Abstract Submitted
for the NWS11 Meeting of
The American Physical Society

Computational Studies of Protein Folding ADDISON WISTHOFF, ANDREW CLELAND, JOELLE MURRAY, Linfield College — Proteins are known to fold into tertiary structures that determine their functionality in living organisms. The goal of our research is to better understand the protein folding process. Using MATLAB, we created an algorithm that models the folding process via a Monte Carlo time step approach. Specifically, amino acids in the chain at each time step are allowed to fold to certain locations according to a set of rules. These rules are based on two main criteria: folds must maintain bond length and should be thermally and energetically favorable. One central goal of our research is to examine whether the folding process can be viewed through the lens of self-organized criticality. In particular we are interested in whether there are features of the folding process that are independent of the size of the protein.

Addison Wisthoff
Linfield College

Date submitted: 12 Oct 2011 Electronic form version 1.4