

Christopher M Sassetti

List of Publications by Year in descending order

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106
papers

14,048
citations

44444

50
h-index

37326

100
g-index

125
all docs

125
docs citations

125
times ranked

13680
citing authors

#	ARTICLE	IF	CITATIONS
1	Host-pathogen genetic interactions underlie tuberculosis susceptibility in genetically diverse mice. <i>ELife</i> , 2022, 11, .	2.8	44
2	Chemicalâ€“genetic interaction mapping links carbon metabolism and cell wall structure to tuberculosis drug efficacy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2201632119.	3.3	20
3	Cell Wall Damage Reveals Spatial Flexibility in Peptidoglycan Synthesis and a Nonredundant Role for RodA in <i>Mycobacteria</i> . <i>Journal of Bacteriology</i> , 2022, 204, e0054021.	1.0	11
4	Granulocytes act as a niche for <i>Mycobacterium tuberculosis</i> growth. <i>Mucosal Immunology</i> , 2021, 14, 229-241.	2.7	43
5	Two-Way Regulation of MmpL3 Expression Identifies and Validates Inhibitors of MmpL3 Function in <i>Mycobacterium tuberculosis</i> . <i>ACS Infectious Diseases</i> , 2021, 7, 141-152.	1.8	13
6	Phosphorylation on PstP Regulates Cell Wall Metabolism and Antibiotic Tolerance in <i>Mycobacterium smegmatis</i> . <i>Journal of Bacteriology</i> , 2021, 203, .	1.0	6
7	Sirtuin 3 Downregulation in <i>Mycobacterium tuberculosis</i> -Infected Macrophages Reprograms Mitochondrial Metabolism and Promotes Cell Death. <i>MBio</i> , 2021, 12, .	1.8	21
8	Characterization of Drug-Resistant Lipid-Dependent Differentially Detectable <i>Mycobacterium tuberculosis</i> . <i>Journal of Clinical Medicine</i> , 2021, 10, 3249.	1.0	5
9	Host immunity increases <i>Mycobacterium tuberculosis</i> reliance on cytochrome bd oxidase. <i>PLoS Pathogens</i> , 2021, 17, e1008911.	2.1	8
10	An improved statistical method to identify chemical-genetic interactions by exploiting concentration-dependence. <i>PLoS ONE</i> , 2021, 16, e0257911.	1.1	1
11	Type I Interferon and Interleukin-1 Driven Inflammatory Pathways as Targets for HDT in Tuberculosis. , 2021, , 219-232.		1
12	Mitochondrial respiration contributes to the interferon gamma response in antigen-presenting cells. <i>ELife</i> , 2021, 10, .	2.8	14
13	Cell-Cycle-Associated Expression Patterns Predict Gene Function in <i>Mycobacteria</i> . <i>Current Biology</i> , 2020, 30, 3961-3971.e6.	1.8	13
14	A natural polymorphism of <i>Mycobacterium tuberculosis</i> in the <i>esxH</i> gene disrupts immunodomination by the TB10.4-specific CD8 T cell response. <i>PLoS Pathogens</i> , 2020, 16, e1009000.	2.1	22
15	Content and Performance of the MiniMUGA Genotyping Array: A New Tool To Improve Rigor and Reproducibility in Mouse Research. <i>Genetics</i> , 2020, 216, 905-930.	1.2	58
16	Distinct Bacterial Pathways Influence the Efficacy of Antibiotics against <i>Mycobacterium tuberculosis</i> . <i>MSystems</i> , 2020, 5, .	1.7	37
17	<i>M.Â</i> tuberculosis Reprograms Hematopoietic Stem Cells to Limit Myelopoiesis and Impair Trained Immunity. <i>Cell</i> , 2020, 183, 752-770.e22.	13.5	148
18	Evaluation of IL-1 Blockade as an Adjunct to Linezolid Therapy for Tuberculosis in Mice and Macaques. <i>Frontiers in Immunology</i> , 2020, 11, 891.	2.2	25

