Abstract Submitted
for the MAR10 Meeting of
The American Physical Society

Determining the Structure of a Cytoplasmic Polyadenylation Element Binding Protein via AMBER9 ALISON SAUNDERS, Reed College — The neurons of *Aplysia californica* contain cytoplasmic polyadenylation element binding protein (CPEB). CPEB shows prion-like properties when expressed in yeast cells. Because prions have misfolded and normally folded forms, prions can code in neurons like binary codes in computers, with "present" and "not present" signals available. CPEB thus provides a candidate protein for the molecular basis of memory. I attempt to determine CPEB's structure, by first threading the known protein sequence around a β-helical structure. Threading is preformed by hand, and by a program written to minimize the energy cost of building the structure. I then analyze the stability of the thread using the molecular dynamics program AMBER9. I also analyze a protein of only glutamine (PolyQ) in a β-helical structure to substantiate my use of a β-helix with the glutamine-rich CPEB. I found PolyQ to be stable in a left-handed β-helical structure with eighteen residues per turn. A candidate structure for CPEB was located with the same β-helical structure.

Alison Saunders
Reed College

Date submitted: 18 Nov 2009 Electronic form version 1.4