JAMES R. VALCOURT

jrvalcourt@gmail.com~(978) 870-5393

SUMMARY Interdisciplinary researcher with experience marshalling both experimental and computational techniques to tackle problems in drug discovery, development, and regenerative medicine.

EDUCATION Harvard University: Cambridge, Massachusetts

- Ph.D. in Systems, Synthetic, and Quantitative Biology, 2020
- Advisor: Sharad Ramanathan, Dissertation: Predicting and controlling mesendoderm competence in human embryonic stem cells
- Discovered and manipulated novel modes of cell state control with applications in regenerative medicine and developmental biology

Princeton University: Princeton, New Jersey

- A.B. in Molecular Biology, magna cum laude, 2012
- Certificate in Quantitative and Computational Biology

WORK EXPERIENCE D. E. Shaw Research: New York, New York

Drug Discovery Fellow, 2020 - present

- Leading two internal drug discovery projects that identified and leveraged novel mechanisms on previously intractable targets
- Internal lead for a collaboration with Relay Therapeutics
- Leveraging techniques such as molecular dynamics, FEP, virtual screening/docking, and machine learning to discover small molecules with novel binding modes and mechanisms
- Directed *in vitro* work by several CRO partners to validate computational predictions

Scientific Associate, 2012 - 2014

- Conducted basic research using long-timescale molecular dynamics simulations of pharmaceutically relevant biological systems
- Special focus on the mechanisms of allosteric modulation in GPCRs and on the structural basis of neutralization breadth of HIV antibodies

PUBLICATIONS	Valcourt, J.R., Huang, R.E., Kundu, S., Venkatasubramanian, D., Kingston,
(ACADEMIC)	R.E., Ramanathan, S. Changing the Waddington landscape to control
	mesendoderm competence. <i>bioRxiv</i> 867010 [Preprint]. December 6, 2019.
	https://doi.org/10.1101/867010
	Bokoch, M. P., Jo, H. I., Valcourt, J. R., Srinivasan, Y., Pan, A. C.,

Bokoch, M. P., Jo, H. I., Valcourt, J. R., Srinivasan, Y., Pan, A. C., Capponi, S., Grabe, M., Dror, R. O., Shaw, D. E., DeGrado, W. F., Coughlin, S. R. (2018). Entry from the lipid bilayer: a possible pathway for inhibition of a peptide G protein-coupled receptor by a lipophilic small molecule. *Biochemistry*, 57(39), 5748–58.

	Dror, R. O., Green, H. F., Valant, C., Borhani, D. W., Valcourt, J. R. , Pan, A. C., Shaw, D. E. (2013). Structural basis for modulation of a G-protein-coupled receptor by allosteric drugs. <i>Nature</i> , 503(7475), 295–299.
	Valcourt, J. R., Lemons, J. M. S., Haley, E. M., Kojima, M., Demuren, O. O., & Coller, H. A. (2012). Staying alive: Metabolic adaptations to quiescence. <i>Cell Cycle</i> , 11(9), 1680–1696.
PUBLICATIONS (TRADE)	Valcourt, J. R. "Systematic: How Systems Biology is Transforming Modern Medicine." New York: Bloomsbury, 2017.
AWARDS AND DISTINCTIONS	 Peralta Award, Department of Molecular and Cellular Biology, Harvard University, 2019 Quantitative Biology Fellowship, NSF-Simons Center for the Mathematical & Statistical Analysis of Biology at Harvard University, 2019 National Defense Science and Engineering Graduate Fellowship, 2014 (declined) National Science Foundation Graduate Research Fellowship, 2014 Fannie and John Hertz Foundation Graduate Fellowship, 2012 Moses Taylor Pyne Honor Prize, the highest general distinction conferred on an undergraduate by Princeton University, 2012 Phi Beta Kappa, 2012 Society of Sigma Xi, 2012 Alberto Santos-Dumont Prize for Innovation (accepted on behalf of The Princeton Tiger Magazine), Princeton University, 2011 Shapiro Prize for Academic Excellence, Princeton University, 2009
TECHNICAL SKILLS	Wet lab: RNA/ATAC/ChIP-seq, quantitative live cell microscopy, mammalian cell culture, immunofluorescence, fluorescence-activated cell sorting, microfluidics
	Dry lab: molecular dynamics; numerical modeling; analysis of RNA/ATAC/ChIP-seq and genomic data, both bulk and single-cell; image analysis; statistical methods
	Languages and Platforms: Python, Bash, Matlab, R, Linux, Slurm, LaTeX, some PyTorch, some Julia, Adobe Illustrator
TEACHING EXPERIENCE	Teaching Fellow, LS50 Integrated Science, Harvard University, 2016 Served as one of the inaugural teaching fellows for a new, intense double course for first-year undergraduates. Taught weekly sections, gave input on overall course structure, co-developed weekly problem sets, and co-wrote exams.
	Volunteer Tutor, Star Learning Center, New York City, 2013-2014

Taught high school chemistry for underprivileged students.

Peer Tutor, Wilson College, Princeton University, 2009-2012 Tutored other students in entry-level science courses.

ADDITIONAL RESEARCH EXPERIENCE Interactions between microRNA and RNA-binding proteins, 2010-2012 Worked with Professor Hilary Coller at Princeton University to investigate novel post-transcriptional regulatory networks

Quantifying *D. melanogaster* embryo morphogenesis, 2008-2010 Worked with Professor Eric Wieschaus at Princeton University to study the genetic and morphological processes of cephalic furrow formation and develop software to analyze morphogenesis in three dimensions

Hotspots of structural variation in the human genome, 2009 Worked with Dr. Jan Korbel at the European Molecular Biology Laboratories to investigate the origins of differing structural variation rates in the genome

OTHER **D. E. Shaw Research:** Diversity, Equity and Inclusion Working Group member; co-designed and co-led multi-day technical workshops for undergraduates; new-hire mentor.

Harvard University: co-founder and co-organizer of the Quantitative Biology Series; Hertz Foundation in-school representative for Harvard and organizer of events and retreats for in-school fellows; miscellaneous public outreach including publishing a non-fiction book about systems biology intended for general audiences.

Princeton University: Chair of second-oldest college humor magazine in the country; outdoor orientation program leader trainer and member of governing body; tour guide; Speakers Chair of Student Bioethics Forum.

Outdoors: Eagle Scout and Order of the Arrow, avid backpacker