Dynamics of membrane proteins in biological cells.

Robinson Zhou*

Department of Chemistry, Physical and Theoretical Chemistry Laboratory, University of Oxford, Oxford OX1, UK

Abstract

Membrane proteins mediate actions that are essential for biological cells to thrive. Receptors facilitate communication between the cell and its surroundings, membrane-embedded enzymes catalyse chemical reactions, and transporters that are embedded in membranes carry ions and bigger solutes across membranes. Understanding how the proteins link to their fluid, hydrated lipid membrane environment is necessary to comprehend these methods of action. Here, we present recent research on the structure, function, and dynamics of membrane proteins using computational and experimental methods. We also demonstrate how these studies address important issues in understanding the complex environmental influences on these properties.

Keywords: Membrane proteins, lipids, Protein structure, Protein function, Protein dynamics, Membrane-mediated interactions.

Introduction

Proteins that carry out crucial tasks for cell physiology and disease progression are housed in the different compartments and lipid membranes surrounding cells. According to recent research, lipid membranes have a significant impact on the local structure, dynamics, and even activity of a membrane protein. Membrane proteins mediate processes that are fundamental for the flourishing of biological cells. Membrane-embedded transporters move ions and larger solutes across membranes; receptors mediate communication between the cell and its environment and membrane-embedded enzymes catalyze chemical reactions [1].

Understanding these mechanisms of action requires knowledge of how the proteins couple to their fluid, hydrated lipid membrane environment. We present here current studies in computational and experimental membrane protein biophysics, and show how they address outstanding challenges in understanding the complex environmental effects on the structure, function, and dynamics of membrane proteins [2].

Given the advances in computational methodologies and computer power, theoretical approaches are likely to become increasingly important in the study of membrane proteins and their reactions. Studying the potential energy landscape provides both conceptual and computational tools for understanding a wide range of observable properties in membrane protein science. In particular, we can exploit stationary points (minima and transition states) for structure prediction and analysis of global thermodynamic and kinetic properties [3].

Cells sense and respond to the external environment, mainly through proteins presented on the membrane where their expression and conformation are dynamically regulated *via* intracellular programs. Here, we engineer a cell–surface nanoarchitecture that realizes molecular-recognition-initiated DNA assembly to mimic the dynamic behavior of membrane proteins, enabling the manipulation of cellular interaction in response to environmental changes. Our results show that this membrane-anchored DNA nanoarchitecture can be specifically activated by cell-responsive signals to external stimulation [4].

Detection of weak ligand binding to membrane-spanning proteins, such as receptor proteins at low physiological concentrations, poses serious experimental challenges. Saturation transfer difference nuclear magnetic resonance (STD-NMR) spectroscopy offers an excellent way to surmount these problems. As the name suggests, magnetization transferred from the receptor to its bound ligand is measured by directly observing NMR signals from the ligand itself. Low-power irradiation is applied to a 1H NMR spectral region containing protein signals but no ligand signals. This irradiation spreads quickly throughout the membrane protein by the process of spin diffusion and saturates all protein 1H NMR signals [5].

Conclusion

Reconstituting functional transmembrane (TM) proteins into model membranes is challenging due to the difficulty of expressing hydrophobic TM domains, which often require stabilizing detergents that can perturb protein structure and function. Recent model systems solve this problem by linking the soluble domains of membrane proteins to lipids, using noncovalent conjugation.

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***Correspondence to:** Robinson Zhou, Department of Chemistry, Physical and Theoretical Chemistry Laboratory, University of Oxford, Oxford OX1, UK, E-mail: Zhou.robinson@chem.ox.ac.uk

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