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| University of California, San FranciscoDepartment of Pharmaceutical ChemistryCardiovascular Research Institute555 Mission Bay Blvd South, Room 452T, MC 3211San Francisco, California 94158-9001 | t 415.502.2874 (office)f 415.476.8173michael.grabe@ucsf.eduhttp://grabelab.ucsf.edu/ |

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| POSITIONS |
| 2013 – | Associate Professor, Cardiovascular Research Institute and Department of Pharmaceutical Chemistry, University of California, San Francisco |
| 2012 – 2013 | Visiting Associate Professor, Cardiovascular Research Institute, University of California, San Francisco |
| 2012 – 2013 | Associate Professor of Biological Sciences, University of Pittsburgh, Pittsburgh, Pennsylvania |
| 2008 – 2012 | Assistant Professor (secondary appointment), Department of Computational & Systems Biology, University of Pittsburgh School of Medicine, Pittsburgh, Pennsylvania |
| 2006 – 2012 | Assistant Professor of Biological Sciences, University of Pittsburgh, Pittsburgh, Pennsylvania  |

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| EDUCATION |
| 1996 – 2002 | Ph.D., Physics, University of California, Berkeley, Berkeley, California  |
| 1992 – 1996 | Sc.B., Mathematics-Physics,*magna cum laude* with departmental honors, Brown University, Providence, Rhode Island  |

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| RESEARCH TRAINING |
| 2002 – 2006 | Postdoctoral research, University of California, San Francisco*Advisor Lily Y. Jan, Howard Hughes Medical Institute and Department of Biophysics* |
|  | * quantified energies of voltage-gating in molecular models of ion channels
* used molecular dynamics and bioinformatic analysis to develop a model of the voltage-gated channel KAT1 using data from a high-throughput yeast screen
* discovered a novel method of ion selectivity in potassium channels
 |
| 1997 – 2002 | Doctoral research, University of California, Berkeley*Advisor George F. Oster, Department of Molecular and Cellular Biology* |
|  | * formulated a theoretical framework for mechanochemical systems and used this framework to describe rotary ATPase motors
* developed an elastic theory of membrane-protein interactions that describes the crystallization of bacteriorhodopsin from cubic phase membranes
* used systems modeling in combination with fluorescence labeling to understand pH regulation in cellular compartments
 |
| 1995 – 1996 | Undergraduate research, Brown University *Advisor Herbert M. Fried, Department of Physics* |
|  | * applied Green’s function techniques to study non-perturbative solutions to field theories
 |
| 1993 – 1996 | Undergraduate research (summers), University of Pittsburgh *Advisor David N. Beratan, Department of Chemistry* |
|  | * used phenomenological models of electron transport to understand the role of proteinarchitecture in mediating donor-acceptor electronic coupling
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| AWARDS and HONORS |
| 2012 | Shining Star Award for community outreach, Oakland Planning and Development Corporation, Pittsburgh, PA |
| 2011 | Senior Vice Chancellor’s Research Seminar, University of Pittsburgh |
| 2009 – 2014 | NSF CAREER award |
| 2009 – 2011 | Alfred P. Sloan Research Fellow in Molecular Biology |
| 2009 | Finalist in 2009 Howard Hughes Medical Institute Early Career Scientist Competition(150 finalists were chosen from over 2000 applications) |
| 2008 | Appointed to the Graduate Faculty, University of Pittsburgh |
| 2002 – 2003  | Howard Hughes Medical Institute Computational Postdoctoral Fellowship |
| 1997 – 1998 | University of California, Berkeley *Outstanding Graduate Student Instructor* Award |
| 1998 | Santa Fe Institute Complex Systems Summer School |

