

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Chakrapani, Sudha

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

POSITION TITLE: Professor

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 Madras, Chennai, India	B.S.	06/1995	Chemistry
University of Pune, India	M.S.	06/1997	Biochemistry
Indian Institute of Technology, India	M.Tech.	02/1999	Biomedical Engineering
University at Buffalo, Buffalo, NY	Ph.D.	05/2004	Physiology & Biophysics
University of Virginia, Charlottesville, VA	Postdoctoral	01/2006	Physiology & Biophysics
University of Chicago, Chicago, IL	Postdoctoral	07/2008	Physiology & Biophysics

A. Personal Statement

My long-standing scientific interest has been in developing a molecular-level understanding of ion-transport phenomenon across cellular membranes that occurs under normal and pathophysiological conditions. My research over the last 20 years has focused on ion channels that mediate fast synaptic transmission at the neuronal and neuromuscular junction; namely, ligand- and voltage- gated ion channels. My scientific approach is a combination of cutting-edge multidisciplinary tools that includes Cryo-EM and X-ray crystallography for high-resolution structure determination, EPR spectroscopy for protein dynamic measurements, and electrophysiology for functional characterization of ion channels.

We solved the first cryo-EM structure of the full-length 5-HT_{3A}R channel in its resting conformation (*Nature Communications*, 2018), in serotonin-bound states that revealed the conformational changes underlying channel activation (*Nature*, 2018), bound to setrons, clinically used drugs in the treatment of nausea and vomiting in patients undergoing cancer treatments, revealing the mechanism of setron-mediated inhibition in these channels (*Nature Communications*, 2019; *eLife* 2020). Together, these structures represent the first set of gating conformational states along the ligand-driven activation pathway described for a full-length pentameric-ligand gated ion channel (pLGIC). We recently developed a comprehensive structural scheme of glycine receptors gating by determining cryo-EM structures of the channel in the apo, open, and desensitized conformations in a lipid bilayer environment (*Nature Communications*, 2020). In summary, with the experience I have gained in diverse structural, dynamics, and functional approaches, and further equipped with the cutting-edge cryo-EM technique, we are now poised to address some of the fundamental questions in the membrane protein field that have remained elusive so far.

Teaching and Mentoring: I have been extremely fortunate to work with and mentor extremely talented individuals who have helped build my research program and are an integral part of what we have achieved as a team. In the last 10 years, *I have trained 7 graduate students (past and current) of which 5 are female.* All my predoctoral trainees and postdoctoral trainees have remained in biomedical science professions. Among past trainees from the lab, two of the three predoctoral trainees hold leadership positions in pharmaceutical industries and two of

the three postdoctoral trainees are independent PIs with faculty positions. In addition, I have participated in 24 graduate student thesis progress committees, of which I am Chair on 7 of them. I am on the mentoring Committee for 6 Junior faculty members to provide them guidance on grants, tenure, promotion, and professional growth. Since 2012, I serve on the Graduate Education Committee at the Department of Physiology and Biophysics and in 2019 was appointed to the MSTP Steering Committee. Among the accolades won by my trainees, the notable ones include postdoctoral fellowships from the American Heart Association by Dr. Basak, and Dr. Arvind Kumar; NIH F32 Fellowship by Dr. Eric Gibbs, Biophysical Society Student Travel Award and the University of Chicago postdoctoral Fellowship by Dr. Nicholas Schmandt, and the *Recknagel Award* from the DPB by Ms. Yvonne Gicheru and Ms. Kayla Kindig. Over the last ten years my lab has hosted nine students from the DPB Summer Undergraduate Research Program and the Heart Lung Blood Summer Research Program. Two of these students, Ross Bonner and Lauren Talley (URM), are contributing authors on a paper in *Journal of General Physiology*, 2015.

Ongoing and recently completed projects that I would like to highlight include:

NIH R35 GM134896

Chakrapani (PI)

01/01/20 – 12/31/24

Structure and Function of Pentameric Ligand-Gated Ion Channels

Completed Research Support

NIH R01 GM131216

Chakrapani (PI)

01/1/19 – 12/31/22

Structure, Function, and Modulation of Serotonin (3A) receptors"

(Rolled into R35 MIRA Award).

