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logo
NTDB id 985958 MHH61 RS14180 WP 125586545.1  MQIPKPNNSTWTDDQWEAIVSEGQDILVAAAAGSGKTAVLVERLIRKMTRPEDPVDVDRLLVVTFTNASAAEMKHRITEA   80
NTDB id 119 BSU 10630 NP 388944.2            MNIPKPADSTWTDDQWNAIVSTGQDILVAAAAGSGKTAVLVERMIRKITAEENPIDVDRLLVVTFTNASAAEMKHRIAEA   80
consensus                                    !*!!!!  !!!!!!!! !!!! !!!!!!!!!!!!!!!!!!!!*!!!*! *! !*!!!!!!!!!!!!!!!!!!!!!! !!

logo
NTDB id 985958 MHH61 RS14180 WP 125586545.1  LEKELVKNPGSLHMRRQLSLMNRANISTLHSFCLQVLRTFYYEIDLDPGFRLADQTEGELLGDEVLDELFEDEYKAGKPA  160
NTDB id 119 BSU 10630 NP 388944.2            LEKELVQRPGSLHIRRQLSLLNRASISTLHSFCLQVLKKYYYLIDLDPGFRIADQTEGELIGDEVLDELFEDEYAKGEKA  160
consensus                                    !!!!!!  !!!!!*!!!!!!*!!! !!!!!!!!!!!!* *!! !!!!!!!!*!!!!!!!!*!!!!!!!!!!!!!  ! *!

logo
NTDB id 985958 MHH61 RS14180 WP 125586545.1  FFELVDRYTSDRHDLDLQWLVKRIYEFSRSHPSPDQWMRAFLSLYDVDAQTKVEQLPFYPYIKEDLSLVFRSCLELLERA  240
NTDB id 119 BSU 10630 NP 388944.2            FFELVDRYTTDRHDLDLQFLVKQVYEYSRSHPNPEAWLESFVHLYDVSEKSAIEELPFYQYVKEDIAMVLNGAKEKLLRA  240
consensus                                    !!!!!!!!!*!!!!!!!!*!!! *!!*!!!!! !* !*  !**!!!!   * *! !!!!*!*!!!* *!   * ! ! !!

logo
NTDB id 985958 MHH61 RS14180 WP 125586545.1  LALSKEPGGPAPRAENFIDDLEQVNELIRHQDDFSKLYKRVPNVSFKRLKTVKGDEYDPVLLEKATDARNQAKKQLEKLK  320
NTDB id 119 BSU 10630 NP 388944.2            LELTKAPGGPAPRADNFLDDLAQIDELIQHQDDFSELYKRVPAVSFKRAKAVKGDEFDPALLDEATDLRNGAKKLLEKLK  320
consensus                                    ! !*! !!!!!!!!*!!*!!! !* !!! !!!!!  !!  *! * !!! ! *!!!!*!! !!* !!! !! !!! !!!!!

logo
NTDB id 985958 MHH61 RS14180 WP 125586545.1  DEYFMRSPAQHLKSLAEMKPVVETLVELVIQFGQRFERAKQEKSIVDFSDLEHYCLRILAEQDAEGNLIETEAAKYYQQQ  400
NTDB id 119 BSU 10630 NP 388944.2            TDYFTRSPEQHLKSLAEMKPVIETLVQLVISYGKRFEAAKQEKSIIDFSDLEHYCLAILTAENDKGEREPSEAARFYQEQ  400
consensus                                     *!! !!! !!!!!!!!!!!!*!!!! !!! *! !!! !!!!!!!*!!!!!!!!!! !!      !   **!!!**!! !

logo
NTDB id 985958 MHH61 RS14180 WP 125586545.1  FEEVLVDEYQDTNLVQETILKLVSKGEHAAEGNLFMVGDVKQSIYRFRLAEPMLFLNKYKQFKPDGKETGKRIDLNKNFR  480
NTDB id 119 BSU 10630 NP 388944.2            FHEVLVDEYQDTNLVQESILQLVTSGPE.ETGNLFMVGDVKQSIYRFRLAEPLLFLSKYKRFTESGEGTGRKIDLNKNFR  479
consensus                                    !*!!!!!!!!!!!!!!!!*!! !!* !***  !!!!!!!!!!!!!!!!!!!!!*!!! !!! ! * !  !!**!!!!!!!!

logo
NTDB id 985958 MHH61 RS14180 WP 125586545.1  SRSDVLDSTNFLFKQLMGETVGEIEYDEQAELKLGASYPESKDTTTEMLLVHLDQQEAESDEEREELETVQLEARVIAKK  560
NTDB id 119 BSU 10630 NP 388944.2            SRADILDSTNFLFKQLMGGKIGEVDYDEQAELKLGAAYPDNDETETELLLIDNA.EDTDASEEAEELETVQFEAKAIAKE  558
consensus                                    !! !*!!!!!!!!!!!!!  *!!**!!!!!!!!!!! !!*  *! !!*!!**  * * *  !! !!!!!!! !!* !!!
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logo
NTDB id 985958 MHH61 RS14180 WP 125586545.1  IRELVEQPFQVYDAKQQLTRNLQYRDIVILLRSMPWAPQMMEELKKQGIPVYANLSSGYFEATEVSVILSLLKVIDNPYQ   640
NTDB id 119 BSU 10630 NP 388944.2            IRKLISSPFKVYDGKKKTHRNIQYRDIVILLRSMPWAPQIMEELRAQGIPVYANLTSGYFEAVEVAVALSVLKVIDNPYQ   638
consensus                                    !! !*  !! !!!*!    *!!*!!!!!!!!!!!!!!!!*!!!!* !!!!!!!!!*!!!!!! !! ! !!*!!!!!!!!!

