```
logo
NTDB id 401405 GKC25 RS15810 WP 316250400.1  ......MNMDKAMELRQQLQSRHLLTAETRCSQSDLDWLEEKGFVIRTPAIERKANGLTCCRCGVSKKRYFAHTPCDMCQ   74
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYH..SSG   78
consensus                                    ****** !     !! ! ! !!!!!  !  *!   **!*   !**   * !        !*!!! *  !!! *  ** *

logo
NTDB id 401405 GKC25 RS15810 WP 316250400.1  KDCVYCRSCIMMGKTTECGFLYEWTGPQMEETCHTELTWQGNLSKGQKRASEKLIEAIKKKSDLLIWAVCGAGKTEVLFY  154
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP  158
consensus                                    ! **!!!!!*!!!* *!* *!! !  **    **  !!! ! !! !! *!   !!!!! !! *!!!!!!!!!!!!!*!!*

logo
NTDB id 401405 GKC25 RS15810 WP 316250400.1  GIKYALHQGMSVCIATPRTDVVLELEPRLKKAFQGMKIAVLYGGSPQRFQIAPLVIATTHQLMRYKHAFDVLIIDEVDAF  234
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF  238
consensus                                    !!   !!*!!* !!!!!!!!!!!!!!! !!!! !!!!   !  !!!!!* *   * !!*! !!!!!*!!!*! !!*!!!!!!!!

logo
NTDB id 401405 GKC25 RS15810 WP 316250400.1  PYSIDERLQFAVLKAMRKKGVRVYLSATPSKKMKRDVSRGQLEAIKIPLRFHKQPLPVPSFQWIGHWKKKLKKNQLPPKV  314
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV  318
consensus                                    !!! !  !!!!! !! *!    !!!!!!!*! *!!    !!!* **!! !*!* !!! ! ! !*!*!!!!! *! *!! !

logo
NTDB id 401405 GKC25 RS15810 WP 316250400.1  MNWMQKHITKKRRILLFVPSISTMKKVTKVLREHRLNVEGVSADDPDRKQKVQHFRDYKYDVLVTTTILERGVTIPNVQV  394
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT  398
consensus                                      !*  !*   !** !!!!!*! * !   * * ***    !*!*!**!! !!!*!!!   !*!*!!!!!!!!!!*! !!

logo
NTDB id 401405 GKC25 RS15810 WP 316250400.1  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