

Christopher J. Benway

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Summary

I am currently a computational biologist at Boston Children's Hospital in the Division of Nephrology. As a member of the Sampson Lab I am presently leveraging genetic, genomic and RNA-seq expression data to identify novel eQTLs the glomerulus and renal tubule to further uncover the heritable factors contributing to nephrotic syndrome. This work will further provide insight into the pathogenesis of other renal diseases, as well as broad renal function. I am also involved in the design, troubleshooting, and analysis of various other genomic efforts to understand podocyte biology in health and disease using state-of-the-art technologies such as scRNA-seq/sc-ATAC-seq, MPRA, and organ-on-a-chip. I completed my post-doctoral training at Brigham and Women's Hospital and Harvard Medical School Channing Division of Network Medicine investigating the genetics and functional genomics of chronic obstructive pulmonary disease (COPD). This research involved genome-wide association studies, statistical genetics and fine-mapping, transcriptomics, and chromatin accessibility assays. During my Ph.D. in the lab of John Iacomini at Tufts University Sackler School of Biomedical Sciences I worked on *in vivo* and cell-based models of calcineurin inhibitor nephrotoxicity, using transcriptomics and sequencing methods to detect *in vivo* miRNA:mRNA targeting. In prior work as a research technician I have largely worked on molecular and cell biology projects related to immune function, ER stress, gene therapy, and high throughput chemical biology screens.

Education

2011–2017	Ph.D. in Genetics, Tufts University, Boston, MA. PhD thesis: <i>Defining a microRNA-mRNA targetome for calcineurin inhibitor induced nephrotoxicity</i>
2004–2008	A.B. in Biology, Harvard University, Cambridge, MA.

Past Scientific Positions

2020–present	Computational Biologist Boston Children's Hospital, Division of Nephrology, Boston, MA. Adviser: Matt Sampson, M.D., M.S.C.E.
2017–2020	Postdoctoral Research Fellow Brigham and Women's Hospital and Harvard Medical School, Channing Division of Network Medicine, Boston, MA. Advisers: Edwin K. Silverman, M.D., Ph.D. and Xiaobo Zhou, Ph.D.
2011–2017	Graduate Research Assistant Tufts University Sackler School of Biomedical Sciences, Department of Developmental, Molecular and Chemical Biology, Boston, MA. Adviser: John Iacomini, Ph.D.
2009–2011	Research Assistant Harvard Medical School, Department of Genetics, Boston, MA. Richard C. Mulligan, Ph.D. Laboratory
2008–2009	Research Assistant

	Harvard School of Public Health, Department of Immunology and Infectious Diseases, Boston, MA. Laurie H. Glimcher, M.D. Laboratory
2007	Research Assistant Harvard University, Department of Organismic and Evolutionary Biology, Cambridge, MA. Noel Michele Holbrook, Ph.D. Laboratory
2006	Research Assistant Harvard University, Department of Molecular and Cellular Biology, Cambridge, MA. Sam Kunes, Ph.D. Laboratory
2005–2006	Research Assistant Brigham and Women's Hospital and Harvard Medical School, Division of Genetics, Department of Medicine, Cambridge, MA. Alan M. Michelson, M.D., Ph.D. Laboratory

Research Interests

- Dissecting the genetic contributions to complex disease
- Investigating the biological role of genetic variation associated with complex diseases and decoding the functional role of sequence variation in biological pathways
- Genomics, epigenomics, transcriptomics; special interest in small non-coding RNAs such as microRNAs.
- Integration of multiple 'omic datatypes; network medicine

