

logo

```
NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 1030784 AB3D65 RS04330 WP 012117985.1
NTDB id 96 BSU 24730 NP 390353.1
consensus
```

MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGS LAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK 80
MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGS LAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK 0
..... 0
..... 0
..... 0

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NTDB id 1030784 AB3D65 RS04330 WP 012117985.1
NTDB id 96 BSU 24730 NP 390353.1
consensus
```

ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLDTLSEEEVDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPPSG 160
ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLDTLSEEEVDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPPSG 0
..... 0
..... 0
..... 0

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

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consensus

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

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consensus

KEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAQAVATMLGPTCDPEEDPI
 KEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAQAVATQLGYPYVDPEEDP. 399
MSQYTICQQTTERI 14
 0
 0

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```

FDISPSRWQPNLLKQLRLRYLVYPVRLTECHLWLVKDERNLTLALELYRMLTRKGLNKYEIPVWITSDEITYLLINALS
 ...PDPGAPLLLPEDLCRRYGVFPHRLGNRLVLLKDPRLNLACDDFAFLKPKGLNKEIAIAAAEAAATIKLLINALS 471
 FDISPSRWQKNCEEKQLLLRYLAVPVQETEHKLWLVADDENNLTAEIFAFM.TH...KQIEPVVIASDEIKYLLINALS 89
 0
 0

 non conserved
 similar
 $\geq 50\%$ conserved