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logo
NTDB id 26772 LWE RS07665 WP 011702312.1  MAEQESLALFDDTPEELFMKGTMLSTIFYNAENLFSVVRILVKETNADWDEKDIIVTGFFPALHEQEVYTFYGKMQEHAKFGQQF   85
NTDB id 355 BSU 27480 NP 390625.1         MQQHP...DQLKLEEEPYLKGTVNTVIYHNDTNLYTVLKVKVTETSEAIEDKAVSVTGYFPALQEEETYTFYGKIVTHPKFGLQF   82
consensus                                 !  *****     *!!***!!!* * !**!  !!**!*** ! !!    **! * !!!*!!!!*! ! !!!!!!*  !*!!! !!

logo
NTDB id 26772 LWE RS07665 WP 011702312.1  KADRFRKEMPQSRAGLINYLSGELFKGIGKVTAENIVDTIGDDAITKILSDPSLLNTVPKLPSGAAESLLASLRENQGLEHVMVG  170
NTDB id 355 BSU 27480 NP 390625.1         QAEHFKKEIPTTKEGIIQYLSSDLFEGIGKKTAEEIVKKLGDSAINKILADASVLYDVPRLSKKKADTLAGALQRHQGLEQIMIS  167
consensus                                  !**!*!!*! ** !*!*!!! *!! !!!! !!! !!  *!! !! !!! !*!*!  !!*!*   !**! * !  *!!!!**!*

logo
NTDB id 26772 LWE RS07665 WP 011702312.1  LNEYGFGPQLSMKIFQVYKQNATEVLENNPYKLIEDVKGIGFQRADELGRKLGLGGNHPERLRAGVLFMLDSVCMQQGHVYMEKE  255
NTDB id 355 BSU 27480 NP 390625.1         LNQFGFGPQLSMKIYQAYESETLEKIQENPYQLVKDVEGIGFGKADELGSRMGLSGNHPERVKAAILYTLETTCLSEGHTYIETE  252
consensus                                 !! *!!!!!!!!!!*! !    *! *  !!! !* !! !!!! *!!!!! **!! !!!!!!**!**!* !** !*  !! !*! !

logo
NTDB id 26772 LWE RS07665 WP 011702312.1  VLLGEVTYLLEES..EGIRIDQAILLQQVEKLAEEQKIITENTRVYMPSLYYSESGFAYHVKRMLKQTEYQEQFPQSEFLLALGE  338
NTDB id 355 BSU 27480 NP 390625.1         QLIIDTQSLLNQSAREGQRITEMDAANAIIALGENKDIVIEDGRCYFPSLFYAEQNVAKRVKHIASQTEYENQFPESEFLLALGE  337
consensus                                  !* *   !!  !**!! !!      * *  !*!   !* !  !*! !!!*! !   ! *!!**  !!!!  !!! !!!!!!!!!

logo
NTDB id 26772 LWE RS07665 WP 011702312.1  LEERIGVHYGDSQREALEQALMSPMLVLTGGPGTGKTTVIKGIVELYAELNGLSLDPHAYKDGATFPVLLAAPTGRAAKRMSEST  423
NTDB id 355 BSU 27480 NP 390625.1         LEERMDVQYAPSQKEAIQKALSSPMLLLTGGPGTGKTTVIRGIVELYGELHGVSLDPSAYKKDEAFPIVLAAPTGRAAKRMSEST  422
consensus                                 !!!!* !*!**!!*!!*  !! !!!!*!!!!!!!!!!!!!!*!!!!!!*!!*!*!!!!*!!!    !!**!!!!!!!!!!!!!!!!!

logo
NTDB id 26772 LWE RS07665 WP 011702312.1  GLPAMTIHRLLGMNGQEQMDDDAERLIDGRLLIVDEMSMVDIWLANQLFRALPAHMQVVLVGDQDQLPSVGPGQVLKDILHSEQI  508
NTDB id 355 BSU 27480 NP 390625.1         GLPAVTIHRLLGWNGAEGFTHTEDQPIEGKLLIIDEASMLDIWLANHLFKAIPDHIQIIIVGDEDQLPSVGPGQVLRDLLASQVI  507
consensus                                 !!!!*!!!!!!! !! !   *  * *!*!*!!!*!! !!*!!!!!!*!!*!*! !*!***!!! !!!!!!!!!!!!*!*!*!  !

logo
NTDB id 26772 LWE RS07665 WP 011702312.1  PTVALSDIYRQKDGSSIIEMAHYIKEGMLPTDFAKNSADRSFFHCTVNQIGDVVEQVVKNAKNKGFRAKDIQVLAPMYRGPAGID  593
NTDB id 355 BSU 27480 NP 390625.1         PTVRLTDIYRQAEGSSIVELAHQMKNGLLPNNLTAPTKDRSFIRCGGSQIKEVVEKVVANALKKGYTAKDIQVLAPMYRGKAGIN  592
consensus                                 !!! !*!!!!! *!!!!*!*!! *! !*!!     ** !!!! *!   !! *!!! !! !!  !!* !!!!!!!!!!!!!*!!!
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logo
NTDB id 26772 LWE RS07665 WP 011702312.1  ILNKKLQEIFNPNDTGRRKEVQFGEIKYRVHDKVLQLINQPEKNVFNGDIGEIVSIIYAKENTEKQDLIVVQFDQTEVSYYRQEF   678
NTDB id 355 BSU 27480 NP 390625.1         ELNVMLQDILNPPKE.KRRELKFGDVVYRTGDKILQLVNQPENNVFNGDIGEITSIFYAKENTEKEDMAVVSFDGNEMTFTKKDF   676
consensus                                  !!   !!*! !!*  **!*!* !!** !! *!!*!!!*!!!! !!!!!!!!!! !! !!!!!!!! !* !! !!   !*** * *!

logo
NTDB id 26772 LWE RS07665 WP 011702312.1  NQLTHAYCCSIHKAQGSEFPIVIMPIVRSYYRMLRRDLLYTGVTRSKQFLILCGEEEAFRMGVERVDENKRNTTLSERLMSEDVM   763
NTDB id 355 BSU 27480 NP 390625.1         NQFTHAYCCSIHKSQGSEFPIVVLPVVKGYYRMLRRNLLYTAITRAKKFLILCGEEEALEWGVKNNDATVRQTSLKNRLSVQVEE   761
consensus                                 !! !!!!!!!!!! !!!!!!!!**!*!* !!!!!!! !!!!**!! ! !!!!!!!!!!   !!   !   !*!*!  !!

logo
NTDB id 26772 LWE RS07665 WP 011702312.1  LEQMTNKRILTTENITEIDPMIGMEGITPEQFMVG...   798
NTDB id 355 BSU 27480 NP 390625.1         MDA.ELEALQKELPFSVHDANIGMEGITPFDFMKEEQQ   798
consensus                                 ** *    *    * * *!* !!!!!!!!  !!  ***
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X non conserved

X similar

X $\geq$ 50% conserved