Scientific Meetings

2019	COPDGene Investigators Meeting Boston, MA Attendee
2019	American Society of Human Genetics (ASHG) Annual Meeting Houston, TX Poster Presentation: <i>Assaying lung-specific accessible chromatin to predict the causal variants in COPD</i> . C. J. Benway, J. Liu, F. Du, M. H. Cho, E. K. Silverman, X. Zhou. (abstract , poster)
2019	HMS Epigenetics and Gene Dynamics Symposium Boston, MA Poster Presentation: <i>Assaying lung-specific accessible chromatin to predict the causal variants in COPD</i> . C. J. Benway, J. Liu, F. Du, M. H. Cho, E. K. Silverman, X. Zhou. (poster)
2019	American Thoracic Society (ATS) Conference Dallas, TX Poster Presentation: <i>Genome-Wide Association Study of Parametric Response Mapping in the COPDGene Study Dissects Genetic Contributions to Emphysema and Functional Small Airway Disease</i> . C. J. Benway, P. Sakornsakolpat, J. Ross, B.D. Hobbs, M.H. Cho, E.K. Silverman. (abstract , poster)
2018	COPDGene Investigators Meeting

	Denver, CO Attendee
2018	Discover Brigham Boston, MA Poster presentation: <i>Chromatin accessibility landscapes of large and small airway cells annotate multiple COPD susceptibility GWAS regions.</i> C. J. Benway, F. Du, M. H. Cho, E. K. Silverman, X. Zhou. (e-poster) Research Open Mic: <i>From GWAS to Function: Uncovering the causal genetic variants in COPD</i>
2018	American Society of Human Genetics (ASHG) Annual Meeting San Diego, CA Poster Presentation: <i>Chromatin accessibility landscapes of large and small airway cells annotate multiple COPD susceptibility GWAS regions.</i> C. J. Benway, F. Du, M. H. Cho, E. K. Silverman, X. Zhou. Reviewer's Choice Abstract (abstract , poster)
2017	American Society of Human Genetics (ASHG) Annual Meeting Orlando, FL Attendee
2017	COPDGene Investigators Meeting Boston, MA Attendee
2016	Tufts Charlton Poster Competition Boston, MA Poster Presentation: <i>Ago-PAR-CLIP Defines Targetome and Role of MicroRNAs in Cyclosporine-induced Nephrotoxicity.</i> C. J. Benway, J. Iacomini (poster)
2015	EMBO/EMBL Symposium: The Non-Coding Genome Heidelberg, Germany Poster Presentation: <i>Ago-PAR-CLIP Defines MicroRNA Targets in Human Proximal Tubule Epithelial Kidney Cells.</i> C.J. Benway, J. Iacomini (poster)
2015	24th Short Course on Experimental Models of Human Cancer The Jackson Laboratory, Bar Harbor, Maine Attendee
2015	Non-Coding RNA: New Mechanisms and Approaches Boston, MA Attendee

Bioinformatic and Computer Skills

- Data analysis of high-throughput sequencing data including DNA-seq, RNA-seq, ATAC-seq, and ChIP-seq.
- Knowledge and ability to use various bioinformatic databases, APIs, repositories, and tools.
- Knowledge and and ability to script in R and use reproducible research tools such as Markdown/R Markdown.
- Ability to implement bioinformatic pipelines using pipelining tools.

Academic References

Edwin Kepner Silverman, Ph.D., M.D.
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John Iacomini, Ph.D.
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Publications

