Title:	Protein Contact Network analysis and atomistic Molecular Dynamics simulation study of various thermostable mutant proteins
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Abstract:	Thermal stability of protein means to be resistant to changes in protein structure due to applied heat. in this thesis, our interest has been to study, those proteins and their mutants, having indistinguishable ordered crystallographic structures, but exhibiting large changes in functions mostly in thermostability. Here in our analysis we take five different wild type proteins and their thermostable mutants and we analyse residue specific network parameters of each one using Residue Interaction Network(RIN) to know role of such parameters in determining it's thermostability thereafter we have done Atomistic Molecular Dynamics Simulation study of three selected proteins to know RMSD, Radius of gyration and Hydrogen-Bond analysis which are factors that can give us comparative measure to know how small changes in protein can affect its function majorly its melting temperature .
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