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Do lattice protein simulations exhibit self-organized criticality? ADDISON WISTHOFF[1], JOELLE MURRAY[2], Linfield College — Proteins are known to fold into tertiary structures that determine their functionality in living organisms. The goal of my research is to better understand the protein folding process through a lattice Monte-Carlo simulation. Specifically, amino acids in the chain at each time step are allowed to fold to certain locations according to two main criteria: folds must maintain bond length and should be thermally and energetically favorable. This simulation will then be used to examine whether the folding process can be viewed through the lens of self-organized criticality (SOC). In particular I am interested in whether there are features of the folding process that are independent of the size of the protein.

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