Mackenzie Noon

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EDUCATION

Yale University, New Haven, CT *Fall 2022 – present*

Ph.D. Candidate, Department of Genetics (admitted to candidacy)

M.Phil., Genetics *2024*

- Advisor: Steven K. Reilly, Ph.D.

University of California, Berkeley *2019 – 2021*

B.A., awarded with Honors *2021*

- GPA 3.888/4.0. Coursework: biochemistry, genetics, developmental biology, immunology, physiology, data science, computational biology.

University of California, Davis *2017 – 2019*

- Provost's Undergraduate Fellowship. Foundational coursework in chemistry, physics, calculus, biology, and computer science.

FELLOWSHIPS AND HONORS

- **Gruber Science Fellowship**, Yale University
- **Boehringer Ingelheim BEST Program** Emerging Scientific Talent awardee
- **NSF Graduate Research Fellowship Program**, Honorable Mention
- **Provost's Undergraduate Fellowship**, UC Davis

PUBLICATIONS

Author order reflects contribution; asterisks (*) denote equal contribution.

- Butts JC, Rong S, Gosai SJ, Castro RI, **Noon M**, Adeniran K, Ghosh R, Sabeti PC, Tewhey R, Reilly SK. *Identifying non-coding variant effects at scale via machine learning models of cis-regulatory reporter assays.* bioRxiv (2025). In revision at *Nature*. doi:10.1101/2025.04.16.648420.
- Jensen TB[†], Zhong L[†], Zhu L, Chitrakar A, Ming H, Dias N, Li Y, Balowski J, Gbyli R, **Noon M**, Hou TJ, Ardestani G, Starble R, Sun E, Scatolin GN, Sakkas D, Smith ZD, Wang S, Jiang Z*, Sozen B*, Xiao AZ*. *Histone variant H2A.J regulates trophoblast development through ribosome biogenesis in early human development.* (In revision, 2026). *Contribution:* Performed single-cell RNA-seq analysis of human embryo datasets; contributed to hESC engineering experiments.
- Rodríguez-Martínez J, Peña-Martínez E, Sharma S, Medina-Feliciano J, Root E, Parks L, Granitto M, Pomales-Matos D, Messon-Bird J, Barreiro-Rosario A, Sanabria-Alberto L, Rivera-Madera A, Rodríguez-Ríos J, Velázquez-Roig R, Figueroa-Rosado J, **Noon M**, Donmez O, Forney C, Hesse H, Dunn K, Chen X, Hass M, Lawson L, Weirauch M, Kottyan L, Reilly S, Bhimsaria D. *Global evaluation of congenital heart disease-associated non-coding variants.* bioRxiv (2026). In review at *Nature Communications*. doi:10.64898/2025.12.02.691900. *Contribution:* MPRA data analysis.
- Chitrakar A, **Noon M**, Xiao AZ. *Taming the transposon: H3K9me3 turns foe to friend in human development. Cell Stem Cell* (2022). doi:10.1016/j.stem.2022.06.010.
- Modzelewski AJ, Shao W, Chen J, Lee A, Qi X, **Noon M**, Tjokro K, Sales G, Biton A, Anand A, Speed TP, Xuan Z, Wang T, Risso D, He L. *A mouse-specific retrotransposon drives a conserved Cdk2ap1 isoform essential for development. Cell* (2021). doi:10.1016/j.cell.2021.09.021.

Software (first author / maintainer):

- `scMPRAforge`: Python package for simulation, hypothesis testing, and design of single-cell massively parallel reporter assays (scMPRA). Manuscript in preparation; open-source release pending.
- `tensorzinb-plusplus`: Fork of the TensorZINB solver adding modern-TensorFlow support, sparse input matrices, and sample-weighted zero-inflated negative binomial regression, enabling scalable modeling of single-cell reporter-

assay count data.

RESEARCH EXPERIENCE

Graduate Researcher, Reilly Lab, Yale Department of Genetics *Fall 2022 – present*

- Developing scMPRAforge: a statistical framework and software suite for single-cell massively parallel reporter assays, including novel zero-inflation correction, hypothesis testing (Wald, Mann–Whitney U, bootstrap), and power-analysis tooling.
- Applied deep convolutional neural network ensembles to predict transcriptional-modulatory effects of non-coding human variants at genome scale (MPAC / Butts et al., 2025).
- Developing and optimizing a combinatorial-barcoding scMPRA experimental protocol for cell-type-resolved measurement of cis-regulatory element activity.

