

logo

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NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 1019322 AB0R81 RS12045 WP 012117985.1
NTDB id 96 BSU 24730 NP 390353.1
consensus
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MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGS LAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK 80
MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGS LAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK 0
..... 0
..... 0
..... 0

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consensus
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ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLDTLSEEEVDLTGLVVEPYQTKSAFLYALAKHYPELGLPVPPPPSG 160
ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLDTLSEEEVDLTGLVVEPYQTKSAFLYALAKHYPELGLPVPPPPSG 0
..... 0
..... 0
..... 0

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EGQKDLKLGELLLQKGWISREALVEEQEKTGDLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAALLL 240
EGQKDLKLGELLLQKGWISREALVEEQEKTGDLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAALLL 0
..... 0
..... 0
..... 0

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L R S D A L R Y G A V P I G F Q N G E V E V V L S D P R H K E A V A Q L L N R P A R F Y L A L P Q A W E E L F R R A Y P Q K N R L G E V L V Q E G K L S R E A L 320
 L R S D A L R Y G A V P I G F Q N G E V E V V L S D P R H K E A V A Q L L N R P A R F Y L A L P Q A W E E L F R R A Y P Q K N R L G E V L V Q E G K L S R E A L 0
 0
 0
 0

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KEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAAQAVATMLGYPVDEEDP
KEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAAQAVATMLGYPVDEEDP
.....MSQYTICQQTETRI
.....
.....

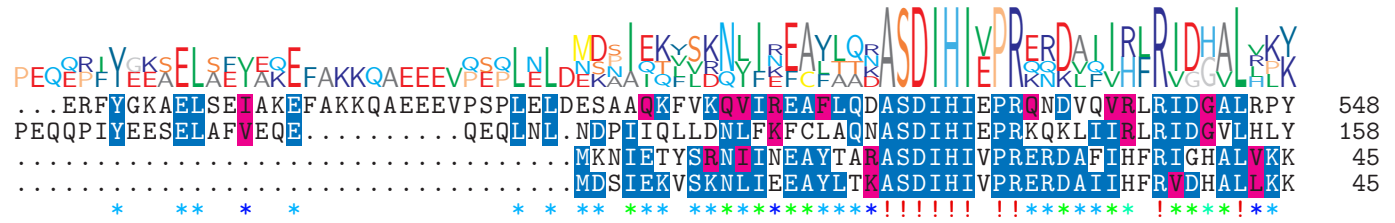
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FDISPSRWQPNLLPKQLLRRYLWYPVRLTECHRLWLVKDERNLTALCEIFAFMTRKGLNKEIAIAAAEAATKLLINALS
 ...PDPGAPLLLPEDLCRRYGVFPHRLEGNRIWLLMKDPRNLTALCDVRLALKRKGLNVEVAPAVEATAAIIKKLLI... 471
 FDISPSRWQKNCEEKQLLLRYLAVPVQETEHKLWLVADDENLTACEIFAFM.TH...KQIEPVVIASDEIKYLLINALS 89
 0
 0

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 non conserved
 similar
 $\geq 50\%$ conserved