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logo
NTDB id 392101 GA646 RS13270 WP 104498470.1  MPNSPVHPAPIYRVRVAVPVYLYDGFDYMLSAAEYQQAAVGARVLVSFGRQNLVGIIIEKLPPDHPLDPKIKLKAISELL   80
NTDB id 1072 ABD1 RS01805 WP 000156662.1     MTITPKPDSVVYRVRVAVPVHLYDTFDYTLTQAQYERAHVGSRVAISFGRQNLIGIITEKVDPSESFTGTFQLKAISDLL   80
consensus                                    !* *!   * **!!!!!!!!!*!!! !!! !* ! !  !*!! !! *!!!!!!!*!!! !!**! **  *   !!!!!*!!

logo
NTDB id 392101 GA646 RS13270 WP 104498470.1  DQQPILDQKVLTLLTWSAQYYQFPIGEVMHSALPSLLRQGRPYNLLARMWKLLD.DQAEAKLKRSEKQQEAYKVLKLHPS  159
NTDB id 1072 ABD1 RS01805 WP 000156662.1     DEQPILDEQVLSLLTWSAQYYQFPIGEVMQTALPALLRQGKPMDVLFHLWKITPCDNVEALLKRSGKQQDAYQILKLHPA  160
consensus                                    ! !!!!!  !!*!!!!!!!!!!!!!!!!!**!!! !!!!!*!  *! **!!* **!* !! !!!! !!!*!! *!!!!!

logo
NTDB id 392101 GA646 RS13270 WP 104498470.1  GTSENILNLAGIETATLKALEKKQICCCDLEQQDFSPVPMTLAQMPLTPNSDQKQAIETVLKAQHRYQAFLLDGLTGSGK  239
NTDB id 1072 ABD1 RS01805 WP 000156662.1     GTTENILNLSGVETATLKALQKKGLVDCTLEPHDFSPSPVQLAQMPLTLNEDQKKATQYVVNAQHQYQAFLLDGLTGSGK  240
consensus                                    !!*!!!!!! !*!!!!!!!! !! ***! !!**!!!! !* !!!!!!!*! !!! !   !* !!! !!!!!!!!!!!!!!

logo
NTDB id 392101 GA646 RS13270 WP 104498470.1  TEVYLQIMQEVLKQGKQVLVLVPEIGLTPQTISRFQSRFHCHIALLHSGLNDSKRLQAWQAAQTGKASIILGTRSAIYTP  319
NTDB id 1072 ABD1 RS01805 WP 000156662.1     TEVYLHIMHEVLKQGKQVLVLVPEIGLTPQTISRFKSRFNCDIALLHSGLNDSKRLQAWQQAQTGKASIILGTRSAIYTP  320
consensus                                    !!!!!*!!*!!!!!!!!!!!!!!!!!!!!!!!!!!! !!!*!*!!!!!!!!!!!!!!!!!!! !!!!!!!!!!!!!!!!!!!

logo
NTDB id 392101 GA646 RS13270 WP 104498470.1  LPNLGLIILDEEHDLSFKQQEGFRYHARDVALYRAHLEHCPVILGSATPSIDSYALTEQGKMTRLELNQRAGPALMPKIH  399
NTDB id 1072 ABD1 RS01805 WP 000156662.1     LPRLGLIILDEEHDLSYKQQEGFRYHARDVALYRGHLQGCPVLLGSATPSIDSYHLVETGKLTALQLNQRAGHALLPKMH  400
consensus                                    !! !!!!!!!!!!!!!*!!!!!!!!!!!!!!!!!*!! *!!!*!!!!!!!!!!!*! ! !!*! ! !!!!!! !!*!!*!

logo
NTDB id 392101 GA646 RS13270 WP 104498470.1  IIDLKVAQKQLGLSLLLIQEIKKCLQKKEQVLIFLNRRGYAPVLVCDSCGWQAQCPHCDANFTLHHSPYTHLHCHHCGTI  479
NTDB id 1072 ABD1 RS01805 WP 000156662.1     LIDLKIVKKQHGISQPLIEQIKNTLARKEQVLIFLNRRGYAPVLVCESCGWQANCPHCDAHFTLHTQPYSYLHCHHCGTV  480
consensus                                    *!!!!*  !!*!*! *!!  !! *! *!!!!!!!!!!!!!!!!!!!!*!!!!!!*!!!!!!*!!!!* !!**!!!!!!!!*

logo
NTDB id 392101 GA646 RS13270 WP 104498470.1  HRKPEQCPQCQHSELKTLGMGTAKVEENLQQLFPDYEVVRVDRDSTSRVGSWQKIYDRIQTSQPLILLGTQMLAKGHHFP  559
NTDB id 1072 ABD1 RS01805 WP 000156662.1     HRLPDHCPECQQKSLKTLGAGTAKVEEHLQELFPDHDVIRVDRDSTSRVGSWQKIYDRIQQNKPSILLGTQMLAKGHHFP  560
consensus                                    !! !**!! !!*  !!!!! !!!!!!!*!! !!!!**!*!!!!!!!!!!!!!!!!!!!!!!    ! !!!!!!!!!!!!!!!
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logo

NTDB id 392101 GA646 RS13270 WP 104498470.1  YVTLVAILDIDAGLLSVDIRAPERTAQLIVQVAGRAGRGEHKGDVYLQTLRPDHPLLSTLVEQDYRAFARQTLKERQAAL   639
NTDB id 1072 ABD1 RS01805 WP 000156662.1     HVTLVAILDIDAGLLSVDIRAPERTAQLIVQVAGRAGRGEHKGHVYLQTLRPDHPLLTTLIEKDYRAVAKQTLAERKVAL   640
consensus                                    *!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!*!!!!!!!!!!!!!!*!!*! !!!! !*!!! !!   !!

logo

NTDB id 392101 GA646 RS13270 WP 104498470.1  LPPFRYTALIRCESKSQEQNQQFLQQHAQWLRENSEQLIDIWGPIPAPMERKAGRYQAHLVLLSQDRARLHFYLRAWWQN   719
NTDB id 1072 ABD1 RS01805 WP 000156662.1     LPPYRYAVLIRAESKDRDYTLHFLNEAAEQLRQIAGDIVDIWGPIPAPMERKAGRYRAHMVILSADRARLHFYLRQWWAQ   720
consensus                                    !!!*!!  !!!*!!!  *   *!!* *!  !!     **!!!!!!!!!!!!!!!!!! !!*!*!! !!!!!!!!!! !! *

logo

NTDB id 392101 GA646 RS13270 WP 104498470.1  MLHHK.PSNMKLSLDIDPQEFS   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