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19	CD11c ^{hi} monocyte-derived macrophages are a major cellular compartment infected by Mycobacterium tuberculosis. PLoS Pathogens, 2020, 16, e1008621.	2.1	36
20	Title is missing!. , 2020, 16, e1008621.		0
21	Title is missing!. , 2020, 16, e1008621.		0
22	Title is missing!. , 2020, 16, e1008621.		0
23	Title is missing!. , 2020, 16, e1008621.		0
24	Common Variants in the Glycerol Kinase Gene Reduce Tuberculosis Drug Efficacy. MBio, 2019, 10, .	1.8	80
25	Large-scale chemical genetics yields new M. tuberculosis inhibitor classes. Nature, 2019, 571, 72-78.	13.7	119
26	Functionally Overlapping Variants Control Tuberculosis Susceptibility in Collaborative Cross Mice. MBio, 2019, 10, .	1.8	36
27	Statistical analysis of variability in TnSeq data across conditions using zero-inflated negative binomial regression. BMC Bioinformatics, 2019, 20, 603.	1.2	15
28	Advancing Translational Science for Pulmonary Nontuberculous Mycobacterial Infections. A Road Map for Research. American Journal of Respiratory and Critical Care Medicine, 2019, 199, 947-951.	2.5	53
29	The structure of the endogenous ESX-3 secretion system. ELife, 2019, 8, .	2.8	61
30	Consequence of enhanced LC3-trafficking for a live, attenuated M. tuberculosis vaccine. Vaccine, 2018, 36, 939-944.	1.7	7
31	CNBP controls IL-12 gene transcription and Th1 immunity. Journal of Experimental Medicine, 2018, 215, 3136-3150.	4.2	36
32	ORBIT: a New Paradigm for Genetic Engineering of Mycobacterial Chromosomes. MBio, 2018, 9, .	1.8	86
33	A Lysine Acetyltransferase Contributes to the Metabolic Adaptation to Hypoxia in Mycobacterium tuberculosis. Cell Chemical Biology, 2018, 25, 1495-1505.e3.	2.5	33
34	Tolerating the Unwelcome Guest; How the Host Withstands Persistent Mycobacterium tuberculosis. Frontiers in Immunology, 2018, 9, 2094.	2.2	20
35	The Phagocyte Oxidase Controls Tolerance to Mycobacterium tuberculosis Infection. Journal of Immunology, 2018, 201, 1705-1716.	0.4	25
36	Modeling Diversity: Do Homogeneous Laboratory Strains Limit Discovery?. Trends in Microbiology, 2018, 26, 892-895.	3.5	14

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37	Comprehensive Essentiality Analysis of the <i>Mycobacterium tuberculosis</i> Genome via Saturating Transposon Mutagenesis. MBio, 2017, 8, .	1.8	496
38	Programmable transcriptional repression in mycobacteria using an orthogonal CRISPR interference platform. Nature Microbiology, 2017, 2, 16274.	5.9	368
39	Nitric oxide prevents a pathogen-permissive granulocytic inflammation during tuberculosis. Nature Microbiology, 2017, 2, 17072.	5.9	222
40	Unravelling the pleiotropic role of the <i>MceG</i> ATPase in <i>Mycobacterium smegmatis</i> . Environmental Microbiology, 2017, 19, 2564-2576.	1.8	20
41	Statistical analysis of genetic interactions in Tn-Seq data. Nucleic Acids Research, 2017, 45, e93-e93.	6.5	31
42	Role of Granulocyte-Macrophage Colony-Stimulating Factor Production by T Cells during <i>Mycobacterium tuberculosis</i> Infection. MBio, 2017, 8, .	1.8	65
43	A Parallel Adder Coordinates Mycobacterial Cell-Cycle Progression and Cell-Size Homeostasis in the Context of Asymmetric Growth and Organization. Current Biology, 2017, 27, 3367-3374.e7.	1.8	62
44	<i>Mycobacterium tuberculosis</i> is protected from NADPH oxidase and LC3-associated phagocytosis by the LCP protein CpsA. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E8711-E8720.	3.3	138
45	Molecular and functional analysis of the <i>mce4</i> operon in <i>Mycobacterium smegmatis</i> . Environmental Microbiology, 2017, 19, 3689-3699.	1.8	21
46	Fine-tuning of Substrate Affinity Leads to Alternative Roles of Mycobacterium tuberculosis Fe ²⁺ -ATPases. Journal of Biological Chemistry, 2016, 291, 11529-11539.	1.6	36
47	Spatially distinct and metabolically active membrane domain in mycobacteria. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 5400-5405.	3.3	78
48	Tuberculosis Susceptibility and Vaccine Protection Are Independently Controlled by Host Genotype. MBio, 2016, 7, .	1.8	116
49	Structural and Genetic Analyses of the Mycobacterium tuberculosis Protein Kinase B Sensor Domain Identify a Potential Ligand-binding Site. Journal of Biological Chemistry, 2016, 291, 22961-22969.	1.6	27
50	Metabolic crosstalk between host and pathogen: sensing, adapting and competing. Nature Reviews Microbiology, 2016, 14, 221-234.	13.6	166
51	Chewing the fat: lipid metabolism and homeostasis during M. tuberculosis infection. Current Opinion in Microbiology, 2016, 29, 30-36.	2.3	118
52	xCT increases tuberculosis susceptibility by regulating antimicrobial function and inflammation. Oncotarget, 2016, 7, 31001-31013.	0.8	24
53	A cytoplasmic peptidoglycan amidase homologue controls mycobacterial cell wall synthesis. ELife, 2016, 5, .	2.8	82
54	TRANSIT - A Software Tool for Himar1 TnSeq Analysis. PLoS Computational Biology, 2015, 11, e1004401.	1.5	170

