```
logo
NTDB id 401465 GKC27 RS17290 WP 269457875.1  ......MNMDKAMELGQHLQSRHLLTAETRCSQSDLDWLEEKGLVIRTPAIERKANGLICCRCGVSKNRYFAHSSCDKCQ   74
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYH..SSG   78
consensus                                    ****** !     !! !*! !!!!!  !  *!   **!*   ! *   * !        !*!!! * *!!! * *** *

logo
NTDB id 401465 GKC27 RS17290 WP 269457875.1  KDCVYCRSCIMMGKTTECGFLYEWTGPQMEEACHSELTWQGNLSKGQKRASEKLIEAIKNKSDLLIWAVCGAGKTEVLFH  154
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP  158
consensus                                    ! **!!!!!*!!!* *!* *!! !  **    **  !!! ! !! !! *!   !!!!!  ! *!!!!!!!!!!!!!*!!

logo
NTDB id 401465 GKC27 RS17290 WP 269457875.1  GIEYALHQGMSVCIATPRTDVVLELEPRLKKAFQGMKIAVLYGGSPQRFQIAPLVIATTHQLMRYKHAFDVLIIDEVDAF  234
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF  238
consensus                                    !!! !!*!!* !!!!!!!!!!!!!! !!!! !!!!  !  !!!!!* *  * !!*! !!!!!*!!!*! !!*!!!!!!!!

logo
NTDB id 401465 GKC27 RS17290 WP 269457875.1  PYSIDERLQFAVLKAMRKKGVRVYLSATPSKKMIRDVSRGQLEAIKIPLRFHQQPLPVPSFQWIGHWKKKLKKNQLPPKV  314
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV  318
consensus                                    !!! !  !!!!! !! *!    !!!!!!!*! * !    !!!* **!! !*!  !!! ! ! !*!*!!!!! *! *!! !

logo
NTDB id 401465 GKC27 RS17290 WP 269457875.1  MNLMQKHITKKRRVLLFVPSISTMKKVTKVLRKHHLNVEGVSADDPDRKQKVQQFRDYKYDVLVTTTILERGVTISNVQV  394
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT  398
consensus                                       *  !*   !*! !!!!!*! * !   * * *!*    !*!*!**!! !!!!!!!   !*!*!!!!!!!!!!** !!

logo
NTDB id 401465 GKC27 RS17290 WP 269457875.1  GVLGAESTIFTESALVQISGRAGRHPDFFKGDVFFFHFGLTRSMKQAKKHIVKMNDTAEKEFSEK  459
NTDB id 108 BSU 35470 NP 391427.1            GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD  463
consensus                                    !!!!!!!*!!!!!!!!!!! !! !!!***  !!! *!!!! !*!!  !*!!!  !!* ! !  *
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X non conserved

X similar

X ≥ 50% conserved