NIH R01 GM108921

Chakrapani (PI)

09/1/14 – 08/31/20

Molecular Mechanisms of Desensitization and Drug Modulation in Ligand-Gated Ion Channels.

(Renewal funded as R35 MIRA Award)

Citations:

1. Schmandt, N., P. Velisetty, S. V. Chalamalasetti, R. A. Stein, R. Bonner, L. Talley, M. D. Parker, H. S. McHaourab, V. C. Yee, D. T. Lodowski and **S. Chakrapani*** (2015). "A chimeric prokaryotic pentameric ligand-gated channel reveals distinct pathways of activation." *J Gen Physiol* **146**(4): 323-340.
2. Basak S, Gicheru Y, Rao S, Sansom MSP, **Chakrapani S***. (2018) Cryo-EM reveals two distinct serotonin-bound conformations of full-length 5-HT3A receptor. *Nature*;563(7730):270-4. doi: 10.1038/s41586-018-0660-7. PubMed PMID: 30401837; PMCID:PMC6237196 (*Article Recommended by Faculty 1000*)
3. Kumar A, Basak S, Rao S, Gicheru Y, Mayer ML, Sansom MSP, **Chakrapani S***. (2020) Mechanisms of activation and desensitization of full length glycine receptors in lipid nanodisc. *Nature Communications* Jul 27;11(1):3752. doi: 10.1038/s41467-020-17364-5. PMID: 32719334
4. Basak S, Kumar A, Ramsey S, Gibbs E, Kapoor A, Filizola M, Chakrapani S. High-resolution structures of multiple 5-HT3AR-serotonin complexes reveal a novel mechanism of competitive inhibition. *eLife*. 2020;9. Epub 2020/10/17. doi: 10.7554/eLife.57870. PubMed PMID: 33063666.

B. Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments

- 2020-present Director, Cleveland Center for Membrane and Structural Biology, , Case Western Reserve University, Cleveland, OH
- 2020-present Professor, Department of Physiology and Biophysics, Case Western Reserve University, Cleveland, OH
- 2018-present Director, Cryo-Electron Microscopy Core, Case Western Reserve University, Cleveland, OH
- 2017-2020 Associate Professor (Tenured), Department of Physiology and Biophysics, Case Western Reserve University, Cleveland, OH
- 2010-2017 Assistant Professor (Tenure-track), Department of Physiology and Biophysics, Case Western Reserve University, Cleveland, OH
- 2008-2010 Research Assistant Professor, Department of Biochemistry and Molecular Biology, University of Chicago, Chicago, IL

Other Experience and Professional Memberships

- 2019-2023 *Permanent Member*, Biochemistry and Biophysics of Membranes, NIH Study Section.
- 2019 Editorial Board, Biophysical Journal
- 2018-2020 Reviewer, United States-Israel Binational Science Foundation
- 2018 Editorial Advisory Board, Journal of General Physiology
- 2018 Reviewer, United States-Israel Binational Science Foundation
- 2018 Reviewer, French National Research Agency (ANR), France
- 2018 Reviewer, MCMB grant proposal, Medical Research Council (MRC) UK
- 2018 Ad hoc Reviewer, NIH BPNS study Section (Feb cycle).
- 2017 Reviewer, MCMB grant proposal, Medical Research Council (MRC) UK
- 2016 Ad hoc Reviewer, NIH BBM study Section (Feb and Sep cycles).
- 2015-2018 Councilor (elected to office), Society for General Physiologists.
- 2015-2021 Committee for Professional Opportunities for Women Committee (CPOW), Biophysical Society
- 2015-2017 Reviewer, American Heart Association (Basic Cell, Proteins & Crystallography1 and Proteins & Crystallography 1 and 3)
- 2015-present Member, Society for General Physiology
- 2014 Reviewer, NIGMS Program Projects Grants (P01) special emphasis panel
- 2012-2013 Panelist, Early Career Development Committee, Biophysical Society
- 2005 Early Career Committee, Biophysical Society
- 2010-present Member, American Heart Association
- 2003-present Member, Biophysical Society

