James C Sacchettini

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/367166/publications.pdf

Version: 2024-02-01

112 papers	14,084 citations	57758 44 h-index	24982 109 g-index
117 all docs	117 docs citations	117 times ranked	18164 citing authors

#	Article	IF	Citations
1	In Vitro and In Vivo Inhibition of the <i>Mycobacterium tuberculosis</i> Phosphopantetheinyl Transferase PptT by Amidinoureas. Journal of Medicinal Chemistry, 2022, 65, 1996-2022.	6.4	10
2	Interplay between an ATP-binding cassette F protein and the ribosome from Mycobacterium tuberculosis. Nature Communications, 2022, 13, 432.	12.8	16
3	A portable brightfield and fluorescence microscope toward automated malarial parasitemia quantification in thin blood smears. PLoS ONE, 2022, 17, e0266441.	2.5	2
4	Optimization of TAM16, a Benzofuran That Inhibits the Thioesterase Activity of Pks13; Evaluation toward a Preclinical Candidate for a Novel Antituberculosis Clinical Target. Journal of Medicinal Chemistry, 2022, 65, 409-423.	6.4	15
5	CinA mediates multidrug tolerance in Mycobacterium tuberculosis. Nature Communications, 2022, 13, 2203.	12.8	22
6	Structural Basis of Agonist Capture by Regulatory C1 Domain of PKC. FASEB Journal, 2022, 36, .	0.5	0
7	Structural anatomy of Protein Kinase C C1 domain interactions with diacylglycerol and other agonists. Nature Communications, 2022, 13, 2695.	12.8	17
8	Covalent Inactivation of <i>Mycobacterium tuberculosis</i> Isocitrate Lyase by <i>cis</i>-2,3-Epoxy-Succinic Acid. ACS Chemical Biology, 2021, 16, 463-470.	3.4	6
9	Development of single-cell-level microfluidic technology for long-term growth visualization of living cultures of Mycobacterium smegmatis. Microsystems and Nanoengineering, 2021, 7, 37.	7.0	7
10	Metabolic bifunctionality of Rv0812 couples folate and peptidoglycan biosynthesis in <i>Mycobacterium tuberculosis</i>. Journal of Experimental Medicine, 2021, 218, .	8.5	4
11	The Tuberculosis Drug Accelerator at year 10: what have we learned?. Nature Medicine, 2021, 27, 1333-1337.	30.7	32
12	Characterization of Phosphopantetheinyl Hydrolase from Mycobacterium tuberculosis. Microbiology Spectrum, 2021, 9, e0092821.	3.0	1
13	Mechanism-Based Inactivation of <i>Mycobacterium tuberculosis</i> Isocitrate Lyase 1 by (2<i>R</i>,3<i>S</i>)-2-Hydroxy-3-(nitromethyl)succinic acid. Journal of the American Chemical Society, 2021, 143, 17666-17676.	13.7	4
14	Second-Shell Amino Acid R266 Helps Determine <i>N</i>-Succinylamino Acid Racemase Reaction Specificity in Promiscuous <i>N</i>-Succinylamino Acid Racemase/<i>o</i>-Succinylbenzoate Synthase Enzymes. Biochemistry, 2021, 60, 3829-3840.	2.5	2
15	Structural insights into phosphopantetheinyl hydrolase PptH from Mycobacterium tuberculosis. Protein Science, 2020, 29, 744-757.	7.6	6
16	Mutations in <i>fbiD</i> (<i>Rv2983</i>) as a Novel Determinant of Resistance to Pretomanid and Delamanid in Mycobacterium tuberculosis. Antimicrobial Agents and Chemotherapy, 2020, 65, .	3.2	48
17	Bedaquiline reprograms central metabolism to reveal glycolytic vulnerability in Mycobacterium tuberculosis. Nature Communications, 2020, 11, 6092.	12.8	34
18	A low-cost, novel endoscopic repeated-access port for small animal research. MethodsX, 2020, 7, 101049.	1.6	0

