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logo
NTDB id 1135606 DQL80 RS08150 WP 111680369.1  ....MSDPTLFDYSMIKGTVEAILFQNSDNFYTVLKVDTIETNEDFD.TMPTVVGFLPNIVEGDVYTFKGQVVDHPRYGK   75
NTDB id 355 BSU 27480 NP 390625.1             MQQHPDQLKLEEEPYLKGTVNTVIYHNDTNLYTVLKVKVTETSEAIEDKAVSVTGYFPALQEEETYTFYGKIVTHPKFGL   80
consensus                                     *****  * ! * * *!!!!  ****!  ! !!!!!!  !! !  **  **! !* ! * ! * !!! ! *! !!**!

logo
NTDB id 1135606 DQL80 RS08150 WP 111680369.1  QLKAETFEKEMPQTKEAIISYLSSDLFKGVGKKTAQNIVNTLGDNAINDILDDHSVLEKVSGLSKKKQKQIAEQISANQE  155
NTDB id 355 BSU 27480 NP 390625.1             QFQAEHFKKEIPTTKEGIIQYLSSDLFEGIGKKTAEEIVKKLGDSAINKILADASVLYDVPRLSKKKADTLAGALQRHQG  160
consensus                                     !  !!*! !!*! !!!*!! !!!!!!! !*!!!!!  !!  !!! !!! !! !*!!!  !* !!!!!   *!  *  *!

logo
NTDB id 1135606 DQL80 RS08150 WP 111680369.1  SEKIMIRLHDLGFGPKLSMAIYQFYLGDTLTILDRNPYQLIYDIKGIGFNKADQLARNIGIAYNDNERLKAALLYTLEEE  235
NTDB id 355 BSU 27480 NP 390625.1             LEQIMISLNQFGFGPQLSMKIYQAYESETLEKIQENPYQLVKDVEGIGFGKADELGSRMGLSGNHPERVKAAILYTLETT  240
consensus                                      ! !!! !*  !!!! !!! !!! !  *!!  *  !!!!!* !* !!!! !!! !*  *!*  !**!!*!!!*!!!!!

logo
NTDB id 1135606 DQL80 RS08150 WP 111680369.1  CIKQGHTYLPINVVIDLTVDVLNYQDEEVI..EPEKLDEMLQYLNEEKRLIIDNEQVAIPSLYYSEIKSVQNLFRIKTHT  313
NTDB id 355 BSU 27480 NP 390625.1             CLSEGHTYIETEQLIIDTQSLLNQSAREGQRITEMDAANAIIALGENKDIVIEDGRCYFPSLFYAEQNVAKRVKHIASQT  320
consensus                                     !*  !!!!**   *!  !  *!!    !  ** *     *  ! ! ! **!*   *  !!!*! !      * *! **!

logo
NTDB id 1135606 DQL80 RS08150 WP 111680369.1  NKLTEIEQSDLQMHIGEIEDTNQVNYAASQKEALQTAINSKVMLLTGGPGTGKTTVIKGIVELYAEIHGLSLDYDDYVN.  392
NTDB id 355 BSU 27480 NP 390625.1             EYENQFPESEFLLALGELEERMDVQYAPSQKEAIQKALSSPMLLLTGGPGTGKTTVIRGIVELYGELHGVSLDPSAYKKD  400
consensus                                           * !*  ***!!*!*   !*!!*!!!!!*! !* !***!!!!!!!!!!!!!!*!!!!!*!*!!*!!!*  !  *

logo
NTDB id 1135606 DQL80 RS08150 WP 111680369.1  DDYPVVLAAPTGRASKRLQESTGLEAMTIHRLIGWNQDTKPEDILENEINARLIIIDEMSMVDTWLFHQFLSAVPLDAQL  472
NTDB id 355 BSU 27480 NP 390625.1             EAFPIVLAAPTGRAAKRMSESTGLPAVTIHRLLGWNGAEGFTHTEDQPIEGKLLIIDEASMLDIWLANHLFKAIPDHIQI  480
consensus                                     * *!*!!!!!!!!! !!* !!!!!*!*!!!!!*!!!    * *  ***! **!*!!!! !!*! !! **   !*! * !*

logo
NTDB id 1135606 DQL80 RS08150 WP 111680369.1  IFVGDEDQLPSVGPGQVFKDLIESKAIPRVNLTEVYRQQDGSSIIELAHRMKLGQKI.DITQRFHDRSFINCQANQIPTV  551
NTDB id 355 BSU 27480 NP 390625.1             IIVGDEDQLPSVGPGQVLRDLLASQVIPTVRLTDIYRQAEGSSIVELAHQMKNGLLPNNLTAPTKDRSFIRCGGSQIKEV  560
consensus                                     ! !!!!!!!!!!!!!!! *!!* !  !! ! !!**!!! *!!!!*!!!! !! !  ** *! * *!!!!! ! * !!* !
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logo
NTDB id 1135606 DQL80 RS08150 WP 111680369.1  VEKVVTSAVNKGYTMADIQVLAPMYKGNAGIKRLNQVLQDILNPKKKDTREIEFGDVVFRKGDKVLQLVNRPNDNIFNGD   631
NTDB id 355 BSU 27480 NP 390625.1             VEKVVANALKKGYTAKDIQVLAPMYRGKAGINELNVMLQDILNPPKEKRRELKFGDVVYRTGDKILQLVNQPENNVFNGD   640
consensus                                     !!!!!  !* !!!!  !!!!!!!!!*! !!!  !! *!!!!!!!*!   !!* !!!!!*! !!!*!!!!! !  !*!!!!

logo
NTDB id 1135606 DQL80 RS08150 WP 111680369.1  IGVIVGIFWAKENALNKDVLVVDFEGNEITFTKQDMMELTHAYCTSIHKSQGSEFPIVIMPIVKQYFRMLQRPILYTGLT   711
NTDB id 355 BSU 27480 NP 390625.1             IGEITSIFYAKENTEKEDMAVVSFDGNEMTFTKKDFNQFTHAYCCSIHKSQGSEFPIVVLPVVKGYYRMLRRNLLYTAIT   720
consensus                                     !! !  !!*!!!!    !* !! !*!!!*!!!! !    !!!!!*!!!!!!!!!!!!!**!*!! !*!!! !**!!!**!

logo
NTDB id 1135606 DQL80 RS08150 WP 111680369.1  RAKTSLVLLGDPEAFDIGLKINGQARLTQLCTLLKNYFNSEDEEILENTATNDTGASQTTINDQVEAPISSNDSEEVTSD   791
NTDB id 355 BSU 27480 NP 390625.1             RAKKFLILCGEEEALEWGVKNNDATVRQ...TSLKNRLSVQVEE.....................................   761
consensus                                     !!!  !*!*!**!! * !*! !      ***! !!!      !!*************************************

logo
NTDB id 1135606 DQL80 RS08150 WP 111680369.1  SIETDTNVL.TEATMFKIDPMINMGEITPYDFIER...   825
NTDB id 355 BSU 27480 NP 390625.1             .MDAELEALQKELPFSVHDANIGMEGITPFDFMKEEQQ   798
consensus                                     *** *    !* ! *    *!* ! !  !!!*!!*  ***
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X non conserved

X similar

X $\geq$ 50% conserved