
BIOGRAPHICAL SKETCH

NAME: Daniel Louis Minor, Jr., Ph.D.

POSITION TITLE:

Professor, Departments of Biochemistry and Biophysics, & Cellular and Molecular Pharmacology
Investigator, Cardiovascular Research Institute, University of California San Francisco
Faculty Scientist, Molecular Biophysics & Integrated Imaging Division, Lawrence Berkeley National Laboratory, Berkeley

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
University of Pennsylvania, Philadelphia, PA	B.A. magna cum laude	05/1989	Biochemistry (Honors)
Massachusetts Institute of Technology, Cambridge, MA	Ph.D.	02/1996	Biophysics (Honors) Chemistry
MRC Laboratory of Molecular Biology, Cambridge, UK	postdoc	09/1996	Ion channel structure
University of California, San Francisco, CA	postdoc	12/2000	Ion channel structure and function

A. Personal Statement

I have a broad background in ion channel structural biology and functional characterization, with specific expertise and prior accomplishments directly relevant to this application. My interest in the physical chemistry of biological phenomena began with my undergraduate study in biophysics and biochemistry at the University of Pennsylvania. As a graduate student in the Department of Chemistry at MIT with Prof. Peter S. Kim, I focused on understanding the basic principles of protein folding and molecular interactions. While at MIT, I developed a keen interest in the proteins involved in electrical signaling. To pursue this interest, I was a postdoctoral fellow with Dr. Nigel Unwin at the LMB Cambridge and with Prof. Lily Y. Jan at UCSF where I applied my structural biology background to questions regarding ion channel structure and regulation. As a PI, I have focused my laboratory's efforts on structural and mechanistic understanding of ion channels. My lab is pursuing a research program that combines structural biology, functional studies of ion channels, and development of novel means to control channel function, and studies of toxin resistance. Our central goals are to obtain a structural understanding of ion channel action and regulation and to leverage this knowledge to gain control of channel function. We have had a long-standing effort on $\text{Ca}_{\text{v}}\text{s}$ and K_{2ps} that has made seminal contributions to our understanding of how they function and in the development of new channel modulators. I am a Professor of Biochemistry and Biophysics and Cellular and Molecular Pharmacology, an Investigator in the Cardiovascular Research Institute at UCSF, and a Faculty Scientist at LBNL.

My laboratory has made many contributions to structural understanding of the function of various classes of ion channels, ion channel:small molecule interactions, and the first ion channel:chaperone complex exemplified by:

1. Arrigoni, C., Rohaim, A., Shaya, D., Findeisen, F., Stein, R.A., Reddy Nurva, S., Mishra, S., Mchaourab, H.S., **Minor, D. L., Jr.** 'Unfolding of a temperature-sensitive domain controls voltage-gated channel activation' *Cell* **164** 922-936 (2016) PMID: 26919429 PMCID: PMC4769381
2. Lolicato, M., Arrigoni, C., Mori, T., Sekioka, Y., Bryant, C., Clark, K.A., **Minor, D.L., Jr.** ' $\text{K}_{\text{2p}2.1}(\text{TREK-1})$:activator complexes reveal a cryptic selectivity filter binding site' *Nature* **547** 364-368 (2017) PMID: 28693035 PMCID: PMC5778891
3. Chen, Z., Mondal, A., Abderemane-Ali, F., Jang, S., Niranjan, S., Montaño, J.L., Zaro, B.W. and **Minor, D.L., Jr.**, 'EMC chaperone- Ca_{v} structure reveals an ion channel assembly intermediate' *Nature* **619** 410-419 (2023) PMID: 37196677 PMCID: In Progress
4. Chen, Z., Mondal, A., and **Minor, D.L., Jr.**, 'Structural basis for $\text{Ca}_{\text{v}}\alpha_2\delta$:gabapentin binding' *Nature Struct. & Mol. Biol.* **30** 735-739 (2023) PMID: 36973510 PMCID: In Progress

B. Positions and Honors:

Positions and Employment

1990-1996	Graduate Student, Department of Chemistry, Massachusetts Institute of Technology Advisor: Peter S. Kim, Ph.D.
1996	Postdoctoral Fellow, MRC-Laboratory of Molecular Biology Cambridge, England Advisor: Nigel Unwin, Ph.D.

