Amelia Weber Hall, PhD

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Education

Ph.D. **Microbiology** (2017),
University of Texas at Austin, Austin, TX

B.S. **Molecular Genetics** (2007),
University of Rochester, Rochester, NY

Honors and Awards

Broad Institute Excellence Award in Mentorship, Teaching, or Training, 2024
NSF reviewer, 2023, 2024
Broad Institute Staff Scientists Distinction Award in Management and Mentorship, 2022
AHA GPM Young Investigator Award, 2019
AHA Atrial Fibrillation SFRN Fellowship, 2018, 2019

Experience

Research Scientist II, Advised by Dr. Charles Epstein, Epigenomic Platform and Gene Regulation Observatory, the Broad Institute of MIT and Harvard, Cambridge, MA. 07/2021 – present

- Standardized a protocol for performing SHARE-seq (a single cell multiomic protocol that profiles ATAC and RNA sequencing data at the same time) with members of the Buenrostro laboratory
- Developed and refined a protocol for isolating intact nuclei from frozen cadaveric human tissue
- Trained five research assistants in the above protocols as well as basic molecular biology and epigenetic techniques (RNA extractions, qPCR usage, basics of data analysis for ChIP).
- Lead an informal computational biology training group on analysis of NGS data using the Google cloud platform Terra, focus was wetbench scientists with minimal computational biology knowledge. Topics covered: R: ggplot2, ArchR, DEseq2, Seurat. Python: scanpy.
- In July 2023, promoted to Research Scientist II, directly managing 3 research assistants

Research Fellow, Advised by Dr. Patrick Ellinor, Cardiovascular Research Center, Massachusetts General Hospital, Boston, MA and the Broad Institute of MIT and Harvard, Cambridge, MA. 11/2017 – 07/2021

- Conducted bench and computational research on the genetics of cardiovascular disease, with particular attention to atrial arrhythmias
- Developed a computational pipeline for processing ChIP-seq data using Unix, bash scripting, Python, R
- Developed a pipeline for processing RNA-seq data using Kallisto, DEseq2, tximport and R Bioconductor
- Annotated SNP data using external databases to provide genomic context for disease associated SNPs identified in genome wide association studies
- Implemented initial computational processing pipeline for single cell RNA-seq data (10X Genomics), developed transcriptome gtfs for non-model organisms such as rat and pig

Graduate Research Assistant, Advised by Dr. Vishwanath Iyer, Department of Molecular Biosciences, The University of Texas at Austin, Austin, TX 5/2011 – 7/2017

- Directed research on profiling the epigenome and transcriptome of primary human glioblastoma samples
- Established and optimized protocol for performing ChIP in primary brain tumors
- Developed a pipeline for primary analysis of ChIP sequence data (alignment, peak calling, quality control metrics), and visualization of ChIP data using R and Python
- Collaborated on computational modelling of amino acid conservation in calmodulin across a large set of phyla with the Aldrich laboratory

Laboratory Technician, Advised by Dr. Richard Aldrich, Section of Neurobiology, The University of Texas at Austin, Austin, TX 2007 – 2010

- Developed protein mutagenesis protocol to selectively add non-natural amino acids to calcium binding sites for optical measurement of calcium binding strength

Undergraduate Research Assistant, Advised by Dr. Vera Gorbunova, University of Rochester, Rochester, NY 2006 – 2007

- Defended undergraduate thesis: The Effects of Irradiation, Oxidative Damage and Oncogenic Senescence on DNA Repair Efficiency in Human Dermal Fibroblasts, Spring 2007

Student Technician, Educational Technology Center, University of Rochester, Rochester, NY 2003 – 2007

Summer Programming Intern, IntrinsiQ Research, Inc., Waltham, MA 2004 – 2006

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Selected Publications

Weng LC, Rämö JT, Jurgens SJ, Khurshid S, Chaffin M, **Hall AW**, et al. The impact of common and rare genetic variants on bradyarrhythmia development. *Nature Genetics,* 2025. PMID: 39747593.

Arduini A, Fleming SJ, Xiao L, **Hall AW**, et al. Transcriptional profile of the rat cardiovascular system at single cell resolution. *Cell Reports,* 2025. PMID: 39709602.

