Michael P. Meers

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RESEARCH EXPERIENCE AND EDUCATION

Assistant Professor Washington University School of Medicine

Epigenome profiling to study transcription factor function in development

Postdoctoral Fellow Fred Hutchinson Cancer Research Center

2017-2022

2022-

Design of high-throughput chromatin profiling and analysis tools

Study of pioneer transcription factor molecular function in development

Advisor: Steven Henikoff, PhD

Graduate Student University of North Carolina at Chapel Hill

2010-2017

Implementation of metazoan histone replacement genetic models

Study of the function of histone H3 lysine 36 methylation in RNA processing

Advisor: A. Gregory Matera, PhD

Undergraduate Research Duke University

2007-2010

Advisor: Claudia Gunsch, PhD, Duke University

Study of mechanisms of bacterial toluene biosynthesis (2009-2010)

Advisor: Nathan Yee, PhD, Rutgers University

Genomic analysis of *E. cloacae* pathways conferring selenium compound reducing activity (2007)

FELLOWSHIPS AND AWARDS

Cancer Research Foundation Young Investigator Award	2023
K99/R00 Pathway to Independence Award, NIGMS	2021-Present
William Guy Forbeck Foundation Scholar	2021-Present
Intersections Science Symposium Fellow	2021-2022
Ruth N. Kirchstein NRSA F32 Postdoctoral Fellowship, NIGMS	2020-2021
Washington Research Foundation Postdoctoral Fellowship: Finalist	2018
Ruth N. Kirchstein NRSA F31 Predoctoral Fellowship, NCI	2014-2017

FEATURED PUBLICATIONS (Google Scholar)

- Meers MP, Llagas G, Janssens DH, Codomo CA, Henikoff S. Multifactorial profiling of epigenetic landscapes at single-cell resolution using MulTI-Tag. *Nature Biotechnology* 2022, doi: <u>10.1038/s41587-022-01522-9</u>
- Janssens DH, Meers MP, Wu SJ, Babaeva E, Meshinchi S, Sarthy JF, Ahmad K, Henikoff S. Automated CUT&Tag profiling of chromatin heterogeneity in KMT2Ar leukemia. *Nature Genetics* 2021, doi: 10.1038/s41588-021-00941-9
- **3.** Sarthy JF, **Meers MP**, Janssens DH, Henikoff JG, Feldman H, Paddison PJ, Lockwood CM, Vitanza NA, Olson JM, Ahmad K, Henikoff S. Histone deposition pathways determine the chromatin landscapes of H3.1 and H3.3 K27M oncohistones. **eLife** 2020, doi: 10.7554/eLife.61090
- **4. Meers MP**, Janssens DH, Henikoff S. Pioneer factor-nucleosome binding events during differentiation are motif-encoded. *Molecular Cell* 2019, doi: 10.1016/j.molcel.2019.05.025
- **5. Meers MP**, Tenenbaum D, Henikoff S. Peak calling by Sparse Enrichment Analysis for CUT&RUN chromatin profiling. *Epigenetics Chromatin* 2019, doi: 10.1186/s13072-019-0287-4
- Meers MP, Bryson TD, Henikoff JG, Henikoff S. Improved CUT&RUN chromatin profiling tools. eLife 2019, doi: 10.7554/eLife.46314
- 7. Meers MP, Henriques T, Lavender CA, McKay DJ, Strahl BD, Duronio RJ, Adelman K, Matera AG. Histone gene replacement reveals a post-transcriptional role for H3K36 in maintaining metazoan transcriptome fidelity. eLife 2017, doi: 10.7554/eLife.23249

REVIEWS AND BOOK CHAPTERS

- 1. Talbert PB, **Meers MP**, Henikoff S. Old cogs, new tricks: the evolution of gene expression in a chromatin context. *Nature Reviews Genetics* 2019, doi: 10.1038/s41576-019-0105-7
- Meers MP, Leatham-Jensen M, Penke TJR, McKay DJ, Duronio RJ, Matera AG. An Animal Model for Genetic Analysis of Multi-Gene Families: Cloning and Transgenesis of Large Tandemly Repeated Histone Gene Clusters. *Methods in Molecular Biology* 2018, doi: 10.1007/978-1-4939-8663-7_17
- 3. Wigington CP, Williams KR, Meers MP, Bassell GJ, Corbett AH. Poly(A) RNA-binding proteins and polyadenosine RNA: new members and novel functions. *Wiley Inderdisciplinary Reviews: RNA* 2014, doi: 10.1002/wrna.1233

SELECTED ORAL PRESENTATIONS

Gordon Research Seminar: Cancer Genetics and Epigenetics Forbeck Scholars Fall Retreat ASBMB Special Symposium: Transcriptional Regulation by Chromatin and RNA Polymerase I Forbeck Forum in Dynamic Histone Methylation and Chromatin Organization in Tumor Suppre Chan Zuckerberg Initiative Single Cell Biology Symposium Next Generation Genomics Symposium Intersections Science Fellows Symposium	
Cell Symposia: Transcriptional Regulation in Evolution, Development, and Disease Penn State Summer Symposium: Chromatin and Epigenetic Regulation of Transcription	2019 2019
SELECTED POSTER PRESENTATIONS	
EMBL Chromatin and Epigenetics Conference HHMI Annual Science Meeting Annual ENCODE Users Meeting Cold Spring Harbor: Epigenetics & Chromatin The 21 st Annual RNA Society Meeting	2023 2019 2019 2018 2016
TEACHING AND MENTORING EXPERIENCE	
Washington University School of Medicine in St. Louis Lecturer for core Genomics course (Bio 5488)	2023
University of North Carolina at Chapel Hill Co-instructed Advanced Biochemistry Lab	2010
Mentored Trainees: Arnold Federico, PhD Graduate Student (Washington University School of Medicine) Yu-Liang Yeh, PhD Graduate Student (Washington University School of Medicine) Brittany Johnson, Research Technician (Washington University School of Medicine) Trizia Llagas, Research Technician (Fred Hutchinson Cancer Research Center) Kirsten Adams, Undergraduate Assistant (UNC Chapel Hill) Nathan Spain, Undergraduate Assistant (UNC Chapel Hill) Katie Bolling, Rotation Graduate Student (UNC Chapel Hill) Casey Schmidt, Rotation Graduate Student (UNC Chapel Hill) Stephen Cooper, Undergraduate Assistant (UNC Chapel Hill) PROFESSIONAL AFFILIATIONS AND SERVICE	2023-Present 2023-Present 2022-Present 2020-2022 2016-2017 2014-2016 2013 2012 2011-2014

PROFESSIONAL AFFILIATIONS AND SERVICE

Reviewer : Science, Molecular Cell, Nature Cell Biology, Nature Genetics, Nature Structural &	
Molecular Biology, Genome Biology, Genome Research, Communications Biology	2018-Present
Member, The Genetics Society of America	2014-2017
Graduate Student Representative, The International RNA Society	2012-2015
Organized/coordinated Junior Scientist social and professional development programmin	a

Organized/coordinated Junior Scientist social and professional development programming at annual International RNA Society meetings

Member, The International RNA Society

2012-2017