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logo
NTDB id 299098 DOU34 RS04035 WP 113629830.1  MQIPKPKDSIWTDDQWSAIVSSGRDILVAAAAGSGKTAVLVERMIRKITAEEDPIDVDRLLVVTFTNASAAEMKHRIAEA   80
NTDB id 119 BSU 10630 NP 388944.2            MNIPKPADSTWTDDQWNAIVSTGQDILVAAAAGSGKTAVLVERMIRKITAEENPIDVDRLLVVTFTNASAAEMKHRIAEA   80
consensus                                    !*!!!! !! !!!!!! !!!!*! !!!!!!!!!!!!!!!!!!!!!!!!!!!! !!!!!!!!!!!!!!!!!!!!!!!!!!!!

logo
NTDB id 299098 DOU34 RS04035 WP 113629830.1  LEKELAKNPGSLHIRRQLSLLNRASISTLHSFCLQVLKKYYYMIDLDPGFRMADQTEGELLGDEVLDELFEDEYAKGNQA  160
NTDB id 119 BSU 10630 NP 388944.2            LEKELVQRPGSLHIRRQLSLLNRASISTLHSFCLQVLKKYYYLIDLDPGFRIADQTEGELIGDEVLDELFEDEYAKGEKA  160
consensus                                    !!!!!   !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!

logo
NTDB id 299098 DOU34 RS04035 WP 113629830.1  FFELADRYTTDRHDLDLQDLVKRVYEYSRSHPDPEVWLQSFVRLYDVTEESKMEELPFYQYVKEDAEMALFGAKQKLEKA  240
NTDB id 119 BSU 10630 NP 388944.2            FFELVDRYTTDRHDLDLQFLVKQVYEYSRSHPNPEAWLESFVHLYDVSEKSAIEELPFYQYVKEDIAMVLNGAKEKLLRA  240
consensus                                    !!!! !!!!!!!!!!!!! !!! !!!!!!!!! !! !! !!!*!!!!*! ! *!!!!!!!!!!!!  ! ! !!! !! *!

logo
NTDB id 299098 DOU34 RS04035 WP 113629830.1  LELTKAPGGPAPRADNFLDDLQQIEELISCRHDFDALYERVPAVSFKRAKAVKGDEFDKALLDEATDLRNGAKKLIEKVK  320
NTDB id 119 BSU 10630 NP 388944.2            LELTKAPGGPAPRADNFLDDLAQIDELIQHQDDFSELYKRVPAVSFKRAKAVKGDEFDPALLDEATDLRNGAKKLLEKLK  320
consensus                                    !!!!!!!!!!!!!!!!!!!!! !!*!!!   *!!  !! !!!!!!!!!!!!!!!!!!!*!!!!!!!!!!!!!!!!!*!!*!

logo
NTDB id 299098 DOU34 RS04035 WP 113629830.1  TDYFTRSPQDHLKSLTDMKPVIETLVQLVISYGKRFEAAKQEKSIIDFSDLEHYCLAILTAVDEEGRRVPSEAAVYYQDQ  400
NTDB id 119 BSU 10630 NP 388944.2            TDYFTRSPEQHLKSLAEMKPVIETLVQLVISYGKRFEAAKQEKSIIDFSDLEHYCLAILTAENDKGEREPSEAARFYQEQ  400
consensus                                    !!!!!!!!  !!!!!! *!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!  * ! ! !!!!! *!!*!

logo
NTDB id 299098 DOU34 RS04035 WP 113629830.1  FHEVLVDEYQDTNLVQESILQLVTSGPEETGNLFMVGDVKQSIYRFRLAEPLLFLGKYKRFTESGEGTGRKIDLNQNFRS  480
NTDB id 119 BSU 10630 NP 388944.2            FHEVLVDEYQDTNLVQESILQLVTSGPEETGNLFMVGDVKQSIYRFRLAEPLLFLSKYKRFTESGEGTGRKIDLNKNFRS  480
consensus                                    !!!!!!!!!!!!!!!!!!!!!!!!  !!*!!  !!!!!!!!!!!!!!!!!!!!!!!!!!!!  !!!!!!!!!!!  !  !!!!!  !!!!

logo
NTDB id 299098 DOU34 RS04035 WP 113629830.1  RSDILDSTNFLFKQLMGGKIGEVDYDEQAALKLGASYPPNDAAKTELLLIDSADGADSSEDAEDFETVHWEAKAIAGEIR  560
NTDB id 119 BSU 10630 NP 388944.2            RADILDSTNFLFKQLMGGKIGEVDYDEQAELKLGAAYPDNDETETELLLIDNAEDTDASEEAEELETVQFEAKAIAKEIR  560
consensus                                    ! !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
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logo

NTDB id 299098 DOU34 RS04035 WP 113629830.1  KLVSSPFKVYDGKTKTHRNIQYRDIVILLRSMPWAPQLMEELKNQGIPVYANLTSGYFEAVEVAAALSVLKVIDNPYQDI   640
NTDB id 119 BSU 10630 NP 388944.2            KLISSPFKVYDGKKKTHRNIQYRDIVILLRSMPWAPQIMEELRAQGIPVYANLTSGYFEAVEVAVALSVLKVIDNPYQDI   640
consensus                                    !!*!!!!!!!!!! !!!!!!!!!!!!!!!!!!!!!!!*!!!!* !!!!!!!!!!!!!!!!!!!! !!!!!!!!!!!!!!!!

