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logo

NTDB id 423189 G4D59 RS05100 WP 017366975.1  MQIPKPNNSTWTDDQWNAIVSEGQDILVAAAAGSGKTAVLVERLIRKMTRPEQPVDVDRLLVVTFTNASAAEMKHRITEA   80
NTDB id 119 BSU 10630 NP 388944.2            MNIPKPADSTWTDDQWNAIVSTGQDILVAAAAGSGKTAVLVERMIRKITAEENPIDVDRLLVVTFTNASAAEMKHRIAEA   80
consensus                                    !*!!!!  !!!!!!!!!!!!! !!!!!!!!!!!!!!!!!!!!!!*!!!*! *!*!*!!!!!!!!!!!!!!!!!!!!!!! !!

logo

NTDB id 423189 G4D59 RS05100 WP 017366975.1  LEKELSKNPGSLHMRRQLSLMNRANISTLHSFCLQVLRTFYYEIDLDPGFRLADQTEGELLGDEVLDELFEDEYKAGKPS  160
NTDB id 119 BSU 10630 NP 388944.2            LEKELVQRPGSLHIRRQLSLLNRASISTLHSFCLQVLKKYYYLIDLDPGFRIADQTEGELIGDEVLDELFEDEYAKGEKA  160
consensus                                    !!!!!   !!!!!*!!!!!!*!!! !!!!!!!!!!!!* *!! !!!!!!!!*!!!!!!!!*!!!!!!!!!!!!!  ! *

logo

NTDB id 423189 G4D59 RS05100 WP 017366975.1  FFELVDRYTSDRHDLDLQWLVKRIYEFSRSHPAPEQWMRAFLSLYDVDTQTKVEELPFYPYIKEDLSLVLRSCQELLEQA  240
NTDB id 119 BSU 10630 NP 388944.2            FFELVDRYTTDRHDLDLQFLVKQVYEYSRSHPNPEAWLESFVHLYDVSEKSAIEELPFYQYVKEDIAMVLNGAKEKLLRA  240
consensus                                    !!!!!!!!!*!!!!!!!!*!!! *!!*!!!!! !! !*  !**!!!!   * *!!!!!!*!*!!!* *!!  * ! !  !

logo

NTDB id 423189 G4D59 RS05100 WP 017366975.1  LTLSKEPGGPAPRAENFIDDLEQVNELIRHQDDFGTLYELLPNINFKRLKTCKGDDYDPALLEKATDARNQAKKQLEKLK  320
NTDB id 119 BSU 10630 NP 388944.2            LELTKAPGGPAPRADNFLDDLAQIDELIQHQDDFSELYKRVPAVSFKRAKAVKGDEFDPALLDEATDLRNGAKKLLEKLK  320
consensus                                    ! !*! !!!!!!!!*!!*!!! !* !!! !!!!!  !!  *! * !!! ! *!!!**!!!!!* !!! !! !!! !!!!!

logo

NTDB id 423189 G4D59 RS05100 WP 017366975.1  DEYFMRSPDQHLKSLAEMKPVVETLVELVIQYGERFERAKQEKSIVDFSDLEHYCLRILAKQDAEGNLIETEAAKYYQQQ  400
NTDB id 119 BSU 10630 NP 388944.2            TDYFTRSPEQHLKSLAEMKPVIETLVQLVISYGKRFEAAKQEKSIIDFSDLEHYCLAILTAENDKGEREPSEAARFYQEQ  400
consensus                                     *!! !!!*!!!!!!!!!!!!!*!!!! !!! !! !!! !!!!!!!*!!!!!!!!!! !!      !   **!!!**!! !

logo

NTDB id 423189 G4D59 RS05100 WP 017366975.1  FEEVLVDEYQDTNLVQETILKLVSKGKHPAEGNRFMVGDVKQSIYRFRLAEPMLFLNKYKQFKADSNEIGKRIDLNKNFR  480
NTDB id 119 BSU 10630 NP 388944.2            FHEVLVDEYQDTNLVQESILQLVTSGPE.ETGNLFMVGDVKQSIYRFRLAEPLLFLSKYKRFTESGEGTGRKIDLNKNFR  479
consensus                                    !*!!!!!!!!!!!!!!!!*!! !!* !***  !! !!!!!!!!!!!!!!!!!!*!!! !!! !       !**!!!!!!!!

logo

NTDB id 423189 G4D59 RS05100 WP 017366975.1  SRADVLDSTNFLFKQLMGETVGEIEYDEQAELKLGASYPQSEDTTTEMLLVHLDQHDTESDEEREELETVQFEARVIAKK  560
NTDB id 119 BSU 10630 NP 388944.2            SRADILDSTNFLFKQLMGGKIGEVDYDEQAELKLGAAYPDNDETETELLLIDN.AEDTDASEEAEELETVQFEAKAIAKE  558
consensus                                    !!!!*!!!!!!!!!!!!!  *!!**!!!!!!!!!!! !!  **! !!*!!** * *!!*  !! !!!!!!!!!* !!!
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logo

NTDB id 423189 G4D59 RS05100 WP 017366975.1  IKELVEQPFQVYDAKQQLTRNLQYRDIVILLRSMPWAPQMMEELKKQGIPVYANLSSGYFEATEVSVILSLLKVIDNPYQ   640
NTDB id 119 BSU 10630 NP 388944.2            IRKLISSPFKVYDGKKKTHRNIQYRDIVILLRSMPWAPQIMEELRAQGIPVYANLTSGYFEAVEVAVALSVLKVIDNPYQ   638
consensus                                    !* !*  !! !!!*!   *!!*!!!!!!!!!!!!!!!!*!!!!* !!!!!!!!!*!!!!!! !! ! !!*!!!!!!!!!

