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Tyler Hansen

PhD Candidate
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EDUCATION

Ph.D. Candidate • Vanderbilt University • Nashville, TN 2017-present
Advisor: Emily Hodges, Ph.D
Thesis Project: Development and use of ATAC-STARR-seq to investigate cis and trans effects on human gene regulatory evolution.

Bachelor of Science • University of Wisconsin • Madison, WI 2011-2015
Major: Biochemistry
Advisor: Judith Kimble, Ph.D

RESEARCH EXPERIENCE

Ph.D. Candidate • Vanderbilt University • Nashville, TN 2017-present
- Wet/dry lab researcher in Prof. Emily Hodges' Lab in the Department of Biochemistry.
- Overall, I apply functional genomic technologies to understand gene regulatory evolution of humans.
- I developed ATAC-STARR-seq to measure regulatory element activity, chromatin accessibility, and TF footprinting from a single DNA fragment source.
- I then applied ATAC-STARR-seq and other functional genomic technologies to investigate *cis* and *trans* effects on human gene regulatory evolution.
- As part of *cis/trans* project, I have been collaborating Prof. John A. Capra's Lab at University of California – San Francisco.
- I have skills in both wet/dry lab techniques that allow me to both generate and analyze functional genomic data.

Post-Baccalaureate IRTA Fellow • NIDDK | NIH • Bethesda, MD 2015-2017
- Researcher in Dr. Andy Golden's Lab in the Laboratory of Biochemistry and Genetics within the National Institute of Diabetes and Digestive and Kidney Disease at the National Institutes of Health Intramural Campus.
- I used CRISPR/Cas9 genome editing to generate molecular models of rare human monogenic diseases in *C. elegans* for purposes of elucidating unknown disease mechanisms and developing potential drug treatments.
- I developed disease models for NGLY1 deficiency and four craniofacial disorders.
- I also generated CRISPR mutants for a variety of collaborations.

Undergraduate Researcher • University of Wisconsin • Madison, WI 2012-2015
- Researcher in Prof. Judith Kimble's Lab in the Department of Biochemistry.
- Investigated genetic regulation of stem cell fate using *C. elegans* as a model.

TEACHING AND MENTORING EXPERIENCE

Assistant Facilitator • Vanderbilt University • Nashville, TN Fall 2021
- Lead a first-year graduate student discussion group as a key contributor to the first-year IGP program.
- Teaching duties involved facilitating discussion of journal articles, assisting with problem set questions, and grading various assessments.

Undergraduate Mentor • Vanderbilt University • Nashville, TN 2018-2021
- Mentored two undergraduate researchers in relevant techniques, such as: ATAC-seq, electroporation transfection, flow cytometry, western blotting, human embryonic stem cell culture, and standard mammalian tissue culture.

PUBLICATIONS

Vanderbilt University

PLACEHOLDER for the cis/trans paper. Hansen, T., and Hodges, E. (2022). ATAC-STARR-seq reveals transcription factor-bound activators and silencers across the chromatin accessible human genome. *Genome Research* 32, 1529-1541. doi: 10.1101/gr.276766.122. PMID: 35858748.

PLACEHOLDER for tims paper. Hansen, T., and Hodges, E. (2022). ATAC-STARR-seq reveals transcription factor-bound activators and silencers across the chromatin accessible human genome. *Genome Research* 32, 1529-1541. doi: 10.1101/gr.276766.122. PMID: 35858748.

Hansen, T., and Hodges, E. (2022). ATAC-STARR-seq reveals transcription factor-bound activators and silencers across the chromatin accessible human genome. *Genome Research* 32, 1529-1541. doi: 10.1101/gr.276766.122. PMID: 35858748.

Barnett, K. R., Decato, B., Scott, T., Hansen, T., Chen, B., Attalla, J., Smith, A., & Hodges, E. (2020). ATAC-Me Captures Prolonged DNA Methylation of Dynamic Chromatin Accessibility Loci During Cell Fate Transitions. *Molecular Cell*. *77*(6), 1350–1364. doi: https://doi.org/10.1016/j.molcel.2020.01.004. PMID: 31999955.

Guarnaccia, A. D., … Hansen, T., … Tansey, W. P. (2021) Impact of WIN site inhibitor on the WDR5 interactome. *Cell Reports.* 34(3), 108636. doi: 10.1016/j.celrep.2020.108636. PMID: 33472061.

NIDDK | NIH

Eustice, M., Konzman, D., Reece, J.M., Ghosh, S., Alston, J., Hansen, T., Golden, A., Bond, M.R., Abramowitz, L.K., and Hanover, J.A. (2022). Nutrient sensing pathways regulating adult reproductive diapause in C. elegans. *PLoS One.* 17, e0274076. doi: 10.1371/journal.pone.0274076. PMID: 36112613.

Rourke, C.K., Murat, D., Hansen, T., and Jaramillo-Lambert, A. (2021) Endogenous localization of TOP-2 in C. elegans using a C-terminal GFP-tag. *microPublication Biology*. doi: 10.17912/micropub.biology.000402. PMID: 34095779.

Fernando, L., Nguyen, V., Hansen, T., Golden, A., & Allen, A. (2020). Loss of proteasome subunit RPN-12 causes an increased mean lifespan at a higher temperature in C. elegans. *microPublication Biology*. doi: 10.17912/micropub.biology.000234. PMID: 32550497.

