```
logo
NTDB id 252177 CG477 RS20920 WP 109090172.1  ...................MQKGRQMLLHELSWSKEQLHDFISRGEIVLEKGIVRKSSNYICQRCGNQEKRLFASFLCKRCN   63
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHSS..G   78
consensus                                    *****************  * !**! *!!!*! ! ** *!  ! !  !  !      ! !*!!!* * ! !  *** **

logo
NTDB id 252177 CG477 RS20920 WP 109090172.1  QVCAYCRKCIMMGRVSECTMLVRSVCEGKQECFPHALQWKGVLSPGQNRAAKGVVEAIKQKESFFIWAVCGAGKTEMLFS  143
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP  158
consensus                                      * !!! !*!!!!!!!* *!    *!    * ** ! ! ! !!*!!**!!  **!!!  !!   !!!!!!!!!!!!!!*

logo
NTDB id 252177 CG477 RS20920 WP 109090172.1  GIDEALKNGKRVCIATPRKDVVLELAPRLQEVFPDIPFATLYGGSKEYEKEAMLIVTTTHQLLRYYRAFDVMIIDEIDAF  223
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF  238
consensus                                    !!* !! *! !!!!!!!! !!!!!!!!!!    !*  *   !!!!! *  *  *!***!!!!!!!!  ! !!!!!!!*!!!

logo
NTDB id 252177 CG477 RS20920 WP 109090172.1  PYAMDHMLHEAVRKAAKEDASYIYLTATPEEKWKQSVQNGKQKGVIISGRYHRHPLPVPKLKWCGNWRKLLRRKQIPQVL  303
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV  318
consensus                                    !!  !* !* !! !! !   * *!!*!!!*   !    !!  * ! !**!*!!*!!! !*  !!!!!*! ! !  !!* *

logo
NTDB id 252177 CG477 RS20920 WP 109090172.1  LDWLLIYLQKHYPIFLFVPHICYVEEVTAVLQRLHHKIAGVHAEDPMRKEKVEAFRKCDIPLLITTTILERGVTVTNLQV  383
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDCQLDLLITTTILERGVTVPKVQT  398
consensus                                     !*  **  * !*!!!!*** *!   !*   *! * ! !!!!!**!!!!!  !! ! **!!!!!!!!!!!!!!!* *!

logo
NTDB id 252177 CG477 RS20920 WP 109090172.1  AVLGAEEDIFSESALVQIAGRVGRSSHNPKGEVIYFHYGKTKAMTAAKKHIQFMNKRAKQEGLID   448
NTDB id 108 BSU 35470 NP 391427.1            GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                                    *!!!!!  !!*!!!!!!!!!! !!* * * !*!!!!!*!!!! !  !*!!!  !!  !    * !
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X non conserved

X similar

X $\geq$ 50% conserved