

logo

NTDB id 185123 AS012 RS01970 WP 012503449.1
NTDB id 1132 OK783 RS01905 WP 010951035.1
consensus

MSAP|RAFDPLTAPI|SGTNL|EASAGTGKTYG|AALFTRL|IVLEQKSVERVLV|VFTKAATAELKTRLR|ARLDDVLQVLE
MSAPIRAFDPLTAPISGTNLEASAGTGKTYGIAALFTRLIVLEQKSVERVLVVTFTKAATAELKTRLRRLRLLDDVLQVLE
MSAPIRAFDPLTAPISGTNLEASAGTGKTYGIAALFTRLIVLEQKSVERVLVVTFTKAATAELKTRLRRLRLLDDVLQVLE
!!

80
80

logo

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consensus

SKEIAELGDDT|LSDG|AAYCAEHHEGDT|FLPALLEQALQKESRTRL|IVRLKAAIGQFDNAAIYTIHGFCQRI|LRDYAFLC
SKEIAELGDDT|LSDG|AAYCAEHHEGDT|FLPALLEQALQKESRTRL|IVRLKAAIGQFDNAAIYTIHGFCQRI|LRDYAFLC
SKEIAELGDDT|LSDG|AAYCAEHHEGDT|FLPALLEQALQKESRTRL|IVRLKAAIGQFDNAAIYTIHGFCQRI|LRDYAFLC
!!

160
160

logo

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consensus

QAPFDVELTEEDG|DRLLVPAQDF|WRERVS|GDPVLAALAFK|RKAVPQTVL|AQIRAYLSR|PYNFRFPQADL|KQAQRDAETS
QAPFDVELTEEDGDRLLVPAQDFWRERVS|GDPVLAALAFK|RKAVPQTVL|AQIRAYLSR|PYNFRFPQADL|KQAQRDAETS
QAPFDVELTEEDGDRLLVPAQDFWRERVS|GDPVLAALAFK|RKAVPQTVL|AQIRAYLSR|PYNFRFPQADL|KQAQRDAETS
!!

240
240

logo

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consensus

WQTVCRLLPELEAG|FWR|HPDL|NGNSYRKNS|FGNLFKELAQKSAAG|QLPEL|DKD|THERLLKLSSDKLEAGL|KKGKTPDAA
WQTVCRLLPELEAGFWR|HPDL|NGNSYRKNS|FGNLFKELAQKSAAG|QLPEL|DKD|THERLLKLSSDKLEAGL|KKGKTPDAA
WQTVCRLLPELEAGFWR|HPDL|NGNSYRKNS|FGNLFKELAQKSAAG|QLPEL|DKD|THERLLKLSSDKLEAGL|KKGKTPDAA
!!

320
320

logo

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VFAELQKLAD|FGRDLN|ALEEAEETM|IRLQLD|LIEYLNSS|LAEMKKSRRRER|GFDDLLLDVHTAL|TDNPHAETPARAVAEN
VFAELQKLAD|FGRDLN|ALEEAEETM|IRLQLD|LIEYLNSS|LAEMKKSRRRER|GFDDLLLDVHTAL|TDNPHAETPARAVAEN
VFAELQKLAD|FGRDLN|ALEEAEETM|IRLQLD|LIEYLNSS|LAEMKKSRRRER|GFDDLLLDVHTAL|TDNPHAETPARAVAEN
!!

400
400

logo

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WEIALID|EFQD|TDPLQYE|IFQK|FIARNR|PFLV|GDPKQAIYS|FRGADIYAYL|QAAEDARHRYT|LATNYRSHAAL|IGSIG
WEIALID|EFQD|TDPLQYE|IFQK|FIARNR|PFLV|GDPKQAIYS|FRGADIYAYL|QAAEDARHRYT|LATNYRSHAAL|IGSIG
WEIALID|EFQD|TDPLQYE|IFQK|FIARNR|PFLV|GDPKQAIYS|FRGADIYAYL|QAAEDARHRYT|LATNYRSHAAL|IGSIG
!!

480
480

logo

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ALFRLK|ERP|VLENI|GYSEVGAARA|ESRLSPKRP|AVQLR|WLHENDNEK|KANKDVLRRRAADY|CADEIARALNEASG|GRLNF
ALFRLK|ERP|VLENI|GYSEVGAARA|ESRLSPKRP|AVQLR|WLHENDNEK|KANKDVLRRRAADY|CADEIARALNEASG|GRLNF
ALFRLK|ERP|VLENI|GYSEVGAARA|ESRLSPKRP|AVQLR|WLHENDNEK|KANKDVLRRRAADY|CADEIARALNEASG|GRLNF
!!

