```
logo
NTDB id 403931 GD442 RS25340 WP 000879430.1  ................MLAGKQLLLEELSSDLQRELNDLKKKGEIVCVQGVKKKNSKYMCQRCGNVDRWLFASFLCKRC   63
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFS.DEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHS..S   77
consensus                                    ***************** !  **!!  !!!  *   *  * ! ! ! * * *     *! !*!!!* !   !  ******

logo
NTDB id 403931 GD442 RS25340 WP 000879430.1  SKVCTYCRKCIAMGRVSECAVLVRGIAERKREKNSNLLQWNGTLSTGQNLAAQGVIEAIKQKESFFIWAVCGAGKTEMLF   143
NTDB id 108 BSU 35470 NP 391427.1            GKNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLF   157
consensus                                     ! * !!! !* !!!!!!* *!     !       !  ! ! ! !!*!!* !!* *!!!!  !!   !!!!!!!!!!!!!!

logo
NTDB id 403931 GD442 RS25340 WP 000879430.1  YGINEALQKGERVCIATPRTDVVLELAPRLQEVFPYIKVAALYGGSVDKEKDAVLVVATTHQLLRYYRAFHVIVVDEIDA   223
NTDB id 108 BSU 35470 NP 391427.1            PGIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDA   237
consensus                                    *!!   !!* ! !!!!!!!!!!!!!!!!!!!!   !!*   * !!!!!! !! *  *!** !!!!!!!!  ! *!***!!*!!

logo
NTDB id 403931 GD442 RS25340 WP 000879430.1  FPYCADQMLQYAVKQAMKEKAARIYLTATPDETWKRKLKQGKQKGVIVSGRYHRHPLPVPLFCWCGNWKKSLNHERIPRV   303
NTDB id 108 BSU 35470 NP 391427.1            FPYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPA   317
consensus                                    !!!*!!! !!*!!  ! !     *!!*!!!*   !!!  *!  * ! ***!*!!*!!! ! !*!!!!!!! !!* *!!*

logo
NTDB id 403931 GD442 RS25340 WP 000879430.1  LLQWLKMYLNKKYPVFLFVPHIRYIEEISSLLKSLHNKVEGVHAEDPMRKEKVAAFRKGEIPLLVTTTILERGVTVKNLQ   383
NTDB id 108 BSU 35470 NP 391427.1            VKRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQ   397
consensus                                    *  !*  **    !!!!!!!**  *!    * ! *!**   !!!!!**!!!!!  !! ! **!!*!!!!!!!!!!!* *!

logo
NTDB id 403931 GD442 RS25340 WP 000879430.1  VAVLGAEEEIFSESALVQIAGRAGRSFEAPYGEVIYFHYGKTEAMVRAKKHIQGMNKNAKEQGLID   449
NTDB id 108 BSU 35470 NP 391427.1            TGVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                                     *!!!!!  !!*!!!!!!!!!! !!* ! * !*!!!!!*!!!  !* !*!!!  !!  !    * !
```

X non conserved

X similar

X $\geq$ 50% conserved