

## Kathryn Monopoli – CURRICULUM VITAE

PERSONAL INFORMATION	368 Plantation Street Worcester, MA 01605 <a href="mailto:krmonopoli@gmail.com">krmonopoli@gmail.com</a> +1-508-367-9077 Code repository: <a href="https://kmonopoli.github.io/">https://kmonopoli.github.io/</a>	
EDUCATION	<i>UMass Chan Medical School &amp; Worcester Polytechnic Institute (WPI)</i> <b>PhD Candidate Computational Biosciences &amp; Bioengineering</b> , GPA 4.0 <i>University of Massachusetts Amherst</i> <b>MS Molecular and Cellular Biology</b> , <i>thesis-based</i> , GPA 4.0 <b>BS Biochemistry &amp; Molecular Biology</b> , Honors College, GPA 4.0, <i>summa cum laude</i>	2019-present   2015 2014
RESEARCH EXPERIENCE	<b>UMass Chan Medical School &amp; Worcester Polytechnic Institute, Worcester, MA</b> <b>Graduate Researcher, Bioinformatics</b> <i>Principal Investigator</i> – Anastasia Khvorova, PhD   UMass Chan   RNA Therapeutics Institute (RTI) <i>Co-advisor</i> – Dmitry Korkin, PhD   WPI   Bioinformatics & Computer Science <ul style="list-style-type: none"><li>• Apply and develop advanced machine learning (ML) models informed by biological context</li><li>• Build algorithms and software tools for design of therapeutic small RNAs (siRNAs &amp; ASOs)</li><li>• Built first semi-supervised learning model employing processes uniquely inherent to siRNA biology</li><li>• Routinely effectively communicate advanced machine learning and computational topics to non-experts through talks and poster presentations</li><li>• Developed novel sequence feature embedding method applying deep learning to enable efficient capture of short (&lt;30nts) sequence relationships transcriptome-wide, significantly enhancing siRNA efficacy prediction</li><li>• Oversaw the design and selection for 1000's of siRNAs for both research and therapeutic applications</li><li>• Coordinated development of the first web application for therapeutic fully modified siRNA design software<ul style="list-style-type: none"><li>◦ Beta version of application available here: <a href="https://tinyurl.com/sirna-designer-ai">https://tinyurl.com/sirna-designer-ai</a></li></ul></li><li>• Participated in many collaborations both industry and academic advising in siRNA design and selection</li><li>• Co-inventor 13 patents – including three licensed – for therapeutic siRNA design</li><li>• Published first-author manuscript on machine learning for siRNA design; co-authored five manuscripts</li></ul>	2019-present
	<b>Associate Scientist, Bioinformatics   Advirna, Cambridge, MA</b> <i>Principal Investigator</i> – Alexey Wolfson, PhD <ul style="list-style-type: none"><li>• Developed improved software for therapeutic siRNA design, increasing speed of design 5-fold</li><li>• Trained a model improving siRNA efficacy prediction accuracy using an easy to tune linear model</li><li>• Developed database system using SQL to classify large, diverse datasets on the web</li><li>• Performed statistical analysis on siRNA efficacy data to identify and evaluate potency predictors</li><li>• Developed database system using SQL to classify large, diverse datasets on the web</li><li>• Published first author paper detailing algorithm for therapeutic siRNA design</li></ul>	2016-2018
	<b>Researcher, Institute for Protein Design   University of Washington, Seattle, WA</b> <i>Principal Investigator</i> : David Baker, PhD   <i>Co-advisor</i> : Frank DiMaio, PhD <ul style="list-style-type: none"><li>• Integrated entropy modeling into Rosetta software to enhance protein complex energy determination</li><li>• Performed molecular modeling simulations to improve protein structure interaction prediction models</li></ul>	2016
	<b>Graduate &amp; Undergraduate Researcher   University of Massachusetts, Amherst, MA</b> <i>Principal Investigator</i> – Alejandro Heuck, PhD <ul style="list-style-type: none"><li>• Developed and applied biophysical assays to probe membrane protein structure and assembly</li><li>• Optimized techniques for purification of untagged membrane protein complexes from cell membranes</li></ul> <i>Laboratory techniques</i> : fluorescence spectroscopy, membrane protein purification, western blot, blue native PAGE, fluorescent protein tagging, sucrose gradient ultracentrifugation	2012-2015
	<b>Intern, Antibody Discovery Group   Biogen, Cambridge, MA</b> <ul style="list-style-type: none"><li>• Identified and characterized antibodies for a clinical trial assay</li><li>• Developed computational parser algorithm for antigen-binding site analysis</li></ul> <i>Laboratory techniques</i> : Bio-layer interferometry (BLI), ELISA, phage display	2013

