

Mason D. Andrus, PhD

Behavioral Neuroscientist · Computational Biologist · Writer

Portland, OR (Open to Remote) • masondandrus@gmail.com
[linkedin.com/in/masondandrus](https://www.linkedin.com/in/masondandrus) • github.com/masondandrus

SUMMARY

Computational biologist and behavioral neuroscientist who connects experimental neuroscience with transcriptomics, machine learning, and human genetics. Leads projects from study design and molecular data generation through reproducible analysis, biological validation, and target prioritization in stress- and addiction-related psychiatric disease.

EDUCATION

Ph.D., Behavioral Neuroscience

September 2025

Oregon Health & Science University, School of Medicine — Portland, OR

B.A., Psychology, *cum laude*

June 2018

University of California, Los Angeles — Los Angeles, CA

CORE SKILLS

Genomics: RNA-seq (Salmon/tximport → DESeq2, edgeR/limma), ATAC-seq, CUT&RUN; WGCNA; fgsea; VIPER/DoRothEA; BayesPrism/InstaPrism

Statistics & Machine Learning: GLMs and mixed-effects models; LASSO with bootstrap stability selection; pose estimation (DeepLabCut, SLEAP); experimental design and power analysis

Human Genetics: GWAS Catalog; GTEx and RatGTEx eQTL; Allen Brain Cell Atlas; cross-species ortholog mapping

Programming & Bench: R, Python, SQL (BigQuery), Bash; Snakemake, Conda, Git/GitHub, GitHub Actions; RNA-seq/ATAC-seq/CUT&RUN library preparation; RT-qPCR; Pavlovian fear conditioning and extinction

EXPERIENCE

Postdoctoral Scientist — Computational Biology & Behavioral Neuroscience

September 2025 – Present

Lattal Lab, Oregon Health & Science University — Portland, OR

- Prioritized 19 candidate targets from 15,547 genes as computational lead of a UCSD (Palmer Lab) collaboration; each carries convergent co-expression, differential-expression, GWAS, and eQTL support that holds under resampling
- Replaced manual freezing scoring with custom DeepLabCut and SLEAP pose-estimation networks, benchmarked against human-scored data before adoption; now the lab default across hundreds of recorded sessions
- Vetted transcriptome-wide findings with LASSO stability selection, cell-type deconvolution (InstaPrism/BayesPrism), and transcription-factor activity inference (VIPER/DoRothEA); showed cell composition did not drive the gene-by-stress signal
- Designed a computational phenotyping approach that fits latent learning and extinction parameters from trial-level data and runs the transcriptomic analysis against them
- Design and run behavioral studies the computational work rests on
- Advise other labs in the department on RNA-seq, ATAC-seq, CUT&RUN, jetPEI transfection, and RT-qPCR, from experimental design through analysis
- Trained a graduate student and two research technicians to run the pose-estimation and RNA-seq pipelines independently

Doctoral Researcher — Transcriptomics & Computational Biology

September 2020 – September 2025

Walker Lab, OHSU School of Medicine — Portland, OR

- Led a five-year multi-cohort study of adolescent social isolation from design through library preparation to analysis, across three brain regions and multiple developmental timepoints
- Showed that adolescent isolation disrupts medial amygdala and ventral tegmental area maturation and sex-specifically dysregulates transcriptional responses to cocaine and stress (*Neuropharmacology*, 2025)
- Wrote the RNA-seq analysis pipeline the lab still runs (DESeq2, WGCNA, rank-based cross-cohort comparison), now applied to hundreds of samples across multiple projects by other analysts

- Standardized RNA-seq, ATAC-seq, and CUT&RUN library preparation so multi-cohort data stayed comparable, and built the RT-qPCR validation workflow
- Managed sequencing-core submissions and vendor selection; trained lab members and undergraduates in library preparation and analysis
- Deposited sequencing data to GEO/SRA (Gene Expression Omnibus / Sequence Read Archive) with full metadata; maintained version-controlled analysis code and written standard operating procedures (SOPs)

Social Editor

October 2021 – January 2023

RETURN Magazine — Portland, OR

- Grew the publication from launch to ~20,000 subscribers and 500K+ monthly impressions in 16 months; ran the newsletter, long-form features, and podcast through the publication's acquisition

Research Technician — Behavioral & Systems Neuroscience

July 2017 – May 2020

Craske, Lau, Wassum & Fanselow Labs, UCLA — Los Angeles, CA

- Ran human fMRI and rodent conditioning studies across four labs; performed fMRI preprocessing and group-level statistics

OPEN-SOURCE CODE

- **snakemake-sra-rnaseq** — public Snakemake workflow carrying SRA accessions through fastp, decoy-aware Salmon quantification, tximport, and DESeq2 to fgsea, WGCNA, and a config-driven multi-evidence convergence module. Per-rule pinned conda environments, BigQuery-generated sample sheets, GitHub Actions CI (continuous integration); validated on GSE42805. github.com/masondandrus/snakemake-sra-rnaseq

PEER-REVIEWED PUBLICATIONS

- **Andrus, M. D.**, Vu, T., Juarez, B., & Walker, D. M. (2025). Adolescent isolation disrupts medial amygdala and ventral tegmental area maturation and sex-specifically dysregulates transcriptional responses to cocaine and stress. *Neuropharmacology*, 279, 110629. <https://doi.org/10.1016/j.neuropharm.2025.110629>
- Williams, B. E., Martin, S. A., Hoffman, K. A., **Andrus, M. D.**, Dellabough-Gormley, E., & Buchheit, B. M. (2025). "It's within your own power": shared decision-making to support transitions to buprenorphine. *Addiction Science & Clinical Practice*, 20(1), 22. <https://doi.org/10.1186/s13722-025-00555-0>
- Bendersky, C. J., Milian, A. A., **Andrus, M. D.**, De La Torre, U., & Walker, D. M. (2021). Long-term impacts of post-weaning social isolation on nucleus accumbens function [Review]. *Frontiers in Psychiatry*, 12, 745406. <https://doi.org/10.3389/fpsy.2021.745406>

MANUSCRIPTS IN PREPARATION

- **Andrus, M. D.**, Vu, T., Bell, M., & Walker, D. M. Sex-specific disruption of prefrontal maturation following adolescent isolation: behavioral, hormonal, and transcriptional consequences. *First author; in preparation.*
- **Andrus, M. D.**, Lattal, M. Genetic predisposition to cue reactivity conditions behavioral and basolateral amygdala transcriptomic responses to trauma in heterogeneous stock rats. *First author; in preparation.*

GRANTS, TEACHING & SERVICE

- Wrote sections of, and generated pilot data for, funded NIH R01 and R21 applications totaling \$2.275M (Walker Lab, 2021–2025)
- Author and maintain the lab's IACUC animal-use protocols and amendments
- Designed and taught *Advanced Cellular Neurophysiology*, an original undergraduate course at Portland State University (2023–2024); guest lectures across departments
- Review manuscripts for *Learning & Memory* (Cold Spring Harbor Laboratory Press)
- Presented *Regulation of reward-related behaviors by D1 receptors in the main intercalated cell cluster of the amygdala* at the Society for Neuroscience and Pavlovian Society annual meetings (2022)