Honors

- 2019-present Joseph T. Wearn, MD, University Professorship in Medicine
- 2018 CWRU nominee for the Mallinckrodt Scholar Program.
- 2012-2016 Scientist Development Grant, American Heart Association.
- 2007-2008 Postdoctoral Fellowship (Competitive Renewal), American Heart Association
- 2005-2008 Postdoctoral Fellowship, American Heart Association
- 2004 University at Buffalo nominee for the CGS/UMI Distinguished Dissertation award.
- 2004 Dean's Award for Outstanding Dissertation, First Prize. University at Buffalo, SUNY.
- 2004 Herbert Schuel Award for outstanding research in the field of Cell and Developmental Biology, University at Buffalo, SUNY.
- 1999 Selected for the Cambridge Commonwealth Trust Scholarship and Overseas Research Scholar Award.
- 1997-1999 Biomedical Engineering Scholarship, Indian Institute of Technology, Bombay, India
- 1997 Selected for Junior Research Fellowship, Council for Scientific and Industrial Research, India
- 1995-1997 National Chemical Laboratory Scholarship, Pune, India

C. Contributions to Science

1. Structure-function relationships in nicotinic Acetylcholine receptors. One of the fundamental challenges in the ion channel field is to understand how spatially-separated structural motifs of the channel communicate in order to fine-tune its function. In my doctoral research, I addressed this question in nicotinic acetylcholine receptor-channels (nAChR) that belong to the neurotransmitter gated Cys-loop receptor family. These channels are responsible for mediating fast synaptic transmission in neuronal and neuronal muscular junctions. Through single-channel current measurements of over 100 mutations and extensive model-based kinetic analysis within the framework of linear free energy relationships, I found that signal transduction occurs as a sequential movement of rigid “blocks” or “micro-domain” originating at the extracellular ligand-binding domain and culminating at the gate within the transmembrane region. Such an organized and linked motion of rigid bodies may underlie fast dynamics of the allosteric conformational change in these channels. This system also proved ideal to probe the speed-limits of global protein motions in the membrane. This finding has implications on barrier-less transitions in large multimeric membrane proteins.

- a. **Chakrapani, S.**, T.D. Bailey, and A. Auerbach. (2003). The role of loop 5 in acetylcholine receptor channel gating. *J Gen Physiol.* 122:521-539. PMID:PMC2229574
- b. **Chakrapani, S.**, T.D. Bailey, and A. Auerbach. (2004). Gating Dynamics of the Acetylcholine Receptor Extracellular Domain. *J Gen Physiol.* 123: 341-356. (Featured on the Cover). PMID:PMC2217457
- c. **Chakrapani, S.**, and A. Auerbach. (2005). A speed limit for conformational change of an allosteric membrane protein. *Proc Natl Acad Sci U S A*, 2005. 102(1): p. 87-92. PMID:PMC544059

2. C-type inactivation and modal gating behavior in K⁺ channels. Studying prokaryotic channels provides a unique advantage to draw direct information from structural, dynamics, and functional measurements. However, unlike eukaryotic channels most of the bacterial members were not well-characterized at the functional level, this was particularly the case for KcsA, a pH-activated K⁺ channel. As a part of my postdoctoral training, I carried out extensive kinetic analysis both at the macroscopic and single-channel level to characterize C-type inactivation and fast gating events that underlie KcsA function. To obtain high resolution structure of KcsA in multiple conformational states, I crystallized the channel in various mutant forms and in the presence of several modulators. Equating functional states to structural snapshots from crystallography, have led to a better understanding of the structural basis for inactivation from pre-open states, interaction of ions with the channel, modal gating behavior, and transitions that lead to fast gating events.

