

Michael A Dejesus

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

2,178
citations

758635

12
h-index

996533

15
g-index

21
all docs

21
docs citations

21
times ranked

2740
citing authors

#	ARTICLE	IF	CITATIONS
1	CRISPR Interference Reveals That All- <i>Trans</i> -Retinoic Acid Promotes Macrophage Control of <i>Mycobacterium tuberculosis</i> by Limiting Bacterial Access to Cholesterol and Propionyl Coenzyme A. <i>MBio</i> , 2022, 13, e0368321.	1.8	19
2	CRISPRi chemical genetics and comparative genomics identify genes mediating drug potency in <i>Mycobacterium tuberculosis</i> . <i>Nature Microbiology</i> , 2022, 7, 766-779.	5.9	68
3	Genome-wide gene expression tuning reveals diverse vulnerabilities of <i>M. tuberculosis</i> . <i>Cell</i> , 2021, 184, 4579-4592.e24.	13.5	131
4	An improved statistical method to identify chemical-genetic interactions by exploiting concentration-dependence. <i>PLoS ONE</i> , 2021, 16, e0257911.	1.1	1
5	Statistical analysis of variability in TnSeq data across conditions using zero-inflated negative binomial regression. <i>BMC Bioinformatics</i> , 2019, 20, 603.	1.2	15
6	Comprehensive Essentiality Analysis of the <i>Mycobacterium tuberculosis</i> Genome via Saturating Transposon Mutagenesis. <i>MBio</i> , 2017, 8, .	1.8	496
7	Statistical analysis of genetic interactions in Tn-Seq data. <i>Nucleic Acids Research</i> , 2017, 45, e93-e93.	6.5	31
8	Chemical Genetic Interaction Profiling Reveals Determinants of Intrinsic Antibiotic Resistance in <i>Mycobacterium tuberculosis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	70
9	Normalization of transposon-mutant library sequencing datasets to improve identification of conditionally essential genes. <i>Journal of Bioinformatics and Computational Biology</i> , 2016, 14, 1642004.	0.3	12
10	Trehalose-6-Phosphate-Mediated Toxicity Determines Essentiality of OtsB2 in <i>Mycobacterium tuberculosis</i> In Vitro and in Mice. <i>PLoS Pathogens</i> , 2016, 12, e1006043.	2.1	35
11	TRANSIT - A Software Tool for Himar1 TnSeq Analysis. <i>PLoS Computational Biology</i> , 2015, 11, e1004401.	1.5	170
12	Capturing Uncertainty by Modeling Local Transposon Insertion Frequencies Improves Discrimination of Essential Genes. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 92-102.	1.9	7
13	Reannotation of translational start sites in the genome of <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2013, 93, 18-25.	0.8	27
14	A Hidden Markov Model for identifying essential and growth-defect regions in bacterial genomes from transposon insertion sequencing data. <i>BMC Bioinformatics</i> , 2013, 14, 303.	1.2	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. <i>Bioinformatics</i> , 2013, 29, 695-703.	1.8	74
17	High-Resolution Phenotypic Profiling Defines Genes Essential for <i>Mycobacterial</i> Growth and Cholesterol Catabolism. <i>PLoS Pathogens</i> , 2011, 7, e1002251.	2.1	935