

# Thomas R Ioerger

## List of Publications by Year in descending order

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128  
papers

12,838  
citations

47006

47  
h-index

26613

107  
g-index

150  
all docs

150  
docs citations

150  
times ranked

16758  
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of Gene Essentiality from TnSeq Data Using Transit. <i>Methods in Molecular Biology</i> , 2022, 2377, 391-421.	0.9	7
2	A d-Phenylalanine-Benzoxazole Derivative Reveals the Role of the Essential Enzyme Rv3603c in the Pantothenate Biosynthetic Pathway of <i>Mycobacterium tuberculosis</i> . <i>ACS Infectious Diseases</i> , 2022, 8, 330-342.	3.8	1
3	Host-pathogen genetic interactions underlie tuberculosis susceptibility in genetically diverse mice. <i>ELife</i> , 2022, 11, .	6.0	44
4	PPE51 mediates uptake of trehalose across the mycomembrane of <i>Mycobacterium tuberculosis</i> . <i>Scientific Reports</i> , 2022, 12, 2097.	3.3	12
5	Chemical 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.	7.1	20
6	Multiplexed Strain Phenotyping Defines Consequences of Genetic Diversity in <i>Mycobacterium tuberculosis</i> for Infection and Vaccination Outcomes. <i>MSystems</i> , 2022, 7, e0011022.	3.8	3
7	Structure-Activity Relationships of Pyrazolo[1,5-a]pyrimidin-7(4H)-ones as Antitubercular Agents. <i>ACS Infectious Diseases</i> , 2021, 7, 479-492.	3.8	9
8	The Conserved Translation Factor LepA Is Required for Optimal Synthesis of a Porin Family in <i>Mycobacterium smegmatis</i> . <i>Journal of Bacteriology</i> , 2021, 203, .	2.2	5
9	Deletion of Rv2571c Confers Resistance to Arylamide Compounds in <i>Mycobacterium tuberculosis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	3.2	1
10	Developing Synergistic Drug Combinations To Restore Antibiotic Sensitivity in Drug-Resistant <i>Mycobacterium tuberculosis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	3.2	16
11	Genetic models of latent tuberculosis in mice reveal differential influence of adaptive immunity. <i>Journal of Experimental Medicine</i> , 2021, 218, .	8.5	6
12	Characterization of Drug-Resistant Lipid-Dependent Differentially Detectable <i>Mycobacterium tuberculosis</i> . <i>Journal of Clinical Medicine</i> , 2021, 10, 3249.	2.4	5
13	Resistance of <i>Mycobacterium tuberculosis</i> to indole 4-carboxamides occurs through alterations in drug metabolism and tryptophan biosynthesis. <i>Cell Chemical Biology</i> , 2021, 28, 1180-1191.e20.	5.2	5
14	An improved statistical method to identify chemical-genetic interactions by exploiting concentration-dependence. <i>PLoS ONE</i> , 2021, 16, e0257911.	2.5	1
15	6-Fluorophenylbenzohydrazides inhibit <i>Mycobacterium tuberculosis</i> growth through alteration of tryptophan biosynthesis. <i>European Journal of Medicinal Chemistry</i> , 2021, 226, 113843.	5.5	1
16	Modeling Site-Specific Nucleotide Biases Affecting Himar1 Transposon Insertion Frequencies in TnSeq Data Sets. <i>MSystems</i> , 2021, 6, e0087621.	3.8	7
17	Cell-Cycle-Associated Expression Patterns Predict Gene Function in <i>Mycobacteria</i> . <i>Current Biology</i> , 2020, 30, 3961-3971.e6.	3.9	13
18	Mutations in <i>fbiD</i> ( <i>Rv2983</i> ) as a Novel Determinant of Resistance to Pretomanid and Delamanid in <i>Mycobacterium tuberculosis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 65, .	3.2	48