- a. **Chakrapani, S.**, Cordero-Morales, J. F., and Perozo, E. (2007a). A quantitative description of KcsA gating I: macroscopic currents. *J Gen Physiol* 130, 465-478. PMID:PMC2151670
- b. **Chakrapani, S.**, Cordero-Morales, J. F., and Perozo, E. (2007b). A quantitative description of KcsA gating II: single-channel currents. *J Gen Physiol* 130, 479-496. PMID:PMC2151667
- c. **Chakrapani, S.^a**, Cordero-Morales, J. F.^a, Jogini, V., Pan, A. C., Cortes, D. M., Roux, R., and Perozo, E. (2011) On the structural basis for modal gating in K⁺ channels *Nature Structure & Molecular Biology* 18 (1), PMID:PMC3059741. ^aequal contribution.
- d. Ostmeyer J, **Chakrapani S**, Pan AC, Perozo E, Roux B. (2013) Recovery from slow inactivation in K⁺ channels is controlled by water molecules. *Nature*. 501(7465):121-4. PubMed PMID: 23892782; PMID:PMC3799803

3. Voltage-sensing mechanism and slow-inactivation in ion channels. Voltage-gated channels play a critical role in cellular excitability and thereby form the basis for initiation and propagation of nerve impulses. The structure of the voltage-sensor and the mechanisms underlying gating-charge movement have been areas intensively studied. Both the structure and the protein motions in the sensor are critically governed by the local membrane environment. Also as a part of my postdoctoral training, I used site-directed spin labeling and electron paramagnetic resonance (EPR) spectroscopy to directly investigate the architecture of the sensor in a reconstituted system. I studied the dynamics of the isolated voltage-sensors of prokaryotic K⁺ (KvAP) and Na⁺ (NaChBac) channels by EPR spectroscopy. These findings provided an in-depth view of the architecture of this domain on the membrane along with insights into the open-inactivated state of the channel. More recently, my lab characterized the molecular motions underlying slow-inactivation in voltage-gated Na⁺ channel (NavSp1) by pulsed-EPR spectroscopy.

- a. **Chakrapani, S.**, Cuello, L.G., Cortes, D.M., and Perozo, E. (2008). Structural dynamics of an isolated-voltage sensor domain in lipid bilayer. *Structure* 16, 398-409 PMID:PMC2703488

- b. **Chakrapani, S.**, Sompornpisut, P., Intharathep, P., Roux, B. & Perozo, E. (2010). The activated state of a sodium channel voltage sensor in a membrane environment. *Proc Natl Acad Sci U S A* 107, 5435-40. PMID:PMC2851821
- c. **Chakrapani, S.** (2015) EPR studies of gating mechanisms in ion channels *Methods in Enzymology* 557:279-306 PMID:PMC4503332
- d. Chatterjee S, Vyas R, Chalamalasetti SV, Sahu ID, Clatot J, Wan X, Lorigan GA, Deschenes I, **Chakrapani S***. The voltage-gated sodium channel pore exhibits conformational flexibility during slow inactivation. *J Gen Physiol.* 2018;150(9):1333-47. doi: 10.1085/jgp.201812118. PubMed PMID: 30082431; PMID: PMC6122925.
 *This article was featured in a commentary "Progress in Understanding Slow Inactivation Speeds up" Payandeh, J *Journal of General Physiology* (2018)

4. Gating mechanisms in pentameric ligand-gated ion channels. Since joining the faculty at Case Western Reserve University as an Assistant professor in 2010, a major research focus of my lab has been to understand allosteric mechanisms in pentameric ligand-gated ion channels (pLGIC). Using prokaryotic homologues GLIC and ELIC as model systems, we elucidated the ligand-induced pore opening mechanism by EPR spectroscopy. Patch-clamp measurements from reconstituted channels were used to show the salient features of desensitization in GLIC that bears resemblance to the mechanism observed in the eukaryotic counterpart. These methods have allowed us to directly measure the effect of membrane lipid constituents on channel function and to determine the underlying changes in protein dynamics under these conditions. In addition, we studied long-range allosteric communications by engineering functional chimeric channels that incorporates domains from different members of the family. By using X-ray crystallography and pulse-EPR measurement, we determined the crystal structure of the chimera and measured ligand-induced structural changes which reveal conformational coupling between domains. More recently, my lab is geared towards applying these approaches in combination with cryo-EM to complex eukaryotic pLGIC. We recently determined the structures of the full-length 5-HT_{3A}R in the apo, and serotonin-bound conformations by single-particle cryo-EM. The structure reveals salient features of the resting, state and the conformational changes underlying serotonin-mediated activation. I served as the principal investigator in all these studies.

