

logo

NTDB id 87352 K6K00 RS05655 WP 014479389.1  
NTDB id 119 BSU 10630 NP 388944.2  
consensus

MNIPKPADSTWTDQWNIVSTGQDILVAAAAGSGKTAVLVERMIRKITAEENPIDVDRLLVVTFTNASAAEMKHRIAEALEKEL

MNIPKPADSTWTDQWNIVSTGQDILVAAAAGSGKTAVLVERMIRKITAEENPIDVDRLLVVTFTFTNASAAEMKHRIAEALEKEL

MNIPKPADSTWTDQWNIVSTGQDILVAAAAGSGKTAVLVERMIRKITAEENPIDVDRLLVVTFTFTNASAAEMKHRIAEALEKEL

85  
85

logo

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VQRP<sup>g</sup>SLH<sup>i</sup>RR<sup>q</sup>LS<sup>l</sup>LN<sup>r</sup>AS<sup>s</sup>IS<sup>t</sup>LS<sup>h</sup>FS<sup>f</sup>CL<sup>q</sup>VL<sup>k</sup>K<sup>k</sup>Y<sup>y</sup>YL<sup>l</sup>IDL<sup>d</sup>DP<sup>p</sup>GF<sup>r</sup>IAD<sup>q</sup>TE<sup>g</sup>EL<sup>l</sup>+G<sup>g</sup>DE<sup>v</sup>LD<sup>l</sup>EL<sup>f</sup>FE<sup>d</sup>E<sup>y</sup>AK<sup>g</sup>EKA<sup>f</sup>FF<sup>e</sup>LV<sup>d</sup>RY<sup>t</sup>

170  
170

logo

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DRHDLDLQFLVKQVVEYSRSHPNPEAWLESFVHLYDVSEKSAIEELPFYQYVKEDIAMVLNGAKEKLLRALELTKAPGGPAPRAD  
DRHDLDLQFLVKQVVEYSRSHPNPEAWLESFVHLYDVSEKSAIEELPFYQYVKEDIAMVLNGAKEKLLRALELTKAPGGPAPRAD  
DRHDLDLQFLVKQVVEYSRSHPNPEAWLESFVHLYDVSEKSAIEELPFYQYVKEDIAMVLNGAKEKLLRALELTKAPGGPAPRAD

255  
255

logo

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NFLDDLAQIDELIQHQQDFSELYKRVPAVSFKRAKAVKGDEFDPALLDEATDLRNGAKKLEKLKTDYFTRSPEQHLKS LAEMKP  
NFLDDLAQIDELIQHQQDFSELYKRVPAVSFKRAKAVKGDEFDPALLDEATDLRNGAKKLEKLKTDYFTRSPEQHLKS LAEMKP  
NFLDDLAQIDELIQHQQDFSELYKRVPAVSFKRAKAVKGDEFDPALLDEATDLRNGAKKLEKLKTDYFTRSPEQHLKS LAEMKP

340  
340

logo

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VIETLVQLVISYGKRFEAAKQEKSIIDFSDLEHYCLAILTAENDKGEREPSEAAIFYQQFHEVLVDEYQDTNLVQESILQLVTS  
VIETLVQLVISYGKRFEAAKQEKSIIDFSDLEHYCLAILTAENDKGEREPSEAAIFYQQFHEVLVDEYQDTNLVQESILQLVTS  
VIETLVQLVISYGKRFEAAKQEKSIIDFSDLEHYCLAILTAENDKGEREPSEAAIFYQQFHEVLVDEYQDTNLVQESILQLVTS

425  
425

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GPEETGNLFMVGDVKQSIYRFRLAEPLFLSKYKRFTESGEGTGRKIDLNKNFRSRADILDSTNFLFKQLMGGKIGVDYDEQAE  
 GPEETGNLFMVGDVKQSIYRFRLAEPLFLSKYKRFTESGEGTGRKIDLNKNFRSRADILDSTNFLFKQLMGGKIGVDYDEQAE  
 GPEETGNLFMVGDVKQSIYRFRLAEPLFLSKYKRFTESGEGTGRKIDLNKNFRSRADILDSTNFLFKQLMGGKIGVDYDEQAE

510  
510

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LKLGAAYPDNDDETETELLIDNAEDTDASEEAAELETQFEAKAIAKEIRKLSSPFKVYDGKKKTHRNQYRDIVILLRSMPTWALKLGAAYPDNDDETETELLIDNAEDTDASEEAAELETQFEAKAIAKEIRKLSSPFKVYDGKKKTHRNQYRDIVILLRSMPTWALKLGAAYPDNDDETETELLIDNAEDTDASEEAAELETQFEAKAIAKEIRKLSSPFKVYDGKKKTHRNQYRDIVILLRSMPTWAL