logo

NTDB id 423189 G4D59 RS05100 WP 017366975.1  DIPLAAVLRSPIVHLDENEMALIRTSDKKGTYYDAVKAFMSVTHSDHPTCRKLERFFLQLRKWRDFSIQHSVAELIWEVY   720
NTDB id 119 BSU 10630 NP 388944.2            DIPLASVLRSPIVGADENELSLIRLENKKAPYYEAMKDYLAAGDRSDELYQKLNTFYGHLQKWRAFSKNHSVSELIWEVY   718
consensus                                    !!!!! !!!!!!!* !!!!* !!!   !!**!!*!*! **   *  ** * !!  !* *! !!! !! *!!! !!!!!!!

logo

NTDB id 423189 G4D59 RS05100 WP 017366975.1  RDTQYLDYVGGMPGGKQRQANLRALYDRAKQYEKAAFRGLFRFLRFIERMQERGDDLGAAKTFSETEDVVRMMTIHSSKG   800
NTDB id 119 BSU 10630 NP 388944.2            RDTKYMDYVGGMPGGKQRQANLRVLYDRARQYESTAFRGLFRFLRFIERMQERGDDLGTARALSEQEDVVRLMTIHSSKG   798
consensus                                    !!! !*!!!!!!!!!!!!!!!!!! !!!!!*!!!  !!!!!!!!!!!!!!!!!!!!!!! !*  !! !!!!!*!!!!!!!!

logo

NTDB id 423189 G4D59 RS05100 WP 017366975.1  LEFPVVFTAGLGRNFNMMDLNQSYLLDKELGFGSKYIHPELRISYATLPLIAMKKKMRKELLSEELRVLYVALTRAKEKL   880
NTDB id 119 BSU 10630 NP 388944.2            LEFPVVFVAGLGRNFNMMDLNKSYLLDKELGFGTKYIHPQLRISYPTLPLIAMKKKMRRELLSEELRVLYVALTRAKEKL   878
consensus                                    !!!!!!! !!!!!!!!!!!!!! !!!!!!!!!!!*!!!!! !!!!!*!!!!!!!!!!!!!*!!!!!!!!!!!!!!!!!!!!

logo

NTDB id 423189 G4D59 RS05100 WP 017366975.1  FLVGSVKNQVKALSKWQNAAKGDDWLLPDFERYQARTYLDFIGPALIRHQAMSSLLEESR.EVVLSHPSSFSITFHQASD   959
NTDB id 119 BSU 10630 NP 388944.2            FLIGSCKDHQKQLAKWQASASQTDWLLPEFDRYQARTYLDFIGPALARHRDLGDLAGVPAHADISGHPARFAVQMIHSYD   958
consensus                                    !!*!!*! * ! ! !!!   !    !!!!!*!*!!!!!!!!!!!!!!! !!  *  !   * *  *  !!  ! *  **  !

logo

NTDB id 423189 G4D59 RS05100 WP 017366975.1  LLQEDMSLEKQKQDEVVQALMEGVPVQGYGNYEEEVKERLSWRYPYLAASQVGTKQSVSEIKRMKEIQDEYSVPSSVRKA   1039
NTDB id 119 BSU 10630 NP 388944.2            LLDDDLEERMEEKSERLEAIRRGEPVPGSFAFDEKAREQLSWTYPHQEVTQIRTKQSVSEIKRKREYEDEYSGRAPVKPA   1038
consensus                                    !! *!*         ! * !*  ! !!*!   **!  *! !!! !!*   *!* !!!!!!!!!! *!  !!!! * *!**!

logo

NTDB id 423189 G4D59 RS05100 WP 017366975.1  R.ATLYERPAFMKKKTLTAAEQGTAMHTVMQHIPLPSNESYDESRVEELLHSLKEKDLLTDEQIQSINREGIVAFFSTAI   1118
NTDB id 119 BSU 10630 NP 388944.2            DGSILYRRPAFMMKKGLTAAEKGTAMHTVMQHIPLSHVPSIEE..AEQTVHRLYEKELLTEEQKDAIDIEEIVQFFHTEI   1116
consensus                                     *  !! !!!!! !! !!!!! !!!!!!!!!!!!!** *! *!** !  *! ! !!*!!!*!!   !  ! !! !!*! !
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logo
NTDB id 423189 G4D59 RS05100 WP 017366975.1  GQKLRKADWVKREVSFSMVLPVKEVYSHIDAEGEPVLIQGMIDCLFEADGKLYLLDYKTDRVTGRFSGGLEEAEAMLKKR  1198
NTDB id 119 BSU 10630 NP 388944.2            GGQLIGAKWKDREIPFSLALPAKEIYPDAHEADEPLLVQGIIDCLYETEDGLYLLDYKSDRIEGKFQHGFEGAAPILKKR  1196
consensus                                    !  !  ! !  !!**!!* !! !!*!** *   !!*!*!!*!!!!*! *  !!!!!!!*!!* !*! *! ! ! **!!!!
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logo
NTDB id 423189 G4D59 RS05100 WP 017366975.1  YETQISLYTAAVERLTNRTLEEKILYFFDGNLEISL  1234
NTDB id 119 BSU 10630 NP 388944.2            YETQIQLYTKAVEQIAKTKVKGCALYFFDGGHILTL  1232
consensus                                    !!!!! !!! !!! *    *  * !!!!!! * **!
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X non conserved

X similar

X $\geq$ 50% conserved