560
560

logo

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KGRPLQSGDI AVLVRTHNEAVMISAALKKRQVQSVLLSRESVFASPEAAALSALIGFWLEPRRAGTLRFVLTSGIFGYDA
KGRPLQSGDI AVLVRTHNEAVMISAALKKRQVQSVLLSRESVFASPEAAALSALIGFWLEPRRAGTLRFVLTSGIFGYDA
KDRPLQSGDI AVLVRTHNEAVMISAALKKRQVQSVLLSRESVFASPEAAALSALIGFWLEPRRAGTLRFVLTSGIFGYDA
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640
640

logo

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consensus

QQLHDFNQNESEILHWAESARTALDIWQKYGIFAAMQQFSQTHGIETRLLSRNNGRSLTNYFQLLELLAAEDAQNRNPAA
QQLHDFNQNESEILHWAESARTALDIWQKYGIFAAMQQFSQTHGIETRLLSRNNGRSLTNYFQLLELLAAEDAQNRNPAA
QQLHDFNQNESEILHWAESARTALDIWQKYGIFAAMQQFSQTHGIETRLLSRNNGRSLTNYFQLLELLAAEDAQNRNPAA
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720
720

logo

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consensus

LHKWLRDQISLAGNNGGDNRAIRLESDDELVKIVTMHASKGLQYPLVYCPFAWDAQDTGPSDWQILHQQANRAELLAKAQ
LHKWLRDQISLAGNNGGDNRAIRLESDDELVKIVTMHASKGLQYPLVYCPFAWDAQDTGPSDWQILHQQANRAELLAKAQ
LHKWLRDQISLAGNNGGDNRAIRLESDDELVKIVTMHASKGLQYPLVYCPFAWDAQDTGPSDWQILHQQANRAELLAKAQ
!!

800
800

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LSESEKQYADEEMAERLRLLYVALTRAEELNIYAAYSSDTADNPLAYLIEGLPQDSRETVRRTYACEKDGITMLKRNW
LSESEKQYADEEMAERLRLLYVALTRAEELNIYAAYSSDTADNPLAYLIEGLPQDSRETVRRTYACEKDGITMLKRNW
LSESEKQYADEEMAERLRLLYVALTRAEELNIYAAYSSDTADNPLAYLIEGLPQDSRETVRRTYACEKDGITMLKRNW
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880
880

logo

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consensus

RRVADNAPAGTDF_AFTEDAPPPAAYRGNADQAAEFAANSIPERGFVRHTSFTALSR_QTQTPDGGEEDACPSLDAAETS
RRVADNAPAGTDF_AFTEDAPPPAAYRGNADQAAEFAANSIPERGFVRHTSFTALSR_QTQTPDGGEEDACPSLDAAETS
RRVADNAPAGTDF_TFTEDAPPPAAYRGNADQAAEFAANSIPERGFVRHTSFTALSR_HTQTPDGGEEDACPSLDAAETS
!!

960
960

logo

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consensus

VPAMPSETPTASDGI_SIHDFPKGTQAGLCLHEILEDFKFGQAAAEQETLIADKLKKGFFEEIWLPAVAEMAEACRKTPLT
VPAMPSETPTASDGI_SIHDFPKGTQAGLCLHEILEDFKFGQAAAEQETLIADKLKKGFFEEIWLPAVAEMAEACRKTPLT
VPAMPSETPTASDGI_SIHDFPKGTQAGLCLHEILEDFKFGQAAAEQETLIADKLKKGFFEEIWLPAVAEMAEACRKTPLT
!!

1040
1040

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consensus

GAYGLSDIPPGCRRPEMGFTLHTEDFGLKRLRDWLARDDIRLPEVCRAAAETLDFHTVNGFLNGFIDMVCQDPDGNICII
GAYGLSDIPPGCRRPEMGFTLHTEDFGLKRLRDWLARDDIRLPEVCRAAAETLDFHTVNGFLNGFIDMVCQDPDGNICII
GAYGLSDIPPGCRRPEMGFTLHTEDFGLKRLRDWLARDDIRLPEVCRAAAETLDFHTVNGFLNGFIDMVCQDPDGNICII
!!

1120
1120

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consensus



1200
1200

- non conserved
- similar
- ≥ 50% conserved