

Michael A. DeJesus, Ph.D.

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github.com/mad-lab | github.com/rock-lab |

Education

Ph.D., Computer Science , Texas A&M University	2016
M.S., Computer Science , Texas A&M University	2012
B.S., Computer Science , Universidad de Puerto Rico, Mayagüez	2008

Academic and Research Appointments

Senior Computational Biologist , Laboratory of Host-Pathogen Biology, The Rockefeller University	Aug 2020–present
Bioinformatics Specialist II	Nov 2018–Jul 2020
Bioinformatics Specialist	Jun 2018–Oct 2018
Postdoctoral Fellow , Ioerger Laboratory, Texas A&M University	Dec 2016–Jun 2018
Advisor: Thomas R. Ioerger	
Graduate Research Assistant , Ioerger Laboratory, Texas A&M University	Jul 2010–Dec 2016

Research Support

Status	Sponsor	Role	Period	Awarded
Current	Potts Memorial Foundation	Principal Investigator	Oct 2025–2026	\$50,000
Completed	Robertson Therapeutic Development Fund	Co-Principal Investigator	Jan–Jul 2024	\$50,000
Completed	Potts Memorial Foundation	Principal Investigator	2019–2021	\$100,000
Completed	Robertson Therapeutic Development Fund	Co-Principal Investigator	Jan–Jul 2020	\$50,000

Honors and Awards

- Best Paper Award, 7th International Conference on Bioinformatics and Computational Biology (BICoB), 2015
- Best Paper Award, ACM Conference on Bioinformatics, Computational Biology, and Biomedical Informatics (ACM-BCB), 2013
- Lechner Graduate Scholarship, Texas A&M University, 2012

Software and Research Resources

TRANSIT - developed statistical methods and graphical software for Himar1 transposon-sequencing analysis; associated peer-reviewed software paper listed below. transit.readthedocs.io | github.com/mad-lab/transit

Pebble - developed the Rock Laboratory’s public web portal for designing, analyzing, visualizing, and sharing mycobacterial functional-genomics, genetic-interaction, and systems-biology data. pebble.rockefeller.edu

Teaching and Mentoring

Madelaine Leitman, Ph.D. student, Computational Biology and Medicine (CBM)
Computational advisor, Rock lab, The Rockefeller University.

Current

Sam Nitz, CBM Ph.D. student
Computational advisor, Rock lab, The Rockefeller University.

Current

Alexis Schneider, Summer Undergraduate Research Fellowship (SURF) student
Supervised summer research at The Rockefeller University.

2021

Teaching Assistant, CSCE 625: Artificial Intelligence, Texas A&M University
Mentored students on assignments and course material; evaluated projects and home-work.

Fall 2015

Peer-Reviewed Journal Articles

*Reverse chronological. Michael A. DeJesus is shown in bold. *Co-first author. †Co-senior author.*