The IGVF Consortium. Deciphering the impact of genomic variation on function. *Nature,* 2024. PMID: 39232149.

Weng L-C*, Khurshid S*, **Hall AW***, et al. Meta-Analysis of Genome-Wide Association Studies Reveals Genetic Mechanisms of Supraventricular Arrhythmias. *Circulation: Precision and Genomic Medicine,* 2024. PMID: 38804128; PMCID: PMC11187659.

Jameson HS, Hanley A, Hill MC, Xiao L, Ye JC, Bapat A, Ronzier E, **Hall AW**, et al. Loss of the Atrial Fibrillation-Related Gene, Zfhx3, Results in Atrial Dilation and Arrhythmias. *Circulation Research,* 2023. PMID: 37449401; PMCID: PMC10527554.

Khurshid S, Lazarte J, Pirrucello JP, Weng L-C, Choi SC, **Hall AW**, et al. Clinical and genetic associations of deep learning-derived cardiac magnetic resonance-based left ventricular mass. *Nature Communications,* 2023. PMID: 36944631; PMCID: PMC10030590.

Simonson B, Chaffin M, Hill MC, Atwa O, Guedira Y, Bhasin H, **Hall AW**, et al. Single-nucleus RNA sequencing in ischemic cardiomyopathy reveals common transcriptional profile underlying end-stage heart failure. *Cell Reports,* 2023. PMID: 36790929; PMCID: PMC10423750.

Nauffal V, Morrill VN, Jurgens SJ, Choi SC, **Hall AW**, et al. Monogenic and Polygenic Contributions to QTc Prolongation in the Population. *Circulation,* 2022. PMID: 35389749; PMCID: PMC9117504.

O'Brien S, Holmes AP, Johnson D, Kabir SN, O'Shea C, O'Rielly M, Avezzu A, Reyat JS, **Hall AW**, et al. Increased atrial effectiveness of flecainide conferred by altered biophysical properties of sodium channels. *J Mol Cell Cardiol.,* 2022. PMID: 35114252.

Jurgens SJ, Choi SC, Morrill VN, Chaffin MD, Pirrucello JP, Halford JL, Weng LC, Nauffal V, Roselli CR, **Hall AW**, et al. Analysis of rare genetic variation underlying cardiometabolic diseases and traits among 200,000 individuals in the UK Biobank. *Nature Genetics,* 2022. PMID: 35177841; PMCID: PMC8930703.

Choi SC, Jurgens SJ, Haggerty CM, **Hall AW**, et al. Rare Coding Variants Associated With Electrocardiographic Intervals Identify Monogenic Arrhythmia Susceptibility Genes: A Multi-Ancestry Analysis. *Circulation: Precision and Genomic Medicine,* 2021. PMID: 34319147; PMCID: PMC8373440

Hall AW, Chaffin M, Roselli C, et al. Epigenetic Analyses of Human Left Atrial Tissue Identifies Gene Networks Underlying Atrial Fibrillation. *Circulation: Precision and Genomic Medicine,* 2020. PMID: 33155827.

Weng L-C*, **Hall AW***, Choi SC, Jurgens SJ, et al. Genetic Determinants of Electrocardiographic P-wave Duration and Relation to Atrial Fibrillation. *Circulation: Precision and Genomic Medicine,* 2020. PMID: 32822252.

Tucker NR, Chaffin M, Fleming SJ, **Hall AW**, et al. Transcriptional and Cellular Diversity of the Human Heart. *Circulation,* 2020. PMID: 32403949.

Ntalla I, Weng L-C, Cartwright JH, **Hall AW**, et al. Multi-ancestry GWAS of the electrocardiographic PR interval identifies 210 loci underlying cardiac conduction. *Nature Communications, 2020*. PMID: 32439900.

Choi SC, Jurgens SJ, Weng L-C, Pirruccello JP, Roselli C, Chaffin M, Lee C, **Hall AW**, Khera AV, Lunetta K, Lubitz SA, Ellinor PT. Monogenic and Polygenic Contributions to Atrial Fibrillation Risk: Results from a National Biobank. *Circulation Research*, 2019. PMID: 31691645.

