BIOGRAPHICAL SKETCH

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NAME: Olga Boudker

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

POSITION TITLE: Professor / HHMI Investigator

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
Novosibirsk State University, Russia	B.Sc.	05/1990	Biochemistry
Weizmann Institute of Science, Israel	M.Sc.	02/1993	Biochemistry
The Johns Hopkins University, Baltimore, MD	Ph.D.	06/1999	Biophysics
Whitehead Institute/HHMI, Boston, MA	postdoctoral	01/2001	Biochemistry
Columbia University/HHMI, New York, NY	postdoctoral	09/2005	Structural Biology

A. Personal Statement

I have broadly trained in physical protein chemistry, membrane biochemistry, and structural biology. Since starting my research program at Weill Cornell Medicine (WCM), I have employed these skills to study the mechanism of membrane transporters by a combination of X-ray crystallography, cryo-EM, and a battery of biophysical approaches. Highly productive collaborations enhanced our studies. Over the years, my laboratory has made seminal contributions to the studies of biomedically important glutamate transporters. These transporters are critical for healthy glutamatergic neurotransmission that underlies learning and cognition. Our efforts on this project initially focused on an archaeal homolog, GltPh, that shares significant structural, functional, and mechanistic similarities with human transporters. We have delineated critical structural transitions defining the molecular mechanism of these transporters, uncovered the structural basis of transporter specificity, and established the link between its dynamics and function. We have developed structural and mechanistic studies of human homologs, termed excitatory amino acid transporters (EAATs). In our studies, we aim to understand the role of multi-scale protein dynamics in setting the functional properties of transporters, including transport rates, substrate and ion specificity, and allosteric regulation. To enable these studies, we develop new methods, including single-molecule FRET-based protein dynamics and activity assays and ^{19}F NMR. Our studies have revealed that archaeal and human homologs have complex kinetics dynamics and that these dynamics determine the rate of transport. These studies lay the foundation for understanding the transporters' kinetic mechanisms, which may open new avenues for therapies aiming to enhance glutamate transporter function in the brain.

Mentoring and the educational components of scientific activities are important to me. Together with David Eliezer, we launched a Molecular Biophysics Training Program. Started as a grassroots initiative to build a community for the students, postdocs, and faculty perusing structural biology and biophysics at WCM and the neighboring Sloan Kettering Institute, the program is now supported by an NIH T32 grant. The Program, largely run by students and postdocs with faculty oversight, organizes several events, including symposia, research-in-progress seminars, and invited speakers' seminars. Additionally, we developed a new Core Principles of Molecular Biophysics course as a flagship of the Training Program. Recently, together with Dr. Radda Rusinova, we launched Molecular Biophysics Core to open access to diverse biochemistry and biophysics equipment to the broader community at WCM. Building a strong, integrated, equitable community of scientists at all ranks pursuing biophysical and structural research is one of the main goals of my career.

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

HHMI Investigator 2015-2029

R01 NS111767-01A1 12/01/19 – 11/30/24
Mortenson and Boudker (co-PI)
Positive Allosteric Modulation of Glutamate Transporters: Biophysical and Structure-function Relationship Studies

R37 NS134865-01 09/2023 – 08/2030
Boudker (PI)
Ion coupling, permeation, and regulation in glutamate transporters

Citations most relevant to the current proposal

a. Akyuz, N., Altman, R., Blanchard, S.*, **Boudker, O**.* (2013) Transport dynamics in a glutamate transporter homologue. *Nature,* 502:114-8. PMID: 23792560
b. Akyuz, N., Georgieva, E. R., Zhou, Z., Altman, R. B., Cuendet, M. A., Khelashvili, G., Stolzenberg, S., Terry, D. S., Freed, J. H., Weinstein, H., **Boudker, O**.*, Blanchard, S.C.* (2015) Transport domain
c. Huysmans, G.H.M., Ciftci, D., Wang, X., Blanchard, S.C., & **Boudker, O**. (2021). The high-energy transition state of a membrane transporter. *EMBO J* 40:e105415. PMID: 33185289
d. Ciftci D, Martens C, Ghani VG, Blanchard SC, Politis A, Huysmans GHM*, **Boudker O.*** (2021) Linking function to global and local dynamics in an elevator-type transporter. *Proc Natl Acad Sci U S A*. 2021 PMID: 34873050

B. Positions, Scientific Appointments, and Honors

Positions

2021 – 2025	Interim Chair of the Department of Physiology and Biophysics, WCM
2020 – present	Co-director of Molecular Biophysics Training Program at Weill Cornell Graduate School
2015 – present	Professor/HHMI Investigator, Department of Physiology and Biophysics, WCM
2012 – 2015	Associate Professor, Department of Physiology and Biophysics, WCM
2005 – 2012	Assistant Professor, Department of Physiology and Biophysics, WCM

Scientific Appointments

2019 – 2021	Senior Editor, eLife
2019 – 2021	Chair of NIH BBM scientific review panel
2018 – present	Biophysical Journal: Member of the editorial board
2016 – 2021	Member (permanent) of NIH BBM scientific review panel (*ad hoc*, since 2014)
2016 – 2019	Board of Reviewing Editors, eLife
2014 – present	Journal of General Physiology: Member of the editorial board
2014 – 2017	Biophysical Society: Member of the Society Council
2011 – 2017	Biophysical Society: Officer of the Permeation and Transport Subgroup

Honors

2023	NINDS Javits Neuroscience Award from NINDS (R37)
2022	Elected member of the American Academy of Science
2021	Renewed HHMI Investigator
2017	Siegel Family Award for Outstanding Medical Research
2017	Cole Award from the Membrane Biophysics Subgroup of the Biophysical Society
2016	Michael and Kate Bárány Award for Young Investigators, Biophysical Society
2014	NINDS Javits Neuroscience Award from NINDS (R37)
2008 – 2010	Stanley Stahl Fellow of the American Heart Association

