```
logo

NTDB id 50428 HPB14 RS00225 WP 001045836.1  MNKWLKGAIVFIGGFATITTISLVYHQKPKAPLNNQPSLLNDDEVKYPLQDYTFTQNPQPTNTESSKDATIKALQEQLKAALKAL   85
NTDB id 1218 CAA10657.1 2413..3543( )       MNKWLKGVIVFIGGFATITTISLVYHQKPKAPLNNQPSLLNDDEVKYPLQDYTFTQNPQPTNTESSKDATIKALQEQLKAALKAL   85
consensus                                   !!!!!!! !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!

logo

NTDB id 50428 HPB14 RS00225 WP 001045836.1  NSKEMNYSKEETFKSPPMDSKTNTTPPKKDFSLKQLDLLAARITPFKQSPKNYEENLIFPMDNPNGIDGFTNLKEKDIATNENKL   170
NTDB id 1218 CAA10657.1 2413..3543( )       NSKEMNYSKEETFKSPPIDP..NTTPPKKDFSLKQLDLLAARITPFKQSPKNYEENLIFPVDNPKGIDGFTNLKEKDIATNENKL   168
consensus                                   !!!!!!!!!!!!!!!!!!*!***!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!*!!! !!!!!!!!!!!!!!!!!!!!

logo

NTDB id 50428 HPB14 RS00225 WP 001045836.1  LRTITADKMIPAFLITPISSQIAGKVIAQVESDIFASMGKAVLIPKGSKVIGYYSNNNKMGEYRLDIVWSRIITPHGINIMLTNA   255
NTDB id 1218 CAA10657.1 2413..3543( )       LRTITADKMIPAFLITPISSQIAGKVIAQVESDIFAHMGKAVLIPKGSKVIGYYSNNNKMGEYRLDIVWSRIITPHGINIMLTNA   253
consensus                                   !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!*!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!

logo

NTDB id 50428 HPB14 RS00225 WP 001045836.1  KGADIKGYNGLVGELIERNFQRYGVPLLLSTLTNGLLIGITSALNNRGNKEEITNFFGDYLLLQLMRQSGMGINQVVNQILRDKS   340
NTDB id 1218 CAA10657.1 2413..3543( )       KGADIKGYNGLVGELIERNFQRYGVPLLLSTLTNGLLIGITSALNNRGNKEGATNFFGDYLLMQLMRQSGMGINQVVNQILRDKS   338
consensus                                   !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!  !!!!!!!!!*!!!!!!!!!!!!!!!!!!!!!!!!

   <0

logo

NTDB id 50428 HPB14 RS00225 WP 001045836.1  KIAPIVVIREGSRVFISPNTDIFFPIPRENEVIAEFLK.   378
NTDB id 1218 CAA10657.1 2413..3543( )       KIAPIVVIREGSRVFISPNTDIFFPIPRENEVIAEFLK*   376
consensus                                   !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
```

X non conserved
X similar
X ≥ 50% conserved