BIOGRAPHICAL SKETCH

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NAME: Maria Falzone

eRA COMMONS USER NAME (credential, e.g., agency login): mfalzone15

POSITION TITLE: Postdoctoral Fellow

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Start Date MM/YYYY	Completion Date MM/YYYY	FIELD OF STUDY
Drew University	B.A.	08/2010	05/2014	Biochemistry and Molecular Biology
Weill Cornell Graduate School	Ph.D.	08/2014	10/2019	Biomedical Sciences
Rockefeller University	n/a (Postdoc)	12/2019	Present	Molecular Neurobiology and Biophysics

A. Personal Statement

My overall research interest is the lipid regulation of membrane proteins and the physiological roles and manifestation of this regulation. My long-term career goal is to establish an independent research group pursuing these studies and my scientific training has been geared towards this goal. One focus of my dissertation research was the regulation of TMEM16 scramblases by bulk properties the membrane including thickness and rigidity. The proposed project for my postdoctoral studies includes the regulation of ion channels by PIP2, which acts as an allosteric modulator. This project also encompasses the physiological context of this regulation by studying the G protein-dependent activation of one family of enzymes that controls PIP2 concentration in membrane, PLCβ's. By studying these G protein-coupled receptor (GPCR) pathways from signal initiation to channel function, I will gain an understanding of both the specific lipid regulation of ion channels and its associated physiological context. A proposal for this project was awarded a three-year Kirschstein-NRSA postdoctoral fellowship (F32) from the NIH.

The present application for electron microscope access through the National Center for CryoEM Access and Training (NCCAT) will contribute to the completion of my proposed postdoctoral project, specifically the structure determination of PLCβ-G protein complexes. Skills I acquired during my dissertation training will be essential to these experiments including, membrane protein purification from bacteria, yeast, and mammalian cells, reconstitution of purified proteins into membrane environments including liposomes and nanodiscs, functional evaluation of reconstituted proteins, including fluorescence-based measurements and flux assays, and cryoEM of membrane proteins. Further, the proposed experiments are well-suited to the technical and conceptual expertise of my sponsor, Dr. Roderick MacKinnon, and his group. They have extensive experience studying ion channels and their regulation, including by GPCR signaling.

1. **Falzone, M.**, Rheinberger, J., Lee, B. C., Peyear, T., Sasset, L., Raczkowski, A., Eng, E., Di Lorenzo, A., Anderson, O. S., Nimigean, C., Accardi, A. Structural basis of Ca^{2+}-dependent activation and lipid transport by a TMEM16 scramblase. *Elife*. 2019,8:e43229, doi: 10.7554/eLife.43229, PMID: 30648972. PMCID: PMC6355197.
2. Khelashvili, G*., **Falzone, M***., Cheng, X., Lee, B. C., Accardi, A., Weinstein, H. Dynamic modulation of the lipid translocation groove generates a conductive ion channel in Ca2+-bound nhTMEM16. *Nature*

Communications. 2019,10(1):4972. doi: 10.1038/s41467-019-12865-4, PMID: 31672969. PMCID: PMC6823365

3. **Falzone, M*.,** Feng, Z*., Alvarenga, O., Pan, Y., Lee, B. C., Cheng, X., Fortea, E., Scheuring, S., Accardi, A. TMEM16 scramblases thin the membrane to enable lipid scrambling. ResearchSquare [Preprint]. October 8, 2021 [cited 2022 Apr 1]. Available from: https://doi.org/10.21203/rs.3.rs-955726/v1 (accepted at *Nature Communications)*

*denotes equal authorship

B. Positions and Honors

Positions and Employment

POSITION	START DATE MM/YYY	END DATE MM/YY	INSTITUTION	SUPERVISOR
Undergraduate researcher	05/2011	08/2011	Drew University: Drew Summer Science Institute	Dr Arnold Demain
Undergraduate researcher	05/2012	08/2012	Drew University: Drew Summer Science Institute	Dr Arnold Demain
Undergraduate researcher	06/2013	08/2013	Albert Einstein College of Medicine: Summer Undergraduate Research Program	Dr. Steve Almo
Graduate Student	08/2014	12/2019	Weill Cornell Graduate School	Dr. Alessio Accardi
Postdoctoral Fellow	12/2019	present	Rockefeller University	Dr. Roderick MacKinnon

