

# James C Sacchetti

## List of Publications by Citations

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107  
papers

11,470  
citations

40  
h-index

107  
g-index

117  
ext. papers

12,925  
ext. citations

11.7  
avg, IF

5.69  
L-index

#	Paper	IF	Citations
107	PHENIX: building new software for automated crystallographic structure determination. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2002</b> , 58, 1948-54		3477
106	Persistence of Mycobacterium tuberculosis in macrophages and mice requires the glyoxylate shunt enzyme isocitrate lyase. <i>Nature</i> , <b>2000</b> , 406, 735-8	50.4	1091
105	Crystal structure of a plant catechol oxidase containing a dicopper center. <i>Nature Structural Biology</i> , <b>1998</b> , 5, 1084-90		671
104	Modification of the NADH of the isoniazid target (InhA) from Mycobacterium tuberculosis. <i>Science</i> , <b>1998</b> , 279, 98-102	33.3	563
103	Enzymatic characterization of the target for isoniazid in Mycobacterium tuberculosis. <i>Biochemistry</i> , <b>1995</b> , 34, 8235-41	3.2	348
102	Sterilization of granulomas is common in active and latent tuberculosis despite within-host variability in bacterial killing. <i>Nature Medicine</i> , <b>2014</b> , 20, 75-9	50.5	327
101	Use of whole genome sequencing to estimate the mutation rate of Mycobacterium tuberculosis during latent infection. <i>Nature Genetics</i> , <b>2011</b> , 43, 482-6	36.3	319
100	Multivalent protein-carbohydrate interactions. A new paradigm for supermolecular assembly and signal transduction. <i>Biochemistry</i> , <b>2001</b> , 40, 3009-15	3.2	263
99	Transfer of a point mutation in Mycobacterium tuberculosis inhA resolves the target of isoniazid. <i>Nature Medicine</i> , <b>2006</b> , 12, 1027-9	50.5	226
98	Mechanism of thioamide drug action against tuberculosis and leprosy. <i>Journal of Experimental Medicine</i> , <b>2007</b> , 204, 73-8	16.6	223
97	Tryptophan biosynthesis protects mycobacteria from CD4 T-cell-mediated killing. <i>Cell</i> , <b>2013</b> , 155, 1296-308	30.2	222
96	Inactivation of the inhA-encoded fatty acid synthase II (FASII) enoyl-acyl carrier protein reductase induces accumulation of the FASII end products and cell lysis of Mycobacterium smegmatis. <i>Journal of Bacteriology</i> , <b>2000</b> , 182, 4059-67	3.5	212
95	Therapeutic strategies for human amyloid diseases. <i>Nature Reviews Drug Discovery</i> , <b>2002</b> , 1, 267-75	64.1	205
94	Drugs versus bugs: in pursuit of the persistent predator Mycobacterium tuberculosis. <i>Nature Reviews Microbiology</i> , <b>2008</b> , 6, 41-52	22.2	191
93	Structure of isocitrate lyase, a persistence factor of Mycobacterium tuberculosis. <i>Nature Structural Biology</i> , <b>2000</b> , 7, 663-8		187
92	Global assessment of genomic regions required for growth in Mycobacterium tuberculosis. <i>PLoS Pathogens</i> , <b>2012</b> , 8, e1002946	7.6	181
91	Variation among genome sequences of H37Rv strains of Mycobacterium tuberculosis from multiple laboratories. <i>Journal of Bacteriology</i> , <b>2010</b> , 192, 3645-53	3.5	173