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19	Biological Profiling Enables Rapid Mechanistic Classification of Phenotypic Screening Hits and Identification of KatG Activation-Dependent Pyridine Carboxamide Prodrugs With Activity Against Mycobacterium tuberculosis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 582416.	3.9	6
20	Distinct Bacterial Pathways Influence the Efficacy of Antibiotics against Mycobacterium tuberculosis. <i>MSystems</i> , 2020, 5, .	3.8	37
21	Exploiting Homoplasmy in Genome-Wide Association Studies to Enhance Identification of Antibiotic-Resistance Mutations in Bacterial Genomes. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693432094493.	1.2	8
22	Nature-Inspired (di)Azine-Bridged Bisindole Alkaloids with Potent Antibacterial <i>In Vitro</i> and <i>In Vivo</i> Efficacy against Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>Journal of Medicinal Chemistry</i> , 2020, 63, 12623-12641.	6.4	26
23	Natural brominated phenoxyphenols kill persistent and biofilm-incorporated cells of MRSA and other pathogenic bacteria. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 5985-5998.	3.6	5
24	Synthesis, Structure-Activity Relationship, and Mechanistic Studies of Aminoquinazolinones Displaying Antimycobacterial Activity. <i>ACS Infectious Diseases</i> , 2020, 6, 1951-1964.	3.8	16
25	Comprehensive analysis of iron utilization by Mycobacterium tuberculosis. <i>PLoS Pathogens</i> , 2020, 16, e1008337.	4.7	58
26	Comprehensive analysis of iron utilization by Mycobacterium tuberculosis. , 2020, 16, e1008337.		0
27	Comprehensive analysis of iron utilization by Mycobacterium tuberculosis. , 2020, 16, e1008337.		0
28	Comprehensive analysis of iron utilization by Mycobacterium tuberculosis. , 2020, 16, e1008337.		0
29	Comprehensive analysis of iron utilization by Mycobacterium tuberculosis. , 2020, 16, e1008337.		0
30	Inhibition of CorA-Dependent Magnesium Homeostasis Is Cidal in Mycobacterium tuberculosis. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	9
31	Genome-wide Phenotypic Profiling Identifies and Categorizes Genes Required for Mycobacterial Low Iron Fitness. <i>Scientific Reports</i> , 2019, 9, 11394.	3.3	36
32	Novel Pyrazole-Containing Compounds Active against <i>Mycobacterium tuberculosis</i> . <i>ACS Medicinal Chemistry Letters</i> , 2019, 10, 1423-1429.	2.8	37
33	Opposing reactions in coenzyme A metabolism sensitize <i>Mycobacterium tuberculosis</i> to enzyme inhibition. <i>Science</i> , 2019, 363, .	12.6	53
34	3- <i>O</i> -Methyl-Alkylgallates Inhibit Fatty Acid Desaturation in Mycobacterium tuberculosis. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	8
35	Large-scale chemical-genetics yields new <i>M. tuberculosis</i> inhibitor classes. <i>Nature</i> , 2019, 571, 72-78.	27.8	119
36	<i>Mycobacterium smegmatis</i> HtrA Blocks the Toxic Activity of a Putative Cell Wall Amidase. <i>Cell Reports</i> , 2019, 27, 2468-2479.e3.	6.4	16

