

logo

NTDB id 264981 BS11774 RS11680 WP 128473792.1
NTDB id 120 BSU 10620 NP 388943.2
consensus



80
80

logo

NTDB id 264981 BS11774 RS11680 WP 128473792.1
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consensus



160
160

logo

NTDB id 264981 BS11774 RS11680 WP 128473792.1
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240
240

logo

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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

SLDLFQQMI EAGAESLTFSLIPPALDQV FVGNM DLSRMYGTSCTFVLGANDGVL PARPDENGLSDDDREWLKTI GVELS
SLDLFQQMI EAGAESLTFSLIPPALDQV FVGNM DLSRMYGTSCTFVLGANDGVL PARPDENGLSDDDREWLKTI GVELS
SLDLFQQMI EAGAESLTFSLIPPALDQV FVGNM DLSRMYGTSCTFVLGANDGVL PARPDENGLSDDDREWLKTI GVELS
!!

640
640

logo

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SGGRERLLDEHFLIYMAFSSPSDRLYVSYPIADAEGKTL LPSMIVKRLEELFPHHKERLLTNEPEQVSDEEQLMYVVKNS
SGGRERLLDEHFLIYMAFSSPSDRLYVSYPIADAEGKTL LPSMIVKRLEELFPHHKERLLTNEPEQVSDEEQLMYVVKNS
SGGRERLLDEHFLIYMAFSSPSDRLYVSYPIADAEGKTL LPSMIVKRLEELFPHHKERLLTNEPEQVSDEEQLMYVVKNS
!!

720
720

logo

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VAQSFTASQLRLWTREYDISDVWVWSTYNVLMSE^QDR LQSKKLFSSLFFRNEVKQLERSVSRQLYGERIQGSVSRMETFNA
VAQSFTASQLRLWTREYDISDVWVWSTYNVLMSE^PDR LQSKKLFSSLFFRNEVKQLERSVSRQLYGERIQGSVSRMETFNA
VAQSFTASQLRLWTREYDISDVWVWSTYNVLMSE^QDR LQSKKLFSSLFFRNEVKQLERSVSRQLYGERIQGSVSRMETFNA
!!

800
800

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CPFSHFASHGLHLKERQFFKLEAPDIGQLFHSSKLI SDRLREQKLDWRDLTKEQCELFSDAVERLAPKLQKEILLSSN
CPFSHFASHGLHLKERQFFKLEAPDIGQLFHSSKLI SDRLREQKLDWRDLTKEQCELFSDAVERLAPKLQKEILLSSN
CPFSHFASHGLHLKERQFFKLEAPDIGQLFHSSKLI SDRLREQKLDWRDLTKEQCELFSDAVERLAPKLQKEILLSSN
!!

880
880

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RHYVKEKLQKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGCTMELVGRIDRVDKAESSKGLLLRIV
RHYVKEKLQKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGCTMELVGRIDRVDKAESSKGLLLRIV
RHYVKEKLQKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGCTMELVGRIDRVDKAESSKGLLLRIV
!!

960
960

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DYKSSDKGLDLAEVYGLALQMLTYLDLSITHSADWLGMRATPAGVLYFHIDHDPMIQSNLPLGLDEIEQEIFKKFKMKGL
DYKSSDKGLDLAEVYGLALQMLTYLDLSITHSADWLGMRATPAGVLYFHIDHDPMIQSNLPLGLDEIEQEIFKKFKMKGL
DYKSSDKGLDLAEVYGLALQMLTYLDLSITHSADWLGMRATPAGVLYFHIDHDPMIQSNLPLGLDEIEQEIFKKFKMKGL
!!

1040
1040

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LLGDQEVRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITDGRVSI EPYKMKNKTP
LLGDQEVRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITDGRVSI EPYKMKNKTP
LLGDQEVRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITDGRVSI EPYKMKNKTP
!!

1120
1120

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CTYCAFKSVCCFDESLEENEYRPLKAEKDKTILEWIKKEADGNEHS
CTYCAFKSVCCFDESLEENEYRPLKAEKDKTILEWIKKEADGNEHS
!!

1166
1166

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