

Sequence logo visualization of the protein sequence alignment. The y-axis represents information content in bits. The x-axis shows the sequence position from 1 to 60. The legend indicates the amino acids: Y (yellow), F (blue), G (green), D (red), Y (orange), D (purple), A (brown), D (pink), G (grey), V (light blue), S (light green), T (light orange), S (light purple), V (light brown), L (light pink), M (light grey), Y (light blue), L (light green), H (light orange), A (light purple), L (light brown), Q (light pink), K (light grey), E (light blue), L (light green), S (light orange), A (light purple), Q (light brown), V (light pink), D (light grey), F (light blue), Y (light green), I (light orange), P (light purple), N (light brown), R (light pink), F (light grey), T (light blue), E (light green), G (light orange), Y (light purple), G (light brown), P (light pink), N (light grey), E (light blue), E (light green), A (light orange), F (light purple), H (light brown), W (light pink), A (light grey), H (light blue), S (light green), A (light orange), G (light purple), F (light brown), S (light pink), L (light grey), I (light blue), I (light green), T (light orange), V (light purple), D (light brown), T (light pink), G (light grey), I (light blue), A (light green), A (light orange), V (light purple), H (light brown), E (light pink), A (light grey), K (light blue), V (light green), A (light orange), K (light purple), E (light brown), L (light pink), G (light grey), I (light blue), D (light green), L (light orange), I (light purple), I (light brown), T (light pink), D (light grey), H (light blue), H (light green).

L K E L F V S N V S Q S E I T E E T V G F S L A P R L N A V G R L E A T P A V H L L M S E D S F E A K E L A E I D Q L N K L R Q K M V S Q M T E A L E M V E Q Q
L K A L F K V A N V S Q S E I T E E S I G F S I A P R I N A V G R L E D A T P A V H L L L S E D P E E A K E L A E E I D E L N K L R K D I V K Q I T E E A I A E V E N N F
L K E L I K I S G G D I G E A N E E T V G F Q L A P R L N A V G R I E Q A D P A V H L L M S E D S F E A E E L A A E I D Q L N K E R Q K M V S K M T D E A I E M V E Q Q

[illegible]595
593

logo

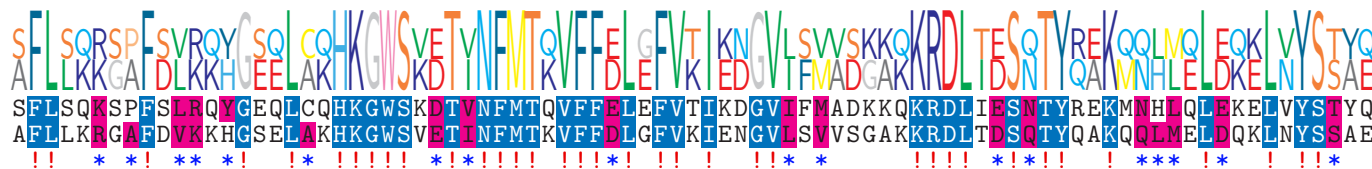
NTDB id 79767 L6477 RS21590 WP 236797220.1
NTDB id 354 BSU 27620 NP 390640.1
consensus



675
678

logo

NTDB id 79767 L6477 RS21590 WP 236797220.1
NTDB id 354 BSU 27620 NP 390640.1
consensus



760
763

logo

NTDB id 79767 L6477 RS21590 WP 236797220.1
NTDB id 354 BSU 27620 NP 390640.1
consensus



779
786

-  non conserved
-  similar
-  $\geq 50\%$ conserved