Professional Memberships

2018-present	Biophysical Society
2018-prsent	Society of General Physiologists

Academic and Professional Honors

2010	Induction into Baldwin Honors Program
2012	Selected for Who's Who in America's Colleges and Universities
2013	Induction into Phi Beta Kappa National Honor Society
2013	George de Stevens Award for research (Drew University)
2014	Induction into Gamma Sigma Epsilon Chemistry Honor Society
2014	American Institute of Chemists' Award (Drew University)
2014	B.A. awarded with specialized honors and *summa cum laude* (Drew University)
2018	Margaret & Herman Sokol Fellowship (Weill Cornell Graduate School)
2018	First Place Poster Prize - COMPPA Symposium on Membrane Protein Production & Analysis
2021	Kirschstein-NRSA postdoctoral fellowship (F32)

C. Contributions to Science

Early Career

For my undergraduate thesis, I worked in the laboratory of Dr. Arnold Demain at Drew University and studied the natural product antibiotics platensimycin and platencin. Antibiotic resistant pathogens are a significant global health problem, emphasizing the need for new antibiotics. Platensimycin and platencin were discovered by Merck & Co in the early 2000's and are produced by the soil actinomycete *Streptomyces platensis*. They were shown to be active against *Mycobacterium tuberculosis* and gram-positive bacteria including antibiotics resistant strains. These compounds inhibit fatty acid synthesis, specifically the FabF and FabH enzymes which are not present in Eukaryotic cells, making them non-toxic to humans. Due to poor pharmacokinetics, these compounds were not further pursued as marketable antibiotics. However, the Demain lab continued to study

the biosynthesis of these compounds by *S. platensis.* During my time in the lab, I contributed to the development of a semi-defined and fully-defined culture medium for *S. plateneis* that supports production of these compounds (A, B). In addition, I contributed to showing that addition of aspartic acid to the chemically defined medium increases antibiotic production, consistent with its role in the biosynthetic pathway (C).

1. Aluotto S., Tynan H., Maggio C., **Falzone M**., Mukherjee A, Gullo V., Demain AL. Development of a semi-defined medium supporting production of platensimycin and platencin by *Streptomyces platensis*. *Journal of Antibiotics*. 2012,66(2):51-54, doi: 10.1038/ja.2012.97, PMID: 23188381.
2. **Falzone M**., Martens E., Tynan H., Maggio C., Golden S., Nayda V., Crespo E., Inamine G., Gelber M., Lemence R., Chiappini N., Friedman E., Shen B., Gullo V., Demain AL. Development of a chemically defined medium for the production of the antibiotic platensimycin by *Streptomyces platensis*. *Appl Microbiol Biotechnol*. 2013,97(21):9535-9, doi: 10.1007/s00253-013-5201-6, PMID: 24022611.
3. **Falzone, M**., Crespo, E., Jones, K., Khan, G., Korn, V. L., Patel, A., Demain, A. L. Nutritional control of antibiotic production by *Streptomyces platensis* MA7327: Importance of l-aspartic acid. *Journal of Antibiotics*. 2017,70(7):828-831, doi: 10.1038/ja.2017.49, PMID: 28465627. PMCID: PMC5642980.

Graduate Career

I carried out my doctoral dissertation work in the laboratory of Dr. Alessio Accardi studying the TMEM16 phospholipid scramblases. In eukaryotic cells, scramblases flip lipids between the leaflets of the membrane down their concentration gradients. Increases in cytosolic Ca^{2+} activate plasma membrane TMEM16 scramblases, which collapse the lipid asymmetry exposing phosphatidylserine (PS) on the extracellular surface. Externalized PS serves as a signaling initiator for many processes including blood coagulation, and apoptosis, highlighting the importance of scramblases. Using fungal TMEM16 model systems, it was shown that lipids are translocated through a large hydrophilic cavity directly exposed to the membrane. Many TMEM16 scramblases are also non-selective ion channels, in which ions are transported through the same region of the protein as lipids. My contributions are related to understanding the mechanism of scrambling, Ca^{2+}-dependent gating, and modulation by membrane properties.

