Thomas R Ioerger

List of Publications by Year
in descending order

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	PHENIX: building new software for automated crystallographic structure determination. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1948-1954.	2.5	3,979
2	High-Resolution Phenotypic Profiling Defines Genes Essential for Mycobacterial Growth and Cholesterol Catabolism. PLoS Pathogens, 2011, 7, e1002251.	4.7	935
3	Comprehensive Essentiality Analysis of the <i>Mycobacterium tuberculosis</i> Genome via Saturating Transposon Mutagenesis. MBio, 2017, 8, .	4.1	496
4	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
5	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
6	FLAMEâ€"Fuzzy Logic Adaptive Model of Emotions. Autonomous Agents and Multi-Agent Systems, 2000, 3, 219-257.	2.1	319
7	Recent developments in thePHENIXsoftware for automated crystallographic structure determination. Journal of Synchrotron Radiation, 2004, 11, 53-55.	2.4	319
8	Tryptophan Biosynthesis Protects Mycobacteria from CD4 T-Cell-Mediated Killing. Cell, 2013, 155, 1296-1308.	28.9	296
9	Identification of New Drug Targets and Resistance Mechanisms in Mycobacterium tuberculosis. PLoS ONE, 2013, 8, e75245.	2.5	223
10	Global Assessment of Genomic Regions Required for Growth in Mycobacterium tuberculosis. PLoS Pathogens, 2012, 8, e1002946.	4.7	220
11	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
12	Leaderless Transcripts and Small Proteins Are Common Features of the Mycobacterial Translational Landscape. PLoS Genetics, 2015, 11, e1005641.	3.5	207
13	MmpL3 Is the Cellular Target of the Antitubercular Pyrrole Derivative BM212. Antimicrobial Agents and Chemotherapy, 2012, 56, 324-331.	3.2	190
14	TRANSIT - A Software Tool for Himar1 TnSeq Analysis. PLoS Computational Biology, 2015, 11, e1004401.	3.2	170
15	Mutations in <i>pepQ</i> Confer Low-Level Resistance to Bedaquiline and Clofazimine in Mycobacterium tuberculosis. Antimicrobial Agents and Chemotherapy, 2016, 60, 4590-4599.	3.2	165
16	Genome Analysis of Multi- and Extensively-Drug-Resistant Tuberculosis from KwaZulu-Natal, South Africa. PLoS ONE, 2009, 4, e7778.	2.5	144
17	Development of a Novel Lead that Targets M.Âtuberculosis Polyketide Synthase 13. Cell, 2017, 170, 249-259.e25.	28.9	124
18	Large-scale chemicalâ€"genetics yields new M. tuberculosis inhibitor classes. Nature, 2019, 571, 72-78.	27.8	119

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19	GWAS for quantitative resistance phenotypes in Mycobacterium tuberculosis reveals resistance genes and regulatory regions. Nature Communications, 2019, 10, 2128.	12.8	111
20	Maturing Mycobacterium smegmatis peptidoglycan requires non-canonical crosslinks to maintain shape. ELife, 2018, 7, .	6.0	108
21	Discovery of Novel Nitrobenzothiazole Inhibitors for *Mycobacterium tuberculosis* ATP Phosphoribosyl Transferase (HisG) through Virtual Screening. Journal of Medicinal Chemistry, 2008, 51, 5984-5992.	6.4	102
22	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
23	Crystal Structure of Circadian Clock Protein KaiA from Synechococcus elongatus. Journal of Biological Chemistry, 2004, 279, 20511-20518.	3.4	93
24	Diarylcoumarins inhibit mycolic acid biosynthesis and kill *Mycobacterium tuberculosis* by targeting FadD32. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11565-11570.	7.1	89
25	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
26	*N*-methylation of a bactericidal compound as a resistance mechanism in *Mycobacterium tuberculosis*. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4523-30.	7.1	88
27	A comprehensive characterization of PncA polymorphisms that confer resistance to pyrazinamide. Nature Communications, 2017, 8, 588.	12.8	87
28	A vitamin B$_{12}$ transporter in *Mycobacterium tuberculosis*. Open Biology, 2013, 3, 120175.	3.6	83
29	Peptidoglycan synthesis in *Mycobacterium tuberculosis* 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
30	Glyoxylate detoxification is an essential function of malate synthase required for carbon assimilation in *Mycobacterium tuberculosis*. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2225-E2232.	7.1	82
31	A cytoplasmic peptidoglycan amidase homologue controls mycobacterial cell wall synthesis. ELife, 2016, 5, .	6.0	82
32	TnSeq of Mycobacterium tuberculosis clinical isolates reveals strain-specific antibiotic liabilities. PLoS Pathogens, 2018, 14, e1006939.	4.7	78
33	Essential but Not Vulnerable: Indazole Sulfonamides Targeting Inosine Monophosphate Dehydrogenase as Potential Leads against *Mycobacterium tuberculosis*. ACS Infectious Diseases, 2017, 3, 18-33.	3.8	77
34	Identifying Essential Genes in Mycobacterium tuberculosis by Global Phenotypic Profiling. Methods in Molecular Biology, 2015, 1279, 79-95.	0.9	75
35	Bayesian analysis of gene essentiality based on sequencing of transposon insertion libraries. Bioinformatics, 2013, 29, 695-703.	4.1	74
36	Conservation of cysâ€"cys trp structural triads and their geometry in the protein domains of immunoglobulin superfamily members. Molecular Immunology, 1999, 36, 373-386.	2.2	72

