Abstract Submitted
for the MAR15 Meeting of
The American Physical Society

**Energetic modeling and single-molecule verification of dynamic regulation on receptor protein diffusion by actin corrals and lipid raft domains receptor** CHIEN YU LIN, JUNG Y. HUANG, Department of Photonics, Chiao Tung University, LEU-WEI LO, Institute of Biomedical Engineering and Nanomedicine, National Health Research Institutes — To faithfully estimate a signal that varies in both space and time, the optimization strategy used by a live cell is to organize a collection of distributed and mobile receptors into a mobile active clustering. However, living eukaryotic cells are highly heterogeneous and stochastically dynamic. It is therefore important to develop an energetic model based on fundamental laws to verify that the underlying processes are energetically favorable. We developed an energetic model based on the generalized Langevin equation and the Cahn-Hilliard equation to simulate the diffusive behaviors of receptor proteins in the plasma membrane with a hierarchical structure of actin corrals, lipid domains, and receptor proteins. Single-molecule tracking data of EGFR acquired on live HeLa cells agrees with the simulation results. We discovered that after ligand binding, EGFR molecules move into lipid nanodomains. The transition rates between different diffusion states of liganded EGFR molecules are regulated by the lipid domains. Our method captures both the sensitivity of single-molecule processes, statistic accuracy of data analysis, and the hierarchical structure of plasma membranes.

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Date submitted: 10 Nov 2014 Electronic form version 1.4