

logo

NTDB id 31217 NGK RS02305 WP 012503449.1
NTDB id 1132 OK783 RS01905 WP 010951035.1
consensus



85
85

logo

NTDB id 31217 NGK RS02305 WP 012503449.1
NTDB id 1132 OK783 RS01905 WP 010951035.1
consensus



170
170

logo

NTDB id 31217 NGK RS02305 WP 012503449.1
NTDB id 1132 OK783 RS01905 WP 010951035.1
consensus



255
255

logo

NTDB id 31217 NGK RS02305 WP 012503449.1
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consensus



340
340

logo

NTDB id 31217 NGK RS02305 WP 012503449.1
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consensus



425
425

logo

NTDB id 31217 NGK RS02305 WP 012503449.1
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consensus



510
510

logo

NTDB id 31217 NGK RS02305 WP 012503449.1
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consensus



595
595

logo

NTDB id 31217 NGK RS02305 WP 012503449.1
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consensus

LLSRESVFASPEAAALSALIGFWLEPRRAGTLRFVLTSGIFGYDAQQLHDFNQNESEILHWAESARTALDIWQKYGIFAAMQQFS
LLSRESVFASPEAAALSALIGFWLEPRRAGTLRFVLTSGIFGYDAQQLHDFNQNESEILHWAESARTALDIWQKYGIFAAMQQFS
!!

680
680

logo

NTDB id 31217 NGK RS02305 WP 012503449.1
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consensus

QTHGIETRLLSRNGRSLTNYFQLELLAEDAQNRNPAALHKWLRDQISLAGNNGDNRAIRLESDEDLVKIVTMHASKGLQYP
QTHGIETRLLSRNGRSLTNYFQLELLAEDAQNRNPAALHKWLRDQISLAGNNGDNRAIRLESDEDLVKIVTMHASKGLQYP
QTHGIETRLLSRNGRSLTNYFQLELLAEDAQNRNPAALHKWLRDQISLAGNNGDNRAIRLESDEDLVKIVTMHASKGLQYP
!!

765
765

logo

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LVYCPFAWDAQDTGPSDWQILHQGANRAELLAKAQLSESEQKQYADEEMAERLRLLYVALTRAEEQLNIYAAYSSDTADNPLAYL
LVYCPFAWDAQDTGPSDWQILHQGANRAELLAKAQLSESEQKQYADEEMAERLRLLYVALTRAEEQLNIYAAYSSDTADNPLAYL
LVYCPFAWDAQDTGPSDWQILHQGANRAELLAKAQLSESEQKQYADEEMAERLRLLYVALTRAEEQLNIYAAYSSDTADNPLAYL
!!

850
850

logo

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IEGLPQDSRETVRRTYACEKDGITMLKRNWRRVADNAPAGTDFAFTEDAPPPAAYRGNADQAEFAANSIPERGFRFVRHTSFTA
IEGLPQDSRETVRRTYACEKDGITMLKRNWRRVADNAPAGTDFAFTEDAPPPAAYRGNADQAEFAANSIPERGFRFVRHTSFTA
IEGLPQDSRETVRRTYACEKDGITMLKRNWRRVADNAPAGTDFAFTEDAPPPAAYRGNADQAEFAANSIPERGFRFVRHTSFTA
!!

935
935

logo

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LSRHTQTPDGGEEDACPSLDAAETSVPAMPSETPTASDGISIHDFPKGTQAGLCLHEILEDFKFGQAAEQETLIADKLKKYGFE
LSRHTQTPDGGEEDACPSLDAAETSVPAMPSETPTASDGISIHDFPKGTQAGLCLHEILEDFKFGQAAEQETLIADKLKKYGFE
LSRHTQTPDGGEEDACPSLDAAETSVPAMPSETPTASDGISIHDFPKGTQAGLCLHEILEDFKFGQAAEQETLIADKLKKYGFE
!!

1020
1020

logo

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EIWLPAVAEMAEACRKTPLTGAYGLSDIPPGCRRPEMGFTLHTEDFGLKRLRDWLARDDIRLPEVCRAAAETLDFHTVNGFLNGF
EIWLPAVAEMAEACRKTPLTGAYGLSDIPPGCRRPEMGFTLHTEDFGLKRLRDWLARDDIRLPEVCRAAAETLDFHTVNGFLNGF
EIWLPAVAEMAEACRKTPLTGAYGLSDIPPGCRRPEMGFTLHTEDFGLKRLRDWLARDDIRLPEVCRAAAETLDFHTVNGFLNGF
!!

1105
1105

logo

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consensus

IDMVCQDPDGNICIIDYKSNHLSAYTRQAMDEAVAHQHYYLQALIYAVAAARYFKLRGQPPAAVSVRYLFLRGLDGKGGGVWRWD
IDMVCQDPDGNICIIDYKSNHLSAYTRQAMDEAVAHQHYYLQALIYAVAAARYFKLRGQPPAAVSVRYLFLRGLDGKGGGVWRWD
IDMVCQDPDGNICIIDYKSNHLSAYTRQAMDEAVAHQHYYLQALIYAVAAARYFKLRGQPPAAVSVRYLFLRGLDGKGGGVWRWD
!!

1190
1190

logo

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consensus



1200
1200

- non conserved
- similar
- ≥ 50% conserved