Kathryn R. Monopoli

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EDUCATION

University of Massachusetts Medical School & Worcester Polytechnic Institute
PhD Candidate Computational Biosciences & Bioengineering*, 2019-present*

University of Massachusetts Amherst
MS Molecular and Cellular Biology thesis-based, GPA 4.0
BS Biochemistry & Molecular Biology Honors College, *Phi Beta Kappa, summa cum laude*, GPA 4.0

EXPERIENCE

UMass Medical School & Worcester Polytechnic Institute, *Worcester, MA 2019-present*
Principal Investigator – Anastasia Khvorova, PhD | UMass Chan | RNA Therapeutics Institute
Co-advisor – Dmitry Korkin, PhD | WPI | Bioinformatics & Computer Science
- Develop and apply advanced machine learning methods to algorithms and software for siRNA design
- Built semi-supervised and deep learning models to accurately predict potent siRNAs
- Developed novel siRNA feature representation scheme to improve machine learning model accuracy
- Collaborate with bench scientists in industry and academia to guide the design of RNA therapeutics
- Designed sequences for 1000's of siRNAs for both research and therapeutic applications
- Co-inventor 13 patents & applications – including three licensed – for therapeutic siRNA design

Advirna (Cambridge, MA) – Associate Scientist | Bioinformatics *2016-2018*
- Developed database system using SQL to classify large, diverse datasets on the web
- Performed statistical analysis on siRNA efficacy data to identify and evaluate potency predictors

University of Massachusetts Amherst – Graduate Researcher *2012-2016*
- Developed and applied biophysical assays to probe Type III Secretion System translocon assembly
- Presented work at Biophysical Society Meeting and co-authored published manuscript

Biogen (Cambridge, MA) – Intern | Antibody Discovery *2013*
- Identified and characterized antibodies used to assess patient immune response in a clinical trial
- Developed sequence parser algorithm increasing efficiency of antigen-binding site analysis

TECHNICAL SKILLS

- Small RNA therapeutic design, computational modeling, bioinformatics, genomic and transcriptomic sequence analysis, data visualization, deep learning, machine learning, RNAseq data analysis, technical/grant writing
- ***Languages***: Expert (10+ years): Python | Advanced (5+ years): Java, Bash | Intermediate (2+ years): R
- ***Software/Tools***: Scikit-Learn, Pandas, Numpy, Vim, Adobe Illustrator, Git, SQL, Excel, Django

SELECTED PUBLICATIONS

- **Monopoli KR,** Korkin D, Khvorova A. (2023) Asymmetric trichotomous data partitioning enables development of predictive machine learning models using limited siRNA efficacy datasets. *Molecular Therapy Nucleic Acids.*
- Shmushkovich T*, **Monopoli KR***, Homsy D, Leyfer D, Betancur-Boissel M, Khvorova A, Wolfson AD. (2018) Algorithm for predicting efficacy of chemically modified siRNAs. *Nucleic Acids Research*. ***Co-first authors**
- Davis SM, Hildebrand S, **Monopoli KR**, et al., (2024) Systematic Analysis of siRNA and mRNA Features Impacting Fully Chemically Modified siRNA Efficacy. *In review with NAR.*
- Tang Q, Fakih H, *et al. [including* **Monopoli KR***].* (2023) Rational design of a JAK1-selective siRNA inhibitor for the modulation of autoimmunity in the skin. *Nature Communications.*
- Hariharan VN, Shin M, Chang CW, O'Reilly D, Biscans A, Yamada K, Guo Z, Somasundaran M, Tang Q, **Monopoli KR**, et al., (2023) Divalent siRNAs are bioavailable in the lung and efficiently block SARS-CoV-2 infection. *PNAS*.
- O'Reilly D, Belgrad J, *et al. [including* **Monopoli KR***].* (2023) Di-valent siRNA Mediated Silencing of MSH3 Blocks Somatic Repeat Expansion in Mouse Models of Huntington's Disease. *Molecular Therapy*

SELECTED CONFERENCE TALKS

- **Monopoli, KR,** Korkin, D, Khvorova, A. Trichotomous classification on small, limited datasets enables predictive model development for therapeutic si RNA. Conference on Intelligent Systems for Molecular Biology; 2022; 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. RNA Therapeutics Symposium; 2022; 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. Oligonucleotide Therapeutics Society Webinar; 2021. *(invited talk)*

SELECTED PATENTS

- Oligonucleotides for SARS-CoV-2 Modulation - US Patent Application No. 17/333,839; 2022
- Oligonucleotides for MSH3 Modulation - US Patent Application No. 63/012,603; 2020
- Oligonucleotides for MAPT Modulation - US Patent Application No. 17/204,480; 2020
- Oligonucleotides for SNCA Modulation - US Patent Application No. 17/204,483; 2020