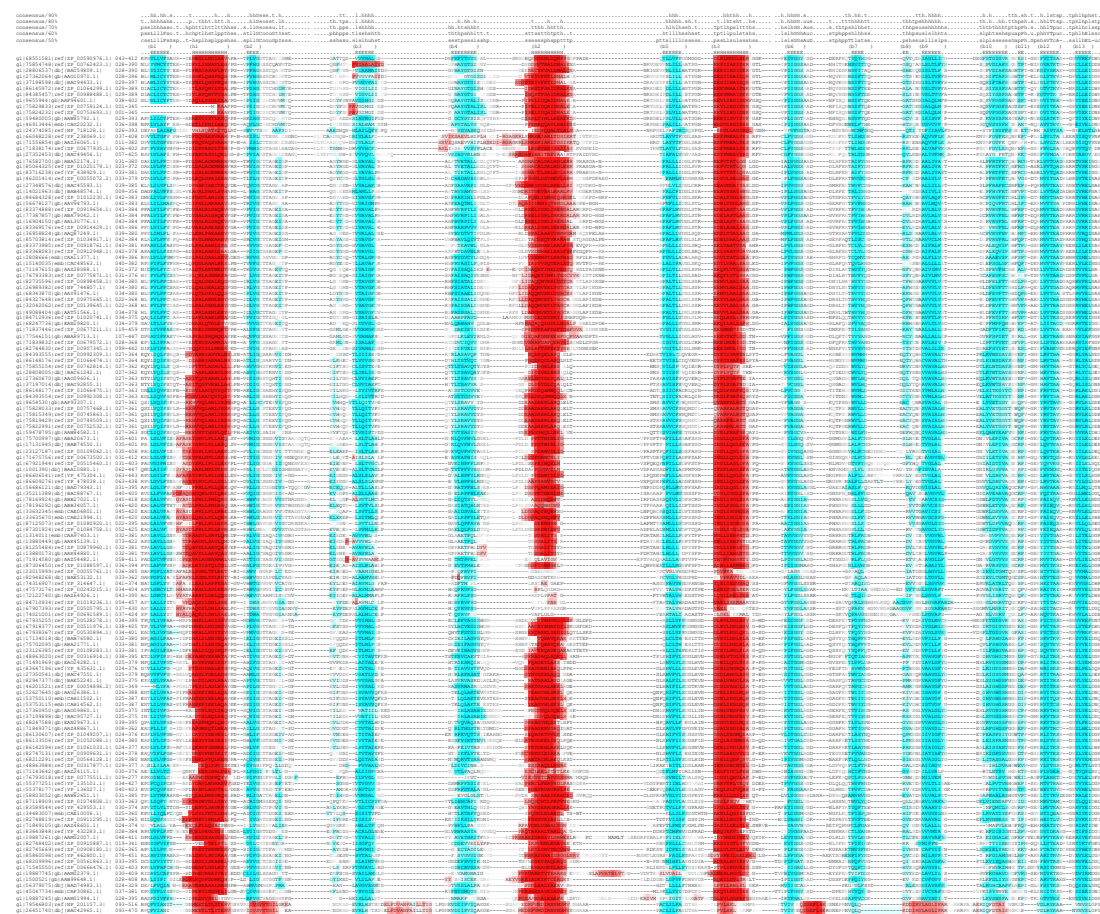
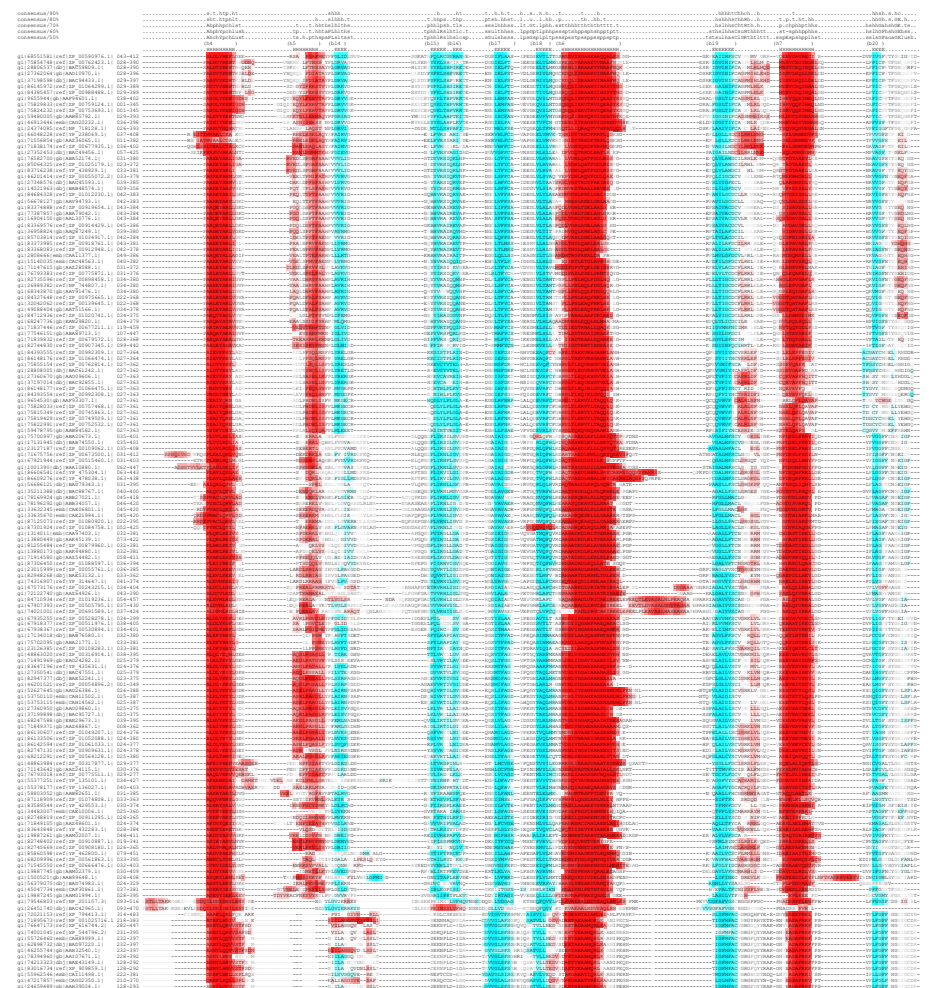


A)



B)



File 1: FIST_N (A) and FIST_C (B) multiple sequence alignments.

Multiple sequence alignment and amino acid consensus of all FIST_N subdomains. Amino acids are colored by secondary structure prediction: (red) alpha helix, (blue) beta strand. The alignments should be viewed at high zoom for detail.