

NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 1063383 ACGLYC RS12000 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 1384 A4U84 RS08525 WP 010787006.1
NTDB id 1063383 ACGLYC RS12000 WP 012117985.1
NTDB id 96 BSU 24730 NP 390353.1
consensus

ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLDTLSEEEVDLTGLWVEPYQTKSAFLYALAKHYPELGLPVPPPPSG 160
 ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLDTLSEEEVDLTGLVVEPYQTKSAFLYALAKHYPELGLPVPPPPSG 0
 0
 0
 0

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consensus

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

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consensus

LRSDALRYGAVPIGFQNGEVEVWLSDPRHKEAVAQLLNRPARFYALALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSREAL 320
 LRSDALRYGAVPIGFQNGEVEVWLSDPRHKEAVAQLLNRPARFYALALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSREAL 0
 0
 0
 0
 0

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consensus

KEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAQAVATMLGPTCDPEEDPI
 KEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAQAVATQLGYPYVDPEEDP. 399
MSQYTICQQTTERI 14
 0
 0

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consensus

FDISPSRWQPNLLKQLRLRYLYVYVRLTECHNLWLVLVKDERNLTLALELYRMLTRKGLNKYEPAVWITSDEITYLINALS
 ...PDPGAPLLLPEDLCRRYGVFPHRLGNRLVLLMKDPRNITLALDDVRLALKRKGLNYEPAVATEAAITKLI... 471
 FDISPSRWQKNCEEKQLLLRYLAVPVQETEHKLWLAVDDENNITACEIFAFM.TH...KQIEPVVIASDEIKYLIINALS 89
 0
 0

 non conserved
 similar
 $\geq 50\%$ conserved