- a. Basak, S.^a, Schmandt, N.^a, Gicheru, Y.^a, and **Chakrapani, S***. (2017) Crystal structure and dynamics of a lipid-induced potential desensitized state of a pentameric ligand-gated channel (*eLIFE*, doi: 10.7554/eLife.23886). PMID:PMC5378477
- b. Basak S, Gicheru Y, Rao S, Sansom MSP, **Chakrapani S***. Cryo-EM reveals two distinct serotonin-bound conformations of full-length 5-HT_{3A} receptor. *Nature*. 2018;563(7730):270-4. doi: 10.1038/s41586-018-0660-7. PubMed PMID: 30401837. PMID:PMC6237196 (*Article Recommended by Faculty 1000*)
- c. Basak S^a, Gicheru Y^a, Kapoor A., Mayer ML., Filizola M, and **Chakrapani S***. (2019) Molecular mechanism of setron-mediated inhibition of full-length 5-HT_{3A} receptors. *Nature Communications* 10, 3225, doi:10.1038/s41467-019-11142-8. PMID:PMC6642186
- d. Kumar A, Basak S, Rao S, Gicheru Y, Mayer ML, Sansom MSP, **Chakrapani S***. (2020) Mechanisms of activation and desensitization of full length glycine receptors in lipid nanodisc. *Nature Communications* Jul 27;11(1):3752. doi: 10.1038/s41467-020-17364-5.PMID: 32719334

Complete List of Published Work in MyBibliography:

<https://www.ncbi.nlm.nih.gov/sites/myncbi/sudha.chakrapani.1/bibliography/50561146/public/?sort=date&direction=ascending>

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Felt, Kevin Christopher

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

POSITION TITLE: PhD Candidate

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	Start Date	Completion Date	FIELD OF STUDY
Skagit Valley College (SVC), Mount Vernon, WA	AA DTA/MRP	09/2013	06/2016	Biology
University of Washington (UW), Seattle, WA	B.S.	09/2016	06/2018	Biochemistry Major, Microbiology Minor
Case Western Reserve University (CWRU), Cleveland, OH	Ph.D.	07/2019	05/2024	Physiology and Biophysics

A. Personal Statement

I became interested in pursuing a research career in high school after the unexpected death of my uncle, which caused me to consider how medicine is advanced and why some disease and injury are still not well understood. Since then, my educational goal has been to obtain a PhD in the biological sciences. I completed the first half of my bachelor's degree at Skagit Valley College due to the high costs of university. I knew I wanted to be a research scientist, so I worked part-time, studied hard, and applied for scholarships so that I could afford transfer to UW. After moving to the UW, I experienced the excellent quality and depth of education being provided and worked hard to overcome the academic and environmental learning curves. I began undergraduate research in the laboratory of Dr. Jim Bruce studying systems structural biology through mass spectrometry-based proteomics. I learned a lot, overcame many academic and life challenges, and graduated UW with a bachelor of science in biochemistry and a minor in microbiology. After a gap year spent recovering from ACL reconstruction surgery and volunteering my time for research experience in the laboratory of Dr. Shane Rea at UW, I was admitted to my PhD program at CWRU. After moving to CWRU and completing my research rotations, I joined the lab of Dr. Sudha Chakrapani in the Department of Physiology and Biophysics. The Chakrapani lab is broadly interested in ion channel structure and physiology, with a focus on cys-loop pentameric ligand gated ion channels (pLGICs). I am excited to contribute to the advancement of health and science as a trained structural biologist.

