## Penner-Andersen's Fatgraph Models of Proteins

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**Abstract.** In 2009, R.C.Penner and J.E.Andersen proposed to classify conformations of proteins by using topological invariants. They introduced the Fatgraph for modeling proteins and constructed an algorithm to calculate those invariants. Their methods are suitable for computation and existing database implies that their invariants could be useful for structural classification of proteins. I would like to introduce their methods and also propose some questions.