Iyer, J., Devaul, N., Hansen, T., & Nebenfuehr, B. (2019). Using Microinjection to Generate Genetically Modified Caenorhabditis elegans by CRISPR/Cas9 Editing. Methods Mol. Biol., 1874, 431—457. doi: 10.1007/978-1-4939-8831-0_25. PMID: 30353529. (Invited book chapter).

Kim, S., Twigg, S. R. F., Scanlon, V. A., Chandra, A., Hansen, T. J., Alsubait, A., … Corsi, A. K. (2017). Localized TWIST1 and TWIST2 basic domain substitutions cause four distinct human diseases that can be modeled in *Caenorhabditis elegans*. *Human Molecular Genetics*, *26*(11), 2118–2132. https://doi.org/10.1093/hmg/ddx107. PMID: 28369379.

Jaramillo-Lambert, A., Fabritius, A. S., Hansen, T. J., Smith, H. E., & Golden, A. (2016). The Identification of a Novel Mutant Allele of topoisomerase II in *Caenorhabditis elegans* Reveals a Unique Role in Chromosome Segregation During Spermatogenesis. *Genetics*, *204*(4), 1407–1422. https://doi.org/10.1534/genetics.116.195099. PMID: 27707787.

University of Wisconsin

Kershner, A. M., Shin, H., Hansen, T. J., & Kimble, J. (2014). Discovery of two GLP-1/Notch target genes that account for the role of GLP-1/Notch signaling in stem cell maintenance. *Proceedings of the National Academy of Sciences of the United States of America*, *111*(10), 3739–3744. https://doi.org/10.1073/pnas.1401861111. PMID: 24567412.

PRESENTATIONS

ORAL PRESENTATIONS:

- *Identifying transcription factor-bound activators and silencers in the chromatin accessible genome using ATAC-STARR-seq.* 2022 Biochemistry Retreat, Chattanooga, TN, April 2022.
- *Investigating gene regulatory mechanisms of human evolution with ATAC-STARR-seq.* Biochemistry Student Association Colloquium, Vanderbilt University, TN, April 2022.
- *Simultaneous profiling of regulatory activity, chromatin accessibility, and transcription factor occupancy with ATAC-STARR-seq.* The 23rd Annual Vanderbilt University Program in Developmental Biology Retreat, Lake Guntersville State Park, AL, September 2021.
- *Investigating gene regulatory differences in primate immune cells with ATAC-STARR-seq.* Stem and Progenitor Cell Interest Group (SPRING) seminar, Vanderbilt University, TN, March 2021.
- *Using ATAC-STARR-seq to identify core units of transcriptional enhancers.* Biochemistry Student Association Colloquium, Vanderbilt University, TN, November 2019.

POSTER PRESENTATIONS:

- *Divergence in both cis and trans drives human gene regulatory evolution.* The 2022 American Society of Human Genetics Conference, Los Angeles, CA, October 2022.
- *A genome-wide reporter assay reveals human specific gene regulation in both cis and trans*. Keystone Symposia: Gene Regulation: From Emerging Technologies to New Models – RESCHEDULED, Santa Fe, NM, June 2022.
- *A genome-wide reporter assay reveals human specific gene regulation in both cis and trans*. The 2022 Biochemistry Retreat, Chattanooga, TN, April 2022.
- *Genome-wide reporter assay reveals human specific gene regulation in both cis and trans*. The Cold Spring Harbor Laboratory Meeting on Systems Biology: Global Regulation of Gene Expression, Cold Spring Harbor, NY, March 2022.
- *ATAC-STARR-seq to quantify the regulatory potential of chromatin accessible genomes.* The 5th Annual Cold Spring Harbor Laboratory Meeting on Epigenetics and Chromatin, Virtual Conference, September 2020.
- *Assaying Enhancer Activity with ATAC-STARR-seq.* The 22st Annual Vanderbilt University Program in Developmental Biology Retreat, Pickwick Landing State Park, TN, September 2019.
- *A Functional and Unbiased Approach to Measure Global Enhancer Activity Dynamics During Cell Fate Transitions.* The 4th Annual Biochemistry Department Retreat, Vanderbilt University, February 2019.
- *A Functional and Unbiased Approach to Measure Global Enhancer Activity Dynamics During Cell Fate Transitions.* The Epithelial Biology Center & Center for Stem Cell Biology Symposium, Vanderbilt University, April 2019.
- *Measuring enhancer activity dynamics during human pluripotent stem cell differentiation using ATAC-STARR.* The 21st Annual Vanderbilt University Program in Developmental Biology Retreat, Montgomery Bell State Park, TN, September 2018.

AWARDS AND HONORS

- Keystone Symposia Travel Scholarship**,** Gene Regulation: From Emerging Technologies to New Models – RESCHEDULED, Santa Fe, NM, June 2022
- Best Poster Award, The 2022 Biochemistry Retreat, Chattanooga, TN, April 2022
- Best Poster Award - Honorable Mention, The 22nd Annual Vanderbilt University Program in Developmental Biology Retreat, Pickwick Landing State Park, TN, September 2019