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logo
NTDB id 1106881 ACLKM6 RS01470 WP 411687305.1  MPNSPVHPAPIYRVRVAVPVYLYDGFDYMLSAAEYQQAAVGARVLVSFGRQNLVGIIIEKLPPDHPLDPKIKLKAISELL   80
NTDB id 1072 ABD1 RS01805 WP 000156662.1       MTITPKPDSVVYRVRVAVPVHLYDTFDYTLTQAQYERAHVGSRVAISFGRQNLIGIITEKVDPSESFTGTFQLKAISDLL   80
consensus                                      !* *!  * **!!!!!!!!!*!!! !!! !* ! !  !*!! !! *!!!!!!!*!!! !!**! **  *   !!!!!*!!

logo
NTDB id 1106881 ACLKM6 RS01470 WP 411687305.1  DQQPILDQKVLTLLTWSAQYYQFPIGEVMHSALPSLLRQGRPYNLLARMWKLLD.DQAEAKLKRSEKQQEAYKVLKLHPS  159
NTDB id 1072 ABD1 RS01805 WP 000156662.1       DEQPILDEQVLSLLTWSAQYYQFPIGEVMQTALPALLRQGKPMDVLFHLWKITPCDNVEALLKRSGKQQDAYQILKLHPA  160
consensus                                      ! !!!!!  !!*!!!!!!!!!!!!!!!!!!**!!! !!!!!*!  *! **!!* **!* !! !!!! !!!*!! *!!!!!

logo
NTDB id 1106881 ACLKM6 RS01470 WP 411687305.1  GTSENILNLAGIETATLKALEKKQICYCDLEQQDFSPVPMTLAQMPLTPNSDQKRAIETVLKAQHRYQAFLLDGLTGSGK  239
NTDB id 1072 ABD1 RS01805 WP 000156662.1       GTTENILNLSGVETATLKALQKKGLVDCTLEPHDFSPSPVQLAQMPLTLNEDQKKATQYVVNAQHQYQAFLLDGLTGSGK  240
consensus                                      !!*!!!!!! !*!!!!!!!! !! ** ! !!**!!!! !* !!!!!!!*! !!!*!   !* !!! !!!!!!!!!!!!!!

logo
NTDB id 1106881 ACLKM6 RS01470 WP 411687305.1  TEVYLQIMQEVLKQGKQVLVLVPEIGLTPQTISRFQSRFHCHIALLHSGLNDSKRLQAWQAAQTGKASIILGTRSAIYTP  319
NTDB id 1072 ABD1 RS01805 WP 000156662.1       TEVYLHIMHEVLKQGKQVLVLVPEIGLTPQTISRFKSRFNCDIALLHSGLNDSKRLQAWQQAQTGKASIILGTRSAIYTP  320
consensus                                      !!!!!*!!*!!!!!!!!!!!!!!!!!!!!!!!!!!! !!!*!*!!!!!!!!!!!!!!!!!!! !!!!!!!!!!!!!!!!!!

logo
NTDB id 1106881 ACLKM6 RS01470 WP 411687305.1  LPNLGMIILDEEHDLSFKQQEGFRYHARDVALYRAHLEHCPVILGSATPSIDSYALTEQGKMIRLELNQRAGPALMPKIH  399
NTDB id 1072 ABD1 RS01805 WP 000156662.1       LPRLGLIILDEEHDLSYKQQEGFRYHARDVALYRGHLQGCPVLLGSATPSIDSYHLVETGKLTALQLNQRAGHALLPKMH  400
consensus                                      !! !!*!!!!!!!!!!*!!!!!!!!!!!!!!!!!!*!! *!!!*!!!!!!!!!!!*! ! !!*  ! !!!!!! !!*!!*!

logo
NTDB id 1106881 ACLKM6 RS01470 WP 411687305.1  IIDLKVAQKQQGLSLLLIQEIKKRLQKKEQVLIFLNRRGYAPVLVCDSCGWQAQCPHCDANFTLHHSPYTHLHCHHCGTI  479
NTDB id 1072 ABD1 RS01805 WP 000156662.1       LIDLKIVKKQHGISQPLIEQIKNTLARKEQVLIFLNRRGYAPVLVCESCGWQANCPHCDAHFTLHTQPYSYLHCHHCGTV  480
consensus                                      *!!!!*  !!*!*! *!!  !!  ! *!!!!!!!!!!!!!!!!!!!!*!!!!!!*!!!!!!*!!!!* !!**!!!!!!!!*

logo
NTDB id 1106881 ACLKM6 RS01470 WP 411687305.1  HRKPEQCPQCQHSELKTLGMGTAKVEENLQHLFPDYEVVRVDRDSTSRVGSWQKIYDRIQTSQPLILLGTQMLAKGHHFP  559
NTDB id 1072 ABD1 RS01805 WP 000156662.1       HRLPDHCPECQQKSLKTLGAGTAKVEEHLQELFPDHDVIRVDRDSTSRVGSWQKIYDRIQQNKPSILLGTQMLAKGHHFP  560
consensus                                      !! !**!! !!*  !!!!! !!!!!!!*!!*!!!!**!*!!!!!!!!!!!!!!!!!!!!!   ! !!!!!!!!!!!!!!!
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logo

NTDB id 1106881 ACLKM6 RS01470 WP 411687305.1  YVTLVAILDIDAGLLSVDIRAPERTAQLIVQVAGRAGRGEHKGDVYLQTLRPDHPLLSTLVEQDYRAFARQTLKERQAAL   639
NTDB id 1072 ABD1 RS01805 WP 000156662.1       HVTLVAILDIDAGLLSVDIRAPERTAQLIVQVAGRAGRGEHKGHVYLQTLRPDHPLLTTLIEKDYRAVAKQTLAERKVAL   640
consensus                                      *!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!*!!!!!!!!!!!!!!*!!*! !!!! !*!!! !!  !!

logo

NTDB id 1106881 ACLKM6 RS01470 WP 411687305.1  LPPFRYTALIRCESKSQEQNQQFLQQHAQWLRENSEQLIDIWGPIPAPMERKAGRYQAHLVLLSQDRARLHFYLRAWWQN   719
NTDB id 1072 ABD1 RS01805 WP 000156662.1       LPPYRYAVLIRAESKDRDYTLHFLNEAAEQLRQIAGDIVDIWGPIPAPMERKAGRYRAHMVILSADRARLHFYLRQWWAQ   720
consensus                                      !!!*!!  !!!*!!!  *   *!!* *!  !!     **!!!!!!!!!!!!!!!!!! !!*!*!! !!!!!!!!!! !! *

logo

NTDB id 1106881 ACLKM6 RS01470 WP 411687305.1  MLHHK.PSNMKLSLDIDPQEFS   740
NTDB id 1072 ABD1 RS01805 WP 000156662.1       LVHAPRQHQLRLSIDVDPQEFS   742
consensus                                      **!********!!*!*!!!!!!
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X non conserved
X similar
X ≥ 50% conserved