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logo

NTDB id 410861 BABF1 RS05705 WP 000970458.1  MMENWPKKPEGSQWTDDQWKAVVATGRDILVAAAAGSGKTAVLVERIIKKIINEENPVDVDRLLVVTFTNAAAQEMKNRI   80
NTDB id 119 BSU 10630 NP 388944.2            ...MNIPKPADSTWTDDQWNAIVSTGQDILVAAAAGSGKTAVLVERMIRKITAEENPIDVDRLLVVTFTNASAAEMKHRI   77
consensus                                    ***  **!!  ! !!!!!! !*! !! !!!!!!!!!!!!!!!!!!*!*!!  !!!!*!!!!!!!!!!!!! ! !!!*!!

logo

NTDB id 410861 BABF1 RS05705 WP 000970458.1  GEALEKVLIDEPGSQHVRKQLSLLNKASISTIHSFCLQVIRGYYYMLDVDPRFRIANQTENELLKEEVLDDILEEEYGIE  160
NTDB id 119 BSU 10630 NP 388944.2            AEALEKELVQRPGSLHIRRQLSLLNRASISTLHSFCLQVLKKYYYLIDLDPGFRIADQTEGELIGDEVLDELFEDEYAKG  157
consensus                                    *!!!!! !*  !!! !*!*!!!!!!*!!!!!*!!!!!!!** !!!**!*!! !!!! !!! !!* *!!!!** !*!!*

logo

NTDB id 410861 BABF1 RS05705 WP 000970458.1  DNTIFFELVDRYTSDRSDDDLQRMILALHTESRAHPNPEKWLDKLVEAYDVEGK.TIEDLVYASYLLEDVKFQLETAEQH  239
NTDB id 119 BSU 10630 NP 388944.2            .EKAFFELVDRYTTDRHDLDLQFLVKQVYEYSRSHPNPEAWLESFVHLYDVSEKSAIEELPFYQYWKEDIAMVLNGAKEK  236
consensus                                    *   !!!!!!!!!*!!*! !!! **  **  !! !!!!! !!*  !* !!!  !* !!*!**  !* !!*   !  !   *

logo

NTDB id 410861 BABF1 RS05705 WP 000970458.1  IRKATELAMLPDGPAPRIETLQADLALLGTLSAAARESWTSVYEAMQNVSWQTLKRIKKSDYNEDIVKQVDSLRNKAKDE  319
NTDB id 119 BSU 10630 NP 388944.2            LLRALELTKAPGGPAPRADNFLDDLAQIDELIQ.HQDDFSELYKRVPAVSFKRAKAVKGDEFDPALLDEATDLRNGAKKL  315
consensus                                    * *! !!   ! !!!!! *    !!! *  !  ** * ** *!  ** !!*   ! *!  ** * **     !!! !!

logo

NTDB id 410861 BABF1 RS05705 WP 000970458.1  VKKLQEELFSRRPESFLRDFQDMHPVLEKLVQLVKVFTERFQAMKRDKGMVDFTDLEHFCLQILSEQSEDGEMKPSAVAL  399
NTDB id 119 BSU 10630 NP 388944.2            LEKLKTDYFTRSPEQHLKSLAEMKPVIETLVQLVISYGKRFEAAKQEKSIIDFSDLEHYCLAILTAENDKGEREPSEAAR  395
consensus                                    * !!  * !*! !! *!*   *!*!!*! !!!!!  *  !! ! ! *! **!!*!!!!*!! !!*   * !!  !!  !

logo

NTDB id 410861 BABF1 RS05705 WP 000970458.1  QYRNKFAEVLVDEYQDTNFVQESIIKFVTKDSESEGNLFMVGDVKQSIYRFRLAEPGLFLGKYKRFTQEGLGGGMKIDLA  479
NTDB id 119 BSU 10630 NP 388944.2            FYQEQFHEVLVDEYQDTNLVQESILQLVTSGPEETGNLFMVGDVKQSIYRFRLAEPLLFLSKYKRFTESGEGTGRKIDLN  475
consensus                                     !   !*!!!!!!!!!!! !!!!!*  !!  *!  !!!!!!!!!!!!!!!!!!!!! !!! !!!!!!  ! ! ! !!!!

logo

NTDB id 410861 BABF1 RS05705 WP 000970458.1  KNFRSRHEVLAGTNFIFKQIMGEEVGEIDYDADAELKLGASYPEGEDVAAELLCIQQTEEEVIDGEEGAEVEKAQLEARL  559
NTDB id 119 BSU 10630 NP 388944.2            KNFRSRADILDSTNFLFKQLMGGKIGEVDYDEQAELKLGAAYPDNDETETELLLIDNAEDT.DASEEAEELETVQFEAKA  554
consensus                                    !!!!!!***!  !!!*!!!*!!  *!!*!!!  !!!!!!! !!* **   !!!*!  * !* *   !!* !*!  ! !!*
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logo
NTDB id 410861 BABF1 RS05705 WP 000970458.1  MAQRIKAMVDSGYEVYDRKTDSMRPVKYRDFVILLRSMPWAPQIMEELKLQGIPVYADLATGYFEATEVNIMMNVFRVID   639
NTDB id 119 BSU 10630 NP 388944.2            IAKEIRKLISSPFKVYDGKKKTHRNIQYRDIVILLRSMPWAPQIMEELRAQGIPVYANLTSGYFEAVEVAVALSVLKVID   634
consensus                                    *!  !* ** !** !!! !  **!** !!! !!!!!!!!!!!!!!!!* !!!!!!! ! *!!!!! !! * * ! *!!!

