```
logo
NTDB id 298563 DOM24 RS01375 WP 111280252.1  MPSSSHNNCCIYRVRVAVPVHLYDSFDYLLSAEQYLQAEVGARVAVSFGRQNLIGIIVEKISPDVMPDPRIKLKAITELL   80
NTDB id 1072 ABD1 RS01805 WP 000156662.1     MTITPKPDSVVYRVRVAVPVHLYDTFDYTLTQAQYERAHVGSRVAISFGRQNLIGITEKVDPSESFTGTFQLKAISDLL   80
consensus                                    !* **** ***!!!!!!!!!!!!!*!!! !*  !!  !*!! !!!*!!!!!!!!!!! !!* !   * *   !!!!**!!

logo
NTDB id 298563 DOM24 RS01375 WP 111280252.1  DKEAIIDSKVLSLLTWSAQYYQFPLGEVMQCALPGLLRQGKPLNLLARVWKVVQPD.AEQLLKRSIKQQDAYKILKLHAA  159
NTDB id 1072 ABD1 RS01805 WP 000156662.1     DEQPILDEQVLSLLTWSAQYYQFPIGEVMQTALPALLRQGKPMDVLFHLWKITPCDNVEALLKRSGKQQDAYQILKLHPA  160
consensus                                    !  *!*!  !!!!!!!!!!!!!!!*!!!!!*!!!*!!!!!!!* *! **!!* * !* ! !!!!! !!!!!! !!!!!*!

logo
NTDB id 298563 DOM24 RS01375 WP 111280252.1  GTTEDILNLSGVETATLKALEKKEIVRCELTAINTTPEPVQLAQMPLTPNEEQHKAIQRILKSLKKFQAFLLDGLTGSGK  239
NTDB id 1072 ABD1 RS01805 WP 000156662.1     GTTENILNLSGVETATLKALQKKGLVDCTLEPHDFSPSPVQLAQMPLTLNEDQKKATQYVVNAQHQYQAFLLDGLTGSGK  240
consensus                                    !!!! !!!!!!!!!!!!!!! !! *! ! ! **  *! !!!!!!!!!!*!!*!*!! ! **   * *!!!!!!!!!!!!!

logo
NTDB id 298563 DOM24 RS01375 WP 111280252.1  TEVYLQVMYEVLKQGKQILVLVPEIGLTPQTISRFKSRFNVDIVLLHSGLSESKRLQAWQHAQTGKASIILGTRSAIYTS  319
NTDB id 1072 ABD1 RS01805 WP 000156662.1     TEVYLHIMHEVLKQGKQVLVLVPEIGLTPQTISRFKSRFNCDIALLHSGLNDSKRLQAWQQAQTGKASIILGTRSAIYTP  320
consensus                                    !!!!!**!*!!!!!!!!*!!!!!!!!!!!!!!!!!!!!!!*!! !!!!!! *!!!!!!!!*!!!!!!!!!!!!!!!!!!*

logo
NTDB id 298563 DOM24 RS01375 WP 111280252.1  LPRLGLIILDEEHDLSFKQQEGFRYHARDVALYRAHLENCPIILGSATPSLDSYHLVEQNKLTRLELNQRAGNAVLPKMQ  399
NTDB id 1072 ABD1 RS01805 WP 000156662.1     LPRLGLIILDEEHDLSYKQQEGFRYHARDVALYRGHLQGCPVLLGSATPSIDSYHLVETGKLTALQLNQRAGHALLPKMH  400
consensus                                    !!!!!!!!!!!!!!!!*!!!!!!!!!!!!!!!!!!*!!  !!**!!!!!!!*!!!!!!!  !!! ! !!!!!!*!*!!!!*

logo
NTDB id 298563 DOM24 RS01375 WP 111280252.1  LIDLKVAKKQHGISEQLIKQIQQRLDKKEQVLVFLNRRGYAPVLVCNHCGWQAKCPHCDAHFTLHTQPYNHLHCHHCGSI  479
NTDB id 1072 ABD1 RS01805 WP 000156662.1     LIDLKIVKKQHGISQPLIEQIKNTLARKEQVLIFLNRRGYAPVLVCESCGWQANCPHCDAHFTLHTQPYSYLHCHHCGTV  480
consensus                                    !!!!!* !!!!!!! *!! !! * ! *!!!!!*!!!!!!!!!!!!!! *!!!!! !!!!!!!!!!!!!! *!!!!!!!**

logo
NTDB id 298563 DOM24 RS01375 WP 111280252.1  HRVPESCPECQQTTLKTLGMGTAKVEETLTELFPDFDVIRVDRDSTSRVGQWDRIYQRIHQSQPAILLGTQMLAKGHHFP  559
NTDB id 1072 ABD1 RS01805 WP 000156662.1     HRLPDHCPECQQKSLKTLGAGTAKVEEHLQELFPDHDVIRVDRDSTSRVGSWQKIYDRIQQNKPSILLGTQMLAKGHHFP  560
consensus                                    !!*!**!!!!!! *!!!!! !!!!!!!*! !!!!!*!!!!!!!!!!!!!! ! *!! !!*!  ! !!!!!!!!!!!!!!!
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logo
NTDB id 298563 DOM24 RS01375 WP 111280252.1  YVTLVAILDIDAGLLSFDFRAPERTAQLIIQVAGRAGRGDRRGEVYLQTLRPDHPLLTTLIEKDYRAFAKQALIERQQAQ   639
NTDB id 1072 ABD1 RS01805 WP 000156662.1     HVTLVAILDIDAGLLSVDIRAPERTAQLIVQVAGRAGRGEHKGHVYLQTLRPDHPLLTTLIEKDYRAVAKQTLAERKVAL   640
consensus                                    *!!!!!!!!!!!!!!! ! !!!!!!!!!!*!!!!!!!!!***!*!!!!!!!!!!!!!!!!!!!!!!! !!! ! !!   !

logo
NTDB id 298563 DOM24 RS01375 WP 111280252.1  LPPYRYTVLVRADSRNQQYSQEFLAEIARKLRELAGSQVDIWGPIPAPMERKAGRYRAHLVLLSADRAQLHFYLRQWWVM   719
NTDB id 1072 ABD1 RS01805 WP 000156662.1     LPPYRYAVLIRAESKDRDYTLHFLNEAAEQLRQIAGDIVDIWGPIPAPMERKAGRYRAHMVILSADRARLHFYLRQWWAQ   720
consensus                                    !!!!!! !!*!!*!*   !* *!! ! !  !! *!!  !!!!!!!!!!!!!!!!!!!!!!*!*!!!!!! !!!!!!!!!

logo
NTDB id 298563 DOM24 RS01375 WP 111280252.1  VVQQPRQHQLKLSIDVDPQELS   741
NTDB id 1072 ABD1 RS01805 WP 000156662.1     LVHAPRQHQLRLSIDVDPQEFS   742
consensus                                    *!* !!!!!!*!!!!!!!!! !
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X non conserved

X similar

X $\geq$ 50% conserved