

logo

NTDB id 209502 AU097 RS03045 WP 000658897.1
NTDB id 1046 HON27 RS03130 WP 168726941.1
consensus

MKEILKTLTEAMLPEDSYSEQDAEFLEIFIEEIEEIEFVDLQPLINKWQSENIATLTEIRRHFTLKGSGRMIGAKSSA
MKEILKTLTEAMLPEDSYSEQDAEFLEIFIEEIEEIEFVDLQPLINKWQSENIATLTEIRRHFTLKGSGRMIGAKSSA
MKEILKTLTEAMLPEDSYSEQDAEFLEIFIEEIEEIEFVDLQPLINKWQSENIATLTEIRRHFTLKGSGRMIGAKSSA
!!

80
80

logo

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consensus

ELAMTVEDTLNRVINQSLQLTPTIQSYVQLVFKFYFLKLVDNFKQKRAHTLDFRPLILLGQQLQQQSSLEPALEELLQLS
ELAWTVEDTLNRVINQSLQLTPTIQSYVQLVFKFYFLKLVDNFKQKRAHTLDFRPLILLGQQLQQQSSLEPALEELLQLS
ELAWTVEDTLNRVINQSLQLTPTIQSYVQLVFKFYFLKLVDNFKQKRAHTLDFRPLILLGQQLQQQSSLEPALEELLQLS
!!

160
160

logo

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consensus

HTLMAETVTGLELDYIEQDSLAEPIIQATHTEIEINLDETTLFMEEAEEHLATHQFLDQELHQYDSYNALIRALHTLR
HTLMAETVTGLELDYIEQDSLAEPIIQATHTEIEINLDETTLFMEEAEEHLATHQFLDQELHQYDSYNALIRALHTLR
HTLMAETVTGLELDYIEQDSLAEPIIQATHTEIEINLDETTLFMEEAEEHLATHQFLDQELHQYDSYNALIRALHTLR
*!!

240
240

logo

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consensus

GSSAMAQVETIFEASTKVEHLFKILLQEELSSHSEEILLQYREFVRDSLELLSRYSSSEQL EARLQFNQSWDASYVEQ
GSSAMAQVETIFEASTKVEHLFKILLQEELSSHSEEILLQYREFVRDSLELLSRYSSSEQL EARLQFNQSWDASYVEQ
GSSAMAQVETIFEASTKVEHLFKILLQEELSSHSEEILLQYREFVRDSLELLSRYSSSEQL EARLQFNQSWDASYVEQ
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320
320

logo

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HGDRTPPLMPHGLVSQLQLDVSSELLDAELDFEKGIRNEFPDYLERLSEQADLLLQHTHSQAMGLHEYTSQLKESYEV
HGDRTPPLMPHGLVSQLQLDVSSELLDAELDFEKGIRNEFPDYLERLSEQADLLLQHTHSQAMGLHEYTSQLKESYEV
HGDRTPPLMPHGLVSQLQLDVSSELLDAELDFEKGIRNEFPDYLERLSEQADLLLQHTHSQAMGLHEYTSQLKESYEV
!!

400
400

logo

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LLDKPALLQSDYIFEIYQKAHQQLQLFDALAAGQRVGVVVKQHQSI EELKLYTQYTPDISNDLPQQDSTSFEPISNIEP
LLDKPALLQSDYIFEIYQKAHQQLQLFDALAAGQRVGVVVKQHQSI EELKLYTQYTPDISNDLPQQDSTSFEPISNIEP
LLDKPALLQSDYIFEIYQKAHQQLQLFDALAAGQRVGVVVKQHQSI EELKLYTQYTPDISNDLPQQDSTSFEPISNIEP
!!

480
480

logo

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EPEWATVENFSDSADWAVLGQSVQQDRQYISSTQVNRNFDADLLDIFLEEAEEELLEGLDITDLNIWVGEQENFAALNNLM
EPEVATVENFSDSADWAVLGQSVQQDRQYISSTQVNRNFDADLLDIFLEEAEEELLEGLDITDLNIWVGEQENFAALNNLM
EPEVATVENFSDSADWAVLGQSVQQDRQYISSTQVNRNFDADLLDIFLEEAEEELLEGLDITDLNIWVGEQENFAALNNLM
!!