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55	The Oxidative Stress Network of Mycobacterium tuberculosis Reveals Coordination between Radical Detoxification Systems. <i>Cell Host and Microbe</i> , 2015, 17, 829-837.	5.1	131
56	New TB treatments hiding in plain sight. <i>EMBO Molecular Medicine</i> , 2015, 7, 125-126.	3.3	6
57	New insights into <i>TB</i> physiology suggest untapped therapeutic opportunities. <i>Immunological Reviews</i> , 2015, 264, 327-343.	2.8	23
58	Label-free Quantitative Proteomics Reveals a Role for the Mycobacterium tuberculosis SecA2 Pathway in Exporting Solute Binding Proteins and Mce Transporters to the Cell Wall*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1501-1516.	2.5	47
59	Peptidoglycan synthesis in <i>Mycobacterium tuberculosis</i> is organized into networks with varying drug susceptibility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13087-13092.	3.3	82
60	Identifying Essential Genes in Mycobacterium tuberculosis by Global Phenotypic Profiling. <i>Methods in Molecular Biology</i> , 2015, 1279, 79-95.	0.4	75
61	Mycobacterial Recombineering. <i>Methods in Molecular Biology</i> , 2015, 1285, 177-199.	0.4	87
62	Phosphorylation of the Peptidoglycan Synthase PonA1 Governs the Rate of Polar Elongation in Mycobacteria. <i>PLoS Pathogens</i> , 2015, 11, e1005010.	2.1	100
63	Allele-Specific Induction of IL-1 β Expression by C/EBP β and PU.1 Contributes to Increased Tuberculosis Susceptibility. <i>PLoS Pathogens</i> , 2014, 10, e1004426.	2.1	94
64	Subpolar addition of new cell wall is directed by DivIVA in mycobacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3243-51.	3.3	159
65	Biochemical and Spatial Coincidence in the Provisional Ser/Thr Protein Kinase Interaction Network of Mycobacterium tuberculosis*. <i>Journal of Biological Chemistry</i> , 2014, 289, 20422-20433.	1.6	56
66	Differential roles for the <i>Co</i> ²⁺ transporting <i>ATP</i> ases, <i>CtpD</i> and <i>CtpJ</i> , in <i>Mycobacterium tuberculosis</i> virulence. <i>Molecular Microbiology</i> , 2014, 91, 185-197.	1.2	52
67	Fixing the odds against tuberculosis. <i>Nature</i> , 2014, 511, 39-40.	13.7	6
68	Genetic Strategies for Identifying New Drug Targets. <i>Microbiology Spectrum</i> , 2014, 2, MGM2-0030-2013.	1.2	5
69	Nitric oxide controls the immunopathology of tuberculosis by inhibiting NLRP3 inflammasome-dependent processing of IL-1 β . <i>Nature Immunology</i> , 2013, 14, 52-60.	7.0	500
70	Infection control in cystic fibrosis: share and share alike. <i>Lancet</i> , The, 2013, 381, 1517-1519.	6.3	2
71	The Normalcy of Dormancy: Common Themes in Microbial Quiescence. <i>Cell Host and Microbe</i> , 2013, 13, 643-651.	5.1	277
72	DNA Methylation Impacts Gene Expression and Ensures Hypoxic Survival of Mycobacterium tuberculosis. <i>PLoS Pathogens</i> , 2013, 9, e1003419.	2.1	132