logo

NTDB id 299098 DOU34 RS04035 WP 113629830.1  PLASVLRSPIVGCDENELALIRLEKKKAPFYEALKAYIANADRHDELYQKLRTFYDSLQKWRSFSTNHSVSELIWEVYRD   720
NTDB id 119 BSU 10630 NP 388944.2            PLASVLRSPIVGADENELSLIRLENKKAPYYEAMKDYLAAGDRSDELYQKLNTFYGHLQKWRAFSKNHSVSELIWEVYRD   720
consensus                                    !!!!!!!!!!!!*!!!!! !!!!! !!!!*!!!*! !*! *!!*!!!!!!! !!! *!!!!! !! !!!!!!!!!!!!!!

logo

NTDB id 299098 DOU34 RS04035 WP 113629830.1  TGYFDYAGGMPGGKQRQANLRVLYDRARSYESTAFRGLFRFLRFIERMQERGDDLGTARAFSEQEDVVRLMTIHSSKGLE   800
NTDB id 119 BSU 10630 NP 388944.2            TKYMDYVGGMPGGKQRQANLRVLYDRARQYESTAFRGLFRFLRFIERMQERGDDLGTARALSEQEDVVRLMTIHSSKGLE   800
consensus                                    ! ! !! !!!!!!!!!!!!!!!!!!!!! !! !!!!!!!!!!!!!!!!!!!!!!!!!!!! !!!!!!!!!!!!!!!!!!!

logo

NTDB id 299098 DOU34 RS04035 WP 113629830.1  FPVVFTAGLGRSFNMMDLNKSYLLDKELGFGTKYIHPELRISYPTLPLVAMKKKMRRELLSEELRVLYVALTRAKEKLFL   880
NTDB id 119 BSU 10630 NP 388944.2            FPVVFVAGLGRNFNMMDLNKSYLLDKELGFGTKYIHPQLRISYPTLPLIAMKKKMRRELLSEELRVLYVALTRAKEKLFL   880
consensus                                    !!!!! !!!!! !!!!!!!!!!!!!!!!!!!!!!!!! !!!!!!!!!!*!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!

logo

NTDB id 299098 DOU34 RS04035 WP 113629830.1  VGSCKNREKQLAKWQAQADRADWLLSEFDRYQASSYLDFIGPALIRHRDMEAHRTPGLSSSEDIARDPSRFHIRMLQQSE   960
NTDB id 119 BSU 10630 NP 388944.2            IGSCKDHQKQLAKWQASASQTDWLLPEFDRYQARTYLDFIGPALARHRDLGD..LAGVPAHADISGHPARFAVQMIHSYD   958
consensus                                    *!!!! * !!!!!!!! !   !!!!*!!!!!!! *!!!!!!!!! !!!!*  ** *!** * !!   *! !!** !**   *

logo

NTDB id 299098 DOU34 RS04035 WP 113629830.1  LLEENPKERAEEKSKRLKAIQQGEPIPDSFSFDDQARRLLEWEYPYRELTAIRTKQSVSELKRKQEYEDEYSGRSLIKPS   1040
NTDB id 119 BSU 10630 NP 388944.2            LLDDDLEERMEEKSERLEAIRRGEPVPGSFAFDEKAREQLSWTYPHQEVTQIRTKQSVSEIKRKREYEDEYSGRAPVKPA   1038
consensus                                    !!** * !! !!!! !! !!   !!!*! !! !!* !!   ! ! !!* !*! !!!!!!!!!*!!! !!!!!!!!! **!!

logo

NTDB id 299098 DOU34 RS04035 WP 113629830.1  GDTLLYRRPGFMMKKGLTAAEKGTAMHTVMQHIPLTHVPTAEEAERTVRMLYEKELLTEEQQEAIDIEEIVQFFGTEIGK   1120
NTDB id 119 BSU 10630 NP 388944.2            DGSILYRRPAFMMKKGLTAAEKGTAMHTVMQHIPLSHVPSIEEAEQTVHRLYEKELLTEEQKDAIDIEEIVQFFHTEIGG   1118
consensus                                      **!!!!!*!!!!!!!!!!!!!!!!!!!!!!!!!!*!!!* !!!! !!* !!!!!!!!!!! *!!!!!!!!!!!*!!!!
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logo
NTDB id 299098 DOU34 RS04035 WP 113629830.1  DLLGALRIDREVPFSMALPAGEVYKDAETAGEPLLVQGIIDCLYETADGLYLLDYKTDRIEGKFRNGFEGAAPILQKRYE  1200
NTDB id 119 BSU 10630 NP 388944.2            QLIGAKWKDREIPFSLALPAKEIYPDAHEADEPLLVQGIIDCLYETEDGLYLLDYKSDRIEGKFQHGFEGAAPILKKRYE  1198
consensus                                     !*!!   !!!*!!!*!!!! !*!*!!* ! !!!!!!!!!!!!!!! !!!!!!!!!!*!!!!!!! *!!!!!!!!!! !!!!

logo
NTDB id 299098 DOU34 RS04035 WP 113629830.1  TQIELYTKAVEQITKTKVKGRALYFFDGGHVLTL  1234
NTDB id 119 BSU 10630 NP 388944.2            TQIQLYTKAVEQIAKTKVKGCALYFFDGGHILTL  1232
consensus                                    !!! !!!!!!!!! !!!!!!!*!!!!!!!!!!*!!!
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X non conserved

X similar

X $\geq$ 50% conserved