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37	GWAS for quantitative resistance phenotypes in <i>Mycobacterium tuberculosis</i> reveals resistance genes and regulatory regions. <i>Nature Communications</i> , 2019, 10, 2128.	12.8	111
38	Global Assessment of <i>Mycobacterium avium</i> subsp. <i>hominissuis</i> Genetic Requirement for Growth and Virulence. <i>MSystems</i> , 2019, 4, .	3.8	31
39	Statistical analysis of variability in TnSeq data across conditions using zero-inflated negative binomial regression. <i>BMC Bioinformatics</i> , 2019, 20, 603.	2.6	15
40	Mutations in the anti-sigma H factor RshA confer resistance to econazole and clotrimazole in <i>Mycobacterium smegmatis</i> . <i>Access Microbiology</i> , 2019, 1, e000070.	0.5	0
41	Identification of a Mycothiol-Dependent Nitroreductase from <i>Mycobacterium tuberculosis</i> . <i>ACS Infectious Diseases</i> , 2018, 4, 771-787.	3.8	19
42	2-Mercapto-Quinazolinones as Inhibitors of Type II NADH Dehydrogenase and <i>Mycobacterium tuberculosis</i> : Structure-Activity Relationships, Mechanism of Action and Absorption, Distribution, Metabolism, and Excretion Characterization. <i>ACS Infectious Diseases</i> , 2018, 4, 954-969.	3.8	49
43	Targeting protein biotinylation enhances tuberculosis chemotherapy. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	24
44	Discovery of Antimicrobial Lipodepsipeptides Produced by a <i>Serratia</i> sp. within Mosquito Microbiomes. <i>ChemBioChem</i> , 2018, 19, 1590-1594.	2.6	26
45	Chlorflavin Targets Acetohydroxyacid Synthase Catalytic Subunit IlvB1 for Synergistic Killing of <i>Mycobacterium tuberculosis</i> . <i>ACS Infectious Diseases</i> , 2018, 4, 123-134.	3.8	26
46	The 7-phenyl benzoxaborole series is active against <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2018, 108, 96-98.	1.9	22
47	A statistical method to identify recombination in bacterial genomes based on SNP incompatibility. <i>BMC Bioinformatics</i> , 2018, 19, 450.	2.6	7
48	Identification of cyclic hexapeptides natural products with inhibitory potency against <i>Mycobacterium tuberculosis</i> . <i>BMC Research Notes</i> , 2018, 11, 416.	1.4	1
49	Altered <i>Mycobacterium tuberculosis</i> Cell Wall Metabolism and Physiology Associated With RpoB Mutation H526D. <i>Frontiers in Microbiology</i> , 2018, 9, 494.	3.5	28
50	Impact of immunopathology on the antituberculous activity of pyrazinamide. <i>Journal of Experimental Medicine</i> , 2018, 215, 1975-1986.	8.5	29
51	Anion- $\pi$ Interactions in Computer-Aided Drug Design: Modeling the Inhibition of Malate Synthase by Phenyl-Diketo Acids. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 2085-2091.	5.4	21
52	TnSeq of <i>Mycobacterium tuberculosis</i> clinical isolates reveals strain-specific antibiotic liabilities. <i>PLoS Pathogens</i> , 2018, 14, e1006939.	4.7	78
53	Maturing <i>Mycobacterium smegmatis</i> peptidoglycan requires non-canonical crosslinks to maintain shape. <i>ELife</i> , 2018, 7, .	6.0	108
54	Comprehensive Essentiality Analysis of the <i>Mycobacterium tuberculosis</i> Genome via Saturating Transposon Mutagenesis. <i>MBio</i> , 2017, 8, .	4.1	496

