

logo

NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 1468 ASU2 RS05090 WP 014991734.1
NTDB id 96 BSU 24730 NP 390353.1
NTDB id 1028 TT RS08215 WP 011173991.1
consensus

MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVKALLPA
.....
.....
MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVKALLPA

0
0
0
85

logo

NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 1468 ASU2 RS05090 WP 014991734.1
NTDB id 96 BSU 24730 NP 390353.1
NTDB id 1028 TT RS08215 WP 011173991.1
consensus

EKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPPSGEGQKDLKLGE
.....
.....
EKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPPSGEGQKDLKLGE

0
0
0
170

logo

NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 1468 ASU2 RS05090 WP 014991734.1
NTDB id 96 BSU 24730 NP 390353.1
NTDB id 1028 TT RS08215 WP 011173991.1
consensus

LLLQKGWISREALEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAALLLLRSDALRYGAVPIGF
.....
.....
LLLQKGWISREALEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAALLLLRSDALRYGAVPIGF

0
0
0
255

logo

NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 1468 ASU2 RS05090 WP 014991734.1
NTDB id 96 BSU 24730 NP 390353.1
NTDB id 1028 TT RS08215 WP 011173991.1
consensus

QNGEVEVWLSDPRHKEAVAQLLNRPARFYALALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSREALKEALEVQKGLPRAKPLGEIL
.....
.....
QNGEVEVWLSDPRHKEAVAQLLNRPARFYALALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSREALKEALEVQKGLPRAKPLGEIL

0
0
0
340

logo

NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 1468 ASU2 RS05090 WP 014991734.1
NTDB id 96 BSU 24730 NP 390353.1
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consensus

VELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAQAVATQ...MSQYITICEQQTERIFDISPSRWQKNCBEKQLLLRYLAVP
.....
.....
VELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAQAVATQ...GYPYVDPEEDPPDPGAPL...LLPEDLCRRYGVPF

39
38
0
420

logo

NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 1468 ASU2 RS05090 WP 014991734.1
NTDB id 96 BSU 24730 NP 390353.1
NTDB id 1028 TT RS08215 WP 011173991.1
consensus

YQETENTLWLAADDNNLACEIFAFMTHK...QIEPVVIASDELKYLLNALSPEQQPIYEESELAFFE...QE.QE
.....
.....
HRLEGNRLVLMKDPNLTALDDVRLALKRGLNYEVAPAVATEAATTKLTI...ERFYGKAETSETAKEFAKKQAEEDVPS

109
109
0
498

