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logo

NTDB id 1010040 ABN702 RS13620 WP 417900905.1  MGMELLPKPVDAQWTDDQWKAIVASGRDILVAAAAGSGKTAVLVERMIHKIVQE..HVDVDRLLVVTFTNASAAEMRHRI   78
NTDB id 119 BSU 10630 NP 388944.2              ...MNIPKPADSTWTDDQWNAIVSTGQDILVAAAAGSGKTAVLVERMIRKITAEENPIDVDRLLVVTFTNASAAEMKHRI   77
consensus                                      ***  *!!! !  !!!!!! !!! *! !!!!!!!!!!!!!!!!!!!!*!!  !** *!!!!!!!!!!!!!!!!!!*!!!

logo

NTDB id 1010040 ABN702 RS13620 WP 417900905.1  GEALEKQLEKRPASLHLRRQLSLLNRASISTIHSFCLDVVRKYYYLIDIDPSFRIADTTEIQLMQEEVLENVFEEEYGKE  158
NTDB id 119 BSU 10630 NP 388944.2              AEALEKELVQRPGSLHIRRQLSLLNRASISTLHSFCLQVLKKYYYLIDLDPGFRIADQTEGELIGDEVLDELFEDEYAK.  156
consensus                                      *!!!!! !  !!*!!!*!!!!!!!!!!!!!!*!!!!! !**!!!!!!!*!! !!!!! !!  !* *!!!* *!!*!!*!*

logo

NTDB id 1010040 ABN702 RS13620 WP 417900905.1  GNDAFFDLVDRYTNDRTDGALQKLVLDLHEFSRANPAPEKWLEDIAAFYQSTSQLPIDELPFISMLKREMELQFLGAKSL  238
NTDB id 119 BSU 10630 NP 388944.2              GEKAFFELVDRYTTDRHDLDLQFLVKQVYEYSRSHPNPEAWLESFVHLYDVSEKSAIEELPFYQYVKEDIAMVLNGAKEK  236
consensus                                      !  !!!*!!!!!! !!*!  !! !!  **!*!! *! !! !!!   * !  *   *!*!!!!   *! ** *   !!!

logo

NTDB id 1010040 ABN702 RS13620 WP 417900905.1  LEKAMEITLEPGGPAPRSVNIEEDTEQLARLQAALGESWDVLYEEMQSLDFPRAKTCRGDEYDKELIESWTKVRNKAKGI  318
NTDB id 119 BSU 10630 NP 388944.2              LLRALELTKAPGGPAPRADNFLDDLAQIDELIQ.HQDDFSELYKRVPAVSFKRAKAVKGDEFDPALLDEATDLRNGAKKL  315
consensus                                      ! *!*!*!  !!!!!!!  !  *!  !*  !  ** * *  !!  ** * !*!!! **!!!*!* !**  ! *!! !! *

logo

NTDB id 1010040 ABN702 RS13620 WP 417900905.1  VQGIKDELFSRRPESFLKDLEELAPVMSTLVGLVKEYGRQFSMLKQEKGLVDFSDLEHLCLSILRTPTGSGF.ERSEAAL  397
NTDB id 119 BSU 10630 NP 388944.2              LEKLKTDYFTRSPEQHLKSLAEMKPVIETLVQLVISYGKRFEAAKQEKSIIDFSDLEHYCLAILTAENDKGEREPSEAAR  395
consensus                                      *  *! * !*! !! *!! ! !* !!* !!! !!  !!* !   !!!! **!!!!!!! !! !!  *   ! *!*!!!!

logo

NTDB id 1010040 ABN702 RS13620 WP 417900905.1  RYQATFKEVMVDEYQDTNMVQEAILKLVTKEEEEAGNMFMVGDVKQSIYRFRLAEPFLFLSKYKRFDTKGEDGGLRIDLN  477
NTDB id 119 BSU 10630 NP 388944.2              FYQEQFHEVLVDEYQDTNLVQESILQLVTSGPEETGNLFMVGDVKQSIYRFRLAEPLLFLSKYKRFTESGEGTGRKIDLN  475
consensus                                       !!  !*!!*!!!!!!!!*!!! !! !!!  *!! !!*!!!!!!!!!!!!!!!!!! !!!!!!!!!   !!  ! *!!!!

logo

NTDB id 1010040 ABN702 RS13620 WP 417900905.1  RNFRSRTEVLDATNFIFKQIMGETVGEIDYNEAAELKFGAANYPQADDRETELLLVDRSDHSADESFGVSEEDFSPSAFD  557
NTDB id 119 BSU 10630 NP 388944.2              KNFRSRADILDSTNFLFKQLMGGKIGEVDYDEQAELKLGA.AYPDNDETETELLLIDNAEDTDA.............SEE  541
consensus                                      *!!!!! **!! !!!*!!!*!!  *!!*!! ! !!!! !!* !!  !* !!!!!!*!  ***  ************  *
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logo
NTDB id 1010040 ABN702 RS13620 WP 417900905.1  KVELETAQVEAKLIARKIKKLIQSGYKIYDKDEKRMRPVTYRDFVILMRSMPWAPQFMEEFKQEGLPLYANLSTGYFEAT   637
NTDB id 119 BSU 10630 NP 388944.2              AEELETVQFEAKAIAKEIRKLISSPFKVYDGKKKTHRNIQYRDIVILLRSMPWAPQIMEELRAQGIPVYANLTSGYFEAV   621
consensus                                        !!!! ! !!! !!* !*!!! !**!*!!   ! *!** !!! !!!*!!!!!!!! !!! *  !*!*!!!!**!!!!!

