```
logo
NTDB id 392595 GA693 RS00725 WP 104489142.1  MR.KPSLK.FICTSILGLTLVVSGGCQTTG.AKGDPEKAVKVRTQLAAEYIKVNNFDAAKRALDQALEINSRDATANMMM   77
NTDB id 1051 ABD1 RS02465 WP 004738086.1     MS.TPKLKIMLCMGVAVA..LLASGCQTSQTVKKDPEKAVKVRTQLAAEYIRSGDLDSAKRSLDQALSVDSRDATANMMM   77
NTDB id 1017 ACIAD RS02540 WP 011182074.1    MSKWTINKTLGCAAIVGA..FILSGCQTVPT.TKDPEKGVKVRTQLAAEYIKSGDLDSAKRALDQALKVNPKDSSANMMM   77
consensus                                    !*  * *! **! *****  ** *!!!!* * **!!!!*!!!!!!!!!!!!*****!*!!!*!!!!! ****!**!!!!!

logo
NTDB id 392595 GA693 RS00725 WP 104489142.1  GVLLQQEGSKFNVERAERYFKQALSIEPKNAQARNNYGTYLYQVGRYNDAIEHLQIAGTTLGYDQRFRALENLGRAYVQL  157
NTDB id 1051 ABD1 RS02465 WP 004738086.1     GILLQQEGSKPNLEKAEHYFKRAISSEPDNAQARNNYGTYLYQMERYNDAIEQFRIAGATLGYDQRYQALENLGRIYLKL  157
NTDB id 1017 ACIAD RS02540 WP 011182074.1    GVLLQQEGSRPNLEKADAYFERAVQLDPENAQAHNNYGTYLYQMKRYHDAIQQLTLAGSSLGYDQRYRALENIGRIYLHL  157
consensus                                    !*!!!!!!!**!*!*!* !!**!*****!*!!!!*!!!!!!!!!* !!*!!!*** *!!**!!!!!!**!!!!*!!*!* !

logo
NTDB id 392595 GA693 RS00725 WP 104489142.1  GKLKEAEQAFIQALQINRDAYIAMLELAELKYFNQQQAMATELYEDFVRGVGQNNQDARALWIGIRIARANQDNLGTQVL  237
NTDB id 1051 ABD1 RS02465 WP 004738086.1     GDIASAEKTFKQALLANRDSYISMLELAEIFYLQQQIPAATQMYEQYVRTVGQKNQGARALWIGLRVARANADKMGMQVL  237
NTDB id 1017 ACIAD RS02540 WP 011182074.1    GGVANAEKMFSQALQANRDSSVSMLELAEIYYLQQRIPAATGMYEQYVRTVGQKNQGARALWIGIRVARANADRTGVQVL  237
consensus                                    ! ** !!* ! !!!**!!!****!!!!!!*!**!****!! *!!**!!*!!!*!!*!!!!!!!*!*!!!!!*!**!*!!!

logo
NTDB id 392595 GA693 RS00725 WP 104489142.1  VNQLRALYPESQEYQRYLQLKYSTEAVWK   266
NTDB id 1051 ABD1 RS02465 WP 004738086.1     VNQLRALFPESPEYQRYLQLQYSTEAVWK   266
NTDB id 1017 ACIAD RS02540 WP 011182074.1    VNQLRIFYPDSSEYQRYLKLQYSTEAVWK   266
consensus                                    !!!!!***!*! !!!!!!*!*!!!!!!!!
```

X non conserved

X similar

X ≥ 50% conserved