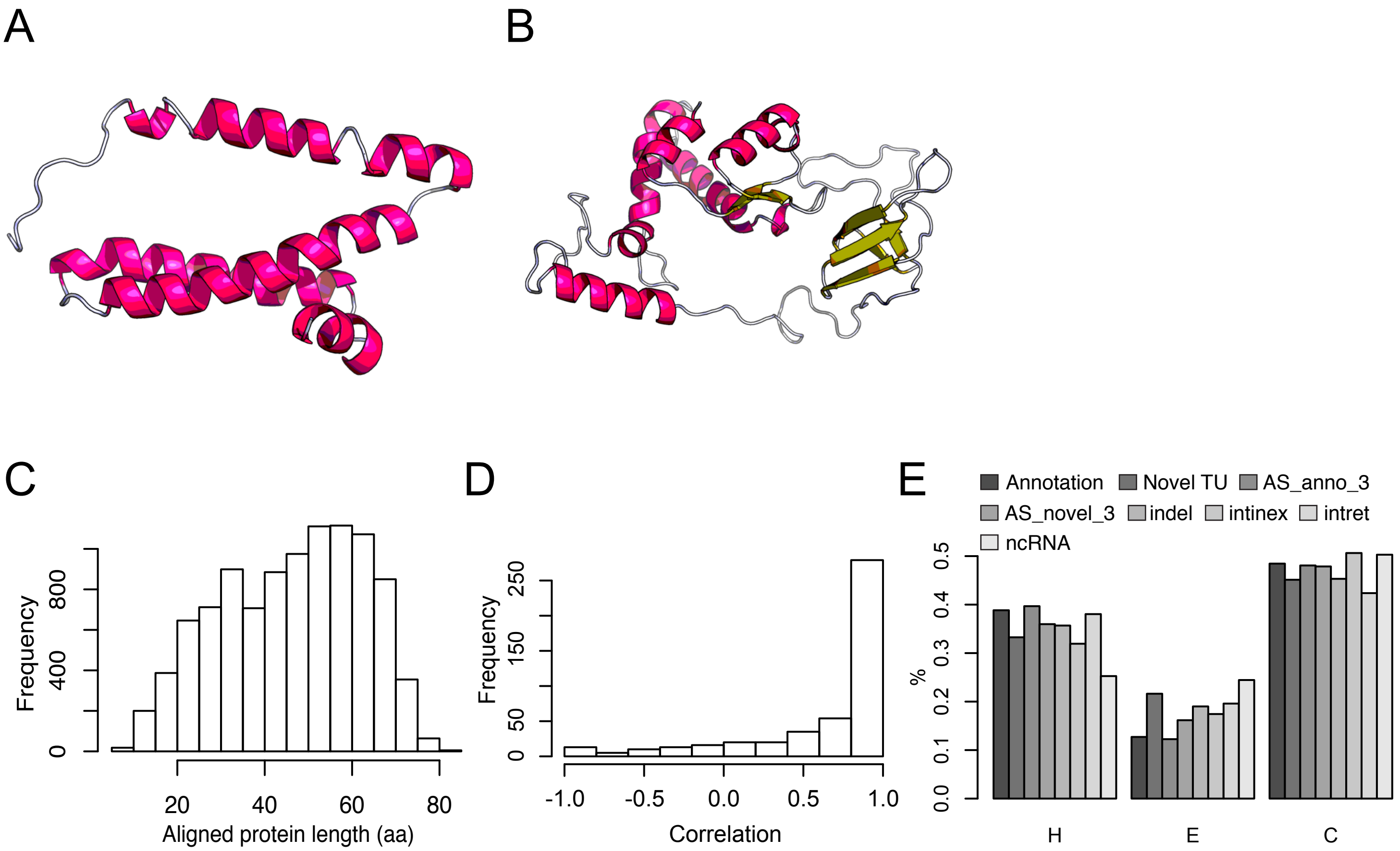

Supplemental Figure S7. Secondary structure prediction. (A) Structure predicted for NG554. (B) Structure predicted for NG569. (C) Lengths of aligned proteins predicted from novel TUs. (D) Correlation of the ratios of α-helix (H), β-sheet (E) and coil (C) predicted from C terminus annotated or amino acid sequence starting at first alteration in AS isoforms. (E) Percentages of α-helix (H), β-sheet (E) and coil (C) predicted for different classes of proteins.