

A New Model for Myosin Motors Incorporating Brownian Ratchet and Powerstroke Mechanisms

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Abstract:

Myosin proteins encompass a diverse group of molecular motors that convert the energy stored in ATP directly into mechanical work. In recent years, the microscopic mechanism that these motors use to move has come under scrutiny. Many researches maintain that the well established powerstroke mechanism developed to explain muscle contractions is still the best theory to explain the behavior of these proteins. With the advent of new single molecule experiments used for studying these proteins, new mechanisms such as the Brownian ratchet have been proposed to explain behaviors inconsistent with a powerstroke mechanism. A Brownian ratchet moves by rectifying the thermal fluctuations that all motor proteins experience, as opposed to the deterministic mechanism of a powerstroke. Unfortunately, neither of these models sufficiently explains the behavior of all myosin motor proteins.

We will investigate a new motor protein model that uses rotational-translational coupling to incorporate both a Brownian ratchet mechanism (diffusion driven) and a powerstroke mechanism (drift driven). With a given set of physical parameters, this stochastic model can utilize either of the mechanisms to do work. While this model can be used to explain the observed behavior of a wide variety of motor proteins, we will look specifically at how this model relates to the particular characteristics of Myosins II, V, and VI. These proteins are usually considered to operate very differently, but with computer simulations of this hybrid model we can explore the efficiency, velocity and step size for both loaded and unloaded cases for each motor protein.