90	Identification of new drug targets and resistance mechanisms in Mycobacterium tuberculosis. <i>PLoS ONE</i> , <b>2013</b> , 8, e75245	3.7	165
89	Dual role of isocitrate lyase 1 in the glyoxylate and methylcitrate cycles in Mycobacterium tuberculosis. <i>Molecular Microbiology</i> , <b>2006</b> , 61, 940-7	4.1	142
88	Gene-target recognition among members of the myc superfamily and implications for oncogenesis. <i>Nature Genetics</i> , <b>2000</b> , 24, 113-9	36.3	122
87	Biochemical and structural studies of malate synthase from Mycobacterium tuberculosis. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 1735-43	5.4	109
86	Crystal structure of the human 20S proteasome in complex with carfilzomib. <i>Structure</i> , <b>2015</b> , 23, 418-24	5.2	101
85	TB drug discovery: addressing issues of persistence and resistance. <i>Tuberculosis</i> , <b>2004</b> , 84, 45-55	2.6	98
84	Development of a Novel Lead that Targets M. tuberculosis Polyketide Synthase 13. <i>Cell</i> , <b>2017</b> , 170, 249-259	5.2	88
83	Structure-guided discovery of phenyl-diketo acids as potent inhibitors of M. tuberculosis malate synthase. <i>Chemistry and Biology</i> , <b>2012</b> , 19, 1556-67		80
82	Structural and functional analyses of the severe acute respiratory syndrome coronavirus endoribonuclease Nsp15. <i>Journal of Biological Chemistry</i> , <b>2008</b> , 283, 3655-3664	5.4	80
81	Structure-Based Design of N-Phenyl Phenoxazine Transthyretin Amyloid Fibril Inhibitors. <i>Journal of the American Chemical Society</i> , <b>2000</b> , 122, 2178-2192	16.4	74
80	Binding of fatty acids and peroxisome proliferators to orthologous fatty acid binding proteins from human, murine, and bovine liver. <i>Biochemistry</i> , <b>2000</b> , 39, 1469-74	3.2	67
79	Mycobacterial Metabolic Syndrome: LprG and Rv1410 Regulate Triacylglyceride Levels, Growth Rate and Virulence in Mycobacterium tuberculosis. <i>PLoS Pathogens</i> , <b>2016</b> , 12, e1005351	7.6	65
78	Peptidoglycan synthesis in Mycobacterium tuberculosis is organized into networks with varying drug susceptibility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 13087-92	11.5	64
77	A comprehensive characterization of PncA polymorphisms that confer resistance to pyrazinamide. <i>Nature Communications</i> , <b>2017</b> , 8, 588	17.4	64
76	Discovery of Novel Oral Protein Synthesis Inhibitors of Mycobacterium tuberculosis That Target Leucyl-tRNA Synthetase. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2016</b> , 60, 6271-80	5.9	61
75	Phosphorylation of InhA inhibits mycolic acid biosynthesis and growth of Mycobacterium tuberculosis. <i>Molecular Microbiology</i> , <b>2010</b> , 78, 1591-605	4.1	55
74	Glyoxylate detoxification is an essential function of malate synthase required for carbon assimilation in. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E2225-E2232	11.5	53
73	Selective Inactivity of Pyrazinamide against Tuberculosis in C3HeB/FeJ Mice Is Best Explained by Neutral pH of Caseum. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2016</b> , 60, 735-43	5.9	47