- PUBLICATIONS**
- **Monopoli KR**, Sostek B, Gross K, Alterman J, Korkin D, Khvorova A. MODsiGNER: fully modified siRNA design application applying artificial intelligence with deep sequence feature embedding. *In preparation for submission to Nature Methods*.
  - Weiss A, Gilbert JW, Flores IVR, Belgrad J, Ferguson C, Dogan EO, Wightman N, Mocarski K, Echeverria D, Summers A, Bramato B, McHugh N, Furgal R, Yamada N, Cooper D, **Monopoli KR**, Godinho BMDC, Hassler MR, Yamada K, Greer P, Henninger N, Brown RH Jr, Khvorova A. (2024) RNAi-mediated silencing of SOD1 profoundly extends survival and functional outcomes in ALS mice. *bioRxiv [Preprint]*.
  - Rivera Flores IV, **Monopoli KR**, Jackson S, Echeverria D, O'Reilly D, Brown RH, Khvorova A. (2024) Near Sequence Homology Does Not Guarantee siRNA Cross-Species Efficacy. *Nucleic Acid Therapeutics*.
  - Tang Q, Gross KY, Fakih HH, Jackson SO, UI Abideen MZ, **Monopoli KR**, Blanchard C, Bouix-Peter C, Portal T, Harris JE, Khvorova A, Alterman JF. (2024) Multispecies-targeting siRNAs for the modulation of JAK1 in the skin. *Molecular Therapy Nucleic Acids*.
  - **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*.
  - Davis SM, Hildebrand S, **Monopoli KR**, MacMillan H, Sousa J, Cooper D, Ly Socheata; Echeverria D, *et al.* (2023) Guidelines for Designing Therapeutic siRNA. *Under review with NAR*.
  - Hariharan VN, Shin M, Chang CW, O'Reilly D, Biscans A, Yamada K, Guo Z, Somasundaram M, Tang Q, **Monopoli KR**, Krishnamurthy PM, Devi G, McHugh N, Cooper DA, Echeverria D, Cruz J, Chan IL, Liu P, Lim SY, McConnell J, Singh SP, Hildebrand S, Sousa J, Davis SM, Kennedy Z, Ferguson C, Godinho BMDC, Thillier Y, Caiazza J, Ly S, Muhuri M, Kelly K, Humphries F, Cousineau A, Parsi KM, Li Q, Wang Y, Maehr R, Gao G, Korkin D, McDougall WM, Finberg RW, Fitzgerald KA, Wang JP, Watts JK, Khvorova A. (2023) Divalent siRNAs are bioavailable in the lung and efficiently block SARS-CoV-2 infection. *PNAS*.
  - O'Reilly D, Belgrad J, Ferguson C, Summers A, Sapp E, McHugh C, Mathews E, Boudi A, Buchwald J, Ly S, Moreno D, Furgal R, Luu E, Kennedy Z, Hariharan V, **Monopoli KR**, Yang XW, Carroll J, DiFiglia M, Aronin N, Khvorova A. (2023) Divalent siRNA Mediated Silencing of MSH3 Blocks Somatic Repeat Expansion in Mouse Models of Huntington's Disease. *Molecular Therapy*.
  - Tang Q, Fakih HH, Zain UI Abideen M, Hildebrand SR, Afshari K, Gross KY, Sousa J, Maebius AS, Bartholdy C, Søgaard PP, Jackerott M, Hariharan V, Summers A, Fan X, Okamura K, **Monopoli KR**, Cooper DA, Echeverria D, Bramato B, McHugh N, Furgal RC, Dresser K, Winter SJ, Biscans A, Chuprin J, Haddadi NS, Sherman S, Yıldız-Altay Ü, Rashighi M, Richmond JM, Bouix-Peter C, Blanchard C, Clauss A, Alterman JF, Khvorova A, Harris JE. (2023) Rational design of a JAK1-selective siRNA inhibitor for the modulation of autoimmunity in the skin. *Nature Communications*.
  - Tang Q, Sousa J, Echeverria D, Fan X, Hsueh YC, Afshari K, McHugh N, Cooper DA, Vangjeli L, **Monopoli KR**, *et al.* (2022) RNAi-based modulation of IFN- $\gamma$  signaling in skin. *Molecular Therapy*.
  - 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 authors*
  - Romano FB, Rossi KC, Tang Y, **Monopoli KR**, Ross JL, Heuck AP. (2016) Type 3 Secretion translocators spontaneously assemble a hexadecameric transmembrane complex. *JBC*.

