```
logo

NTDB id 39077 NLA RS08010 WP 013449299.1   MSENKQNEVLTGYEQLKRRNRRRLVTASCLVAASCILLAAALSSDPADSNPAPQAGETGATENQTANAAQAPALKSAAGNGEIAA   85
NTDB id 1129 NGFG RS01435 WP 003687618.1   MSENKQNEVLTGYEQLKRRNRRRLVTASSLVAASCILLAAALSSDPADSNPAPQAGETGATESQTANTAQTPALKSAAENGETAA   85
consensus                                  !!!!!!!!!!!!!!!!!!!!!!!!!!!!!*!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!! !!!!  !! !!!!!!! !!!  !!

logo

NTDB id 39077 NLA RS08010 WP 013449299.1   GKPQDAAGVGKPA.DDGGISEPEDIGAPLVIINNRLDDSNIKGLEASAKPQPQEAAEKPQPEETAATAQAEAKQGAAEKVPATAD   169
NTDB id 1129 NGFG RS01435 WP 003687618.1   DKPQDLAGEDKPSAADSEISEPENVGAPLVLINDRLEDSNIKGLEESEKLQQAE.........TAKTEPKQAKQRAAEKVSATAD   161
consensus                                   !!!! !!  !! * !  !!!!! *!!!!!*!! !!*!!!!!!!!! ! !*!* !*********!! ! *  !!! !!!!!*!!!!

logo

NTDB id 39077 NLA RS08010 WP 013449299.1   STDTAAVEKPKRTAETKPQKAERAAEAKPKAKETKTAEKVADKPKTAAEKTKPDTAKSDKPVKEPKKSDKAESKKPAEKDSSDGK   254
NTDB id 1129 NGFG RS01435 WP 003687618.1   STDTVAVEKPKRSAEPKPQKAERTAEAKPKAKETKTAEKVADKPKTAAEKTKPDTAKSDSAVKEAKKADKAEGKKTAEKDRSDGK   246
consensus                                  !!!! !!!!!!!*!!*!!!!!!! !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!! *!!!*!! !!!! !!*!!!! !!!!

logo

NTDB id 39077 NLA RS08010 WP 013449299.1   KHETAQKTDKADKAKTAGPGKTAEKEKSDKTGKKAAIQAGYAEKERALSLQRKMKAAGIDSTITEIMTDNGKVYRVKSSNYKNAR   339
NTDB id 1129 NGFG RS01435 WP 003687618.1   KHETAQKTDKADKTK......TAEKEKSGKAGKKAAIQAGYAEKERALSLQRKMKAAGIDSTITEIMTDNGKVYRVKSSNYKNAR   325
consensus                                  !!!!!!!!!!!!! !******!!!!!!! ! !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!

logo

NTDB id 39077 NLA RS08010 WP 013449299.1   DAERDLNKLRVHGIAGQVTNE   360
NTDB id 1129 NGFG RS01435 WP 003687618.1   DAERDLNKLRVHGIAGQVTNE   346
consensus                                  !!!!!!!!!!!!!!!!!!!!!
```

X non conserved
X similar
X ≥ 50% conserved