# Jared Andrews

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## Education

**Washington University in St. Louis** | St. Louis, MO | July 2014 - May 2020 (anticipated)

- Ph.D. in Molecular Genetics and Genomics
- Thesis Mentor: Dr. Jacqueline Payton
- Thesis: Defining New Pathways of Lymphoma Pathogenesis Through Integrated 'omics

**University of Louisville** | Louisville, KY **|** September 2010 **-** May 2014

- B.S. in Biology, subcellular/genetics concentration
- Honors: *summa cum laude,* Honor's Scholar, Grawemeyer Scholar (research scholarship)
- Thesis Mentor: Dr. Michael Perlin
- Senior Honors Thesis: Identification and Expression Analysis of Sugar Transporters in *Microbotryum violaceum*

## Research Experience

**Ph.D. Graduate Student** | July 2014 - Present **|** 40+ hours/week
Lab of Dr. Jacqueline Payton | Washington University | St. Louis, MO

Project: Defining key super enhancers that drive oncogene expression and regulate tumor suppressive regulatory feedback programs in Non-Hodgkin's Lymphoma (NHL).

- Processed, sorted, organized, and banked >50 primary blood draws and tumor biopsies of Chronic Lymphocytic Leukemia (CLL), Follicular Lymphoma (FL), and Diffuse Large B Cell Lymphoma (DLBCL) patients to isolate malignant B cells.
- Performed integrative analyses combining epigenomic (histone ChIP-seq/FAIRE-seq), transcriptomic (RNA-seq), and genomic (SNP microarray) assays to define comprehensive multi-omics profiles and differences between NHL subtypes and healthy B cells.
- Identified numerous super enhancer driven transcriptional feedback programs that power expression of tumor suppressors such as RUNX3, SPI1 (PU.1), TCF3 (E2A), and USF2 that are absent in NHL.
- Defined the keystone constituent element of a super enhancer driving aberrant NHL expression of two Ig receptors, *FCMR* and *PIGR*, using reporter assays. Validated expression of PIGR in CLL via immunofluorescence.
- A manuscript describing the findings from this study is in preparation for submission to a peer-reviewed journal.

Project: Tracking cutaneous T cell lymphoma (CTCL) pathogenesis over time via single-cell sequencing technologies.

- Sorted and prepared >100k cells for single-cell RNA and immune repertoire sequencing.
- Guided study design and project direction to ensure data generated was sufficient to achieve all project goals.
- Analyzed and integrated multimodal bulk and single-cell data (RNA-seq, immune repertoire information, and mutations) to elucidate how CTCL progresses over time, how this progression may impact treatment efficiency, and how this progression differs between patients.
- A manuscript describing the findings from this study is in preparation for submission to a peer-reviewed journal.

Project: Identifying novel predictors of histone deacetylase inhibitor resistance in cutaneous T cell lymphoma (CTCL).

- Processed >100 primary blood draws and skin biopsies of CTCL patients to isolate malignant cell populations.
- Tracked specimen information and ensured organized, proper storage of hundreds of cryopreserved samples.
- Performed large-scale comparative 'omics analyses to identify transcriptomic and epigenetic differences between HDACi-resistant and sensitive patients, resulting in the discovery of novel pathways and a potential biomarker associated with HDACi-resistance in CTCL.
- Validated analyses findings via functional reporter assays, qRT-PCR, and ELISA assays in CTCL cell lines and patient samples.
- Summarized findings in a manuscript for peer review and publication (Andrews JM, et al. *EBioMedicine* 2019).

Project: Developing computational tools, storage practices, and workflows for processing large-scale sequencing data.

- Developed computational workflows to automate RNA-seq, ChIP-seq, and exome/whole-genome sequencing analyses using best practices, reducing hands-on time of basic analyses by more than 80% and dramatically reducing the entry barrier for new bioinformaticians.
- Provide extensive documentation to serve as a knowledgebase and entry guide for lab members and collaborators new to bioinformatics.
- Serve as the lab's data steward, ensuring all data is perpetually available, organized, secure, and redundantly backed up.
- Created a tool conglomerating information from dozens of sources for ultra-quick, comprehensive gene lookup that is used daily by every member of the lab (Andrews JM, et al. *JOSS* 2018).
- Analyze large-scale sequencing data for collaborators that lack computational skillsets, often expediting paper submissions and revisions by weeks (Morales AJ, et al. *eLife* 2017; Deepti S, et al. *Cell Reports* 2019).

