

logo

NTDB id 283407 C7M30 RS04965 WP 160244064.1  
NTDB id 120 BSU 10620 NP 388943.2  
consensus



80  
80

logo

NTDB id 283407 C7M30 RS04965 WP 160244064.1  
NTDB id 120 BSU 10620 NP 388943.2  
consensus



160  
160

logo

NTDB id 283407 C7M30 RS04965 WP 160244064.1  
NTDB id 120 BSU 10620 NP 388943.2  
consensus



240  
240

logo

NTDB id 283407 C7M30 RS04965 WP 160244064.1  
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consensus



320  
320

logo

NTDB id 283407 C7M30 RS04965 WP 160244064.1  
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consensus



400  
400

logo

NTDB id 283407 C7M30 RS04965 WP 160244064.1  
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consensus



480  
480

logo

NTDB id 283407 C7M30 RS04965 WP 160244064.1  
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consensus



560  
560

logo

NTDB id 283407 C7M30 RS04965 WP 160244064.1  
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consensus

SLDLFQQMIEAGAESLTFSLIPPALDQVFVGNMDSLRYMGTSCFVLGANDGVLPARPDENGVLSDDDREWLKTI GVELS  
SLDLFQQMIEAGAESLTFSLIPPALDQVFVGNMDSLRYMGTSCFVLGANDGVLPARPDENGVLSDDDREWLKTI GVELS  
!!

640  
640

logo

NTDB id 283407 C7M30 RS04965 WP 160244064.1  
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consensus

SGGRERLLDEHFLIYMAFSSPSDRLVSYPIADAEGKTL LPSMIVKRLEELFPHHKERLLTNEPEQVSDEEQLMYVVKNS  
SGGRERLLDEHFLIYMAFSSPSDRLVSYPIADAEGKTL LPSMIVKRLEELFPHHKERLLTNEPEQVSDEEQLMYVVKNS  
!!

720  
720

logo

NTDB id 283407 C7M30 RS04965 WP 160244064.1  
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consensus

VAQSFTASQLRLWTR EYDISDVVWSTYNVLMSE<sup>Q</sup>DRLQSKKLFSSLFFRNEVKQLERSVSRQLYGERIQGSVSRMETFNA  
VAQSFTASQLRLWTR EYDISDVVWSTYNVLMSE<sup>Q</sup>DRLQSKKLFSSLFFRNEVKQLERSVSRQLYGERIQGSVSRMETFNA  
!!

800  
800

logo

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CPFSHFASHGLHLKERQFFKLEAPDIGQLFHSSLKLISDRLREQKLDWRDLTKEQCELFSDAVERLAPKLQKEILLSSN  
CPFSHFASHGLHLKERQFFKLEAPDIGQLFHSSLKLISDRLREQKLDWRDLTKEQCELFSDAVERLAPKLQKEILLSSN  
!!

880  
880

logo

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RHYVKEKLVKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGCTMELVGRIDRVDKAESSKGLLLRIV  
RHYVKEKLVKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGCTMELVGRIDRVDKAESSKGLLLRIV  
!!

960  
960

logo

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DYKSSDKGLDLAEVYGLALQMLTYLDSLITHSADWLGMRATPAGVLYFHIHDPMIQSNLPLGLDEIEQEIFKFKMKGL  
DYKSSDKGLDLAEVYGLALQMLTYLDSLITHSADWLGMRATPAGVLYFHIHDPMIQSNLPLGLDEIEQEIFKFKMKGL  
!!

1040  
1040

logo

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LLGDQEVVRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITDGRVSI EPYKMKNKTP  
LLGDQEVVRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITDGRVSI EPYKMKNKTP  
!!

1120  
1120

