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logo

NTDB id 1011630 ABS324 RS24515 WP 098616878.1  MIENWPKKKPEDSQWTDDQWKAVVANGRDILVAAAAGSGKTAVLVERIIKKIINEENPVDVDRLLVVTFTNAAAQEMKNRI   80
NTDB id 119 BSU 10630 NP 388944.2              ...MNIPKPADSTWTDDQWNAIVSTGQDILVAAAAGSGKTAVLVERMIRKITAEENPIDVDRLLVVTFTNASAAEMKHRI   77
consensus                                      ***  **!! !! !!!!!! !*!  ! !!!!!!!!!!!!!!!!!!*!*!!  !!!!*!!!!!!!!!!!!! ! !!!*!!

logo

NTDB id 1011630 ABS324 RS24515 WP 098616878.1  GEALEKVLIDEPGSQHVRKQLSLLNKASISTIHSFCLQVIRGYYYMLDVDPRFRIANQTENELLKEEVLDDILEEEYGIE  160
NTDB id 119 BSU 10630 NP 388944.2              AEALEKELVQRPGSLHIRRQLSLLNRASISTLHSFCLQVLKKYYYLIDLDPGFRIADQTEGELIGDEVLDELFEDEYAKG  157
consensus                                      *!!!!! !*  !!! !*!*!!!!!!*!!!!!*!!!!!!!** !!!**!*!! !!!! !!! !!* *!!!!** !*!!*

logo

NTDB id 1011630 ABS324 RS24515 WP 098616878.1  DNTIFFELVDRYTSDRSDDDLQRMILALHTESRAHPNPEKWLDKLVEAYDVEGK.TIEDLVYASYLLEDVKFQLETAEQH  239
NTDB id 119 BSU 10630 NP 388944.2              .EKAFFELVDRYTTDRHDLDLQFLVKQVYEYSRSHPNPEAWLESFVHLYDVSEKSAIEELPFYQYVKEDIAMVLNGAKEK  236
consensus                                      *   !!!!!!!!!*!!*! !!! **  **  !! !!!!! !!*  !* !!!  !* !!*!**  !* !!*   !  !  *

logo

NTDB id 1011630 ABS324 RS24515 WP 098616878.1  IRKATELAMLPDGPAPRIETLQADVALLGTLSSAAHESWTSLYEAMQNVSWQTLKRIKKSDYNEDVVKQVDSLRNKAKDE  319
NTDB id 119 BSU 10630 NP 388944.2              LLRALELTKAPGGPAPRADNFLDDLAQIDELIQ.HQDDFSELYKRVPAVSFKRAKAVKGDEFDPALLDEATDLRNGAKKL  315
consensus                                      * *! !!   ! !!!!! *    !*! *  !  **** ** !!  ** !!*   ! *!  ** * **     !!! !!

logo

NTDB id 1011630 ABS324 RS24515 WP 098616878.1  VKKLQEELFSRKPESFLRDFQDMHPVLEKLVQLVKVFTERFQAMKRDKGMVDFTDLEHFCLQILSEQSENGEMNPSAVAL  399
NTDB id 119 BSU 10630 NP 388944.2              LEKLKTDYFTRSPEQHLKSLAEMKPVIETLVQLVISYGKRFEAAKQEKSIIDFSDLEHYCLAILTAENDKGEREPSEAAR  395
consensus                                      * !!  * !*! !! *!*   *!*!!*! !!!!!  *  !! ! ! *! **!!*!!!!*!! !!*   * !!  !!  !

logo

NTDB id 1011630 ABS324 RS24515 WP 098616878.1  QYRNKFAEVLVDEYQDTNFVQESIIKFVTKDSESEGNLFMVGDVKQSIYRFRLAEPGLFLGKYKRFTQEGLGGGMKIDLA  479
NTDB id 119 BSU 10630 NP 388944.2              FYQEQFHEVLVDEYQDTNLVQESILQLVTSGPEETGNLFMVGDVKQSIYRFRLAEPLLFLSKYKRFTESGEGTGRKIDLN  475
consensus                                       !   !*!!!!!!!!!!! !!!!!*  !!   *!  !!!!!!!!!!!!!!!!!!!!! !!! !!!!!!  ! ! ! !!!!

logo

NTDB id 1011630 ABS324 RS24515 WP 098616878.1  KNFRSRHEVLAGTNFIFKQIMGEEVGEIDYDADAELKLGATYPEGEDVAAELLCIQQTEEEVIDGEEGAEVEKAQLEARL  559
NTDB id 119 BSU 10630 NP 388944.2              KNFRSRADILDSTNFLFKQLMGGKIGEVDYDEQAELKLGAAYPDNDETETELLLIDNAEDT.DASEEAEELETVQFEAKA  554
consensus                                      !!!!!!***!  !!!*!!!*!!  *!!*!!!  !!!!!!! !!* **   !!!*! * !* *   !!* !*!  ! !!*
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NTDB id 1011630 ABS324 RS24515 WP 098616878.1  MAQRIKAMVDSGYEVYDRKNDSMRPVQYRDFVILLRSMPWAPQIMEELKLQGIPVYADLATGYFEATEVNIMMNVFRVID   639
NTDB id 119 BSU 10630 NP 388944.2              IAKEIRKLISSPFKVYDGKKKTHRNIQYRDIVILLRSMPWAPQIMEELRAQGIPVYANLTSGYFEAVEVAVALSVLKVID   634
consensus                                      *!   !* ** !** !!! !   **!**!!!! !!!!!!!!!!!!!!!!* !!!!!!! ! *!!!!! !! * * ! *!!!