C. Contributions to Science

# represents equal contributions

* represents co-corresponding authors

1. As a postdoctoral fellow and a starting independent faculty, I made key contributions to the structural studies of a glutamate transporter homologue, GltPh. In the brain, glutamate transporters clear the neurotransmitter from the synaptic cleft to allow repeated neurotransmission rounds and prevent excitotoxicity. To maintain up to a million-fold concentration gradient of glutamate between extracellular space and cytoplasm, these transporters couple the uptake of each amino acid molecule to the symport of three sodium ions and a proton and counter-transport of one potassium ion. We determined a series of crystal structures of an archaeal homologue GltPh, which allowed us to propose a novel mechanism of transport, now termed the elevator mechanism, which since then has been found in several other families of transporters. Our structures further suggested how members of this family conduct anions, an important functional feature in some subtypes of mammalian glutamate transporters.
    a. Yernool, D.#, Boudker, O.#, Jin, Y. & Gouaux, E. (2004) Structure of a glutamate transporter homologue from Pyrococcus horikoshii. *Nature* 431, 811-818. PMID: 15483603
    b. Boudker, O.#, Ryan, R.#, Shimamoto, K, Yernool, D. Gouaux, E. (2007) Coupling substrate and ion binding to extracellular gate of sodium-dependent aspartate transporter. *Nature* 445: 387-93. PMID: 17230192
    c. Reyes, N., Ginter, C., Boudker, O. (2009) Transport mechanism of a bacterial homologue of glutamate transporters. *Nature* 462: 880-885. PMID: 19924125
    d. Verdon G., Boudker, O. (2012) Crystal structure of an asymmetric trimer of a bacterial glutamate transporter homolog. *Nature Structural and Molecular Biology* Feb 12;19(3):355-7. PMID: 22343718
2. We further elaborated on the mechanisms of substrate specificity, gating, and structural features that might control substrate affinity and selectivity in this family of transporters.
    a. Scopelliti AJ, Font J, Vandenberg RJ, Boudker O*, Ryan RM*. (2018) Structural characterisation reveals insights into substrate recognition by the glutamine transporter ASCT2/SLC1A5. *Nat Commun*. 9:38. PMID: 29295993.
    b. Wang X, Boudker O. (2020) Large domain movements through the lipid bilayer mediate substrate release and inhibition of glutamate transporters. *eLlife*. ;9:e58417. PMID: 33155546
    c. Oh, S., Boudker, O. (2018) Kinetic mechanism of coupled binding in sodium-aspartate symporter GltPh. *eLife*. 2018 Sep 26;7. pii: e37291. doi: 10.7554/eLife.37291. PubMed PMID: 30255846.
    d. Reddy KD, Ciftci D, Scopelliti AJ, Boudker O. (2022) The archaeal glutamate transporter homologue GltPh shows heterogeneous substrate binding. *J Gen Physiol*. 154:e202213131. PMID: 35452090
3. We deciphered the mechanism by which archaeal and human glutamate transporters harvest the energy of ionic gradients to drive concentrative uptake of their substrates.
    a. Reyes, N.*, Oh, S., Boudker, O.* (2013) Binding thermodynamics of a glutamate transporter homologue. *Nature Structural and Molecular Biology* 20, 634-40. PMID: 23563139
    b. Verdon, G.*, Oh, SeCheol, Serio, R., Boudker, O.* (2014) Coupled ion binding and structural transitions along the transport cycle of glutamate transporters. *eLife* May 19; 3:e02283. PMID: 24842876
    c. Qiu B, Matthies D, Fortea E, Yu Z, Boudker O. (2021) Cryo-EM structures of excitatory amino acid transporter 3 visualize coupled substrate, sodium, and proton binding and transport. *Sci Adv*. 2021 7:eabf5814PMID: 33658209
    d. Qiu, B.*, & Boudker, O.* (2023). Symport and antiport mechanisms of human glutamate transporters. *Nature communications*, *14*(1), 2579. PMID: 37142617
4. We developed an experimental platform to study the dynamics of archaeal transporters using single-molecule FRET TIRF microscopy, defined the nature of the rate-limiting high-energy translocation intermediate, and related the observed dynamics to transport activity rates.
    a. Akyuz, N., Altman, R., Blanchard, S.* Boudker, O.* (2013) Transport dynamics in a glutamate transporter homologue. *Nature,* 502: 114-8. PMID: 23792560
    b. Akyuz, N., Georgieva, E. R., Zhou, Z., Altman, R. B., Cuendet, M. A., Khelashvili, G., Stolzenberg, S., Terry, D. S., Freed, J. H., Weinstein, H., Boudker, O.*, Blanchard, S.C.* (2015) Transport domain unlocking sets the uptake rate of an aspartate transporter. *Nature*, 518: 68-73. PMID: 25652997
    c. Huysmans, G.H.M., Ciftci, D., Wang, X., Blanchard, S.C., & Boudker, O. (2021). The high-energy transition state of a membrane transporter. *EMBO J* 40:e105415. PMID: 33185289

d. Ciftci D, Martens C, Ghani VG, Blanchard SC, Politis A, Huysmans GHM*, **Boudker O.*** (2021) Linking function to global and local dynamics in an elevator-type transporter. *Proc Natl Acad Sci U S A*. 2021 PMID: 34873050

5. We expanded the methodological toolkit to study state distributions, dynamics, and activity of membrane transporters in collaborative studies. Most recently, we developed a novel ^{19}F NMR approach and a novel ^{19}F probe to study transporter dynamics, which revealed greater flexibility of the transporter than anticipated. We compared the populations measured spectroscopically in solution to those observed in cryo-EM.
    a. Georgieva, E., Borbat, P, Ginter, C., Freed, J.*, Boudker, O.* (2013) Conformational ensemble of the sodium-coupled aspartate transporter, *Nature Structural Molecular Biology* 20: 215-21. PMID: 23334289)
    b. Ciftci, D., Huysmans, G.H.M., Wang, X., He, C., Terry, D., Zhou, Z., Fitzgerald, G., Blanchard, S.C.*, Boudker, O.* (2020). Single-molecule transport kinetics of a glutamate transporter homolog shows static disorder. *Sci Adv*. 6(22):eaaz1949. doi: 10.1126/sciadv.aaz1949. PMID: 32523985
    c. Huang, Y., Wang, X., Lv, G., Razavi, A.M., Huysmans, G.H.M., Weinstein, H., Bracken, C., Eliezer, D.*, Boudker, O.* (2020) Use of paramagnetic ^{19}F NMR to monitor domain movement in a glutamate transporter homolog. *Nat Chem Biol*. 2020 16:1006-1012. PMID: 32514183
    d. Huang, Y.*, Reddy, K. D., Bracken, C., Qiu, B., Zhan, W., Eliezer, D.*, & Boudker, O.* (2023). Environmentally Ultrasensitive Fluorine Probe to Resolve Protein Conformational Ensembles by ^{19}F NMR and Cryo-EM. *Journal of the American Chemical Society*, *145*(15), 8583–8592. PMID: 37023263

