```
NTDB id 964454 NSU02 RS03375 WP 339194222.1 .........MHDHDLQKHLLGRHLLSNELPFSMDAVQ...NAPFVEIEQGVVKKSGIFYCNRCGNDQPFLFAGFDCARCK   68
NTDB id 108 BSU 35470 NP 391427.1           MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHSS..G   78
consensus                                    ********* * **!! *!  !!!!  !!*!! * * ***  ***  !* *      * !!!!!*  *  !  *** **
```

```
NTDB id 964454 NSU02 RS03375 WP 339194222.1 KFCHYCRNCIMMGRVSECSKLVSFPRRDKEEKHSIQSDQTNFLQWDGELSPAQKRASDRIAESVLQRTDCLIWAVCGAGK  148
NTDB id 108 BSU 35470 NP 391427.1           KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWK......SIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGK  152
consensus                                   ! **!!! !*!!!!!!!* *! !**       ********  ! !!! !!**! *!   * ! *  * **!!!!!!!!!!
```

```
NTDB id 964454 NSU02 RS03375 WP 339194222.1 TEVLFAGINTALQKGLFVCIAAPRTDVVLELGPRLKNVFPSIDVAVLYGGSEDRLKLSPITISTTHQLLRYKEAFDVVIL  228
NTDB id 108 BSU 35470 NP 391427.1           TEMLFPGIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMII  232
consensus                                   !!*!!*!! *!!* !! !!!! !!!!!!!!!*!!!!  !*  !*  !!!!!*!* *!!!* !!!!!!!!!!!*! !!*!*
```

```
NTDB id 964454 NSU02 RS03375 WP 339194222.1 DEVDAFPYSVDPALQFAVEKARKRNSSLIYLTATPSSAIKRHFKPS..EIVKIPARYHGYPLPVPEFKWCGNWKKRLEKG  306
NTDB id 108 BSU 35470 NP 391427.1           DEVDAFPYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRN  312
consensus                                   !!!!!!!!! !* !!!!! !!!!*!!*!*!!*!!!*  *!!*  * *** !*!!!!*!  !!! ! ! !!!!!!!*! *
```

```
NTDB id 964454 NSU02 RS03375 WP 339194222.1 KLPKNIITWAAEQMQKERQAFLFVPEIKVLHDVVPLLKKLNSAVEGVHAEDPQRKEKVRAFRNGRIPIIVTTTILERGVT  386
NTDB id 108 BSU 35470 NP 391427.1           KIPPAVKRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVT  392
consensus                                   !*!* *  !   **   !* !!!!! * *!*  ** ! ***    !!!!!**!!!!!  !! ! *****!!!!!!!!!!
```

```
NTDB id 964454 NSU02 RS03375 WP 339194222.1 VPGTDAAVLGAEETIFTESALVQISGRVGRSMNNPTGSVIFFHYGKTNEMIAAKHHILAMNREAAKEDLLKR  458
NTDB id 108 BSU 35470 NP 391427.1           VPKVQTGVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD.  463
consensus                                   !!    *!!!!! *!!!!!!!!!! !! !!*   * ! !!*!!*!!!  !* !**!!  !!  !!! **  *
```

X non conserved
X similar
X ≥ 50% conserved