

logo

NTDB id 328378 EGH17 RS02625 WP 047923872.1
NTDB id 1132 OK783 RS01905 WP 010951035.1
consensus

MSAP|RAFDPLTAP|ISGTN|IEASAGTGKTYG|AALFTRL|IVLEQKSVERVLV|VFTKAATAELKTR|LRARLDDVLQVLE
MSAPIRAFDPLTAPISGTN|IEASAGTGKTYG|AALFTRL|IVLEQKSVERVLV|VFTKAATAELKTR|LRARLDDVLQVLE
!!

80
80

logo

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consensus

SKE|AELGDDT|LSDG|AAYCAEH|HEGDTFL|PALLEQALQKESRTR|LIVRLKAA|GQFDNAA|YTIHGFCQR|LRDYAFLC
SKEIAELGDDT|LSDG|AAYCAEH|HEGDTFL|PALLEQALQKESRTR|LIVRLKAA|GQFDNAA|YTIHGFCQR|LRDYAFLC
SKEIAELGDDT|LSDG|AAYCAEH|HEGDTFL|PALLEQALQKESRTR|LIVRLKAA|GQFDNAA|YTIHGFCQR|LRDYAFLC
!!

160
160

logo

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consensus

QAPFDV|ELTEEDG|DRLLVPAQDF|WRERVS|GDPVLAALAF|KRVKAVPQTVL|AQIRAYLSR|PYNFRFPQADL|KQAQRDAETS
QAPFDV|ELTEEDG|DRLLVPAQDF|WRERVS|GDPVLAALAF|KRVKAVPQTVL|AQIRAYLSR|PYNFRFPQADL|KQAQRDAETS
QAPFDV|ELTEEDG|DRLLVPAQDF|WRERVS|GDPVLAALAF|KRVKAVPQTVL|AQIRAYLSR|PYNFRFPQADL|KQAQRDAETS
!!

240
240

logo

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consensus

WQTVCR|LLPELEAG|FWR|HPDLN|GNSYRKNS|FGNLFKELAQK|SAAGQLPEL|DKD|THERLLKL|SSDKLEAGL|KKGKTPDAA
WQTVCR|LLPELEAG|FWR|HPDLN|GNSYRKNS|FGNLFKELAQK|SAAGQLPEL|DKD|THERLLKL|SSDKLEAGL|KKGKTPDAA
WQTVCR|LLPELEAG|FWR|HPDLN|GNSYRKNS|FGNLFKELAQK|SAAGQLPEL|DKD|THERLLKL|SSDKLEAGL|KKGKTPDAA
!!

320
320

logo

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VFAELQK|LADFRDLN|ALEEA|EETMIRL|QLDLIEYLN|SSLAEMK|KSRERGFDD|LLLDVHTAL|TDNPHAET|PARAVAEN
VFAELQK|LADFRDLN|ALEEA|EETMIRL|QLDLIEYLN|SSLAEMK|KSRERGFDD|LLLDVHTAL|TDNPHAET|PARAVAEN
VFAELQK|LADFRDLN|ALEEA|EETMIRL|QLDLIEYLN|SSLAEMK|KSRERGFDD|LLLDVHTAL|TDNPHAET|PARAVAEN
!!

400
400

logo

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consensus

WEIALI|DEFQD|TDPLQYE|IFQKIFI|ARNRPL|FLVGD|PKQAIYS|FRGADIYAYL|QAAEDAR|HRYTLATN|YRSHAAL|IGSIG
WEIALI|DEFQD|TDPLQYE|IFQKIFI|ARNRPL|FLVGD|PKQAIYS|FRGADIYAYL|QAAEDAR|HRYTLATN|YRSHAAL|IGSIG
WEIALI|DEFQD|TDPLQYE|IFQKIFI|ARNRPL|FLVGD|PKQAIYS|FRGADIYAYL|QAAEDAR|HRYTLATN|YRSHAAL|IGSIG
!!

480
480

logo

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consensus

ALFRLK|ERP|VLENI|GYSEV|GAARAE|SRLSPKRP|AVQLR|WLHEND|NEKANKD|VLRRAADY|CADEIARAL|NEASGGRLNF
ALFRLK|ERP|VLENI|GYSEV|GAARAE|SRLSPKRP|AVQLR|WLHEND|NEKANKD|VLRRAADY|CADEIARAL|NEASGGRLNF
ALFRLK|ERP|VLENI|GYSEV|GAARAE|SRLSPKRP|AVQLR|WLHEND|NEKANKD|VLRRAADY|CADEIARAL|NEASGGRLNF
!!

