

logo

NTDB id 87099 BsBEST3145 RS05665 WP 003244988.1
NTDB id 120 BSU 10620 NP 388943.2
consensus

SLDLFQQMI EAGAESLTFSLIPPALDQVFVGNM DLSRMYGTSCTFVLGANDGVL PARPDENGVL SDDDREWLKTI GVELS
SLDLFQQMI EAGAESLTFSLIPPALDQVFVGNM DLSRMYGTSCTFVLGANDGVL PARPDENGVL SDDDREWLKTI GVELS
SLDLFQQMI EAGAESLTFSLIPPALDQVFVGNM DLSRMYGTSCTFVLGANDGVL PARPDENGVL SDDDREWLKTI GVELS
!!

640
640

logo

NTDB id 87099 BsBEST3145 RS05665 WP 003244988.1
NTDB id 120 BSU 10620 NP 388943.2
consensus

SGGRERLLDEHFLIYMAFSSPSDRLYVSYPIADAEGKTL LPSMIVKRLEELFPHHKERLLTNEPEQVSDEEQLMYVVKNS
SGGRERLLDEHFLIYMAFSSPSDRLYVSYPIADAEGKTL LPSMIVKRLEELFPHHKERLLTNEPEQVSDEEQLMYVVKNS
SGGRERLLDEHFLIYMAFSSPSDRLYVSYPIADAEGKTL LPSMIVKRLEELFPHHKERLLTNEPEQVSDEEQLMYVVKNS
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720
720

logo

NTDB id 87099 BsBEST3145 RS05665 WP 003244988.1
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consensus

VAQSFTASQLRLWTREYDISDVVWSTYNVLMSEQDRLQSKKLFSSLFFRNEVKQLERSVSRQLYGERIQGSVSRMETFNA
VAQSFTASQLRLWTREYDISDVVWSTYNVLMSEQDRLQSKKLFSSLFFRNEVKQLERSVSRQLYGERIQGSVSRMETFNA
VAQSFTASQLRLWTREYDISDVVWSTYNVLMSEQDRLQSKKLFSSLFFRNEVKQLERSVSRQLYGERIQGSVSRMETFNA
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800
800

logo

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consensus

CPFSHFASHGLHLKERQFFKLEAPDIGQLFHSSLKLISDRLEQKLDWRDLTKEQCELFSDAVERLAPKLQKEILLSSN
CPFSHFASHGLHLKERQFFKLEAPDIGQLFHSSLKLISDRLEQKLDWRDLTKEQCELFSDAVERLAPKLQKEILLSSN
CPFSHFASHGLHLKERQFFKLEAPDIGQLFHSSLKLISDRLEQKLDWRDLTKEQCELFSDAVERLAPKLQKEILLSSN
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880
880

logo

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consensus

RHYVYKEKLQKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGCTMELVGRIDRVDKAESSKGLLLRIV
RHYVYKEKLQKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGCTMELVGRIDRVDKAESSKGLLLRIV
RHYVYKEKLQKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGCTMELVGRIDRVDKAESSKGLLLRIV
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960
960

logo

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consensus

DYKSSDKGLDLAEVYVYGLALQMLTYDLSITHSADWLGMRATPAGVLYFHIHDPMIQSNLPLGLDEIEQEIFKKFKMKGL
DYKSSDKGLDLAEVYVYGLALQMLTYDLSITHSADWLGMRATPAGVLYFHIHDPMIQSNLPLGLDEIEQEIFKKFKMKGL
DYKSSDKGLDLAEVYVYGLALQMLTYDLSITHSADWLGMRATPAGVLYFHIHDPMIQSNLPLGLDEIEQEIFKKFKMKGL
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1040
1040

logo

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consensus

LLGDQEVVRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITDGRVSI EPYKMKNKTP
LLGDQEVVRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITDGRVSI EPYKMKNKTP
LLGDQEVVRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITDGRVSI EPYKMKNKTP
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1120
1120