1996-2000 Postdoctoral Fellow, Howard Hughes Medical Institute, Department of Physiology, University of California, San Francisco, Advisor: Lily Y. Jan, Ph.D.
 2000-2007 Assistant Professor, Department of Biochemistry and Biophysics, UCSF
 2002-2007 Assistant Professor, Department of Cellular and Molecular Pharmacology, UCSF
 2000-present Investigator, Cardiovascular Research Institute, UCSF
 2007-2011 Associate Professor (w/ tenure), Departments of Biochemistry and Biophysics & Cellular and Molecular Pharmacology, UCSF
 2009-present Biochemist, Faculty Scientist, Physical Biosciences Division, Lawrence Berkeley National Laboratory (as of 2016, renamed as Molecular Biophysics & Integrated Imaging Division)
 2011-present Professor (w/ tenure), Cardiovascular Research Institute, Departments of Biochemistry and Biophysics & Cellular and Molecular Pharmacology, UCSF

Other experience and Professional Memberships

2000-present Member, Graduate Programs in Biological Sciences: Biochemistry, Biophysics, Chemistry and Chemical Biology, Neuroscience, Program in Molecular Medicine, UCSF
 2000-2006 Member, Graduate program in Biomedical Science
 2001-present Protein Society, Member
 2001- present Biophysical Society, Member
 2001- present Society for Neuroscience, Member
 2007 NIH BST-Q Study Section (*ad hoc* member)
 2007 NIH NTRC Study Section (*ad hoc* member)
 2008 NIH BPNS Study Section (*ad hoc* member)
 2008- present Member, Graduate program in Biomedical Science
 2008 -present Society of General Physiologists, Member
 2009 NIH NIDA CEBRA Study Section (*ad hoc* member)
 2011-present NIH BPNS Study Section (permanent member)
 2012-2015 Biophysical Society Council Member
 2013-2014 US-Israel Binational Science Foundation – Scientific Advisory Board Member
 2015-2016 Beckman Young Investigator, Beckman Foundation - Selection Committee Member
 2016 NIH ZEY1 VSN Study Section (*ad hoc* member)
 2016 NSF CAREER Review Study Section, MCB Division, Molecular Biophysics Cluster
 2017 NIH: Special Emphasis Panel 'Biophysics' ZRG1 MDCN-R(04) (*ad hoc* member)
 2017 NSF Biomolecular Dynamics and Function II Study Section, MCB Division, Molecular Biophysics Cluster

 2016-present *Neuron* Editorial Board
 2017-present *Journal of Molecular Biology* Editorial Board
 2020- present *The EMBO Journal* Editorial Board

Honors:

1985 ILGWU Scholarship
 1986, 1987, 1988 Dean's list, University of Pennsylvania,
 1988-89 Penn Student Agencies Scholarship, University of Pennsylvania
 1989 Helix Prize in Biochemistry, University of Pennsylvania
 1989 Phi Beta Kappa
 1996 Burroughs Wellcome Hitchings-Elion Fellowship
 2001-2004 McKnight Scholar in Neuroscience
 2001-2005 Rita Allen Scholar
 2002-2004 Alfred P. Sloan Research Fellow
 2002-2005 Beckman Young Investigator
 2002-2004 March of Dimes, Basil O'Connor Scholar
 2002-2005 Searle Scholar
 2004-2006 McKnight Technological Innovations in Neuroscience Award
 2007-2011 Established Investigator, American Heart Association
 2010-2012 Fellow of the American Asthma Foundation
 2011 Weizmann Institute of Science, Feinberg Visiting Faculty Fellowship
 2023 Fellow of the Biophysical Society, Biophysical Society
 2023 Visiting Professor, Dipartimento di Scienze Chimiche, Università degli Studi di Napoli Federico II, ITALY

