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logo
NTDB id 87603 TOL5 RS19535 WP 151780662.1  MPNTIVTPQTIYRVQVAVPVYLNDCFDYQVSAEQYAQAEIGARVAVSFGRQNLVGVIVKKIPIDEPIDSHFKLKAITKLLDDHAI   85
NTDB id 1072 ABD1 RS01805 WP 000156662.1   MTITPKPDSVVYRVRVAVPVHLYDTFDYTLTQAQYERAHVGSRVAISFGRQNLIGIITEKVDPSESFTGTFQLKAISDLLDEQPI   85
consensus                                  !* !* **  *!!! !!!!!*! !*!!! **  !!  !**! !!!*!!!!!!!*!*!  !*** !*   *! !!!!* !!!***!

logo
NTDB id 87603 TOL5 RS19535 WP 151780662.1  LDSKVLNLLTWSSQYYQFPIGEVIQTALPTLLRQGKPYDLLARVWKVIDLHA.EDKVKRSEKQQDAYKILKLHPKGTQENILNLS  169
NTDB id 1072 ABD1 RS01805 WP 000156662.1   LDEQVLSLLTWSAQYYQFPIGEVMQTALPALLRQGKPMDVLFHLWKITPCDNVEALLKRSGKQQDAYQILKLHPAGTTENILNLS  170
consensus                                  !!  !! !!!!! !!!!!!!!!!*!!!!! !!!!!!! !*! **!* *** *!  *!!! !!!!!! !!!!!! !! !!!!!!!

logo
NTDB id 87603 TOL5 RS19535 WP 151780662.1  GIETATLKVLEKKAIIQFALEPQNTQPEPVQLAQLPLTPNEDQKKAIQTILKALKKYQAFLLDGLTGSGKTEVYLQVMHEVLKQG  254
NTDB id 1072 ABD1 RS01805 WP 000156662.1   GVETATLKALQKKGLVDCTLEPHDFSPSPVQLAQMPLTLNEDQKKATQYVVNAQHQYQAFLLDGLTGSGKTEVYLHIMHEVLKQG  255
consensus                                  !*!!!!!! ! !!*** * !!!*   ! !!!!!!*!!!*!!!!!!! ! ** ! * !!!!!!!!!!!!!!!!!!!**!!!!!!!!

logo
NTDB id 87603 TOL5 RS19535 WP 151780662.1  KQVLVLVPEIGLTPQTISRFQSRFHCNIALLHSGLNDSKRLQAWQHAQTGKASIILGTRSAIYTPLPNLGLIILDEEHDLSFKQQ  339
NTDB id 1072 ABD1 RS01805 WP 000156662.1   KQVLVLVPEIGLTPQTISRFKSRFNCDIALLHSGLNDSKRLQAWQQAQTGKASIILGTRSAIYTPLPRLGLIILDEEHDLSYKQQ  340
consensus                                  !!!!!!!!!!!!!!!!!!!! !!!*! !!!!!!!!!!!!!!!!!!!*!!!!!!!!!!!!!!!!!!!! !!!!!!!!!!!!!*!!!

logo
NTDB id 87603 TOL5 RS19535 WP 151780662.1  EGFRYHARDVALYRAHLENCPIILGSATPSIESYYLARQEKLTRIELNQRAGVALMPKMHLIDLKVAKKQHGLSDVLIGEIKKRL  424
NTDB id 1072 ABD1 RS01805 WP 000156662.1   EGFRYHARDVALYRGHLQGCPVLLGSATPSIDSYHLVETGKLTALQLNQRAGHALLPKMHLIDLKIVKKQHGISQPLIEQIKNTL  425
consensus                                  !!!!!!!!!!!!!!*!!  !!**!!!!!!!!*!!*!    !!! * !!!!!!*!!*!!!!!!!!!* !!!!!*! *!!  !!  !

logo
NTDB id 87603 TOL5 RS19535 WP 151780662.1  DKKEQVLIFLNRRGYAPVLICESCGWQANCPNCDAHFTLHLKPYQHLHCHHCGTINRLPDACPQCNQQQLKPIGMGTAKVEETLT  509
NTDB id 1072 ABD1 RS01805 WP 000156662.1   ARKEQVLIFLNRRGYAPVLVCESCGWQANCPHCDAHFTLHTQPYSYLHCHHCGTVHRLPDHCPECQQKSLKTLGAGTAKVEEHLQ  510
consensus                                   *!!!!!!!!!!!!!!!!!*!!!!!!!!!!*!!!!!!!!  !! *!!!!!!!!**!!!!*!! !*!  !!**! !!!!!!!*!

logo
NTDB id 87603 TOL5 RS19535 WP 151780662.1  ELFPNFPVLRVDRDSTSRVGSWQKIYDQIQKSEPTILLGTQMLAKGHHFPYVTLVAILDIDAGLLSVDFRATERTAQLIIQVAGR  594
NTDB id 1072 ABD1 RS01805 WP 000156662.1   ELFPDHDVIRVDRDSTSRVGSWQKIYDRIQQNKPSILLGTQMLAKGHHFPHVTLVAILDIDAGLLSVDIRAPERTAQLIVQVAGR  595
consensus                                  !!!! **!*!!!!!!!!!!!!!!!!!!!! !!   !*!!!!!!!!!!!!!!!!*!!!!!!!!!!!!!!!!!! !!*!!!!!!!*!!!!!
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logo

NTDB id 87603 TOL5 RS19535 WP 151780662.1   AGRGENKGEVYLQTLRPDHPLLNTLIHNDYRTFAKQTLKDRQAALLPPFRYASLIRCESKHQEENLKFLTEMTQLLRQMSESHLI   679
NTDB id 1072 ABD1 RS01805 WP 000156662.1    AGRGEHKGHVYLQTLRPDHPLLTTLIEKDYRAVAKQTLAERKVALLPPYRYAVLIRAESKDRDYTLHFLNEAAEQLRQIA.GDIV   679
consensus                                   !!!!!*!!*!!!!!!!!!!!!! !!!* !!!  !!!!! *!  !!!!!*!!! !!!*!!!* *  !*!! !    !!!* * ***
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logo

NTDB id 87603 TOL5 RS19535 WP 151780662.1   DIWGPIPAPMERKAGRYQAHVVLLSQDRAKMHFYVHQWWAQLLQQK.PSTMKVTIDVDPQELS   741
NTDB id 1072 ABD1 RS01805 WP 000156662.1    DIWGPIPAPMERKAGRYRAHMVILSADRARLHFYLRQWWAQLVHAPRQHQLRLSIDVDPQEFS   742
consensus                                   !!!!!!!!!!!!!!!!!! !!*!*!! !!!**!!!**!!!!!!** **** ****!!!!!!! !
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X non conserved

X similar

X $\geq$ 50% conserved