

logo

NTDB id 46872 HPF32 RS04045 WP 000774362.1
NTDB id 1206 C694 RS04180 WP 000774319.1
consensus

MADLLSSLK^{SH}NLSSGVYQYFDK^{SH}NRQLLYIGKAKNLKKRIKSYFSYRNNEITPNH^{AS}RLRIQMMVKQIAFLETILVENEQDALIL
MADLLSSLK^{SH}NLSSGVYQYFDK^{SH}NRQLLYIGKAKNLKKRIKSYFSYRNNEITPNH^{AS}RLRIQMMVKQIAFLETILVENEQDALIL
MADLLSSLK^{SH}NLSSGVYQYFDK^{SH}NRQLLYIGKAKNLKKRIKSYFSYRNNEITPNH^{AS}RLRIQMMVKQIAFLETILVENEQDALIL
* * * * *

85
85

logo

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consensus

ENSLIKQLKPKYNILLRDDKTYPIYIMDFSTDFPIPLITRKILKQPGVKYFGPFTSGAKDILDSLYELLPLVQKKNCIKDKKACM
 ENSLIKQLKPKYNILLRDDKTYPIYIMDFSTDFPIPLITRKILKQPGVKYFGPFTSGAKDILDSLYELLPLVQKKNCIKDKKACM
 ENSLIKQLKPKYNILLRDDKTYPIYIMDFSTDFPIPLITRKILKQPGVKYFGPFTSGAKDILDSLYELLPLVQKKNCIKDKKACM

170
170

logo

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consensus

FYQIERCKAPCENKITKEEYLKIAKECLEMIENKDKLKELELKMERSNNLRFEELIYRDRIAKIQKIAPFTCMDLAKLYDLD
 FYQIERCKAPCENKITKEEYLKIAKECLEMIENKDKLKELELKMERSNNLRFEELIYRDRIAKIQKIAPFTCMDLAKLYDLD
 FYQIERCKAPCENKITKEEYLKIAKECLEMIENKDKLKELELKMERSNNLRFEELIYRDRIAKIQKIAPFTCMDLAKLYDLD

255
255

logo

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consensus

IFAFYSGSNKAVLVKMFMRGGKIISSAFEKIHSLNGFDTDEAMKQAIINHYQSHLPLMPEQILLNACSNETLKELQEFISHQYSK
 IFAFYSGSNKAVLVKMFMRGGKIISSAFEKIHSLNGFDTDEAMKQAIINHYQSHLPLMPEQILLNACSNETLKELQEFISHQYSK
 IFAFYGSNKA^{*}VLVKMFMRGGKIISSAFEKIHSLNGFDTDEAMKQAIINHYQSHLPLMPEQILLNACSNETLKELQEFISHQYSK

340
340

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K I A L S I P K K G D K L A L I E I A M K N A Q E I F S Q E K T S N E D L I L E E A R S L F K L E C M P Y R V E I F D ^V S H ^A N S S Q C V G G M V V Y E N ^H E F Q K N S Y
 K I A L S I P K K G D K L A L I E I A M K N A Q E I F S Q E K T S N E D L I L E E A R S L F K L E C M P Y R V E I F D T S H H S S S Q C V G G M V V Y E N ^A F Q K N S Y
 K I A L S I P K K G D K L A L I E I A M K N A Q E I F S Q E K T S N E D L I L E E A R S L F K L E C M P Y R V E I F D T S H H S S S Q C V G G M V V Y E N ^A F Q K N S Y

425
425

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consensus

RRYHLKGS^NEYTMSELLTRRALDFAKEPPPNLWIDGGRAQLNIALEILKSSGSFVEVIAISKEKRDSKAYRSKGGAKDIHTP
RRYHLKGS^NEYTMSELLTRRALDFAKEPPPNLWIDGGRAQLNIALEILKSSGSFVEVIAISKEKRDSKAYRSKGGAKDIHTP
RRYHLKGS^DEYTMSELLTRRALDFAKEPPPNLWIDGGRAQLNIALEILKSSGSFVEVIAISKEKRDSKAYRSKGGAKDIHTP

510
510

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consensus

SDTFKLLPSDKRLQWVQKL RDESHRYAINFHRSTKLKMMQIAL LKEKGI GEASVKKLLDYFGSFEAIEKASEQEKNAVLKKRI
SDTFKLLPSDKRLQWVQKL RDESHRYAINFHRSTKLKMMQIAL LKEKGI GEASVKKLLDYFGSFEAIEKASEQEKNAVLKKRI
SDTFKLLPSDKRLQWVQKL RDESHRYAINFHRSTKLKMMQIAL LKEKGI GEASVKKLLDYFGSFEAIEKASEQEKNAVLKKRI

94
94

 non conserved
 similar
 $\geq 50\%$ conserved