- PATENTS**
- *Oligonucleotides for MAPT Modulation - US Utility Patent Application No. 62/991,405*
  - *Oligonucleotides for SNCA Modulation - US Utility Patent Application No. 62/991,406*
  - *Oligonucleotides for MSH3 Modulation\* - US Patent Application No. 63/012,603*
  - *Oligonucleotides for MAPT Modulation - US Utility Patent Application No. 63/071,106*
  - *Oligonucleotides for SNCA Modulation - US Utility Patent Application No. 63/071,115*
  - *Oligonucleotides for SARS-CoV-2 Modulation - US Utility Patent Application No. 63/031,222*
  - *Oligonucleotides for SARS-CoV-2 Modulation - US Utility Patent Application No. 63/084,817*
  - *Oligonucleotides for MAPT Modulation\* - US Patent Application No. 17/204,480*
  - *Oligonucleotides for MAPT Modulation - Intl Patent Application No. PCT/US2021/022688*
  - *Oligonucleotides for SNCA Modulation\* - US Patent Application No. 17/204,483*
  - *Oligonucleotides for SNCA Modulation - Intl Patent Application No. PCT/US2021/022748*
  - *Oligonucleotides for SARS-CoV-2 Modulation - US Patent Application No. 17/333,839*
  - *Oligonucleotides for SARS-CoV-2 Modulation - Intl Patent App No. PCT/US2021/035002*

\*Licensed with Atalanta Therapeutics, Boston, MA

TECHNICAL SKILLS	<ul style="list-style-type: none"> <li>• <i>Languages:</i> Advanced (5+ years): Python, Java, R Intermediate/Proficient (&lt;3 years): C++, SQL, Perl</li> <li>• <i>Software/Tools:</i> Vim, Git, Django, Scikit-Learn, Matplotlib, IntelliJ, Jupyter, MATLAB, AWS, Adobe Illustrator</li> </ul>
ORAL PRESENTATIONS	<ul style="list-style-type: none"> <li>• <b>Monopoli, KR</b>, 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.</li> <li>• <b>Monopoli, KR</b>, 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.</li> <li>• <b>Monopoli, KR</b>, Korkin, D, Khvorova, A. Methods to apply and evaluate machine learning models on limited biological datasets through the lens of siRNA design. Presented at Oligonucleotide Therapeutics Society Webinar; 2021 Oct 29.</li> </ul>
TEACHING EXPERIENCE	<p><b>Computer Science Teaching Assistant – Worcester Polytechnic Institute</b></p> <ul style="list-style-type: none"> <li>• <i>Introduction to Programming Design</i>: held recitations, lectured 2018</li> <li>• <i>Object-Oriented Program Design</i>: developed lesson plans and assessments, led recitations 2018</li> </ul> <p><b>Biochemistry Teaching Assistant – University of Massachusetts Amherst</b></p> <ul style="list-style-type: none"> <li>• <i>Physical Chemistry</i>: team-based learning instructor 2014</li> <li>• <i>General Genetics</i>: held recitations, lectured 2013</li> </ul> <p><b>Instructor Biogen Community Lab</b></p> <ul style="list-style-type: none"> <li>• Instructed high school students on lab-based molecular biology projects 2013</li> </ul> <p><b>Mathematics Tutor (Calculus I, II, III, &amp; Differential Equations) – Colorado School of Mines</b> 2012</p>
CONFERENCE POSTERS	<ul style="list-style-type: none"> <li>• <b>Monopoli KR</b>, Sostek B, Korkin D, Khvorova A. Advanced machine learning approach for accurate prediction of functional fully modified siRNAs. Poster presented at the Oligonucleotide Therapeutics Society Meeting; 2024 Oct 7; Montreal, QC.</li> <li>• <b>Monopoli KR</b>, Korkin D, Khvorova A. Artificial intelligence-based nonlinear sequence environment encapsulation yields robust native context therapeutic siRNA potency prediction algorithm. Poster presented at the Oligonucleotide Therapeutics Society Meeting; 2023 Oct 14; Barcelona, Spain.</li> <li>• <b>Monopoli KR</b>, Korkin D, Khvorova A. Method for encapsulating transcript sequence environment information boosts siRNA potency prediction accuracy of supervised machine learning models. Poster presented at the RNA Therapeutics Symposium; 2023 Jun 23; Worcester, MA.</li> <li>• <b>Monopoli KR</b>, Korkin D, Khvorova A. Trichotomous classification on small, limited datasets enables predictive model development for therapeutic small interfering RNA. Poster presented at the Conference on Intelligent Systems for Molecular Biology; 2022 Jul 11; Madison, WI.</li> <li>• <b>Monopoli KR</b>, Korkin D, Khvorova A. Data Partitioning to Enable Application of Machine Learning Models to Limited Biological Datasets Using SiRNA Design as an Example Case. Poster at the Oligonucleotide Therapeutics Society Meeting; Sep 2021; virtual.</li> <li>• <b>Monopoli KR</b>, siRNA Screening Consortium, Korkin D, Khvorova A. Predicting siRNA Silencing Efficacy using Supervised Machine Learning. Poster presented at the RNA Therapeutics Symposium; 2021 Jun 22; Worcester, MA.</li> <li>• <b>Monopoli KR</b>, Heuck AP. Forming the <i>Pseudomonas aeruginosa</i> translocon requires simultaneous incorporation of PopB and PopD. Poster presentation at the Biophysical Society Annual Meeting; 2015 Feb 6-11; Baltimore, MD.</li> <li>• <b>Monopoli KR</b>, Romano FB, Heuck AP. Structural Studies of the Membrane Bound Translocon of the <i>Pseudomonas aeruginosa</i> Type III Secretion System. Poster presented at the Undergraduate Symposium for the American Chemical Society; 2014 April 26; Amherst, MA.</li> </ul>
THESES	<p><b>Monopoli KR</b>. Advised by Prof. Anastasia Khvorova and Prof. Dmitry Korkin. Advanced machine learning methods for therapeutic fully modified siRNA design. University of Massachusetts Chan Medical School, RNA Therapeutics Institute, Worcester Polytechnic Institute Department of Bioinformatics. <i>PhD Thesis in preparation, defense date set for January 17, 2025.</i></p>

