```
logo

NTDB id 1017 ACIAD RS02540 WP 011182074.1        MSKWTINKTLGCAAIV.GAFILSGCQTVPTTKDPEKGVKVRTQLAAEYIKSGDLDSAKRALDQALKVNPKDSSANMMMGV    79
NTDB id 1069991 ACIHQS RS02140 WP 007482693.1    MNTTR.SKTIIATTILFTVLGLTACQSTKTTKDPEKAVQVRTQLAAEYIRTRDLDSAKRSLDQALKIDSRDANANMMMGI    79
NTDB id 1051 ABD1 RS02465 WP 004738086.1         MSTPK.LKIMLCMGVAVALLASGCQTSQTVKKDPEKAVKVRTQLAAEYIRSGDLDSAKRSLDQALSVDSRDATANMMMGI    79
consensus                                        !** *  !**** *** **********  **!!!!!*!*!!!!!!!!!!***!!!!!!!*!!!!!*****!**!!!!!!*

logo

NTDB id 1017 ACIAD RS02540 WP 011182074.1        LLQQEGSRPNLEKADAYFERAVQLDPENAQAHNNYGTYLYQMKRYHDAIQQLTLAGSSLGYDQRYRALENIGRIYLHLGG   159
NTDB id 1069991 ACIHQS RS02140 WP 007482693.1    LLQQEGSKTNMEKAESYFKRAISSEPDNAQARNNYGTYLYQMERYNEAIEQFTIAGATLGYDQRFQSLENLGRIYLKLGD   159
NTDB id 1051 ABD1 RS02465 WP 004738086.1         LLQQEGSKPNLEKAEHYFKRAISSEPDNAQARNNYGTYLYQMERYNDAIEQFRIAGATLGYDQRYQALENLGRIYLKLGD   159
consensus                                        !!!!!!!**!*!!!* !!*!!****!*!!!!*!!!!!!!!!!*!!**!!*!***!!**!!!!!!***!!!*!!!!!*!!*

logo

NTDB id 1017 ACIAD RS02540 WP 011182074.1        VANAEKMFSQALQANRDSSVSMLELAEIYYLQQRIPAATGMYEQYVRTVGQKNQGARALWIGIRVARANADRTGVQVLVN   239
NTDB id 1069991 ACIHQS RS02140 WP 007482693.1    VANAEKAFKQALQANRNATISMLELSEIFYLQQNNRDASQLYEQYVRNVGQKNQGARALWIGLRIARANADQLGMQVLVN   239
NTDB id 1051 ABD1 RS02465 WP 004738086.1         IASAEKTFKQALLANRDSYISMLELAEIFYLQQQIPAATQMYEQYVRTVGQKNQGARALWIGLRVARANADKMGMQVLVN   239
consensus                                        *!*!!! !*!!!*!!!**!!!!!*!!*!!!!****!***!!!!!!*!!!!!!!!!!!!!!!!*!*!!!!!!**!*!!!!!

logo

NTDB id 1017 ACIAD RS02540 WP 011182074.1        QLRIFYPDSSEYQRYLKLQYSTEAVWK   266
NTDB id 1069991 ACIHQS RS02140 WP 007482693.1    QLRALFPDSPEYQRYLQLQYSTEAVWK   266
NTDB id 1051 ABD1 RS02465 WP 004738086.1         QLRALFPESPEYQRYLQLQYSTEAVWK   266
consensus                                        !!!***!*!*!!!!!!*!!!!!!!!!!
```

X non conserved
X similar
X ≥ 50% conserved