Mallory Ann Freeberg, Ph.D.

CONTACT INFORMATION	3400 N Charles Street Mudd Hall 144 Baltimore, MD 21218 USA	*Phone:* (724) 840-6294 *Email:* mallory dot freeberg at gmail dot com

EDUCATION

University of Michigan, Ann Arbor, MI USA
Department of Computational Medicine and Bioinformatics
Ph.D. Bioinformatics, May 2015

Saint Vincent College, Latrobe, PA USA
The Herbet M. Boyer School of Natural Science, Mathematics, and Computing
B.S. Bioinformatics, May 2009

RESEARCH EXPERIENCE

Galaxy Project and **Galaxy Training Network**, Baltimore, MD USA
Team Member — Jan 2017 - present
Research: Development of workflows, training materials, and best practices for transcriptomics and genomics-related research

Johns Hopkins University, Baltimore, MD USA
Postdoctoral Research Fellow — Jun 2015 - present
Research: Investigating post-transcriptional gene regulation via next gen and nanopore sequencing
Advisor: Dr. James Taylor

University of Michigan, Ann Arbor, MI USA
Graduate Student — Jul 2009 - May 2015
Dissertation: Computational analysis of the post-transcriptional gene regulatory network
Advisor: Dr. John K. Kim

Saint Vincent College, Latrobe, PA USA
Undergraduate Student — Aug 2005 - May 2009
Dissertation: Functional annotation of non-coding elements in the Amphioxus genome
Advisor: Dr. Michael L. Sierk

Boyce Thompson Institute for Plant Research, Ithaca, NY USA
Summer Research Intern — May - Aug 2008
Research: Designed motif discovery tool to identify conserved DNA motifs in *Solanaceae* genomes
Advisor: Dr. Lukas A. Mueller

Johns Hopkins University Applied Physics Laboratory, Laurel, MD USA
Summer Research Intern — May - Aug 2007
Research: Developed computational pipeline for microorganism identification by mass spectrometry
Advisors: Drs. Plamen A. Demirev and Richard S. Potember

FUNDING AND AWARDS

Extreme Science and Engineering Discovery Environment (XSEDE), Startup Computational Resource Allocation (2017)
XSEDE, Educational Computational Resource Allocation (2017)
Galaxy Community Fund, Travel Award (2017)
Rackham Predoctoral Fellowship (2013-2014)
NSF Open Data IGERT Fellowship (2010-2013)
Rackham Graduate Student Research Grant (2010, 2012)
NIH Bioinformatics Training Grant (2009-2010)

COMPUTING AND
DATA ANALYSIS
SKILLS

Operating Systems: MacOS X, Linux/Unix (limited Windows)
Languages: Python, Perl, SQL, Unix shell (limited C++, Java, Javascript, PHP/HTML, CWL)
Statistical Packages: R, Bioconductor (limited MatLab)
Applications: Galaxy, LaTeX, GitHub, NGS analysis tools and methodologies, MySQL
Laboratory Techniques: Nanopore sequencing (Oxford Nanopore Technologies), general molecular biology techniques

PUBLICATIONS

Freeberg MA, Han T, Taylor J, and Kim JK. Transcriptome-wide identification and comparative target analysis of the Pumilio family of RNA-binding proteins in *S. cerevisiae*. (in revision)

Jin M*, Fuller G*, Han T*, Yao Y, Alessi AF, **Freeberg MA**, Roach N, Moresco JJ, Karnovsky A, Baba M, Yates JR III, Gitler AD, Inoki K, Klionsky DJ, and Kim JK. (2017) Glycolytic Enzyme Coalescence in G bodies is Essential for Cell Proliferation in Hypoxia. *Cell Reports* (in press)

Hong S, **Freeberg MA***, Han T*, Kamath A*, Yao Y, Fukuda T, Suzuki T, Kim JK, and Inoki K. (2017) LARP-1 functions as a molecular switch for mTORC1-mediated translation of an essential class of mRNAs. *eLife* 6:e25237. DOI:10.7554/eLife.25237

Weiser NE, Yang DX, Feng S, Kalinava N, Brown KC, Khanikar J, **Freeberg MA**, Snyder MJ, Csankovszki G, Chan RC, Gu SG, Montgomery TA, Jacobsen SE, and Kim JK. (2017) MORC-1 Integrates Nuclear RNAi and Transgenerational Chromatin Architecture to Promote Germline Immortality. *Dev Cell* 41(4):408-23. DOI:10.1016/j.devcel.2017.04.023

Turaga N, **Freeberg MA**, Baker D, Chilton J, The Galaxy Team, Nekrutenko A, and Taylor J. (2016) A guide and best practices for R/Bioconductor tool integration in Galaxy [version 1; referees: 1 approved, 1 approved with reservations]. *F1000Research* 5:2757. DOI:10.12688/f1000research.9821.1

Freeberg MA and Kim JK. (2016) Mapping the Transcriptome-Wide Landscape of RBP Binding Sites using gPAR-CLIP-seq: Bioinformatic Analysis. Invited chapter in *Methods in Mol Biol* 1361(6):91-104. DOI:10.1007/978-1-4939-3079-1

Alessi AF*, Khivansara V*, Han T*, **Freeberg MA**, Moresco JJ, Tu PG, Montoye E, Yates JR III, Karp X, and Kim JK. (2015) Casein kinase II promotes target silencing by miRISC through direct phosphorylation of the DEAD-box RNA helicase CGH-1. *PNAS* 112(49):E6789. DOI:10.1073/pnas.1509499112

