**Introduction**

Mutation in the coding regions for metabolic enzymes can lead to altered kinetic properties. Its effect on the entire network can be more complex. The correlation analysis between mutation and in silico GEM simulation could help to provide some clues.(2000)

Combine the structural genomics and system biology, we can observe how biological networks developed. Proteins in the network are dominated by a limited number of folds (it should be domain). Most of these folds occurred in the essential core (-30%) of the network. Few additional folds can be found from non-essential proteins(2009).

Reference

(2000). "In Silico Model-Driven Assessment of the Effects of Single Nucleotide Polymorphisms (SNPs) on

Human Red Blood Cell Metabolism." Genome Research.

(2009). "Three-Dimensional Structural View of the Central Metabolic Network of Thermotoga maritima."