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55	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
56	Statistical analysis of genetic interactions in Tn-Seq data. Nucleic Acids Research, 2017, 45, e93-e93.	14.5	31
57	Introduction to selected papers from the 8th International Conference on Bioinformatics and Computational Biology (BICOB 2016). Journal of Bioinformatics and Computational Biology, 2017, 15, 1702002.	0.8	0
58	Improved Phenoxyalkylbenzimidazoles with Activity against <i>Mycobacterium tuberculosis</i> Appear to Target QcrB. ACS Infectious Diseases, 2017, 3, 898-916.	3.8	54
59	Chemical Genetic Interaction Profiling Reveals Determinants of Intrinsic Antibiotic Resistance in <i>Mycobacterium tuberculosis</i> . Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	70
60	A comprehensive characterization of PncA polymorphisms that confer resistance to pyrazinamide. Nature Communications, 2017, 8, 588.	12.8	87
61	Susceptibility of <i>Mycobacterium tuberculosis</i> Cytochrome <i>bd</i> Oxidase Mutants to Compounds Targeting the Terminal Respiratory Oxidase, Cytochrome <i>c</i> . Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	49
62	Development of a Novel Lead that Targets <i>M. tuberculosis</i> Polyketide Synthase 13. Cell, 2017, 170, 249-259.e25.	28.9	124
63	Essential but Not Vulnerable: Indazole Sulfonamides Targeting Inosine Monophosphate Dehydrogenase as Potential Leads against <i>Mycobacterium tuberculosis</i> . ACS Infectious Diseases, 2017, 3, 18-33.	3.8	77
64	Ribosomal mutations promote the evolution of antibiotic resistance in a multidrug environment. ELife, 2017, 6, .	6.0	53
65	Mutations in <i>pepQ</i> Confer Low-Level Resistance to Bedaquiline and Clofazimine in <i>Mycobacterium tuberculosis</i> . Antimicrobial Agents and Chemotherapy, 2016, 60, 4590-4599.	3.2	165
66	Behavioral and transcriptomic profiling of mice null for <i>Lphn3</i> , a gene implicated in ADHD and addiction. Molecular Genetics & Genomic Medicine, 2016, 4, 322-343.	1.2	40
67	Discovery of Novel Oral Protein Synthesis Inhibitors of <i>Mycobacterium tuberculosis</i> That Target Leucyl-tRNA Synthetase. Antimicrobial Agents and Chemotherapy, 2016, 60, 6271-6280.	3.2	88
68	First Evaluation of GenoType MTBDR <i>plus</i> 2.0 Performed Directly on Respiratory Specimens in Central America. Journal of Clinical Microbiology, 2016, 54, 2498-2502.	3.9	8
69	<i>N</i> -methylation of a bactericidal compound as a resistance mechanism in <i>Mycobacterium tuberculosis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4523-30.	7.1	88
70	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
71	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
72	Structural Similarities and Differences between Two Functionally Distinct SecA Proteins, <i>Mycobacterium tuberculosis</i> SecA1 and SecA2. Journal of Bacteriology, 2016, 198, 720-730.	2.2	19

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73	Metabolic Network for the Biosynthesis of Intra- and Extracellular Î±-Glucans Required for Virulence of Mycobacterium tuberculosis. PLoS Pathogens, 2016, 12, e1005768.	4.7	46
74	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
75	A cytoplasmic peptidoglycan amidase homologue controls mycobacterial cell wall synthesis. ELife, 2016, 5, .	6.0	82
76	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
77	TRANSIT - A Software Tool for Himar1 TnSeq Analysis. PLoS Computational Biology, 2015, 11, e1004401.	3.2	170
78	Leaderless Transcripts and Small Proteins Are Common Features of the Mycobacterial Translational Landscape. PLoS Genetics, 2015, 11, e1005641.	3.5	207
79	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
80	A Novel Antimycobacterial Compound Acts as an Intracellular Iron Chelator. Antimicrobial Agents and Chemotherapy, 2015, 59, 2256-2264.	3.2	33
81	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
82	Identifying Essential Genes in Mycobacterium tuberculosis by Global Phenotypic Profiling. Methods in Molecular Biology, 2015, 1279, 79-95.	0.9	75
83	Functional Genomics Screening Utilizing Mutant Mouse Embryonic Stem Cells Identifies Novel Radiation-Response Genes. PLoS ONE, 2015, 10, e0120534.	2.5	5
84	The Copper-Responsive RicR Regulon Contributes to Mycobacterium tuberculosis Virulence. MBio, 2014, 5, .	4.1	61
85	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
86	Synthesis and evaluation of the 2,4-diaminoquinazoline series as anti-tubercular agents. Bioorganic and Medicinal Chemistry, 2014, 22, 6965-6979.	3.0	27
87	Reannotation of translational start sites in the genome of <i>Mycobacterium tuberculosis</i> . Tuberculosis, 2013, 93, 18-25.	1.9	27
88	Diarylcoumarins inhibit mycolic acid biosynthesis and kill <i>Mycobacterium tuberculosis</i> by targeting FadD32. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11565-11570.	7.1	89
89	Tryptophan Biosynthesis Protects Mycobacteria from CD4 T-Cell-Mediated Killing. Cell, 2013, 155, 1296-1308.	28.9	296
90	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

