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logo
NTDB id 60408 HK87 RS05860 WP 003727413.1  MAEQESLALFNDTPEELFMKGTMLSTIFYNAENLFSVVRILVKETNADWDEKDIIVTGFFPALHEQEVYTFYGKMQEHAKFGQQF   85
NTDB id 355 BSU 27480 NP 390625.1          MQQH...PDQLKLEEEPYLKGTVNTVIYHNDTNLYTVLKVKVTETSEAIEDKAVSVTGYFPALQEEETYTFYGKIVTHPKFGLQF   82
consensus                                  !  *****     *!!***!!!* * !**!  !!**!*** ! !!    **! * !!!*!!!!*! ! !!!!!!*  !*!!! !!

logo
NTDB id 60408 HK87 RS05860 WP 003727413.1  KADRFRKEMPQSRAGLINYLSGELFKGIGKVTAENIVDTIGDDAITKILSDPSLLNTVPKLPSGAAESLLASLRENQGLEHVMVG  170
NTDB id 355 BSU 27480 NP 390625.1          QAEHFKKEIPTTKEGIIQYLSSDLFEGIGKKTAEEIVKKLGDSAINKILADASVLYDVPRLSKKKADTLAGALQRHQGLEQIMIS  167
consensus                                   !**!*!!*! ** !*!*!!! *!! !!!! !!! !!  *!! !! !!! !*!*!  !!*!*   !**! * !  *!!!!**!*

logo
NTDB id 60408 HK87 RS05860 WP 003727413.1  LNEYGFGPQLSMKIFQAYKQNAIEVLENNPYKLIEDIKGIGFQRADELGRKLGLGGNHPERLRAGILFMLDSVCMQQGHVYMEQE  255
NTDB id 355 BSU 27480 NP 390625.1          LNQFGFGPQLSMKIYQAYESETLEKIQENPYQLVKDVEGIGFGKADELGSRMGLSGNHPERVKAAILYTLETTCLSEGHTYIETE  252
consensus                                  !! *!!!!!!!!!!*!!!    *! *  !!! !* !* !!!! *!!!!! **!! !!!!!!**!*!!* !** !*  !! !*! !

logo
NTDB id 60408 HK87 RS05860 WP 003727413.1  VLLGEVTYLLEES..EGIRIDQNILVAQVEKLAEEQKIITENTRVYMPSLYYSESGFAYHVKRMLKQTEYQEQFPQSEFLLALGE  338
NTDB id 355 BSU 27480 NP 390625.1          QLIIDTQSLLNQSAREGQRITEMDAANAIIALGENKDIVIEDGRCYFPSLFYAEQNVAKRVKHIASQTEYENQFPESEFLLALGE  337
consensus                                   !* *   !!  !**!! !!        *  !*!   !* !  !*! !!!*! !   ! *!!**  !!!!  !!! !!!!!!!!!

logo
NTDB id 60408 HK87 RS05860 WP 003727413.1  LEERIGVHYGDSQRQALEQALMSPMLVLTGGPGTGKTTVIKGIVELYAELNGVSLDPHAYKDGATFPVLLAAPTGRAAKRMSEST  423
NTDB id 355 BSU 27480 NP 390625.1          LEERMDVQYAPSQKEAIQKALSSPMLLLTGGPGTGKTTVIRGIVELYGELHGVSLDPSAYKKDEAFPIVLAAPTGRAAKRMSEST  422
consensus                                  !!!!* !*!**!!* !*  !! !!!!*!!!!!!!!!!!!!*!!!!!!*!!*!!!!!!*!!!    !!**!!!!!!!!!!!!!!!!

logo
NTDB id 60408 HK87 RS05860 WP 003727413.1  GLPAMTIHRLLGMNGQEQMDDDAERLIDGRLLIVDEMSMVDIWLANQLFRALPAHMQVVLVGDQDQLPSVGPGQVLKDILQSEQI  508
NTDB id 355 BSU 27480 NP 390625.1          GLPAVTIHRLLGWNGAEGFTHTEDQPIEGKLLIIDEASMLDIWLANHLFKAIPDHIQIIVGDEDQLPSVGPGQVLRDLLASQVI  507
consensus                                  !!!!*!!!!!!! !! !   *  * *!*!*!!!*!! !!*!!!!!!*!!*!*! !*!***!!! !!!!!!!!!!!!*!*! !   !

logo
NTDB id 60408 HK87 RS05860 WP 003727413.1  PTVALSDIYRQKDGSSIIEMAHYIKEGMLPADFTKNSADRSFFHCTVNQIGDVVEQVVKNAKNKGFRAKDIQVLAPMYRGPAGID  593
NTDB id 355 BSU 27480 NP 390625.1          PTVRLTDIYRQAEGSSIVELAHQMKNGLLPNNLTAPTKDRSFIRCGGSQIKEVVEKVVANALKKGYTAKDIQVLAPMYRGKAGIN  592
consensus                                  !!! !*!!!!! *!!!!*!*!! *! !*!!   ! ** !!!! *!   !! *!!! !! !!  !!* !!!!!!!!!!!!!*!!!
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logo
NTDB id 60408 HK87 RS05860 WP 003727413.1  ILNKKLQEIFNPNDTGRRKEVQFGDIKYRVHDKVLQLINQPEKNVFNGDIGEIVSIIYAKENTEKQDLIVVQFDQTEVSYYRQEF   678
NTDB id 355 BSU 27480 NP 390625.1          ELNVMLQDILNPPKE.KRRELKFGDVVYRTGDKILQLVNQPENNVFNGDIGEITSIFYAKENTEKEDMAVVSFDGNEMTFTKKDF   676
consensus                                   !!  !!*! !!*  **!*!* !!!* !! *!!*!!!*!!!! !!!!!!!!!! !! !!!!!!!! !* !! !!  !*** * *!

logo
NTDB id 60408 HK87 RS05860 WP 003727413.1  NQLTHAYCCSIHKAQGSEFPIVIMPIVRSYYRMLRRDLLYTGVTRSKQFLILCGEEEAFRMGIERIDENKRNTTLSERLMSEDVL   763
NTDB id 355 BSU 27480 NP 390625.1          NQFTHAYCCSIHKSQGSEFPIVVLPVVKGYYRMLRRNLLYTAITRAKKFLILCGEEEALEWGVKNNDATVRQTSLKNRLSVQVEE   761
consensus                                  !! !!!!!!!!!! !!!!!!!!**!*!* !!!!!!! !!!!**!! ! !!!!!!!!!!   !*   !   !*!*!  !!

logo
NTDB id 60408 HK87 RS05860 WP 003727413.1  LEQMTNKRILTAENITEIDPMIGMEGITPEQFMAG...   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