72	TnSeq of Mycobacterium tuberculosis clinical isolates reveals strain-specific antibiotic liabilities. <i>PLoS Pathogens</i> , <b>2018</b> , 14, e1006939	7.6	47
71	Structural insights into species-specific features of the ribosome from the human pathogen Mycobacterium tuberculosis. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, 10884-10894	20.1	41
70	Folate pathway disruption leads to critical disruption of methionine derivatives in Mycobacterium tuberculosis. <i>Chemistry and Biology</i> , <b>2014</b> , 21, 819-30		41
69	Antitubercular drugs for an old target: GSK693 as a promising InhA direct inhibitor. <i>EBioMedicine</i> , <b>2016</b> , 8, 291-301	8.8	41
68	Solution structure of ileal lipid binding protein in complex with glycocholate. <i>FEBS Journal</i> , <b>2000</b> , 267, 2929-38		40
67	Opposing reactions in coenzyme A metabolism sensitize to enzyme inhibition. <i>Science</i> , <b>2019</b> , 363,	33.3	37
66	Structure of Ribosomal Silencing Factor Bound to Mycobacterium tuberculosis Ribosome. <i>Structure</i> , <b>2015</b> , 23, 1858-1865	5.2	37
65	Ribosomal mutations promote the evolution of antibiotic resistance in a multidrug environment. <i>ELife</i> , <b>2017</b> , 6,	8.9	34
64	An Antibacterial $\beta$ -Lactone Kills Mycobacterium tuberculosis by Disrupting Mycolic Acid Biosynthesis. <i>Angewandte Chemie - International Edition</i> , <b>2018</b> , 57, 348-353	16.4	34
63	The TB Structural Genomics Consortium: a decade of progress. <i>Tuberculosis</i> , <b>2011</b> , 91, 155-72	2.6	33
62	High resolution crystal structures of Mycobacterium tuberculosis adenosine kinase: insights into the mechanism and specificity of this novel prokaryotic enzyme. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 27334-27342	5.4	31
61	Advancing Translational Science for Pulmonary Nontuberculous Mycobacterial Infections. A Road Map for Research. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2019</b> , 199, 947-951	10.2	31
60	Structural insights into the mechanism of the allosteric transitions of Mycobacterium tuberculosis cAMP receptor protein. <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 36581-36591	5.4	30
59	A novel antimycobacterial compound acts as an intracellular iron chelator. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2015</b> , 59, 2256-64	5.9	27
58	Mechanisms for isoniazid action and resistance. <i>Novartis Foundation Symposium</i> , <b>1998</b> , 217, 209-20; discussion 220-1		24
57	Synthesis and evaluation of the 2,4-diaminoquinazoline series as anti-tubercular agents. <i>Bioorganic and Medicinal Chemistry</i> , <b>2014</b> , 22, 6965-79	3.4	21
56	A comparative study of the backbone dynamics of two closely related lipid binding proteins: Bovine heart fatty acid binding protein and porcine ileal lipid binding protein. <i>Molecular and Cellular Biochemistry</i> , <b>1999</b> , 192, 109-121	4.2	21
55	N-Benzyl-4-((heteroaryl)methyl)benzamides: A New Class of Direct NADH-Dependent 2-trans Enoyl-Acyl Carrier Protein Reductase (InhA) Inhibitors with Antitubercular Activity. <i>ChemMedChem</i> , <b>2016</b> , 11, 687-701	3.7	21

54	Elesclomol alleviates Menkes pathology and mortality by escorting Cu to cuproenzymes in mice. <i>Science</i> , <b>2020</b> , 368, 620-625	33.3	20
53	The molecular basis of pyrazinamide activity on Mycobacterium tuberculosis PanD. <i>Nature Communications</i> , <b>2020</b> , 11, 339	17.4	20
52	Impact of immunopathology on the antituberculous activity of pyrazinamide. <i>Journal of Experimental Medicine</i> , <b>2018</b> , 215, 1975-1986	16.6	19
51	Mechanism-based inactivator of isocitrate lyases 1 and 2 from. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, 7617-7622	11.5	19
50	Deletion of SenX3-RegX3, a key two-component regulatory system of Mycobacterium smegmatis, results in growth defects under phosphate-limiting conditions. <i>Microbiology (United Kingdom)</i> , <b>2012</b> , 158, 2724-2731	2.9	19
49	Genome-wide Phenotypic Profiling Identifies and Categorizes Genes Required for Mycobacterial Low Iron Fitness. <i>Scientific Reports</i> , <b>2019</b> , 9, 11394	4.9	18
48	Targeting protein biotinylation enhances tuberculosis chemotherapy. <i>Science Translational Medicine</i> , <b>2018</b> , 10,	17.5	17
47	Anion-Interactions in Computer-Aided Drug Design: Modeling the Inhibition of Malate Synthase by Phenyl-Diketo Acids. <i>Journal of Chemical Information and Modeling</i> , <b>2018</b> , 58, 2085-2091	6.1	17
46	A Lysine Acetyltransferase Contributes to the Metabolic Adaptation to Hypoxia in Mycobacterium tuberculosis. <i>Cell Chemical Biology</i> , <b>2018</b> , 25, 1495-1505.e3	8.2	17
45	Aspartate aminotransferase Rv3722c governs aspartate-dependent nitrogen metabolism in Mycobacterium tuberculosis. <i>Nature Communications</i> , <b>2020</b> , 11, 1960	17.4	16
44	Structure, activity, and inhibition of the Carboxyltransferase $\beta$ subunit of acetyl coenzyme A carboxylase (AccD6) from Mycobacterium tuberculosis. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2014</b> , 58, 6122-32	5.9	16
43	Identification of compounds with potential antibacterial activity against Mycobacterium through structure-based drug screening. <i>Journal of Chemical Information and Modeling</i> , <b>2013</b> , 53, 1200-12	6.1	16
42	The effect of hinge mutations on effector binding and domain rotation in Escherichia coli D-3-phosphoglycerate dehydrogenase. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 18418-18426	5.4	15
41	Mutations in () as a Novel Determinant of Resistance to Pretomanid and Delamanid in Mycobacterium tuberculosis. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2020</b> , 65,	5.9	15
40	Discovery of InhA inhibitors with anti-mycobacterial activity through a matched molecular pair approach. <i>European Journal of Medicinal Chemistry</i> , <b>2015</b> , 94, 378-85	6.8	14
39	Discovery of Antimicrobial Lipodepsipeptides Produced by a Serratia sp. within Mosquito Microbiomes. <i>ChemBioChem</i> , <b>2018</b> , 19, 1590-1594	3.8	14
38	Binding Mechanism of the N-Terminal SH3 Domain of CrkII and Proline-Rich Motifs in cAbl. <i>Biophysical Journal</i> , <b>2016</b> , 110, 2630-2641	2.9	14
37	Structural Similarities and Differences between Two Functionally Distinct SecA Proteins, Mycobacterium tuberculosis SecA1 and SecA2. <i>Journal of Bacteriology</i> , <b>2015</b> , 198, 720-30	3.5	14