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| PUBLICATIONS (1600 total citations, Hirsch index = 22, based on Google Scholar)† - equal authors, ‡ - co-corresponding authors |
|  | Sun, J. and M. Grabe. Cooperativity Can Enhance Cellular Signal Detection. (*in review Physical Review Letters E*) |
|  | Choudhary, O.P., A. Paz, J.L. Adelman, J.P. Coulletier, J. Abramson‡, and M. Grabe‡ (2014). Structure guided simulations illuminate the Mechanism of ATP transport through VDAC1. (*in press Nature Structure & Molecular Biology*) |
|  | TT. Hong†, H. Yang†, SS. Zhang, M. Grabe, L.Y. Jan, and R.M. Shaw (2014). BIN1 Splicing and Actin Shape Cardiac T-tubule Membrane. (*in press Nature Medicine*) |
|  | Adelman, J.L., Y. Sheng, Y., S. Choe, J. Abramson, E. Wright, J.M. Rosenberg‡, and M. Grabe‡ (2014). Structural determinants of water permeation through the sodium-galactose transporter vSGLT. *Biophys. J.* **106**:1280-1289*News and Views* by Dr. Fangqiang Zhu in same issue. |
|  | N.R. Latorraca†, K.M. Callenberg†, J.P. Boyle, and M. Grabe (2014). Continuum approaches to understanding ion and peptide interactions with the membrane.*J. Memb. Biol.* **247**:395-408 |
|  | S. Mukherjee, H. Zheng, M. Derebe, K.M. Callenberg, C.L. Partch, D. Rollins, D.C. Propheter, J. Rizo, M. Grabe, Q.X. Jiang, and L.V. Hooper (2014). Antibacterial membrane attack by a pore-forming intestinal C-type lectin. *Nature*. **505**:103-107Citations: 5 |
|  | Y. Ishida, S. Nayak, J.A. Mindell‡, and M. Grabe‡ (2013). A model of lysosomal pH regulation. *J. Gen. Physiol.* **141**:705-720Citations: 1 |
|  | J.L. Adelman‡ and M. Grabe‡ (2013). Simulating rare events using a Weighted Ensemble-based string method. *J. Chem. Phys.* **138**:044105Citations: 1 |
|  | K.M. Callenberg, N.R. Latorraca, and M. Grabe (2012). Membrane shape optimization for examining the energetics of transmembrane protein insertion. *J. Gen. Physiol.* **140**:55-68Citations: 5 |
|  | J.L. Adelman, A.L. Dale, M.C. Zwier, D. Bhatt, L.T. Chong, D.M. Zuckerman, and M. Grabe (2011). Simulations of the alternating access mechanism of the sodium symporter Mhp1. *Biophys. J.* **101**:2399-2407Citations: 9 |
|  | P.G. Cantalupo, B. Calgua, G. Zhao, A. Hundesa, A.D. Wier, J.P. Katz, M. Grabe, R.W. Hendrix, R. Girones, D. Wang, and J.M. Pipas (2011). Raw Sewage Harbors Diverse Viral Populations. *mBio* **2**(5):e00180-11Citations: 29 |
|  | O.B. Kashlan, J.L. Adelman, S. Okumora, B.M. Blobner, Z. Zuzek, R.P. Hughey, T.R. Kleyman, and M. Grabe (2011). Constraint-based, homology model of the extracellular domain of the epithelial Na+ channel  subunit reveals a mechanism of channel activation by proteases.   *J. Biol. Chem.* **286**:649-660Citations: 20 |
|  | O.B. Kashlan, C.R. Boyd, C. Argyropoulos, S. Okumora, R.P. Hughey, M. Grabe, and T.R. Kleyman (2010). Allosteric inhibition of the epithelial Na+ channel through peptide binding at peripheral finger and thumb domains.  *J. Biol. Chem.* **285**:35216-35223Citations: 14 |
|  | A. Watanabe†, S. Choe†, V. Chaptal, J.M. Rosenberg, E.M. Wright, M. Grabe‡, and J. Abramson‡(2010).  The mechanism of sodium and substrate release from the binding pocket of vSGLT.  *Nature* **468**:988-991Citations: 50 |
|  | S. Choe, J.M. Rosenberg, J. Abramson, E.M. Wright‡, and M. Grabe‡(2010). Water permeation through the sodium-dependent galactose cotransporter vSGLT.   *Biophys. J.* **99**:L56-L58**Cover Article**Citations: 18 |
|  | K.M. Callenberg, O.P. Choudhary, G.L. de Forest, D.W. Gohara, N.A. Baker, and M. Grabe (2010). APBS membrane tool: a graphical tool for electrostatics calculations at the membrane.  *PLoS ONE* **5**(9): e12722Citations: 15 |
|  | Bailey, M.A., M. Grabe, and D.C. Devor (2010). Characterization of the PCMBS-dependent modification of KCa3.1 channel gating.   *J. Gen. Physiol.* **136**: 367-387Citations: 4 |
|  | O.P. Choudhary, R. Ujwal, W. Kowallis, R. Coalson, J. Abramson, and M. Grabe (2010). The electrostatics of VDAC: implications for selectivity and gating. *J. Mol. Biol.* **396**: 580-592Citations: 33 |
|  | S. Choe and M. Grabe (2009). Conformational dynamics of the inner pore helix of voltage-gated potassium channels. *J. Chem. Phys.* **130**: 215103-215115**Highlighted in Virtual Journal of Biological Physics Research (2009). 17(12)**Citations: 6 |
|  | S. Choe, K.A. Hecht, and M. Grabe (2008). A continuum method for determining membrane protein insertion energies and the problem of charged residues. *J. Gen. Physiol.* **131**: 563-573**Faculty of 1000 Factor 9 Must Read**: http://f1000.com/1108693Citations: 31 |