1. Kresse IJ*, Sayegh NY*, Munsamy-Govender V, Na A, Nitz S, Ozakman Y, Bosch B, Gonzalez S, Poulton NC, Reddy A, Wallach JB, Aguilera Olvera R, Castro A, Kim H, Wong AI, Tornow N, Bueler SA, Law WWH, Glickman MS, Rubinstein JL, Schnappinger D, **DeJesus MA**†, Rock JM†. Genetic interaction mapping of essential genes reveals the functional organization of the mycobacterial cell. *Nature*. **Accepted in principle**. *Co-first authors. †Co-senior authors.
2. Theriault ME, Wong AI, **DeJesus MA**, Pisu D, Lee BNR, Kirukubar G, Li S, Wallach JB, Schnappinger D, Lê-Bury G, Russell DG, Rock JM. 2026. Utilization of a CRISPRi-based ex vivo challenge model to reveal temporally dependent gene essentiality in intracellular Mycobacterium tuberculosis. *mBio* 17(5):e0061026. DOI: [10.1128/mbio.00610-26](https://doi.org/10.1128/mbio.00610-26).
3. Eckart KA, Munsamy-Govender V, Quiñones-Garcia S, **DeJesus MA**, Ju X, Liu S, Rock JM. 2026. Transcription attenuation amplifies collateral vulnerabilities in rifampicin-resistant Mycobacterium tuberculosis. *Nature Microbiology* 11:1696–1710. DOI: [10.1038/s41564-026-02357-9](https://doi.org/10.1038/s41564-026-02357-9).
4. Jinich A, Zaveri A, **DeJesus MA**, Spencer A, Almada-Monter R, Flores-Bautista E, Smith CM, Sassetti CM, Rock JM, Ehrt S, Schnappinger D, Ioerger TR, Rhee KY. 2025. The Mycobacterium tuberculosis Transposon Sequencing Database (MtbTnDB): A large-scale guide to genetic conditional essentiality. *Molecular Microbiology* 124(1):91–101. DOI: [10.1111/mmi.15370](https://doi.org/10.1111/mmi.15370).
5. Mishra S, Singh PR, Hu X, Lopez-Quezada L, Jinich A, Jahn R, Geurts L, Shen N, **DeJesus MA**, Hartman T, Rhee K, Zimmerman M, Dartois V, Jones RM, Jiang X, Almada-Monter R, Bourouiba L, Nathan C. 2025. Candidate transmission survival genome of Mycobacterium tuberculosis. *Proceedings of the National Academy of Sciences* 122(10):e2425981122. DOI: [10.1073/pnas.2425981122](https://doi.org/10.1073/pnas.2425981122).
6. Eckart KA, Delbeau M, Munsamy-Govender V, **DeJesus MA**, Azadian ZA, Reddy AK, Chandanani J, Poulton NC, Quiñones-Garcia S, Bosch B, Landick R, Campbell EA, Rock JM. 2024. Compensatory evolution in NusG improves fitness of drug-resistant M. tuberculosis. *Nature* 628(8006):186–194. DOI: [10.1038/s41586-024-07206-5](https://doi.org/10.1038/s41586-024-07206-5).
7. Poulton NC, **DeJesus MA**, Munsamy-Govender V, Kanai M, Roberts CG, Azadian ZA, Bosch B, Lin KM, Li S, Rock JM. 2024. Beyond antibiotic resistance: The whiB7 transcription factor coordinates an adaptive response to alanine starvation in mycobacteria. *Cell Chemical Biology* 31(4):669–682.e7. DOI: [10.1016/j.chembiol.2023.12.020](https://doi.org/10.1016/j.chembiol.2023.12.020).
8. Choudhery S, **DeJesus MA**, Srinivasan A, Rock JM, Schnappinger D, Ioerger TR. 2024. A dose-response model for statistical analysis of chemical genetic interactions in CRISPRi screens. *PLOS Computational Biology* 20(5):e1011408. DOI: [10.1371/journal.pcbi.1011408](https://doi.org/10.1371/journal.pcbi.1011408).
9. Bosch B, **DeJesus MA**, Schnappinger D, Rock JM. 2024. Weak links: Advancing target-based drug discovery by identifying the most vulnerable targets. *Annals of the New York Academy of Sciences* 1535(1):10–19. DOI: [10.1111/nyas.15139](https://doi.org/10.1111/nyas.15139).
10. Babunovic GH, **DeJesus MA**, Bosch B, Chase MR, Barbier T, Dickey AK, Bryson BD, Rock JM, Fortune SM. 2022. CRISPR interference reveals that all-trans-retinoic acid promotes macrophage control of Mycobacterium tuberculosis by limiting bacterial access to cholesterol and propionyl coenzyme A. *mBio* 13:e03683-21. DOI: [10.1128/mbio.03683-21](https://doi.org/10.1128/mbio.03683-21).
11. Li S, Poulton NC, Chang JS, Azadian ZA, **DeJesus MA**, Ruecker N, Zimmerman MD, Eckart KA, Bosch B, Engelhart CA, Sullivan DF, Gengenbacher M, Dartois VA, Schnappinger D, Rock JM. 2022. CRISPRi chemical genetics and comparative genomics identify genes mediating drug potency in Mycobacterium tuberculosis. *Nature Microbiology* 7(6):766–779. DOI: [10.1038/s41564-022-01130-y](https://doi.org/10.1038/s41564-022-01130-y).

