

NTDB id 972665 WQC64 RS08080 WP 001805151.1
NTDB id 22 SA RS07995 WP 001557362.1
NTDB id 38 MW RS08220 WP 001566670.1
consensus



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logo

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consensus

LYEGGKNQNVLDITGGKVDDTKQPSYSISKYHILPTLNERGINELEYLILTHPHNDHIGVEEYIISHIKIKHIVLYNKG
LYEGGKNQNVLDITGGKVDDTKQPSYSISKYHILPTLNERGINELEYLILTHPHNDHIGVEEYIISHIKIKHIVLYNKG
LYEGGKNQNVLDITGGKVDDTKQPSYSISKYHILPTLNERGINELEYLILTHPHNDHIGVEEYIISHIKIKHIVLYNKG
LYEGGKNQNVLDITGGKVDDTKQPSYSISKYHILPTLNERGINELEYLILTHPHNDHIGVEEYIISHIKIKHIVLYNKG

560
560
560

logo

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consensus

YSSNTLM LLSKLSHKYNIKLMDVRQVSSFKLGSSSFLFFDSFIPNSRDKNEYSIITMTITYQNKVKVLLMGDASKNNESLLL
YSSNTLM LLSKLSHKYNIKLMDVRQVSSFKLGSSSFLFFDSFIPNSRDKNEYSIITMTITYQNKVKVLLMGDASKNNESLLL
YSSNTLM LLSKLSHKYNIKLMDVRQVSSFKLGSSSFLFFDSFIPNSRDKNEYSIITMTITYQNKVKVLLMGDASKNNESLLL
YSSNTLM LLSKLSHKYNIKLMDVRQVSSFKLGSSSFLFFDSFIPNSRDKNEYSIITMTITYQNKVKVLLMGDASKNNESLLL

640
640
640

logo

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consensus

KKYNLPEIDILKVGHHGSKTSSSKEFIEMIKPKISLISSGKNMYHLPNIEVVKRLQRIIRSRIYNSQQNGQVTIDLDDNL
 KKYNLPEIDILKVGHHGSKTSSSKEFIEMIKPKISLISSGKNMYHLPNIEVVKRLQRIIRSRIYNSQQNGQVTIDLDDNL
 KKYNLPEIDILKVGHHGSKTSSSKEFIEMIKPKISLISSGKNMYHLPNIEVVKRLQRIIRSRIYNSQQNGQVTIDLDDNL
 KKYNLPEIDILKVGHHGSKTSSSKEFIEMIKPKISLISSGKNMYHLPNIEVVKRLQRIIRSRIYNSQQNGQVTIDLDDNL

720
720
720

logo

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consensus

Sequence logo for the motif KVDSNSYGNASGL. The top row shows the consensus sequence with amino acid side chains. The bottom row shows the information content in bits for each position, with a green asterisk under the 6th position (S) indicating the most conserved site.

733
733
733

-  non conserved
-  similar
-  $\geq 50\%$ conserved