logo


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NTDB id 107844 A214 RS26615 WP 003113873.1  ....MTDLSQHTPMMQQYFKLKHQHPDQLMFYRMGDFYELFYEDAKKAAKLLDITLTARGQSGGKAIPMAGIPFHSAEGYLAKLV  81
NTDB id 1201 CAH03854.1 414..2993( )        MTKPNADLSAHTPMMQQYWRLKREHPDQLMFYRMGDFYELFYDDAKKAAALLDITLTARGQSAGTAIPMAGIPFHSAEGYLARLV  85
consensus                                   ****  !!! !!!!!!!!**!!* !!!!!!!!!!!!!!!!!!*!!!!!! !!!!!!!!!!!!*! !!!!!!!!!!!!!!!!!*!!
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NTDB id 107844 A214 RS26615 WP 003113873.1  KLGESVAICEQIGDPATSKGPVERQVVRIITPGTVSDEALLDERRDNLLAAILGDERLFGLAVLDITSGRFSVQEIKGWETLLAE  166
NTDB id 1201 CAH03854.1 414..2993( )        KLGESVVICEQIGDPAASKGPVERQVVRIITPGTVSDEALLDERRDNLLAAVVGDERLFGLSVLDIASGRFSVQELKGWETLLAE  170
consensus                                   !!!!!! !!!!!!!!! !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!**!!!!!!!! !!!! !!!!!!!!*!!!!!!!!!
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NTDB id 107844 A214 RS26615 WP 003113873.1  LERLNPAELLIPDDWPQGLPAEKRRGVRRRAPWDFDRDSAHKSLCQQFGTQDLKGFGCQNLTLAIGAAGCLLAYAKETQRTALPH  251
NTDB id 1201 CAH03854.1 414..2993( )        LERLSPAELLIPDDWPQGLPLEKRRGVRRRAPWDFDRDSAFKSLCQQFSTQDLKGFGCENLTLAIGAAGCLLAYAKETQRTALPH  255
consensus                                   !!!! !!!!!!!!!!!!!!! !!!!!!!!!!!!!!!!!!!*!!!!!!! !!!!!!!!! !!!!!!!!!!!!!!!!!!!!!!!!!!
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logo


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NTDB id 107844 A214 RS26615 WP 003113873.1  LRSLRHDRLDDTVILDGASRRNLELDINLSGGRENTLQSVVDRCQTAMASRLMSRWLNRPLRDRAVLEARQESIACLLERYRFEN  336
NTDB id 1201 CAH03854.1 414..2993( )        LRSLRHERLADTVILDGASRRNLELDVNLSGGRDNTLQSVMDRCQTAMGSRLLTRWLNRPLRNREILEARQDSITCLLEHYRFEQ  340
consensus                                   !!!!!!*!! !!!!!!!!!!!!!!!!*!!!!!!*!!!!!!*!!!!!!!*!!!**!!!!!!!! ! *!!!!!*!! !!!!*!!!!*
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NTDB id 107844 A214 RS26615 WP 003113873.1  LQPQLKEIGDLERILARIGLRNARPRDLARLRDALAALPDLQNAMTELEAPHLQALATTIGTYPELAELLAKAIIDNPPAVIRDG  421
NTDB id 1201 CAH03854.1 414..2993( )        LQPQLKDIGDLERILARIGLRNARPRDLARLRDALAALPQLQAGMQDLVAPHLLELATSISTYPELAELLARAIIDNPPAVIRDG  425
consensus                                   !!!!!!*!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!! !! *! *! !!!!  !!!*! !!!!!!!!!!*!!!!!!!!!!!!!
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NTDB id 107844 A214 RS26615 WP 003113873.1  GVIKTGYDAELDELQALSENAGQFLMDLEAREKARTGLPNLKVGYNRIHGYFIELPRVQAEQAPADYIRRQTLKGAERFITPELK  506
NTDB id 1201 CAH03854.1 414..2993( )        GVLKTGYDPELDELQSLSENAGQYLMDLETREKARTGLANLKVGYNRVHGYFIELPSKQAESAPADYIRRQTLKGAERFITPELK  510
consensus                                   !!*!!!!!*!!!!!! !!!!!!!*!!!!! !!!!!!!!*!!!!!!!!*!!!!!!!!  !!! !!!!!!!!!!!!!!!!!!!!!!!
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NTDB id 107844 A214 RS26615 WP 003113873.1  AFEDKALSAQSRALAREKALYEELLERLIGHLAPLQDSASALAELDVLANLAERALNLDLNRPRFVEHTCLHIEQGRHPVVEQVL  591
NTDB id 1201 CAH03854.1 414..2993( )        EFEDKALSAKSRALAREKLLYDELLEMLIGHLAPLQESAAALAELDMLSNLAERALNLDLNRPRFVEQPCMRIEQGRHPVVEQVL  595
consensus                                    !!!!!!!! !!!!!!!! !!*!!!! !!!!!!!!!*!! !!!!!!*! !!!!!!!!!!!!!!!!!!**!**!!!!!!!!!!!!!
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NTDB id 107844 A214 RS26615 WP 003113873.1  ETPFVANDLALDADTRMLVITGPNMGGKSTYMRQTALIVLLAHIGSFVPAARCELSLVDRIFTRIGSSDDLAGGRSTFMVEMSET  676
NTDB id 1201 CAH03854.1 414..2993( )        ETPFVANDLGLDDATRMLVITGPNMGGKSTYMRQTALIVLLAQIGSFVPAAACELSLVDRIFTRIGSSDDLAGGRSTFMVEMSET  680
consensus                                   !!!!!!!!!*!!  !!!!!!!!!!!!!!!!!!!!!!!!!!!!*!!!!!!!! !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!

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NTDB id 107844 A214 RS26615 WP 003113873.1  ANILHNATDKSLVLMDEVGRGTSTFDGLSLAWAAAEDLARTRAFTLFATHYFELTVLPESQPAVANVHLNATEHNERIVFLHHVL  761
NTDB id 1201 CAH03854.1 414..2993( )        ANILHNASDRSLVLMDEVGRGTSTFDGLSLAWAAAEHLAKLRAFTLFATHYFELTVLPESEPVVANVHLSATEHNERIVFLHHVL  765
consensus                                   !!!!!!!*!*!!!!!!!!!!!!!!!!!!!!!!!!!!*!!* !!!!!!!!!!!!!!!!!! ! !!!!!! !!!!!!!!!!!!!!!

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NTDB id 107844 A214 RS26615 WP 003113873.1  PGPASQSYGLAVAQLAGVPAPVIQRAREHLKRLETTSLPHEMPSQQSGKPASPMQSDLFASLPHPVIDELSRINPDDISPRQALD  846
NTDB id 1201 CAH03854.1 414..2993( )        PGPASQSYGLAVAQLAGVPGEVIQRARDHLSRLETTSLSHEAPRITPGQPAPPMQSDMFASLPHPVLEELGRINPDDVTPRQALE  850
consensus                                   !!!!!!!!!!!!!!!!!!!!**!!!!!!*!! !!!!!!!*!! !   *! !!*!!!!!*!!!!!!!!**!! !!!!!!**!!!!!*

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NTDB id 107844 A214 RS26615 WP 003113873.1  LLYAWKMRV.   855
NTDB id 1201 CAH03854.1 414..2993( )        LLYSLKTRI*   859
consensus                                   !!!  ! !*
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X non conserved
X similar
X ≥50% conserved