560
560

logo

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consensus

RYLH TLKGGANMVQATYLGLIAHELES IYERLIQKQLVATSDLIDFIRLVQDDLADRLQY MREQQLDYAAPYTINALKRA
RYLH TLKGGANMVQATYLGLIAHELES IYERLIQKQLVATSDLIDFIRLVQDDLADRLQY MREQQLDYAAPYTINALKRA
RYLH TLKGGANMVQATYLGLIAHELES IYERLIQKQLVATSDLIDFIRLVQDDLADRLQY MREQQLDYAAPYTINALKRA
!!

640
640

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consensus

GQNSNFQPLPW EAFDAESEYFSEQEVI SEI I DEI PVELEPALAELETHHDQVFD TAVTE LATPVEMITTVTSQES EYA
GQNSNFQPLPVVEAFDT ESEYFSEQEVI SEI I DEI PVELEPALAELETHHDQVFD TAVTE LATPVEMITTVTSQES EIA
GQNSNFQPLPVVEAFDAESEYFSEQEVI SEI I DEI PVELEPALAELETHHDQVFD TAVTE LATPVEMITTVTSQENEVA
!!

720
720

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consensus

AN EQDI EAWVEQTFLEEATELLEMAESLLKQWF EQRTNRS ILLQLQRAVHSLKGGARMVGL EAVQAIAYQLEN AFEQFAL
AN EQDI EAVVEQTFLEEATELLEMAESLLKQWF EQRTNRS ILLQLQRAVHSLKGGARMVGL EAVQAIAYQLEN AFEQFAL
AN EQDI EAVVEQTFLEEATELLEMAESLLKQWF EQRTNRS ILLQLQRAVHSLKGGARMVGL EAVQAIAYQLEN AFEQFAL
!!

800
800

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HHFNSNIYDHLLES AIAWLKDAIFNHNYQHFDGLQQSLENIQFFETT I QIP TKL TRADLFSSEPVM TFIQGDGTEPPPM
HHFNSNIYDHLLES AIAWLKDAIFNHNYQHFDGLQQSLENIQFFETT I QIP TKL TRADLFSSEPVM TFIQGDGTEPPPM
HHFNSNIYDHLLES AIAWLKDAIFNHNYQHFDGLQQSLENIQFFETT I QIP TKL TRADLFSSEPVM TFIQGDGTEPPPM
!!

880
880

logo

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GAWEQTERLDQNNEMIRVSADLIEKMIDLSGENSINRSRIEMDLSQFSHTLVEMELAIQRLADQLRRMEGELETQIIAKH
GAWEQTERLDQNNEMIRVSADLIEKMIDLSGENSINRSRIEMDLSQFSHTLVEMELAIQRLADQLRRMEGELETQIIAKH
GAWEQTERLDQNNEMIRVSADLIEKMIDLSGENSINRSRIEMDLSQFSHTLVEMELAIQRLADQLRRMEGELETQIIAKH
!!

960
960

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GIEHSRYTDFDPLEMDQYSSLNQLSKSLAESASDLVDFKNTLSDKIRD TESLLLQQSRIQAEIQEGLMRTRLV PFSRLLP
GIEHSRYTDFDPLEMDQYSSLNQLSKSLAESASDLVDFKNTLSDKIRD TESLLLQQSRIQAEIQEGLMRTRLV PFSRLLP
GIEHSRYTDFDPLEMDQYSSLNQLSKSLAESASDLVDFKNTLSDKIRD TESLLLQQSRIQAEIQEGLMRTRLV PFSRLLP
!!

1040
1040

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RLQRIVRQTSTALNRP AELFVNNT EGELDRN ILERLVTPL EHLRVAIDHGLEDRAQRQQANKPETGR IELNIQRQGT DV
RLQRIVRQTSTALNRP AELFVNNT EGELDRN ILERLVTPL EHLRVAIDHGLEDRAQRQQANKPETGR IELNIQRQGT DV
RLQRIVRQTSTALNRP AELFVNNT EGELDRN ILERLVTPL EHLRVAIDHGLEDRAQRQQANKPETGR IELNIQRQGT DV
!!

1120
1120

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1200
1200

logo

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consensus



1280
1280

logo

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consensus



1360
1360

logo

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consensus



1440
1440

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consensus



1506
1506

non conserved
 similar
 ≥ 50% conserved