```
logo

NTDB id 1165933 AB3Y92 RS16780 WP 342498014.1  ......MNMDKAMELGQHLQSRHLLTAETRCSQSDLDWLEEKGLVMRTPAIERKANGLICCRCGVSKNRYFAHSPCDKCQ   74
NTDB id 108 BSU 35470 NP 391427.1              MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYH..SSG   78
consensus                                       ****** !     !! !*! !!!!!  !  *!   **!*   ! *   * !        !*!!! * *!!! *  ** *

logo

NTDB id 1165933 AB3Y92 RS16780 WP 342498014.1  KDCVYCRSCIMMGKTKECGFLYEWTGPQMEETCHTELTWQGNLSKGQKRASEKLIKAIKSKSDLLIWAVCGAGKTEVLFH   154
NTDB id 108 BSU 35470 NP 391427.1              KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP   158
consensus                                      ! **!!!!!*!!!*  !* *!! !  **    **  !!! ! !! !! *!   !! !!  ! *!!!!!!!!!!!!!*!!

logo

GIEYALHQGMSVCIATPRTDVVLELEPRLKKAFQGLNIAVLYGGSPQRFQIAPLVIATTHQLMRYKHAFDVLIIDEVDAF   234
GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF   238
consensus                                      !!! !!*!!* !!!!!!!!!!!!!! !!!! !!!!  !  !!!!!* *  * !!*! !!!!!*!!!*! !!*!!!!!!!!

logo

PYSIDERLQFAVLKAMRKKGVRVYLSATPSKKMIKDVFRGQLEAIKIPLRFHQQPLPVPSFHWVGNWKKKLKKNQLPSKV   314
PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV   318
consensus                                      !!! !  !!!!! !! *!    !!!!!!!*! * *    !!!* **!! !*!  !!! ! !*!*!!!!!!! *! *!* !

logo

MRWMQNHYTKKRRVLLFVPSYSTMKKVTKVLRKVHLRVESVSAEDPHRKQKVQQFRDGQYDVLYTTTILERGVTYPNVQV   394
KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT   398
consensus                                        !*  !*   !*   !!!!*! * !   * * *!*    !*!!!**!! !!!!!!!   !*!*!!!!!!!!!!*! !!

logo

GVLGAESTIFTESALVQISGRAGRHPDFFKGDVFFFYFGLTRNMKQAKKHIVKMNDTAEKEFSEK   459
GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                      !!!!!!!*!!!!!!!!!! !! !!!***  !!! *!*!! !* !  !*!!!  !!* ! !  *
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X non conserved

X similar

X $\geq$ 50% conserved