12. Poulton NC, Azadian ZA, **DeJesus MA**, Rock JM. 2022. Mutations in rv0678 confer low-level resistance to benzothiazine DprE1 inhibitors in Mycobacterium tuberculosis. *Antimicrobial Agents and Chemotherapy* 66:e00904-22. DOI: [10.1128/aac.00904-22](https://doi.org/10.1128/aac.00904-22).
13. Dutta E, **DeJesus MA**, Ruecker N, Zaveri A, Koh EI, Sassetti CM, Schnappinger D, Ioerger TR. 2021. An improved statistical method to identify chemical-genetic interactions by exploiting concentration-dependence. *PLOS ONE* 16:e0257911. DOI: [10.1371/journal.pone.0257911](https://doi.org/10.1371/journal.pone.0257911).
14. Bosch B*, **DeJesus MA***, Poulton NC, Zhang W, Engelhart CA, Zaveri A, Lavalette S, Ruecker N, Trujillo C, Wallach JB, Li S, Ehrt S, Chait BT, Schnappinger D, Rock JM. 2021. Genome-wide gene expression tuning reveals diverse vulnerabilities of M. tuberculosis. *Cell* 184(17):4579–4592.e24. *Co-first authors. DOI: [10.1016/j.cell.2021.06.033](https://doi.org/10.1016/j.cell.2021.06.033).
15. Subramaniyam S, **DeJesus MA**, Zaveri A, Smith CM, Baker RE, Ehrt S, Schnappinger D, Sassetti CM, Ioerger TR. 2019. Statistical analysis of variability in TnSeq data across conditions using zero-inflated negative binomial regression. *BMC Bioinformatics* 20:603. DOI: [10.1186/s12859-019-3156-z](https://doi.org/10.1186/s12859-019-3156-z).
16. **DeJesus MA**, Nambi S, Smith CM, Baker RE, Sassetti CM, Ioerger TR. 2017. Statistical analysis of genetic interactions in Tn-Seq data. *Nucleic Acids Research* 45(11):e93. DOI: [10.1093/nar/gkx128](https://doi.org/10.1093/nar/gkx128).
17. Xu W, **DeJesus MA**, Ruecker N, Engelhart CA, Wright MG, Healy C, Lin K, Wang R, Park SW, Ioerger TR, Schnappinger D, Ehrt S. 2017. Chemical genetic interaction profiling reveals determinants of intrinsic antibiotic resistance in Mycobacterium tuberculosis. *Antimicrobial Agents and Chemotherapy* 61:e01334-17. DOI: [10.1128/AAC.01334-17](https://doi.org/10.1128/AAC.01334-17).
18. **DeJesus MA**, Gerrick ER, Xu W, Park SW, Long JE, Boutte CC, Rubin EJ, Schnappinger D, Ehrt S, Fortune SM, Sassetti CM, Ioerger TR. 2017. Comprehensive essentiality analysis of the Mycobacterium tuberculosis genome via saturating transposon mutagenesis. *mBio* 8(1):e02133-16. DOI: [10.1128/mBio.02133-16](https://doi.org/10.1128/mBio.02133-16).
19. Korte J, Alber M, Trujillo CM, Syson K, Koliwer-Brandl H, Deenen R, Köhrer K, **DeJesus MA**, Hartman T, Jacobs WR Jr, Bornemann S, Ioerger TR, Ehrt S, Kalscheuer R. 2016. Trehalose-6-phosphate-mediated toxicity determines essentiality of OtsB2 in Mycobacterium tuberculosis in vitro and in mice. *PLOS Pathogens* 12(12):e1006043. DOI: [10.1371/journal.ppat.1006043](https://doi.org/10.1371/journal.ppat.1006043).
