Review of: "Modeling the processive movement of dimerized kinesin-10 NOD motors"

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The author provides a self-consistent model to explain the processive motion of NOD. The method used in the manuscript has been successfully used in lots of the author's motor-related works. The calculation is solid. There is a minor suggestion. The key point of the model is the conformational change of tubulin induced by the binding of NOD. The affinity of NOD in nucleotide-bound state (E_{w2}) to the tubulin with this conformational change is weaker than that to the normal tubulin (E_{w1}). The elastically conformational change of tubulin is rapid (t_f, t_k, in the order of ns or μs). These elements is grafted from the MD simulation results of kinesin-1. Though the experimental results of Refs. [5][9] can provide the evidence that this conformational change-related difference in the binding affinity exist in NOD, a direct structural analysis of the binding conformation of NOD and tubulin in NOD's different nucleotide-binding states will be helpful.