```
logo
NTDB id 419430 GVU25 RS01630 WP 004975947.1  MPDSTLDPQPVYRIRVAVPVYLYDCFDYMLSAAQYQQAEVGARVLVSFGRQNLVGIIVEKLALDTPIDPRFKLKAISELL   80
NTDB id 1072 ABD1 RS01805 WP 000156662.1     MTITPKPDSVVYRVRVAVPVHLYDTFDYTLTQAQYERAHVGSRVAISFGRQNLIGIITEKVDPSESFTGTFQLKAISDLL   80
consensus                                    !* ** ** *!!!*!!!!!!*!!!*!!! !* !!!  !*!! !! *!!!!!!!*!!! !!* *  *  * ! !!!!!*!!

logo
NTDB id 419430 GVU25 RS01630 WP 004975947.1  DEQAILDPKVLTLLTWSAQYYQFPIGEVMQSALPSLLRQAKPYNLLARTWKLLDAH.AEAKITRSEKQQEAYKILKLHPS  159
NTDB id 1072 ABD1 RS01805 WP 000156662.1     DEQPILDEQVLSLLTWSAQYYQFPIGEVMQTALPALLRQGKPMDVLFHLWKITPCDNVEALLKRSGKQQDAYQILKLHPA  160
consensus                                    !!!*!!!* !!*!!!!!!!!!!!!!!!!!!*!!! !!!!*!!  *! * !!* **** !! * !! !!!*!! !!!!!!

logo
NTDB id 419430 GVU25 RS01630 WP 004975947.1  GTSENILNLAGIETATLKALANKEICACVLEAQDFSPMPVTLAQMPLTPNPDQKKAIDSVLKVRQQYKAFLLDGLTGSGK  239
NTDB id 1072 ABD1 RS01805 WP 000156662.1     GTTENILNLSGVETATLKALQKKGLVDCTLEPHDFSPSPVQLAQMPLTLNEDQKKATQYVVNAQHQYQAFLLDGLTGSGK  240
consensus                                    !!*!!!!!! !*!!!!!!!!  ! ** ! !!**!!!! !! !!!!!!!*!*!!!!!   !*   *!! !!!!!!!!!!!!

logo
NTDB id 419430 GVU25 RS01630 WP 004975947.1  TEVYLHIMHEVLKQGKQVLVLVPEIGLTPQTISRFQSRFHCHIALLHSGLNDSKRLQAWQAAQTGKASIILGTRSAIYTP  319
NTDB id 1072 ABD1 RS01805 WP 000156662.1     TEVYLHIMHEVLKQGKQVLVLVPEIGLTPQTISRFKSRFNCDIALLHSGLNDSKRLQAWQQAQTGKASIILGTRSAIYTP  320
consensus                                    !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!! !!!*!*!!!!!!!!!!!!!!!!!! !!!!!!!!!!!!!!!!!!

logo
NTDB id 419430 GVU25 RS01630 WP 004975947.1  LPNLGLIILDEEHDLSFKQQEGFRYHARDVALYRAHLENCPVILGSATPSIDSYALVDQGKMQCLELNQRAGTALMPKIH  399
NTDB id 1072 ABD1 RS01805 WP 000156662.1     LPRLGLIILDEEHDLSYKQQEGFRYHARDVALYRGHLQGCPVLLGSATPSIDSYHLVETGKLTALQLNQRAGHALLPKMH  400
consensus                                    !! !!!!!!!!!!!!!*!!!!!!!!!!!!!!!!!*!! !!!*!!!!!!!!!!!!*!!* !!* *! !!!!!!*!!*!!*!

logo
NTDB id 419430 GVU25 RS01630 WP 004975947.1  LIDLKIAKKQHGISQQLIDEIKKRLAKKEQVLVFLNRRGYAPVLICESCAWQAKCPNCDANFTLHHQPYTHLHCHHCGTI  479
NTDB id 1072 ABD1 RS01805 WP 000156662.1     LIDLKIVKKQHGISQPLIEQIKNTLARKEQVLIFLNRRGYAPVLVCESCGWQANCPHCDAHFTLHTQPYSYLHCHHCGTV  480
consensus                                    !!!!!! !!!!!!!!*!!* !!  !!*!!!!!*!!!!!!!!!!!*!!!!*!!! !!*!!!*!!!!*!!!**!!!!!!!!*

logo
NTDB id 419430 GVU25 RS01630 WP 004975947.1  HRKPEQCPACNHAELKPIGMGTAKVEDSLNELFPNVDVIRVDRDSTSRVGSWQKIYDRIQRSEPLILLGTQMLAKGHHFP  559
NTDB id 1072 ABD1 RS01805 WP 000156662.1     HRLPDHCPECQQKSLKTLGAGTAKVEEHLQELFPDHDVIRVDRDSTSRVGSWQKIYDRIQQNKPSILLGTQMLAKGHHFP  560
consensus                                    !! !**!! !**  !!**! !!!!!**!*!!!! *!!!!!!!!!!!!!!!!!!!!!!!!!!   ! !!!!!!!!!!!!!!
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logo
NTDB id 419430 GVU25 RS01630 WP 004975947.1  YVTLVAILDIDSGLLSVDIRAPERTAQLIVQVAGRAGRGEHKGDVYLQSVRPDHPLLTTLVEGDYRKFAKQSLKERKAAQ  639
NTDB id 1072 ABD1 RS01805 WP 000156662.1     HVTLVAILDIDAGLLSVDIRAPERTAQLIVQVAGRAGRGEHKGHVYLQTLRPDHPLLTTLIEKDYRAVAKQTLAERKVAL  640
consensus                                    *!!!!!!!!!! !!!!!!!!!!!!!!!!!!!!!!!!!!!!!*!!!!**!!!!!!!!!!*! !!!  !!!*! !!! !

logo
NTDB id 419430 GVU25 RS01630 WP 004975947.1  LPPYRYSALIRCESKSQELNQQFLQQHAQWLREHSEQLIEIWGPIPAPMERKAGRFHAHMVLLSKDRARLHFYIRNWWQN  719
NTDB id 1072 ABD1 RS01805 WP 000156662.1     LPPYRYAVLIRAESKDRDYTLHFLNEAAEQLRQIAGDIVDIWGPIPAPMERKAGRYRAHMVILSADRARLHFYLRQWWAQ  720
consensus                                    !!!!!!  !!!*!!!  *   *!!* *!  !! *   ***!!!!!!!!!!!!!!!!**!!!!*!! !!!!!!!!*!*!! *

logo
NTDB id 419430 GVU25 RS01630 WP 004975947.1  MLHEK.PSSMKLSLDIDPQEFS  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