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91	Evaluating minimalist mimics by exploring key orientations on secondary structures (EKOS). <i>Organic and Biomolecular Chemistry</i> , 2013, 11, 7789.	2.8	26
92	Multidrug-Resistant Tuberculosis in Panama Is Driven by Clonal Expansion of a Multidrug-Resistant <i>Mycobacterium tuberculosis</i> Strain Related to the KZN Extensively Drug-Resistant <i>M. tuberculosis</i> Strain from South Africa. <i>Journal of Clinical Microbiology</i> , 2013, 51, 3277-3285.	3.9	41
93	Exploring Key Orientations at Protein-Protein Interfaces with Small Molecule Probes. <i>Journal of the American Chemical Society</i> , 2013, 135, 167-173.	13.7	37
94	Perturbation of Cytochrome <i>c</i> Maturation Reveals Adaptability of the Respiratory Chain in <i>Mycobacterium tuberculosis</i> . <i>MBio</i> , 2013, 4, e00475-13.	4.1	58
95	Structures of <i>Mycobacterium tuberculosis</i> FadD10 Protein Reveal a New Type of Adenylate-forming Enzyme. <i>Journal of Biological Chemistry</i> , 2013, 288, 18473-18483.	3.4	35
96	Identification of New Drug Targets and Resistance Mechanisms in <i>Mycobacterium tuberculosis</i> . <i>PLoS ONE</i> , 2013, 8, e75245.	2.5	223
97	Crystal Structure of <i>Mycobacterium tuberculosis</i> Polyketide Synthase 11 (PKS11) Reveals Intermediates in the Synthesis of Methyl-branched Alkylpyrones. <i>Journal of Biological Chemistry</i> , 2013, 288, 16484-16494.	3.4	21
98	Bayesian analysis of gene essentiality based on sequencing of transposon insertion libraries. <i>Bioinformatics</i> , 2013, 29, 695-703.	4.1	74
99	A vitamin B <sub>12</sub> transporter in <i>Mycobacterium tuberculosis</i> . <i>Open Biology</i> , 2013, 3, 120175.	3.6	83
100	High-Throughput Sequencing Enhanced Phage Display Identifies Peptides That Bind <i>Mycobacteria</i> . <i>PLoS ONE</i> , 2013, 8, e77844.	2.5	22
101	Global Assessment of Genomic Regions Required for Growth in <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2012, 8, e1002946.	4.7	220
102	Deletion of SenX3-RegX3, a key two-component regulatory system of <i>Mycobacterium smegmatis</i> , results in growth defects under phosphate-limiting conditions. <i>Microbiology (United Kingdom)</i> , 2012, 158, 2724-2731.	1.8	23
103	MmpL3 Is the Cellular Target of the Antitubercular Pyrrole Derivative BM212. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 324-331.	3.2	190
104	Structure-Guided Discovery of Phenyl-diketo Acids as Potent Inhibitors of <i>M. tuberculosis</i> Malate Synthase. <i>Chemistry and Biology</i> , 2012, 19, 1556-1567.	6.0	102
105	Use of Multiplex Allele-Specific Polymerase Chain Reaction (MAS-PCR) to Detect Multidrug-Resistant Tuberculosis in Panama. <i>PLoS ONE</i> , 2012, 7, e40456.	2.5	23
106	Pyrrolinone-Pyrrolidine Oligomers as Universal Peptidomimetics. <i>Journal of the American Chemical Society</i> , 2011, 133, 12350-12353.	13.7	55
107	Use of whole genome sequencing to estimate the mutation rate of <i>Mycobacterium tuberculosis</i> during latent infection. <i>Nature Genetics</i> , 2011, 43, 482-486.	21.4	403
108	High-Resolution Phenotypic Profiling Defines Genes Essential for <i>Mycobacterial</i> Growth and Cholesterol Catabolism. <i>PLoS Pathogens</i> , 2011, 7, e1002251.	4.7	935