logo
NTDB id 1010040 ABN702 RS13620 WP 417900905.1  EVAIMLSLLKIIDNPYQDIPLASVLRSPIVGLDSNELALIRIQQRKGNYFDALLVFLNKTPDSVEEKEVVRKVKAFYEML   717
NTDB id 119 BSU 10630 NP 388944.2              EVAVALSVLKVIDNPYQDIPLASVLRSPIVGADENELSLIRLENKKAPYYEAMKDYLAAGD...RSDELYQKLNTFYGHL   698
consensus                                      !!!* !!*!!*!!!!!!!!!!!!!!!!!!! ! !!! !!!* **!**!**!*  *!   ****   !*  !*  !! *!

logo
NTDB id 1010040 ABN702 RS13620 WP 417900905.1  QNWRTSAREGALSELIWQIYQDTHFYDFVGGMPGGKQRQANLRALYDRARQYESTSFRGLFRFLRFIERMQDRGEDLGAA   797
NTDB id 119 BSU 10630 NP 388944.2              QKWRAFSKNHSVSELIWEVYRDTKYMDYVGGMPGGKQRQANLRVLYDRARQYESTAFRGLFRFLRFIERMQERGDDLGTA   778
consensus                                      ! !!   * * *!!!!! *! !!** !*!!!!!!!!!!!!!!! !!!!!!!!!!! !!!!!!!!!!!!!!!*!!*!!! !

logo
NTDB id 1010040 ABN702 RS13620 WP 417900905.1  RALGEQEDVIRLMTIHSSKGLEFPIVFVAGLSRQFNMMDLNSSYLMDKELGFGTKYVNARLRITYPTLLQLALKRKAKAQ   877
NTDB id 119 BSU 10630 NP 388944.2              RALSEQEDVVRLMTIHSSKGLEFPWVFVAGLGRNFNMMDLNKSYLLDKELGFGTKYIHPQLRISYPTLPLIAMKKKMRRE   858
consensus                                      !!! !!!!!*!!!!!!!!!!!!!!!*!!!!!! !*!!!!!!! !!!*!!!!!!!*!!*** !!!*!!!!* *!*!*! *

logo
NTDB id 1010040 ABN702 RS13620 WP 417900905.1  LIAEEMRVLYVALTRAKEKLYLVGTVKDFEKSRLQWNESADTNNWLLPDYARAASKSYIDWVGPALVRHKDADELREGAT   957
NTDB id 119 BSU 10630 NP 388944.2              LLSEELRVLYVALTRAKEKLFLIGSCKDHQKQLAKWQASASQTDWLLPEFDRYQARTYLDFIGPALARHRDLGDLAGVPA   938
consensus                                      !* !!*!!!!!!!!!!!!!!!*!*!**!!* !    !* !!    !!!!** !   **!*!**!!!! !!*!  *!   *

logo
NTDB id 1010040 ABN702 RS13620 WP 417900905.1  STLIPEEITQHPASWKITVTNVQELLE.ELESAKHEENELLEKVKHGLHVNIQSPLFEKVKEQLHWQYPFKEASRHRSKQ  1036
NTDB id 119 BSU 10630 NP 388944.2              ....HADISGHPARFAVQMIHSYDLLDDDLEERMEEKSERLEAIRRGEPVPGSFAFDEKAREQLSWTYPHQEVTQIRTKQ  1014
consensus                                      ****  *!* !!! * * * *  *!!***!!   *!  ! !! ***!  !*   *  !! *!!!*! !!* ! * *!*!!

logo
NTDB id 1010040 ABN702 RS13620 WP 417900905.1  SVSELKRMKEQQDPYADHSLVQT.ERKYFLDRPTFLQKKRLSPSEIGTAMHTVMQNIRLDQSSFTREELQGRILEMVQKE  1115
NTDB id 119 BSU 10630 NP 388944.2              SVSEIKRKREYEDEYSGRAPVKPADGSILYRRPAFMMKKGLTAAEKGTAMHTVMQHIPLSHVPSIE.EAEQTVHRLYEKE  1093
consensus                                      !!!!*!! *!  !*!  * *! ***      !! !* !! !** ! !!!!!!!!!!*!*! * *   *!    ** *  !!
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logo

NTDB id 1010040 ABN702 RS13620 WP 417900905.1  LLTGDQAEVIDMSAVESFFSTPIGKRMLHAEKVHREVPFSFALKGSEIGNDADLEEETVLVQGVIDCLIEDEDGLVLLDY  1195
NTDB id 119 BSU 10630 NP 388944.2              LLTEEQKDAIDIEEIVQFFHTEIGGQLIGAKWKDREIPFSLALPAKEIYPDAHEADEPLLVQGIIDCLYETEDGLYLLDY  1173
consensus                                      !!! *! * !!*  *  !!*!*!!  ***!   *!!*!!! !!** !! *!!*  *!**!!!!*!!!! ! !!!! !!!!

logo

NTDB id 1010040 ABN702 RS13620 WP 417900905.1  KTDTITGRFANGFEEAEPVLRNRYREQVSLYGKAVEQIWNKKLTAKYLYFFDRNHLVKIEE  1256
NTDB id 119 BSU 10630 NP 388944.2              KSDRIEGKFQHGFEGAAPILKKRYETQIQLYTKAVEQIAKTKVKGCALYFFDGGHILTL..  1232
consensus                                      !*! ! !*! *!!! ! !*!* !!  !* !! !!!!!!   !* ** !!!!!  !** ***
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X non conserved

X similar

X $\geq$ 50% conserved