 1092875 ACK25W RS15925 WP 142393300.1  KDCVYCRSCIMMGKTTECGFLYEWTGPQMEETCHTELTWQGNLSKGQKRASEKLIEAIKNKFDLLIWAVCGAGKTEVLFH   154
NTDB id 108 BSU 35470 NP 391427.1              KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP   158
consensus                                      ! **!!!!!*!!!* *!* *!! !  **    **  !!! ! !! !! *!   !!!!!  ! *!!!!!!!!!!!!!*!!

logo
NTDB id 1092875 ACK25W RS15925 WP 142393300.1  GIEYALHQGMSVCIATPRTDVVLELEPRLKKAFQGMKIAVLYGGSPQRFQIAPLVIATTHQLMRYKLAFDVLIIDEVDAF   234
NTDB id 108 BSU 35470 NP 391427.1              GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF   238
consensus                                      !!!  !!*!!* !!!!!!!!!!!!!! !!!!  !!!!   !  !!!!!* *  * !!*! !!!!!*!!!  ! !!*!!!!!!!!

logo
NTDB id 1092875 ACK25W RS15925 WP 142393300.1  PYSIDERLQFAVLKAMRKKGVRVYLSATPSKKMKRDVSRGQLEAIKIPLRFHQQPLPVPSFQWIGHWKKKLKKNQLPPKV   314
NTDB id 108 BSU 35470 NP 391427.1              PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV   318
consensus                                      !!! !  !!!!! !! *!    !!!!!!!*! *!!    !!!* **!! !*!  !!! ! ! !*!*!!!!! *! *!! !

logo
NTDB id 1092875 ACK25W RS15925 WP 142393300.1  MNWMQKHITKKRRILLFVPSISTMKKITKVLREHRLNVEGVSADDPDRKQKVQHFRDYKYDVLVTTTILERGVTIPNVQV   394
NTDB id 108 BSU 35470 NP 391427.1              KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT   398
consensus                                        !*  !*   !** !!!!!*! * !   * * ***    !*!*!**!! !!!*!!!   !*!*!!!!!!!!!!*! !!

logo
NTDB id 1092875 ACK25W RS15925 WP 142393300.1  GVLGAESTIFTESALVQISGRAGRHPDFFKGDVIFFHFGLTRSMKQAKKHIVKMNDTAAKEFSEK   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