

logo

NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 44625 BANAU RS12955 WP 014418378.1
NTDB id 96 BSU 24730 NP 390353.1
consensus

MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVKALLPA
MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVKALLPA
.....

85
0
0
0

logo

NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 44625 BANAU RS12955 WP 014418378.1
NTDB id 96 BSU 24730 NP 390353.1
consensus

EKAKELKAIPFALDEEAGVVRVAFNLPLDTLGLEEVEDLTGLVPEPYQTTKSAFLYALAKHYPELGLPVPPPPSGEGQKDLKLGE
 EKAKELKAIPFALDEEAGVVRVAFNLPLDTLGLEEVEDLTGLVPEPYQTTKSAFLYALAKHYPELGLPVPPPPSGEGQKDLKLGE

170
0
0
0

logo

NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 44625 BANAU RS12955 WP 014418378.1
NTDB id 96 BSU 24730 NP 390353.1
consensus

LLLQKGWISREALEEALVEQEKTDLLGRILVRKGLPEEALYRALAEQKGLFLESTEGIVDPDPSAALLLLRSDALRYGAVPIGF
 LLLQKGWISREALEEALVEQEKTDLLGRILVRKGLPEEALYRALAEQKGLFLESTEGIVDPDPSAALLLLRSDALRYGAVPIGF

255
0
0
0

logo

NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 44625 BANAU RS12955 WP 014418378.1
NTDB id 96 BSU 24730 NP 390353.1
consensus

QNGEVEVVLSDPRHKEAVAQLLNRPARFYLLALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSREALKEALEVQKGLPRAKPLGEIL
QNGEVEVVLSDPRHKEAVAQLLNRPARFYLLALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSREALKEALEVQKGLPRAKPLGEIL
.....

340
0
0
0

logo

NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 44625 BANAU RS12955 WP 014418378.1
NTDB id 96 BSU 24730 NP 390353.1
consensus

VELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAQAVATMLGIPICDPEEDPIFDISDPGAKLCCEEDLCRLRYLYP
VELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAQAVATQLGYPYVDPEEDP...PDPGAPLLLPEDLCRRYGVFP
.....MSQYTICEQQTERIFDISPSRWQKNCEEKQLLLRYLAVP

420
39
0

* * * * *

logo

NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 44625 BANAU RS12955 WP 014418378.1
NTDB id 96 BSU 24730 NP 390353.1
consensus

YRLTISNRLLVLYKDPNRNITALELYRIMLTRKGLNKETAI A AA EAATKKLTNALSP EQEPFEEAAEAKFAKKQAE E E V P S
 HRLEGNRLVLLMKDPRNITALLDVRLLAKRKGLN Y E V A PAVATEAAITKLI ERFYVGKAE L S E I A K E F A K K Q A E E E V P S
 VQETEHKLWLAVDDENNITACEIFAFM.TH . . . KQIEP V V I A S D E L K Y L I L N A L S P E Q Q P I Y E E S E L A F V E Q E Q E

498
109
0

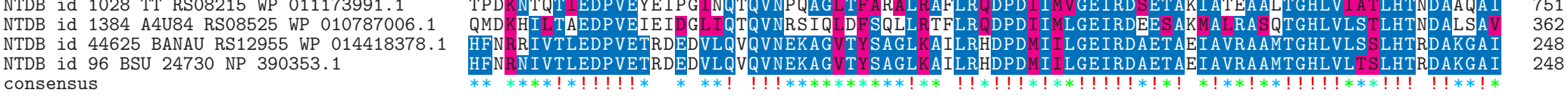
logo



logo



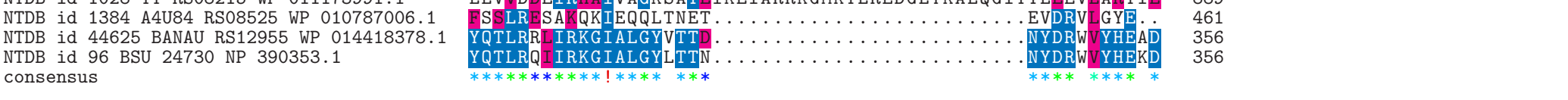
logo



logo



logo



⊠ non conserved
⊠ similar
⊠ ≥ 50% conserved