## BIOGRAPHICAL SKETCH

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

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

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 *(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 |
|---|---|---|---|
| University of Pennsylvania, Philadelphia, PA | B.A. *magna cum laude* | 05/1989 | Biochemistry (Honors) Biophysics (Honors) |
| Massachusetts Institute of Technology, Cambridge, MA | Ph.D. | 02/1996 | 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. 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 worked as a postdoctoral fellow with Dr. Nigel Unwin at the LMB Cambridge and with Prof. Lily Y. Jan at UCSF where I was able to apply my background in structural biology to specific 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 and in the development of new pharmacological tools for orphaned channel classes. My lab is pursing a research program that combines structural biology, ion channel functional studies, and chemical biology approaches to develop new channel pharmacologies. 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 the structural understanding of the function of various classes of ion channels and development of new channel modulators using a multidisciplinary approach employing genetic selections, biophysical approaches, chemical biology, and X-ray crystallography. Our work is exemplified by the following key papers:


1. 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)
2. 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*' *function' The EMBO* Journal **30** 3594-3606 (2011) **PMID: 21765396 PMCID: PMC3181481**
3. 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 or temperature- and mechano-sensitive $K_{2p}$ channels' ACS Chemical Biology **8*** 1841-1851 (2013) **PMID: 23738709PMCID: PMC3747594**
4. Lolicato, M., Riegelhaupt, P.M., Arrigoni, C., Clark, K.A., Minor, D.L., Jr.' *Transmembrane helix straightening and buckling underlies activation of mechanosensitive and thermosensitive $K_{2p}$ channels' Neuron* **84** 1198-1212 (2014) **PMID: 25500157 PMCID: PMC4270892**

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

6. 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* (In Press)

**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

**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

**C. Contributions to science:**

**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*.

**Minor, D. L., Jr.** and Kim P. S. "Measurement of the β-sheet forming propensities of amino acids" *Nature* **367** 660-663 (1994a) **PMID: 810785**

**Minor, D.L., Jr.** and Kim P.S. "Context is a major determinant of β-sheet propensity" *Nature* **371** 264-267 (1994b) **PMID: 8078589**

**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 ($Ca_v$s):** Voltage-gated calcium channels ($Ca_v$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 $Ca_v$s.* My laboratory determined the first high-resolution structure of part of a $Ca_v$, the β-subunit, alone and in complex with its interaction site from the channel (*Van Petegem et al, 2004*). *We subsequently have determined structures for all of the components for which there are presently high-resolution data* including calcium-calmodulin complexes of $Ca_v1$ (*Van Petegem et al, 2005; Kim et al, 2010*) and $Ca_v2$ IQ domains (*Kim et al, 2008*). These studies have established a structural foundation for investigating $Ca_v$ function and have demonstrated the conformational complexities that underlie $Ca_v$ feedback modulation by calcium-calmodulin.

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 PMCID: PMC3076333** (*Research Highlight Nature Rev. Neuroscience* **5:**517, 2004; rated 'Exceptional' Faculty of 1000)

Van Petegem, F, Chatelain, F.C., **Minor, D.L., Jr., "**Insights into voltage-gated calcium channel regulation from the structure of the $Ca_v1.2$ IQ domain-$Ca^{2+}$/calmodulin complex" *Nature Structural & Molecular Biology* **12** 1108-1115 (2005) **PMID: 16299511 PMCID: PMC3020901**

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)

Kim, E.Y., Rumpf, C.H., Fujiwara, Y., Van Petegem, F., Arant, R., Findeisen, F., Cooley, E.S., Isacoff, E.Y. and **Minor, D.L., Jr.,** 'Multiple C-terminal Tail $Ca^{2+}$/CaMs regulate $Ca_v1.2$ function but do not mediate channel dimerization' *The EMBO Journal* **29** 3924-3938 (2010) **PMID: 20953164 PMCID: PMC3020648**

**3) Bacterial voltage gated sodium channels ($BacNa_v$s):** $BacNa_v$s are model systems for understanding the fundamental principles of voltage gated channel function. Using a protein dissection approach, we demonstrated that $BacNa_v$s are modular within the membrane and that the pore domain can be excised from the voltage sensors to produce functional sodium or calcium selective channels. These 'pore-only' proteins establish a general design principle of modularity within voltage-gated ion channel membrane domains and show that the pore domain and voltage sensor domains are separable units (*Shaya et al. 2011*). We determined the structure of a bacterial 'pore-only' sodium channel. *This work uncovered the complete structure of a pore-only $BacNa_v$ and revealed the structure of a crucial part, the cytoplasmic tail that had evaded other structural studies* (*Shaya et al. 2014*). This finding together 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 and

*discovered a previously unknown determinant of ion selectivity in human voltage-gated calcium channels* (*Shaya et al. 2014*).

