

# ERIN WISSINK, PHD

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## EDUCATION

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**Cornell University**, Ithaca, NY 2009 - 2016  
PhD, Biochemistry, Molecular, and Cell Biology

**North Carolina State University**, Raleigh, NC 2004 - 2008  
BS, Biological Sciences  
BA, History

## EXPERIENCE

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**Embark Veterinary** Ithaca, NY  
Senior Scientist, Computational Biology Oct 2022 - Nov 2024  
Research Scientist II, Epigenetics Oct 2021 - Sept 2022

- Co-developed Embark's Dog Age Test by designing experiment for recruiting dogs of known ages, assessing DNA methylation data quality, testing penalized regression and random forest models, writing internal white paper, and explaining claims allowed by our predictive model to stakeholders
- Selected custom markers to add to our DNA methylation microarray, which enabled epigenetic-wide analysis studies for wellness, cancer, and aging
- Led experiments to benchmark QC metrics for custom DNA methylation microarrays
- Acted as lead scientist for creating DNA methylation data ingestion and analysis pipeline
- Managed project to recruit 800+ cats for research, which included planning logistics efforts, creating our sample tracking system, and collaborating with other scientists and software engineers

**Cornell University** Ithaca, NY  
NIH Ruth L. Kirschstein NRSA Postdoctoral Fellow with Prof. John Lis Jul 2017 - Sept 2021

- Used CRISPR-Cas9 genome editing, nascent RNA-seq, and genomics analysis to perturb and measure enhancer RNA transcription
- Discovered interplay between cell type-specific transcription factors and glucocorticoid signaling in enhancer RNA activation, using systems biology analysis of RNA-seq, ChIP-seq, and ATAC-seq data (see Ref. [12](#))
- Investigated transcription changes at estrogen-responsive enhancer RNAs (see Ref. [1](#))
- Optimized PRO-seq assay for low-input samples (see Ref. [13](#))
- Co-first authored highly cited Nature Reviews Genetics paper about nascent RNA-seq methods (see Ref. [4](#))
- Contributed to interdisciplinary collaborations with six research groups (internal and external to Cornell; see Refs. [1](#), [12](#), [13](#))
- Won an NIH postdoctoral fellowship and contributed to several lab grant applications (to NIGMS, NIA, and NHGRI; sections included Research Strategy, Personnel Justification, Facilities, and Equipment)

**University of California, Los Angeles**  
Postdoctoral Associate with Prof. Tracy Johnson

Los Angeles, CA  
Jan 2016 - Jun 2017

- Researched regulation of mammalian co-transcriptional splicing in macrophages by stimulating cells, then preparing rRNA-depleted RNA-sequencing libraries from fractionated chromatin, nucleoplasm, and cytoplasm (see Ref. [2](#))
- Member of the UCLA Ribonomics Group collaboration
- Contributed to Research Strategy section of lab grant application to NIGMS

**Cornell University**  
PhD Student with Prof. Andrew Grimson

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 (see Ref. [6](#))
- Identified how microRNA expression affects CD8+ T cells and how development alters gene regulation in neonatal and adult immune systems, in collaboration with Brian Rudd at Cornell (see Refs. [5](#), [7](#), [8](#), [9](#))

**National Institute of Environmental Health Sciences**  
Undergraduate Researcher with Dr. Serena Dudek

Research Triangle Park, NC  
Jun 2007 - May 2009

- Researched transcription regulation in long-term memory formation, using cortical cell culture and qPCR (see Refs. [10](#), [11](#))

## AWARDS

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|---|----------------|
| • National Merit Scholarship  | 2004 - 2008    |
| • Phi Beta Kappa  | 2007 - present |
| • National Science Foundation Graduate Research Fellowship                    | 2011 - 2014    |
| • Ruth L. Kirschstein Postdoctoral Individual National Research Service Award | 2018 - 2020    |

## ACTIVITIES

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- 2023-present—Volunteer with ASXL Rare Research Endowment, providing critical scientific feedback about rare disease mechanisms and collating research database
- 2018-2019—eLife Ambassador, contributed to projects about meta-research, preprints, and public involvement in research (see Refs. [3](#), [14](#))
- 2015-2020—Letters to a Prescientist, penpal, classroom coordinator, and Scientific Advisory Board Member for an organization that connects students in low socioeconomic areas with STEM professionals
- 2018—Participant in ComSciCon-Cornell, receiving training in communicating science with a lay audience

## COURSEWORK

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- Machine Learning Scientist with Python career track, consisting of >90 hours of videos and hands-on exercises (DataCamp, 2023)
- Data Science Associate with Python Certificate (DataCamp, 2023)
- Leadership Essentials Certificate, including courses in team performance, active listening, and effective hiring (Cornell University, 2022)

- Intergroup Dialogue Workshop, focused on communicating across differences and increasing DEI in academia (Cornell University, 2018)
- Workshops in R, Statistics, and NGS analysis (UCLA Collaboratory, 2016)
- Science Writing for Media (Cornell University, 2012)
- Applied Bioinformatics (Cornell University, 2010)

## PUBLICATIONS

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1. Ginley-Hidinger M, Abewe H, Osborne K, Richey A, Kitchen N, Mortenson KL, **Wissink EM**, Lis J, Zhang X, Gertz J. [Cis-regulatory control of transcriptional timing and noise in response to estrogen](#). *Cell Genomics* 4, 100542 (2024).
2. Lefaudeux 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).
3. Jambor H, Antonietti A, Alicea B, Audisio TL, Auer S, Bhardwaj V, Burgess SJ, Ferling I, Gazda MA, Hoepfner LH, Ilango 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).
4. **Wissink EM\***, Vihervaara A\*, Tippens ND, Lis JT. [Nascent RNA analyses: Tracking transcription and its regulation](#). *Nature Reviews Genetics* 20, 705-523 (2019).
5. 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).
6. **Wissink EM**, Fogarty E, Grimson A. [High-throughput discovery of post-transcriptional cis-regulatory elements](#). *BMC Genomics* 17, 177 (2016).
7. **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).
8. 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).
9. Smith NL, **Wissink E**, Wang J, Pinello JF, Davenport MP, Grimson A, Rudd BD. [Rapid proliferation and differentiation impairs the development of memory CD8+ T cells in early life](#). *Journal of Immunology* 193, 177-84 (2014).
10. 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).
11. Adams JP, Robinson RA, Hudgins ED, **Wissink EM**, Dudek SM. [NMDA receptor-independent control of transcription factors and gene expression](#). *Neuroreport* 16, 1429-33 (2009).

## PREPRINTS

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12. **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).

13. 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).
14. Sarabipour S\*, **Wissink EM\***, Burgess SJ\*, Hensel Z, Debat H, Emmott E, Akay A, Akdemir K, Schwessinger B. [Maintaining confidence in the reporting of scientific outputs](#). PeerJ Preprints (2018).

\* indicates co-first authorship