



logo

NTDB id 320845 D9779 RS06680 WP 121642273.1  
NTDB id 119 BSU 10630 NP 388944.2  
consensus

KLISSPFKVYDGGKTKTHRNIQYRDIVILLRSMPWAPQIMDELRAQGIPVYANLTSGYFDAVEVAVALSVLKVIDNPHYQDI  
KLISSPFKVYDGGKTKTHRNIQYRDIVILLRSMPWAPQIMDELRAQGIPVYANLTSGYFDAVEVAVALSVLKVIDNPHYQDI  
!!

640  
640

logo

NTDB id 320845 D9779 RS06680 WP 121642273.1  
NTDB id 119 BSU 10630 NP 388944.2  
consensus

PLASVLRSPVIGADENELSLIRLENKKAPYYEAMKDYLEAGDRNDELYQKLQTFYTHLQKWRAFASKNHSVSELIWEVYRD  
PLASVLRSPVIGADENELSLIRLENKKAPYYEAMKDYLEAGDRNDELYQKLQTFYTHLQKWRAFASKNHSVSELIWEVYRD  
PLASVLRSPVIGADENELSLIRLENKKAPYYEAMKDYLEAGDRNDELYQKLQTFYTHLQKWRAFASKNHSVSELIWEVYRD  
!!

720  
720

logo

NTDB id 320845 D9779 RS06680 WP 121642273.1  
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consensus

TKYMDYVGGMPGGKQRQANLRVLYDRARQYESTAFRGLFRFLRFIERMQERGDDLGTARALSEQEDVRLMTIHSSKGLE  
TKYMDYVGGMPGGKQRQANLRVLYDRARQYESTAFRGLFRFLRFIERMQERGDDLGTARALSEQEDVRLMTIHSSKGLE  
TKYMDYVGGMPGGKQRQANLRVLYDRARQYESTAFRGLFRFLRFIERMQERGDDLGTARALSEQEDVRLMTIHSSKGLE  
!!

800  
800

logo

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consensus

FPVVFVAGLGRNFMMDLNKSYLLDKELGFGTKYIHPQLRISYPTLPLIAMKKMRRELLSEELRVLYVALTRAKEKLFEL  
FPVVFVAGLGRNFMMDLNKSYLLDKELGFGTKYIHPQLRISYPTLPLIAMKKMRRELLSEELRVLYVALTRAKEKLFEL  
FPVVFVAGLGRNFMMDLNKSYLLDKELGFGTKYIHPQLRISYPTLPLIAMKKMRRELLSEELRVLYVALTRAKEKLFEL  
!!

880  
880

logo

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consensus

IGSCKDHQKQYAKWQASASQTDWLLPEFDYQARTYLDFIGPALARHRLDLAGENVMAPADISSHPARFAVRMIHSYD  
IGSCKDHQKQYAKWQASASQTDWLLPEFDYQARTYLDFIGPALARHRLDLAGENVMAPADISSHPARFAVRMIHSYD  
IGSCKDHQKQLAKWQASASQTDWLLPEFDYQARTYLDFIGPALARHRLDLAG..VPAHADISGHPARFAVRMIHSYD  
!!

960  
958

logo

NTDB id 320845 D9779 RS06680 WP 121642273.1  
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consensus

LLDDDLEERMEEKSERLEAIRRGEVPGSFAFDEKAREQLSWTYPHQEVTHIRTKQSVSEIKRKREYEDEYSGRAPVKPA  
LLDDDLEERMEEKSERLEAIRRGEVPGSFAFDEKAREQLSWTYPHHHEVTHIRTKQSVSEIKRKREYEDEYSGRAPVKPA  
LLDDDLEERMEEKSERLEAIRRGEVPGSFAFDEKAREQLSWTYPHQEVTHIRTKQSVSEIKRKREYEDEYSGRAPVKPA  
!!

1040  
1038

logo

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consensus

DGSMLYRRPAFMMKKGLTAAEKGTAMHTVMQHIPLSHVPSYEEAEQTVHRLYEKELLTEEQKDAIDIEEIVQFFHTEIGG  
DGSMLYRRPAFMMKKGLTAAEKGTAMHTVMQHIPLSHVPSYEEAEQTVHKLFEKELLTEEQKAAIDIEEIVQFFHTEIGG  
DGSILYRRPAFMMKKGLTAAEKGTAMHTVMQHIPLSHVPSIEEAEQTVHRLYEKELLTEEQKDAIDIEEIVQFFHTEIGG  
!!

1120  
1118