Additional responsibilities:

- Mentor and train high school, undergraduate, rotation, and new graduate students. Directly mentored and trained 5 high school and undergraduate students in basic molecular biology, cell culture, and research ethics. Mentored and trained 5 rotation students, 2 of which joined the lab to perform their thesis work. Trained a new lab tech in cell culture, flow cytometry, molecular biology, and common administrative tasks (record keeping, supply ordering, etc).

**Undergraduate Researcher** | August 2011 - August 2012, May 2013 - June 2014 **|** 30-40 hours/week
Lab of Dr. Michael Perlin | University of Louisville | Louisville, KY

Project: Generating the reference genome for *Microbotryum violaceum*

- Infected and maintained dozens of host plants with *Microbotryum violaceum* over two years.
- Tracked, collected, and preserved infected host tissue at 5+ developmental stages.
- Isolated RNA from infected tissues and cultured samples for subsequent RNA-seq.
- Identified putative sugar transporter genes from whole-genome sequencing and RNA-seq data through homology and temporal expression changes.
- Contributed data to a peer-reviewed publication detailing the generation of the reference genome for *Microbotryum violaceum* (Perlin MH, et al. *BMC Genomics* 2015).

Project: Investigating *Microbotryum violaceum* temporal gene expression changes during host invasion

- Performed exhaustive data mining on existing literature to execute comparisons of sugar transporters in *Microbotryum violaceum* and other fungi.
- Elucidated candidate sugar transporters involved in evading host defenses during invasion via qRT-PCR of samples from different stages of plant and flower development.
- Contributed analyses and figures to a peer-reviewed publication describing differences in transporter families among pathogenic fungi (Perlin MH, et al. *Adv Genet* 2014).

**Lab Technician** | August 2012 - May 2013 **|** 15-20 hours/week
Advanced Genomic Technology | Louisville, KY

Project: Development of microRNA-based blood tests for early detection of Alzheimer's Disease

- Genotyped transgenic mice and assigned for use in various experiments or additional breeding.
- Assessed presence of microRNA biomarkers in blood plasma samples via RT-qPCR.

## Funding

- NCI F31 Fellowship (F31CA221012, 2017 – Present)
- Summer Research Opportunity Program (University of Louisville, 2013)
- Undergraduate Research Scholar Grant (University of Louisville, 2013)

## Skills

- Molecular biology (cloning, PCR, RNA/DNA isolation, Western blotting, qRT-PCR, etc)
- Cell culture (cell lines and primary cells)
- Immunofluorescence
- Flow cytometry/sorting
- Science writing (for both expert and lay audiences)
- Public speaking (to both expert and lay audiences)
- Study and project design
- Bioinformatics and big data analysis
    - Competent in R, python, bash, and general UNIX usage
    - Big data handling & analysis (1 TB+ scale)
        - Parallelization and high-performance computing cluster use
    - Advanced data visualization (ggplot2, matplotlib, etc)
    - RNA-seq, ChIP-seq, and WGS analysis
        - Differential gene expression
        - ChIP-seq peak calling and differential binding analyses
        - Variant/copy number alteration calling and comparison
    - Multimodal data integration
    - Single-cell RNA and V(D)J sequencing analysis
    - R and python package development
    - Web development (javascript, web design)
    - Workflow creation
    - Interactive analysis and documentation via Jupyter notebook/Rmarkdown
    - Statistics

## Teaching Experience

**Graduate Teaching Assistant**, Fall 2015, Bio 437
Washington University in St. Louis
Course: Laboratory on DNA Manipulation

**Undergraduate Teaching Assistant**, Fall 2012, Spring 2013
University of Louisville
Course: Principles of Biology - Lab

## Peer-Reviewed Publications

Andrews JM, Schmidt JA, Carson KR, Musiek AC, Mehta-Shah N, Payton JE: Novel cell adhesion/migration pathways are predictive markers of HDAC inhibitor resistance in cutaneous T cell lymphoma. *EBioMedicine* 2019, 46:170–183.