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37	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
38	Chemical Genetic Interaction Profiling Reveals Determinants of Intrinsic Antibiotic Resistance in Mycobacterium tuberculosis. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	70
39	The non-clonality of drug resistance in Beijing-genotype isolates of Mycobacterium tuberculosis from the Western Cape of South Africa. BMC Genomics, 2010, 11, 670.	2.8	69
40	*Mycobacterium tuberculosis* Dihydrofolate Reductase Is Not a Target Relevant to the Antitubercular Activity of Isoniazid. Antimicrobial Agents and Chemotherapy, 2010, 54, 3776-3782.	3.2	67
41	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
42	The Copper-Responsive RicR Regulon Contributes to Mycobacterium tuberculosis Virulence. MBio, 2014, 5, .	4.1	61
43	Perturbation of Cytochrome *c* Maturation Reveals Adaptability of the Respiratory Chain in Mycobacterium tuberculosis. MBio, 2013, 4, e00475-13.	4.1	58
44	Comprehensive analysis of iron utilization by Mycobacterium tuberculosis. PLoS Pathogens, 2020, 16, e1008337.	4.7	58
45	Crystal structures of *Mycobacterium tuberculosis* S‑adenosyl‑L‑homocysteine hydrolase in ternary complex with substrate and inhibitors. Protein Science, 2008, 17, 2134-2144.	7.6	55
46	Pyrrolinone–Pyrrolidine Oligomers as Universal Peptidomimetics. Journal of the American Chemical Society, 2011, 133, 12350-12353.	13.7	55
47	Improved Phenoxyalkylbenzimidazoles with Activity against *Mycobacterium tuberculosis* Appear to Target QcrB. ACS Infectious Diseases, 2017, 3, 898-916.	3.8	54
48	Ribosomal mutations promote the evolution of antibiotic resistance in a multidrug environment. ELife, 2017, 6, .	6.0	53
49	Opposing reactions in coenzyme A metabolism sensitize *Mycobacterium tuberculosis* to enzyme inhibition. Science, 2019, 363, .	12.6	53
50	Susceptibility of Mycobacterium tuberculosis Cytochrome *bd* Oxidase Mutants to Compounds Targeting the Terminal Respiratory Oxidase, Cytochrome *c*. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	49
51	2-Mercapto-Quinazolinones as Inhibitors of Type II NADH Dehydrogenase and *Mycobacterium tuberculosis*: Structure–Activity Relationships, Mechanism of Action and Absorption, Distribution, Metabolism, and Excretion Characterization. ACS Infectious Diseases, 2018, 4, 954-969.	3.8	49
52	Mutations in *fbiD* (*Rv2983*) as a Novel Determinant of Resistance to Pretomanid and Delamanid in Mycobacterium tuberculosis. Antimicrobial Agents and Chemotherapy, 2020, 65, .	3.2	48
53	Metabolic Network for the Biosynthesis of Intra- and Extracellular α-Glucans Required for Virulence of Mycobacterium tuberculosis. PLoS Pathogens, 2016, 12, e1005768.	4.7	46
54	TEXTAL System: Artificial Intelligence Techniques for Automated Protein Model Building. Methods in Enzymology, 2003, 374, 244-270.	1.0	45