560
560

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KGRPLQSGDIAVLVRTHNEAVMISAALKKRQVQSVLLSRESVFASPEAAALSALIGFWLEPRRAGTLRFVLTSGIFGYDA
KGRPLQSGDIAVLVRTHNEAVMISAALKKRQVQSVLLSRESVFASPEAAALSALIGFWLEPRRAGTLRFVLTSGIFGYDA
KDRPLQSGDIAVLVRTHNEAVMISAALKKRQVQSVLLSRESVFASPEAAALSALIGFWLEPRRAGTLRFVLTSGIFGYDA
!!

640
640

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consensus

QQLHDFNQNESEILHWAESARTALDIWQKYGIFAAMQQFSQTHGIETRLLSRNNGRSLTNYFQLLELLAAEDAQNRNPAA
QQLHDFNQNESEILHWAESARTALDIWQKYGIFAAMQQFSQTHGIETRLLSRNNGRSLTNYFQLLELLAAEDAQNRNPAA
QQLHDFNQNESEILHWAESARTALDIWQKYGIFAAMQQFSQTHGIETRLLSRNNGRSLTNYFQLLELLAAEDAQNRNPAA
!!

720
720

logo

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LHKWLRDQISLAGNNGGDNRAIRLESDDELVKIVTMHASKGLQYPLVYCPFAWDAQDTGPSDWQILHQQANRAELLAKAQ
LHKWLRDQISLAGNNGGDNRAIRLESDDELVKIVTMHASKGLQYPLVYCPFAWDAQDTGPSDWQILHQQANRAELLAKAQ
LHKWLRDQISLAGNNGGDNRAIRLESDDELVKIVTMHASKGLQYPLVYCPFAWDAQDTGPSDWQILHQQANRAELLAKAQ
!!

800
800

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LSESEKQYADEEMAERLRLLYVALTRAEELNIYAAYSSDTADNPLAYLIEGLPQDSRETVRRTYACEKDGITMLKRNW
LSESEKQYADEEMAERLRLLYVALTRAEELNIYAAYSSDTADNPLAYLIEGLPQDSRETVRRTYACEKDGITMLKRNW
LSESEKQYADEEMAERLRLLYVALTRAEELNIYAAYSSDTADNPLAYLIEGLPQDSRETVRRTYACEKDGITMLKRNW
!!

880
880

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RRVADNAPAGTDF_AFTEDAPPPAAYRGNADQAAEFAANSIPERGFVRHTSFTALSRHTQTPDGGEEDACPSLDAAETS
RRVADNAPAGTDF_AFTEDAPPPAAYRGNADQAAEFAANSIPERGFVRHTSFTALSRHTQTPDGGEEDACPSLDAAETS
RRVADNAPAGTDF_TFTEDAPPPAAYRGNADQAAEFAANSIPERGFVRHTSFTALSRHTQTPDGGEEDACPSLDAAETS
!!

960
960

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VPAMPSETPTASDGI_SIHDFPKGTQAGLCLHEILEDFKFGQAAAEQETLIADKLKKGFFEEIWLPAVAEMAEACRKTPLT
VPAMPSETPTASDGI_SIHDFPKGTQAGLCLHEILEDFKFGQAAAEQETLIADKLKKGFFEEIWLPAVAEMAEACRKTPLT
VPAMPSETPTASDGI_SIHDFPKGTQAGLCLHEILEDFKFGQAAAEQETLIADKLKKGFFEEIWLPAVAEMAEACRKTPLT
!!

1040
1040

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GAYGLSDIPPGCRRPEMGFTLHTEDFGLKRLRDWLARDDIRLPEVCRAAAETLDFHTVNGFLNGFIDMVCQDPDGNICII
GAYGLSDIPPGCRRPEMGFTLHTEDFGLKRLRDWLARDDIRLPEVCRAAAETLDFHTVNGFLNGFIDMVCQDPDGNICII
GAYGLSDIPPGCRRPEMGFTLHTEDFGLKRLRDWLARDDIRLPEVCRAAAETLDFHTVNGFLNGFIDMVCQDPDGNICII
!!

1120
1120

logo

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DYKSNHLSAYTRQAMDEAVAHQHYYLQALYAVAAARYFKLRGQPPAAVSVRYLFLRGLDGKGGGVWRWDIDAAALEQIK
DYKSNHLSAYTRQAMDEAVAHQHYYLQALYAVAAARYFKLRGQPPAAVSVRYLFLRGLDGKGGGVWRWDIDAAALEQIK
!!

1200
1200

- non conserved
- similar
- ≥ 50% conserved