Full list of published work:
https://www.ncbi.nlm.nih.gov/myncbi/18107EN35cAQF/bibliography/public/

BIOGRAPHICAL SKETCH

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NAME: Wu, Qianyi

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

POSITION TITLE: Postdoctoral Associate

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

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Start Date MM/YYYY	Completion Date MM/YYYY	FIELD OF STUDY
The University of Sydney (Australia)	B.Sc.	03/2013	11/2015	Pharmacology and Nutrition and Dietetics
The University of Sydney (Australia)	B.Sc. Hons.	02/2016	11/2016	Pharmacology
The University of Sydney (Australia)	Ph.D.	03/2017	03/2021	Electrophysiology and Pharmacology
Weill Cornell Medicine (NY, USA)	Postdoc	06/2021	Present	Physiology and Biophysics

A. Personal Statement

Trained as a pharmacologist and electrophysiologist, I was immersed in structural biology during my Ph.D. I was also involved part-time in a pharmaceutical company (MetabloQ, AU), where I was exposed to the field of membrane proteins, particularly transporters, in modern drug development. Brain glutamate transporters (termed excitatory amino acid transporters, EAATs), which clear most of the excitatory neurotransmitter glutamate from the synaptic cleft, have a coexisting chloride channel. My doctoral studies under the supervision of Prof Renae Ryan investigated how glutamate transport and chloride channel activity are functionally and structurally integrated, focusing on their physiological relevance under pathological conditions. I also developed a passion for studying the glutamatergic and other neurological networks in the central nervous system.

My broad interest in the molecular basis of neurotransmission led to my postdoctoral position at Weill Cornell Medicine under the supervision of Prof. Olga Boudker. As one of the leaders in the field, she has made seminal contributions to the studies of prokaryotic and eukaryotic glutamate transporters. During post-doctoral training, I extended my skill set to various biophysical approaches, including single-molecule FRET (smFRET) and CryoEM, which together allow me to untangle the mechanistic relation between conformational dynamics, atomic structures, transport kinetics, and pathology. I was awarded an American Heart Association Postdoctoral Fellowship and a Charles Revson Postdoctoral Fellowship to support the early stages of this work.

Teaching is an important component of my training as I aim to help educate a new generation of scientists during my academic career. I have developed my skills through teaching undergraduate classes during my Ph.D. and supervising rotations and summer students in the Boudker lab.

B. Positions, Scientific Appointments and Honors

Positions and Scientific Appointment

2021 – Present Postdoctoral Associate, Weill Cornell Medicine, NY, USA
2017 – 2021 Ph.D. candidate at the University of Sydney, Australia
2017 – 2019 Research Assistant, MetaBloQ Pharmaceuticals (the Centenary Institute), Australia

2018 – 2020 Casual Academic (laboratory demonstrator, marker, and teacher), Discipline of Pharmacology, The University of Sydney, Australia

2021 – 2024 Member, American Heart Association
2022 – Present Early Career Member, the Biophysical Society
2023 – Present Member, Society of General Physiologists
2022 – 2024 Reviewer, *Nature Communications*, *Nature Cardiovascular Research, Cell Reports, and Biophysical CoLab*
2017 – 2018 Member, Australia Society for Medical Research
2016 – 2021 Member, the Australian Society for Biophysics

Honors

2024 – 2026 Senior Fellow, Charles H. Revson Senior Fellowship in Biomedical Sciences Program, USA
2022 – 2023 Awardee, American Heart Association Postdoctoral Fellowship, USA (ranked 5.97%)
2024 Speaker, Membrane Transport Proteins Gordon Research Conference, USA
2023 Speaker, New York City Integrative Structural Biology Symposium, USA
2023 Speaker, the 28th International Workshop on "Single Molecule Spectroscopy and Super-resolution Microscopy," Germany
2021 Higher Degree by Research Newsletter Spotlight, Faculty of Medicine and Health, University of Sydney, Australia
2019 Poster Fellowship, the Cold Spring Harbor Laboratory Asia Conference, China
2018 Best Student Talk, the Asian Biophysics Symposium, Australia
2017 – 2019 Postgraduate Research Support Scheme, University of Sydney, Australia
2017 Speaker, Annual meeting of the Australian Society for Biophysics, Australia
2016 Speaker, Joint meeting of the Australian Physiology Society and the Australian Society for Biophysics, Australia
2016, 2018 Travel Awards, the Australian Society for Biophysics
2016 Honors Class I in Pharmacology, School of Medical Sciences, University of Sydney, Australia

Teaching

Weill Cornell Medical College of Cornell University, NY, USA
2021 - 2024 Trained four rotations and a summer graduate student
2025 Mentoring a starting PhD student

The University of Sydney, NSW, Australia
(course code: course name – class name (teaching hours / marking student assignments)
2018 BMED2403: Cardiovascular and Respiratory Systems – Respiratory pharmacology (8)
2018 BMED2405: Pharmacokinetics and Pharmacodynamics – Pharmacokinetics (14)
2019 PCOL3x12: Drug Design and Development (Advanced) – Molecular Modelling (marking)
2019 PCOL2605: Pharmacology for Pharmacy – EYE Practical (24)
2020 MEDS2002: Foundations of Pharmacology – Experiments on Bovine Trachea Exercises (marking)

C. Contributions to Science

1. My undergraduate research characterized transporters that utilize an elevator-like movement for substrate transport, including the bacterial glutamate transporter Glt_{Ph}, a human concentrative nucleoside transporter hCNT3, and a dicarboxylate transporter NaDC3 using disulfide crosslinks. I was awarded First-Class Honours with a thesis focusing on the latter two transporters. The work on Glt_{Ph} extended to

the study of chloride channel properties in the mammalian glutamate transporter (Excitatory Amino Acid Transporter 1, EAAT1), which became one of the main foci of my graduate career and led to three major publications. We described the structural determination of the chloride-conducting pathway (a), revealed a potential pathologic mechanism for the channelopathy episodic ataxia type 6 (EA6), which is a neurological disorder caused by mutations in the gene that encodes EAAT1 (b), and in collaboration with computational biologists, determined the mechanism of ion permeation through the chloride channel (c).

a. Chen I *, Pant S *, **Wu Q** *, Cater R, Sobti M, Vandenberg RJ, Stewart A, Tajkhorshid E **, Font J ** & Ryan RM **. (2021) Glutamate transporters have a chloride channel with two hydrophobic gates. *Nature*, 591(7849):327-331.

b. **Wu Q** *, Akhter A *, Pant S, Cho E, Zhu JX, Garner A, Ohyama T, Tajkhorshid E, van Meyel D ** & Ryan RM **. (2022) Ataxia-linked SLC1A3 mutations alter EAAT1 chloride channel activity and glial regulation of CNS function. *Journal of Clinical Investigation*, 132(7):e154891.

c. Pant S, **Wu Q**, Ryan RM **, & Tajkhorshid E **. (2022) Microscopic Characterization of the Chloride Permeation Pathway in the Human Excitatory Amino Acid Transporter 1 (EAAT1). *ACS Chemical Neuroscience*, 13(6), 776–785.

