

logo

NTDB id 339840 ES968 RS05895 WP 129134247.1  
NTDB id 120 BSU 10620 NP 388943.2  
consensus



80  
80

logo

NTDB id 339840 ES968 RS05895 WP 129134247.1  
NTDB id 120 BSU 10620 NP 388943.2  
consensus



160  
160

logo

NTDB id 339840 ES968 RS05895 WP 129134247.1  
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consensus



240  
240

logo

NTDB id 339840 ES968 RS05895 WP 129134247.1  
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consensus



320  
320

logo

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consensus



400  
400

logo

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consensus



480  
480

logo

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consensus



560  
560

logo

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consensus

SLDLFQQMIEAGAESLTFSLIPPALDQVFGNMDLSRMYGTSCTFVLGANDGVLPARPDENGVLSDDDREWLKTI GVELS  
SLDLFQQMIEAGAESLTFSLIPPALDQVFGNMDLSRMYGTSCTFVLGANDGVLPARPDENGVLSDDDREWLKTI GVELS  
!!

640  
640

logo

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consensus

SGGRERLLDEHFLIYMAFSSPSDRLVSYPIADAEGKTL LPSMIVKRLEELFPHHKERLLTNEPEQVSDEEQLMYVVKNS  
SGGRERLLDEHFLIYMAFSSPSDRLVSYPIADAEGKTL LPSMIVKRLEELFPHHKERLLTNEPEQVSDEEQLMYVVKNS  
!!

720  
720

logo

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consensus

VAQSFTASQLRLWTREYDISDVMWSTYNVLMSE<sup>EQ</sup>AP<sup>AP</sup>DRLQSKKLFSSLFFRNEVKQLERSVSRQLYGERIQGSVSRMETFNA  
VAQSFTASQLRLWTREYDISDVMWSTYNVLMSE<sup>EQ</sup>AP<sup>AP</sup>DRLQSKKLFSSLFFRNEVKQLERSVSRQLYGERIQGSVSRMETFNA  
!!

800  
800

logo

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CPFSHFASHGLHLKERQFFKLEAPDIGQLFHSSLKLISDRLREQKLDWRDLTKEQCELFSDAVERLAPKLQKEILLSSN  
CPFSHFASHGLHLKERQFFKLEAPDIGQLFHSSLKLISDRLREQKLDWRDLTKEQCELFSDAVERLAPKLQKEILLSSN  
!!

880  
880

logo

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RHYVVK<sup>E</sup>KLQKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGCTMELVGRIDRVDKAESSKGLLLRIV  
RHYVVK<sup>E</sup>KLQKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGCTMELVGRIDRVDKAESSKGLLLRIV  
RHYVVK<sup>E</sup>KLQKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGCTMELVGRIDRVDKAESSKGLLLRIV  
!!

960  
960

logo

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DYKSSDKGLDLAEVYGLALQMLTYLDSLITHSADWLGM<sup>R</sup>RATPAGVLYFHIHDPMIQSNLPLGLDEIEQEIFKKFKMKGL  
DYKSSDKGLDLAEVYGLALQMLTYLDSLITHSADWLGM<sup>R</sup>RATPAGVLYFHIHDPMIQSNLPLGLDEIEQEIFKKFKMKGL  
DYKSSDKGLDLAEVYGLALQMLTYLDSLITHSADWLGM<sup>R</sup>RATPAGVLYFHIHDPMIQSNLPLGLDEIEQEIFKKFKMKGL  
!!

1040  
1040

logo

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LLGDQEWRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITDGRVSI EPYKMKNKTP  
LLGDQEWRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITDGRVSI EPYKMKNKTP  
LLGDQEWRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITDGRVSI EPYKMKNKTP  
!!

1120  
1120

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CTYCAFKSVCFDESLEENEYRPLKAEKDKTILEWIKKEADGNEHS  
CTYCAFKSVCFDESLEENEYRPLKAEKDKTILEWIKKEADGNEHS  
CTYCAFKSVCFDESLEENEYRPLKAEKDKTILEWIKKEADGNEHS  
!!

1166  
1166

- non conserved
- similar
- ≥ 50% conserved