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logo
NTDB id 99400 DPADHS01 RS08055 WP 003113873.1   ....MTDLSQHTPMMQQYFKLKHQHPDQLMFYRMGDFYELFYEDAKKAAKLLDITLTARGQSGGKAIPMAGIPFHSAEGY   76
NTDB id 1201 CAH03854.1 414..2993( )            MTKPNADLSAHTPMMQQYWRLKREHPDQLMFYRMGDFYELFYDDAKKAAALLDITLTARGQSAGTAIPMAGIPFHSAEGY   80
consensus                                       ****  !!! !!!!!!!!**!!* !!!!!!!!!!!!!!!!!!*!!!!!! !!!!!!!!!!!!*! !!!!!!!!!!!!!!!

logo
NTDB id 99400 DPADHS01 RS08055 WP 003113873.1   LAKLVKLGESVAICEQIGDPATSKGPVERQVVRIITPGTVSDEALLDERRDNLLAAILGDERLFGLAVLDITSGRFSVQE   156
NTDB id 1201 CAH03854.1 414..2993( )            LARLVKLGESVVICEQIGDPAASKGPVERQVVRIITPGTVSDEALLDERRDNLLAAVVGDERLFGLSVLDIASGRFSVQE   160
consensus                                       !!*!!!!!!!! !!!!!!!!! !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!**!!!!!!!! !!!! !!!!!!!!

logo
NTDB id 99400 DPADHS01 RS08055 WP 003113873.1   IKGWETLLAELERLNPAELLIPDDWPQGLPAEKRRGVRRRAPWDFDRDSAHKSLCQQFGTQDLKGFGCQNLTLAIGAAGC   236
NTDB id 1201 CAH03854.1 414..2993( )            LKGWETLLAELERLSPAELLIPDDWPQGLPLEKRRGVRRRAPWDFDRDSAFKSLCQQFSTQDLKGFGCENLTLAIGAAGC   240
consensus                                       *!!!!!!!!!!!!! !!!!!!!!!!!!!!! !!!!!!!!!!!!!!!!!!!*!!!!!!! !!!!!!!!! !!!!!!!!!!!

logo
NTDB id 99400 DPADHS01 RS08055 WP 003113873.1   LLAYAKETQRTALPHLRSLRHDRLDDTVILDGASRRNLELDINLSGGRENTLQSVVDRCQTAMASRLMSRWLNRPLRDRA   316
NTDB id 1201 CAH03854.1 414..2993( )            LLAYAKETQRTALPHLRSLRHERLADTVILDGASRRNLELDVNLSGGRDNTLQSVMDRCQTAMGSRLLTRWLNRPLRNRE   320
consensus                                       !!!!!!!!!!!!!!!!!!!!!*!! !!!!!!!!!!!!!!!!*!!!!!!*!!!!!!*!!!!!!!*!!!**!!!!!!!! ! 

logo
NTDB id 99400 DPADHS01 RS08055 WP 003113873.1   VLEARQESIACLLERYRFENLQPQLKEIGDLERILARIGLRNARPRDLARLRDALAALPDLQNAMTELEAPHLQALATTI   396
NTDB id 1201 CAH03854.1 414..2993( )            ILEARQDSITCLLEHYRFEQLQPQLKDIGDLERILARIGLRNARPRDLARLRDALAALPQLQAGMQDLVAPHLLELATSI   400
consensus                                       *!!!!!*!! !!!!*!!!!*!!!!!!*!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!! !! *! *! !!!!  !!!*!

logo
NTDB id 99400 DPADHS01 RS08055 WP 003113873.1   GTYPELAELLAKAIIDNPPAVIRDGGVIKTGYDAELDELQALSENAGQFLMDLEAREKARTGLPNLKVGYNRIHGYFIEL   476
NTDB id 1201 CAH03854.1 414..2993( )            STYPELAELLARAIIDNPPAVIRDGGVLKTGYDPELDELQSLSENAGQYLMDLETREKARTGLANLKVGYNRVHGYFIEL   480
consensus                                        !!!!!!!!!!*!!!!!!!!!!!!!!!*!!!!!*!!!!!! !!!!!!!*!!!!! !!!!!!!!*!!!!!!!!*!!!!!!!

logo
NTDB id 99400 DPADHS01 RS08055 WP 003113873.1   PRVQAEQAPADYIRRQTLKGAERFITPELKAFEDKALSAQSRALAREKALYEELLERLIGHLAPLQDSASALAELDVLAN   556
NTDB id 1201 CAH03854.1 414..2993( )            PSKQAESAPADYIRRQTLKGAERFITPELKEFEDKALSAKSRALAREKLLYDELLEMLIGHLAPLQESAAALAELDMLSN   560
consensus                                       !  !!! !!!!!!!!!!!!!!!!!!!!!!! !!!!!!!! !!!!!!!! !!*!!!! !!!!!!!!!*!! !!!!!!*! !
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logo

NTDB id 99400 DPADHS01 RS08055 WP 003113873.1  LAERALNLDLNRPRFVEHTCLHIEQGRHPVVEQVLETPFVANDLALDADTRMLVITGPNMGGKSTYMRQTALIVLLAHIG   636
NTDB id 1201 CAH03854.1 414..2993( )           LAERALNLDLNRPRFVEQPCMRIEQGRHPVVEQVLETPFVANDLGLDDATRMLVITGPNMGGKSTYMRQTALIVLLAQIG   640
consensus                                      !!!!!!!!!!!!!!!!!**!**!!!!!!!!!!!!!!!!!!!!!!!*!!  !!!!!!!!!!!!!!!!!!!!!!!!!!!!*!!

logo

NTDB id 99400 DPADHS01 RS08055 WP 003113873.1  SFVPAARCELSLVDRIFTRIGSSDDLAGGRSTFMVEMSETANILHNATDKSLVLMDEVGRGTSTFDGLSLAWAAAEDLAR   716
NTDB id 1201 CAH03854.1 414..2993( )           SFVPAAACELSLVDRIFTRIGSSDDLAGGRSTFMVEMSETANILHNASDRSLVLMDEVGRGTSTFDGLSLAWAAAEHLAK   720
consensus                                      !!!!!! !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!*!*!!!!!!!!!!!!!!!!!!!!!!!!!!*!!*

logo

NTDB id 99400 DPADHS01 RS08055 WP 003113873.1  TRAFTLFATHYFELTVLPESQPAVANVHLNATEHNERIVFLHHVLPGPASQSYGLAVAQLAGVPAPVIQRAREHLKRLET   796
NTDB id 1201 CAH03854.1 414..2993( )           LRAFTLFATHYFELTVLPESEPVVANVHLSATEHNERIVFLHHVLPGPASQSYGLAVAQLAGVPGEVIQRARDHLSRLET   800
consensus                                       !!!!!!!!!!!!!!!!!!! ! !!!!!! !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!**!!!!!!*!! !!!!

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NTDB id 99400 DPADHS01 RS08055 WP 003113873.1  TSLPHEMPSQQSGKPASPMQSDLFASLPHPVIDELSRINPDDISPRQALDLLYAWKMRV.   855
NTDB id 1201 CAH03854.1 414..2993( )           TSLSHEAPRITPGQPAPPMQSDMFASLPHPVLEELGRINPDDVTPRQALELLYSLKTRI*   859
consensus                                      !!!*!! !   *! !!*!!!!!*!!!!!!!!**!! !!!!!!**!!!!!*!!!  !  !*
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X non conserved

X similar

X ≥ 50% conserved