Using cryo-EM I determined structures of a fungal TMEM16 in a membrane environment in the presence and absence of Ca^{2+}. The structures showed that Ca^{2+}-dependent gating occurs via movements in two helices that are part of the permeation pathway. Through a collaboration with the lab of Dr. Harel Weinstein at Weill Cornell, we showed that a hydrophobic lock between two pathway helices also plays a role in gating, including regulating the equilibrium between a scramblase and channel-only conformation. Through a collaboration with the laboratory of Dr. Elisabeth Carpenter at Oxford, I characterized the function of hTMEM16K *in vitro,* which is localized in the endoplasmic reticulum, making its characterization in cells challenging. I showed that hTMEM16K is a scramblase and non-selective channel with properties very similar to the fungal model systems. Accompanying structures revealed that the Ca^{2+}-dependent gating mechanism is conserved in some mammalian scramblases.

In addition, my structures of the fungal scramblase in a membrane environment revealed that TMEM16 scramblases disrupt the organization of the surrounding membrane, inducing a pronounced bending. Additional, higher resolution structures revealed specific protein-lipid interactions providing molecular details to the observed membrane bending. Accompanying *in vitro* functional experiments showed that scrambling is inhibited by thicker membranes and by ceramide lipids which rigidify the membrane, consistent with the observed altered membrane organization. The mechanism of this modulation was further investigated to reveal that is it not dependent on conformational changes of the protein but rather changes in lipid permeation. Additional functional experiments suggest that lipids do not need to enter the scrambling cavity to be transported, challenging the paradigm of the credit card mechanism in the field. We proposed that scrambling requires local membrane thinning imposed by the scramblase and in environments that reduce thinning, like thicker or more rigid bilayers, scrambling is reduced.

1. **Falzone, M.**, Rheinberger, J., Lee, B. C., Peyear, T., Sasset, L., Raczkowski, A., Eng, E., Di Lorenzo, A., Anderson, O. S., Nimigean, C., Accardi, A. Structural basis of Ca2+-dependent activation and lipid transport by a TMEM16 scramblase. *Elife*. 2019,8:e43229, doi: 10.7554/eLife.43229, PMID: 30648972. PMCID: PMC6355197.

2. Khelashvili, G*., **Falzone, M***., Cheng, X., Lee, B. C., Accardi, A., Weinstein, H. Dynamic modulation
of the lipid translocation groove generates a conductive ion channel in Ca2+-bound nhTMEM16. *Nature Communications*. 2019,10(1):4972. doi: 10.1038/s41467-019-12865-4, PMID: 31672969. PMCID: PMC6823365.
3. Bushell, S. R*., Pike, A. C. W*., **Falzone, M*.,** Rorsman, N. J. G., Ta, C. M., Corey, R. A., Newport, T. D., Shintre, C. A., Tessitore, A., Chu, A., Wang, Q., Shrestha, L., Mukhopadhyay, S. M. M., Love, J., Burgess-Brown, N. A., Sitsapesan, R., Sttansfeld, P. J., Huiskonen, J. T., Tammaro, P., Accardi, A., Carpenter, E. P. The structural basis of lipid scrambling and inactivation in the endoplasmic reticulum scramblase TMEM16K. *Nature Communications*. 2019,10(1):3956. doi: 10.1038/s41467-019-11753-1, PMID: 31477691. PMCID: PMC6718402.
4. **Falzone, M*.,** Feng, Z*., Alvarenga, O., Pan, Y., Lee, B. C., Cheng, X., Fortea, E., Scheuring, S., Accardi, A. TMEM16 scramblases thin the membrane to enable lipid scrambling. ResearchSquare [Preprint]. October 8, 2021 [cited 2022 Apr 1]. Available from: https://doi.org/10.21203/rs.3.rs-955726/v1 (accepted at *Nature Communications)*

*denotes equal authorship

Complete list of Published work:
https://pubmed.ncbi.nlm.nih.gov/?term=Falzone%20Maria&sort=date&pos=9

D. Scholastic Performance

Weill Cornell Graduate School

YEAR	COURSE TITLE	GRADE
2014	Molecular Genetics	HP
2014	Biochemistry and Structural Biology Core	HP
2015	Cell Biology and Development	H
2015	Gene Structure and Function	H
2015	Logic and Critical Analysis	HP
2015	Quantitative Understanding in Biology	H
2017	Molecular Mechanisms of membrane transport	H

