```
logo
NTDB id 251890 CG483 RS20720 WP 109090172.1  ................MQKGRQMLLHELSWSKEQLHDFISRGEIVLEKGIVRKSSNYICQRCGNQEKRLFASFLCKRCN   63
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHSS..G   78
consensus                                    ****************  * !**! *!!!*! ! ** *!  ! !  !  !      ! !*!!!* * ! !  *** **

logo
NTDB id 251890 CG483 RS20720 WP 109090172.1  QVCAYCRKCIMMGRVSECTMLVRSVCEGKQECFPHALQWKGVLSPGQNRAAKGVVEAIKQKESFFIWAVCGAGKTEMLFS   143
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP   158
consensus                                      * !!! !*!!!!!!!* *!    *!    * ** ! ! ! !!*!!**!!  **!!!  !!   !!!!!!!!!!!!!!*

logo
NTDB id 251890 CG483 RS20720 WP 109090172.1  GIDEALKNGKRVCIATPRKDVVLELAPRLQEVFPDIPFATLYGGSKEYEKEAMLIVTTTHQLLRYYRAFDVMIIDEIDAF   223
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF   238
consensus                                    !!* !! *! !!!!!!!! !!!!!!!!!!    !*  *   !!!!! *  *  *!***!!!!!!!!  ! !!!!!!!*!!!

logo
NTDB id 251890 CG483 RS20720 WP 109090172.1  PYAMDHMLHEAVRKAAKEDASYIYLTATPEEKWKQSVQNGKQKGVIISGRYHRHPLPVPKLKWCGNWRKLLRRKQIPQVL   303
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV   318
consensus                                    !!  !* !* !! !! !   * *!!*!!!*   !    !!  * ! !**!*!!*!!! !*  !!!!!*! ! !  !!* *

logo
NTDB id 251890 CG483 RS20720 WP 109090172.1  LDWLLIYLQKHYPIFLFVPHICYVEEVTAVLQRLHHKIAGVHAEDPMRKEKVEAFRKCDIPLLITTTILERGVTVTNLQV   383
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDCQLDLLITTTILERGVTVPKVQT   398
consensus                                     !*  **  * !*!!!!*** *!   !*   *! * ! !!!!!**!!!!!  !! ! **!!!!!!!!!!!!!!* *!

logo
NTDB id 251890 CG483 RS20720 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 ≥ 50% conserved