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73	Identification of New Drug Targets and Resistance Mechanisms in <i>Mycobacterium tuberculosis</i> . <i>PLoS ONE</i> , 2013, 8, e75245.	1.1	223
74	A Novel P1B-type Mn ²⁺ -transporting ATPase Is Required for Secreted Protein Metallation in <i>Mycobacteria</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 11334-11347.	1.6	86
75	Bayesian analysis of gene essentiality based on sequencing of transposon insertion libraries. <i>Bioinformatics</i> , 2013, 29, 695-703.	1.8	74
76	Global Assessment of Genomic Regions Required for Growth in <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2012, 8, e1002946.	2.1	220
77	A Phosphorylated Pseudokinase Complex Controls Cell Wall Synthesis in <i>Mycobacteria</i> . <i>Science Signaling</i> , 2012, 5, ra7.	1.6	151
78	Cyclic AMP regulation of protein lysine acetylation in <i>Mycobacterium tuberculosis</i> . <i>Nature Structural and Molecular Biology</i> , 2012, 19, 811-818.	3.6	46
79	Cholesterol Catabolism by <i>Mycobacterium tuberculosis</i> Requires Transcriptional and Metabolic Adaptations. <i>Chemistry and Biology</i> , 2012, 19, 218-227.	6.2	270
80	Role in metal homeostasis of CtpD, a Co ²⁺ transporting P _{1B4} -ATPase of <i>Mycobacterium smegmatis</i> . <i>Molecular Microbiology</i> , 2012, 84, 1139-1149.	1.2	50
81	Depletion of antibiotic targets has widely varying effects on growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4176-4181.	3.3	141
82	<i>Mycobacterium tuberculosis</i> Induces an Atypical Cell Death Mode to Escape from Infected Macrophages. <i>PLoS ONE</i> , 2011, 6, e18367.	1.1	108
83	Metabolic Regulation of <i>Mycobacterial</i> Growth and Antibiotic Sensitivity. <i>PLoS Biology</i> , 2011, 9, e1001065.	2.6	255
84	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
85	Relics of selection in the <i>mycobacterial</i> genome. <i>Nature Genetics</i> , 2010, 42, 476-478.	9.4	2
86	Increased NOD2-mediated recognition of <i>N</i> -glycolyl muramyl dipeptide. <i>Journal of Experimental Medicine</i> , 2009, 206, 1709-1716.	4.2	203
87	NOD2, RIP2 and IRF5 Play a Critical Role in the Type I Interferon Response to <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2009, 5, e1000500.	2.1	239
88	Phthiocerol Dimycocerosate Transport Is Required for Resisting Interferon-Independent Immunity. <i>Journal of Infectious Diseases</i> , 2009, 200, 774-782.	1.9	55
89	<i>igr</i> Genes and <i>Mycobacterium tuberculosis</i> Cholesterol Metabolism. <i>Journal of Bacteriology</i> , 2009, 191, 5232-5239.	1.0	142
90	Nitrile-inducible gene expression in <i>mycobacteria</i> . <i>Tuberculosis</i> , 2009, 89, 12-16.	0.8	71

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91	Inducible Expression Systems for Mycobacteria. <i>Methods in Molecular Biology</i> , 2009, 465, 255-264.	0.4	3
92	Role of cholesterol in Mycobacterium tuberculosis infection. <i>Indian Journal of Experimental Biology</i> , 2009, 47, 407-11.	0.5	67
93	Mycobacterial persistence requires the utilization of host cholesterol. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 4376-4380.	3.3	900
94	NOD2 Pathway Activation by MDP or Mycobacterium tuberculosis Infection Involves the Stable Polyubiquitination of Rip2. <i>Journal of Biological Chemistry</i> , 2007, 282, 36223-36229.	1.6	199
95	The open book of infectious diseases. <i>Nature Medicine</i> , 2007, 13, 279-280.	15.2	18
96	Characterization of mycobacterial virulence genes through genetic interaction mapping. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 11760-11765.	3.3	187
97	A new site-specific integration system for mycobacteria. <i>Tuberculosis</i> , 2005, 85, 317-323.	0.8	20
98	The folate pathway is a target for resistance to the drug para-aminosalicylic acid (PAS) in mycobacteria. <i>Molecular Microbiology</i> , 2004, 53, 275-282.	1.2	158
99	Genes required for mycobacterial growth defined by high density mutagenesis. <i>Molecular Microbiology</i> , 2003, 48, 77-84.	1.2	2,302
100	Endoglycan, a Member of the CD34 Family, Functions as an L-selectin Ligand through Modification with Tyrosine Sulfation and Sialyl Lewis x. <i>Journal of Biological Chemistry</i> , 2003, 278, 27390-27398.	1.6	65
101	Genetic requirements for mycobacterial survival during infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 12989-12994.	3.3	1,208
102	Genomic analyses of microbial virulence. <i>Current Opinion in Microbiology</i> , 2002, 5, 27-32.	2.3	24
103	Mast cells migrate, but do not degranulate, in response to fractalkine, a membrane-bound chemokine expressed constitutively in diverse cells of the skin. <i>European Journal of Immunology</i> , 2000, 30, 2355-2361.	1.6	80
104	Identification of Endoglycan, a Member of the CD34/Podocalyxin Family of Sialomucins. <i>Journal of Biological Chemistry</i> , 2000, 275, 9001-9010.	1.6	95
105	Identification of Podocalyxin-like Protein as a High Endothelial Venule Ligand for L-selectin: Parallels to CD34. <i>Journal of Experimental Medicine</i> , 1998, 187, 1965-1975.	4.2	230
106	Genetic Strategies for Identifying New Drug Targets. , 0, , 493-509.		0