#	Article	IF	Citations
19	Elesclomol alleviates Menkes pathology and mortality by escorting Cu to cuproenzymes in mice. Science, 2020, 368, 620-625.	12.6	66
20	Activity-Based Protein Profiling Reveals That Cephalosporins Selectively Active on Non-replicating Mycobacterium tuberculosis Bind Multiple Protein Families and Spare Peptidoglycan Transpeptidases. Frontiers in Microbiology, 2020, 11, 1248.	3.5	11
21	The Structural Basis of T4 Phage Lysis Control: DNA as the Signal for Lysis Inhibition. Journal of Molecular Biology, 2020, 432, 4623-4636.	4.2	16
22	Improvement of the novel inhibitor for Mycobacterium enoyl-acyl carrier protein reductase (InhA): a structureâ€"activity relationship study of KES4 assisted by in silico structure-based drug screening. Journal of Antibiotics, 2020, 73, 372-381.	2.0	3
23	The molecular basis of pyrazinamide activity on Mycobacterium tuberculosis PanD. Nature Communications, 2020, 11, 339.	12.8	37
24	Aspartate aminotransferase Rv3722c governs aspartate-dependent nitrogen metabolism in Mycobacterium tuberculosis. Nature Communications, 2020, 11, 1960.	12.8	44
25	A Sec14-like phosphatidylinositol transfer protein paralog defines a novel class of heme-binding proteins. ELife, 2020, 9, .	6.0	10
26	Genome-wide Phenotypic Profiling Identifies and Categorizes Genes Required for Mycobacterial Low Iron Fitness. Scientific Reports, 2019, 9, 11394.	3.3	36
27	Structural and functional insight into the Mycobacterium tuberculosis protein PrpR reveals a novel type of transcription factor. Nucleic Acids Research, 2019, 47, 9934-9949.	14.5	18
28	Opposing reactions in coenzyme A metabolism sensitize <i>Mycobacterium tuberculosis</i> to enzyme inhibition. Science, 2019, 363, .	12.6	53
29	A DNA-Binding Protein Tunes Septum Placement during <i>Bacillus subtilis</i> Sporulation. Journal of Bacteriology, 2019, 201, .	2.2	10
30	Structure-Guided Drug Design of 6-Substituted Adenosine Analogues as Potent Inhibitors of <i>Mycobacterium tuberculosis</i> Adenosine Kinase. Journal of Medicinal Chemistry, 2019, 62, 4483-4499.	6.4	11
31	Minocycline and Silver Dual-Loaded Polyphosphoester-Based Nanoparticles for Treatment of Resistant <i>Pseudomonas aeruginosa</i>. Molecular Pharmaceutics, 2019, 16, 1606-1619.	4.6	22
32	R pyocin tail fiber structure reveals a receptor-binding domain with a lectin fold. PLoS ONE, 2019, 14, e0211432.	2.5	21
33	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.	5.6	53
34	Mycobacterium tuberculosis SatS is a chaperone for the SecA2 protein export pathway. ELife, 2019, 8, .	6.0	12
35	Targeting protein biotinylation enhances tuberculosis chemotherapy. Science Translational Medicine, 2018, 10, .	12.4	24
36	Structure-guided design of a potent peptide inhibitor targeting the interaction between CRK and ABL kinase. MedChemComm, 2018, 9, 519-524.	3.4	1

