

Kathryn Monopoli

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Adaptable computational scientist with expertise in machine learning and high-throughput analysis. Proven track record developing models for therapeutic applications and efficient pipelines for data processing. Prior bench experience provides me a deep understanding of experimental design, enabling efficient raw data validation, and the ability to communicate seamlessly across teams to drive research forward.

Key Expertise

- Extensive knowledge of RNA Biology and experience developing RNA therapeutics, with expertise in siRNAs
- AI/Machine Learning model development and application to drug design and sequence data analysis
- Python for bioinformatics applications and extensive experience with relevant data analysis packages
- Data analysis, cleaning, preprocessing, and feature selection including for high-throughput pipelines
- Data Visualization to effectively communicate high dimensional data and concepts
- Communication computational concepts to broad audiences orally and written (patents, grants, manuscripts)
- Software development for drug design, sequence analysis, and pipeline development
- **Languages & Tools:** Python (10+ years), R, Java, SQL, Git, Docker, Bash, AWS, linux, Django, MATLAB

EDUCATION:

UMass Chan Medical School & Worcester Polytechnic Institute (WPI)

PhD Computational Biosciences & Bioengineering Aug. 2025 (expected)

PIs: Anastasia Khvorova - RNA Therapeutics Institute | Dmitry Korkin - Bioinformatics & Computer Science

Thesis: Advanced machine learning methods for therapeutic fully modified siRNA design

University of Massachusetts Amherst

MS Molecular and Cellular Biology, thesis-based, Phi Beta Kappa, GPA 4.0 2015

BS Biochemistry & Molecular Biology, Honors College, GPA 4.0, summa cum laude 2014

RESEARCH EXPERIENCE:

Graduate Researcher, Bioinformatics - UMass Chan Medical School, Worcester, MA 2019-2025

- Developed and implemented ML models for therapeutic small RNA (siRNAs, ASOs) design, directing the design of 2000+ highly potent siRNAs, 34 currently applied in drug discovery and therapeutic pipelines
- Developed frameworks for statistical analysis, cleaning, and parameter optimization of wide array of data
- Created data pipelines for high-throughput sequencing data preprocessing ensuring accuracy and reliability
- Pioneered novel feature embedding and engineering method applying deep learning to capture transcriptome-wide sequence relationships, improving siRNA potency prediction 5-fold
- Collaborated extensively with cross-functional teams to drive data analysis and model development

Associate Scientist, Bioinformatics - Advirna, Cambridge, MA 2016-2018

- Developed improved software for therapeutic siRNA design, increasing speed of design 5-fold
- Trained a model improving siRNA efficacy prediction accuracy using an easy to tune linear model
- Developed MySQL database application to streamline organization, classification, and storage; deployed as web platform on the cloud to simplify access and maintenance and minimize costs

Graduate & Undergraduate Researcher, Biochemistry - UMass Amherst, MA 2012-2015

- Developed and applied biophysical and fluorescence assays to probe membrane protein structure
- Optimized methods for purification of untagged membrane protein complexes from cell membranes

Intern, Antibody Discovery Group - Biogen, Cambridge, MA 2013

- Identified, purified, and characterized antibodies later utilized in an assay for a clinical trial
- Resolved challenges in antigen-binding site analysis process by developing computational (Python) parser

SELECTED PUBLICATIONS

for more see: scholar.google.com/citations?user=fYt4EYcAAAAAJ&hl

- Davis SM, Hildebrand S, Monopoli KR, et al. (2025) Systematic Analysis of siRNA and mRNA Features Impacting Fully Chemically Modified siRNA Efficacy. *Nucleic Acids Research*.
- Monopoli KR, Korkin D, Khvorova A. (2023) Asymmetric trichotomous data partitioning enables development of predictive machine learning models using limited siRNA efficacy datasets. *MTNA*.
- Shmushkovich T*, Monopoli KR*, Homsy D, Leyfer D, Betancur-Boissel M, Khvorova A, Wolfson A. (2018) Functional features defining the efficacy of cholesterol-conjugated, self-deliverable, chemically modified siRNAs. *NAR*. ***equally contributing first authors**

PATENTS:

- Oligonucleotides for MAPT modulation US Patent Application No. 17/204,480 MAR-17-2020
- Oligonucleotides for SNCA modulation US Patent Application No. 17/204,483 MAR-17-2020
- Oligonucleotides for MSH3 modulation US Patent Application No. 63/012,603 APR-20-2020
- Oligonucleotides for SARS-CoV-2 modulation US Patent Application No. 17/333,839 MAY-28-2021

ORAL PRESENTATIONS:

- Monopoli, KR, Korkin, D, Khvorova, A. Trichotomous classification on small, limited datasets enables predictive model development for therapeutic small interfering RNA. Talk presented at the Conference on Intelligent Systems for Molecular Biology; 2022 Jul 10; Madison, WI.
- Monopoli, KR, Korkin, D, Khvorova, A. Evaluation-centric method for extracting base preferences from siRNA prediction models identifies features consistent with established mechanisms and is adaptable to examine any machine learning model. On-demand talk presented at the RNA Therapeutics Symposium; 2022 Jun 22; Worcester, MA.
- Monopoli, KR, Korkin, D, Khvorova, A. Methods to apply and evaluate machine learning models on limited biological datasets through the lens of siRNA design. Talk presented at Oligonucleotide Therapeutics Society Webinar; 2021 Oct 29.

TEACHING & MENTORING EXPERIENCE:**Computer Science Teaching Assistant** – Worcester Polytechnic Institute*Introduction to Programming Design*: held recitations, lectured

2018

Object-Oriented Program Design: developed lesson plans and assessments, led recitations

2018

Biochemistry Teaching Assistant – University of Massachusetts Amherst

Physical Chemistry: team-based learning instructor

2014

General Genetics: held recitations, lectured

2013

Instructor Biogen Community Lab

Instructed high school student on independent lab-based molecular biology projects

2013

References available upon request