C. Contributions to science:

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1) Protein folding: I established the experimental scale for β -sheet formation (*Minor and Kim, 1994a*) and uncovered that this property is context dependent (*Minor and Kim, 1994b*). Previously, there were no experimental measures of β -sheet formation. The observation of the effect of context led us to design an 11-residue sequence, the ‘chameleon’ sequence whose folding was entirely context dependent (*Minor and Kim, 1996*). *This work established that context could drive the formation of entire secondary structures, a demonstration that had implications for understanding structural transitions in amyloid and other fibril-forming proteins.*

- a) Minor, D. L., Jr. and Kim P. S. ‘Measurement of the β -sheet forming propensities of amino acids’ *Nature* **367** 660-663 (1994) PMID: 810785
- b) Minor, D.L., Jr. and Kim P.S. ‘Context is a major determinant of β -sheet propensity’ *Nature* **371** 264-267 (1994) PMID: 8078589
- c) Minor, D.L., Jr. and Kim P.S. ‘Context-dependent secondary structure formation of a designed protein sequence’ *Nature* **380** 730-734 (1996) PMID: 8614471

2) Voltage-gated calcium channels (Cav_S): Voltage-gated calcium channels (Cav_S) are central components of excitable tissues in the brain and heart. *When my laboratory started working on this channel family there were no high-resolution data for Cav_S.* My laboratory determined the first high-resolution structure of part of a Cav_S, the β -subunit, alone and in complex with its interaction site from the channel (Van Petegem *et al.*, *Nature*, 2004) and a suite of calcium-calmodulin complexes of Cav1 (Van Petegem *et al.*, *NSMB* 2005; Kim *et al.*, *EMBO J.* 2010) and Cav2 IQ domains (Kim *et al.*, *EMBO J.* 2008) that established a structural foundation for investigating Cav_S feedback modulation by calcium-calmodulin. We showed that the Cav_S selectivity filter (SF) is the endpoint of calcium-dependent inactivation (CDI) (Abderemane-Ali *et al.*, *Neuron*, 2019) bringing Cav_S inactivation into a larger set of mechanisms shared by the VGIC superfamily. *Recently, we determined the structure of the first known ionchannel:chaperone interaction (Chen *et al.* *Nature*, 2023), the first structure of human Cav1.2 (Chen *et al.* *Nature* 2023), and defined the structural basis for Cav_S interaction with gabapentinoid class of anti-nociceptive and anti-epileptic drugs (Chen *et al.* *NSMB*, 2023).*

- a) Van Petegem, F., Clark, K.A., Chatelain, F.C., and Minor, D.L., Jr., ‘Structure of a complex between a voltage-gated calcium channel β -subunit and an α -subunit domain’ *Nature* **429** 671-675 (2004) PMID:15141227 PMC3076333 (Research Highlight *Nature Rev. Neuroscience* 5:517, 2004; rated ‘Exceptional’ Faculty of 1000)
- b) Abderemane-Ali, F., Findeisen, F., Rossen, N.D., and Minor, D.L. Jr., ‘A selectivity filter gate controls voltage-gated calcium channel (Cav_S) calcium-dependent inactivation’ *Neuron* **101** 1134-1149 (2019) PMID: 30733149 PMCID: PMC8878153
- c) Chen, Z., Mondal, A., Abderemane-Ali, F., Jang, S., Niranjan, S., Montaño, J.L., Zaro, B.W. and Minor, D.L., Jr., ‘EMC chaperone-Cav structure reveals an ion channel assembly intermediate’ *Nature* **619** 410-419 (2023) PMID: 37196677 PMCID: In Progress
- d) Chen, Z., Mondal, A., and Minor, D.L., Jr., ‘Structural basis for Cav_S α δ :gabapentin binding’ *Nature Struct. & Mol. Biol.* **30** 735-739 (2023). PMID: 36973510 PMCID: In Progress