Hall AW, Battenhouse AM, Shivram H, Morris AR, Cowperthwaite MC, Shpak M, Iyer VR. Bivalent Chromatin Domains in Glioblastoma Reveal a Subtype-Specific Signature of Glioma Stem Cells. *Cancer Res*. 2018. PMID: 29549165; PMCID: PMC5955797.

Halling DB, Liebeskind BJ, **Hall AW**, Aldrich RW. Conserved properties of individual Ca2+-binding sites in calmodulin. *Proc Natl Acad Sci USA*. 2016. PMID: 26884197; PMCID: PMC4780646.

Ni Y, **Hall AW**, Battenhouse A, Iyer VR. Simultaneous SNP identification and assessment of allele-specific bias from ChIP-seq data. *BMC Genet.* 2012. PMID: 22950704; PMCID: PMC3434080.

Li W, Halling DB, **Hall AW**, Aldrich RW. EF hands at the N-lobe of calmodulin are required for both SK channel gating and stable SK-calmodulin interaction. *J Gen Physiol.* 2009. PMID: 19752189; PMCID: PMC2757765.

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Teaching Experience

Intermediate Unix. Co-taught internally at Broad Institute with Kate Bowers. Course taught May 2025.

Unix 101: A practical guide. Co-taught internally at Broad Institute with Jean Chang. Courses taught June, October 2024.

A practical guide to bulk RNA-seq analysis (plus a little on eQTL analysis). Medical and Population Genetics Primer Series at the Broad Institute. Lecture given on April 4th, 2024.

So you've generated the data … now what? Bioinformatics and data science for the bench scientist. Breakout session conducted at the Broad Institue of MIT and Harvard 19th annual retreat, on December 12, 2023.

Single cell and single nucleus RNA sequencing experiments: an updated practical guide to design and analysis American Heart Association: Conference on Vascular Discovery, May 12, 2023.

Single cell and single nucleus RNA sequencing experiments: a practical guide to design and analysis. American Heart Association: Conference on Vascular Discovery, September 21, 2021.

RNA-seq: A practical guide to differential gene expression and pathway analysis. Medical and Population Genetics Primer Series at the Broad Institute. Lecture given on October 1st, 2020.

Using tximport and DEseq2 to identify differentially expressed genes: an interactive Terra tutorial. Medical and Population Genetics Primer Series at the Broad Institute. Lecture given on October 8th, 2020.

Core Next Generation Sequencing Tools on Stampede. Big Data Summer School at UT Austin, Co-instructor May 2017, May 2016, May 2015. Teaching assistant May 2014.

Public Health Bacteriology Laboratory. Teaching assistant under Dr. Suzanne Barth, (BIO361L, Spring, Fall 2016). **Awarded Outstanding Teaching Assistant Award, April 2017**

Working with MySQL Databases. Short Course for Center for Computational Biology and Bioinformatics. Teaching assistant: December 2015, October 2014.

Invited Talks and Posters

Epigenetic Analyses Of Human Left Atrial Tissue Identifies Gene Networks Underlying Atrial Fibrillation, Presented webinar for Diagenode. January 2021

Epigenetic Analyses Of Human Left Atrial Tissue Identifies Gene Networks Underlying Atrial Fibrillation AHA Scientific Sessions Genomic and Precision Medicine Young Investigator Award Finalist presentation, Philadelphia, PA. November 2019

Glioblastoma enhancers and bivalent chromatin domains are subtype specific, Department of Molecular Biosciences Retreat, March 2017. **Awarded "Best Poster."**

Public Protocols

SHARE-seq protocol v2.2 V.5 (an RNA and ATAC multi-omic method): http://broad.io/shareseq

Nuclear Isolation and Purification Protocol for Single-Cell Methods: http://broad.io/gronuclei

Skills

Molecular biology:

- Protocol development/experimental design
- Single cell methods, ATAC, RNA
- Epigenetics protocols/Chromatin IP
- tissue manipulation, nuclei preparation

Bioinformatics:

- Single cell multi-omics (RNA and ATAC)
- ChIP-seq, RNA-seq, WGS
- Unix, R, HPC (SGE/SLURM), Python
- Cloud computing (Terra, GCP, Jupyter)
- Data analysis and visualization (ggplot, dplyr, tidyr, tidyverse)