#	ARTICLE	IF	CITATIONS
37	Discovery of Antimicrobial Lipodepsipeptides Produced by a <i>Serratia</i> sp. within Mosquito Microbiomes. ChemBioChem, 2018, 19, 1590-1594.	2.6	26
38	An Antibacterial Î²â€Łactone Kills Mycobacterium tuberculosis by Disrupting Mycolic Acid Biosynthesis. Angewandte Chemie - International Edition, 2018, 57, 348-353.	13.8	55
39	Ein antibakterielles Î²â€Łacton bekÃmpft <i>Mycobacterium tuberculosis</i> durch Infiltration der MykolsÃurebiosynthese. Angewandte Chemie, 2018, 130, 354-359.	2.0	3
40	A Lysine Acetyltransferase Contributes to the Metabolic Adaptation to Hypoxia in Mycobacterium tuberculosis. Cell Chemical Biology, 2018, 25, 1495-1505.e3.	5.2	33
41	Impact of immunopathology on the antituberculous activity of pyrazinamide. Journal of Experimental Medicine, 2018, 215, 1975-1986.	8.5	29
42	Anion-Ï€ Interactions in Computer-Aided Drug Design: Modeling the Inhibition of Malate Synthase by Phenyl-Diketo Acids. Journal of Chemical Information and Modeling, 2018, 58, 2085-2091.	5.4	21
43	Construction of an overexpression library for Mycobacterium tuberculosis. Biology Methods and Protocols, 2018, 3, bpy009.	2.2	12
44	TnSeq of Mycobacterium tuberculosis clinical isolates reveals strain-specific antibiotic liabilities. PLoS Pathogens, 2018, 14, e1006939.	4.7	78
45	A strategy for dual inhibition of the proteasome and fatty acid synthase with belactosin C-orlistat hybrids. Bioorganic and Medicinal Chemistry, 2017, 25, 2901-2916.	3.0	14
46	Glyoxylate detoxification is an essential function of malate synthase required for carbon assimilation in <i>Mycobacterium tuberculosis</i>. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2225-E2232.	7.1	82
47	Structural insights into species-specific features of the ribosome from the human pathogen Mycobacterium tuberculosis. Nucleic Acids Research, 2017, 45, 10884-10894.	14.5	77
48	Identification of a novel class of small compounds with anti-tuberculosis activity by in silico structure-based drug screening. Journal of Antibiotics, 2017, 70, 1057-1064.	2.0	6
49	A comprehensive characterization of PncA polymorphisms that confer resistance to pyrazinamide. Nature Communications, 2017, 8, 588.	12.8	87
50	Tetraterpene Synthase Substrate and Product Specificity in the Green Microalga <i>Botryococcus braunii</i> Race L. ACS Chemical Biology, 2017, 12, 2408-2416.	3.4	1
51	Mechanism-based inactivator of isocitrate lyases 1 and 2 from <i>Mycobacterium tuberculosis</i>. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 7617-7622.	7.1	32
52	Development of a Novel Lead that Targets M.Âtuberculosis Polyketide Synthase 13. Cell, 2017, 170, 249-259.e25.	28.9	124
53	Ribosomal mutations promote the evolution of antibiotic resistance in a multidrug environment. ELife, 2017, 6, .	6.0	53
54	High Throughput Screen for Escherichia coli Twin Arginine Translocation (Tat) Inhibitors. PLoS ONE, 2016, 11, e0149659.	2.5	21

#	Article	IF	Citations
55	<i>N</i>â€Benzylâ€4â€((heteroaryl)methyl)benzamides: A New Class of Direct NADHâ€Dependent 2â€<i>trans</i> Enoylâ€“Acyl Carrier Protein Reductase (InhA) Inhibitors with Antitubercular Activity. ChemMedChem, 2016, 11, 687-701.	3.2	28
56	Antitubercular drugs for an old target: GSK693 as a promising InhA direct inhibitor. EBioMedicine, 2016, 8, 291-301.	6.1	60
57	Discovery of Novel Oral Protein Synthesis Inhibitors of Mycobacterium tuberculosis That Target Leucyl-tRNA Synthetase. Antimicrobial Agents and Chemotherapy, 2016, 60, 6271-6280.	3.2	88
58	Binding Mechanism of the N-Terminal SH3 Domain of CrkII and Proline-Rich Motifs in cAbl. Biophysical Journal, 2016, 110, 2630-2641.	0.5	20
59	Structural Insights into <i>Mycobacterium tuberculosis</i> Rv2671 Protein as a Dihydrofolate Reductase Functional Analogue Contributing to <i>para</i>-Aminosalicylic Acid Resistance. Biochemistry, 2016, 55, 1107-1119.	2.5	22
60	Selective Inactivity of Pyrazinamide against Tuberculosis in C3HeB/FeJ Mice Is Best Explained by Neutral pH of Caseum. Antimicrobial Agents and Chemotherapy, 2016, 60, 735-743.	3.2	62
61	Structural Similarities and Differences between Two Functionally Distinct SecA Proteins, Mycobacterium tuberculosis SecA1 and SecA2. Journal of Bacteriology, 2016, 198, 720-730.	2.2	19
62	Mycobacterial Metabolic Syndrome: LprG and Rv1410 Regulate Triacylglyceride Levels, Growth Rate and Virulence in Mycobacterium tuberculosis. PLoS Pathogens, 2016, 12, e1005351.	4.7	79
63	Comparison of transposon and deletion mutants in Mycobacterium tuberculosis : The case of rv1248c , encoding 2-hydroxy-3-oxoadipate synthase. Tuberculosis, 2015, 95, 689-694.	1.9	7
64	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, 2015, 33, 2509-2522.	3.2	1
65	Crystal Structure of the Human 20S Proteasome in Complex with Carfilzomib. Structure, 2015, 23, 418-424.	3.3	130
66	A Novel Antimycobacterial Compound Acts as an Intracellular Iron Chelator. Antimicrobial Agents and Chemotherapy, 2015, 59, 2256-2264.	3.2	33
67	Discovery of InhA inhibitors with anti-mycobacterial activity through a matched molecular pair approach. European Journal of Medicinal Chemistry, 2015, 94, 378-385.	5.5	18
68	Peptidoglycan synthesis in <i>Mycobacterium tuberculosis</i> is organized into networks with varying drug susceptibility. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13087-13092.	7.1	82
69	Structure of Ribosomal Silencing Factor Bound to Mycobacterium tuberculosis Ribosome. Structure, 2015, 23, 1858-1865.	3.3	50
70	Functional Genomics Screening Utilizing Mutant Mouse Embryonic Stem Cells Identifies Novel Radiation-Response Genes. PLoS ONE, 2015, 10, e0120534.	2.5	5
71	Sterilization of granulomas is common in active and latent tuberculosis despite within-host variability in bacterial killing. Nature Medicine, 2014, 20, 75-79.	30.7	442
72	Synthesis and evaluation of the 2,4-diaminoquinazoline series as anti-tubercular agents. Bioorganic and Medicinal Chemistry, 2014, 22, 6965-6979.	3.0	27