There has been much debate about the origins of ion channel thermosensitivity and whether such responses rely on a dedicated sensing to domain or a more distributed property of the channel. *Our recent studies of BacNa$_v$ mechanisms have defined the first authentic temperature-sensitive module in an ion channel and show that it is possible for a single, defined domain to control channel thermal responses.* (Arrigoni *et al.* 2016).

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**

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**

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

**4) K$_{2P}$ channels** K$_{2P}$ channels are a diverse set of potassium channels that produce 'leak' currents that control cellular excitability. K$_{2P}$2.1 (TREK-1) is a classic polymodal channel that is gated by a wide range of stimuli including pH, temperature, and pressure. *When we began studying this channel family, it was unclear whether the various inputs controlled the channel by separate or common mechanisms.* Using a gain-of-function selection that identified K$_{2P}$2.1 (TREK-1) mutants that rescued a potassium transport deficient yeast strain, we identified a key element of the channel gate and established that pH, temperature, and pressure act through a common mechanism to control the gate, which is the channel selectivity filter (*Bagriantsev et al, 2011*). We established that signals from the intracellular sensors for temperature and phosphorylation are relayed to the selectivity filter via transmembrane helix M4 (*Bagriantsev et al. 2012*). Structure determination of two gain-of-function mutants in K$_{2P}$4.1 (TRAAK) revealed an unexpected mechanism that is opposite from prior expectations based on studies of other potassium channel classes (*Lolicato et al. 2014*). Upon activation M4 straightens at a conserved glycine and causes the M2 transmembrane helix to buckle at a conserved 'GXG' sequence. Structure-based functional tests demonstrate that this mechanism operates in the thermosensitive and mechanosensitive K$_{2P}$ subfamily. *Our studies have shown that K$_{2P}$ channels gate at the selectivity filter rather than an intracellular gate. Our latest work has defined the structure of K$_{2P}$2.1 (TREK-1) and uncovered a previously unknown small molecule modulatory site and demonstrates that small molecules can directly activate the selectivity filter gate (Lolicato et al., 2017, In Press).*

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' function' The EMBO* Journal **30** 3594-3606 (2011) **PMID: 21765396 PMCID: PMC3181481**

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**

Lolicato, M., Riegelhaupt, P.M., Arrigoni, C., Clark, K.A., and **Minor, D.L., Jr.** '*Transmembrane helix straightening and buckling underlies activation of mechanosensitive and thermosensitive K$_{2P}$ channels' Neuron* **84** 1198-1212 (2014) **PMID: 25500157 PMCID: PMC4270892**

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* (In Press, 2017)

**5) Ion channel-modulator interactions:** We established a yeast genetic selection system for investigating ion channel-modulator interactions. By selecting for barium resistant mutants of the inward rectifier Kir2.1, we identified a T→K mutant that demonstrated that the pore helix dipole, thought by many to be important for function, is not involved in ion permeation (*Chatelain et al. 2005*). We showed that the yeast system could be used generally to identify residues important for ion channel-small molecule interactions. Recently, we have established this system as a means to identify small molecule modulators of K$_{2P}$ channel function and have developed a novel, selective activator of the K$_{2P}$ subclass of mechanosensitive and thermosensitive channels (*Bagriantsev et al, 2013*). *Our efforts have defined the first set selective K$_{2P}$ activators (patent Bagriantsev et al. 61/785,155).* We have also shown that the yeast system can be used to discover novel protein-based regulators of ion channel function (*Bagriantsev et al, 2014*).

Our structure-based efforts have yielded the first protein-protein interaction inhibitor for an ion channel *(Findeisen et al. 2017)* and *have defined a novel class of $K_{2P}$ activators that bind to a previously unknown site supporting the channel selectivity filter, the '$K_{2P}$ modulator pocket'. (Lolicato et al. In press, 2017). These studies set the stage for the development of a new classes of ion channel modulators*

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 PMCID: PMC3017504 (Preview *Neuron* 47 777-778, 2005)**

Chatelain, F.C., Gazzarrini, S., Fujiwara, Y., Arrigoni, C., Domigan, C., Ferrara, G., Pantoja, C., Thiel, G., Moroni, A., and **Minor, D.L., Jr**., 'Selection of inhibitor-resistant viral potassium channels identifies a selectivity filter site that affects barium and amantadine block' *PLoS ONE* 4 (10) e7496. doi:10.1371/journal.pone.0007496 (2009) **PMID: 19834614; PMCID: PMC2759520**

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 or temperature- and mechano-sensitive $K_{2P}$ channels' ACS Chemical Biology **8*** 1841-1851 (2013) **PMID: 23738709PMCID: PMC3747594**

