WILLIAM MALLARD
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EDUCATION

Harvard University *Cambridge, MA*
PhD, Biochemistry *8/2016 – 5/2025*

University of California, Berkeley *Berkeley, CA*
BSc, Engineering Physics *1/2002 – 5/2007*
Minors in Computer Science and Mathematics

SKILLS

Languages: Python, C, Assembly, Java, Matlab, Simulink, Unix text processing (sed, awk, grep, etc)
Systems: Linux, Xilinx FPGAs, HPC/SLURM, Real-time Signal Processing
Domains: Structural Biology, Genomics, Machine Learning, Computer Vision, Scientific Computing

EXPERIENCE

Independent *Palo Alto, CA*
Research Scientist *6/2025 – 12/2025*

Solved the molecular mechanism of my PhD system, and published a two-author structure-function paper (PLoS One, 2025).
- Performed quantitative analysis of NMR spectra (NOESY and HSQC)
- Independently managed the full manuscript revision process

Tools: Python, NumPy, Pandas, NMRPipe, Poky

Harvard University *Cambridge, MA*
Graduate Student Researcher, Molecular and Cellular Biology *8/2016 – 5/2025*

Discovered a novel regulatory mechanism in bacterial cell division.
- Developed a novel AlphaFold workflow for studying IDR interactions: generated thousands of 3D structural models, extracted 2D contact maps, and clustered to identify binding modes
- Built computer vision pipelines processing tens of thousands of images: memory-efficient parallel processing of multi-GB datasets; computational geometry for cell size measurement
- Built end-to-end microscopy workflows (live-cell fluorescence, TIRF, and confocal imaging)
- Designed and executed biochemical experiments: GTPase assays, PhosTag gels
- Coordinated structural biology data collection: NMR, ITC, proximity proteomics

Tools: Python, NumPy, Pandas, SciPy, scikit-image, Fiji, Bash, SLURM

Broad Institute *Cambridge, MA*
Computational Biologist, Rinn Lab *2/2013 – 7/2016*

Contributed functional genomics analyses to 13 peer-reviewed studies in stem cell biology and developmental epigenetics.
- Built end-to-end NGS pipelines: demux, alignment, quantification, downstream analysis
- Developed custom toolchains for multi-omics integration: RNA-seq, ChIP-seq, ATAC-seq, bisulfite sequencing; differential expression, promoter identification, peak-to-gene mapping
- Partnered with bench scientists to translate experimental questions into computational analyses
- Wrote a Python C extension for automated job monitoring and queue management via LSF

Tools: Python, NumPy, Pandas, SciPy, scikit-learn, Bash, bedtools, Bowtie, TopHat, Cufflinks, C, LSF

Broad Institute of MIT and Harvard *Cambridge, MA*
Software Engineer, The Cancer Genome Atlas *4/2012 – 2/2013*

Maintained and extended production genomics pipelines for the Cancer Genome Atlas, contributing to 4 consortium publications (Nature/Cell, 2013–2014).
- Rewrote memory-intensive R scripts into streaming Python to scale to thousands of samples
- Identified a Python standard library limitation blocking large-dataset processing; contributed fix to CPython 3.4 in zipfile and shutil (issues #17189, #17201)

Tools: Python, NumPy, R, Bash

Space Sciences Laboratory   *Berkeley, CA*
Systems Engineer, Townes Lab   *9/2009 – 8/2011*

Designed the digital backend for the Infrared Spatial Interferometer at Mount Wilson Observatory.
- Built a real-time signal processing system handling 6 GSPS data rates on Xilinx Virtex-5
- Implemented synchronized cross-correlation across three FPGAs via 10 Gbps interconnects
- Extended CASPER's DSP library with DSP48E support for FFTs and polyphase filter banks, enabling higher clock rates across the platform
- Wrote placement constraint tooling to meet timing at near-maximum clock rates
- Developed an end-to-end data acquisition pipeline from FPGA fabric through embedded Linux to networked storage

Tools: Simulink, MATLAB, C, Python

Center for Astronomy Signal Processing and Electronics Research   *Berkeley, CA*
Systems Engineer, Werthimer Lab   *4/2008 – 9/2009*

