

logo

NTDB id 150531 VT05 RS00570 WP 003692769.1
NTDB id 1132 OK783 RS01905 WP 010951035.1
consensus

MSAPIRAFDPLTAPISGTNLEASAGTGKTYGIAALFTRLIVLEQKSVERVLVVTFTKAATAELKTRLRRLDDVLQVLESKEIA
MSAPIRAFDPLTAPISGTNLEASAGTGKTYGIAALFTRLIVLEQKSVERVLVVTFTKAATAELKTRLRRLDDVLQVLESKEIA
MSAPIRAFDPLTAPISGTNLEASAGTGKTYGIAALFTRLIVLEQKSVERVLVVTFTKAATAELKTRLRRLDDVLQVLESKEIA
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85
85

logo

NTDB id 150531 VT05 RS00570 WP 003692769.1
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consensus

ELGDDTSLSDGIAAYCAEHHEGDTFLPALLEQALQKESRTRLIVRLKAAIGQFDNAAIYTIHGFCQRILRDYAFLLCQAPFDVELTE
ELGDDTSLSDGIAAYCAEHHEGDTFLPALLEQALQKESRTRLIVRLKAAIGQFDNAAIYTIHGFCQRILRDYAFLLCQAPFDVELTE
ELGDDTSLSDGIAAYCAEHHEGDTFLPALLEQALQKESRTRLIVRLKAAIGQFDNAAIYTIHGFCQRILRDYAFLLCQAPFDVELTE
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170
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logo

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consensus

EDGDRLLVPAQDFWRERVSGDPVLAALAFKRKAVPQTVLAQIRAYLSRPYLNFRPPQADLKQAQRDAETSWQTVCRLLPELEAGF
EDGDRLLVPAQDFWRERVSGDPVLAALAFKRKAVPQTVLAQIRAYLSRPYLNFRPPQADLKQAQRDAETSWQTVCRLLPELEAGF
EDGDRLLVPAQDFWRERVSGDPVLAALAFKRKAVPQTVLAQIRAYLSRPYLNFRPPQADLKQAQRDAETSWQTVCRLLPELEAGF
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logo

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WRIHDPDLNGNSYRKNSFGNLFKELAQKSAAGQLPCLDKDITHERLLKLSSDKLEAGLKKGKTPDAAVFAELQKLADFGRDNLNALEE
WRIHDPDLNGNSYRKNSFGNLFKELAQKSAAGQLPCLDKDITHERLLKLSSDKLEAGLKKGKTPDAAVFAELQKLADFGRDNLNALEE
WRIHDPDLNGNSYRKNSFGNLFKELAQKSAAGQLPCLDKDITHERLLKLSSDKLEAGLKKGKTPDAAVFAELQKLADFGRDNLNALEE
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logo

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AEETTMIRLQLDLIEYLNSSLAEMKKSRRERGFDDLLLDVHTALTDNPHAETPARAVAENWEIALIDEFQDTPDPLQYEIFQKIFI
AEETTMIRLQLDLIEYLNSSLAEMKKSRRERGFDDLLLDVHTALTDNPHAETPARAVAENWEIALIDEFQDTPDPLQYEIFQKIFI
AEETTMIRLQLDLIEYLNSSLAEMKKSRRERGFDDLLLDVHTALTDNPHAETPARAVAENWEIALIDEFQDTPDPLQYEIFQKIFI
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logo

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consensus

ARNRPLFLVGDPKQAIYSFRGADIYAYLQAAEDARHRYTLATNYRSHAALIGSIGALFRLKERPFVLENIYGYSEVGAARAESRLS
ARNRPLFLVGDPKQAIYSFRGADIYAYLQAAEDARHRYTLATNYRSHAALIGSIGALFRLKERPFVLENIYGYSEVGAARAESRLS
ARNRPLFLVGDPKQAIYSFRGADIYAYLQAAEDARHRYTLATNYRSHAALIGSIGALFRLKERPFVLENIYGYSEVGAARAESRLS
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logo

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consensus

PKRPAVQLRWLHENDNEKANKDVLRRRAADYCADEIARALNEASGGRLNFKGRPLQSGDIAVLVRTHNEAVMISAALKKRQVQSV
PKRPAVQLRWLHENDNEKANKDVLRRRAADYCADEIARALNEASGGRLNFKGRPLQSGDIAVLVRTHNEAVMISAALKKRQVQSV
PKRPAVQLRWLHENDNEKANKDVLRRRAADYCADEIARALNEASGGRLNFKGRPLQSGDIAVLVRTHNEAVMISAALKKRQVQSV
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consensus