3) Bacterial voltage gated sodium channels (BacNavs): BacNavs are model systems for understanding fundamental principles of voltage gated channel (VGIC) function. Using protein dissection, we demonstrated that the pore domain is modular and can be excised to produce functional sodium or calcium selective channels (Shaya *et al.* *PNAS*, 2011). We determined the structure of a bacterial ‘pore-only’ sodium channel. *This work the structure of a crucial BacNay part, the cytoplasmic tail that had evaded other structural studies* and with functional tests resolved controversy over the location of the intracellular gate that controls channel opening and established a role for the cytoplasmic domain in controlling channel opening. Structure determination of a ‘pore-only’ bacterial sodium channel also identified an ion binding site having common to human voltage-gated calcium channel pores. *This work allowed us to discover a previously unknown determinant of ion selectivity in human Cav_S (Shaya *et al.* *JMB*, 2014).* We showed that the intracellular ‘neck’ domain controls channel function, demonstrating that this domain undergoes a thermal-sensitive unfolding reaction coupled to gating. *This work is the first demonstration that a discrete domain can encode the thermal response of an ion channel (Arrigoni *et al.*, *Cell*, 2016).* Our most recent work on BacNavs demonstrated the unexpected ability of pore domains (PDs) to form non-canonical quaternary structures and established that the PD is an autonomously folded domain. This principle manifests in the EMC:Cav complex.

- a) Shaya, D., Kreir, M., Robbins, R.A., Wong, S., Hammon, J., Brüggemann, A., and Minor, D.L., Jr., ‘Voltage-gated sodium channel (Na_V) protein dissection creates a set of functional ‘pore-only’ proteins’ *Proc Natl Acad Sci USA* **108** 12313-12318 (2011) PMID: 21746903: PMCID: PMC3145705
- b) Shaya, D., Findeisen, F., Abderemane-Ali, F., Arrigoni, C., Wong, S., Reddy Nurva, S., Loussouarn, G., and Minor, D.L., Jr., ‘Structure of a prokaryotic sodium channel pore reveals essential gating elements and an

outer ion binding site common to eukaryotic channels' Journal of Molecular Biology **426** 476-483 (2014) PMID: 24120938 PMCID: PMC3947372

c) Arrigoni, C., Rohaim, A., Shaya, D., Findeisen, F., Stein, R.A., Reddy Nurva, S., Mishra, S., Mchaourab, H.S., **Minor, D. L., Jr.** 'Unfolding of a temperature-sensitive domain controls voltage-gated channel activation' *Cell* **164** 922-936 (2016) PMID: 26919429 PMCID: PMC4769381

d) Arrigoni, C., Lolicato, M., Shaya, D., Rohaim, A., Findeisen, F., Fong, L.-K., Colleran, C.M., Dominik, P., Kim, S.S., Schuermann, J., DeGrado, W.F., Grabe, M., Kossiakoff, A.A., and **Minor, D.L., Jr.**, 'Quaternary structure independent folding of voltage-gated ion channel pore domain subunits' *Nature Struct. & Mol. Biol.* **29** 537-548 (2022) PMID: 35655098 PMCID: PMC9809158

