

logo

NTDB id 53843 BsBEST3145 RS05670 WP 003233100.1
NTDB id 119 BSU 10630 NP 388944.2
consensus

MNIPKPADSTWTDDQWNAIVSTGQDILVAAAAGSGKTAVLVERMIRKITAEEENPIDVDRLLVVTFTNASAAEMKHRIA
EA
MNIPKPADSTWTDDQWNAIVSTGQDILVAAAAGSGKTAVLVERMIRKITAEEENPIDVDRLLVVTFTFTNASAAEMKHRIA
EA
!!

80
80

logo

NTDB id 53843 BsBEST3145 RS05670 WP 003233100.1
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consensus

LEKELVQRPGLHRRQLSLLNRASISTLHSFCLQVLKYYLIDLDPGFRIADQTEGELIGDEVLDLFEDEYAKGEKA
LEKELVQRPGLHRRQLSLLNRASISTLHSFCLQVLKYYLIDLDPGFRIADQTEGELIGDEVLDLFEDEYAKGEKA
LEKELVQRPGLHRRQLSLLNRASISTLHSFCLQVLKYYLIDLDPGFRIADQTEGELIGDEVLDLFEDEYAKGEKA
!!

160
160

logo

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consensus

FFELVDRYTDDRHDLDLQFLVKQVVEYSRSHNPPEAWLESFVHLYDVSEKSAIEELPFYQYVKEDIAMVLNGAKEKLLRA
FFELVDRYTDDRHDLDLQFLVKQVVEYSRSHNPPEAWLESFVHLYDVSEKSAIEELPFYQYVKEDIAMVLNGAKEKLLRA
FFELVDRYTDDRHDLDLQFLVKQVVEYSRSHNPPEAWLESFVHLYDVSEKSAIEELPFYQYVKEDIAMVLNGAKEKLLRA
!!

240
240

logo

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LELTKAPGGPAPRADNFLDDLAQIDELIQHQDDFSELYKRVPVAVSFKRAKAVKGDEFDPALLDEATDLRNGAKKLLLEKLK
LELTKAPGGPAPRADNFLDDLAQIDELIQHQDDFSELYKRVPVAVSFKRAKAVKGDEFDPALLDEATDLRNGAKKLLLEKLK
LELTKAPGGPAPRADNFLDDLAQIDELIQHQDDFSELYKRVPVAVSFKRAKAVKGDEFDPALLDEATDLRNGAKKLLLEKLK
!!

320
320

logo

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TDYFTRSPEQHLKSLAEMKPVETLVQLVISYGRFEEAAKQEKSIIDFSDLEHYCLAILTAEENDKGEREPSEAAARFYQEQ
TDYFTRSPEQHLKSLAEMKPVETLVQLVISYGRFEEAAKQEKSIIDFSDLEHYCLAILTAEENDKGEREPSEAAARFYQEQ
TDYFTRSPEQHLKSLAEMKPVETLVQLVISYGRFEEAAKQEKSIIDFSDLEHYCLAILTAEENDKGEREPSEAAARFYQEQ
!!

400
400

logo

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FHEVLVDEYQDTNLVQESILQLVTSGPEETGNLFMVGDKQSIYRFRLAEPLFLSKYKRFTESGEGTGRKIDLNKNFRS
FHEVLVDEYQDTNLVQESILQLVTSGPEETGNLFMVGDKQSIYRFRLAEPLFLSKYKRFTESGEGTGRKIDLNKNFRS
FHEVLVDEYQDTNLVQESILQLVTSGPEETGNLFMVGDKQSIYRFRLAEPLFLSKYKRFTESGEGTGRKIDLNKNFRS
!!

480
480

logo

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RADILDSTNFLFKQLMGGKIGVDYDEQAELKLGAAYPDNDDETETELLLIDNAEDTDASEEAELETQFEAKIAKEIR
RADILDSTNFLFKQLMGGKIGVDYDEQAELKLGAAYPDNDDETETELLLIDNAEDTDASEEAELETQFEAKIAKEIR
RADILDSTNFLFKQLMGGKIGVDYDEQAELKLGAAYPDNDDETETELLLIDNAEDTDASEEAELETQFEAKIAKEIR
!!

