

Mallory A Freeberg, Ph.D.

CONTACT INFORMATION Wellcome Trust Genome Campus *Phone:* + 44 (0) 1223 49 2567
Main Building A2-125 *Email:* mallory dot freeberg at gmail dot com
Hinxton, Cambridgeshire, CB10 1SD, UK

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 AND WORK EXPERIENCE **European Bioinformatics Institute (EMBL-EBI)**, Hinxton, Cambridgeshire UK
Human Cell Atlas Data Coordination Platform
Senior Bioinformatician Oct 2018 - present
Bioinformatician Oct 2017 - Sep 2018
Responsibilities: Metadata curation and data wrangling for cellular-resolution data

The Galaxy Project, Baltimore, MD USA
Team Member Jan 2017 - Sep 2017
Research: Developed workflows, training materials, and best practices for transcriptomics and genomics-related research

Johns Hopkins University, Baltimore, MD USA
Postdoctoral Research Fellow Jun 2015 - Sep 2017
Research: Investigated post-transcriptional gene regulatory networks and developed nanopore direct RNA sequencing protocols
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 Jan 2008 - May 2009
Dissertation: Functional annotation of non-coding elements in the *Amphioxus* genome
Advisor: Dr. Michael L. Sierk

PUBLICATIONS Batut B, Hiltemann S, Bagnacani A, Baker D, Bhardwaj V, Blank C, Bretaudeau A, Brillet-Guguen L, Cech M, Chilton J, Clements D, Doppelt-Azeroual O, Erxleben A, **Freeberg MA**, *et al.* (2018) Community-Driven Data Analysis Training for Biology. *Cell Syst* 6(6):752-758. DOI:10.1016/j.cels.2018.05.012

Lariviere D, Mei H, **Freeberg MA**, Taylor J, Nekrutenko A. (2018) Understanding trivial challenges of microbial genomics: An assembly example. *bioRxiv* (preprint) 347625. DOI:10.1101/347625

Gruning B, Dale R, Sjodin A, Chapman BA, Rowe J, Tomkins-Tinch CH, Valieris R, Koster J, **The Bioconda Team**. (2018) Bioconda: sustainable and comprehensive software distribution for the life sciences. *Nat Meth* 15:475-6. DOI:10.1038/s41592-018-0046-7

Malhotra S, **Freeberg MA**, Winans SJ, Taylor J, Beemon KL. (2018) A Novel Long Non-Coding RNA in the *hTERT* Promoter Region Regulates *hTERT* Expression. *Non-Coding RNA* 4(1). DOI:10.3390/ncrna4010001

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

Jin M*, Fuller GG*, Han T*, Yao Y, Alessi AF, **Freeberg MA**, Roach NP, Moresco JJ, Karnovsky A, Baba M, Yates JR III, Gitler AD, Inoki K, Klionsky DJ, and Kim JK. (2017) Glycolytic Enzymes Coalesce in G Bodies Under Hypoxic Stress. *Cell Reports* 20(4):895-908. DOI:10.1016/j.celrep.2017.06.082

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

INVITED TALKS

Freeberg MA, Yordanova G, and Tickle T. How to engage with the Data Coordination Platform. Human Cell Atlas General Meeting; May 2019; Toyko, Japan

Clarke L, **Freeberg MA**, and Yordonova G. Human Cell Atlas Data Coordination Platform. Pilot Projects for a Human Cell Atlas Europe Retreat; Aug 2018; Stockholm, Sweden

Freeberg MA. Human Cell Atlas: Google Maps for human anatomy. Cambridge UK Computational Biology and Bioinformatics Meetup; Jun 2018; Cambridge, UK

Clarke L, **Freeberg MA**, O'Connor B, Osborn K, and Tickle T. Human Cell Atlas Data Coordination Platform: Status Update. Human Cell Atlas General Meeting; Mar 2018; Hinxton, UK

Freeberg MA. Single molecule RNA sequencing of the *C. elegans* transcriptome. Molecular Biosystems Conference on Eukaryotic Gene Regulation and Functional Genomics; Sep 2017; Puerto Varas, Chile. Sponsored by Oxford Nanopore Technologies

Freeberg MA. From high school to postdoc: lessons from a decade of bioinformatics education. Great Lakes Bioinformatics Conference; May 2017; University of Illinois at Chicago, Chicago, IL. 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

CONFERENCE TALKS AND WORKSHOPS

Freeberg MA. The Data Coordination Platform: Making the Human Cell Atlas data easily accessible. The Biology of Genomes; May 2018; Cold Spring Harbor, NY (Poster)

Freeberg MA and Taylor J. Approaches for small RNA-seq in Galaxy [version 1; not peer reviewed]. Galaxy Community Conference; Jun 2017; Montpellier, France (Talk)
F1000Research 2017, 6:1137. DOI:10.7490/f1000research.1114423.1

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

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. 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. 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)

Freeberg MA. Functional Annotation of Non-Coding Elements in the Amphioxus Genome. Saint Vincent College 6th Annual Undergraduate Conference; Apr 2009; Latrobe, PA. (Talk)

FUNDING AND
AWARDS

XSEDE Educational Computational Resource Allocation (2017)
XSEDE Startup Computational Resource Allocation (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++, Javascript, PHP/HTML, CWL)
Statistical Packages: R, Bioconductor (limited MatLab)
Applications: JSON, GitHub, L^AT_EX, Galaxy, NGS analysis tools and methodologies, MySQL

TEACHING AND
MENTORING
EXPERIENCE

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 - Sep 2017
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