|  | T.C. Krzysiak, M. Grabe, and S.P. Gilbert (2008). Getting in Sync with Dimeric Eg5: Initiation and Regulation of the Processive Run. *J. Biol. Chem.* **283**: 2078-2087Citations: 21 |
|  | M. Grabe**†,** H.C. Lai**†**, M. Jain, Y.N. Jan, and L.Y. Jan (2007). Structure for the down state of a potassium channel voltage sensor. *Nature* **445**: 550-553**Faculty of 1000 Factor 10 Exceptional**: http://f1000.com/1082977Citations: 51 |
|  | M. Grabe, D. Bichet, X. Qian, Y.N. Jan, and L.Y. Jan (2006). K+ channel selectivity depends on kinetic as well as thermodynamic factors. *Proc. Natl. Acad. Sci. USA*. **103**: 14361-14366**Faculty of 1000 Factor 6 Recommended**: http://f1000.com/1071939Citations: 23 |
|  | D. Bichet, M. Grabe, Y.N. Jan, and L.Y. Jan (2006). Electrostatic interactions in the channel cavity as an important determinant of potassium channel selectivity. *Proc. Natl. Acad. Sci. USA*. **103**: 14355-14360Citations: 33 |
|  | Nayak, S., I. Olkin, H. Liu, M. Grabe, M.K. Gould, I.E. Allen, D.K. Owens, and D.M. Bravata (2006). Accuracy of calcaneal quantitative ultrasound for identifying patients meeting the world health organization’s diagnostic criteria for osteoporosis: A systematic review. *Ann. Inter. Med.* **144**: 832-841Citations: 72 |
|  | H.C. Lai, M. Grabe, Y.N. Jan, and L.Y. Jan (2005). The S4 voltage sensor packs against the pore domain in the KAT1 voltage-gated potassium channel. *Neuron* **47**: 395-406 Citations: 34 |
|  | M. Grabe, H. Lecar, Y.N. Jan, and L.Y. Jan (2004). A quantitative assessment of models for voltage-dependent gating of ion channels. *Proc. Natl. Acad. Sci. USA*. **101**: 17640-17645Citations: 65 |
|  | H. Lecar, H.P. Larsson, and M. Grabe (2003). Electrostatic model of S4 motion in voltage-gated ion channels. *Biophys. J.* **85(5)**: 2854-2864Citations: 54 |
|  | B.E. Cohen**†**, M. Grabe**†**, and L.Y. Jan (2003). Answers and questions from the KvAP structures. *Neuron* **39**: 395-400Citations: 76 |
|  | M. Grabe, J. Neu, G. Oster, and P. Nollert (2003). Protein interactions and membrane geometry. *Biophys. J.* **84(2)**: 854-868Citations: 55 |
|  | H-P.H. Moore, J.M. Andersen, B.A. Eaton, M. Grabe, M. Haugwitz, M.M. Wu, and T.E. Machen (2002). Biosynthesis and secretion of pituitary hormones: dynamics and regulation. *Arch. Physiol. Biochem.* **110(1-2):** 16-25Citations: 22 |
|  | T.E. Machen, G. Chandy, M.M. Wu, M. Grabe, and H-P.H. Moore (2001). Cystic fibrosis transmembrane conductance regulator and H+ permeability in regulation of Golgi pH. *J. Pancrease.* **2(4 Suppl):** 229-236Citations: 14 |
|  | M.M. Wu, M. Grabe, S. Adams, R. Tsien, H.-P.H. Moore, and T. Machen (2001). Mechanisms of pH regulation in the regulated secretory pathway. *J. Biol. Chem.* **276(35)**: 33027-33035Citations: 181 |
|  | G. Chandy, M. Grabe, H-P.H. Moore, and T. Machen (2001). Regulation of intra-Golgi pH in respirotary epithelial cells: Does CFTR regulate Golgi pH? *Am. J. Physiol.* **281(3)**: C908-C921Citations: 33 |
|  | M. Grabe and G. Oster (2001). Regulation of organelle acidity. *J. Gen. Physiol.* **117(4)**: 329-344Citations: 189 |
|  | M. Grabe, H. Wang, and G. Oster (2000). Mechanochemistry of the V-ATPase proton pump. *Biophys. J.* **78(6)**: 2798-2813Citations: 75 |
|  | G. Oster, H. Wang, and M. Grabe (2000). How F0-ATPase generates rotary torque. *B: Phil. Trans. Roy. Soc.* **355(1396)**: 523-528Citations: 42 |
|  | P. Dimroth, H. Wang, M. Grabe, and G. Oster (1999). Energy transduction in the sodium F-ATPase of *Propionigenium modestum.* *Proc. Natl. Acad. Sci. USA*. **96**: 4924-4929Citations: 157 |
|  | W.B. Curry, M.D. Grabe, I.V Kurnikov, S.S. Skourtis, D.N. Beratan, J.J. Regan, A.J.A. Aquino, P. Beroza, and J.N. Onuchic (1995). Pathways, pathway tubes, pathway docking, and propagators in electron transfer proteins. *J. Bioenerg. Biomem.* **27(3)**: 285-293Citations: 65 |

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| CURRENT GRANT SUPPORT |
| 2012 – 2014 | *Computational Simulations of Lysosomal and Osteoclast Microphysiology*NIH R21, Role: PI ($414K, R21GM100224-01) |
| 2011 – 2016 | *Computational Studies of Sodium Symporters*NIH R01, Role: PI ($1.4M, 1RO1GM089740-01A1) |
| 2009 – 2014 | *Computational Approaches to Understanding Membrane Protein Energetics and Function* NSF CAREER Award ($932K, MCB0845286) |

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| CURRENT COMPUTATIONAL SUPPORT |
| 2013 – 2014 | *Computational Approaches to Understanding Membrane Protein Function* XSEDE Supercomputing grant, Role: PI (3M hours, MCB080011) |