Shourya Sonkar Roy Burman

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Professional Experience

2019-Present Research Fellow in Cancer Biology
Dana-Farber Cancer Institute, Boston, MD
&
Biological Chemistry & Molecular Pharmacology
Harvard Medical School, Boston, MD

2018-2019 Postdoctoral Fellow in Chemical & Biomolecular engineering
Johns Hopkins University, Baltimore, MD

Education

2012–2018 Ph.D. in Chemical & Biomolecular engineering
Johns Hopkins University, Baltimore, MD

2008–2012 B. Tech. in Biological Sciences & Bioengineering
Indian Institute of Technology Kanpur, India

Awards & Honors

2020–2023 Cancer Research Institute Irvington Postdoctoral Fellowship
2011, 2009 Certificate of Merit for Academic Excellence at IIT Kanpur
2010–2011 Mona and Paramjit Singh Scholarship
2008–2010 Baljit and Nirmal Dhindsa Scholarship
2008–2009 Nitish Thakor Scholarship

Research Experience

PRESENT Research Fellow at Dana-Farber Cancer Institute
Advisor: *Dr. Eric S. Fischer, Department of Cancer Biology*

- Designing synthetic tag proteins that get selectively degraded or stabilized with small molecule drugs.
- Developing a computational pipeline for rational design of hetero-bifunctional compounds called proteolysis inducing chimeras (PROTACs) using RosettaDock.
- Predicted that the positioning of ubiquitination sites on a protein is the single most important intrinsic feature that determines its tractability to targeted degradation approaches in collaboration with *Dr. X. Shirley Liu*.

2013-2018 Graduate Research Assistant at Johns Hopkins University
Thesis: *Modeling Interactions of Flexible Proteins*
Advisor: *Dr. Jeffrey J. Gray, Department of Chemical & Biomolecular Engineering*

- Developed RosettaDock 4.0, a computational tool that efficiently predicts the structure of protein complexes. Tested this tool on a benchmark of flexible proteins to verify a high accuracy on proteins with difficult-to-predict conformational changes.

- Developed Rosetta SymDock2 that enhanced global docking performance of high-order symmetric homomeric complexes by five-fold.
- Led the Gray Lab team in the blind prediction experiment, Critical Assessment of PRediction of Interactions (CAPRI) to predict structures of protein, peptide and oligosaccharide in complex in blind challenges for two years.
- Modeled putative interactions of a drug to demonstrate that it can simultaneously inhibit histone deacetylase and histone demethylase in the CoREST complex in collaboration with *Dr. Philip Cole*.

Publications

1. Zou C, Yoon H, Park PMC, Tsai JM, Li Y-D, **Roy Burman SS**, Nowak RP, Fischer ES, Ebert BL & Slabicki M (2023) "The Human E3 ligase RNF185 is a regulator of the SARS-CoV-2 envelope protein." *Under Review*.

2. Li J*, Wang L*, Hahn Q, Nowak R, Viennet T, Orellana E, **Roy Burman SS**, Yue H, Hunkeler M, Fontana P, Wu H, Arthanari H, Fischer ES & Gregory RI (2023) "Structural basis of regulated m^7G tRNA modification by METTL1-WDR4 ." *Nature*. In Press

3. Zhang W*, **Roy Burman SS***, Chen J, Donovan KA, Cao Y, Shu C, Zhang B, Zeng Z, Gu S, Zhang Y, Li D, Fischer ES, Tokheim C & Liu XS (2022) "Machine learning modeling of protein-intrinsic features predicts tractability of targeted protein degradation." *Genomics, Proteomics & Bioinformatics*. In Press

4. Nitsch L*, Jensen P*, Yoon H, Koeppel J, **Roy Burman SS**, Fischer ES, Scholl C, Fröhling S & Slabicki M (2022) "BTB_{BCL6} dimers as building blocks for reversible drug-induced protein oligomerization." *Cell Reports Methods*. 2, 100193 (**Cover Article**)