* indicates co-first authors and ** indicates co-corresponding authors

2. I co-wrote two reviews describing the structural interplay between glutamate transport and chloride channel activity in glutamate transporters (a) and a general review of the solute carrier family SLC1A and its role in human physiology and pathophysiology (b).

   a. Chen I, **Wu Q**, Font J, & Ryan RM. (2022) The twisting elevator mechanism of glutamate transporters reveals the structural basis for the dual transport-channel functions. *Current Opinion in Structural Biology,* 75, 102405.

   b. Freidman N, Chen I, **Wu Q,** Briot C, Holst J, Font J, Vandenberg RJ, Ryan RM. (2019) Amino Acid Transporters and Exchangers from the SLC1A Family: Structure, Mechanism and Roles in Physiology and Cancer. *Neurochemical Research*, 45: 1268-1286.

3. I collaborated with insect physiologists to functionally characterize and determine the transport mechanism of an insect version of EAAT. We then re-engineered the transporter to closely resemble human homologs. This work helps us better understand what is critical for the ion coupling of the glutamate transporters. The manuscript describing these findings is in the final stages of preparation and is expected to be submitted in 2025.

4. Currently, I employ smFRET to follow the functional dynamics of EAAT1 directly. To my knowledge, no such measurements have been previously performed on any mammalian membrane transporter, and this reflects numerous methodological challenges I had to overcome. Dynamic measurements on single transporters with sub-second temporal resolution reveal an unexpected kinetic complexity, showing that transporters switch between periods of high activity and quiescence. Combined with CryoEM, these experiments are leading me toward understanding the structural underpinnings of the high- and low-activity transporter states. These striking findings open novel possibilities in developing long-sought transporter activators with broad therapeutic potential. This work has been presented at both local and international conferences, and a manuscript detailing it is in production.

BIOGRAPHICAL SKETCH

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NAME: RUPASREE BRAHMA

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

POSITION TITLE: Postdoctoral Associate in the Department of Physiology and Biophysics, Weill Cornell Medicine

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
Asutosh College, University of Calcutta, Kolkata, India	B.Sc.	05/2015	Microbiology
Ballygunge Science College, University of Calcutta, Kolkata, India	M.Sc.	07/2017	Biochemistry
Crystallography and Molecular Biology Division, Saha Institute of Nuclear Physics, Homi Bhabha National Institute, Kolkata, India	Ph.D.	09/2024	Life Sciences

A. Personal Statement

I am currently a postdoctoral researcher in Dr. Olga Boudker's laboratory at Weill Cornell Medical College. My primary research interest lies in elucidating the structural dynamics landscape of membrane proteins in their native lipid environments, with a particular focus on their roles in human health and disease. In line with this interest, I am investigating the structure and conformational dynamics of the glutamate transporter GltPh, a prokaryotic homolog of human excitatory amino acid transporter (EAAT) — using cryo-electron microscopy (cryo-EM) and complementary biophysical techniques. My aim is to understand how physiological lipid membranes modulate the conformational substates and transport mechanism of GltPh. Previously, I completed my Ph.D. in Life Sciences at the Saha Institute of Nuclear Physics, where I studied the gating-related structural dynamics of MgtE magnesium channels. I developed and applied advanced spectroscopic approaches to characterize membrane protein conformation in micelles and membrane mimetics, and successfully purified and characterized a novel MgtE homolog. These studies highlighted the importance of lipid-protein interactions in regulating transporter function and laid the conceptual and technical foundation for my current work. I have extensive experience in membrane protein expression, purification, reconstitution into liposomes and nanodiscs, a range of biophysical assays, and cryo-EM sample preparation and data collection. My combined expertise in transporter biochemistry, structural biology, and membrane biophysics positions me to make significant contributions to the mechanistic understanding of membrane protein function in physiologically relevant contexts.

B. Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments

- 2025–Present: Postdoctoral Associate, Boudker Lab, Weill Cornell Medical College, USA
- 2018–2024: Graduate Student, Saha Institute of Nuclear Physics, India

Honors and Awards

- Travel Award, 67th Biophysical Society Meeting, 2023, San Diego, USA
- Best Poster Award, 1st HBNI Life Sciences Theme Meeting, 2022
- Senior Research Fellowship, Department of Atomic Energy (DAE), India (2020–2024)
- Junior Research Fellowship, DAE, India (2018–2020)
- Qualified JGEEBILS for Ph.D. (2018) and M.Sc.–Ph.D. Integrated Program (2015)

C. Contributions to Science

1. *Functional characterization and gating related structural dynamics of a novel MgtE homolog from Bacillus firmus ($MgtE_{BF}$)*

I characterized a novel homolog of the MgtE magnesium channel from *Bacillus firmus* ($MgtE_{BF}$), which notably lacks the canonical Mg^{2+}-sensing N-terminal domain. I successfully expressed and purified this channel to homogeneity, establishing it as only the second MgtE homolog ever purified. Using microscale thermophoresis (MST) and fluorescence-based transport assays, I demonstrated that $MgtE_{BF}$ retains the ability to bind Mg^{2+} and ATP and mediates Mg^{2+} transport similarly to *T. thermophilus* MgtE, indicating that the N-domain is not essential for channel function. Furthermore, I explored its conformational dynamics in membrane-mimetic environments using intrinsic tryptophan fluorescence. Sophisticated fluorescence techniques—including red edge excitation shift (REES), anisotropy, quenching, and maximum entropy method (MEM)-based lifetime distribution—revealed distinct structural organization and dynamic behavior in liposomes compared to detergent micelles. These findings provide important insight into lipid-dependent gating mechanisms of MgtE channels and the evolutionary flexibility of Mg^{2+} transporters.

a. **Brahma, R.**, and Raghuraman, H. (2024) Characterization of a novel MgtE homolog and its structural dynamics in membrane mimetics. *Biophys. J.* 1968-1983.

b. **Brahma, R.**, Das, A., Raghuraman, H. (2022) Site-directed fluorescence approaches to monitor the structural dynamics of proteins using intrinsic Trp and labeled with extrinsic fluorophores. *STAR Protoc*. 3: 101200.

c. **Brahma, R.**, and Raghuraman, H. (2022) Measuring membrane penetration depth and conformational changes in membrane peptide and proteins. *J. Membr. Biol*. 255: 469-483

d. **Brahma, R.**, and Raghuraman, H. (2021) Novel insights in linking solvent relaxation dynamics and protein conformations utilizing red edge excitation shift approach. *Emerg. Top. Life Sci*. 5: 89-101.