4) K_{2P} channels K_{2P} channels produce 'leak' currents that control cellular excitability. K_{2P}2.1 (TREK-1) is a classic polymodal channel gated by pH, temperature, and pressure. When we began studying this channel family, it was unclear whether the various inputs controlled the channel by separate or common mechanisms. We showed that the channel selectivity filter is the principal gate in K_{2Ps} and that pH, temperature, and pressure act through a common mechanism to control its function (Bagriantsev *et al.*, *The EMBO J* 2011). We established that signals from the intracellular sensors for temperature and phosphorylation are relayed to the selectivity filter via transmembrane helix M4 (Bagriantsev *et al.*, *The EMBO J* 2012) and that movement of the M4 helix influences channel function (Lolicato *et al.*, *Neuron* 2014). These studies established K_{2P} channels gate at the selectivity filter rather than an intracellular gate and set this channel family apart from other well-studied channels that use an intracellular gate. We defined the structure of K_{2P}2.1 (TREK-1) alone and in complex with two types of activators, uncovered a previously unknown small molecule modulatory site, and showed that small molecules can directly activate the selectivity filter gate (Lolicato *et al.*, *Nature* 2017). We have shown that the K_{2P} selectivity filter gate operates by a combination of pinching and dilation mechanisms that originate from an inherent structural asymmetry found throughout the K_{2P} family (Lolicato *et al.*, *Science Adv.* 2020). Hence, my lab has established the primacy of the selectivity filter gate for K_{2P} function from the functional to the structural level and have exploited this mechanism to develop new K_{2P}-selective pharmacologies.

a) Bagriantsev, S., Clark, K.A., Peyronnet, R., Honoré, E., and **Minor, D.L., Jr.**, 'Multiple modalities act through a common gate to control K_{2P} channel function' *The EMBO Journal* **30** 3594-3606 (2011) PMID: 21765396 PMCID: PMC3181481

b) Bagriantsev, S., Clark, K.A., and **Minor, D.L., Jr.**, 'Metabolic and thermal stimuli control K_{2P}2.1 (TREK-1) through modular sensory and gating domains' *The EMBO Journal* **31** 3297-3308 (2012) PMID: 22728824 PMCID: PMC3411076

c) Lolicato, M., Arrigoni, C., Mori, T., Sekioka, Y., Bryant, C., Clark, K.A., **Minor, D.L., Jr.**, 'K_{2P}2.1(TREK-1):activator complexes reveal a cryptic selectivity filter binding site' *Nature* **547** 364-368 (2017) PMID: 28693035 PMCID: PMC5778891

d) Lolicato, M., Natale, A., Abderemane-Ali, F., Crottès, D., Capponi, S., Duman, R., Wagner, A., Rosenberg, J.M., Grabe, M., and **Minor, D.L., Jr.**, 'K_{2P}2.1 channel C-type gating involves asymmetric selectivity filter order-disorder transitions' *Science Advances* **6** eabc9174 (2020)

5) Ion channel-modulator interactions: We established a yeast genetic selection system for investigating ion channel-modulator interactions. By selecting for inward rectifier Kir2.1 barium resistant mutants, we identified a T→K mutant that demonstrated that the pore helix dipole, thought to be important for function, is not involved in ion permeation (Chatelain *et al.*, *Neuron*, 2005). We showed that the yeast system could be used generally to identify residues important for ion channel-small molecule interactions. We used this system to identify small molecules that bind to the K_{2P} selectivity filter (Lolicato *et al.*, *Nature*, 2017) and have determined the structural basis for K_{2P} block polyruthenium amines (Pope *et al.*, *Cell Chemical Biology*, 2020).

a) Chatelain, F.C., Alagem, N., Xu, Q., Pancaroglu, R., Reuveny, E., and **Minor, D.L., Jr.**, 'The pore helix dipole has a minor role in inward rectifier channel function' *Neuron* **47** 833-843 (2005) PMID: 16157278 PMC3017504 (Preview *Neuron* **47** 777-778, 2005)

b) Bagriantsev, S. N., Ang, K.H., Gallardo-Godoy, A., Clark, K.A., Arkin, M.R., Renslo, A.R., and **Minor, D.L., Jr.**, 'A high-throughput functional screen identifies small molecule regulators of temperature- and mechano-sensitive K_{2P} channels' *ACS Chemical Biology* **8** 1841-1851 (2013) PMID: 23738709 PMCID: PMC3747594

