```
logo
NTDB id 411665 GRT08 RS05370 WP 377803168.1  MQIPKPKDSIWTDDQWSAIVSSGRDILVAAAAGSGKTAVLVERMIRKITAEEDPVDVDRLLVVTFTNASAAEMKHRIAEA   80
NTDB id 119 BSU 10630 NP 388944.2            MNIPKPADSTWTDDQWNAIVSTGQDILVAAAAGSGKTAVLVERMIRKITAEENPIDVDRLLVVTFTNASAAEMKHRIAEA   80
consensus                                    !*!!!! !! !!!!!! !!!!*! !!!!!!!!!!!!!!!!!!!!!!!!!!!! !*!!!!!!!!!!!!!!!!!!!!!!!!!!

logo
NTDB id 411665 GRT08 RS05370 WP 377803168.1  LEKELAKNPGSLHIRRQLSLLNRASISTLHSFCLQVLKKYYYMIDLDPGFRMADQTEGELLGDEVLDELFEDEYAKGNQA  160
NTDB id 119 BSU 10630 NP 388944.2            LEKELVQRPGSLHIRRQLSLLNRASISTLHSFCLQVLKKYYYLIDLDPGFRIADQTEGELIGDEVLDELFEDEYAKGEKA  160
consensus                                    !!!!!   !!!!!!!!!!!!!!!!!!!!
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logo
NTDB id 411665 GRT08 RS05370 WP 377803168.1  KLVSSPFKVYDGKTKTHRNIQYRDIVILLRSMPWAPQLMEELKNQGIPVYANLTSGYFEAVEVAAALSVLKVIDNPYQDI   640
NTDB id 119 BSU 10630 NP 388944.2            KLISSPFKVYDGKKKTHRNIQYRDIVILLRSMPWAPQIMEELRAQGIPVYANLTSGYFEAVEVAVALSVLKVIDNPYQDI   640
consensus                                    !!*!!!!!!!!!! !!!!!!!!!!!!!!!!!!!!!!!*!!!!* !!!!!!!!!!!!!!!!!!!! !!!!!!!!!!!!!!!!

logo
NTDB id 411665 GRT08 RS05370 WP 377803168.1  PLASVLRSPIVGCDENELALIRLEKKKAPFYEALKAYIANADRHDELYQKLRTFYDSLQKWRSFSTNHSVSELIWEVYRD   720
NTDB id 119 BSU 10630 NP 388944.2            PLASVLRSPIVGADENELSLIRLENKKAPYYEAMKDYLAAGDRSDELYQKLNTFYGHLQKWRAFSKNHSVSELIWEVYRD   720
consensus                                    !!!!!!!!!!!!*!!!!! !!!!! !!!!*!!!*! !*! *!!*!!!!!!! !!! *!!!!! !! !!!!!!!!!!!!!!

logo
NTDB id 411665 GRT08 RS05370 WP 377803168.1  TGYFDYAGGMPGGKQRQANLRVLYDRARSYESTAFRGLFRFLRFIERMQERGDDLGTARALSEQEDVVRLMTIHSSKGLE   800
NTDB id 119 BSU 10630 NP 388944.2            TKYMDYVGGMPGGKQRQANLRVLYDRARQYESTAFRGLFRFLRFIERMQERGDDLGTARALSEQEDVVRLMTIHSSKGLE   800
consensus                                    ! ! !! !!!!!!!!!!!!!!!!!!!!! !! !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!

logo
NTDB id 411665 GRT08 RS05370 WP 377803168.1  FPVVFTAGLGRSFNMMDLNKSYLLDKELGFGTKYIHPELRISYPTLPLVAMKKKMRRELLSEELRVLYVALTRAKEKLFL   880
NTDB id 119 BSU 10630 NP 388944.2            FPVVFVAGLGRNFNMMDLNKSYLLDKELGFGTKYIHPQLRISYPTLPLIAMKKKMRRELLSEELRVLYVALTRAKEKLFL   880
consensus                                    !!!!! !!!!! !!!!!!!!!!!!!!!!!!!!!!!! !!!!!!!!!!*!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!

logo
NTDB id 411665 GRT08 RS05370 WP 377803168.1  VGSCKNREKQLAKWQAQADRADWLLSEFDRYQASSYLDFIGPALIRHRDMEAHRTPGLSSSEDIARDPSRFHIRMLQQSE   960
NTDB id 119 BSU 10630 NP 388944.2            IGSCKDHQKQLAKWQASASQTDWLLPEFDRYQARTYLDFIGPALARHRDLGD..LAGVPAHADISGHPARFAVQMIHSYD   958
consensus                                    *!!!! * !!!!!!!!! !   !!!!*!!!!!!! *!!!!!!!!! !!!!*  ** *!** * !!  *! !!** !**   *

logo
NTDB id 411665 GRT08 RS05370 WP 377803168.1  LLEENPKERAEEKSKRLKAIQQGEPIPDSFSFDDQARRLLEWEYPYRELTAIRTKQSVSELKRKQEYEDEYSGRSLIKPS   1040
NTDB id 119 BSU 10630 NP 388944.2            LLDDDLEERMEEKSERLEAIRRGEPVPGSFAFDEKAREQLSWTYPHQEVTQIRTKQSVSEIKRKREYEDEYSGRAPVKPA   1038
consensus                                    !!** * !! !!!! !! !!   !!!*! !! !!* !!   ! ! !!* !*! !!!!!!!!!*!!! !!!!!!!!! **!!

logo
NTDB id 411665 GRT08 RS05370 WP 377803168.1  GDTLLYRRPGFMMKKGLTAAEKGTAMHTVMQHIPLTHVPTAEEAERTVRMLYEKELLTEEQQEAIDIEEIVQFFGTEIGK   1120
NTDB id 119 BSU 10630 NP 388944.2            DGSILYRRPAFMMKKGLTAAEKGTAMHTVMQHIPLSHVPSIEEAEQTVHRLYEKELLTEEQKDAIDIEEIVQFFHTEIGG   1118
consensus                                      **!!!!!*!!!!!!!!!!!!!!!!!!!!!!!!!!*!!!* !!!! !!* !!!!!!!!!!! *!!!!!!!!!!!*!!!!
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logo
NTDB id 411665 GRT08 RS05370 WP 377803168.1  DLLRALRIDREVPFSMALPAGEVYKDAETAGEPLLVQGIIDCLYETADGLYLLDYKTDRIEGKFRNGFEGAAPILQKRYE  1200
NTDB id 119 BSU 10630 NP 388944.2            QLIGAKWKDREIPFSLALPAKEIYPDAHEADEPLLVQGIIDCLYETEDGLYLLDYKSDRIEGKFQHGFEGAAPILKKRYE  1198
consensus                                     !* !   !!!*!!!*!!!! !*!*!!* ! !!!!!!!!!!!!!!! !!!!!!!!!!*!!!!!!! *!!!!!!!!!! !!!!

logo
NTDB id 411665 GRT08 RS05370 WP 377803168.1  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