logo
NTDB id 985958 MHH61 RS14180 WP 125586545.1  DIPLAAVLRSPIVHLDENEMALIRTSDKKGTYYDAVKAFMSVTHSDHPTCKKLERFFRLLRKWRDFSMNHSVAELIWEVY   720
NTDB id 119 BSU 10630 NP 388944.2            DIPLASVLRSPIVGADENELSLIRLENKKAPYYEAMKDYLAAGDRSDELYQKLNTFYGHLQKWRAFSKNHSVSELIWEVY   718
consensus                                    !!!!! !!!!!!!* !!!!* !!!   !!**!!*!*! **   *  ** * !!  !* *! !!! !! !!!! !!!!!!!

logo
NTDB id 985958 MHH61 RS14180 WP 125586545.1  RDTQYLDYVGGMPGGKQRQANLRALYDRAKQYEKAAFRGLFRFLRFIERMQERGDDLGAAKTFSETEDVVRMMTIHSSKG   800
NTDB id 119 BSU 10630 NP 388944.2            RDTKYMDYVGGMPGGKQRQANLRVLYDRARQYESTAFRGLFRFLRFIERMQERGDDLGTARALSEQEDVVRLMTIHSSKG   798
consensus                                    !!! !*!!!!!!!!!!!!!!!!!! !!!!!*!!!  !!!!!!!!!!!!!!!!!!!!!!! !*  !! !!!!!*!!!!!!!!

logo
NTDB id 985958 MHH61 RS14180 WP 125586545.1  LEFPIVFTAGLGRNFNMMDLNQSYLLDKELGFGSKYIHPELRISYATLPLVAMKKKMRKELLSEELRVLYVALTRAKEKL   880
NTDB id 119 BSU 10630 NP 388944.2            LEFPVVFVAGLGRNFNMMDLNKSYLLDKELGFGTKYIHPQLRISYPTLPLIAMKKKMRRELLSEELRVLYVALTRAKEKL   878
consensus                                    !!!!*!! !!!!!!!!!!!!! !!!!!!!!!!!*!!!!! !!!!!*!!!!*!!!!!!!*!!!!!!!!!!!!!!!!!!!!!

logo
NTDB id 985958 MHH61 RS14180 WP 125586545.1  FLVGSVKNQVKALSKWQNAANGEDWLIPDFERYQSKTYLDFIGPALIRHQAMSSILEETGN.VVLSHPSVFTISFTQASD   959
NTDB id 119 BSU 10630 NP 388944.2            FLIGSCKDHQKQLAKWQASASQTDWLLPEFDRYQARTYLDFIGPALARHRDLGDLAGVPAHADISGHPARFAVQMIHSYD   958
consensus                                    !!*!!*! * ! ! !!!   !    !!!*!*!*!!! *!!!!!!!!!! !!  *  *   **** *  !!   ! *   *  !

logo
NTDB id 985958 MHH61 RS14180 WP 125586545.1  LLKEDMSLEKKQQDEVVQALMDGLPVEGYGDADEKVAERLSWRYPYLAASQVGTKQSVSEIKRMKEIQDEYSVPSSLRRA   1039
NTDB id 119 BSU 10630 NP 388944.2            LLDDDLEEERMEEKSERLEAIRRGEPVPGSFAFDEKAREQLSWTYPHQEVTQIRTKQSVSEIKRKREYEDEYSGRAPVKPA   1038
consensus                                    !! *!*         ! * !*  ! !!*!    !!!  ! !!! !!*   *!* !!!!!!!!!! *!  !!!! * ****!

logo
NTDB id 985958 MHH61 RS14180 WP 125586545.1  H.ATLYDRPAFMKKKALTAAEQGTAMHTVMQHIPLSSDEPLDEIHIHQLLDSLQQRDLLTNEQVQSIDQEGISAFFSTSI   1118
NTDB id 119 BSU 10630 NP 388944.2            DGSILYRRPAFMMKKGLTAAEKGTAMHTVMQHIPLSHVPSIEEA..EQTVHRLYEKELLTEEQKDAIDIEEIVQFFHTEI   1116
consensus                                    **  !! !!!!! !!*!!!!! !!!!!!!!!!!!!!* ****! ***! ** !  **!!! !!   !! ! !  !!*! !
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logo
NTDB id 985958 MHH61 RS14180 WP 125586545.1  GQKLLKADWVKREMSFSMVLPVKEVYSHIDAEGEPVLIQGMIDCLFETDGKLYLLDYKTDRVQGRYTGGLEAAVPILKKR  1198
NTDB id 119 BSU 10630 NP 388944.2            GGQLIGAKWKDREIPFSLALPAKEIYPDAHEADEPLLVQGIIDCLYETEDGLYLLDYKSDRIEGKFQHGFEGAAPILKKR  1196
consensus                                    !  !* ! !  !!**!!* !! !!*!** *   !!*!*!!*!!!!*!!*  !!!!!!!*!!* !** *! !*! !!!!!!
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logo
NTDB id 985958 MHH61 RS14180 WP 125586545.1  YETQIALYAQAVERLTNRTLEEKILYFFDGNLEISL  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