LLSRESVFASPEAAALSALIGFWLEPRRAGTLRFVLTSGIFGYDAQQLHDFNQNESEILHWAESARTALDIWQKYGIFAAMQQFS
LLSRESVFASPEAAALSALIGFWLEPRRAGTLRFVLTSGIFGYDAQQLHDFNQNESEILHWAESARTALDIWQKYGIFAAMQQFS
LLSRESVFASPEAAALSALIGFWLEPRRAGTLRFVLTSGIFGYDAQQLHDFNQNESEILHWAESARTALDIWQKYGIFAAMQQFS
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680
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logo

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consensus

QTHGIETRLLSRNNGRSLTNYFQLLELLAAEDAQNRNPAALHKWLRDQISLAGNNGDNRAIRLESDEDLVKIVTMHASKGLQYP
QTHGIETRLLSRNNGRSLTNYFQLLELLAAEDAQNRNPAALHKWLRDQISLAGNNGDNRAIRLESDEDLVKIVTMHASKGLQYP
QTHGIETRLLSRNNGRSLTNYFQLLELLAAEDAQNRNPAALHKWLRDQISLAGNNGDNRAIRLESDEDLVKIVTMHASKGLQYP
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765
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logo

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consensus

LVYCPFAWDAQDTGPSDWQILHQQANRAELLAKAQLSESEKQYADEEMAERLRLLYVALTRAEEQLNIYAAYSSDTADNPLAYL
LVYCPFAWDAQDTGPSDWQILHQQANRAELLAKAQLSESEKQYADEEMAERLRLLYVALTRAEEQLNIYAAYSSDTADNPLAYL
LVYCPFAWDAQDTGPSDWQILHQQANRAELLAKAQLSESEKQYADEEMAERLRLLYVALTRAEEQLNIYAAYSSDTADNPLAYL
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850
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logo

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consensus

IEGLPQDSRETVRRTYACEKDGITMLKRNWRRVADNAPAGTDF_AFTEDAPPPAAYRGNADQAAEFAANSIPERGFRFVRHTSFTA
IEGLPQDSRETVRRTYACEKDGITMLKRNWRRVADNAPAGTDF_AFTEDAPPPAAYRGNADQAAEFAANSIPERGFRFVRHTSFTA
IEGLPQDSRETVRRTYACEKDGITMLKRNWRRVADNAPAGTDF_TFTEDAPPPAAYRGNADQAAEFAANSIPERGFRFVRHTSFTA
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935
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logo

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consensus

LSRHTQTPDGGEEDACPSLDAAETSVAMPSETPTASDGISIHDFPKGTQAGLCLHEILEDFKFGQAAAEQETLIADKLKKGFE
LSRHTQTPDGGEEDACPSLDAAETSVAMPSETPTASDGISIHDFPKGTQAGLCLHEILEDFKFGQAAAEQETLIADKLKKGFE
LSRHTQTPDGGEEDACPSLDAAETSVAMPSETPTASDGISIHDFPKGTQAGLCLHEILEDFKFGQAAAEQETLIADKLKKGFE
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1020
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logo

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EIWLPAVAEMAEACRKTPLTGAYGLSDIPPGCRRPEMGFTLHTEDFGLKRLRDWLRDDIRLPEVCRAAAE_TDFHTVNGFLNGF
EIWLPAVAEMAEACRKTPLTGAYGLSDIPPGCRRPEMGFTLHTEDFGLKRLRDWLRDDIRLPEVCRAAAE_TDFHTVNGFLNGF
EIWLPAVAEMAEACRKTPLTGAYGLSDIPPGCRRPEMGFTLHTEDFGLKRLRDWLRDDIRLPEVCRAAAE_LDFHTVNGFLNGF
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1105
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logo

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IDMVCQDPDGNICIIDYKSNHLSAYTRQAMDEAVAHQHYYLQALYAVAAARYFKLRGQPPAAVSVRYLFLRGLDGKGGGVWRWD
IDMVCQDPDGNICIIDYKSNHLSAYTRQAMDEAVAHQHYYLQALYAVAAARYFKLRGQPPAAVSVRYLFLRGLDGKGGGVWRWD
IDMVCQDPDGNICIIDYKSNHLSAYTRQAMDEAVAHQHYYLQALYAVAAARYFKLRGQPPAAVSVRYLFLRGLDGKGGGVWRWD
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1190
1190

logo

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consensus



1200
1200

- X non conserved
- X similar
- X $\geq 50\%$ conserved