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Protein Dynamics, Ligand Binding, and Biological Function

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Dynamics is essential for protein function. To demonstrate this point, this talk presents three studies. (1) For a ligand-gated ion channel, ligand binding leads to channel activation by modulating the dynamics of the channel protein. A common theme that emerges from different families of ligand-gated ion channels is that agonist binding closes the ligand-bidning domain (LBD), leading to pore opening in the transmembrane domain (TMD); in contrast, antagonist binding opens the LBD, leading to pore closing in the TMD [1]. (2) When the structure [2] and gating dynamics [3] of the influenza M2 proton channel are accounted for, the calculated rate of ion transport is in quantitative agreement with experimental data [4]. (3) In enzymes, gating dynamics afford substrate selectivity [5].

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[3] M. Yi, T. A. Cross, and H.-X. Zhou (2009). Conformational heterogeneity of the M2 proton channel and a structural model for channel activation. Proc. Natl. Acad. Sci. USA 106, 13311-13316.
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