Grading Scheme: H=Honors, HP=High Pass, LP=Low Pass, P=Pass, F=Fail

BIOGRAPHICAL SKETCH

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NAME: MacKinnon, Roderick

eRA COMMONS USER NAME (credential, e.g., agency login): MACKINNONR

POSITION TITLE: Professor of Molecular Neurobiology and Biophysics

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Brandeis University, Waltham, MA	B.A.	06/1978	Biochemistry
Tufts University School of Medicine, Boston, MA	M.D.	06/1982	Medicine
Beth Israel Hospital, Harvard Univ., Boston, MA	Postdoctoral Fellowship (NIH)	09/1985-09/1986	Medicine
Brandeis University, Waltham, MA	Postdoctoral Fellowship (NIH)	09/1986-09/1989	Biochemistry

A. Personal Statement

I am a professor at Rockefeller University in the Laboratory of Molecular Neurobiology and Biophysics and an investigator with the Howard Hughes Medical Institute.

B. Positions and Honors

Positions and Employment

1982-85 Medical House Officer, Internal Medicine, Beth Israel Hospital/Harvard Medical School, Boston, MA
1985-86 NIH Postdoctoral Fellow, Dept. of Medicine, Beth Israel Hospital, Harvard University, Boston, MA
1986-89 NIH Postdoctoral, Dept. of Biochemistry, Brandeis University, Waltham, MA
1989-91 Assistant Professor, Dept. of Cellular and Molecular Physiology, Harvard Med. School, Boston, MA
1991-92 Assistant Professor, Department of Neurobiology, Harvard Medical School, Boston, MA
1992-95 Associate Professor, Department of Neurobiology, Harvard Medical School, Boston, MA
1995-96 Professor, Department of Neurobiology, Harvard Medical School, Boston, MA
1996- Professor, Laboratory of Mol. Neurobiology and Biophysics, Rockefeller University, New York, NY
1997- Investigator, Howard Hughes Medical Institute

Other Experience and Professional Memberships

2000 Member, The U.S. National Academy of Sciences
2005 Member, The American Philosophical Society
2007 Foreign Member, The Royal Netherlands Academy of Arts and Sciences

Honors

1978 High Honors in Biochemistry, Brandeis University
1982 Alpha Omega Alpha Medical Honors Society, Tufts University School of Medicine
1992 PEW Scholar in the Biomedical Sciences

1992 McKnight Scholars Award
1995 Biophysical Society Young Investigator Award
1997 McKnight Investigator Award
1998 W. Alden Spencer Award, Columbia University
1998 AAAS Newcomb Cleveland Prize
1999 Albert Lasker Basic Medical Research Award
2000 Lewis S. Rosenstiel Award for Distinguished Work in Basic Medical Research
2000 Hodgkin-Huxley-Katz Prize
2000 Alexander M. Cruickshank Award
2000 Membership to the U.S. National Academy of Sciences
2001 Gairdner Foundation International Award
2001 George Harvey Miller Distinguished Lecturer Award, University of Illinois, Chicago
2002 Perl-UNC Neuroscience Prize
2002 The Degree of Doctor of Science, Honoris Causa – Tufts University
2003 Fritz Lipmann Memorial Lectureship Award
2003 Nobel Prize in Chemistry
2003 Louisa Gross Horwitz Prize
2003 Scientific American Research Leader of the Year
2004 Max Tishler Prize – Harvard University
2004 National Lecturer, Biophysical Society Annual Meeting
2004 Bijvoet Medal for Outstanding Research – The Netherlands
2005 The Hans Neurath Award-Protein Society
2005 The Degree of Doctor of Science, Honoris Causa – Brandeis University
2005 Membership to the American Philosophical Society
2006 Rolf Sammet Honorary Lectureship –J.W. Goethe University, Frankfurt, Germany
2006 The Degree of Doctor of Science, Honoris Causa – Pohang Univ. of Science & Technology, Korea
2007 Wolfgang Pauli Lectureship - ETH, Zurich, Switzerland
2007 Foreign Membership to the Royal Netherlands Academy of Arts and Sciences
2007 The Degree of Doctor of Science, Honoris Causa – Rene Descartes University, France
2008 Pauling Legacy Award
2013 Max Tishler Lecturer Award, Tufts University
2015 Kenneth S. Cole Award, Biophysical Society