20. Orsini C, Setlow B, **DeJesus MA**, Galaviz S, Loesch K, Ioerger TR, Wallis D. 2016. Behavioral and transcriptomic profiling of mice null for Lphn3, a gene implicated in ADHD and addiction. *Molecular Genetics & Genomic Medicine* 4(3):322–343. DOI: [10.1002/mgg3.207](https://doi.org/10.1002/mgg3.207).
21. **DeJesus MA**, Ioerger TR. 2016. Normalization of transposon-mutant library sequencing datasets to improve identification of conditionally essential genes. *Journal of Bioinformatics and Computational Biology* 14(3):1642004. DOI: [10.1142/S021972001642004X](https://doi.org/10.1142/S021972001642004X).
22. **DeJesus MA**, Ambadipudi C, Baker R, Sassetti C, Ioerger TR. 2015. TRANSIT - A software tool for Himar1 TnSeq analysis. *PLOS Computational Biology* 11(10):e1004401. DOI: [10.1371/journal.pcbi.1004401](https://doi.org/10.1371/journal.pcbi.1004401).
23. Wallis D, Loesch K, Galaviz S, Sun Q, **DeJesus MA**, Ioerger TR, Sacchettini JC. 2015. High-throughput differentiation and screening of a library of mutant stem cell clones defines new host-based genes involved in rabies virus infection. *Stem Cells* 33(8):2509–2522. DOI: [10.1002/stem.1983](https://doi.org/10.1002/stem.1983).
24. Loesch K, Galaviz S, Hamoui Z, Clanton R, Akabani G, Deveau M, **DeJesus MA**, Ioerger TR, Sacchettini JC, Wallis D. 2015. Functional genomics screening utilizing mutant mouse embryonic stem cells identifies novel radiation-response genes. *PLOS ONE* 10(4):e0120534. DOI: [10.1371/journal.pone.0120534](https://doi.org/10.1371/journal.pone.0120534).
25. **DeJesus MA**, Ioerger TR. 2015. Capturing uncertainty by modeling local transposon insertion frequencies improves discrimination of essential genes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 12(1):92–102. DOI: [10.1109/TCBB.2014.2326857](https://doi.org/10.1109/TCBB.2014.2326857).
26. **DeJesus MA**, Ioerger TR. 2013. A hidden Markov model for identifying essential and growth-defect regions in bacterial genomes from transposon insertion sequencing data. *BMC Bioinformatics* 14:303. DOI: [10.1186/1471-2105-14-303](https://doi.org/10.1186/1471-2105-14-303).
27. **DeJesus MA**, Zhang YJ, Sassetti CM, Rubin EJ, Sacchettini JC, Ioerger TR. 2013. Bayesian analysis of gene essentiality based on sequencing of transposon insertion libraries. *Bioinformatics* 29(6):695–703. DOI: [10.1093/bioinformatics/btt043](https://doi.org/10.1093/bioinformatics/btt043).
28. **DeJesus MA**, Sacchettini JC, Ioerger TR. 2013. Reannotation of translational start sites in the genome of Mycobacterium tuberculosis. *Tuberculosis* 93:18–25. DOI: [10.1016/j.tube.2012.11.012](https://doi.org/10.1016/j.tube.2012.11.012).
29. Griffin JE, Gawronski JD, **DeJesus MA**, Ioerger TR, Akerley BJ, Sassetti CM. 2011. High-resolution phenotypic profiling defines genes essential for mycobacterial growth and cholesterol catabolism. *PLOS Pathogens* 7:e1002251. DOI: [10.1371/journal.ppat.1002251](https://doi.org/10.1371/journal.ppat.1002251).

