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**Biological molecules are the elementary building blocks comprising organelles, cells, and life forms. We seek to understand how these building blocks assemble into higher-order, mesoscale patterns from which cellular structure and function emerge. To this aim we exploit the inherent 2-dimensionality of membranes to analyze protein interactions using various biophysical methods including electron and fluorescence microscopy.**

For several decades the MacKinnon lab focused on the structures and mechanisms of membrane proteins called ion channels. These proteins underlie the electrical system of life by converting chemical and mechanical stimuli into electrical signals and propagating those signals in the form of electrical impulses. The lab determined the first structures of a selective ion channel, the  $K^+$  channel, to understand how it discriminates between  $K^+$  and other ions, especially the closely related alkali metal ion  $Na^+$ . Following this work on ion conduction and selectivity, the MacKinnon lab sought to understand how ion channels gate their pores so that their activity can be regulated by specific stimuli. They determined the first structures of voltage-dependent ion channels, which underlie the propagation of action potentials, showing how the movement of charged amino acids within the membrane electric field is coupled to opening the pore. They also showed how the binding of ligands, including  $Ca^{2+}$ , PIP2, and G proteins, regulate gating through allosteric conformational changes. Most recently, through atomic structures of Piezo ion channels and quantitative analysis of membrane vesicle shapes, they put forth the membrane dome model to explain how these channels sense mechanical force.

Until recently, work in the MacKinnon lab was best described as trying to understand how individual proteins function as 'molecular machines' to accomplish their required tasks. Presently, work in the MacKinnon lab is directed at understanding how different molecules interact with each other to fulfill their biological functions. Such interactions are important for the regulatory control exhibited when G protein coupled receptors (GPCRs) are stimulated, for example. Indeed, all of cell biology depends on the interactions between proteins, mostly non-covalent, to build up every macroscopic component of a cell. To understand how biomolecules assemble to form 'mesoscale' structures we remain focused on the cell membrane to exploit its approximate 2-dimensionality, which makes it easier to quantify interactions. The methods we use include electron microscopy and fluorescence microscopy for imaging, and mass spectrometry, NMR and other biophysical methods for compositional analysis.

Exemplar current projects include: 1) When you have a signal pathway traditionally described as protein1  $\rightarrow$  protein2  $\rightarrow$  protein3, with arrows to be read as 'communicate with', what do the arrows physically mean? We have recently discovered that weak, yet specific protein-protein interactions produce clusters that we call higher-order transient structures (HOTS). These bring the 'right' proteins in transient proximity, thus connecting the proteins on average, i.e., statistically. We call this new concept dynamic connectivity and examine its applicability to numerous GPCR pathways. 2) We have found that cell membranes spontaneously segregate into protein rich islands with intervening protein poor regions, which we can isolate and examine compositionally. These appear to support unique cellular functions. We seek to understand how and why cell membranes organize this way. 3) Cellular structures emerge through the spontaneous self-assembly of proteins, lipids and other molecules. We posit the existence of non-covalent chemical rules that permit this to occur and seek to discover these rules. 4) Using cryo-EM tomography we are determining the structure of the node of Ranvier, which is the specialized structure in myelinated nerve fibers that permits rapid nerve conduction.

## EDUCATION

B.A. in biochemistry, 1978  
Brandeis University

M.D., 1982  
Tufts University School of Medicine

## MEDICAL TRAINING

Residency in internal medicine, 1982–1985  
Beth Israel Hospital, Harvard Medical School

## POSTDOC

Harvard University, 1985–1986  
Brandeis University, 1986–1989

## POSITIONS

Assistant Professor, 1989–1992  
Associate Professor, 1992–1995  
Professor, 1995–1996  
Harvard Medical School  
Professor, 1996–  
The Rockefeller University  
Investigator, 1997–  
Howard Hughes Medical Institute  
Senior Advisor, Kavli Neural Systems Institute, 2016–

## AWARDS

Albert Lasker Basic Medical Research Award, 1999  
Lewis S. Rosenstiel Award, 2000  
Canada Gairdner International Award, 2001  
Peri-UNC Neuroscience Prize, 2001  
Nobel Prize in Chemistry, 2003  
Louisa Gross Horwitz Prize, 2003

## HONORARY SOCIETIES

National Academy of Sciences  
American Philosophical Society

## SELECTED PUBLICATIONS

Mandala, V. et al. Spatial deconstruction of the plasma membrane. *bioRxiv* DOI: 10.1101/2025.11.14.688519 (2025).  
Mandala, V. et al. Molecular contacts in self-assembling clusters of membrane proteins. *Proc. Natl. Acad. Sci. U.S.A.* 122, e2507112122 (2025).  
Mandala, V. and MacKinnon, R. Electric field-induced pore constriction in the human Kv2.1 channel. *Proc. Natl. Acad. Sci. U.S.A.* 122, e2426744122 (2025).  
Zhang, Y. et al. Higher-order transient membrane protein structures. *Proc. Natl. Acad. Sci. U.S.A.* 122, e2421275121 (2025).  
Zhang, Y. and MacKinnon, R. Higher-order transient structures and the principle of dynamic connectivity in membrane signaling. *Proc. Natl. Acad. Sci. U.S.A.* 122, e2421280121 (2025).