595  
595

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PQIMEELRA<sup>g</sup>IPVYANLTSGYFEAVEVAVALSVLKVIDNPYQDIPLASVLRSPIVGADENELSLIRLENKKAPYYEAMKDYLAA  
 PQIMEELRA<sup>H</sup>GIPVYANLTSGYFEAVEVAVALSVLKVIDNPYQDIPLASVLRSPIVGADENELSLIRLENKKAPYYEAMKDYLAA  
 PQIMEELRA<sup>Q</sup>GIPVYANLTSGYFEAVEVAVALSVLKVIDNPYQDIPLASVLRSPIVGADENELSLIRLENKKAPYYEAMKDYLAA  
 \*

680  
680

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GDR<sup>S</sup>DELYQKLNTFYGHLQKWRAFSKNHSVSELIWEVYRDTKYM<sup>D</sup>YVGGMPGGKQRQANLRVLYDRARQYESTAFRGLFRFLRFI  
 GDR<sup>N</sup>DELYQKLNTFYGHLQKWRAFSKNHSVSELIWEVYRDTKYM<sup>D</sup>YVGGMPGGKQRQANLRVLYDRARQYESTAFRGLFRFLRFI  
 GDR<sup>S</sup>DELYQKLNTFYGHLQKWRAFSKNHSVSELIWEVYRDTKYM<sup>D</sup>YVGGMPGGKQRQANLRVLYDRARQYESTAFRGLFRFLRFI

765  
765

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850  
850

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MKKKMRRELLSEELRVLYVALTRAKEKFLIGSCKDHQQLAKWQASASQTDWLLPEFDTRYQARTYLDFIGPALARHRDLGDLG  
 MKKKMRRELLSEELRVLYVALTRAKEKFLIGSCKDHQQLAKWQASASQTDWLLPEFDTRYQARTYLDFIGPALARHRDLGDLG  
 MKKKMRRELLSEELRVLYVALTRAKEKFLIGSCKDHQQLAKWQASASQTDWLLPEFDTRYQARTYLDFIGPALARHRDLGDLG

935  
935

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VPAHADISGHPARFAVQMIHSYDLLDDDL EERMEEKSERLEAIRRGEPVPGSF AFDEKAREQLSWTYPHQEVTQIRTKQSVSEIK  
 VPAHADISGHPARFAVQMIHSYDLLDDDL EERMEEKSERLEAIRRGEPVPGSF AFDEKAREQLSWTYPHQEVTQIRTKQSVSEIK  
 VPAHADISGHPARFAVQMIHSYDLLDDDL EERMEEKSERLEAIRRGEPVPGSF AFDEKAREQLSWTYPHQEVTQIRTKQSVSEIK

1020  
1020

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RKREYEDEYSGRAPVKPADGSILYRRPAFMMKKGLTAAEKGTAHMTVMQHIPLSHVPSIEEAEQTVHRLYEKELLTEEQKDAIDI  
 RKREYEDEYSGRAPVKPADGSILYRRPAFMMKKGLTAAEKGTAHMTVMQHIPLSHVPSIEEAEQTVHRLYEKELLTEEQKDAIDI  
 RKREYEDEYSGRAPVKPADGSILYRRPAFMMKKGLTAAEKGTAHMTVMQHIPLSHVPSIEEAEQTVHRLYEKELLTEEQKDAIDI

1105  
1105

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EEIVQFFHTEIGGQLGAKWKDREIPFSLALPAKEIYPDA<sup>h</sup>EADEPLL<sup>h</sup>VQGIIDCLYETEDGLYL<sup>h</sup>LDYKSDRIEGKFQHGFE<sup>h</sup>GAA<sup>h</sup>  
EEIVQFFHTEIGGQLGAKWKDREIPFSLALPAKEIYPDA<sup>h</sup>EADEPLL<sup>h</sup>VQGIIDCLYETEDGLYL<sup>h</sup>LDYKSDRIEGKFQHGFE<sup>h</sup>GAA<sup>h</sup>  
EEIVQFFHTEIGGQLGAKWKDREIPFSLALPAKEIYPDA<sup>h</sup>EADEPLL<sup>h</sup>VQGIIDCLYETEDGLYL<sup>h</sup>LDYKSDRIEGKFQHGFE<sup>h</sup>GAA<sup>h</sup>

1190  
1190

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