

Hydrodynamic Collective Effects of Active Protein Machines in Solution and Lipid Bilayers

Alexander S. Mikhailov (FHI)

The cytoplasm and biomembranes in biological cells contain large numbers of proteins that cyclically change their shapes. They are molecular machines that can function as molecular motors or carry out many other tasks in the cell. Many enzymes are also undergoing conformational changes within their turnover cycles. We analyze the effects that hydrodynamic flows induced by active proteins have on other passive molecules in solution or membranes. We show [1] that the diffusion constants of passive particles are enhanced substantially.

Furthermore, when gradients of active proteins are present, a chemotaxis-like drift of passive particles takes place. In lipid bilayers, the effects are strongly nonlocal, so that active inclusions in the entire membrane contribute to local diffusion enhancement and the drift. Thus, active proteins generate fluctuating hydrodynamic fields that span the entire biological cell. Because such fluctuating fields are non-thermal, they can be further rectified so that energy or work is extracted from them.

[1] A.S. Mikhailov and R. Kapral, arXiv: 1503.02610v1. [cond-mat.soft]

9 Mar 2015