560
560

logo

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consensus

KLISSPFKVYDGKKKT-HRNIQYRDIVILLRSMWPAPQIMEELRAQGIPVYANLTSGYFEAVEVAVALSVLKVIDNPYQDI
KLISSPFKVYDGKKKT-HRNIQYRDIVILLRSMWPAPQIMEELRAQGIPVYANLTSGYFEAVEVAVALSVLKVIDNPYQDI
!!

640
640

logo

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PLASVLRSPIVGADENELSLIRLENKKAPYYEAMKDYLEAGDRSDELYQKLNTFYGHLQKWRAF-SKNH-SVSELIWEVYRD
PLASVLRSPIVGADENELSLIRLENKKAPYYEAMKDYLEAGDRSDELYQKLNTFYGHLQKWRAF-SKNH-SVSELIWEVYRD
PLASVLRSPIVGADENELSLIRLENKKAPYYEAMKDYLEAGDRSDELYQKLNTFYGHLQKWRAF-SKNH-SVSELIWEVYRD
!!

720
720

logo

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consensus

TKYMDYVGGMPGGKQRQANLRVLYDRARQYESTAFRGLFRFLRFIERMQERGDDLGTARALSEQEDVRLMTIHSSKGLE
TKYMDYVGGMPGGKQRQANLRVLYDRARQYESTAFRGLFRFLRFIERMQERGDDLGTARALSEQEDVRLMTIHSSKGLE
TKYMDYVGGMPGGKQRQANLRVLYDRARQYESTAFRGLFRFLRFIERMQERGDDLGTARALSEQEDVRLMTIHSSKGLE
!!

800
800

logo

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consensus

FPWFVAGLGRNFMMDLNKSYLLDKELGFGTKYIHPQLRISYPTLPLIAMKKKMRRELLSEELRVLYVALTRAKEKFLFL
FPVVFVAGLGRNFMMDLNKSYLLDKELGFGTKYIHPQLRISYPTLPLIAMKKKMRRELLSEELRVLYVALTRAKEKFLFL
FPVVFVAGLGRNFMMDLNKSYLLDKELGFGTKYIHPQLRISYPTLPLIAMKKKMRRELLSEELRVLYVALTRAKEKFLFL
!!

880
880

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IGSCKDHQKQLAKWQASASQTDWLLPEFDYQARTYLDFIGPALARHRDLGDLAGVPAHADISGHPARFAVQMIHSYDLL
IGSCKDHQKQLAKWQASASQTDWLLPEFDYQARTYLDFIGPALARHRDLGDLAGVPAHADISGHPARFAVQMIHSYDLL
IGSCKDHQKQLAKWQASASQTDWLLPEFDYQARTYLDFIGPALARHRDLGDLAGVPAHADISGHPARFAVQMIHSYDLL
!!

960
960

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DDDLEERMEEKSERLEAIRRGEPVPGSFADFDEKAREQLSWTYPHQEV-TQIRTKQSVSEIKRKREYEDEYSGRAPVKPADG
DDDLEERMEEKSERLEAIRRGEPVPGSFADFDEKAREQLSWTYPHQEV-TQIRTKQSVSEIKRKREYEDEYSGRAPVKPADG
DDDLEERMEEKSERLEAIRRGEPVPGSFADFDEKAREQLSWTYPHQEV-TQIRTKQSVSEIKRKREYEDEYSGRAPVKPADG
!!

1040
1040

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SILYRRPAFMMKKGLTAAEKGTAMHTVMQHIPLSHVPSIEEAEQTVHRLYEKELLTEEQKDAIDIEEIVQFFHTEIGGQL
SILYRRPAFMMKKGLTAAEKGTAMHTVMQHIPLSHVPSIEEAEQTVHRLYEKELLTEEQKDAIDIEEIVQFFHTEIGGQL
SILYRRPAFMMKKGLTAAEKGTAMHTVMQHIPLSHVPSIEEAEQTVHRLYEKELLTEEQKDAIDIEEIVQFFHTEIGGQL
!!

1120
1120

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consensus



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