c) Lolicato, M., Arrigoni, C., Mori, T., Sekioka, Y., Bryant, C., Clark, K.A., **Minor, D.L., Jr.**, 'K_{2P}2.1(TREK-1):activator complexes reveal a cryptic selectivity filter binding site' *Nature* **547** 364-368 (2017) PMID: 28693035 PMCID: PMC5778891

d) Pope, L., Lolicato, M., **Minor, D.L., Jr.** 'Polynuclear ruthenium amines inhibit K_{2P} channels via a 'Finger in the dam' mechanism' *Cell Chemical Biology* **27** 511-524 (2020) **PMCID: PMC7245552**

5) **Toxin resistance mechanisms:** Saxitoxin (STX) produced by oceanic red tides is one of the most lethal paralytic neurotoxins due to its ability to inhibit voltage-gated sodium channels (Navs), is a chemical weapon, and has no antidote. Select frog species are resistant to STX poisoning, but how these creatures evade the lethal effects of STX remains unknown. We determined the structure of a bullfrog soluble, high affinity STX binding protein, saxiphilin (Sxph), thought to contribute to natural STX resistance (Yen *et al.*, *Science Adv.*, 2019) and discovered that Sxph engages STX in a manner very similar to Navs. This key step in understanding natural defenses to STX holds important lessons for STX antidote design as demonstrated in our demonstration of the role of 'toxin sponge' proteins in toxin resistance (Abderemane-Ali *et al.* *J. Gen. Physiol.*, 2020). We recently defined the STX binding code and discovered that Sxphs are found among anurans separated by ~140 million years of evolution (Chen *et al.* *PNAS*, 2022). This area of research is a new focus supported by (HDTRA11910040 and HDTRA12110011).

a) Yen, T.-J., Lolicato, M., Thomas-Tran, R., Du Bois, J., and **Minor, D.L. Jr.**, 'Structure of the saxiphilin:saxitoxin (STX) complex reveals a convergent molecular recognition strategy for paralytic toxins' *Science Advances* **5** eaax2650 (2019) **PMID: 31223657** **PMCID: PMC6584486** (News coverage: *KQED Public Media, San Francisco; Hakai Coastal Magazine*)

b) Abderemane-Ali, F., Rossen, N.D., Kobiela, M.E., Craig, R.A., Garrison, C.E., Chen, Z., Colleran, C.M., O'Connell, L.A., Du Bois, J., Dumbacher, J.P., and **Minor, D.L. Jr.**, 'Evidence that toxin resistance in poison birds and frogs is not rooted in sodium channel mutations and may rely on "toxin sponge" proteins' *J. Gen. Physiol.* **153** e202112872 (2021) **PMID: 34351379** **PMCID: PMC8348241** (News coverage: *Nature Highlights, National Geographic, The Times UK*)

c) Chen, Z., Zakrzewska, S., Hajare, H., Alvarez-Buluya, A., Abderemane-Ali, F., Bogan, M., Ramirez, D., O'Connell, L.A., Du Bois, J., and **Minor, D.L. Jr.**, 'Definition of a saxitoxin (STX) binding code enables discovery and characterization of the Anuran saxiphilin family' *Proceedings of the National Academy of Sciences, USA* **119**:e2210114119 (2022) **PMID: 36279441** **PMCID: PMC9636910**

URL to myNCBI a full list of published work

<http://www.ncbi.nlm.nih.gov/sites/myncbi/daniel.minor.1/bibliography/41458029/public/?sort=date&direction=ascending>

Complete list of Peer-reviewed publications (in chronological order):