Post-baccalaureate Research Associate, Xiao Lab, Yale *Summer 2021 – Fall 2022*

- Investigated the role of Alkbh1 in early mammalian development using cell culture and mouse models.

Undergraduate Researcher, He Lab, UC Berkeley *Fall 2019 – Summer 2021*

- Characterized retrotransposon-derived chimeric gene isoforms (Cdk2ap1, Rpl41) in human and murine development through transcriptomic analysis and mouse knockout models; established and applied a single-embryo qPCR protocol; wrote software to evaluate evolutionary conservation of novel retrotransposon-derived isoforms.

Undergraduate Researcher, Kaplan Lab, UC Davis *Winter 2018 – 2019*

- Investigated the role of autophagy in chromosome segregation during anaphase in *S. cerevisiae*.

TEACHING AND MENTORSHIP

- **Teaching Assistant, GENE 760: Genomic Methods for Genetic Analysis**, Yale (Winter 2025). Lecturing and curriculum refinement.
- **Teaching Assistant, Bioinformatics Bootcamp**, Yale (Winter 2024, Winter 2025). Introduced graduate students and postdoctoral fellows to bioinformatic analysis.
- **Instructor, Yale Pathways to Science** (Spring 2024). Designed and taught biology curriculum to middle- and high-school students as part of Yale's community outreach program.
- **Graduate Student Instructor, MCB 141: Developmental Biology**, UC Berkeley (Spring 2021). Discussion sections, curriculum design, quiz writing, and office hours.
- **Instructor, Redlands Conservatory** (Oct. 2014 – Sept. 2018). Designed and taught multi-year courses in Python programming, Scratch, robotics, and animation for K–12 students.
- **Python Course Instructor, Grove High School** (Spring 2017). Designed and taught a Python programming course.

SERVICE AND OUTREACH

- **Yale Center for Research Computing (YCRC), collaborator** (2023 – present). Worked with YCRC staff to improve cluster support for data-intensive biology workflows, including configuration and troubleshooting of distributed-computing and large-scale analysis tooling in response to the needs of my own and other groups' research.
- **Open Insulin Project**, wet-lab and science-outreach working group (2020). Contributed to plasmid construction for distributed insulin production; built web tools and content-management system.
- **IGI-Fast COVID-19 testing study**, UC Berkeley (Summer 2020). Volunteer and paid kiosk worker supporting a campus SARS-CoV-2 testing program.
- **iGEM UC Berkeley**, computational team (2020). Contributed to development of a machine-learning literature-search tool.
- **Davis Community Meals**, Dining Room Coordinator (2018 – 2019). Managed volunteer groups at a community soup kitchen.
- **Citizens Who Care, Saturday Club**, Davis, CA (2018 – 2019). Provided care and companionship for community members with dementia.
- **Synthetic Biology Club, UC Davis**, build team (2017 – 2018). Designed, 3D-printed, and assembled microfluidic drop-seq devices.

TECHNICAL SKILLS

Programming: Python (extensive), C++ (extensive), Rust (intermediate), R, Bash, common Linux and bioinformatics utilities.

Machine learning and statistics: PyTorch, TensorFlow (including custom low-level GradientTape pipelines), deep convolutional networks, zero-inflated / negative binomial regression, likelihood-based inference, Mann–Whitney and bootstrap testing, Dask-distributed HPC pipelines.

Genomics: Design and execution of MPRA and scMPRA experiments, Illumina library preparation (NextSeq 2000), Oxford Nanopore assay design, single-cell RNA-seq analysis.

Molecular and cell biology: Molecular cloning, transfection, tissue culture, mouse colony establishment and management, mouse embryo manipulation, fluorescence microscopy. Model systems: *E. coli*, *S. cerevisiae*, *M. musculus*, human cell lines.

Certifications: Cisco Certified Network Associate (CCNA), Cisco Certified Design Associate (CCDA), Cisco Data Center Networking Infrastructure Design Specialist, Cisco Unified Computing Technology Design Specialist.

Other: FCC amateur radio license (Technician class; call sign KM6KZY).