

ERIN WISSINK, PHD

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SUMMARY

- Genomics and molecular biology expert with 13+ years bioinformatics and NGS experience
- Co-author of ten peer-reviewed articles (five first-author) and four preprints
- Cross-functional scientist and communicator who turns big data into discoveries

EDUCATION

Cornell University, Ithaca, NY 2009-2016

PhD, Biochemistry, Molecular, and Cell Biology

National Science Foundation Graduate Research Fellow

Dissertation: "Post-transcriptional gene regulation: Roles for microRNAs in CD8+ T cells and discovery of novel cis-regulatory elements"

North Carolina State University, Raleigh, NC 2004 - 2008

BS, Biological Sciences; BA, History

National Merit Scholarship, Phi Beta Kappa

Graduated with honors and *summa cum laude*

EXPERIENCE

Embark Veterinary Ithaca, NY

Senior Scientist, Epigenetics

Research Scientist II, Epigenetics

Oct 2022 - present

Oct 2021 - Sept 2022

- Established epigenomics research program at Embark, using predictive models and machine learning
- Used DNA methylation data from thousands of dogs to investigate epigenetic signatures of aging and wellness
- Developed QC metrics and data analysis pipelines for custom DNA methylation microarrays
- Communicated complex science to a cross-functional team with Product and Engineering

Cornell University Ithaca, NY

NIH Ruth L. Kirschstein NRSA Postdoctoral Fellow

Jul 2017 - Sept 2021

- Used CRISPR-Cas9 genome editing, nascent RNA-seq, and genomics analysis to investigate enhancer RNAs
- Discovered interplay between cell type-specific gene expression and small molecule signaling, using systems biology analysis of RNA-seq, ChIP-seq, and ATAC-seq data
- Contributed to interdisciplinary collaborations with six research groups (internal and external to Cornell)
- Successfully applied for postdoctoral research funding and contributed to several lab grant applications

University of California, Los Angeles

Postdoctoral Associate

Los Angeles, CA

Jan 2016 - Jun 2017

- Researched regulation of mammalian co-transcriptional splicing, using RNA-sequencing, cell culture, CRISPR-Cas9 genome editing, and data analysis as a member of the UCLA Ribonomics Group collaboration

Cornell University

PhD Student

Ithaca, NY

Aug 2009 - Nov 2015

- Developed a high-throughput screen to discover novel post-transcriptional regulatory sequences, using cell culture and high-throughput sequencing
- Led collaboration with immunologists to identify how microRNA expression affects the neonatal immune system

SKILLS

- Scripting with Python (scikit-learn, pandas, numpy, matplotlib), R (Bioconductor, tidyverse, ggplot), and Linux
- Creating bioinformatics pipelines and analyzing genomics data (Tuxedo suite, HT-seq, HOMER)
- Using AWS for storage and computing and Git for version control
- Generating and analyzing high-throughput sequencing libraries (mRNA, small RNA, and nascent RNA)
- Communicating scientific findings to cross-functional and interdisciplinary audiences

SELECTED PUBLICATIONS

1. Lefaudeaux D, Sen S, Jiang K, Hoffmann A, **UCLA Ribonomics Group**. Kinetics of mRNA nuclear export regulate innate immune response gene expression. *Nature Communications* 13, 7197 (2022).
2. Jambor H, Antonietti A, Alicea B, Audisio TL, Auer S, Bhardwaj V, Burgess SJ, Ferling I, Gazda MA, Hoepfner LH, Ilangovan V, Lo H, Olson M, Mohamed SY, Sarabipour S, Varma A, Walavalkar K, **Wissink EM**, Weissgerber TL. Creating clear and informative image-based figures for scientific publications. *PLOS Biology* 19, e3001161 (2021).
3. **Wissink EM***, Vihervaara A*, Tippens ND, Lis JT. Nascent RNA analyses: Tracking transcription and its regulation. *Nature Reviews Genetics* 20, 705-523 (2019).
4. Wang J*, **Wissink EM***, Watson N*, Smith NL, Grimson A, Rudd BD. Fetal and adult progenitors give rise to unique populations of CD8+ T cells. *Blood* 128, 3073-3082 (2016).
5. **Wissink EM**, Fogarty E, Grimson A. High-throughput discovery of post-transcriptional cis-regulatory elements. *BMC Genomics* 17, 177 (2016).
6. **Wissink EM***, Smith NL*, Spektor R, Rudd BD, Grimson A. MicroRNAs and their targets are differentially regulated in adult and neonatal mouse CD8+ T cells. *Genetics* 201, 1017-1030 (2015).
7. Smith NL*, **Wissink EM***, Grimson A, Rudd BD. miR-150 regulates differentiation and cytolytic effector function in CD8+ T cells. *Scientific Reports* 5, 16399 (2015).
8. Saha RN, **Wissink EM**, Bailey ER, Zhao M, Fargo DC, Hwang JY, Daigle KR, Fenn DJ, Adelman K, Dudek SM. Rapid activity-induced transcription of arc and other IEGs relies on poised RNA polymerase II. *Nature Neuroscience* 14, 848-856 (2011).

* indicates co-first authorship

SELECTED PREPRINTS

1. **Wissink EM**, Martinez DM, Ehmsen KT, Yamamoto KR, Lis JT. Glucocorticoid receptor collaborates with pioneer factors and AP-1 to execute genome-wide regulation. *bioRxiv* (2021) doi: 10.1101/2021.06.01.444518.
2. Judd J, Wojenski LA, Wainman LA, Tippens ND, Rice EJ, Dziubek A, Villafano GJ, **Wissink EM**, Versluis P, Bagepalli L, Shah SR, Mahat DB, Tome JM, Danko CG, Lis JT, Core LJ. A rapid, sensitive, scalable method for Precision Run-On sequencing (PRO-seq). *bioRxiv* (2020) doi: 10.1101/2020.05.18.102277.

COURSEWORK

- Data Science Associate with Python Certificate (DataCamp, 2023)
- Machine Learning Fundamentals with Python track (DataCamp, 2023)
- Leadership Essentials Certificate (Cornell University, 2022)
- Workshops in R, Statistics, and NGS analysis (UCLA Collaboratory, 2016)
- Science Writing for Media (Cornell University, 2012)
- Applied Bioinformatics (Cornell University, 2010)