```
logo

NTDB id 120315 NMA510612 RS05595 WP 002246120.1  MRRKMLNVPKGSYDGMKGFTIIEFLVAGMLSMIVLMAVGSSYFTSRKLNDAANERLAIQQDLRNAATLIVRDARMAGSFG   80
NTDB id 1138 NGFG RS02430 WP 003694978.1         MKRKMLNVPKGGYDGMKGFTIVEFLVAGLLSVIVLIAVVSSYFTSRKLNDAANERLAEQQDLRNAATLIVRDARMAGSFG   80
consensus                                        !*!!!!!!!!! !!!!!!!!!*!!!!!!*!!*!!!*!! !!!!!!!!!!!!!!!!!! !!!!!!!!!!!!!!!!!!!!!!

logo

NTDB id 120315 NMA510612 RS05595 WP 002246120.1  CFNMSEHIGSDVVSNVVQKNPLFSLKKR..NSTNKLIPITESSNIGYPGFTQRLNALIFQYGIDDVNASADTTVVSSCAK  158
NTDB id 1138 NGFG RS02430 WP 003694978.1         CFNMSEHIGNDVVFNVAQKNALFSLKRNSTNSTNKLIPITESPNINYQNFFQVSSALIFQYGIDDVDASADTTVVSSCAA  160
consensus                                        !!!!!!!!! !!! !! !!!*!!!!!* **!!!!!!!!!!!!*!! !* ! !   !!!!!!!!!!! !!!!!!!!!!!!

logo

NTDB id 120315 NMA510612 RS05595 WP 002246120.1  IAKPGKKISTLQEAKSALQITNDD.KQNGNITRQRHVVNAYAVGRIAGEEGLFRFQLNDDGQWGNPQLLVKKINKMDIRY  237
NTDB id 1138 NGFG RS02430 WP 003694978.1         ISKPGKQIPTLENAKKELKIQNSDKEQNGNIARQRHVVNAYAVGKIAGEEGLFRFQLDDKGKWGNPQLLAKKVKRMRVRY  240
consensus                                        ! !!!! !*!!  !!  ! ! ! !* !!!!! !!!!!!!!!!!!*!!!!!!!!!!!! ! ! !!!!!!! !!* *! *!!

logo

NTDB id 120315 NMA510612 RS05595 WP 002246120.1  IYLLVENPGIPPTNSPRYIYGCPEDDDAGKEETFKYTDKFDSSTNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDAT  317
NTDB id 1138 NGFG RS02430 WP 003694978.1         IY................VSGCPEDEDAGKEEQFKYTDKFDSS...VTPAGVEVLLDSGSDAKIAASSDNIIYAYRINAT  301
consensus                                        !!***************** !!!!!*!!!!!! !!!!!!!!!!***!!!!!!!!!! !!*! !!!!!!!!*!!!!!! !!

logo

NTDB id 120315 NMA510612 RS05595 WP 002246120.1  IRGGNVCANRTL   329
NTDB id 1138 NGFG RS02430 WP 003694978.1         IRGGNVCANRTL   313
consensus                                        !!!!!!!!!!!!
```

X non conserved

X similar

X ≥ 50% conserved