

## Jordan Eli Rossen

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Contact Information	jordanerossen@gmail.com github.com/jordanero	319-541-0640
Education	<b>Harvard University</b> PhD in Epidemiology - Statistical genetics PhD advisor: Alkes Price	2020 - 2025
	<b>Harvard University</b> M.S. in Biostatistics	2020 - 2025
	<b>Tufts University</b> B.S. with majors in Computer Science and Chemistry Major GPA: 3.95, GPA: 3.89	2013 - 2017
Professional Experience	<b>Harvard University</b> PhD Researcher	Alkes Price Group 2020-2025
	<ul style="list-style-type: none"><li>• Developed MultiSuSiE, an open source Python package for multi-ancestry fine-mapping with higher power and lower computational cost than alternative methods (Rossen et al. 2024 bioRxiv).</li><li>• Studied differences in heritability components across ancestries using hundreds of thousands of whole genome sequences from All of Us (Rossen and Price 2024 American Society of Human Genetics Conference).</li></ul>	
	<b>Broad Institute of MIT and Harvard</b> Associate Computational Biologist II Associate Computational Biologist I	Cancer Data Science Group 2019 - 2020 2017 - 2019
	<ul style="list-style-type: none"><li>• Developed data processing methodology for DepMap Achilles, a public, high-throughput CRISPR-Cas9 genome-scale knockout dataset (Dempster et al. 2019 BioRxiv, &gt;1,000 cell lines x 20,000 genes).</li><li>• Lead assay development analyst for PRISM, a high-throughput, in-vitro drug screening platform (Corsello et al. 2020 Nature Cancer, &gt;500 cell lines x 4,500 drugs).</li><li>• Analyzed public high-throughput drug screening datasets to identify promising small molecules (Tsvetkov et al. 2019 Nature Chemical Biology, Tsvetkov et al. 2022 Science).</li></ul>	
	<b>Pfizer Inc.</b> Molecular Data Intern	Precision Medicine Summer 2016
	<ul style="list-style-type: none"><li>• Designed and implemented an internal metabolomics biomarker database using RShiny.</li></ul>	
	<b>University of Illinois</b> REU researcher	Kami Hull Organometallic Catalysis Group Summer 2015
	<ul style="list-style-type: none"><li>• Expanded the reaction scope of ex-situ, Pd-catalyzed, chloroform-based alkoxycarbonylation reactions.</li></ul>	
	<b>Tufts University</b> Research Assistant	Lin Computational Chemistry Group 2013 - 2014
	<ul style="list-style-type: none"><li>• Programmed molecular dynamics simulations of liquid argon, oxygen, and water using Fortran.</li></ul>	

Teaching Assistant	<b>Harvard University</b>	Department of Epidemiology
	Causal Inference (EPI207), Jamie Robbins Advanced Population and Medical Genetics (EPI511), Alkes Price	Fall 2022, Fall 2023 Spring 2023
	<b>Tufts University</b>	Department of Computer Science
	Algorithms (COMP160), Gregory Aloupis	Fall 2017, Spring 2017
Awards	<b>Platform Talk</b> - American Society for Human Genetics	2023
	<b>F31 Grant</b> - National Institutes of Health	2023
	<b>Spot Award</b> - Broad Institute, Level 2	2019
	<b>Deans List</b> - Tufts University	2013 - 2017
	<b>Snyder Scholarship</b> - UIUC, Department of Organic Chemistry	2015
	<b>Iowa State Policy Debate Tournament</b> - 2nd place	2013
Programming	<ul style="list-style-type: none"> <li>• Proficiency in R and Python</li> <li>• Experience in C, C++, and Matlab</li> </ul>	
Publications	Cited more than 3,700 times across six publications	
	<p>Rossen, J., Shi, H., Strober, B., Zhang, M.J., Kanai, M., McCaw, Z.R., Liang, L., Weissbrod, O., Price, A.L., 2024. MultiSuSiE improves multi-ancestry fine-mapping in All of Us whole-genome sequencing data. medRxiv.</p> <p>Strober, B.J., Zhang, M.J., Amariuta, T., Rossen, J., Price, A.L., 2024, Fine-mapping causal tissues and genes at disease-associated loci. in press at Nature Genetics.</p> <p>Tsvetkov, P., Coy, S., Petrova, B., Dreishpoon, M., Verma, A., Abdusamad, M., Rossen, J., Joesch-Cohen, L., Humeidi, R., Spangler, R.D. and Eaton, J.K., Frenkel, E., Kocak, M., Corsello, S.M., Lutsekno, S., Kanarek, NM., Santagata, S., Golub, T.R., 2022. Copper induces cell death by targeting lipoylated TCA cycle proteins. Science, 375(6586), pp.1254-1261.</p> <p>Dempster, J.M., Rossen, J., Kazachkova, M., Pan, J., Kugener, G., Root, D.E. and Tsherniak, A., 2019. Extracting biological insights from the project achilles genome-scale CRISPR screens in cancer cell lines. BioRxiv, p.720243.</p> <p>Corsello, S.M., Nagari, R.T., Spangler, R.D., Rossen, J., [33 others], Golub, T.R., 2020. Discovering the anticancer potential of non-oncology drugs by systematic viability profiling. Nature Cancer, 1(2), pp.235-248.</p> <p>Tsvetkov, P., Detappe, A., Cai, K., Keys, H.R., Brune, Z., Ying, W., Thiru, P., Reidy, M., Kugener, G., Rossen, J., Kockac, M., Kory, N., Tsherniak, A., Santagata, S., Whitesell, Luke., Ghobrial, I.M., Markley, J.L., Lindquist, S., Golub, T.R., 2019. Mitochondrial metabolism promotes adaptation to proteotoxic stress. Nature Chemical Biology, 15(7), pp.681-689.</p>	