Contributed to CASPER, an open-source FPGA toolkit for radio astronomy signal processing.
- Developed a 10 Gbps UDP receiver with a synchronized ring buffer; core architecture adopted into PySPEAD, the data transport layer for the Square Kilometre Array
- Extended DSP libraries for real-time spectrometry and correlation
- Deployed an instrument at Arecibo Observatory

Tools: Simulink, MATLAB, C, Python

MusicianLink, Inc.   *San Jose, CA*
Software Engineer   *6/2007 – 3/2008*

Developed network software for JamLink, a real-time music collaboration device.
- Designed the binary protocol: packet format, session negotiation, master election
- Built a multi-threaded connection manager in Java using raw TCP sockets

Tools: Java

UC Berkeley Clustered Computing   *Berkeley, CA*
Unix Systems Administrator   *1/2006 – 8/2006*

Administered Unix systems and job schedulers for scientific HPC clusters.

Massachusetts Institute of Technology   *Cambridge, MA*
Research Assistant, Chuang Lab   *6/2005 – 8/2005*

Built instrumentation to characterize planar ion traps for quantum computation.
- Wrote a programmable pulse sequencer in 1k lines of Scenix microcontroller assembly
- Designed a serial protocol for laptop-to-microcontroller communication
- Fabricated a custom NIM enclosure housing microcontroller and buffer electronics

Tools: Assembly, C, Python

University of California, Berkeley   *Berkeley, CA*
Research Assistant, Holzapfel Lab   *6/2004 – 5/2005*

Wrote software to thermocycle a helium dilution fridge to cool millimeter-wave detectors to 250mK.
- Rewrote LabView control system from scratch in C++ for robustness and remote deployment
- Interfaced with Linux Comedi drivers for ADC thermometer readout and DIO heater control

Tools: C++, Linux, Comedi

Teaching Fellow. *MCB 112: Biological Data Analysis*. Fall 2017, Fall 2021, Harvard University.

Lecturer. *MCB Matlab Bootcamp*. Fall 2017, Spring 2019, Harvard University.

Guest Lecturer. *SCRB 157: The Noncoding Genome*. Spring 2014, Harvard University.

Lab Teaching Assistant. *CS 61B: Data Structures*. Fall 2007, UC Berkeley.

Mallard WJ, Pham VV. "FtsZ phosphorylation modulates tail-core binding to tune cell division in *Bacillus subtilis*." **PLoS One** (2025).

Mallard WJ. "FtsZ phosphorylation modulates tail-core binding to tune cell division in *Bacillus subtilis*." PhD thesis, Harvard University (2025).

Erber J, Stecher C, Plajer V, Braun N, **Mallard W**, Goff LA, Barozzi I, Mohr T, Rinn JL, Flavell RA, Herndler-Brandstetter D. "*Rroid2* regulates effector-to-memory CD8+ T cell differentiation during infection *in vivo*." **Proc Natl Acad Sci** (2025).

Teo AKK, Nguyen L, Gupta MK, Lau HH, Loo LSW, Jackson N, Lim CS, **Mallard W**, Gritsenko MA, Rinn JL, Smith RD, Qian WJ, Kulkarni RN. "Defective insulin receptor signaling in hPSCs skews pluripotency and negatively perturbs neural differentiation." **Journal of Biological Chemistry** (2021).

Choudhuri A, Trompouki E, Abraham BJ, Colli LM, Kock KH, **Mallard W**, Yang ML, Vinjamur DS, Ghamari A, Sporrij A, Hoi K, Hummel B, Boatman S, Chan V, Tseng S, Nandakumar SK, Yang S, Lichtig A, Superdock M, Grimes SN, Bowman TV, Zhou Y, Takahashi S, Joehanes R, Cantor AB, Bauer DE, Ganesh SK, Rinn J, Albert PS, Bulyk ML, Chanock SJ, Young RA, Zon LI. "Common variants in signaling transcription-factor-binding sites drive phenotypic variability in red blood cell traits." **Nature Genetics** (2020).

Lewandowski JP, Lee JC, Hwang T, Sunwoo H, Goldstein JM, Groff AF, Chang NP, **Mallard W**, Williams A, Henao-Meija J, Flavell RA, Lee JT, Gerhardinger C, Wagers AJ, Rinn JL. "The Firre locus produces a trans-acting RNA molecule that functions in hematopoiesis." **Nature Communications** (2019).

