Abstract Submitted
for the NWS10 Meeting of
The American Physical Society

**Dynamic and static fluorescence quenching of bovine serum albumin**[1] JACOB FRIDAY, JEREMIAH BABCOCK, LORENZO BRANCALEON — Protein folding dynamics studies can benefit from the knowledge of specific binding-site availabilities, which aid the detection of protein structural changes and, possibly, protein structure. Fluorescence quenching (FQ) spectroscopy can be used to detect binding site variations arising from evolving protein conformational changes over time. Use of the Stern-Volmer and modified Stern-Volmer equations shows the divergence of the bimolecular quenching constant from the diffusion-limited constant, which can be indicative of bimolecular binding. The study is part of a larger effort to understand early structural events that lead to the aggregation of partly unfolded proteins. In this study, bovine serum albumin (BSA), a globular alpha-helix plasma transport protein, was complexed with the fluorescent ligand fluorescein in phosphate buffer at pH 7.4 and subjected to FQ spectroscopy. Stern-Volmer plots demonstrated an upward quadratic relationship, indicating the presence of dynamic and static quenching factors. Data-fitting showed that multiple binding sites were available. With these results, further studies will be undertaken, where BSA will be subjected to varied denaturing conditions, including pH changes and urea solvent addition. The change of available binding sites could reveal BSA structural patterns.

[1]Partially supported by MBRS-RISE GM60655

Jacob Friday

Date submitted: 24 Sep 2010 Electronic form version 1.4