```
NTDB id 392098 GA646 RS12325 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                                    !*  * *! **! *****  ** *!!!!* * **!!!!*!!!!!!!!!!!!!*****!*!!!*!!!!! ****!**!!!!!
```

```
NTDB id 392098 GA646 RS12325 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                                    !*!!!!!!!**!*!*!* !!**!*****!*!!!!*!!!!!!!!!* !!*!!!*** *!!**!!!!!!**!!!!*!!*!* !
```

```
NTDB id 392098 GA646 RS12325 WP 104489142.1  GKLKEAEQAFIQALQINRDAYIAMLELAELKKYFNQQQAMATELYEDFVRGVGQNNQDARALWIGIRIARANQDNLGTQVL  237
NTDB id 1051 ABD1 RS02465 WP 004738086.1     GDIASAEKTFKQALLANRDSYISMLELAEIFYLQQQIPAATQMYEQYVRTVGQKNQGARALWIGLRVARANADKMGMQVL  237
NTDB id 1017 ACIAD RS02540 WP 011182074.1    GGVANAEKMFSQALQANRDSSVSMLELAEIYYLQQRIPAATGMYEQYVRTVGQKNQGARALWIGIRVARANADRTGVQVL  237
consensus                                    ! **  !!* ! !!!**!!!****!!!!!!*!**!****!! *!!**!!*!!!*!!*!!!!!!!*!*!!!!*!**!*!!!
```

```
NTDB id 392098 GA646 RS12325 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