B. Positions, Scientific Appointments and Honors

2021	Chair, Graduate Student Research Talks, Department of Physiology and Biophysics Retreat
2020	Student Representative, Biomedical graduate student organization, CWRU
2019 – 2020	Recknagel Academic Award for the Department of Physiology and Biophysics
2017	Herschel Roman Undergraduate Science Scholarship (<i>Competitive</i>), UW
2016	Sydney S. McIntyre Jr. Scholarship (<i>Competitive</i>), SVC
2015 – 2016	President, Phi Theta Kappa Honor Society, SVC
2015	Richard and Jean Nowadnick Life Sciences Scholarship (<i>Competitive</i>), SVC
2015	William D. Werner Memorial Scholarship (<i>Competitive</i>), SVC
2015	Esther Woodford Taylor Scholarship (<i>Competitive</i>), SVC

C. Contributions to Science

Undergraduate Research

Upon transferring to the University of Washington to complete my degree, I joined the laboratory of Dr. James Bruce in the Department of Genome Sciences as an undergraduate researcher. During my time at the Bruce lab, I gained experience in proteomics research through my own project investigating molecular crowding, defined as the summation of molecular forces acting on polypeptides when in high concentrations, a condition endogenous to membrane-bound structures. We hypothesized that molecular crowding is an important consideration for understanding protein conformations and interactions in vivo, particularly for proteins that require high flexibility to recognize and bind many interactors, like the chaperone Hsp90. Understanding if protein structures or interactions change under different crowding conditions is relevant to the accuracy of protein studies, since many are performed in diluted, in vitro environments. To study these effects, we applied lysine-reactive chemical cross-linking to proteins under conditions that exert different levels of molecular crowding, and analyzed the results using mass spectrometry. These conditions included cross-linking of living cells where high protein density causes high levels of crowding, and cross-linking of cellular lysates where protein density and molecular crowding effects are reduced. The linkage sites provided physical distance constraints useful for structural predictions, and the observed changes in cross-link site abundances within and between proteins predicted possible conformation and interaction changes. My project produced some evidence of specific protein interactions occurring at increased frequencies in different molecular crowding conditions, including some data on Hsp90, but more replicates are required to determine consistent trends. Additionally, the data revealed an increase in the fraction of interprotein cross-links to intraprotein cross-links present in vivo vs lysate, respectively, suggesting that endogenous protein interactions are better retained during in vivo cross-linking. These data were presented at the 2017 Cascadia Proteomics Symposium (Seattle, WA) and 2018 Undergraduate Research Symposium (University of Washington, Seattle, WA), as well as included in a 2019 Journal of Proteome Research publication, on which I am a co-author.

1. Keller A, Chavez JD, **Felt KC**, Bruce JE. Prediction of an Upper Limit for the Fraction of Interprotein Cross-Links in Large-Scale In Vivo Cross-Linking Studies. *J Proteome Res.* 2019 Aug 2;18(8):3077-3085. doi: 10.1021/acs.jproteome.9b00189. Epub 2019 Jul 17. PMID: 31267744; PMCID: PMC6777711.

Graduate Research

My current research focus in the Chakrapani lab is the 5-HT₃ receptor, one of the seven 5-hydroxytryptamine (serotonin) receptors found in eukaryotes, and the only pLGIC serotonin receptor. The 5-HT₃R is an important drug target due to its implication in chemotherapy-induced nausea and vomiting, irritable bowel syndrome, depression, anxiety, bipolar disorder, and pain perception. My dissertation research plan is comprised of several related research projects that utilize cryoEM to analyze the structure of the 5-HT₃R. One project focuses on structural analysis of drug-target interactions between the 5-HT₃R and the partial agonist SMP100 at the orthosteric binding site and how subtle changes in drug-target interactions can lead to agonism, partial agonism, or antagonism of the 5-HT₃R. Another project utilizes cryoEM and electrophysiology to investigate allosteric modulation of the 5-HT₃R by lipids and lipidic ligands such as Δ -9-tetrahydrocannabinol (THC). The last project in my dissertation research plan is to solve the structure of the 5-HT₃R heteropentamer comprised of the A and B subunits, for which there is presently no high-resolution structural information. Preliminary results include 3D charge density maps of the 5-HT_{3A}R in complex with the partial agonist SMP-100, as well as the 5-HT_{3A}R in complex with the lipidic ligand THC, with each map showing novel conformations of the receptor. Solving the structure of the 5-HT₃R in complex with these ligands would provide novel insights into the molecular mechanism of partial agonism and allosteric modulation, as well as assist in assigning functional annotations to previously solved structures.

