```
logo
NTDB id 292680 DKE43 RS12320 WP 276318041.1  ......MNMDKAMELRQQLQSRHLLTAETRCSQSDLDWLVEKGLVIRTPAIERKANGLTCCRCGVSKKRYFAHTPCDMCQ   74
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYH..SSG   78
consensus                                    ****** !     !! ! ! !!!!!  !  *!   **!**  ! *   * !        !*!!! *  !!! *  ** *

logo
NTDB id 292680 DKE43 RS12320 WP 276318041.1  KDCAYCRSCIMMGKTTECGFLYEWTGPQMEETCHTELTWQGNLSKGQKRASEKLIEAIKNKFDLLIWAVCGAGKTEVLFH  154
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP  158
consensus                                    ! * !!!!!*!!!* *!* *!! !  **    **  !!! ! !! !! *!   !!!!!  ! *!!!!!!!!!!!!!*!!

logo
NTDB id 292680 DKE43 RS12320 WP 276318041.1  GIEYALHQGMSVCIATPRTDVVLELEPRLKKAFQGMKIAVLYGGSPQRFQIAPLVIATTHQLMRYKLAFDVLIIDEVDAF  234
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF  238
consensus                                    !!! !!*!!* !!!!!!!!!!!!!! !!!! !!!!  !  !!!!!* *  * !!*! !!!!!*!!! ! !!*!!!!!!!!

logo
NTDB id 292680 DKE43 RS12320 WP 276318041.1  PYSIDERLQFAVLKAMRKKGVRVYLSATPSKKMKRDVSRGQLEAIKIPLRFHQQPLPVPSFQWIGHWKKKLKKNQLPPKV  314
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV  318
consensus                                    !!! !  !!!!! !! *!    !!!!!!!*! *!!    !!!* **!! !*!  !!! ! ! !*!*!!!!! *! *!! !

logo
NTDB id 292680 DKE43 RS12320 WP 276318041.1  MNWMQKHITKKRRILLFVPSISTMKKITKVLREHRLNVEGVSADDPDRKQKVQHFRDYKYDVLVTTTILERGVTIPNVQV  394
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT  398
consensus                                      !*  !*   !** !!!!!*! * !   * * ***    !*!*!**!! !!!*!!!   !*!*!!!!!!!!!!*! !!

logo
NTDB id 292680 DKE43 RS12320 WP 276318041.1  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