5. Meyerhardt JA, Yue H, Nowak RP, Brais L, Ma C, Johnson S, Harrod J, **Roy Burman SS**, Hendrickson L, Fischinger S, Alter G, Hahn W, Johnson BE & Fischer ES (2022) "Serological testing for SARS-CoV-2 antibodies of employees shows low transmission working in a cancer center." *PLoS One*. 17(4), e0266791

6. Koehler Leman J*, Lyskov S*, Lewis S*, Adolf-Bryfogle J, Alford RF, Barlow K, Ben-Aharon Z, Farrell D, Fell J, Hansen WA, Harmalkar A, Jeliazkov J, Kuenze G, Krys JD, Ljubetic A, Loshbaugh AL, Maguire J, Moretti R, Mulligan VK, Nguyen PT, Ó Conchúir S, **Roy Burman SS**, Smith ST, Teets F, Tiemann JKS, Watkins A, Woods H, Yachnin BJ, Bahl CD, Bailey-Kellogg C, Baker D, Das R, DiMaio F, Khare SD, Kortemme T, Labonte JW, Lindorff-Larsen K, Meiler J, Schief W, Schueler-Furman O, Siegel J, Stein A, Yarov-Yarovoy V, Kuhlman B, Leaver-Fay A, Gront D, Gray JJ & Bonneau R (2021) "Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks." *Nature Communications*. 12, 6947

7. Le KH, Adolf-Bryfogle J, Klima JC, Lyskov S, Labonte J, Bertolani S, **Roy Burman SS**, Leaver-Fay A, Weitzner B, Maguire J, Rangan R, Adrianowycz MA, Alford RF, Adal A, Nance ML, Wu Y, Willis J, Kulp D, Das R, Dunbrack RL Jr, Schief W, Kuhlman B, Siegel JB & Gray JJ (2021) "PyRosetta jupyter notebooks teach biomolecular structure prediction and design." *The Biophysicist*. 2(1), 108–122

8. Slabicki M*, Yoon H*, Koeppel J*, Nitsch L, **Roy Burman SS**, Di Genua CA, Donovan KA, Sperling AS, Hunkeler M, Tsai JM, Sharma R, Guirguis A, Zou C, Chudasama P, Gasser JA, Miller PG, Scholl C, Fröhling S, Nowak RP, Fischer ES & Ebert BL (2020) "Small molecule-induced polymerization triggers degradation of BCL6." *Nature*. 588, 164–168

9. Koehler Leman J, Weitzner BD, Lewis SM, Adolf-Bryfogle J, Alam N, Alford RF, Aprahamian M, Baker D, Barlow KA, Barth P, Basanta B, Bender BJ, Blacklock K, Bonet J, Boyken S, Bradley P, Bystroff C, Conway P, Cooper S, Correia BE, Coventry B, Das R, De Jong RM, DiMaio F, Dsilva L, Dunbrack R, Ford A, Frenz B, Fu DY, Geniesse C, Goldschmidt L, Gowthaman R, Gray JJ, Gront D, Guffy S, Horowitz S, Huang P-S, Huber T, Jacobs TM, Jeliazkov JR, Johnson DK, Kappel K, Karanicolas J, Khakzad H, Khar KR, Khare SD, Khatib Firas, Khramushin A, King IC, Kleffner R, Koepnick B, Kortemme T, Kuenze G, Kuhlman B, Kuroda D, Labonte JW, Lai JK, Lapidoth G, Leaver-Fay A, Lindert S, Linsky T, London N, Lubin JH, Lyskov S, Maguire J, Malmström L, Marcos E, Marcu O, Marze NA, Meiler J, Moretti R, Mulligan VK, Nerli S, Norn C, Ó'Conchúir S, Ollikainen N, Ovchinnikov S, Pacella MS, Pan X, Park H, Pavlovicz RE, Pethe M, Pierce BG, Pilla KB, Raveh B, Renfrew PD, **Roy Burman SS**, Rubenstein A, Sauer MF, Scheck A, Schief W, Schueler-Furman O, Sedan Y, Sevy AM, Sgourakis NG, Shi L, Siegel J, Silva D-A,

Smith S, Song Y, Stein A, Szegedy M, Teets FD, Thyme SB, Wang RY-R, Watkins A, Zimmerman L & Bonneau R (2020) "Macromolecular modeling and design in Rosetta: new methods and frameworks." *Nature Methods*. 17, 665–680

