Michael A Dejesus

List of Publications by Year
in descending order

17 papers	2,178 citations	759233 12 h-index	996975 15 g-index
21 all docs	21 docs citations	21 times ranked	2740 citing authors

#	Article	IF	Citations
1	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, 2022, 13, e0368321.	4.1	19
2	CRISPRi chemical genetics and comparative genomics identify genes mediating drug potency in Mycobacterium tuberculosis. Nature Microbiology, 2022, 7, 766-779.	13.3	68
3	Genome-wide gene expression tuning reveals diverse vulnerabilities of M.Âtuberculosis. Cell, 2021, 184, 4579-4592.e24.	28.9	131
4	An improved statistical method to identify chemical-genetic interactions by exploiting concentration-dependence. PLoS ONE, 2021, 16, e0257911.	2.5	1
5	Statistical analysis of variability in TnSeq data across conditions using zero-inflated negative binomial regression. BMC Bioinformatics, 2019, 20, 603.	2.6	15
6	Comprehensive Essentiality Analysis of the Mycobacterium tuberculosis Genome via Saturating Transposon Mutagenesis. MBio, 2017, 8, .	4.1	496
7	Statistical analysis of genetic interactions in Tn-Seq data. Nucleic Acids Research, 2017, 45, e93-e93.	14.5	31
8	Chemical Genetic Interaction Profiling Reveals Determinants of Intrinsic Antibiotic Resistance in Mycobacterium tuberculosis. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	70
9	Normalization of transposon-mutant library sequencing datasets to improve identification of conditionally essential genes. Journal of Bioinformatics and Computational Biology, 2016, 14, 1642004.	0.8	12
10	Trehalose-6-Phosphate-Mediated Toxicity Determines Essentiality of OtsB2 in Mycobacterium tuberculosis In Vitro and in Mice. PLoS Pathogens, 2016, 12, e1006043.	4.7	35
11	TRANSIT - A Software Tool for Himar1 TnSeq Analysis. PLoS Computational Biology, 2015, 11, e1004401.	3.2	170
12	Capturing Uncertainty by Modeling Local Transposon Insertion Frequencies Improves Discrimination of Essential Genes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 92-102.	3.0	7
13	Reannotation of translational start sites in the genome ofÂMycobacterium tuberculosis. Tuberculosis, 2013, 93, 18-25.	1.9	27
14	A Hidden Markov Model for identifying essential and growth-defect regions in bacterial genomes from transposon insertion sequencing data. BMC Bioinformatics, 2013, 14, 303.	2.6	72
15	Improving discrimination of essential genes by modeling local insertion frequencies in transposon mutagenesis data. , 2013, , .		0
16	Bayesian analysis of gene essentiality based on sequencing of transposon insertion libraries. Bioinformatics, 2013, 29, 695-703.	4.1	74
17	High-Resolution Phenotypic Profiling Defines Genes Essential for Mycobacterial Growth and Cholesterol Catabolism. PLoS Pathogens, 2011, 7, e1002251.	4.7	935