36	Structural Insights into Mycobacterium tuberculosis Rv2671 Protein as a Dihydrofolate Reductase Functional Analogue Contributing to para-Aminosalicylic Acid Resistance. <i>Biochemistry</i> , <b>2016</b> , 55, 1107-1119	3.2	13
35	Minocycline and Silver Dual-Loaded Polyphosphoester-Based Nanoparticles for Treatment of Resistant Pseudomonas aeruginosa. <i>Molecular Pharmaceutics</i> , <b>2019</b> , 16, 1606-1619	5.6	13
34	Bedaquiline reprograms central metabolism to reveal glycolytic vulnerability in Mycobacterium tuberculosis. <i>Nature Communications</i> , <b>2020</b> , 11, 6092	17.4	11
33	A strategy for dual inhibition of the proteasome and fatty acid synthase with belactosin C-orlistat hybrids. <i>Bioorganic and Medicinal Chemistry</i> , <b>2017</b> , 25, 2901-2916	3.4	10
32	Mycobacterium tuberculosis acyl carrier protein synthase adopts two different pH-dependent structural conformations. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2011</b> , 67, 657-69		10
31	High Throughput Screen for Escherichia coli Twin Arginine Translocation (Tat) Inhibitors. <i>PLoS ONE</i> , <b>2016</b> , 11, e0149659	3.7	10
30	R pyocin tail fiber structure reveals a receptor-binding domain with a lectin fold. <i>PLoS ONE</i> , <b>2019</b> , 14, e0211432	3.7	9
29	SatS is a chaperone for the SecA2 protein export pathway. <i>ELife</i> , <b>2019</b> , 8,	8.9	8
28	Structural and functional insight into the Mycobacterium tuberculosis protein PrpR reveals a novel type of transcription factor. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 9934-9949	20.1	7
27	Structure-Guided Drug Design of 6-Substituted Adenosine Analogues as Potent Inhibitors of Mycobacterium tuberculosis Adenosine Kinase. <i>Journal of Medicinal Chemistry</i> , <b>2019</b> , 62, 4483-4499	8.3	7
26	The Tuberculosis Drug Accelerator at year 10: what have we learned?. <i>Nature Medicine</i> , <b>2021</b> , 27, 1333-1337	33.5	7
25	The Structural Basis of T4 Phage Lysis Control: DNA as the Signal for Lysis Inhibition. <i>Journal of Molecular Biology</i> , <b>2020</b> , 432, 4623-4636	6.5	6
24	Construction of an overexpression library for. <i>Biology Methods and Protocols</i> , <b>2018</b> , 3, bpy009	2.4	6
23	Activity-Based Protein Profiling Reveals That Cephalosporins Selectively Active on Non-replicating Bind Multiple Protein Families and Spare Peptidoglycan Transpeptidases. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 1248	5.7	5
22	Functional genomics screening utilizing mutant mouse embryonic stem cells identifies novel radiation-response genes. <i>PLoS ONE</i> , <b>2015</b> , 10, e0120534	3.7	5
21	A Sec14-like phosphatidylinositol transfer protein paralog defines a novel class of heme-binding proteins. <i>ELife</i> , <b>2020</b> , 9,	8.9	5
20	Subfamily-specific adaptations in the structures of two penicillin-binding proteins from Mycobacterium tuberculosis. <i>PLoS ONE</i> , <b>2014</b> , 9, e116249	3.7	4
19	Structural insights into phosphopantetheinyl hydrolase PptH from Mycobacterium tuberculosis. <i>Protein Science</i> , <b>2020</b> , 29, 744-757	6.3	4

