

logo

```
NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 1107247 ACM5XX RS12195 WP 003153083.1
NTDB id 96 BSU 24730 NP 390353.1
consensus
```

MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGS LAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPVKV 80
MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGS LAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPVKV 0
..... 0
..... 0
..... 0

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

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

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LRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARFYALALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSREAL 320
 LRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARFYALALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSREAL 0
 0
 0
 0

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KEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAQAVATMLGYPVDPEDDP
 KEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAQAVATQLGYYPVDPEDDP
MSQYTICQQQTERI

399
 14
 0
 0

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FDISPSRWQPNLLPKQLRLRYLYVPHVLTENRVLWLKVDERNLTLACDDFYRFMLTRBKGLNKEIAVA AAEAAITKLINALS
...PDPGAPALLLPEDLCRRYGVFPHRLGNRIIVLLMKDPRNTLALDDVRLALKRKGLNYEAVAPATEAAAITKLI... 471
FDISPSRWQKNCEEKQLLLRYLAVPVQETEHKLWLVADDENNLTACEIFAFM.TH...KQIEPVVIASDEIKYLIINALS 89
. 0
. 0

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 non conserved
 similar
 $\geq 50\%$ conserved