

logo

NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 418615 SynRS9909 RS00100 WP 007101116.1
NTDB id 1410 SGL RS13950 WP 010873519.1
consensus

MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGS LAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK
MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGS LAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK
.....
.....

80
0
0

logo

NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 418615 SynRS9909 RS00100 WP 007101116.1
NTDB id 1410 SGL RS13950 WP 010873519.1
consensus

ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPPSG
ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPPSG
.....
.....

160
0
0

logo

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NTDB id 418615 SynRS9909 RS00100 WP 007101116.1
NTDB id 1410 SGL RS13950 WP 010873519.1
consensus

EGQKDLKLGELLLQKGWISREALEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKLEFLESTEGIVPDPSAALLL
EGQKDLKLGELLLQKGWISREALEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKLEFLESTEGIVPDPSAALLL
.....
.....

240
0
0

logo

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consensus

LRSDALRYGAVPIGFQNGEVEVMTSSSSSKK EAVAQLLNRPARFYALPQAWHEELFRVAQKNRLGEVLVQEGKLSREAL
LRSDALRYGAVPIGFQNGEVEVMTSDPRHKEAVAQLLNRPARFYALPQAWHEELFRVAQKNRLGEVLVQEGKLSREAL
.....
.....
MTSSSSSKK SRAVA

320
0
14

logo

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consensus

KEALEVQKGLNRAKIFQETLVAGHADA LDLEELQKQKKGGRLEDELKAVTSRKLSPEELLROY VKVOYGYT
KEALEVQKGLPRAKPLGEI LVELGLARPEDEVEALQKQKRGGRLEDTL VQSGKLRPEALQA VATQLGYP
.....
.....
LRNYFSPFCNKLVAGCHVDAEQLRQALVQVKKTCRSLPPELKA VGTGRELSPELRLRQYKKNQLFELKVLYGVD

391
2
86

logo

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consensus

YVDPEEADPAIQSADAAQMAELAGLFFEDLCRRYKQYVWRQQRLPPNRLEPSSLLLQWDPNLLALDDVRLQRKRRLNLMVLYNYEVRRLVVT
SVDPEEADPAIQSADAAQMAELAGLFFEDLCRRYKQYVWRQQRLPPNRLEPSSLLLQWDPNLLALDDVRLQRKRRLNLMVLYNYEVRRLVVT
YVDPEEDPPDPC.....APLLLPEDL CRRYGVFPHRL...EGNRLVILMKDPRNLLALDDVRLALKRKGLNYEVAPAVAT
V...HAPAAAA.....QNPWHQQRLE.LELLLQVPVPERLDAADAQLQEAMR.....
SVDPEVAPIATQQMAELIGRFFPLDTCRRYKFLPLAQQEGDPPSVLVAMVDPDNLAA..QDELNRI LRVKGFELRRLVVT

463
46
164

logo

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NTDB id 1410 SGL RS13950 WP 010873519.1
consensus



889
545
672

X non conserved
X similar
X ≥ 50% conserved