- [1] C. J. Benway, J. Liu, F. Guo, F. Du, M. H. Cho, E. K. Silverman, and X. Zhou. Chromatin Landscapes of Lung Cell Types Predict Functional COPD GWAS Variants. Manuscript in preparation.
- [2] Y. Hao*, S. Bates*, B. Pham, H. Mou, J. Liu, W. Qiu, J. D. Morrow, C. P. Hersh, L. Gong, F. Guo, C. J. Benway, I. O. Rosas, M. H. Cho, J. Park, P. J. Castaldi, F. Du, and X. Zhou. Idiopathic pulmonary fibrosis (IPF) functional variant rs2076295 regulates Desmoplakin (DSP) gene-mediated cell migration. *Am. J. Respir. Cell Mol. Biol.*, under review.
- [3] K. E. Lowe, E. A. Regan, A. Anzueto, E. Austin, J. H. M. Austin, T. H. Beaty, P. V. Benos, C. J. Benway, S. P. Bhatt, E. R. Bleecker, S. Bodduluri, J. Bon, A. M. Boriek, A. R. Boueiz, R. P. Bowler, M. Budoff, R. Casaburi, P. J. Castaldi, J. P. Charbonnier, M. H. Cho, A. Comellas, D. Conrad, C. Costa Davis, G. J. Criner, D. Curran-Everett, J. L. Curtis, D. L. DeMeo, A. A. Diaz, M. T. Dransfield, J. G. Dy, A. Fawzy, M. Fleming, E. L. Flenaugh, M. G. Foreman, S. Fortis, H. Gebrekristos, S. Grant, P. A. Grenier, T. Gu, A. Gupta, M. K. Han, N. A. Hanania, N. N. Hansel, L. P. Hayden, C. P. Hersh, B. D. Hobbs, E. A. Hoffman, J. C. Hogg, J. E. Hokanson, K. F. Hoth, A. Hsiao, S. Humphries, K. Jacobs, F. L. Jacobson, E. A. Kazerooni, V. Kim, W. J. Kim, G. L. Kinney, H. Koegler, S. M. Lutz, D. A. Lynch, N. R. MacIntye, B. J. Make, N. Marchetti, F. J. Martinez, D. J. Maselli, A. M. Mathews, M. C. McCormack, M. N. McDonald, C. E. McEvoy, M. Moll, S. S. Molye, S. Murray, H. Nath, J. D. Newell, M. Occhipinti, M. Paoletti, T. Parekh, M. Pistolesi, K. A. Pratte, N. Putcha, M. Ragland, J. M. Reinhardt, S. I. Rennard, R. A. Rosiello, J. C. Ross, H. B. Rossiter, I. Ruczinski, R. San Jose Estepar, F. C. Sciruba, J. C. Sieren, H. Singh, X. Soler, R. M. Steiner, M. J. Strand, W. W. Stringer, R. Tal-Singer, B. Thomashow, G. Vegas Sanchez-Ferrero, J. W. Walsh, E. S. Wan, G. R. Washko, J. Michael Wells, C. H. Wendt, G. Westney, A. Wilson, R. A. Wise, A. Yen, K. Young, J. Yun, E. K. Silverman, and J. D. Crapo. COPDGene® 2019: Redefining the Diagnosis of Chronic Obstructive Pulmonary Disease. *Chronic Obstr Pulm Dis*, 6(5):384–399, Nov 2019. [DOI:[10.15326/jcopdf.6.5.2019.0149](https://doi.org/10.15326/jcopdf.6.5.2019.0149)] [PubMed:[31710793](https://pubmed.ncbi.nlm.nih.gov/31710793/)].
- [4] C. J. Benway, P. Sakornsakolpat, J. Ross, B. D. Hobbs, M. H. Cho, and E. K. Silverman. Genome-Wide Association Study of Parametric Response Mapping in the COPDGene Study Dissects Genetic Contributions to Emphysema and Functional Small Airway Disease. *American Thoracic Society*, May 2019.

- [5] M. F. Ragland*, C. J. Benway*, S. M. Lutz, R. P. Bowler, J. Hecker, J. E. Hokanson, J. D. Crapo, P. J. Castaldi, D. L. DeMeo, C. P. Hersh, B. D. Hobbs, C. Lange, T. H. Beaty, M. H. Cho, and E. K. Silverman. Genetic Advances in Chronic Obstructive Pulmonary Disease. Insights from COPDGene. *Am. J. Respir. Crit. Care Med.*, 200(6):677–690, Sep 2019. [PubMed Central:[PMC6775891](#)] [DOI:[10.1164/rccm.201808-1455SO](#)] [PubMed:[26221665](#)].
- [6] C. J. Benway and J. Iacomini. Defining a microRNA-mRNA interaction map for calcineurin inhibitor induced nephrotoxicity. *Am. J. Transplant.*, 18(4):796–809, 04 2018. [DOI:[10.1111/ajt.14503](#)] [PubMed:[28925592](#)].
- [7] J. Yuan, C. J. Benway, J. Bagley, and J. Iacomini. MicroRNA-494 promotes cyclosporine-induced nephrotoxicity and epithelial to mesenchymal transition by inhibiting PTEN. *Am. J. Transplant.*, 15(6):1682–1691, Jun 2015. [DOI:[10.1111/ajt.13161](#)] [PubMed:[25854542](#)].