C. Contributions to Science

1. I began my scientific career as an electrophysiologist. The first main question I focused on was how do K+ channels select for K+ over Na+? Two things intrigued me about K+ selectivity. First, K+ is larger than Na+. How can the larger ion conduct and the smaller ion not? Second, high selectivity, it seemed to me, would ordinarily be associated with high affinity and yet K+ diffuses through the channel at near diffusion-limited rates (i.e. as fast as physically possible). Thus, the K+ channel was a paradox in my mind. Using electrophysiological methods I could observe this remarkable behavior and using mutagenesis I could even identify particular amino acids that were responsible for it. But it soon became clear to me that in order to answer the question I would have to see what the channel looked like. But no one had ever determined the atomic structure of a selective ion channel, and moreover I was not trained in that sort of work. I decided to do it anyway, learned x-ray crystallography, and solved the structure of a K+ channel. The structure was very revealing because it contained a selectivity filter with structural and chemical properties that explained selectivity for K+ over Na+ and simultaneous high conduction rates. This was a good advance for our understanding of electrical impulse formation because since the famous work of Hodgkin and Huxley in 1952 scientists had wondered what does an ion channel really look like.

    a) Doyle, D.A., Cabral, J.M., Pfuetzner, R.A., Kuo, A., Gulbis, J.M., Cohen, S.L., Chait, B.T., MacKinnon, R. (1998). The structure of the potassium channel: molecular basis of K+ conduction and selectivity. *Science,* 280(5360), 69-77. PubMed PMID: 9525859.
    b) Zhou, M., Morais-Cabral, J., Mann, S., MacKinnon, R. (2001). Potassium channel receptor site for the inactivation gate and quaternary amine inhibitors. *Nature*, 411(6838), 657-661. PubMed PMID: 11395760.

2. If the first major question driving my scientific studies is how do ion channels conduct ions selectively, the second is how do ion channels turn conduction off and on in a process known as gating? My laboratory determined the first voltage-gated ion channel structure and the first ligand-gated K+ channel structure. Our studies of voltage-dependent gating led us to determine the first eukaryotic membrane protein structure from recombinant expression.

    a) Jiang, Y., Lee, A., Chen, J., Ruta, V., Cadene, M., Chait, B.T., MacKinnon, R. (2003). X-ray structure of a voltage-dependent K+ channel. *Nature*, *423*(6935), 33-41. PubMed PMID: 12721618.
    b) Jiang, Y., Lee, A., Chen, J., Cadene, M., Chait, B.T., MacKinnon, R. (2002). Crystal structure and mechanism of a calcium-gated potassium channel. *Nature*, *417*(6888), 515-522. PubMed PMID: 12037559.
    c) Long, S.B., Campbell, E.B., MacKinnon, R. (2005). Voltage sensor of Kv1.2: structural basis of electromechanical coupling. *Science, 309*(5736), 903-908. PubMed PMID: 16002579.
    d) Long, S.B., Tao X., Campbell, E.B., MacKinnon, R. (2007). Atomic structure of a voltage-dependent K+ channel in a lipid membrane-like environment. *Nature*, *450*(7168), 376-382. PubMed PMID: 18004376.

3. The K+ channel family is extraordinarily diverse. In humans there are more than 70 K+ channels. While these share the highly-conserved selectivity filter observed in the first K+ channel structure KcsA, they are architecturally distinct. As function follows form, these distinct K+ channels have evolved under the control of different stimuli: membrane voltage, intracellular Ca2+, G proteins and mechanical forces. To better understand this marvelous family of proteins we have determined structures and studied the behaviors of far-ranging members of the K+ channel family tree.

    a) Brohawn, S.G., Campbell, E.B., MacKinnon, R. (2014). Physical mechanism for gating and mechanosensitivity of the human TRAAK K+ channel. *Nature*, 516 (7529), 126-30. PubMed Central PMCID: 468236. HHMIMSID: HHMIMS639323.
    b) Tao, X., Hite, R., MacKinnon, R. (2017). Cryo-EM structure of the open high-conductance Ca^{2+}-activated K^+ channel**.** *Nature*, *541*(7635*)*, 46-51. PubMed Central PMCID: 5500982.
    c) Sun, Ji, MacKinnon, R. (2017). Cryo-EM structure of a KCNQ1/CaM complex reveals insights into congenital long QT syndrome. *Cell*, *169*(6), 1042-1050. PubMed Central PMCID: 5562354.
    d) Lee, Chia-Hsueh, MacKinnon, R. (2018). Activation mechanism of a human SK/calmodulin channel complex elucidated by cryo-EM structures. *Science* 360, 508-513. PubMed Central PMCID: 6241251.