1. **Minor, D. L., Jr.** and Kim P. S. 'Measurement of the β -sheet forming propensities of amino acids' *Nature* **367** 660-663 (1994) **PMID: 810785**
2. **Minor, D.L., Jr.** and Kim P.S. 'Context is a major determinant of β -sheet propensity' *Nature* **371** 264-267 (1994) **PMID: 8078589**
3. Schumacher, T.N.M., Mayr, L.M., **Minor, D.L., Jr.**, Milhollen, M.A., Burgess, M.W. and Kim, P.S. 'Identification of (D)-peptide ligands through Mirror-Image phage display' *Science* **271** 1854-1857 (1996) **PMID: 8596952**
4. **Minor, D.L., Jr.** and Kim P.S. 'Context-dependent secondary structure formation of a designed protein sequence' *Nature* **380** 730-734 (1996) **PMID: 8614471**
5. **Minor, D.L., Jr.**, Masseling, S.J., Jan, Y.N. and Jan, L.Y. 'Transmembrane structure of an inwardly rectifying potassium channel' *Cell* **96** 879-891 (1999) **PMID: 10102275**
6. **Minor, D.L., Jr.**, Lin, Y.F., Mobley, B.C., Avelar, A., Jan, Y.N., Jan, L.Y. and Berger, J.M. 'The polar T1 interface is linked to conformational changes that open the voltage-gated potassium channel' *Cell* **102** 657-670 (2000) **PMID: 11007484**
7. Mosavi, L. K., Minor, D.L., Jr., and Peng, Z.-y., 'Consensus-derived structural determinants of the ankyrin repeat motif' *Proceedings of the National Academy of Sciences, USA* **99** 16029-16034 (2002) **PMID: 12461176; PMCID: PMC138559**
8. Walden, H., Podgorski, M.S., Huang, D.T., Miller, D.W., Howard, R.J., **Minor, D.L., Jr.**, Holton, J.M., and Schulman, B.A., 'The structure of APPBP-1UBA3-NEDD8-ATP complex reveals the basis for selective ubiquitin-like protein activation by an E1' *Molecular Cell* **12** 1427-1437 (2003) **PMID: 14690597**
9. Van Petegem, F., Clark, K.A., Chatelain, F.C., and **Minor, D.L., Jr.**, 'Structure of a complex between a voltage-gated calcium channel β -subunit and an α -subunit domain' *Nature* **429** 671-675 (2004) **PMID: 15141227** (Research Highlight *Nature Rev. Neuroscience* **5**:517, 2004; rated 'Exceptional' Faculty of 1000)

