

NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 1019626 AB0R88 RS11740 WP 003153083.1
NTDB id 96 BSU 24730 NP 390353.1
consensus

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

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NTDB id 96 BSU 24730 NP 390353.1
consensus

ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLD~~TL~~SL~~EE~~VEDLTGLVVEPYQT~~TK~~SAFLYALAKHYPELGLPVP~~PP~~PSG 160
ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLD~~TL~~SL~~EE~~VEDLTGLVVEPYQT~~TK~~SAFLYALAKHYPELGLPVP~~PP~~PSG 0
..... 0
..... 0
..... 0

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consensus

EGQKDLKLGELLQKGWISREALEEALVEQEKTDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAALLL 240
EGQKDLKLGELLQKGWISREALEEALVEQEKTDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAALLL
.....
.....
.....
.....
.....

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consensus

LRSDALRYGAVPIGFQNGEVEVWLSDFRHKEAVAQLLNRPARFYALALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSREAL 320
 LRSDALRYGAVPIGFQNGEVEVWLSDFRHKEAVAQLLNRPARFYALALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSREAL 0
 0
 0
 0

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KEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAQAVATMLGYPYVDPPEEDP
KEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAQAVATMLGYPYVDPPEEDP
MSQYTICQQTETRI
* * *

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FDISPSRWQPNLLPEKQLRLRYLWVPVRLTEENRVLWLVDERNFLALELYRMTRKGLNKYEYEPVVIASDEITKLINALS
...PDPGAPLLLLPEDLCRRYGVFPHRLEGNRIIVLNKDPRNILLADVRLALKRKGLNYEYAPAVATEAAITKKLI.... 471
FDISPSRWQKNCEEKQLLLRYLAVPVQETEHKLWLAVDDENNLTACEIFAFM.TH...KQIEPVVIASDEIKYLINALS 89
..... 0
..... 0

* * * * *

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 non conserved
 similar
 $\geq 50\%$ conserved