4. G protein coupled receptor signaling controls heart rate and neuronal activity through the activity of K+ channels known as G protein gated inward rectifier K+ (GIRK) channels. We have discovered how the G proteins regulate GIRK activity through atomic structural and functional studies.

    a) Whorton, M.R., MacKinnon, R. (2011). Crystal structure of the mammalian GIRK2 K+ channel and gating regulation by G proteins, PIP(2), and sodium. *Cell*, 147(1), 199-208. PubMed Central PMCID: 3243363.
    b) Whorton, M.R., MacKinnon, R. (2013). X-ray structure of the mammalian GIRK2-βγ G-protein complex. *Nature*, published online June 5. PubMed Central PMCID: 4654628.
    c) Wang, W., Touhara, K.K., Weir, K., Bean, B.P., MacKinnon, R. (2016). Cooperative regulation by G proteins and Na+ of neuronal GIRK2 K+ channels. *eLife*, April 2016:*5*:e15751. PubMed Central PMCID: 4866826.
    d) Touhara, K, MacKinnon, R. (2018) Molecular basis of signaling specificity between GIRK channels and GPCRs. *eLife,* Dec. 2018:7:e42908. PubMed Central PMCID: 6335053.

5. Mechanosensitive ion channels allow living organisms to sense mechanical forces. These underlie touch sensation and other cellular processes. We have proposed the membrane dome model of mechanosensitive gating in Piezo1, a mechanosensitive ion channel.

    a) Guo, Y.R., MacKinnon, R. (2017). Structure-based membrane dome mechanism for Piezo mechanosensitivity. *eLife*, Dec. 2017, el.33660. PubMed Central PMCID: 5788504.

b) Haselwandter, Christoph, MacKinnon, R. (2018). Piezo's membrane footprint and its contribution to mechanosensitivity. *eLife*, Nov. 2018:7:e41968. PubMed Central PMCID: 6317911.
c) Del Marmol, J., Touhara, K.K., Croft, G., MacKinnon, R. (2018). Piezo1 forms a slowly-inactivating mechanosensory channel in mouse embryonic stem cells. ***eLife,*** Aug. 2018; 7:e33149. PubMed Central PMCID: 6128688.
d) Lin, Y.C., Guo, Y.R., Mayagi, A., Levering, J., MacKinnon, R., Scheuring, S. (2019). Force-induced conformational changes in Piezo1. ***Nature***, *573*, 230-244. PMID: 31435018. PMCID: in process.

Complete list of published work available publicly:

https://www.ncbi.nlm.nih.gov/sites/myncbi/1ZOcxVvzmaekv/bibliography/50241239/public/?sort=date&direction=ascending

or

https://www.ncbi.nlm.nih.gov/myncbi/1ZOcxVvzmaekv/bibliography/public/

or
http://lab.rockefeller.edu/mackinnon/publications

D. Research Support

Ongoing Research Support

R01 GM043949 MacKinnon (PI) 04/01/1990 - 11/30/2024
NIH/NIGMS
"Mechanisms of K+ channel gating"
The major goal of this project is to understand the structural basis of voltage-dependent channel gating.

HHMI MacKinnon (PI) 1997 – Present
(a) "The structural basis of ion selectivity in channels"
The major goal of this project is to understand how channels select K^+ and Cl^- ions and conduct them rapidly across the membrane.
(b) "The structural basis of gating in K^+ channels"
The major goal of this project is to understand how Ca^{2+}, G-protein subunits, and cyclic nucleotides open channels. Funding also contributes to the voltage-dependent channel studies by providing equipment and antibodies for protein crystallization.
(c) "Development of new methods for the expression and crystallization of membrane proteins"
The major goal of this project is to understand the structural basis and function of CLC chloride channels.

Completed Research Support

Robertson Therapeutic Development Fund MacKinnon (PI) 9/1/2015 – 12/31/2017
Project description: hERG channel – cell-free high throughput screening method development.