10. **Roy Burman SS**, Jeliazkov JR, Labonte JW, Nance ML, Lubin JH, Biswas N & Gray JJ (2020) "Novel sampling strategies and a coarse-grained score function for docking homomers, flexible heteromers, and oligosaccharides using Rosetta in CAPRI Rounds 37–45." *Proteins*. 88(8), 973–985
11. **Roy Burman SS**, Yovanno RA & Gray JJ (2019) "Flexible backbone assembly and refinement of symmetrical homomeric complexes." *Structure*. 27, 1041–1051
12. Marze NA*, **Roy Burman SS***, Sheffler W & Gray JJ (2018) "Efficient flexible backbone protein-protein docking for challenging targets." *Bioinformatics*. 34(20), 3461-3469
13. Kalin JH*, Wu M*, Gomez AV*, Song Y*, Das J, Hayward D, Adejola N, Wu M, Panova I, Chung HJ, Kim E, Roberts HJ, Roberts JM, Prusevich P, Jeliazkov JR, **Roy Burman SS**, Fairall L, Milano C, Eroglu A, Proby CM, Dinkova-Kostova AT, Hancock WW, Gray JJ, Bradner JE, Valente S, Mai A, Anders NM, Rudek MA, Hu Y, Ryu B, Schwabe J, Mattevi A, Alani RM & Cole PA (2018) "Targeting the CoREST complex with dual histone deacetylase and demethylase inhibitors" *Nature Communications*. 9, 53
14. Marze NA*, Jeliazkov JR*, **Roy Burman SS**, Boyken SE, DiMaio F & Gray JJ (2017) "Modeling oblong proteins and water-mediated interfaces with RosettaDock in CAPRI rounds 28–35" *Proteins*. 85(3), 479-486
15. Lensink MF, Velankar S, Kryshtafovych A, Huang SY, Schneidman-Duhovny D, Sali A, Segura J, Fernandez-Fuentes N, Viswanath S, Elber R, Grudinin S, Popov P, Neveu E, Lee H, Baek M, Park S, Heo L, Rie Lee G, Seok C, Qin S, Zhou HX, Ritchie DW, Maigret B, Devignes MD, Ghoorah A, Torchala M, Chaleil RA, Bates PA, Ben-Zeev E, Eisenstein M, Negi SS, Weng Z, Vreven T, Pierce BG, Borrman TM, Yu J, Ochsenbein F, Guerois R, Vangone A, Rodrigues JP, van Zundert G, Nellen M, Xue L, Karaca E, Melquiond AS, Visscher K, Kastritis PL, Bonvin AM, Xu X, Qiu L, Yan C, Li J, Ma Z, Cheng J, Zou X, Shen Y, Peterson LX, Kim HR, Roy A, Han X, Esquivel-Rodriguez J, Kihara D, Yu X, Bruce NJ, Fuller JC, Wade RC, Anishchenko I, Kundrotas PJ, Vakser IA, Imai K, Yamada K, Oda T, Nakamura T, Tomii K, Pallara C, Romero-Durana M, Jiménez-García B, Moal IH, Férnandez-Recio J, Joung JY, Kim JY, Joo K, Lee J, Kozakov D, Vajda S, Mottarella S, Hall DR, Beglov D, Mamonov A, Xia B, Bohnuud T, Del Carpio CA, Ichiishi E, Marze N, Kuroda D, **Roy Burman SS**, Gray JJ, Chermak E, Cavallo L, Oliva R, Tovchigrechko A & Wodak, SJ (2016) "Prediction of homo- and hetero-protein complexes by ab-initio and template-based docking: a CASP-CAPRI experiment" *Proteins*. 84(Suppl 1), 323-48

* These authors contributed equally.