10. Chatelain, F.C., Alagem, N., Xu, Q., Pancaroglu, R., Reuveny, E., and **Minor, D.L., Jr.**, 'The pore helix dipole has a minor role in inward rectifier channel function' *Neuron* **47** 833-843 (2005) **PMID: 16157278** (Preview *Neuron* **47** 777-778, 2005)
11. Van Petegem, F., Chatelain, F.C., **Minor, D.L., Jr.**, 'Insights into voltage-gated calcium channel regulation from the structure of the $\text{Ca}_v1.2$ IQ domain- Ca^{2+} /calmodulin complex' *Nature Structural & Molecular Biology* **12** 1108-1115 (2005) **PMID: 16299511** **PMCID: PMC3020901**
12. Tsuruda, P., Julius, D., and **Minor, D.L., Jr.**, 'Identification and characterization of a domain required for assembly of a cold-activated TRP channel' *Neuron* **51** 201-212 (2006) **PMID: 16846855** **PMCID: PMC3014052**
13. Michelsen, K., Mrowiec, T., Duderstadt, K.E., Frey, S., **Minor, D.L., Jr.**, Mayer, M.P., Schwappach, B., 'A multimeric membrane protein reveals 14-3-3 isoform specificity in forward transport in yeast' *Traffic* **7** 903-916 (2006) **PMID: 16734667**
14. Pioletti, M., Findeisen, F., Hura, G.L., and **Minor, D.L., Jr.**, 'Three-dimensional structure of the $\text{KChIP1}/\text{Kv}4.3$ T1 domain complex reveals a cross-shaped octamer' *Nature Structural & Molecular Biology* **13** 987-995 (2006) **PMID: 17057713** **PMCID: PMC3018330**
15. Howard, R.J., Clark, K.A., Holton, J.M., and **Minor, D.L., Jr.**, 'Structural insight into KCNQ (Kv7) channel assembly and channelopathy' *Neuron* **53** 663-675 (2007) **PMID: 17329207** **PMCID: PMC3011230**
16. Balss, J., Paptheodorou, P., Mehmel, M., Baumeister, D., Hertel, B., Delaroque, N., Chatelain, F. C., **Minor, D.L., Jr.**, Van Etten, J.L., Rassaw, J., Moroni, A., and Thiel, G. 'Transmembrane Domain Length of Viral Potassium Ion Channels is a Signal for Mitochondria Targeting' *PNAS* **105** 12313-12318 (2008) **PMID: 18719119**; **PMCID: PMC2518832**
17. Van Petegem, F., Duderstadt, K.E., Clark, K.A., Wang, M., **Minor, D.L., Jr.**, 'Alanine-scanning mutagenesis defines a conserved energetic hotspot in the Ca_{v1} AID- $\text{Ca}_{v\beta}$ interaction site that is critical for channel modulation' *Structure* **14** 280-294 (2008) **PMID: 18275819** **PMCID: PMC3018278**
18. Fujiwara, Y. and **Minor, D.L., Jr.**, 'X-ray crystal structure of a TRPM assembly domain reveals an antiparallel four-stranded coiled-coil' *Journal of Molecular Biology* **383** 854-870 (2008) **PMID: 18782578**; **PMCID: PMC2630241**
19. Kim, E.Y., Rumpf, C.H., Fujiwara, Y., Cooley, E.S., Van Petegem, F., and **Minor, D.L., Jr.**, 'Structures of Ca_v2 Ca^{2+} /CaM-IQ domain complexes reveal binding modes that underlie calcium-dependent inactivation and facilitation' *Structure* **16** 1455-1467 (2008) **PMID: 18940602**; **PMCID: PMC2701236** (Rated 'Must Read' by Faculty of 1000)
20. Hammon, J., Palanivelu, D.V., Chen, J., Patel, C., and Minor, D.L., Jr., 'A green fluorescent protein screen for identification of well-expressed membrane proteins' *Protein Science* **18** 121-133 (2009) **PMID: 19177357**; **PMCID: PMC2708023** (Rated 'Recommended' by Faculty of 1000)
21. Findeisen, F. and **Minor, D.L., Jr.**, 'Disruption of the IS6-AID linker affects voltage-gated calcium channel inactivation and facilitation' *Journal of General Physiology* **133** 327-343 (2009) **PMID: 19237593**; **PMCID: PMC2654080**
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Patents issued or pending

Patent US9862684B2 'Modulation of K_{2P} channels' Bagriantsev, S.N., Renslo, A.R., and **Minor, D. L., Jr.**

D. Research Support.

Ongoing Research Support:

R01 HL080050	Minor (PI)	05/01/05-03/31/24
Structure and function of voltage-gated calcium channels		
Role: PI		
R01 DC007664	Minor (PI)	07/01/05-01/31/24 (NCE)
Structural studies of ion channel assembly and signaling complexes		
Role: PI		
R01 MH093603	Minor (PI)	03/01/11-02/28/27
Genetic and chemical biological studies of K_{2P} structure, function, and modulation		
Role: PI		
HDTRA11910040	Minor (PI)	09/25/2019-09/24/2024
High-resolution characterization of saxitoxin (STX) recognition		
Role: PI		
HDTRA12110011	Minor (PI)	03/31/2021-03/31/2026
Development of biologic countermeasures for saxitoxin (STX) poisoning		
Role: PI		