

logo

NTDB id 302582 DS740 RS05675 WP 114168442.1
NTDB id 120 BSU 10620 NP 388943.2
consensus



80
80

logo

NTDB id 302582 DS740 RS05675 WP 114168442.1
NTDB id 120 BSU 10620 NP 388943.2
consensus



160
160

logo

NTDB id 302582 DS740 RS05675 WP 114168442.1
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consensus



240
240

logo

NTDB id 302582 DS740 RS05675 WP 114168442.1
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consensus



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

SLDLFQQMIEAGAESLTFSLIPPALDQVFGNMDLSRMYGTSCTFVLGANDGVLPARPDENGVLSDDDREWLKTI GVELS
SLDLFQQMIEAGAESLTFSLIPPALDQVFGNMDLSRMYGTSCTFVLGANDGVLPARPDENGVLSDDDREWLKTI GVELS
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640
640

logo

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SGGRERLLDEHFLIYMAFSSPSDRLVSYPIADAEGKTL LPSMIVKRLEELFPHHKERLLTNEPEQVSDEEQLMYVNVKQS
SGGRERLLDEHFLIYMAFSSPSDRLVSYPIADAEGKTL LPSMIVKRLEELFPHHKERLLTNEPEQVSDEEQLMYVNVKQS
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720
720

logo

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VAQSFTASQLRLWTR EYDISDVMWSTYNVLMSE^QDRLQSKKLFSSLFFRNEVKQLERSVSRQLYGERIQGSVSRMETFNA
VAQSFTASQLRLWTR EYDISDVMWSTYNVLMSE^QDRLQSKKLFSSLFFRNEVKQLERSVSRQLYGERIQGSVSRMETFNA
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800
800

logo

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CPFSHFASHGLHLKERQFFKLEAPDIGQLFHSSLKLISDRLREQKLDWRDLTKEQCELFSDAVERLAPKLQKEILLSSN
CPFSHFASHGLHLKERQFFKLEAPDIGQLFHSSLKLISDRLREQKLDWRDLTKEQCELFSDAVERLAPKLQKEILLSSN
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880
880

logo

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RHYVKEKLVKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGCTMELVGRIDRVDKAESSKGLLLRIV
RHYVKEKLVKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGCTMELVGRIDRVDKAESSKGLLLRIV
RHYVKEKLVKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGCTMELVGRIDRVDKAESSKGLLLRIV
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960
960

logo

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DYKSSDKGLDLAEVYGLALQMLTYLDSLITHSADWLGMRATPAGVLYFHIHDPMIQSNLPLGLDEIEQEIFKFKMKKGL
DYKSSDKGLDLAEVYGLALQMLTYLDSLITHSADWLGMRATPAGVLYFHIHDPMIQSNLPLGLDEIEQEIFKFKMKKGL
DYKSSDKGLDLAEVYGLALQMLTYLDSLITHSADWLGMRATPAGVLYFHIHDPMIQSNLPLGLDEIEQEIFKFKMKKGL
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1040
1040

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LLGDQEVVRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITDGRVSI EPYKMKKNTKTP
LLGDQEVVRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITDGRVSI EPYKMKKNTKTP
LLGDQEVVRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITDGRVSI EPYKMKKNTKTP
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1120
1120

