Abstract Submitted
for the MAR16 Meeting of
The American Physical Society

Single molecule analysis of B cell receptor motion during signaling activation IVAN REY SUAREZ, Biophysics Program, University of Maryland, PETER KOO, SIMON MOCHRIE, Department of Physics, Yale University, WENXIA SONG, Dept. of Cell Biology and Molecular Genetics, University of Maryland, ARPITA UPADHYAYA, Department of Physics, University of Maryland — B cells are an essential part of the adaptive immune system. They patrol the body looking for signs of infection in the form of antigen on the surface of antigen presenting cells. The binding of the B cell receptor (BCR) to antigen induces signaling cascades that lead to B cell activation and eventual production of high affinity antibodies. During activation, BCR organize into signaling microclusters, which are platforms for signal amplification. The physical processes underlying receptor movement and aggregation are not well understood. Here we study the dynamics of single BCRs on activated murine primary B cells using TIRF imaging and single particle tracking. The tracks obtained are analyzed using perturbation expectation-maximization (pEM) a systems-level analysis that allows the identification of different short-time diffusive states from a set of single particle tracks. We identified five different diffusive states on wild type cells, which correspond to different molecular states of the BCR. By using actin polymerization inhibitors and mutant cells lacking important actin regulators we were able to identify the BCR molecule configuration associated with each diffusive state.

Arpita Upadhyaya
Department of Physics, University of Maryland

Date submitted: 24 Nov 2015 Electronic form version 1.4