US patent application number 61/785,155 'Modulation of $K_{2P}$ channels' Bagriantsev, S.N., Renslo, A.R., and **Minor, D. L., Jr.**

Bagriantsev, S.N., Chatelain, F.C., Clark, K.A., Alagem, N., Reuveny, E., Minor, D.L., Jr. *'Tethered protein display identifies a novel Kir3.2 (GIRK2) regulator from protein scaffold libraries' ACS Chemical Neuroscience* **5** 812-822 (2014) **PMID: 25028803 PMCID: PMC4176385**

Findeisen, F., Campiglio, M., Jo, H., Abderemane-Ali, F., Rumpf, C.H., Pope, L., Rossen, N.D., Flucher, B.E., DeGrado, W.F., and **Minor D.L., Jr.**, '*Stapled voltage-gated calcium channel ($Ca_V$) α-Interaction Domain (AID) peptides act as selective protein-protein interaction inhibitors of $Ca_V$ Function' ACS Chemical Neuroscience* (2017) Mar 17. doi: 10.1021/acschemneuro.6b00454. [*Epub ahead of print*]

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* (In Press, 2017)

**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 $Ca_v1.2$ 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 KChIP1/Kv4.3 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., Papthеodorou, 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 $Ca_v\alpha_1$ AID-$Ca_v\beta$ 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**

22. Xu, Q. and **Minor, D.L., Jr.,** 'Crystal structure of a trimeric form of the Kv7.1 (KCNQ1) A domain Tail coiled coil reveals structural plasticity and context dependent changes in a putative coiled-coil trimerization motif' ***Protein Science*** **18** 2100-2114 (2009) **PMID 19693805 PMCID: PMC2786974**

23. Chatelain, F.C., Gazzarrini, S., Fujiwara, Y., Arrigoni, C., Domigan, C., Ferrara, G., Pantoja, C., Thiel, G., Moroni, A., and **Minor, D.L., Jr.,** 'Selection of inhibitor-resistant viral potassium channels identifies a selectivity filter site that affects barium and amantadine block' *PLoS ONE* **4 (10)** e7496. doi:10.1371/journal.pone.0007496 **(2009) PMID: 19834614; PMCID: PMC2759520**

24. Kohout S.C., Bell S.C., Liu L., Xu Q., **Minor, D.L., Jr.,** and Isacoff, E.Y., "Electrochemical coupling in the voltage-dependent phosphatase Ci-VSP *Nature Chemical Biology* **6** 369-375 (2010) **PMID: 20364128; PMCID: PMC2857593** (Preview *Nature Chemical Biology* **6 315-316, 2010)**

25. Kim, E.Y., Rumpf, C.H., Fujiwara, Y., Van Petegem, F., Arant, R., Findeisen, F., Cooley, E.S., Isacoff, E.Y. and **Minor, D.L., Jr**., 'Multiple C-terminal Tail $Ca^{2+}$/CaMs regulate $Ca_v1.2$ function but do not mediate channel dimerization' *The EMBO Journal* **29** 3924-3938 (2010) **PMID: 20953164 PMCID: PMC3020648**

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**Reviews, Book Chapters, and commentaries**

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**Patents issued or pending**

Application number 61/785,155 'Modulation of K2P channels' Bagriantsev, S.N., Renslo, A.R., and **Minor, D. L., Jr.**

**D. Research Support.**
**Ongoing Research Support:**

R01HL080050 NIH/NHLBI Minor (PI) 5/1/05-3/31/18
Structure and function of voltage-gated calcium channels $388,174
The major goals of this project are to investigate the molecular origins of calcium channel function.
Role: PI

R01 MH093603-01 NIH/NIMH Minor (PI) 03/01/11 – 02/28/21
Genetic and chemical biological studies of $K_{2P}$ structure, function, and modulation $400,000
The major goals are to develop genetic selection-based, approaches to define and characterize essential elements of $K_{2P}$ channel gating and to discover and characterize small molecule $K_{2P}$ modulators.
Role: PI

R01DC007664 NIH/NIDCD Minor (PI) 07/01/05-01/31/17 (NCE)
Structure and function of ion channel assembly and signaling complexes $210,375
The major goal of this project is to study the structural biology of potassium channel regulation.
Role: PI

U.S.-Israel Binational Science Foundation Grant 2011124 Minor/Reuveny (PI) 10/1/16 – 09/30/20
'Molecular Mechanisms of the regulation of SOCE regulation by SARAF' $13,376
The major goals of this project are to an understanding the interactions between SOCE channels and calcium regulation
Role: Co-PI with E. Reuveny, Weizmann Institute