Connor J. Kenny, PhD

Scientist, RNA Therapeutics & Computational Genomics
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Scientist combining computational genomics, assay development, and high-throughput functional validation to identify disease mechanisms and therapeutic opportunities. Builds interpretable models from large genomics datasets and translates sequence-level insights into experimentally testable mechanisms, with a publication record linking RNA mechanisms, human genetics, and cancer biology.

SELECTED IMPACT

- **First-author mechanism paper:** defined LUC7-regulated 5' splice-site classes in *Nature Communications*.
- **Therapeutic relevance:** identified leukemia/MDS splice signatures linked to splicing-modulator sensitivity.
- **Platform scale:** built pipelines spanning 2,500+ RNA-seq datasets and ~14,000 clinical DNA samples.
- **Deep-learning platform development**: experience with building interpretable deep learning models for RNA sequence design.

TECHNICAL TOOLBOX

Computational: Python, R, Bash; Snakemake; ML/Bayesian modeling; SLURM/HPC; genomics database curation

Experimental: robotic liquid handling, platform development and optimization, reporter design; cell culture

Translational: clinical genomics; patient cohort analysis; mechanism-of-action studies; SOPs

Disease areas: RNA biology; neurodevelopmental genetics; myeloid neoplasms/leukemia; cancer genomics

RESEARCH EXPERIENCE

University of Chicago | Yang I. Li Lab — **Postdoctoral Scholar**
Section for Precision Medicine, Chicago, IL — Sep 2025 - Present
Therapeutic targeting of pre-mRNA splicing

- **Therapeutic modeling:** built interpretable convolutional neural networks for *de novo* learning of sequence determinants of splicing-modulating ASOs, small molecules, and cancer-associated non-coding RNAs.
- **Large-scale genomics:** map splicing-factor loss/mutation to stage-specific error signatures across 2,500+ RNA-seq datasets.
- **Statistical modeling:** designed Bayesian models to identify sequence features linked to splicing-modulator activity.

Massachusetts Institute of Technology | Christopher B. Burge Lab — **Graduate Student**
Department of Biology, Cambridge, MA — Sep 2020 - Aug 2025
Quantitative modeling of 5' splice site subclass regulation and evolution

- **First-author discovery:** defined LUC7-regulated 5' splice-site classes in *Nature Communications*.
- **Wet/dry validation:** combined RNA-seq, motif modeling, splicing reporter design/cloning, and cross-species validation.
- **Therapeutic relevance:** identified leukemia/MDS cohorts with signatures linked to splicing-modulator sensitivity.

Boston Children's Hospital / HHMI | Christopher A. Walsh Lab — **Research Assistant II**
Division of Genetics and Genomics, Boston, MA — June 2016 - May 2019
Rare disease genetics, functional genomics, and neurodevelopmental model systems

- **NGS scale-up:** established robotic liquid-handling protocols for targeted sequencing of ~14,000 human clinical DNA samples.
- **Variant validation:** partnered with clinicians and genetic counselors to validate rare-disease mutations.
- **Functional genomics:** performed transcriptome analysis and devised assays for rare human brain cell types.
- **Team enablement:** created SOPs and accessible analysis tools for somatic and germline variant validation.

THERAPEUTIC TARGET CONSULTING

Independent consultant: assessed therapeutic viability of *SCN1A* poison exon modulation for treating genetic epilepsy.

TECHNICAL METHODS

Genomics analysis: bulk RNA-seq, single-cell transcriptomics, alternative splicing analysis, targeted DNA-seq, eCLIP interpretation, public cohort analysis, and human variant interpretation.

Modeling and statistics: machine learning, Bayesian modeling, probabilistic sequence models, statistical analysis, data visualization, and scalable Snakemake/HPC workflows.

Experimental biology: cell culture, minigene/splicing reporter design and cloning, RT-PCR/ddPCR, NGS library preparation, FACS/flow sorting, robotic liquid handling, and fluorescence microscopy.

Research operations: SOP development, reproducible pipelines, technical documentation, mentorship, manuscript writing, and collaboration across computational and experimental teams.

EDUCATION

Massachusetts Institute of Technology | 2025

PhD, Biology; PhD Presidential Fellow

Boston University, College of Arts and Sciences | 2016

BA, Neuroscience with Honors; magna cum laude; GPA 3.83

SELECTED PUBLICATIONS

14 peer-reviewed publications; selected examples:

Kenny, C.J. et al. LUC7 proteins define two major classes of 5' splice sites in animals and plants. *Nature Communications*, 2025. Featured in MIT News: *MIT biologists discover a new type of control over RNA splicing.*

Shin, T. et al. Rare variation in non-coding regions with evolutionary signatures contributes to autism risk. *Cell Genomics*, 2024.

McDonough, G. et al. Neuropathologically directed profiling of *PRNP* somatic and germline variants in sporadic human prion disease. *Acta Neuropathologica*, 2024.

Kodani, A., Kenny, C.J. et al. Posterior neocortex-specific regulation of neuronal migration by *CEP85L* identifies maternal centriole-dependent activation of CDK5. *Neuron*, 2020.

Smith, R.S., Kenny, C.J. et al. Sodium Channel *SCN3A* regulation of human cerebral cortical folding and oral motor development. *Neuron*, 2018.

Ganz, J. et al. Rates and patterns of clonal oncogenic mutations in normal human brain. *Cancer Discovery*, 2022.

AWARDS & RECOGNITION

RNA Canada ARN Conference for RNA Therapeutics: Top 5% Poster Prize.

RNA Society: Selected speaker.

MIT: Praecis Presidential Fellowship.

Boston Children's Hospital: SPOT Award for outstanding employees.

LEADERSHIP & COLLABORATION

Scientific mentorship: supervised undergraduate, graduate, and visiting PhD researchers on computational biology, machine learning, probabilistic modeling, and evolutionary genomics projects.

Cross-functional work: extensive experience collaborating with clinical, computational, and experimental teams.

Communication: translated statistical and genomics analyses into assay plans, SOPs, presentations, and manuscript figures.