MECHANICAL ENGINEERING SEMINAR

Computer-Aided Design and Engineering of Molecular Motors

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Molecular motors (~ 10 nm in size) convert ATP chemical energy into mechanical work to perform diverse biological functions. Myosin is a family of molecular motors responsible for many essential biological tasks including muscle contraction, cell division, and vesicle transport. To design and engineer molecular motors such as myosin to perform novel functions, one requires detailed understanding of motor kinematics, dynamics and energy transduction mechanism. Using computational modeling and molecular dynamics simulation, I designed a series of myosin VI motors with artificial lever arms fused at different locations. I measured the single molecule stroke sizes of different designs using optical trapping and characterized the directionalities and velocities using dual-labeled in vitro motility assays. Our results demonstrate the predictive power of computational modeling in myosin kinematics. These engineered myosins helped identify the key functional elements of myosin VI. Furthermore, we were able to reverse the direction that myosin moves on actin filaments with a change of only one 18 amino acid stretch that connects the lever arm to the catalytic domain.

Dr. Jung-Chi Liao is a Research Associate in the Department of Bioengineering at Stanford University. He received his B.S. degree from National Taiwan University and his M.S. and Ph.D. degrees from MIT, all in Mechanical Engineering. His Ph.D. work with Professor Kim Vandiver at MIT was to develop one of the leading modeling tools for the predictions of vortex-induced vibration under unsteady flow for offshore oil industry. After completing his Ph.D. work, he took a postdoctoral position at the University of California at Berkeley to work with Professor George Oster. He developed mechanochemical models for various ATP-driven molecular motors, including F1 Fo ATP synthase (rotary motor), T7 DNA helicase, Rho transcription terminator, and virus packaging motor. After his postdoctoral research, he took a Research Associate position at Stanford University to conduct computational modeling, protein engineering, and single molecule experiments to study kinematics and dynamics of myosin under the guidance of Professor Scott Delp, Professor James Spudich, and Professor Russ Altman. He was an organizer and a co-chair of the conference in Multiscale Modeling and Simulation: from Molecules to Cells to Organisms at the 13th Pacific Symposium of Biocomputing, 2008, and he co-chaired the Platform in Protein Structure and Allosteric Communication at the 52nd Biophysical Society Meeting, 2008. He is a reviewer of Physical Review Letter, Journal of Molecular Biology, and BBA Proteins and Proteomics.

Thursday, FEBRUARY 14th, 2008

12:00 pm Seminar in 233 Mudd
1:00 pm Lunch in ME Lobby