Select Oral Presentations

1. "Estimating target degradability from protein-intrinsic features." *Discovery on Target*, Boston, MA, October 2022
2. "Protein-intrinsic features predict tractability for targeted protein degradation." *Summer RosettaCON*, Leavenworth, WA, August 2022
3. "Leveraging the structure-based design of proximity inducing molecules." Workshop co-leader at *Induced Proximity-based Drug Discovery Summit*, Boston, MA, May 2022
4. "Understanding PROTAC-mediated targeted protein degradation." *BioCompare Webinar Series*, Virtual, December 2021
5. "Docking symmetric homomers with flexible-backbone refinement." *RosettaCON*, Leavenworth, WA, August 2018
6. "Flexible-backbone protein docking using motif scoring and large conformational ensembles." *American Institute of Chemical Engineers Annual Meeting*, Minneapolis, MN, November 2017
7. "Flexible-backbone protein docking." *Lectures in Computational Biophysics* at Johns Hopkins University, Baltimore, MD, October 2017
8. "Efficient flexible-backbone protein docking." *Regional Computational Biophysics Symposium*, Baltimore, MD, June 2017

Select Poster Presentations

1. "Designing compound-dependent binders of E3 ubiquitin ligases." *CRI-ENCI-AACR Sixth International Cancer Immunotherapy Conference*, New York City, NY, September 2022
2. "Efficient flexible backbone protein-protein docking for challenging targets." *Biophysical Society Meeting*, San Francisco, CA, February 2018
3. "Efficient flexible protein-protein docking using a diverse ensemble of monomers." *RosettaCON*, Leavenworth, WA, August 2016
4. "Characterization of peptides designed to control calcite growth." *Gordon Research Conference on Biomineralization*, New London, NH, August 2014
5. "Identification of genes essential for attachment of tendons." *Summer Undergraduate Research Grant for Excellence Poster Session*, Kanpur, India, July 2010 (**Awarded Best Poster**)

Editorship and Peer-review Activities

Guest Editor for Methods for Targeted Protein Degradation collection at *Journal of Visualized Experiments*. Reviewer for *Journal of Chemical Information and Modeling, Computational and Structural Biotechnology Journal, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Proteins* & *PeerJ*. Part of the early-career reviewers pool in structural biology and molecular biophysics at *eLife*.

Teaching Experience

2019 | Organizer & Instructor, PyRosetta Code School
for *RosettaCommons* at *Johns Hopkins University*
Designed, organized, and co-taught a week-long workshop to train scientists from experimental backgrounds or with limited coding experience to write computational protocols in Rosetta. Participants had hands-on programming experience to write custom PyRosetta protocols and use a wide range of Rosetta objects.

2015 | Instructor, Protein Misfolding Diseases: A Molecular Perspective
at *Johns Hopkins University*
Conceptualized and co-taught a one credit undergraduate course on molecular mechanisms of Alzheimer's, Huntington's and prion diseases. Students were encouraged to read, discuss and critique recent scientific literature in the field, and were evaluated based on it.

2013–2015 | Fellow , Preparing Future Faculty Teaching Academy
at *Johns Hopkins University*
Participated in a professional development program to learn pedagogical theory and teach practice modules with feedback from the instructors. The program was designed to introduce course design, pedagogical models and methods, and develop evaluation skills.

2014 | Teaching Assistant, Computational Protein Structure Prediction and Design
Instructor: Dr. Jeffrey J. Gray, Johns Hopkins University
Assisted the students during weekly lab sessions. Designed some exam questions and graded assignments and examinations.

2013 | Teaching Assistant, Introduction to Chemical and Biological Process Analysis
Instructor: Dr. Lise Dahuron, Johns Hopkins University
Conducted peer-led recitations sections, taught as a substitute instructor and graded examinations.

Activities & Outreach

- Member, Applications Committee, RosettaCommons (2022 onwards)
- Wrote tutorials for Rosetta Molecular Modeling Suite. (2016)

- Mentored students in Margaret Brent Elementary School to engineer toy solutions to local problems as a part of the STEM Achievement in Baltimore Elementary Schools Program. (2015)
- Provided one-on-one tutoring to local adults seeking a high school-equivalent degree as a part of Johns Hopkins GED Prep. (2013-2015)
- Coordinated new student orientation, mentored students on academic probation, and organized mental health workshops as Assistant Coordinator of the Counselling Service at Indian Institute of Technology, Kanpur. (2010-2011)

References

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