1. **Kevin Felt**, Sandip Basak, Arvind Kumar, Sudha Chakrapani. Structural studies of 5-HT₃R partial agonism, lipid modulation, and subunit composition. Poster, Sep. 2021, Department of Physiology and Biophysics Annual Retreat.
2. Sandip Basak, **Kevin Felt**, Arvind Kumar, Steven Ramsey, Marta Filizola, Sudha Chakrapani. Structural insights into modulation of 5-HT_{3A}R Function. Presentation, Feb. 2021. Biophysical Society Annual Meeting. doi: 10.1016/j.bpj.2020.11.1223

D. Scholastic Performance

Case Western Reserve University (Cumulative GPA: 3.875)

YEAR	COURSE TITLE	GRADE
2021	Introduction to Data Science Systems	A
2020	Contemporary Approaches to Drug Discovery	B
2020	Physiology and Biophysics 1C	A
2020	Physiology and Biophysics 1B	A
2020	Physiology and Biophysics 1A	A
2020	Cell Signaling	A
2019	Biostatistics to Enhance Research Rigor and Reproducibility	A
2019	Molecular Biology 1	A
2019	Cell Biology 1	A
2019	Noel Prize Research in the Last 21 Years	A

University of Washington (Cumulative GPA: 3.29)

YEAR	COURSE TITLE	GRADE
2018	Medical Virology	B+
2018	Calculus 3 (Repeat)	B
2018	Data Programming in Python	B+
2018	Molecular Biology of Viruses	B+
2018	Bacterial Genetics	A
2018	Physical Chemistry for Biochemists 2	B
2017	Fundamentals of General Microbiology	C+
2017	Physical Chemistry for Biochemists 1	B
2017	Introduction to Structural Biology	A
2017	General Microbiology Lab	B+
2017	Calculus 3	C
2017	Honors Biochemistry 3	B
2017	Honors Biochemistry 2	A-
2017	Environmental Ethics	B+
2016	Biochemistry 1	B-
2016	Genomics and Proteomics	B+
2016	Introduction to African History, C. 1880-Present	B+

Skagit Valley College (Cumulative GPA: 3.87)

YEAR	COURSE TITLE	GRADE
2016	Organic Chemistry 3	A
2016	Organic Chemistry Lab 2	A
2016	Organismal Physiology	B
2016	Art History C. 1300 – 1850	A
2016	Organic Chemistry 2	A
2016	Organic Chemistry Lab 1	A-
2016	Cell/Molecular Biology	A
2016	Introduction to Ethics	A
2015	Ecology/Evolution	A
2015	Organic Chemistry 1	A-
2015	Introduction to Political Science	A
2015	General Chemistry w/ Lab 3	A
2015	General Chemistry w/ Lab 2	A
2015	Chinese 2	A
2015	Calculus 1	B
2015	Cultural Anthropology	B+
2014	General Chemistry w/ Lab 1	A
2014	Chinese 1	A
2014	Precalculus 2	A
2014	English Composition 2	A
2014	Precalculus 1	A
2014	General Psychology	A
2014	English Composition 1	A
2014	Intermediate Algebra	A
2014	Aerobic Weight Training	A
2013	Public Speaking	A-
2013	Beginning Algebra 2	A
2011	First Aid, Safety and CPR	A