Jin M, He D, Backues SK, **Freeberg MA**, Liu X, Kim JK, and Klionsky DJ. (2014) Transcriptional regulation by Pho23 modulates the frequency of autophagosome formation. *Curr Biol* 24(12):1314-22. DOI:10.1016/j.cub.2014.04.048

Freeberg MA*, Han T*, Moresco JJ, Kong A, Yang Y, Lu Z, Yates JR III, and Kim JK. (2013) Pervasive and dynamic protein binding sites on the mRNA transcriptome in *Saccharomyces cerevisiae*. *Gen Biol* 14(2):R13. DOI:10.1186/gb-2013-14-2-r13

Billi AC*, **Freeberg MA***, Day AM, Chun SY, Khivansara V, and Kim JK. (2013) A conserved upstream motif drives autonomous, germline-enriched expression of *Caenorhabditis elegans* piRNAs. *PLoS Genet* 9(3):e1003392. DOI:10.1371/journal.pgen.1003392
Comment in: Burgess DJ. (2013) Small RNAs: Defining piRNA expression. *Nat Rev Genet* 14(5):301.

Billi AC, **Freeberg MA**, and Kim JK. (2012) piRNAs and siRNAs collaborate in *Caenorhabditis elegans* genome defense. *Gen Biol* 13(7):164. DOI:10.1186/gb-2012-13-7-164

Billi AC, Alessi AF, Khivansara V, Han T, **Freeberg M**, Mitani S, and Kim JK. (2012) The *Caenorhabditis elegans* HEN1 ortholog, HENN-1, methylates and stabilizes select subclasses of germline small RNAs. *PLoS Genet* 8(4):e1002617. DOI:10.1371/journal.pgen.1002617

*equal contribution

CONFERENCE PRESENTATIONS AND WORKSHOPS

Freeberg MA and Heydarian M. Galaxy 101: A gentle introduction to Galaxy. Galaxy Community Conference; Jun 2017; Montpellier, France. (Workshop)

Freeberg MA and Heydarian M. RNAseq analysis in Galaxy. Galaxy Community Conference; Jun 2017; Montpellier, France. (Workshop)

Freeberg MA and Taylor J. Approaches for small RNA-seq analysis in Galaxy. Galaxy Community Conference; Jun 2017; Montpellier, France. (Talk)

Freeberg MA and Heydarian M. Introduction to Genomic Data Analysis with Galaxy. U. S. Food and Drug Administration; Mar 2017; Silver Spring, MD. (Workshop)

Freeberg MA and Heydarian M. Introduction to Genomic Data Analysis with Galaxy. 13th KOGO Winter Symposium; Feb 2017; Washington D.C. (Workshop)

Freeberg MA and Heydarian M. Galaxy to Genomics using NGS Data. 13th KOGO Winter Symposium; Feb 2017; Hongcheon, South Korea. (Workshop)

Freeberg MA and Turaga N. Bioinformagic: Marrying Bioconductor and Galaxy. Galaxy Community Conference; Jun 2016; Bloomington, IN. (Workshop)

Freeberg MA. Transcriptome sequencing in nematodes. Oxford Nanopore Technologies London Calling; May 2016; London, UK. (Poster)

Freeberg MA and Taylor J. Probabilistic modeling of protein:RNA interaction data identifies functional Transcript States. CSHL Genome Informatics; Oct 2015; Cold Spring Harbor, NY. (Poster)

Freeberg MA, Han T, and Kim JK. Identification and characterization of the mRNA-binding proteome *in vivo* in *Saccharomyces cerevisiae*. CSHL Systems Biology: Global Regulation of Gene Expression; Mar 2014; Cold Spring Harbor, NY. (Talk)

Freeberg MA, Billi AC, and Kim JK. Germline expression, inheritance, and genomic characteristics of *Caenorhabditis elegans* 21U-RNAs. 18th International *C. elegans* Meeting; Jun 2011; Los Angeles, CA. (Poster)

INVITED TALKS

Freeberg MA. From high school to postdoc: Lessons from a decade of bioinformatics education [version 1; not peer reviewed]. *F1000Research* 2017, **6**(ISCB Comm J):801 (slides). DOI: 10.7490/f1000research.1114161.1

Freeberg MA. A novel pipeline for identifying transcriptome-wide binding sites of RNA-binding proteins from PAR-CLIP sequencing data. NCIBI Tools and Technology Seminar Series; May 2013; University of Michigan, Ann Arbor, MI.

Freeberg MA and Stevenson KR. Recommendations for successful scientific data sharing: Case studies of next-generation sequencing data use and re-use. NSF Open Data IGERT Seminar; Mar 2013; University of Michigan, Ann Arbor, MI.

Freeberg MA. Defending the genome: Computational identification of germline-specific piRNAs in *C. elegans*. Sep 2012; Saint Vincent College, Latrobe, PA.

Freeberg MA. Next-generation sequencing data re-use facilitates studies of small RNAs. NSF Open Data IGERT Research Workshop; Apr 2012; University of Michigan, Ann Arbor, MI.

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Johns Hopkins University, Baltimore, MD USA
Instructor for Advanced Academic Program online course   Jan - May 2017
Course title: *Bioinformatics: Tools for Genome Analysis*

Sisters Circle, Baltimore, MD USA
Mentor/tutor for middle school girls at Henderson-Hopkins Elementary   May 2015 - May 2016
Responsibilities: Co-lead weekly after-school sessions, weekly math tutoring

University of Michigan, Ann Arbor, MI USA
Mentor for a high school student   Jul - Aug 2014
Responsibilities: Designed bioinformatics/genomics research project, taught shell/perl programming

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