

logo

NTDB id 376504 FQZ25 RS27855 WP 346726393.1
NTDB id 119 BSU 10630 NP 388944.2
consensus



55
80

logo

NTDB id 376504 FQZ25 RS27855 WP 346726393.1
NTDB id 119 BSU 10630 NP 388944.2
consensus



61
160

logo

NTDB id 376504 FQZ25 RS27855 WP 346726393.1
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consensus



61
240

logo

NTDB id 376504 FQZ25 RS27855 WP 346726393.1
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61
320

logo

NTDB id 376504 FQZ25 RS27855 WP 346726393.1
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61
400

logo

NTDB id 376504 FQZ25 RS27855 WP 346726393.1
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61
480

logo

NTDB id 376504 FQZ25 RS27855 WP 346726393.1
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61
560

logo

NTDB id 376504 FQZ25 RS27855 WP 346726393.1
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consensus

KL|SSPFKVYDGGKKKTHRNIQYRDIVILLRSMWPAPQIMEELRAQGI PVYANLTSGYFEAVEVAVALSVLKVIDNPYQDI
.....
KLISSPFKVYDGGKKKTHRNIQYRDIVILLRSMWPAPQIMEELRAQGIPVYANLTSGYFEAVEVAVALSVLKVIDNPYQDI

61
640

logo

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consensus

PLASVLRSPIVGADENELSLIRLENKKAPYYEAMKDYLEAGDRSDELYQKLNTFYGHLQKWRAF SKNHVSSEL IWEVYRD
.....
PLASVLRSPIVGADENELSLIRLENKKAPYYEAMKDYLEAGDRSDELYQKLNTFYGHLQKWRAF SKNHVSSEL IWEVYRD

61
720

logo

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consensus

TKYMDYVGGMPGGKQRQANLRVLYDRARQYESTAFRGLFRFLRFIERMQERGDDLGTARALSEQEDVRLMTIHSSKGLE
.....
TKYMDYVGGMPGGKQRQANLRVLYDRARQYESTAFRGLFRFLRFIERMQERGDDLGTARALSEQEDVRLMTIHSSKGLE

61
800

logo

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consensus

FPVVFVAGLGRNFMMDLNKSYLLDKELGFGTKYIHPQLRISYPTLPLIAMKKMRRELLSEELRVLYVALTRAKEKFLFL
.....
FPVVFVAGLGRNFMMDLNKSYLLDKELGFGTKYIHPQLRISYPTLPLIAMKKMRRELLSEELRVLYVALTRAKEKFLFL

61
880

logo

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consensus

IGSCKDHQKQLAKWQASASQTDWLLPEFDYQARTYLDFIGPALARHRDLGDLAGVPAHADISGHPARFAVQMIHSYDLL
.....
IGSCKDHQKQLAKWQASASQTDWLLPEFDYQARTYLDFIGPALARHRDLGDLAGVPAHADISGHPARFAVQMIHSYDLL

61
960

logo

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consensus

DDDL EERMEEKSERLEAIRRGEVPVPGSF AFDEKAREQLSWTYPHQEV TQIRTKQSVSEIKRKREYEDEYSGRAPVKPADG
.....
DDDL EERMEEKSERLEAIRRGEVPVPGSF AFDEKAREQLSWTYPHQEV TQIRTKQSVSEIKRKREYEDEYSGRAPVKPADG

61
1040

logo

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SILYRRPAFMMKKGLTAAEKGTAMHTVMQHIPLSHVPSIEEAEQTVHRLYEKELLTEEQKDAIDIEEIVQFFHTEIGGQL
.....
SILYRRPAFMMKKGLTAAEKGTAMHTVMQHIPLSHVPSIEEAEQTVHRLYEKELLTEEQKDAIDIEEIVQFFHTEIGGQL

61
1120

logo

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consensus

I G A K W K D R E I P F S L A L P A K E I Y P D A H E A D E P L L V Q G I I D C L Y E T E D G L Y L L D Y K S D R I E G K F Q H G F E G A A P I L K K R Y E T Q
.....
I G A K W K D R E I P F S L A L P A K E I Y P D A H E A D E P L L V Q G I I D C L Y E T E D G L Y L L D Y K S D R I E G K F Q H G F E G A A P I L K K R Y E T Q

61
1200

logo

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I Q L Y T K A V E Q I A K T K V K G C A L Y F F D G G H I L T L
.....
I Q L Y T K A V E Q I A K T K V K G C A L Y F F D G G H I L T L

61
1232

- X non conserved
- X similar
- X ≥ 50% conserved