2. *Gating-related structural dynamics of the MgtE magnesium channel in membrane-mimetics utilizing site-directed tryptophan fluorescence*

To better understand how native lipid environments regulate ion channel behavior, I investigated the gating-related structural dynamics of the Mg^{2+}-selective channel MgtE in both detergent micelles and membrane-mimetic systems. Using a series of site-directed single-tryptophan mutants and advanced fluorescence techniques, I showed that Mg^{2+}-induced gating likely involves a ‘conformational wave’ from

the cytosolic sensor domain to the transmembrane region. While MgtE responds to Mg^{2+} in both environments, lipid bilayers significantly altered its conformational heterogeneity, hydration dynamics, and organization compared to micelles. These results demonstrate that physiologically relevant membrane composition plays a central role in modulating MgtE gating and provide a broader framework for understanding lipid-dependent regulation of membrane transport proteins.

a. **Brahma, R.**, and Raghuraman, H. (2022) Cost-effective purification of membrane proteins using a dual-detergent strategy. *Curr. Protoc*. 2: e452.
b. Chatterjee, S., **Brahma, R.**, and Raghuraman, H. (2021) Gating-related structural dynamics of the MgtE magnesium channel in membrane-mimetics utilizing site-directed tryptophan fluorescence. *J. Mol. Biol*. 4: 166691.

BIOGRAPHICAL SKETCH

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NAME: Earsley, Alexander Sebastian

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

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 *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of California, Berkeley	BS	05/2021	Chemical Biology
Weill Cornell Medical School	PhD	05/2028 (Expected)	Biochemistry

A. Personal Statement

I am a third-year PhD candidate in the Biochemistry, Cellular Biology, and Molecular Biology (BCMB) program at Weill Cornell Medical College, where my research centers on the structure and biophysical characterization of membrane transporter proteins. My scientific training has been highly interdisciplinary, spanning several disciplines including synthetic biology, RNA vaccine development, and membrane protein biophysics. This diverse background has shaped me into a versatile scientist capable of integrating approaches across molecular biology, chemistry, and structural biology. My thesis work focuses on studying the mechanisms of small molecule modulators through structural determination using cryo-electron microscopy (cryo-EM). I have extensive experience with membrane protein expression, purification, and functional reconstitution, and I routinely employ advanced biophysical methods to probe protein-ligand interactions. Through these efforts, I have successfully resolved high-resolution structures of modular-bound transporter complexes to study targetable regions in the protein and their mechanism of action. This work has been carried out in close collaboration with other institutes and has involved mentoring new users and colleagues in cryo-EM grid preparation, screening, and data analysis. These experiences have strengthened my technical expertise while also fostering skills in scientific communication and peer training. Our findings have led to the submission of a manuscript and have laid the groundwork for multiple ongoing projects aimed at dissecting the conformational dynamics and pharmacological potential of transporter proteins. As I continue this research, I remain committed to understanding membrane protein function at the molecular level and contributing to the advancement of structure-guided drug discovery.

I was previously funded by a fellowship through the College of Chemistry at the University of California, Berkeley, which provided me early training in synthetic biology using CRISPR/Cas9 for fatty acid production in *E. coli*. Currently, I am funded through the NIH T32 Molecular Biophysics Training Program (07/1/2024 - Present) where I am screening drug candidates and using cryo-EM to structurally determine the mechanism of action on membrane proteins.

B. Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments

2025 - Present PhD Candidate, BCMB Program, Weill Cornell Medicine
2025 Teaching Assistant, BCMB Program, Weill Cornell Medicine

2024 – Present	Trainee, Molecular Biophysics Training Program, Weill Cornell Medicine
2023 – Present	Co-coordinator, BCMB Student Seminar Series, Weill Cornell Medicine
2023 – 2025	Graduate Student, BCMB Program, Weill Cornell Medicine
2022 – 2023	Senior Associate Scientist, Pfizer
2021 – 2023	Lead Organizer, RNA Journal Club, Pfizer
2021 – 2022	Associate Scientist, Pfizer
2019 – 2021	Research Associate, SynBio3, Joint BioEnergy Institute
2019 – 2020	Lead Student Instructor, Organic Chemistry I, University of California, Berkeley
2017 – Present	Member, American Chemical Society, University of California, Berkeley

Honors

2023	Award for Most Promising Emerging Scientist, Pfizer
2022	Best Poster Presentation for Young Scientists, Pfizer
2020	Top Undergraduate Teacher Award, University of California, Berkeley
2019	Award for Best Designed Poster, Joint BioEnergy Institute
2019	College of Chemistry Summer Student Award, University of California, Berkeley

C. Contributions to Science

1. My research career began with a focus on sustainable energy production through microbial bioengineering. While biofuels represent a promising renewable energy alternative, existing production platforms often suffer from limited scalability, low yield, and high production costs. To address these challenges, I worked on a project aimed at enhancing fatty acid biosynthesis in *E. coli* by introducing a heterologous metabolic pathway from yeast capable of producing long-chain fatty acid derivatives suitable for conversion into biofuels. This work demonstrated the feasibility of microbial scaffold-based platforms for renewable biofuel production and contributed to broader efforts in engineering microorganisms for sustainable chemical synthesis.

a. **Earsley, A.**, Goyal, G., Hillson, N. (2019). *Genetic Engineering in E. coli for Enhanced Fatty Acid Production* [Poster Presentation]. Joint BioEnergy Institute, Emeryville, CA, United States.