Deepti S, White LS, Yang W, Johnston R, Andrews JM, Murphy KM, Mosammaparast N, Payton JE, Bednarski JJ: RAG-mediated DNA breaks attenuate PU.1 activity in early B cells through activation of a SPIC-BCLAF1 complex. *Cell Reports* 2019, 29(4):829-843.

Andrews JM, Payton JE: Epigenetic dynamics in normal and malignant B cells: die a hero or live to become a villain. *Current Opinion in Immunology* 2019, 57:15–22.

Andrews JM, El-Alawi M, Payton JE: Genotify: Fast, lightweight gene lookup and summarization. *J Open Source Softw* 2018, 3.

Morales AJ, Carrero JA, Hung PJ, Tubbs AT, Andrews JM, Edelson BT, Calderon B, Innes CL, Paules RS, Payton JE, et al.: A type I IFN-dependent DNA damage response regulates the genetic program and inflammasome activation in macrophages. *eLife* 2017, 6:e24655.

Perlin MH, Amselem J, Fontanillas E, Toh SS, Chen Z, Goldberg J, Duplessis S, Henrissat B, Young S, Zeng Q, Anguileta G, Petit E, Badouin H, Andrews JM, et al.: Sex and parasites: genomic and transcriptomic analysis of Microbotryum lychnidis-dioicae, the biotrophic and plant-castrating anther smut fungus. *BMC Genomics* 2015, 16:1–24.

Perlin MH, Andrews JM, Toh SS: Essential letters in the fungal alphabet: ABC and MFS transporters and their roles in survival and pathogenicity. *Adv Genet* 2014, 85:201–253.

## Manuscripts in Preparation

Andrews JM, Pyfrom SC, Schmidt JA, et al.: Key Super-Enhancers Drive Tumor-Suppressing Transcriptional Feedback Programs and Disease-Defining Oncogenes in B Cell Cancers.

Pei J*, Beri N*, Zou, A, Andrews JM, et al.: Molecular Basis for Nuclear Function of Human Respiratory Syncytial Virus Non-Structural Protein NS1.

Fong J, Gardner JR, Andrews JM, Cashen AF, Payton JE, Weinberger KQ, Edwards JR: Determining subpopulation methylation profiles from bisulfite sequencing data from heterogeneous samples using DXM.

## Conference Posters

Andrews JM, Schmidt J, Payton J: Mapping the transcriptome and epigenomic landscape of HDAC-inhibitor resistant CTCL. *The Journal of Immunology* 2018, 200:123.5-123.5.

Andrews JM*, Zaydman M*, Pyfrom S, Schmidt J, Luo H, Koues O, Oltz E, Payton J: A Precision Medicine Approach Using Whole Transcriptome Profiling by RNA-seq for B Cell Cancers. *Am J Clin Pathol* 2018, 149:S167–S167.

Fennoy A, Fong J, Andrews JM, Gasparrini A, Edwards J: Identifying Potential Drivers of Differential DNA Methylation Patterns in Breast Cancer Cells. *The FASEB Journal* 2015, 29:LB143.

## Selected Talks

Defining New Pathways of Lymphoma Pathogenesis Through Integrated 'omics. Washington University Molecular Genetics and Genomics Retreat. Trout Lodge, MO. October 10th, 2019.

Tracking Lymphoma Pathogenesis Through Integrated 'omics. Washington University Cancer Genomics Group Work-in-Progress. October 7th, 2019.

The Regulation and Roles of Two Ig Receptors in B Cell Cancers. Washington University Pathology and Immunology Work-in-Progress. April 13th, 2018.

## Professional Organizations

- American Association for the Advancement of Science. Member, 2018 – Present.
- American Association of Immunologists. Member, 2018 – 2019.

## References

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