

logo

```
NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 115343 BAMY6614 RS14995 WP 061862635.1
NTDB id 96 BSU 24730 NP 390353.1
consensus
```

MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK 80
MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK 0
..... 0
..... 0
..... 0

logo

NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 115343 BAMY6614 RS14995 WP 061862635.1
NTDB id 96 BSU 24730 NP 390353.1
consensus

ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLDLSLEEVEDLTGLVPEPYQTTKSAFLYALAKHYPELGLPVPPPPSG 160
 ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLDLSLEEVEDLTGLVPEPYQTTKSAFLYALAKHYPELGLPVPPPPSG

logo

```
NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 115343 BAMY6614 RS14995 WP 061862635.1
NTDB id 96 BSU 24730 NP 390353.1
consensus
```

[illegible]

logo

NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 115343 BAMY6614 RS14995 WP 061862635.1
NTDB id 96 BSU 24730 NP 390353.1
consensus

L R S D A L R Y G A V P I G F Q N G E V E V L S D P R H K E A V A Q L L N R P A R F Y L A L P Q A W E E L F R R A Y P Q K N R L G E V L V Q E G K L S R E A L
L R S D A L R Y G A V P I G F Q N G E V E V L S D P R H K E A V A Q L L N R P A R F Y L A L P Q A W E E L F R R A Y P Q K N R L G E V L V Q E G K L S R E A L 320
. 0
. 0
. 0

logo

NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 115343 BAMY6614 RS14995 WP 061862635.1
NTDB id 96 BSU 24730 NP 390353.1
consensus

KEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAQAVATMLGPTCDPEEDP I 399
KEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAQAVATMLGYPYVDPEEDP . 14
.....MSQYTICQQTERTI 0
..... 0
.....*

logo

```
NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 115343 BAMY6614 RS14995 WP 061862635.1
NTDB id 96 BSU 24730 NP 390353.1
consensus
```

FDISPSRWQFNLLCEEKQLLRRYLVPYBLTECHRLVLLVYKDERNTALEIYRIMLTRKGLNKEIAA AAAAAEATTKLNALS
...PDPGAPLLLPEDLCRRYGVPFPHRLEGNRTVLMDPRNILALCDVFALFKHKLNYEPVVIASDELTYLTKLNALS 471
FDISPSRWQKNCEEKQLLLRYLAVPVQETEHKLWLAVDDENNLTACEIFAFM.TH...KQIEPVVIASDELKYLLNALSS 89
..... 0
..... 0

* * * * *

 non conserved
 similar
 $\geq 50\%$ conserved