

Thermal Stability of the IgG-binding regions of streptococcus Protein G for Wild-Type and Mutant Conformations

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The B1 domain of Protein G obtained from streptococcus exhibits thermal stability over a broad range of temperatures. Point mutations were introduced at various residues along the 56 amino acid chain. It was shown through circular dichroism experiment that thermal stability of the protein changed, sometimes dramatically, when a point mutation was introduced at threonine 53. It has been hypothesized that a point mutation at position 53 increases the rigidity of the protein; therefore kinetic-energy cannot be absorbed as effectively resulting in denaturation of the protein at lower temperatures. To explore this possibility, 1.2ns molecular dynamic simulations were run for the wild-type, T53M, T53A, and T53P mutations. Using principal component analysis and Procrustes-Rotation, a variance plot can be obtained (Figure below) which shows the extent of variability in inter- C_{α} distances throughout the simulation. We hope to observe a decrease in variability of inter- C_{α} distances for mutated proteins as compared to the wild-type.

