

primary.tcl finds the amino acid sequence in the given protein and writes the primary structure plus proportion for each in the **primary_structure.txt**.

secStruct.tcl finds the secondary structure for each frame of protein, then calculates the percentage of each secondary structure in the protein and writes it in the **secondry_structure_percentage.txt**

phiPsi.tcl finds phi and psi angles for each carbon-alpha in the protein and writes it in the **phi_psi_angels_for_CA.txt**

rmsd.tcl finds rmsd by comparing frames two by two and writes it in the **rmsd.txt**

omega.tcl finds all atoms in hydrogen bonds and calculates their amino acid dihedral angles, secondary structure, and radius of gyration, then writes it in the **amino_acid_psi_phi_omega.txt**.