

# 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

- AHA GPM Young Investigator Award, 2019  
AHA Atrial Fibrillation SFRN Fellowship, 2018, 2019  
Graduate School Summer Fellowship, 2015, 2016  
Ethel and Robert L. Terry Memorial Scholarship, 2012, 2015  
Joseph F. Short Memorial Endowed Fellowship, 2012  
Graduate Recruitment Fellowship, 2010

## Experience

**Research Scientist I**, Advised by Charles Epstein, Gene Regulation Observatory, the Broad Institute of MIT and Harvard, Cambridge, MA 7/2021 – present

- Optimized protocol for performing ATAC-seq and single cell RNA-seq in single cells to support the efforts of the Impact of Genome Variation on Function (IGVF) project
- Supervised research associates in learning cell culture, single cell transcriptome and epigenomic protocols, and in general molecular biology techniques
- Led research assistants in learning basic computational biology techniques using Terra, the Broad Institute's cloud computing platform

**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

- Standardized a protocol for performing ChIP-seq in frozen human left atrial tissue samples
- Developed a computational pipeline for processing ChIP-seq data using Unix, bash scripting, Python, and R Bioconductor
- Implemented initial computational processing pipeline for single cell RNA-seq data (10X Genomics), developed transcriptome gtf's for non-model organisms such as rat and pig
- Developed a pipeline for processing RNA-seq data using Kallisto, DESeq2, tximport and R Bioconductor
  - Collaborated with other group members in need of transcriptome quantification and differential gene expression analysis, for projects involving mouse knockouts, human heart tissue, and engineered cardiomyocytes
- Annotated SNP data using external databases (eQTLs, epigenomic information, transcription factor binding sites) to provide genomic context for disease associated SNPs from GWAS

**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 (with assistance) primary analysis of ChIP sequence data (alignment, peak calling, quality control metrics)
  - Established visualization of ChIP data using R Bioconductor and Python
- Collaborated on an atrial fibrillation blood genotyping project with the Texas Cardiac Arrhythmia Institute

**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
- Managed the molecular biology and protein expression sections of the laboratory,
  - Optimized a protocol for heterologous expression and purification of calmodulin protein

**Undergraduate Research Assistant**, Advised by Dr. Vera Gorbunova, Department of Biology, 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**, Intrinsic Research, Inc., Waltham, MA 2004 – 2006

## Publications

Choi S, Jurgens J, Haggerty C, **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.

**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.

van Ouwkerk AF, **Hall AW**, Kadow ZA, Lazarevic S, et al. Epigenetic and Transcriptional Networks Underlying Atrial Fibrillation. *Circulation Research*, 2020. PMID: 32717170.

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.

Zhang M, Hill MC, Kadow ZA, Suh JH, Tucker NR, **Hall AW**, et al. Long-range Pitx2c enhancer-promoter interactions prevent predisposition to atrial fibrillation. *Proc Natl Acad Sci USA*. 2019. PMID: 31636200.

**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 Ca<sup>2+</sup>-binding sites in calmodulin. *Proc Natl Acad Sci USA*. 2016. PMID: 26884197; PMCID: PMC4780646.

Mohanty S\*, **Hall AW\***, Mohanty P, Prakash S, Trivedi C, et al. Novel association of polymorphic genetic variants with predictors of outcome of catheter ablation in atrial fibrillation: new directions from a prospective study (DECAF). *J Interv Card Electrophysiol*. 2016. PMID: 26497660.

Shpak M, **Hall AW**, Goldberg MM, Derryberry DZ, Ni Y, Iyer VR, Cowperthwaite MC. An eQTL analysis of the human glioblastoma multiforme genome. *Genomics*. 2014. PMID: 24607568.

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.

Seluanov A, Hine C, Bozzella M, **Hall A**, Sasahara TH, Ribeiro AA, Catania KC, Presgraves DC, Gorbunova V. Distinct tumor suppressor mechanisms evolve in rodent species that differ in size and lifespan. *Aging Cell*. 2008. PMID: 18778411; PMCID: PMC2637185.

## Skills

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### Molecular biology:

- Protocol development/experimental design
- Epigenetics protocols/Chromatin IP
- Single cell sequencing (10x Genomics)
- RNA-seq, EM-seq
- Tissue culture
- Protein expression/purification
- Western blot, column chromatography

### Bioinformatics:

- Genomics pipelines: ChIP-seq, RNA-seq, WGS, Single cell/nucleus RNA-seq
- Unix, R, HPC (SGE/SLURM), Python
- Data analysis and visualization (ggplot, dplyr, tidyr, tidyverse)
- Signal/noise enrichment peak identification (MACS2), pathway analysis, motif enrichment and identification

## Invited Talks

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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

Modeling Chromatin States to Elucidate Transcriptional Regulation in Glioblastoma, Chromatin, Non-coding RNAs and RNAP II Regulation in Development and Disease, Austin, TX. March 2016 \*

Modeling Chromatin States to Elucidate Transcriptional Regulation in Glioblastoma, Department of Molecular Biosciences Retreat. March 2016

Histone Modification Profiling in Glioblastoma Tumors Identifies Enhancer Variability, Big Data in Biology Symposium 2015, Austin, TX. May 2015 \*

Epigenetic Profiling and Chromatin Architecture in Glioblastoma, RNA and DNA Club, UT Austin. Feb. 2015

Histone Modification Profiling in Glioblastoma Tumors Identifies Enhancer Variability, Lost Pines Conference 2014, Smithville, TX. November 2014 \*

Optimizing ChIP in Cell Lines and Solid Tumors, M.D. Anderson Science Park, Smithville, TX. Nov. 2013

\* indicates a poster and talk were presented together.

## Posters

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

*Epigenetic Profiling and Clustering of Glioblastoma Multiforme*, Big Data in Biology Symposium 2014, Austin, TX, May 2014. **Won “Best Graduate Student Poster,” award.**

## Teaching Experience

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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**

Immersive approaches to biological data. Teaching assistant at Cold Spring Harbor Laboratories, December 2016.

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

Introduction to ChIP-seq. Short course for Center for Computational Biology and Bioinformatics. Co-instructor November 2015, December 2014.

Core Next Generation Sequencing Analysis Tools. Center for Computational Biology and Bioinformatics. Instructor October 2016, Teaching assistant October 2015.