2. The COVID-19 pandemic rapidly accelerated advances in mRNA vaccine technologies. During this time, I joined the research and development team at Pfizer, where I contributed to several key initiatives aimed at improving the fidelity, efficiency, and scalability of mRNA-based vaccine platforms. One of my primary roles was independently developing a software script to assess mRNA purity prior to downstream purification and formulation. This system linked liquid handling automation with data-processing algorithms to reduce user bias and streamline quality control workflows. In parallel, I assisted in the development of in-house transcription and translation assays designed to rapidly evaluate the expression efficiency of mRNA vaccine candidates. These assays enabled us to identify the effects of specific untranslated regions (UTRs), coding sequence elements, and overall mRNA integrity on translational performance. Notably, we were able to demonstrate how variations in mRNA quality and regulatory architecture directly impact protein output. Finally, I lead the design and synthesis of a reporter-based mRNA construct to systematically assess the relationship between construct length and mRNA quality from our in-house vaccine development platform. The results of this project led to optimization of both reagents and experimental conditions that contributed to the establishment of a universal platform for rapid mRNA vaccine development across diverse antigen targets.

a. **Earsley, A.**, Jhun, H. (2021). *Standardizing Analysis of Capillary Electrophoresis using Automated Peak Detection* [Poster Presentation]. Pfizer, Pearl River, NY, United States.
b. **Earsley, A.**, Liu, Q., Jhun, H. (2022). *In-vitro Transcription-Translation Assays to Study mRNA Regulatory Elements on Expression* [Poster Presentation]. Pfizer, Pearl River, NY, United States.
c. **Earsley, A.**, Liu, Q., Jhun, H. (2023). *Design and Synthesis of a Giant Reporter Construct for Vaccine Platform Optimization* [Poster Presentation]. Pfizer, Pearl River, NY, United States.

3. As a PhD candidate at Weill Cornell Graduate School, I joined the laboratory of Dr. Olga Boudker, where my research focuses on the conformational dynamics and structural characterization of membrane transporters with the goal of informing small molecule drug development. I have conducted experiments to screen and characterize small molecule modulators in collaboration with partnering institutions. Using purified transporter

proteins, we performed structure-activity relationship (SAR) profiling to evaluate compound binding and functional modulation. We also used cryo-EM for data collection and structural analysis of transporter-ligand complexes to identify an allosteric binding pocket that is pharmacologically relevant. The structural data not only supported rational drug design efforts but also contributed to a deeper understanding of how transporter dynamics can be exploited for therapeutic intervention. These findings have culminated into a manuscript currently under peer review and have laid the groundwork for continued optimization of lead compounds using a structure-guided design approach.

a. **Earsley, A.**, Qiu, B., Boudker, O. (2024). *Identifying Small Molecule Inhibitors and New Allosteric Sites in EAAT3* [Poster Presentation]. BCMB Student Retreat, Weill Cornell Medical School, New York, NY, United States.

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
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NAME: Vishnu Ganesh Ghani

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

POSITION TITLE: PhD Student

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
SUNY: Stony Brook University, Stony Brook NY	BS	05/2016	Mathematics
SUNY: Stony Brook University, Stony Brook, NY	BS	05/2016	Physics
Weill Cornell Graduate School of Medical Sciences (WCGS), New York, NY	PhD	05/2024	Molecular Biophysics

A. Personal Statement

My career path into biological research was very unexpected and not remotely on my radar since my undergraduate studies. No one in my family, or my friends growing up, were involved with science or had any idea of what the academia realm was beyond an undergraduate degree. Even throughout undergraduate, I didn't fully understand it, but wanted to somehow get involved. My background and training from undergraduate studies wasn't directly tied to any of the work I am doing now. I gravitated towards studying theoretical physics and mathematics, to understand systems of all sizes and to describe them, respectively. With this mindset, I like to think of science like I picture other tasks or problems that occur in life, as a jigsaw puzzle. I try to connect the pieces together and create a complete picture and solution. With this mindset, I was ready to take on any challenge or system to further my career, whether it be in research or a traditional industry job.

At Stony Brook University, I took a research opportunity in Dr. Eden Figueroa's Quantum Technology Lab. I, along with two colleagues, was tasked with implementing a rubidium optical cavity into a system to increase the photon-photon interactions within the rubidium cell. I didn't have experience with laser-based systems beyond a textbook but was motivated to search for a solution. My team and I brainstormed ideas to identify and correct the causes of instability. While each of us were given training in free-space optical alignment techniques, I was given the responsibility of working through the ray tracing schematic and thermal stability of the cell itself. Working through optimizing the theoretical interactions of the laser line within the cell and effective ways to stabilize the temperature were both rigorous and rewarding. It closed the gap in narrowing the unknown factors that were troubling the system. This experience was my first exposure to a research lab and saw how science is formulated and conducted outside of a traditional classroom. I absolutely enjoyed the hands-on free-space optical alignment of the project. I wanted to take advantage of my optical skills and training and branch out into a different field.

After graduating, I accepted an offer as a research assistant in Dr. Tarun Kapoor's Lab at Rockefeller University to build a state-of-the-art super resolution optical system, the Lattice Light Sheet Microscope (LLSM). This system has allowed me to both master my optical alignment skills and gain an expertise in electronics and software control of the many different components. Microscopy was an application of optics that I hadn't been exposed to, but quickly grabbed my attention. Initially, I came to Rockefeller University to focus on working on the LLSM. However, I became absorbed in the wonderful field of fluorescent imaging. I

developed a passion for the art of imaging and image acquisition from using Total Internal Reflection Microscopy, Spinning Disk- Confocal Microscopy, and LLS Microscopy. I was fascinated with the basic principles of fluorescence, the methodology used to tag fluorescent markers on proteins, and the datasets that we were collecting. Under the mentorship and guidance of the Kapoor lab members, I kept learning more about the organization of the mitotic spindle. The lab's collection of these datasets involved 4D datasets, which caused a problem of how to process and go about the characterization of this densely defined structure. Being involved with finding a solution on how to approach this was an excellent opportunity to improve my understanding of image processing and programming skills.

I wanted to pursue a PhD to further improve my diverse skillset to expand my knowledge to other applications and fields in the biological world. I had an unnerving fear that I would not be a desirable candidate to programs due to my lack of biology/chemistry background on paper. I had acquired hard-earned lab skills, independently read textbooks, and informal training of how certain molecular and cellular processes worked. Despite these experiences, I understood that there was a gap in my knowledge of even elementary material. This was the reason why I was enthusiastic about obtaining higher education. I wanted to be immersed in an environment with multiple outlets that exposed me to critical thinking of even the fundamental concepts themselves. I wanted to use my diverse skillset and mindset as a different perspective compared to those with traditional training. With the encouragement and support from the lab, I successfully applied to PhD programs and accepted an admission offer at Weill Cornell Graduate School.

