

logo

NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 1009274 ABL091 RS11735 WP 014418378.1
NTDB id 96 BSU 24730 NP 390353.1
consensus

MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGS LAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK 80
MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGS LAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK 0
..... 0
..... 0
..... 0

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NTDB id 1009274 ABL091 RS11735 WP 014418378.1
NTDB id 96 BSU 24730 NP 390353.1
consensus

ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLD~~TL~~SLEEVEDLTGLVVEPYQT~~TK~~SAFLYALAKHYPELGLPVPPPPSG 160
 ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLD~~TL~~SLEEVEDLTGLVVEPYQT~~TK~~SAFLYALAKHYPELGLPVPPPPSG 0
 0
 0
 0

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consensus

EGQKDLKLGELLLQKGWISREALVEEQKTGDLLGRILVRKGLPEEALYRALAEQKGLFLESTEGIVDPDPSAALLL 240
EGQKDLKLGELLLQKGWISREALVEEQKTGDLLGRILVRKGLPEEALYRALAEQKGLFLESTEGIVDPDPSAALLL 0
..... 0
..... 0
..... 0

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[illegible]

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consensus

KEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAAQAVATMLGYPICDPEEDPI
KEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAAQAVATQLGYYPVDPEEDP. 399
.....MSQYTICQQTTERI 14
..... 0
..... 0
.....*

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consensus

FDISPSRWQAKNCEEKQLLRRYLYYPVRLTEENRLVLVMDERNITALELYRFLMTRKGLNKYEYEPVVIATSPDELTLYLNALS
 ...PDPGAPLLLLPEDLCRRYGVPFHRLEGNRIIVLLMKDPRIILALDDVRLALKRKGLNVEYAPAVATEAAITKKLI... 471
 FDISPSRWQKNCEEKQLLLRYLAVPVQETEHKLLWLAVDDENNITACEIFAFM.TH...KQIEPVVIASDELKYLNLALS 89
 0
 0
 0

 non conserved
 similar
 $\geq 50\%$ conserved