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NTDB id 1011630 ABS324 RS24515 WP 098616878.1  NPMQDIPLAAVLRSPIVGLNDEELATLRAHGKKGSFYEVMSSFLKGAPLEEEQELHDKLEWFYNLLQGWREFARQQSLSD   719
NTDB id 119 BSU 10630 NP 388944.2              NPYQDIPLASVLRSPIVGADENELSLIRLENKKAPYYEAMKDYLAAGD..RSDELYQKLNTFYGHLQKWRAFSKNHSVSE   712
consensus                                      !! !!!!!! !!!!!!!!  * !!  *! * !!***!! !  *! *****   !!* !!  !! *!! !! ! ***!*!*

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NTDB id 1011630 ABS324 RS24515 WP 098616878.1  LIWKVYGETGYYDFVGGLPAGKQRQANLRVLYDRARQYEATSFRGLFRFLRFIERILERGDDMGTARALGEQEDVVRIMT   799
NTDB id 119 BSU 10630 NP 388944.2              LIWEVYRDTKYMDYVGGMPGGKQRQANLRVLYDRARQYESTAFRGLFRFLRFIERMQERGDDLGTARALSEQEDVVRLMT   792
consensus                                      !!!  !!  *! ! !*!!!*!*!!!!!!!!!!!!!!!!!! ! !!!!!!!!!!!!!* !!!!!*!!!!!! !!!!!!!*!!

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NTDB id 1011630 ABS324 RS24515 WP 098616878.1  IHKSKGLEFPVVFVAGLGRRFNTQDLMKRFLLHKDFGFGSQFIDPRKRIKYTTLSQLAIKRKMKMELIAEEMRVLYVALT   879
NTDB id 119 BSU 10630 NP 388944.2              IHSSKGLEFPVVFVAGLGRNFNMMDLNKSYLLDKELGFGTKYIHPQLRISYPTLPLIAMKKKMRRELLSEELRVLYVALT   872
consensus                                      !! !!!!!!!!!!!!!!!! !!   !! ! *!!*!* !!!* *!*!  !! !*!!* *!*!*!!* !!* !!*!!!!!!!!

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NTDB id 1011630 ABS324 RS24515 WP 098616878.1  RAKEKLILIGTVKDANKEMEKWLDAREHSEWLLPDHIRAGASCYLDWIAPSLYRHRDSEMLLELGQGSIPDEIYGYDTSW   959
NTDB id 119 BSU 10630 NP 388944.2              RAKEKLFLIGSCKDHQKQLAKWQASASQTDWLLPEFDRYQARTYLDFIGPALARHRDLGDLAGVP...AHADISGHPARF   949
consensus                                      !!!!!! !!!**!!**! * !!      ***!!!!** !  ! *!!!*!*! ! !!!!   !  *****   *! !**  *

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NTDB id 1011630 ABS324 RS24515 WP 098616878.1  KVEVVDGNTLLAPE..PVQEEKQELLEALREKKAVPLQSERKEEVYDRLMWKYGYEDATSHRAKQSVTEIKRNYQSEEG.  1036
NTDB id 119 BSU 10630 NP 388944.2              AVQMIHSYDLLDDDLEERMEEKSERLEAIRRGEPVPGSFAFDEKAREQLSWTYPHQEVTQIRTKQSVSEIKRKREYEDEY  1029
consensus                                       ! ***   !! ***** !!! ! !!!*!   *!!      !   * ! ! !** * ! *! !!!!*!!!!    !* *

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NTDB id 1011630 ABS324 RS24515 WP 098616878.1  .SDNTFIKKLRAPIKTRPRFMEKKGLTYAERGTAVHAVMQHVDLKKPITVEVLQEQIAGMVNKELLTFEQAEEIVIEKVI  1115
NTDB id 119 BSU 10630 NP 388944.2              SGRAPVKPADGSILYRRPAFMMKKGLTAAEKGTAMHTVMQHIPLSHVPSIEEAEQTVHRLYEKELLTEEQKDAIDIEEIV  1109
consensus                                      *   *  *    **  !! !! !!!!! !!*!!!*! !!!!**! *****!     ** *  !!!!! !! * ! !! **
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logo

NTDB id 1011630 ABS324 RS24515 WP 098616878.1  SFFNSDLGKRVLAAKSVEREVPFTMMLAAEEAYQDWQGNSGESILVQGVIDCMIEEEDGITLIDFKTDTIEGKFPGGFEQ  1195
NTDB id 119 BSU 10630 NP 388944.2              QFFHTEIGGQLIGAKWKDREIPFSLALPAKEIYPDAH.EADEPLLVQGIIDCLYETEDGLYLLDYKSDRIEGKFQHGFEG  1188
consensus                                       !!****!   ***!!   *!!*!!** !*! ! !*! **    !**!!!!*!!!* ! !!!* !*!*!*! !!!!!**!!!

logo

NTDB id 1011630 ABS324 RS24515 WP 098616878.1  AKPILEDRYKMQLSLYAKALEKSLQHPVKEKCLYFFDGNHVVNIEE  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