```
logo
NTDB id 136551 EHS42 RS02620 WP 010327532.1  .MKKPVSKLYLALTLGVSVWYLVGCQTVNT.KGDPSKAVQVRTQLAAEYIKSNDYDAAKRTLDQALDIDSRDASANMMMG   78
NTDB id 1051 ABD1 RS02465 WP 004738086.1     MS.TPKLKIMLCM.GVAVALLASGCQTSQTVKKDPEKAVKVRTQLAAEYIRSGDLDSAKRSLDQALSVDSRDATANMMMG   78
NTDB id 1017 ACIAD RS02540 WP 011182074.1    MSKWTINKTLGCA.AIVGAFILSGCQTVPT.TKDPEKGVKVRTQLAAEYIKSGDLDSAKRALDQALKVNPKDSSANMMMG   78
consensus                                    *** ** !***** *** *****!!!!**! **!!*!*!*!!!!!!!!!!*!*!*!!!*!!!!! ****!**!!!!!!

logo
NTDB id 136551 EHS42 RS02620 WP 010327532.1  VLLQREGSPQNVEKAERYFKHAIAAEPKNAQARNNYGTYLYQIGRYNDAIDQLQVAGSTLGYDQRYRALENLGRAYLQVG  158
NTDB id 1051 ABD1 RS02465 WP 004738086.1     ILLQQEGSKPNLEKAEHYFKRAISSEPDNAQARNNYGTYLYQMERYNDAIEQFRIAGATLGYDQRYQALENLGRIYLKLG  158
NTDB id 1017 ACIAD RS02540 WP 011182074.1    VLLQQEGSRPNLEKADAYFERAVQLDPENAQAHNNYGTYLYQMKRYHDAIQQLTLAGSSLGYDQRYRALENIGRIYLHLG  158
consensus                                    *!!!*!!!**!*!!!* !!**!*  *!*!!!!*!!!!!!!!!* !!*!!!*!* *!!**!!!!!!!*!!!!*!!*!! *!

logo
NTDB id 136551 EHS42 RS02620 WP 010327532.1  RVAEAEAAFKQALQVNSGAYLAMIEMAEISYLRQQNAEATQYYEQFVRAVGEKNLDARALWIGIRIARASHDTMGSQVLV  238
NTDB id 1051 ABD1 RS02465 WP 004738086.1     DIASAEKTFKQALLANRDSYISMLELAEIFYLQQQIPAATQMYEQYVRTVGQKNQGARALWIGLRVARANADKMGMQVLV  238
NTDB id 1017 ACIAD RS02540 WP 011182074.1    GVANAEKMFSQALQANRDSSVSMLELAEIYYLQQRIPAATGMYEQYVRTVGQKNQGARALWIGIRVARANADRTGVQVLV  238
consensus                                     *! !!* !*!!!**!****!*!*!!!*!!*!****!**!!!*!!*!!*!!**!!!!!!!*!*!!!**!**!*!!!!

logo
NTDB id 136551 EHS42 RS02620 WP 010327532.1  NQLRALYPDSQEYKRYLQLQYTTEAVWK   266
NTDB id 1051 ABD1 RS02465 WP 004738086.1     NQLRALFPESPEYQRYLQLQYSTEAVWK   266
NTDB id 1017 ACIAD RS02540 WP 011182074.1    NQLRIFYPDSSEYQRYLKLQYSTEAVWK   266
consensus                                    !!!!***!*! !!*!!!*!!!*!!!!!!
```

X non conserved

X similar

X ≥ 50% conserved