#	Article	IF	Citations
73	Structure, Activity, and Inhibition of the Carboxyltransferase Î²-Subunit of Acetyl Coenzyme A Carboxylase (AccD6) from Mycobacterium tuberculosis. Antimicrobial Agents and Chemotherapy, 2014, 58, 6122-6132.	3.2	18
74	Folate Pathway Disruption Leads to Critical Disruption of Methionine Derivatives in Mycobacterium tuberculosis. Chemistry and Biology, 2014, 21, 819-830.	6.0	70
75	Subfamily-Specific Adaptations in the Structures of Two Penicillin-Binding Proteins from Mycobacterium tuberculosis. PLoS ONE, 2014, 9, e116249.	2.5	6
76	Tryptophan Biosynthesis Protects Mycobacteria from CD4 T-Cell-Mediated Killing. Cell, 2013, 155, 1296-1308.	28.9	296
77	Identification of Compounds with Potential Antibacterial Activity against <i>Mycobacterium</i> through Structure-Based Drug Screening. Journal of Chemical Information and Modeling, 2013, 53, 1200-1212.	5.4	20
78	Identification of New Drug Targets and Resistance Mechanisms in Mycobacterium tuberculosis. PLoS ONE, 2013, 8, e75245.	2.5	223
79	Global Assessment of Genomic Regions Required for Growth in Mycobacterium tuberculosis. PLoS Pathogens, 2012, 8, e1002946.	4.7	220
80	Deletion of SenX3â€“RegX3, a key two-component regulatory system of Mycobacterium smegmatis, results in growth defects under phosphate-limiting conditions. Microbiology (United Kingdom), 2012, 158, 2724-2731.	1.8	23
81	Structure-Guided Discovery of Phenyl-diketo Acids as Potent Inhibitors of M.Âtuberculosis Malate Synthase. Chemistry and Biology, 2012, 19, 1556-1567.	6.0	102
82	Use of whole genome sequencing to estimate the mutation rate of Mycobacterium tuberculosis during latent infection. Nature Genetics, 2011, 43, 482-486.	21.4	403
83	The TB Structural Genomics Consortium: A decade of progress. Tuberculosis, 2011, 91, 155-172.	1.9	39
84	<i>Mycobacterium tuberculosis</i>acyl carrier protein synthase adopts two different pH-dependent structural conformations. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 657-669.	2.5	14
85	Phosphorylation of InhA inhibits mycolic acid biosynthesis and growth of <i>Mycobacterium tuberculosis</i>. Molecular Microbiology, 2010, 78, 1591-1605.	2.5	60
86	Variation among Genome Sequences of H37Rv Strains of <i>Mycobacterium tuberculosis</i> from Multiple Laboratories. Journal of Bacteriology, 2010, 192, 3645-3653.	2.2	216
87	Structural Insights into the Mechanism of the Allosteric Transitions of Mycobacterium tuberculosis cAMP Receptor Protein. Journal of Biological Chemistry, 2009, 284, 36581-36591.	3.4	39
88	Drugs versus bugs: in pursuit of the persistent predator Mycobacterium tuberculosis. Nature Reviews Microbiology, 2008, 6, 41-52.	28.6	220
89	Structural and Functional Analyses of the Severe Acute Respiratory Syndrome Coronavirus Endoribonuclease Nsp15. Journal of Biological Chemistry, 2008, 283, 3655-3664.	3.4	106
90	The Effect of Hinge Mutations on Effector Binding and Domain Rotation in Escherichia coli D-3-Phosphoglycerate Dehydrogenase. Journal of Biological Chemistry, 2007, 282, 18418-18426.	3.4	19

