

logo

NTDB id 294107 DL538 RS06140 WP 131227293.1
NTDB id 120 BSU 10620 NP 388943.2
consensus



80
80

logo

NTDB id 294107 DL538 RS06140 WP 131227293.1
NTDB id 120 BSU 10620 NP 388943.2
consensus



160
160

logo

NTDB id 294107 DL538 RS06140 WP 131227293.1
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consensus



240
240

logo

NTDB id 294107 DL538 RS06140 WP 131227293.1
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consensus



320
320

logo

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400
400

logo

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480
480

logo

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560
560

logo

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consensus

SLDLFQQMIEAGAESLTFSLIPPALDQVFGNMDLSRMYGTSCTFVLGANDGVLPARPDENGVLSDDDREWLKTI GVELS
SLDLFQQMIEAGAESLTFSLIPPALDQVFGNMDLSRMYGTSCTFVLGANDGVLPARPDENGVLSDDDREWLKTI GVELS
!!

640
640

logo

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consensus

SGGRERLLDEHFLIYMAFSSPSDRLVSYPIADAEGKTL LPSMIVKRLEELFPHHKERLLTNEPEQVSDEEQLMYVVKNS
SGGRERLLDEHFLIYMAFSSPSDRLVSYPIADAEGKTL LPSMIVKRLEELFPHHKERLLTNEPEQVSDEEQLMYVVKNS
SGGRERLLDEHFLIYMAFSSPSDRLVSYPIADAEGKTL LPSMIVKRLEELFPHHKERLLTNEPEQVSDEEQLMYVVKNS
!!!!!!!!!!!!!!!!*!!

720
720

logo

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VAQSFTASQLRLWTREYDISDVVWSTYNVLMSEQDRLQSKKLFSSLFFRNEVKQLERSVSRQLYGERIQGSVSRMETFNA
VAQSFTASQLRLWTREYDISDVVWSTYNVLMSEQDRLQSKKLFSSLFFRNEVKQLERSVSRQLYGERIQGSVSRMETFNA
VAQSFTASQLRLWTREYDISDVVWSTYNVLMSEQDRLQSKKLFSSLFFRNEVKQLERSVSRQLYGERIQGSVSRMETFNA
!!

800
800

logo

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CPFSHFASHGLHLKERQFFKLEAPDIGQLFHSSLKLISDRLREQKLDWRDLTKEQCELFSDAVERLAPKLQKEILLSSN
CPFSHFASHGLHLKERQFFKLEAPDIGQLFHSSLKLISDRLREQKLDWRDLTKEQCELFSDAVERLAPKLQKEILLSSN
CPFSHFASHGLHLKERQFFKLEAPDIGQLFHSSLKLISDRLREQKLDWRDLTKEQCELFSDAVERLAPKLQKEILLSSN
!!

880
880

logo

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RHYVKEKLVKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGCTMELVGRIDRVDKAESSKGLLLRIV
RHYVKEKLVKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGCTMELVGRIDRVDKAESSKGLLLRIV
RHYVKEKLVKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGCTMELVGRIDRVDKAESSKGLLLRIV
!!*

960
960

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DYKSSDKGLDLAEVYGLALQMLTYLDSLITHSADWLGMRATPAGVLYFHIHDPMIQSNLPLGLDEIEQEIFKKFKMKGL
DYKSSDKGLDLAEVYGLALQMLTYLDSLITHSADWLGMRATPAGVLYFHIHDPMIQSNLPLGLDEIEQEIFKKFKMKGL
DYKSSDKGLDLAEVYGLALQMLTYLDSLITHSADWLGMRATPAGVLYFHIHDPMIQSNLPLGLDEIEQEIFKKFKMKGL
!!

1040
1040

logo

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LLGDQEVRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITDGRVSI EPYKMKNKTP
LLGDQEVRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITDGRVSI EPYKMKNKTP
LLGDQEVRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITDGRVSI EPYKMKNKTP
!!

1120
1120