**Monopoli KR.** Advised by Prof. Alejandro Heuck. (2015) Characterization of the Reconstituted and Native *Pseudomonas aeruginosa* Type III Secretion System Translocon. Master's thesis. University of Massachusetts Amherst.

**Monopoli KR.** Advised by Prof. Alejandro Heuck. (2014) Characterization of the *Pseudomonas aeruginosa* Type III Secretion System Translocon in Model Membranes. Honors undergraduate thesis. University of Massachusetts Amherst.

HONORS & AWARDS	Travel Award – Oligonucleotide Therapeutics Society Annual Meeting	2023
	iRNA COSI Travel Fellowship - Conference on Intelligent Systems for Molecular Biology	2022
	Poster Award – Oligonucleotide Therapeutics Society Annual Meeting	2021
	Teaching Assistant fellowship – Worcester Polytechnic Institute	2018
	Biophysical Society Travel Award	2015
	Henry Little Award for Excellence in Research and Academics	2014
	Honors Research Grant – UMass Amherst	2014
	Undergraduate Research Assistant Fellowship – UMass Amherst	2012
	Kappa Mu Epsilon – Honors Society in Mathematics	2012
	Award for Excellence in Organic Chemistry – ACS	2012
	Presidential Scholarship – Colorado School of Mines	2010
SERVICE ACTIVITIES	Oligonucleotide Therapeutics Society, mentee	2022-2023
	Girls Who Code, instructor and program coordinator	2022-present
	Worcester YMCA Minority Achievers Program, mentor and instructor	2021
	WPI Touch Tomorrow, instructor	2019-present
	Wachusett Regional High School Science Fair, judge	2019
	Bright Spot Therapy Dogs, dog handler	2014-present
	Hector Reyes House Worcester, volunteer	2017-present
	Worcester Roller Derby, skater	2017-present
	Harrington Health Care System, volunteer	2017
	UMass STEM mentor	2014-2015
	UMass Biochemistry Club, volunteer	2012-2015
	Engineering Projects in Community Service Program, designer	2010-2011