#	Article	IF	Citations
91	High Resolution Crystal Structures of Mycobacterium tuberculosis Adenosine Kinase. Journal of Biological Chemistry, 2007, 282, 27334-27342.	3.4	36
92	Mechanism of thioamide drug action against tuberculosis and leprosy. Journal of Experimental Medicine, 2007, 204, 73-78.	8.5	274
93	Database Approaches and Data Representation in Structural Bioinformatics. , 2007, , .		1
94	Dual role of isocitrate lyase 1 in the glyoxylate and methylcitrate cycles in Mycobacterium tuberculosis. Molecular Microbiology, 2006, 61, 940-947.	2.5	170
95	Transfer of a point mutation in Mycobacterium tuberculosisÂinhA resolves the target of isoniazid. Nature Medicine, 2006, 12, 1027-1029.	30.7	281
96	TB drug discovery: addressing issues of persistence and resistance. Tuberculosis, 2004, 84, 45-55.	1.9	112
97	Biochemical and Structural Studies of Malate Synthase fromMycobacterium tuberculosis. Journal of Biological Chemistry, 2003, 278, 1735-1743.	3.4	132
98	PHENIX: building new software for automated crystallographic structure determination. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1948-1954.	2.5	3,979
99	Therapeutic strategies for human amyloid diseases. Nature Reviews Drug Discovery, 2002, 1, 267-275.	46.4	238
100	Multivalent Proteinâ˘'Carbohydrate Interactions. A New Paradigm for Supermolecular Assembly and Signal Transduction. Biochemistry, 2001, 40, 3009-3015.	2.5	283
101	Solution structure of ileal lipid binding protein in complex with glycocholate. FEBS Journal, 2000, 267, 2929-2938.	0.2	48
102	Gene-target recognition among members of the Myc superfamily and implications for oncogenesis. Nature Genetics, 2000, 24, 113-119.	21.4	125
103	Structure of isocitrate lyase, a persistence factor of Mycobacterium tuberculosis. Nature Structural Biology, 2000, 7, 663-668.	9.7	211
104	Persistence of Mycobacterium tuberculosis in macrophages and mice requires the glyoxylate shunt enzyme isocitrate lyase. Nature, 2000, 406, 735-738.	27.8	1,251
105	Binding of Fatty Acids and Peroxisome Proliferators to Orthologous Fatty Acid Binding Proteins from Human, Murine, and Bovine Liverâ€. Biochemistry, 2000, 39, 1469-1474.	2.5	74
106	Inactivation of the <i>inhA</i> -Encoded Fatty Acid Synthase II (FASII) Enoyl-Acyl Carrier Protein Reductase Induces Accumulation of the FASI End Products and Cell Lysis of <i>Mycobacterium smegmatis</i>. Journal of Bacteriology, 2000, 182, 4059-4067.	2.2	251
107	Structure-Based Design of N-Phenyl Phenoxazine Transthyretin Amyloid Fibril Inhibitors. Journal of the American Chemical Society, 2000, 122, 2178-2192.	13.7	81
108	Title is missing!. Molecular and Cellular Biochemistry, 1999, 192, 109-121.	3.1	29

#	Article	IF	Citations
109	Crystal structure of a plant catechol oxidase containing a dicopper center. Nature Structural Biology, 1998, 5, 1084-1090.	9.7	744
110	Mechanisms for Isoniazid Action and Resistance. Novartis Foundation Symposium, 1998, 217, 209-221.	1.1	33
111	Modification of the NADH of the Isoniazid Target (InhA) from Mycobacterium tuberculosis. Science, 1998, 279, 98-102.	12.6	645
112	Enzymic Characterization of the Target for Isoniazid in Mycobacterium tuberculosis. Biochemistry, 1995, 34, 8235-8241.	2.5	390