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logo
NTDB id 1090387 ACJQW4 RS03475 WP 241628382.1  MPNTVSPTLPLYRIRVAVPAHVYDCFDYQISADDYERAQIGARVAVPFGPRNLVGVIMEKLPLDAPSNPKFKLKSIQALL   80
NTDB id 1072 ABD1 RS01805 WP 000156662.1       MTITPKPDSVVYRVRVAVPVHLYDTFDYTLTQAQYERAHVGSRVAISFGRQNLIGIITEKVDPSESFTGTFQLKAISDLL   80
consensus                                      !* !* !  **!!*!!!!! !*!!*!!! **   !!!!**! !!!**!!* !!*!*! !!***  *  * ! !! !  !!

logo
NTDB id 1090387 ACJQW4 RS03475 WP 241628382.1  DDEAILDDKVLTLLTWVAQYYQFPIGEVVQSALPSLLRQGKPYDLLAHMWRLLDQH.AEDKIKRSEKQQHAYKILKLHPT  159
NTDB id 1072 ABD1 RS01805 WP 000156662.1       DEQPILDEQVLSLLTWSAQYYQFPIGEVMQTALPALLRQGKPMDVLFHLWKITPCDNVEALLKRSGKQQDAYQILKLHPA  160
consensus                                      !* *!!!* !!*!!!! !!!!!!!!!!!*!*!!! !!!!!!! !*! !*!** **** !  *!!! !!!*!! !!!!!!

logo
NTDB id 1090387 ACJQW4 RS03475 WP 241628382.1  GTSENILNLAGIETATLRALEKKGICEAYLEQKDFSPQTLSLAQMPLTANPDQKHAIQQVLKSLSSYHAYLLDGLTGSGK  239
NTDB id 1072 ABD1 RS01805 WP 000156662.1       GTTENILNLSGVETATLKALQKKGLVDCTLEPHDFSPSPVQLAQMPLTLNEDQKKATQYVVNAQHQYQAFLLDGLTGSGK  240
consensus                                      !!*!!!!!! !*!!!!!*!! !!!**** !!**!!!! ** !!!!!!! !*!!!*! ! !*   * !*!*!!!!!!!!!!

logo
NTDB id 1090387 ACJQW4 RS03475 WP 241628382.1  TEVYLQIMHEVLKQGKQVLVLVPEIGLTPQTISRFQSRFHCHIALLHSGLTDAKRLQAWQSAQTGKASIILGTRSAIYTP  319
NTDB id 1072 ABD1 RS01805 WP 000156662.1       TEVYLHIMHEVLKQGKQVLVLVPEIGLTPQTISRFKSRFNCDIALLHSGLNDSKRLQAWQQAQTGKASIILGTRSAIYTP  320
consensus                                      !!!!!*!!!!!!!!!!!!!!!!!!!!!!!!!!!!!! !!!*!*!!!!!!!! ! !!!!!!! !!!!!!!!!!!!!!!!!!!

logo
NTDB id 1090387 ACJQW4 RS03475 WP 241628382.1  LHNLGLIILDEEHDLSFKQQEGFRYHARDVALYRAHLENCPIILGSATPSMESYALVNQGKLTCLELNERAGTALLPKLH  399
NTDB id 1072 ABD1 RS01805 WP 000156662.1       LPRLGLIILDEEHDLSYKQQEGFRYHARDVALYRGHLQGCPVLLGSATPSIDSYHLVETGKLTALQLNQRAGHALLPKMH  400
consensus                                      !  !!!!!!!!!!!!!!*!!!!!!!!!!!!!!!!!!*!!  !!**!!!!!!!**!!*!!  !!!!!*! !! !!!*!!!!!*!

logo
NTDB id 1090387 ACJQW4 RS03475 WP 241628382.1  ILDLKLGRKQHGFSQFLLDEMHKRLARKDQVLIFLNRRGYAPVLICESCAWQAKCPHCDANFTLHTQPYQHLHCHHCGTI  479
NTDB id 1072 ABD1 RS01805 WP 000156662.1       LIDLKIVKKQHGISQPLIEQIKNTLARKEQVLIFLNRRGYAPVLVCESCGWQANCPHCDAHFTLHTQPYSYLHCHHCGTV  480
consensus                                      **!!!* *!!!! !!*!** **  !!!!*!!!!!!!!!!!!!!!!*!!!!*!!! !!!!!!*!!!!!!!! *!!!!!!!!*

logo
NTDB id 1090387 ACJQW4 RS03475 WP 241628382.1  HRVPDHCPQCQHTELKPIGMGTAKVEESLKELFPEFDVIRVDRDSTSRVGSWQKIYDRIQKSEPVILLGTQMLAKGHHFP  559
NTDB id 1072 ABD1 RS01805 WP 000156662.1       HRLPDHCPECQQKSLKTLGAGTAKVEEHLQELFPDHDVIRVDRDSTSRVGSWQKIYDRIQQNKPSILLGTQMLAKGHHFP  560
consensus                                      !!*!!!!! !!*  !!**! !!!!!!!*! !!!!**!!!!!!!!!!!!!!!!!!!!!!!!!   ! !!!!!!!!!!!!!!!
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logo
NTDB id 1090387 ACJQW4 RS03475 WP 241628382.1  YVSLVAILDIDSGLLSVDFRAPERTAQLIVQVAGRAGRGEKKGDVYLQTLRPEHPLLHTLVDGDYRQFARQTLKERQQAL   639
NTDB id 1072 ABD1 RS01805 WP 000156662.1       HVTLVAILDIDAGLLSVDIRAPERTAQLIVQVAGRAGRGEHKGHVYLQTLRPDHPLLTTLIEKDYRAVAKQTLAERKVAL   640
consensus                                      *!*!!!!!!!! !!!!!! !!!!!!!!!!!!!!!!!!!!*!!*!!!!!!!!*!!!!*!!** !!!  !*!!! !!  !!

logo
NTDB id 1090387 ACJQW4 RS03475 WP 241628382.1  FPPYRYAALIRCESKSQELNQQYLTEHAQQLRQISELNIDIWGPIPAPMERKAGRYQAHMVLLSKDRARLHYYLRAWWQN   719
NTDB id 1072 ABD1 RS01805 WP 000156662.1       LPPYRYAVLIRAESKDRDYTLHFLNEAAEQLRQIAGDIVDIWGPIPAPMERKAGRYRAHMVILSADRARLHFYLRQWWAQ   720
consensus                                       !!!!!! !!!*!!!  *   **! !*! !!!!!    *!!!!!!!!!!!!!!!!!! !!!!*!! !!!!!!*!!! !! *

logo
NTDB id 1090387 ACJQW4 RS03475 WP 241628382.1  MLQH.KPASMKLSLDIDPQEFS   740
NTDB id 1072 ABD1 RS01805 WP 000156662.1       LVHAPRQHQLRLSIDVDPQEFS   742
consensus                                      ******** **!!*!*!!!!!!
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X non conserved
X similar
X $\geq$ 50% conserved