Preprints and Manuscripts Under Review

Not yet peer reviewed.

1. Todor H, Kim LM, Billings E, Grzegorzewicz AE, Burkhart HN, **DeJesus MA**, Na A, Nitz S, Shell SS, Campbell EA, Jackson M, Mancia F, Rock JM, Gross CA, Chen J. 2026. Predicting the protein interaction landscape of a mycobacterial pathogen. *bioRxiv*. DOI: [10.64898/2026.07.15.738315](https://doi.org/10.64898/2026.07.15.738315).
2. Singh PR, Gengenbacher M, Mishra S, Jinich A, Jiang X, Tsang F, Cristaldo M, **DeJesus MA**, Rhee K, Kaner R, Leopold P, Crystal RG, Kathayat D, VanderVen BC, Nathan CF. 2026. *Mycobacterium tuberculosis* genes needed for intra-alveolar resuscitation after airborne transmission. *bioRxiv*. DOI: [10.1101/2025.09.15.676370](https://doi.org/10.1101/2025.09.15.676370).
3. Gouzy A, Li S, Chen J, Na A, Saleh A, Azadian ZA, Tam K, Munsamy-Govender V, Poulton NC, **DeJesus MA**, Schnappinger D, Rhee KY, Ehrt S, Rock JM. 2026. Metabolic control of drug resistance by a mycobacterial ion channel. *bioRxiv*. DOI: [10.64898/2026.03.10.710584](https://doi.org/10.64898/2026.03.10.710584).
4. Deschner F, Chengalroyen MD, Ames L, Quach D, Aguilera Olvera R, Bosch B, Castro A, Kim H, Raman K, Thornton N, Wallach J, da Costa FR, Allen R, Lupien A, Zuma M, Lynch S, Pogliano J, Sugie J, Rock JM, Schnappinger D, Parish T, Mizrahi V, **DeJesus MA**, Müller R, Herrmann J. 2025. Chlorotonils exhibit potent activity against *Mycobacterium tuberculosis*, while resistance is mediated by MmpR5-MmpL5. *bioRxiv*. DOI: [10.64898/2025.12.09.693342](https://doi.org/10.64898/2025.12.09.693342).

Peer-Reviewed Conference Proceedings

1. **DeJesus MA**, Ioerger TR. 2015. Reducing type I errors in Tn-Seq experiments by correcting the skew in read count distributions. *Proceedings of the 7th International Conference on Bioinformatics and Computational Biology (BICoB)*. **Best Paper Award**.
2. **DeJesus MA**, Ioerger TR. 2013. Improving discrimination of essential genes by modeling local insertion frequencies in transposon mutagenesis data. *Proceedings of the ACM Conference on Bioinformatics, Computational Biology, and Biomedical Informatics (ACM-BCB)*, pp. 144–151. **Best Paper Award**. DOI: [10.1145/2506583.2506610](https://doi.org/10.1145/2506583.2506610).

Book Chapter

1. Long JE, **DeJesus MA**, Ward D, Baker RE, Ioerger TR, Sassetti CM. 2015. Identifying essential genes in *Mycobacterium tuberculosis* by global phenotypic profiling. *Methods in Molecular Biology*, vol. 1279, pp. 79–95. DOI: [10.1007/978-1-4939-2398-4_6](https://doi.org/10.1007/978-1-4939-2398-4_6).

Conference Posters

1. Maxwell SA, Wallis D, Zhou N, Baker D, Mousavi-Fard S, Loesch K, Galaviz S, Sun Q, Threadgill DM, Rojas CM, O'Brien M, Clubb FJ, Ioerger TR, **DeJesus MA**, Dong W, Seemann G, Fossum T, Sacchettini JC. 2017. Development of novel, non-toxic rifamycins that reverse drug resistance in diffuse large B-cell lymphoma (DLBCL). *Hematological Oncology* 35(S2):253–254. DOI: [10.1002/hon.2438_118](https://doi.org/10.1002/hon.2438_118).

Thesis

1. **DeJesus MA**. 2012. Bayesian analysis of transposon mutagenesis data. M.S. thesis, Texas A&M University.