logo
NTDB id 410861 BABF1 RS05705 WP 000970458.1  NPMQDIPLAAVLRSPIVGLNDEELATLRAHGKKGSFYEVMSSFLKGAPLEEEKELHDKLEWFYNLLQGWREFARQQSLSD   719
NTDB id 119 BSU 10630 NP 388944.2            NPYQDIPLASVLRSPIVGADENELSLIRLENKKAPYYEAMKDYLAAGD..RSDELYQKLNTFYGHLQKWRAFSKNHSVSE   712
consensus                                    !! !!!!!! !!!!!!!!  * !!  *! * !!***!! !  *! *****   !!* !!  !! *!! !! ! ***!*!*

logo
NTDB id 410861 BABF1 RS05705 WP 000970458.1  LIWKVYGETGYYDFVGGLPAGKQRQANLRVLYDRARQYEATSFRGLFRFLRFIERILERGDDMGTARALGEQEDVVRIMT   799
NTDB id 119 BSU 10630 NP 388944.2            LIWEVYRDTKYMDYVGGMPGGKQRQANLRVLYDRARQYESTAFRGLFRFLRFIERMQERGDDLGTARALSEQEDVVRLMT   792
consensus                                    !!! !! *! ! !*!!!*!*!!!!!!!!!!!!!!!!!! ! !!!!!!!!!!!!!* !!!!!*!!!!!! !!!!!!!*!!

logo
NTDB id 410861 BABF1 RS05705 WP 000970458.1  IHKSKGLEFPVVFVAGLGRRFNTQDLMKRFLLHKDFGFGSQFIDPRKRIKYTTLSQLAIKRKMKMELIAEEMRVLYVALT   879
NTDB id 119 BSU 10630 NP 388944.2            IHSSKGLEFPVVFVAGLGRNFNMMDLNKSYLLDKELGFGTKYIHPQLRISYPTLPLIAMKKKMRRELLSEELRVLYVALT   872
consensus                                    !! !!!!!!!!!!!!!!! !!  !! ! *!!*!* !!!* *!*!  !! !*!!* *!*!*!!* !!* !!*!!!!!!!!

logo
NTDB id 410861 BABF1 RS05705 WP 000970458.1  RAKEKLILIGTVKDATKEMEKWLDAREHSEWLLPDHVRAGASCYLDWIAPSLYRHRDSEMLLELGQGSIPDEIYGYDTSW   959
NTDB id 119 BSU 10630 NP 388944.2            RAKEKLFLIGSCKDHQKQLAKWQASASQTDWLLPEFDRYQARTYLDFIGPALARHRDLGDLAGVP...AHADISGHPARF   949
consensus                                    !!!!!! !!!**!!* ! * !!     ***!!!!** !  ! *!!!*!*! ! !!!!   !  *****   *! !**   *

logo
NTDB id 410861 BABF1 RS05705 WP 000970458.1  KVEVVDGNTLLAPE..PVQEEKQELLEALREKKAVPLESERKEEVYDRLMWKYGYGEATSHRAKQSVTEIKRNYQSEEG.  1036
NTDB id 119 BSU 10630 NP 388944.2            AVQMIHSYDLLDDDLEERMEEKSERLEAIRRGEPVPGSFAFDEKAREQLSWTYPHQEVTQIRTKQSVSEIKRKREYEDEY  1029
consensus                                     ! ***   !! *****  !!! ! !!!*!   *!!      !   * ! ! !** ! ! *! !!!!*!!!!    !* *

logo
NTDB id 410861 BABF1 RS05705 WP 000970458.1  .SDNAFIKKLRAPIQTRPRFMEKKGLTYAERGTAVHAVMQHVDLKKPITVEILQEQIAGMVNKELLTFEQAEEIAIEKVI  1115
NTDB id 119 BSU 10630 NP 388944.2            SGRAPVKPADGSILYRRPAFMMKKGLTAAEKGTAMHTVMQHIPLSHVPSIEEAEQTVHRLYEKELLTEEQKDAIDIEEIV  1109
consensus                                    *   *  *    **  !! !! !!!!! !!*!!!*! !!!!**! *****!     ** *  !!!!! !! * ! !! **
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logo
NTDB id 410861 BABF1 RS05705 WP 000970458.1  SFFDSDLGKRVLAAKSVEREVPFTMMLAAEEAYQDWQGESGESILVQGVIDCMIEEEDGITLIDFKTDTIEGKFPGGFEQ  1195
NTDB id 119 BSU 10630 NP 388944.2            QFFHTEIGGQLIGAKWKDREIPFSLALPAKEIYPDAH.EADEPLLVQGIIDCLYETEDGLYLLDYKSDRIEGKFQHGFEG  1188
consensus                                     !!****!   ***!!   *!!*!!** !*! ! !*! **!   !**!!!!*!!!* ! !!!* !*!*!*! !!!!!**!!!

logo
NTDB id 410861 BABF1 RS05705 WP 000970458.1  AKPILETRYKVQLSLYAKALEKSLQHPVKEKCLYFFDGNHVIKVEE  1241
NTDB id 119 BSU 10630 NP 388944.2            AAPILKKRYETQIQLYTKAVEQIAKTKVKGCALYFFDGGHILTL..  1232
consensus                                    ! !!!  !!  !* !! !!*!    **!! **!!!!!! !** ***
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X non conserved

X similar

X $\geq$ 50% conserved