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109	The non-clonality of drug resistance in Beijing-genotype isolates of <i>Mycobacterium tuberculosis</i> from the Western Cape of South Africa. <i>BMC Genomics</i> , 2010, 11, 670.	2.8	69
110	Variation among Genome Sequences of H37Rv Strains of <i>Mycobacterium tuberculosis</i> from Multiple Laboratories. <i>Journal of Bacteriology</i> , 2010, 192, 3645-3653.	2.2	216
111	<i>Mycobacterium tuberculosis</i> Dihydrofolate Reductase Is Not a Target Relevant to the Antitubercular Activity of Isoniazid. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 3776-3782.	3.2	67
112	Structural genomics approach to drug discovery for <i>Mycobacterium tuberculosis</i> . <i>Current Opinion in Microbiology</i> , 2009, 12, 318-325.	5.1	31
113	Genome Analysis of Multi- and Extensively-Drug-Resistant Tuberculosis from KwaZulu-Natal, South Africa. <i>PLoS ONE</i> , 2009, 4, e7778.	2.5	144
114	Crystal structure of <i>Mycobacterium tuberculosis</i> LrpA, a leucine-responsive global regulator associated with starvation response. <i>Protein Science</i> , 2008, 17, 159-170.	7.6	23
115	Crystal structures of <i>Mycobacterium tuberculosis</i> adenosylhomocysteine hydrolase in ternary complex with substrate and inhibitors. <i>Protein Science</i> , 2008, 17, 2134-2144.	7.6	55
116	Discovery of Novel Nitrobenzothiazole Inhibitors for <i>Mycobacterium tuberculosis</i> ATP Phosphoribosyl Transferase (HisG) through Virtual Screening. <i>Journal of Medicinal Chemistry</i> , 2008, 51, 5984-5992.	6.4	102
117	Distance Metric Learning through Optimization of Ranking. , 2007, , .		24
118	Database Approaches and Data Representation in Structural Bioinformatics. , 2007, , .		1
119	Crystal Structure of Circadian Clock Protein KaiA from <i>Synechococcus elongatus</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 20511-20518.	3.4	93
120	Recent developments in the PHENIX software for automated crystallographic structure determination. <i>Journal of Synchrotron Radiation</i> , 2004, 11, 53-55.	2.4	319
121	TEXTAL System: Artificial Intelligence Techniques for Automated Protein Model Building. <i>Methods in Enzymology</i> , 2003, 374, 244-270.	1.0	45
122	PHENIX: building new software for automated crystallographic structure determination. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1948-1954.	2.5	3,979
123	Automatic modeling of protein backbones in electron-density maps via prediction of C $\alpha$ coordinates. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 2043-2054.	2.5	20
124	Automatic generation of communication and teamwork within multi-agent teams. <i>Applied Artificial Intelligence</i> , 2001, 15, 875-916.	3.2	7
125	Determining protein structure from electron-density maps using pattern matching. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 722-734.	2.5	21
126	FLAME – Fuzzy Logic Adaptive Model of Emotions. <i>Autonomous Agents and Multi-Agent Systems</i> , 2000, 3, 219-257.	2.1	319



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127	Conservation of cys-trp structural triads and their geometry in the protein domains of immunoglobulin superfamily members. <i>Molecular Immunology</i> , 1999, 36, 373-386.	2.2	72
128	Transposon mutagenesis in <i>Mycobacterium abscessus</i> identifies an essential penicillin-binding protein involved in septal peptidoglycan synthesis and antibiotic sensitivity. <i>ELife</i> , 0, 11, .	6.0	16