My journey into the research field has provided me with experiences, skills, and a refreshing determination of pursuing higher level education and responsibility. It also inspires me to continue to mentor and teach others beyond math and physics concepts, and encourage people who also do not come from biological (or any scientific) background to somehow get involved.

B. Positions, Scientific Appointments and Honors

POSITIONS

08/2019- PRESENT	Graduate Researcher; Mentor: Dr. Olga Boudker; Weill Cornell Medicine Graduate School; Department of Physiology, Biophysics & Systems Biology
09/2016- 08/2019	Research Assistant/Technician; Mentor: Dr. Tarun M. Kapoor; Rockefeller University; Biochemistry, Biophysics, Chemical Biology, and Structural Biology/Cancer Biology/Cell Biology
08/2012- 05/2016	Research Volunteer; Mentor: Dr. Eden Figueroa; SUNY: Stony Brook University; Department of Physics & Astronomy

HONORS, AWARDS, & SCHOLARSHIPS

07/2021-06/2022	WCM Molecular Biophysics Training Program (MBTP) T32 Training Grant GRANT No.: 5T32GM132081-02
02/2015-05/2016, 08/2012-12/2013	Stony Brook University Dean's List Award
08/2012-05/2016	Valedictorian Scholarship
08/2014-05/2016	NYS School Academic Excellence Scholarship
08/2012-05/2014	NY State Scholarship

C. Contributions to Science
Graduate Rotation Research

Since starting my time at Weill Cornell Medicine, I rotated in labs with different efforts for approaching and improving limitations of imaging in biological questions. I rotated in Dr. Olga Boudker's transporter protein dynamics lab and learned of biochemical techniques that can be used to overcome traditional light microscopy limitations. The lab has extensively studied Glt_{ph}, an archaeal glutamate transporter, as a toy model to elucidate function and conformational dynamics of the mammalian glutamate transporters such as Excitatory Amino Acid Transporters (EAATs). Through previous studies, these transporters have been observed to have an elevator-type mechanism of each of their trimeric transport domains to translocate target substrate across membrane bilayers. A recent work that was published was linking local and global conformational dynamics of wildtype Glt_{ph} and three mutated constructs to their substrate uptake activity. These mutations either: i) decreased substrate affinity, ii) increased the local conformationally dynamics, iii) and were combined to have both effects. During my rotation, I collected single molecule Foster Energy Resonance Transfer (smFRET) data that characterize different uptake rates of wildtype Glt_{ph} with these mutations. We showed that there are heterogenous transporter activity rates (>~10^2 s^{-1} apart) of many individual transporters in wildtype Glt_{ph}, while each of the described mutations coalesces the heterogeneity.

Publications
Ciftci, D.*, Martens, C.*, **Ghani, V. G.**, Blanchard, S. C., Politis, A., Huysmans, G. H. M., & Boudker, O. (2021). Linking function to global and local dynamics in an elevator-type transporter. Proceedings of the National Academy of Sciences of the United States of America, 118(49).

*D.C. and C.M. contributed equally to this work

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: **Poonam Dhankhar**

eRA COMMONS USER NAME (credential, e.g., agency login): pod4001

POSITION TITLE: Postdoctoral Scientist 03

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

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Start Date MM/YYYY	Completion Date MM/YYYY	FIELD OF STUDY
1. Indian Institute of Technology Roorkee, Uttarakhand, India	PhD	07/2015	03/2021	Structural Biology
2. Kurukshetra University, Kurukshetra, Haryana, India	MSc	06/2011	05/2013	Biochemistry
3. Kurukshetra University, Kurukshetra, Haryana, India	BSc	06/2008	04/2011	Biotechnology, Zoology, Chemistry

A. Personal Statement

My academic training has provided me with a strong background in multiple biological disciplines, including molecular biology, microbiology, biochemistry, and structural biology. My research career has been driven by a strong foundation, utilizing a combination of experimental and computational approaches to address key biological questions. As an early-stage research trainer, I worked on the proline-specific peptidase gene from *Lactobacillus rhamnosus* GG, and I gained hands-on expertise in gene cloning, bacterial transformation, recombinant protein expression, and solubility optimization. As a graduate student with Dr. Pravindra Kumar, my research focused on elucidating the structure-function relationship of the dye-decolorizing peroxidase (DyP) from *Bacillus subtilis* (*Bs*DyP), a type A bacterial enzyme with broad substrate specificity. Through integrative biochemical assays, X-ray crystallography, site-directed mutagenesis, and advanced computational techniques, three distinct substrate-binding sites have been identified in *Bs*DyP, which were published in a peer-reviewed journal as the first author. This work advanced fundamental knowledge of bacterial DyPs and holds promise for engineering these enzymes for industrial and environmental applications. My graduate studies provided me with extensive knowledge of molecular cloning, protein biochemistry, crystallization, and structural analysis of cytosolic proteins, as well as computational modeling, which helped me build a strong foundation in structural biology. Additionally, I collaborated on projects that identified novel inhibitors against pathogens, such as human coronavirus and *Staphylococcus aureus*, thereby gaining extensive expertise in translational computational biology.

As a postdoctoral fellow, I have expanded my focus to membrane protein biochemistry, applying detergent-free solubilization methods using Native Cell Membrane Nanoparticles (NCMNs), which preserve native lipid environments and improve protein stability. I also utilized lipidic cubic phase crystallization to ascertain the high-resolution structures of membrane proteins. Currently in my second postdoctoral position, my research focuses on the structural and functional characterization of OCA2, a key membrane protein involved in melanin biosynthesis and ion transport within melanosomes. This work integrates cryo-EM and functional liposome assays to unravel mechanisms fundamental to pigmentation biology.

This comprehensive training has equipped me with a unique combination of expertise in molecular cloning, structural biology, computational modeling, and membrane protein biochemistry. I am well-prepared to contribute effectively to interdisciplinary projects addressing fundamental questions in enzyme mechanisms, membrane protein function, and drug discovery.

B. Positions, Scientific Appointments and Honors

Positions, Scientific Appointments

04/2023 – present	Postdoctoral Scientist 03, Department of Physilogy and Biophysics, Weill Cornell Medicine, New York, USA
06/2021 – 04/2023	Postdoctoral Research, Medicinal Chemistry, Virginia Commonwealth University, Richmond, USA
03/2021 –06/2021	Senior research fellow, Indian Institute of Technology Roorkee, India
08/2014 –01/2015	Junior research fellow, National Dairy Research Institute, Karnal, India
01/2014 –05/2014	Intern research, National Dairy Research Institute, Karnal, India

Honors

Dec 2013	Qualified Joint CSIR-UGC National Eligibility Test (NET) with AIR 53
Nov. 12-13, 2010	District-level Science Exhibition in Zoology, Hisar (2nd position)

C. Contributions to Science

1. **Early Career:**

During my early research training, I successfully cloned and expressed the *pepQ* gene from *Lactobacillus rhamnosus GG*, which encodes a proline-specific peptidase. This work provided me with practical expertise in gene cloning, bacterial transformation, recombinant protein production, and solubility optimization, all of which are essential skills that aided.

