

NTDB id 86756 K6J89 RS05750 WP 003233100.1
NTDB id 119 BSU 10630 NP 388944.2
consensus

85
85

NTDB id 86756 K6J89 RS05750 WP 003233100.1
NTDB id 119 BSU 10630 NP 388944.2
consensus

170
170

NTDB id 86756 K6J89 RS05750 WP 003233100.1
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consensus



255
255

NTDB id 86756 K6J89 RS05750 WP 003233100.1
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consensus

340
340

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425
425

NTDB id 86756 K6J89 RS05750 WP 003233100.1
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consensus

510
510

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consensus

595
595

logo

NTDB id 86756 K6J89 RS05750 WP 003233100.1
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consensus

PQIMEELRAQGIPVYANLTSGYFEAVEVAVALSVLKVIDNPYQDIPLASVLRSPIVGADENELSLIRLENKKAPYYEAMKDYLAA
 PQIMEELRAQGIPVYANLTSGYFEAVEVAVALSVLKVIDNPYQDIPLASVLRSPIVGADENELSLIRLENKKAPYYEAMKDYLAA
 PQIMEELRAQGIPVYANLTSGYFEAVEVAVALSVLKVIDNPYQDIPLASVLRSPIVGADENELSLIRLENKKAPYYEAMKDYLAA

680
680

logo

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GDRSDELYQKLNIFYGHLQKWRAFSKNHSVSELIWEVYRDTKYM DYVGGMPGGKQRQANLRVLYDRARQYESTAFRGLFRFLRFI
GDRSDELYQKLNIFYGHLQKWRAFSKNHSVSELIWEVYRDTKYM DYVGGMPGGKQRQANLRVLYDRARQYESTAFRGLFRFLRFI
GDRSDELYQKLNIFYGHLQKWRAFSKNHSVSELIWEVYRDTKYM DYVGGMPGGKQRQANLRVLYDRARQYESTAFRGLFRFLRFI

765
765

logo

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ERMQERGDDLGTARALSEQEDVRLMTIHSSKGLEFPWFVAGLGRNFMMDLNKSYLLDKELGFGTKYIHPQLRISYPTLPLIA
ERMQERGDDLGTARALSEQEDVRLMTIHSSKGLEFPVVFVAGLGRNFMMDLNKSYLLDKELGFGTKYIHPQLRISYPTLPLIA
ERMQERGDDLGTARALSEQEDVRLMTIHSSKGLEFPVVFVAGLGRNFMMDLNKSYLLDKELGFGTKYIHPQLRISYPTLPLIA

850
850

logo

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MKKKMRRELLSEELRVLYVALTRAKEKFLIGSCKDHQQLAKWQASASQTDWLLPEFDYQARTYLDFIGPALARHRDLGDLAQ
 MKKKMRRELLSEELRVLYVALTRAKEKFLIGSCKDHQQLAKWQASASQTDWLLPEFDYQARTYLDFIGPALARHRDLGDLAQ
 MKKKMRRELLSEELRVLYVALTRAKEKFLIGSCKDHQQLAKWQASASQTDWLLPEFDYQARTYLDFIGPALARHRDLGDLAQ

935
935

logo

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VPAHADISGHPARFAVQMIHSYDLLDDDL EERMEEKSERLEAIRRGEPVPGSF AFDEKAREQLSWTYPHQEVTQIRTKQSVSEIK
 VPAHADISGHPARFAVQMIHSYDLLDDDL EERMEEKSERLEAIRRGEPVPGSF AFDEKAREQLSWTYPHQEVTQIRTKQSVSEIK
 VPAHADISGHPARFAVQMIHSYDLLDDDL EERMEEKSERLEAIRRGEPVPGSF AFDEKAREQLSWTYPHQEVTQIRTKQSVSEIK

1020
1020

logo

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RKREYEDEYSGRAPVKPADGSILYRRPAFMMKKGLTAAEKGTAMHTVMQHIIPLSHVPSIEEAEQTVHRLYEKELLTEEQKDAID
 RKREYEDEYSGRAPVKPADGSILYRRPAFMMKKGLTAAEKGTAMHTVMQHIIPLSHVPSIEEAEQTVHRLYEKELLTEEQKDAID
 RKREYEDEYSGRAPVKPADGSILYRRPAFMMKKGLTAAEKGTAMHTVMQHIIPLSHVPSIEEAEQTVHRLYEKELLTEEQKDAID

1105
1105

logo

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EEIVQFFHTEIGGQLGAKWKDREIPFSLALPAKEIYPDAHEADEPLLVGIIIDCLYETEDGLYLLDYKSDRIEGKFQHGFEAA
EEIVQFFHTEIGGQLGAKWKDREIPFSLALPAKEIYPDAHEADEPLLVGIIIDCLYETEDGLYLLDYKSDRIEGKFQHGFEAA
EEIVQFFHTEIGGQLGAKWKDREIPFSLALPAKEIYPDAHEADEPLLVGIIIDCLYETEDGLYLLDYKSDRIEGKFQHGFEAA

1190
1190

logo

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consensus

1232
 1232

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