Kaewsapsak P, Shechner DM, **Mallard W**, Rinn JL, Ting AY. "Live-cell mapping of organelle-associated RNAs via proximity biotinylation combined with protein-RNA crosslinking." *eLife* (2017).

Melé M, Mattioli K, **Mallard W**, Shechner DM, Gerhardinger C, Rinn JL. "Chromatin environment, transcriptional regulation, and splicing distinguish lincRNAs and mRNAs." **Genome Research** (2017).

Ferreira LMR, Meissner TB, Mikkelsen TS, **Mallard W**, O'Donnell CW, Tilburgs T, Camahort R, Sherwood RI, Gifford DK, Rinn JL, Cowan CA, Strominger JL. "A distant trophoblast-specific enhancer controls HLA-G expression at the maternal–fetal interface." **Proc Natl Acad Sci** (2016).

Choi J, Lee S, **Mallard W**, Clement K, Tagliazucchi GM, Lim H, Choi IY, Ferrari F, Tsankov A, Pop R, Lee G, Rinn JL, Meissner A, Park P, Hochedlinger K. "A comparison of genetically matched cell lines reveals the equivalence of human iPSCs and ESCs." **Nature Biotechnology** (2015).

Ziller MJ, Edri R, Yaffe Y, Donaghey J, Pop R, **Mallard W**, Issner R, Gifford CA, Goren A, Xing J, Gu H, Cacchiarelli D, Tsankov AM, Epstein C, Rinn JL, Mikkelsen TS, Kohlbacher O, Gnirke A, Bernstein BE, Elkabetz Y, Meissner A. "Dissecting neural differentiation regulatory networks through epigenetic footprinting." *Nature* (2015).

Liao J, Karnik R, Gu H, Ziller MJ, Clement K, Tsankov AM, Akopian V, Gifford CA, Donaghey J, Galonska C, Pop R, Reyon D, Tsai SQ, **Mallard W**, Joung JK, Rinn JL, Gnirke A, Meissner A. "Targeted disruption of DNMT1, DNMT3A and DNMT3B in human embryonic stem cells." **Nature Genetics** (2015).

Cancer Genome Atlas Research Network. "Comprehensive molecular profiling of lung adenocarcinoma."

Nature (2014).

Sauvageau M, Goff L, Lodato S, Bonev B, Groff A, Gerhardinger C, Sanchez-Gomez D, Hacisuleyman E, Li E, Spence M, Liapis S, **Mallard W**, Morse M, Swerdel M, D'Ecclessis M, Moore J, Lai V, Gong G, Yancopoulos G, Frendewey D, Kellis M, Hart R, Valenzuela D, Arlotta P, Rinn J. "Multiple Knockout Mouse Models Reveal lincRNAs are Required for Life and Brain Development." *eLife* (2013).

Cancer Genome Atlas Research Network. "The somatic genomic landscape of glioblastoma." *Cell* (2013).

Cancer Genome Atlas Research Network. "Comprehensive molecular characterization of clear cell renal cell carcinoma." *Nature* (2013).

Cancer Genome Atlas Research Network. "Integrated genomic characterization of endometrial carcinoma." *Nature* (2013).

Siemion APV, Cobb J, Filiba T, Fries A, Howard A, von Korff J, Korpela E, Lebofsky M, **Mallard W**, Parsons A, Wagner M. "Current and Nascent SETI Instruments in the Radio and Optical." In *Communication with Extraterrestrial Intelligence (CETI)*, p. 19 (2011).

Wishnow EH, **Mallard W**, Ravi V, Lockwood S, Fitelson W, Wertheimer D, Townes CH. "Mid-infrared interferometry with high spectral resolution." *Proc SPIE* (2010).

Filiba T, Chen H, Gowda S, **Mallard W**, Manley J, McMahon P, Siemion A, Spitler L, Wagner M, Werthimer D. "Wideband FPGA Spectrometers and Correlators." *2009 USNC/URSI Annual Meeting* (2009).

Pearson C, Leibrandt D, Bakr W, **Mallard W**, Brown K, Chuang I. "Experimental Investigation of Planar Ion Traps." *Physical Review A* (2006).