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logo

NTDB id 1030810 AB3D65 RS10955 WP 369547618.1  MQIPKPKDSIWTDDQWSAIVSSGRDILVAAAAGSGKTAVLVERMIRKITAEEDPVDVDRLLVVTFTNASAAEMKHRIAEA   80
NTDB id 119 BSU 10630 NP 388944.2              MNIPKPADSTWTDDQWNAIVSTGQDILVAAAAGSGKTAVLVERMIRKITAEENPIDVDRLLVVTFTNASAAEMKHRIAEA   80
consensus                                      !*!!!! !! !!!!!! !!!!*! !!!!!!!!!!!!!!!!!!!!!!!!!!!! !*!!!!!!!!!!!!!!!!!!!!!!!!!!

logo

NTDB id 1030810 AB3D65 RS10955 WP 369547618.1  LEKELAKNPGSLHIRRQLSLLNRASISTLHSFCLQVLKKYYYMIDLDPGFRMTDQTEGELLGDEVLDELFEDEYAKGNQA  160
NTDB id 119 BSU 10630 NP 388944.2              LEKELVQRPGSLHIRRQLSLLNRASISTLHSFCLQVLKKYYYLIDLDPGFRIADQTEGELIGDEVLDELFEDEYAKGEKA  160
consensus                                      !!!!!   !!!!!!!!!!!!!!!!!!!!
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logo
NTDB id 1030810 AB3D65 RS10955 WP 369547618.1  KLVSSPFKVYDGKTKTHRNIQYRDIVILLRSMPWAPQLMEELKNQGIPVYANLTSGYFEAVEVAAALSVLKVIDNPYQDI   640
NTDB id 119 BSU 10630 NP 388944.2              KLISSPFKVYDGKKKTHRNIQYRDIVILLRSMPWAPQIMEELRAQGIPVYANLTSGYFEAVEVAVALSVLKVIDNPYQDI   640
consensus                                      !!*!!!!!!!!!! !!!!!!!!!!!!!!!!!!!!!!!!*!!!!* !!!!!!!!!!!!!!!!!!!! !!!!!!!!!!!!!!!!

logo
NTDB id 1030810 AB3D65 RS10955 WP 369547618.1  PLASVLRSPIVGCDENELALIRLEKKKAPFYEALKAYIANGDRHDDLYQKLRTFYDSLQKWRSFSTNHSVSELIWEVYRD   720
NTDB id 119 BSU 10630 NP 388944.2              PLASVLRSPIVGADENELSLIRLENKKAPYYEAMKDYLAAGDRSDELYQKLNTFYGHLQKWRAFSKNHSVSELIWEVYRD   720
consensus                                      !!!!!!!!!!!!!*!!!!! !!!!! !!!!*!!!*! !*! !!!*!*!!!!! !!! *!!!!! !! !!!!!!!!!!!!!!

logo
NTDB id 1030810 AB3D65 RS10955 WP 369547618.1  TGYFDYAGGMPGGKQRQANLRVLYDRARSYESTAFRGLFRFLRFIERMQERGDDLGTARALSEQEDVVRLMTIHSSKGLE   800
NTDB id 119 BSU 10630 NP 388944.2              TKYMDYVGGMPGGKQRQANLRVLYDRARQYESTAFRGLFRFLRFIERMQERGDDLGTARALSEQEDVVRLMTIHSSKGLE   800
consensus                                      ! ! !! !!!!!!!!!!!!!!!!!!!!! !! !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!

logo
NTDB id 1030810 AB3D65 RS10955 WP 369547618.1  FPVVFTAGLGRSFNMMDLNKSYLLDKELGFGTKYIHPELRISYPTLPLVAMKKKMRRELLSEELRVLYVALTRAKEKLFL   880
NTDB id 119 BSU 10630 NP 388944.2              FPVVFVAGLGRNFNMMDLNKSYLLDKELGFGTKYIHPQLRISYPTLPLIAMKKKMRRELLSEELRVLYVALTRAKEKLFL   880
consensus                                      !!!!! !!!!! !!!!!!!!!!!!!!!!!!!!!!!!! !!!!!!!!!!!*!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!

logo
NTDB id 1030810 AB3D65 RS10955 WP 369547618.1  VGSCKNREKQLAKWQAQADRADWLLSEFDRYQASSYLDFIGPALIRHRDMEAHRTPGLSSSEDIARDPSRFHIRMLQQSE   960
NTDB id 119 BSU 10630 NP 388944.2              IGSCKDHQKQLAKWQASASQTDWLLPEFDRYQARTYLDFIGPALARHRDLGD..LAGVPAHADISGHPARFAVQMIHSYD   958
consensus                                      *!!!! * !!!!!!!! !   !!!!*!!!!!!! *!!!!!!!!! !!!!*  ** *!** * !!  *! !!** !**   *

logo
NTDB id 1030810 AB3D65 RS10955 WP 369547618.1  LLEENPKERAEEKSKRLKAIQQGEPIPDSFSFDDQARRLLEWEYPYRELTAIRTKQSVSELKRKQEYEDEYSGRSLIKPS  1040
NTDB id 119 BSU 10630 NP 388944.2              LLDDDLEERMEEKSERLEAIRRGEPVPGSFAFDEKAREQLSWTYPHQEVTQIRTKQSVSEIKRKREYEDEYSGRAPVKPA  1038
consensus                                      !!** * !! !!!! !! !!   !!!*! !! !!* !!   ! ! !!* !*! !!!!!!!!!*!!! !!!!!!!!! **!!

logo
NTDB id 1030810 AB3D65 RS10955 WP 369547618.1  GDTLLYRRPGFMMKKGLTAAEKGTAMHTVMQHIPLTHVPTAEEAERTVRRMLYEKELLTEEQQEAIDIEEIVQFFGTEIGK  1120
NTDB id 119 BSU 10630 NP 388944.2              DGSILYRRPAFMMKKGLTAAEKGTAMHTVMQHIPLSHVPSIEEAEQTVHRLYEKELLTEEQKDAIDIEEIVQFFHTEIGG  1118
consensus                                        **!!!!!*!!!!!!!!!!!!!!!!!!!!!!!!!!*!!!* !!!! !!* !!!!!!!!!!! *!!!!!!!!!!!*!!!!
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logo
NTDB id 1030810 AB3D65 RS10955 WP 369547618.1  DLLGALRIDREVPFSMALPAGEVYKDAETAGEPLLVQGIIDCLYETADGLYLLDYKTDRIEGKFRNGFEGAAPILQKRYE  1200
NTDB id 119 BSU 10630 NP 388944.2              QLIGAKWKDREIPFSLALPAKEIYPDAHEADEPLLVQGIIDCLYETEDGLYLLDYKSDRIEGKFQHGFEGAAPILKKRYE  1198
consensus                                       !*!!    !!!*!!!*!!!! !*!*!!* ! !!!!!!!!!!!!!!! !!!!!!!!!!*!!!!!!! *!!!!!!!!!! !!!!
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logo
NTDB id 1030810 AB3D65 RS10955 WP 369547618.1  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