2. **Graduate Career:**

A. My PhD research focused on determining the structure and function of the dye-decolorizing peroxidase (DyP) from *Bacillus subtilis* (*Bs*DyP), which is a type A bacterial enzyme. DyPs belong to a unique heme peroxidase family due to their biotechnological potential to oxidize and degrade synthetic dyes, lignin, and other aromatic compounds, including antibiotics and pharmaceutical compounds, which are used on a large scale globally. My research resulted in a deeper understanding of the molecular structure of *Bs*DyP, which can oxidize a broad range of dyes. The crystal structures of *Bs*DyP revealed three key substrate-binding sites—δ-edge, γ-edge, and a surface-exposed site—and each site contributes to its substrate versatility. Using a combination of biochemical assays, X-ray crystallography, and computational techniques—including molecular docking, molecular dynamics (MD) simulations, and free energy calculations (MM/PBSA and MM/GBSA)—the results demonstrated that *Bs*DyP forms stable protein-ligand complexes, thereby supporting its role in oxidative biocatalysis. Site-directed mutagenesis further validated the functional importance of these binding regions. Together, these findings advanced our understanding of substrate recognition and catalysis in bacterial DyPs and might be very useful in the engineering of these enzymes for industrial or environmental applications.

a. **Poonam Dhankhar**, Vikram Dalal, Ashwani Kumar Sharma, and Pravindra Kumar* (2022). Structural insights at acidic pH of Dye-decolorizing peroxidase from *Bacillus subtilis*. *Proteins: Structure, Function, and Bioinformatics,* 91(4), pp. 508-517. 10.1002/PROT.26444.
b. **Poonam Dhankhar**, Vikram Dalal, Vishakha Singh, Ashwani Kumar Sharma, and Pravindra Kumar (2021) "Structure of dye-decolorizing peroxidase from Bacillus subtilis in complex with veratryl alcohol." *International Journal of Biological Macromolecules,* 193: pp. 601-608. 10.1016/J.IJBIOMAC.2021.10.100.
c. **Poonam Dhankhar**, Vikram Dalal, Jai Krishna Mahto, Bhola Ram Gurjar, Shailly Tomar, Ashwani Kumar Sharma, and Pravindra Kumar* (2020). "Characterization of dye-decolorizing peroxidase from *Bacillus subtilis*. *Archives of Biochemistry and Biophysics*. 693:108590. 10.1016/j.abb.2020.108590.

B. Apart from my regular graduate work, my other collaborative projects focused on screening and identifying potent novel compounds against human coronavirus, *Staphylococcus aureus*, and *Klebsiella pneumonia*. The application of extensive structural bioinformatics techniques has led to numerous publications in reputable journals, contributing to the early-stage development of anti-infective agents and enriching my experience in translational computational biology.

a. Vishakha Singh[#], **Poonam Dhankhar**[#], Vikram Dalal[#], Shailly Tomar, Dasantila Golemi-Kotra, Pravindra Kumar (2022). Drug repurposing approach to combat Staphylococcus aureus: biomolecular and binding interactions study. *ACS Omega.* 7(43), pp. 38448-38458 ([#]Contributed Equally) 10.1021/ACSOMEGA.2C03671.
b. Vishakha Singh[#], **Poonam Dhankhar**[#], Vikram Dalal[#], and Pravindra Kumar* (2022). *In-silico* Functional and Structural annotation of Hypothetical Protein from Klebsiella pneumonia: a potential drug target. *Journal of Molecular Graphics and Modelling*. 116: 108262 ([#]Contributed Equally) 10.1016/j.jmgm.2022.108262.
c. **Poonam Dhankhar**[#], Vikram Dalal[#], Dasantila Golemi-Kotra, and Pravindra Kumar* (2020). "In-silico approach to identify novel potent inhibitors against GraR of *S. aureus"*. *Frontiers in Bioscience*. 25(7):pp. 1337-1360. ([#] Contributed Equally) https://doi.org/10.2741/4859.
d. **Poonam Dhankhar**[#], Vikram Dalal[#], Vishakha Singh[#], Shailly Tomar, and Pravindra Kumar* (2020). "Computational guided identification of novel potent inhibitors of N-terminal domain of nucleocapsid protein of severe acute respiratory syndrome coronavirus-2". *Journal of Biomolecular Structure and Dynamics.* 40(9), pp. 4084-4099. ([#] Contributed Equally) 10.1080/07391102.2020.1852968.

3. Postdoctoral Career:

My work as a first postdoctoral fellow focused on the structural and functional characterization of membrane proteins using the Native Cell Membrane Nanoparticles (NCMNs) system, a detergent-free extraction method. This system is built based on the previously established Styrene Maleic Acid Lipid Particles (SMALP) method, which has its limitations. It employs novel membrane-active polymers to isolate membrane proteins while preserving their natural lipid environment. The NCMN platform enhances the stability and functionality of membrane proteins, enabling precise structural studies and the development of robust biochemical and biophysical assays.
In a related project, I applied the lipidic cubic phase (LCP) crystallization method to determine the high-resolution structure of a membrane protein. This approach mimics the natural lipidic environment, which supports the formation of high-quality crystals. These projects provided me with a lot of experience in membrane protein biochemistry, polymer-based solubilization strategies, and structure-guided methods for protein analysis.
My current 2nd postdoctoral work focuses on the structural and functional characterization of the OCA2 membrane protein, which is crucial for melanin biosynthesis and ion transport within melanosomes. I determined the cryo-EM structure of this protein at high resolution in both detergent micelles and lipid nanodiscs, and I am integrating electrophysiological and fluorescence-based assays to investigate its mechanistic role.

a. **Poonam Dhankhar**, Thi Kim Hoang Trinh, Youzhong Guo*, and Weihua Qiu* (2023). "Characterization of Ca^{2+}-ATPase with native cell membrane nanoparticles system". *Biochimica et Biophysica Acta (BBA)-Biomembranes*, *1865*(5), 184143. 10.1016/j.bbamem.2023.184143

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