18	Identification of a novel class of small compounds with anti-tuberculosis activity by in silico structure-based drug screening. <i>Journal of Antibiotics</i> , <b>2017</b> , 70, 1057-1064	3.7	3
17	A DNA-Binding Protein Tunes Septum Placement during Sporulation. <i>Journal of Bacteriology</i> , <b>2019</b> , 201,	3.5	3
16	Ein antibakterielles $\beta$ -Lacton bekämpft Mycobacterium tuberculosis durch Infiltration der Mykolsäurebiosynthese. <i>Angewandte Chemie</i> , <b>2018</b> , 130, 354-359	3.6	3
15	Covalent Inactivation of Isocitrate Lyase by $\alpha$ -2,3-Epoxy-Succinic Acid. <i>ACS Chemical Biology</i> , <b>2021</b> , 16, 463-470	4.9	3
14	Structural anatomy of Protein Kinase C C1 domain interactions with diacylglycerol and other agonists.. <i>Nature Communications</i> , <b>2022</b> , 13, 2695	17.4	3
13	Comparison of transposon and deletion mutants in Mycobacterium tuberculosis: The case of rv1248c, encoding 2-hydroxy-3-oxoadipate synthase. <i>Tuberculosis</i> , <b>2015</b> , 95, 689-694	2.6	2
12	Interplay between an ATP-binding cassette F protein and the ribosome from Mycobacterium tuberculosis.. <i>Nature Communications</i> , <b>2022</b> , 13, 432	17.4	2
11	CinA mediates multidrug tolerance in Mycobacterium tuberculosis.. <i>Nature Communications</i> , <b>2022</b> , 13, 2203	17.4	2
10	Structure-guided design of a potent peptide inhibitor targeting the interaction between CRK and ABL kinase. <i>MedChemComm</i> , <b>2018</b> , 9, 519-524	5	1
9	Tetraterpene Synthase Substrate and Product Specificity in the Green Microalga Botryococcus braunii Race L. <i>ACS Chemical Biology</i> , <b>2017</b> , 12, 2408-2416	4.9	1
8	High-Throughput Differentiation and Screening of a Library of Mutant Stem Cell Clones Defines New Host-Based Genes Involved in Rabies Virus Infection. <i>Stem Cells</i> , <b>2015</b> , 33, 2509-22	5.8	1
7	Metabolic bifunctionality of Rv0812 couples folate and peptidoglycan biosynthesis in Mycobacterium tuberculosis. <i>Journal of Experimental Medicine</i> , <b>2021</b> , 218,	16.6	1
6	Improvement of the novel inhibitor for Mycobacterium enoyl-acyl carrier protein reductase (InhA): a structure-activity relationship study of KES4 assisted by in silico structure-based drug screening. <i>Journal of Antibiotics</i> , <b>2020</b> , 73, 372-381	3.7	0
5	Mechanism-Based Inactivation of Isocitrate Lyase 1 by (2,3)-2-Hydroxy-3-(nitromethyl)succinic acid. <i>Journal of the American Chemical Society</i> , <b>2021</b> , 143, 17666-17676	16.4	0
4	Development of single-cell-level microfluidic technology for long-term growth visualization of living cultures of. <i>Microsystems and Nanoengineering</i> , <b>2021</b> , 7, 37	7.7	0
3	A portable brightfield and fluorescence microscope toward automated malarial parasitemia quantification in thin blood smears.. <i>PLoS ONE</i> , <b>2022</b> , 17, e0266441	3.7	0
2	A low-cost, novel endoscopic repeated-access port for small animal research. <i>MethodsX</i> , <b>2020</b> , 7, 101049	1.9	0
1	Characterization of Phosphopantetheinyl Hydrolase from Mycobacterium tuberculosis. <i>Microbiology Spectrum</i> , <b>2021</b> , 9, e0092821	8.9	0

