

```
NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 1019473 AB0R90 RS12855 WP 012117985.1
NTDB id 96 BSU 24730 NP 390353.1
consensus
```

MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGS LAEVLVDMGLLSERRIAQTIEDRFGIPLVELH RVEIPPVKV
MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGS LAEVLVDMGLLSERRIAQTIEDRFGIPLVELH RVEIPPVKV 80
..... 0
..... 0
..... 0
..... 0

```
NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 1019473 ABOR90 RS12855 WP 012117985.1
NTDB id 96 BSU 24730 NP 390353.1
consensus
```

ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLDTLSEEEVDLTGLVVEPYQTKSAFLYALAKHYPELGLPVPPPPSG 160
ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLDTLSEEEVDLTGLVVEPYQTKSAFLYALAKHYPELGLPVPPPPSG 0
..... 0
..... 0
..... 0

```
NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 1019473 ABOR90 RS12855 WP 012117985.1
NTDB id 96 BSU 24730 NP 390353.1
consensus
```

EGQKDLKLGELLLQKGWISREALVEEQKTGDLLGRILVRKGLPEEALYRALAEQKGLFLESTEGIVPDPSAALLL 240
EGQKDLKLGELLLQKGWISREALVEEQKTGDLLGRILVRKGLPEEALYRALAEQKGLFLESTEGIVPDPSAALLL 0
..... 0
..... 0
..... 0

NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 1019473 AB0R90 RS12855 WP 012117985.1
NTDB id 96 BSU 24730 NP 390353.1
consensus

LRSDALRYGAVPIGFQNGEVEVWLSDPRHKEAVAQLLNRPARFYALALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSREAL	320
LRSDALRYGAVPIGFQNGEVEVWLSDPRHKEAVAQLLNRPARFYALALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSREAL	0
.....	0
.....	0
.....	0

```
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NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 1019473 AB0R90 RS12855 WP 012117985.1
NTDB id 96 BSU 24730 NP 390353.1
consensus
```

KEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAQAVATMLGPTCDPEEDPI
 KEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAQAVATQLGYPYVDPEEDP. 399
MSQYTICQQTTERI 14
 0
 0

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NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 1019473 AB0R90 RS12855 WP 012117985.1
NTDB id 96 BSU 24730 NP 390353.1
consensus

FDISPSRWQPNLLKQLRLRYLYVPYRLTECHNLWLVLVKDERNLTLALELYRMLTRKGLNKYEIPVWITSDEITYLLINALS
PDPGAPLLLPEDLCRRYGVFPHRLGNRLIVLLMKDPRNITLALDDVRLALKRKGLNYEVPAAVEAAITKLLI.... 471
 FDISPSRWQKNCEEKQLLLRYLAVPVQETEHKLWLAVDDENNLTACEIFAFM.TH....KQIEPVVIASDEIKYLLINALS 89
 0
 0

 non conserved
 similar
 $\geq 50\%$ conserved