

logo

NTDB id 229471 CA922 RS09545 WP 106141221.1
NTDB id 1263 GC085 RS09730 WP 080450539.1
consensus

MLKSI GIKYQLRITTLIPAFVLVALLFAFFYNGLFGKDLKQHMSRLGEAYIRQLLPAAQYAMLRNDYRTLQGLINASTINP
MLKSI GIKYQLRITTLIPAFVLVALLFAFFYNGLFGKDLKQHMSRLGEAYIRQLLPAAQYAMLRNDYRTLQGLINASTINP
!!

80
80

logo

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consensus

EVKALAFYNADGRLLIAYRGGKHSIHKPFNPPDYTGDIYESKQINPFTINFIAPITIPKFNLYSSTEFKEPSTPKIFQADD
EVKALAFYNADGRLLIAYRGGKHSIHKPFNPPDYTGDIYESKQINPFTINFIAPITIPKFNLYSSTEFKEPSTPKIFQADD
EVKALAFYNADGRLLIAYRGGKHSIHKPFNPPDYTGDIYESKQINPFTINFIAPITIPKFNLYSSTEFKEPSTPKIFQADD
!!*

160
160

logo

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consensus

ILGWLSIDIDTQSLLIKRYQMLIVTIFITLFGLLMGLTIHYFLSKRIYMPIARLRSSMKQILSNEFETEIRVSSPGELGI
ILGWLSIDIDTQSLLIKRYQMLIVTIFITLFGLLMGLTIHYFLSKRIYMPIARLRSSMKQILSNEFETEIRVSSPGELGI
ILGWLSIDIDTQSLLIKRYQMLIVTIFITLFGLLMGLTIHYFLSKRIYMPIARLRSSMKQILSNEFETEIRVSSPGELGI
!!

240
240

logo

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consensus

IEKGAHLQRQYLNTVRDLNHHIEIATADLQQSLELLEEKNIELSLEKKKTEEKSRQKSEFIANMSHEIRTPMNGVIGFT
IEKGAHLQRQYLNTVRDLNHHIEIATADLQQSLELLEEKNIELSLEKKKTEEKSRQKSEFIANMSHEIRTPMNGVIGFT
IEKGAHLQRQYLNTVRDLNHHIEIATADLQQSLELLEEKNIELSLEKKKTEEKSRQKSEFIANMSHEIRTPMNGVIGFT
!!

320
320

logo

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consensus

NVLESKLDPLQLDYVKTIKSSAQDLSIINDILDFSKIDAGKLNLDICPLD^YRGCIDDEVLSLASPNAHKKGIDLIPITD
NVLESKLDPLQLDYVKTIKSSAQDLSIINDILDFSKIDAGKLNLDICPLD^YRGCIDDEVLSLASPNAHKKGIDLIPITD
NVLESKLDPLQLDYVKTIKSSAQDLSIINDILDFSKIDAGKLNLDICPLD^YRGCIDDEVLSLASPNAHKKGIDLIPITD
!!*

400
400

logo

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consensus

INVPKMWLGDPLRIKQIISNLVTNAVKFTDHGYVLIRTKIEQETDKDYTL^LFAI^ADTGIGISPEDQTKLFTAFNQADTSI
INVPKMWLGDPLRIKQIISNLVTNAVKFTDHGYVLIRTKIEQETDKDYTL^LFAI^ADTGIGISPEDQTKLFTAFNQADTSI
INVPKMWLGDPLRIKQIISNLVTNAVKFTDHGYVLIRTKIEQETDKDYTL^LFAI^ADTGIGISPEDQTKLFTAFNQADTSI
!!

480
480

logo

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consensus

TRRYGSSGLGLVIC^KKLCEEMHGRISLTSEINKGSTFSARIKVEKLVAYEIEKNQTHRFAHLKII^CFDDNPLHLEA^MNGG
TRRYGSSGLGLVIC^KKLCEEMHGRISLTSEINKGSTFSARIKVEKLVAYEIEKNQTHRFAHLKII^CFDDNPLHLEA^MNGG
TRRYGSSGLGLVIC^KKLCEEMHGRISLTSEINKGSTFSARIKVEKLVAYEIEKNQTHRFAHLKII^CFDDNPLHLEA^MNGG
!!*

560
560

logo

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consensus

LGFWGIEAIRVDSFNKLSR^XTLTKHKDCKIAFINVNQGCERQAAELIAKHKQIPFVLIISKWPINDFAALGARGFLYKPI^XSI
LGFWGIEAIRVDSFNKLSR^XTLTKHKDCKIAFINVNQGCERQAAELIAKHKQIPFVLIISKWPINDFAALGARGFLYKPI^XSI
!!

640
640

logo

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consensus

QKLQDLIESIANENQTEKNTNQELDTLREQLRFLHPEILIAEDNPVNKMLLTSLLNANNITTVDDGEMAVTACEDKK^XFD
QKLQDLIESIANENQTEKNTNQELDTLREQLRFLHPEILIAEDNPVNKMLLTSLLNANNITTVDDGEMAVTACEDKK^XFD
QKLQDLIESIANENQTEKNTNQELDTLREQLRFLHPEILIAEDNPVNKMLLTSLLNANNITTVDDGEMAVTACEDKK^XFD
!!

720
720

logo

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consensus

MILLDLHMPKLNGL^XEAAKMIHQKSLMNKHSPIVLITASSSDLSSIDMKKSGVDFCFQKPIDEKQLLIQILRIVDKTKHAA
MILLDLHMPKLNGL^XEAAKMIHQKSLMNKHSPIVLITASSSDLSSIDMKKSGVDFCFQKPIDEKQLLIQILRIVDKTKHAA
MILLDLHMPKLNGL^XEAAKMIHQKSLMNKHSPIVLITASSSDLSSIDMKKSGVDFCFQKPIDEKQLLIQILRIVDKTKHAA
!!

800
800

logo

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consensus

IDWQLCVQKVS^XGNQALAE^XEFLAKFIEELYKNREEFI^XELMHQKNVKGLADLAHKLHGACCF^XCGVPILQKRVAQLEKLARRT
IDWQLCVQKVS^XGNQALAE^XEFLAKFIEELYKNREEFI^XELMHQKNVKGLADLAHKLHGACCF^XCGVPILQKRVAQLEKLARRT
IDWQLCVQKVS^XGNQALAE^XEFLAKFIEELYKNREEFI^XELMHQKNVKGLADLAHKLHGACCF^XCGVPILQKRVAQLEKLARRT
!!

880
880

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consensus

ANADNL^XSEAF^XTDLIQS^XDAVISEYENQYSQ
ANADNL^XSEAF^XTDLIQS^XDAVISEYENQYSQ
ANADNL^XSEAF^XTDLIQS^XDAVISEYENQYSQ
!!

910
910

^X non conserved
^X similar
^X ≥ 50% conserved