

logo

NTDB id 195212 BGM23 RS16340 WP 003233101.1
NTDB id 120 BSU 10620 NP 388943.2
consensus



80
80

logo

NTDB id 195212 BGM23 RS16340 WP 003233101.1
NTDB id 120 BSU 10620 NP 388943.2
consensus



160
160

logo

NTDB id 195212 BGM23 RS16340 WP 003233101.1
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consensus



240
240

logo

NTDB id 195212 BGM23 RS16340 WP 003233101.1
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320
320

logo

NTDB id 195212 BGM23 RS16340 WP 003233101.1
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400
400

logo

NTDB id 195212 BGM23 RS16340 WP 003233101.1
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480
480

logo

NTDB id 195212 BGM23 RS16340 WP 003233101.1
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560
560

logo

NTDB id 195212 BGM23 RS16340 WP 003233101.1
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consensus

SLDLFQQMIEAGAESLTFSLIPPALDQVFVGNMDSLRYMGTSCTFVLGANDGVLPARPDENGVLSDDDREWLKTI GVELS
SLDLFQQMIEAGAESLTFSLIPPALDQVFVGNMDSLRYMGTSCTFVLGANDGVLPARPDENGVLSDDDREWLKTI GVELS
!!

640
640

logo

NTDB id 195212 BGM23 RS16340 WP 003233101.1
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consensus

SGGRERLLDEHFLIYMAFSSPSDRLYVSYPIADAEGKTL LPSMIVKRLEELFPHHKERLLTNEPEQVSDEEQLMYVVKNS
SGGRERLLDEHFLIYMAFSSPSDRLYVSYPIADAEGKTL LPSMIVKRLEELFPHHKERLLTNEPEQVSDEEQLMYVVKNS
!!

720
720

logo

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consensus

VAQSFTASQLRLWTREYDISDVWVSTYNVLMSE^QDRLQSKKLFSSLFFRNEVKQLERSVSRQLYGERIQGSVSRMETFNA
VAQSFTASQLRLWTREYDISDVWVSTYNVLMSE^QDRLQSKKLFSSLFFRNEVKQLERSVSRQLYGERIQGSVSRMETFNA
!!

800
800

logo

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CPFSHFASHGLHLKERQFFKLEAPDIGQLFHSSLKLISDRLREQKLDWRDLTKEQCELFSDAVERLAPKLQKEILLSSN
CPFSHFASHGLHLKERQFFKLEAPDIGQLFHSSLKLISDRLREQKLDWRDLTKEQCELFSDAVERLAPKLQKEILLSSN
!!

880
880

logo

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RHYVKEKLVKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGCTMELVGRIDRVDKAESSKGLLLRIV
RHYVKEKLVKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGCTMELVGRIDRVDKAESSKGLLLRIV
RHYVKEKLVKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGCTMELVGRIDRVDKAESSKGLLLRIV
!!

960
960

logo

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DYKSSDKGLDLAEVYGLALQMLTYLDSLITHSADWLGMRATPAGVLYFHIHDPMIQSNLPLGLDEIEQEIFKKFKMKGL
DYKSSDKGLDLAEVYGLALQMLTYLDSLITHSADWLGMRATPAGVLYFHIHDPMIQSNLPLGLDEIEQEIFKKFKMKGL
DYKSSDKGLDLAEVYGLALQMLTYLDSLITHSADWLGMRATPAGVLYFHIHDPMIQSNLPLGLDEIEQEIFKKFKMKGL
!!

1040
1040

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LLGDQEWRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITDGRVSI EPYKMKNKTP
LLGDQEWRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITDGRVSI EPYKMKNKTP
LLGDQEWRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITDGRVSI EPYKMKNKTP
!!

1120
1120