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55	Host-pathogen genetic interactions underlie tuberculosis susceptibility in genetically diverse mice. ELife, 2022, 11, .	6.0	44
56	Multidrug-Resistant Tuberculosis in Panama Is Driven by Clonal Expansion of a Multidrug-Resistant Mycobacterium tuberculosis Strain Related to the KZN Extensively Drug-Resistant M. tuberculosis Strain from South Africa. Journal of Clinical Microbiology, 2013, 51, 3277-3285.	3.9	41
57	Behavioral and transcriptomic profiling of mice null for <i>Lphn3</i>, a gene implicated in <scp>ADHD</scp> and addiction. Molecular Genetics & Genomic Medicine, 2016, 4, 322-343.	1.2	40
58	Exploring Key Orientations at Protein–Protein Interfaces with Small Molecule Probes. Journal of the American Chemical Society, 2013, 135, 167-173.	13.7	37
59	Novel Pyrazole-Containing Compounds Active against <i>Mycobacterium tuberculosis</i>. ACS Medicinal Chemistry Letters, 2019, 10, 1423-1429.	2.8	37
60	Distinct Bacterial Pathways Influence the Efficacy of Antibiotics against Mycobacterium tuberculosis. MSystems, 2020, 5, .	3.8	37
61	Genome-wide Phenotypic Profiling Identifies and Categorizes Genes Required for Mycobacterial Low Iron Fitness. Scientific Reports, 2019, 9, 11394.	3.3	36
62	Structures of Mycobacterium tuberculosis FadD10 Protein Reveal a New Type of Adenylate-forming Enzyme. Journal of Biological Chemistry, 2013, 288, 18473-18483.	3.4	35
63	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
64	A Novel Antimycobacterial Compound Acts as an Intracellular Iron Chelator. Antimicrobial Agents and Chemotherapy, 2015, 59, 2256-2264.	3.2	33
65	Structural genomics approach to drug discovery for Mycobacterium tuberculosis. Current Opinion in Microbiology, 2009, 12, 318-325.	5.1	31
66	Statistical analysis of genetic interactions in Tn-Seq data. Nucleic Acids Research, 2017, 45, e93-e93.	14.5	31
67	Global Assessment of Mycobacterium avium subsp. <i>hominissuis</i> Genetic Requirement for Growth and Virulence. MSystems, 2019, 4, .	3.8	31
68	Impact of immunopathology on the antituberculous activity of pyrazinamide. Journal of Experimental Medicine, 2018, 215, 1975-1986.	8.5	29
69	Altered Mycobacterium tuberculosis Cell Wall Metabolism and Physiology Associated With RpoB Mutation H526D. Frontiers in Microbiology, 2018, 9, 494.	3.5	28
70	Reannotation of translational start sites in the genome of Mycobacterium tuberculosis. Tuberculosis, 2013, 93, 18-25.	1.9	27
71	Synthesis and evaluation of the 2,4-diaminoquinazoline series as anti-tubercular agents. Bioorganic and Medicinal Chemistry, 2014, 22, 6965-6979.	3.0	27
72	Evaluating minimalist mimics by exploring key orientations on secondary structures (EKOS). Organic and Biomolecular Chemistry, 2013, 11, 7789.	2.8	26

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73	Discovery of Antimicrobial Lipodepsipeptides Produced by a <i>Serratia</i> sp. within Mosquito Microbiomes. ChemBioChem, 2018, 19, 1590-1594.	2.6	26
74	Chlorflavonin Targets Acetohydroxyacid Synthase Catalytic Subunit IlvB1 for Synergistic Killing of <i>Mycobacterium tuberculosis</i>. ACS Infectious Diseases, 2018, 4, 123-134.	3.8	26
75	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>. Journal of Medicinal Chemistry, 2020, 63, 12623-12641.	6.4	26
76	Distance Metric Learning through Optimization of Ranking. , 2007, , .		24
77	Targeting protein biotinylation enhances tuberculosis chemotherapy. Science Translational Medicine, 2018, 10, .	12.4	24
78	Crystal structure of <i>Mycobacterium tuberculosis</i> LrpA, a leucineâ€responsive global regulator associated with starvation response. Protein Science, 2008, 17, 159-170.	7.6	23
79	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
80	Use of Multiplex Allele-Specific Polymerase Chain Reaction (MAS-PCR) to Detect Multidrug-Resistant Tuberculosis in Panama. PLoS ONE, 2012, 7, e40456.	2.5	23
81	High-Throughput Sequencing Enhanced Phage Display Identifies Peptides That Bind Mycobacteria. PLoS ONE, 2013, 8, e77844.	2.5	22
82	The 7-phenyl benzoxaborole series is active against Mycobacterium tuberculosis. Tuberculosis, 2018, 108, 96-98.	1.9	22
83	Determining protein structure from electron-density maps using pattern matching. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 722-734.	2.5	21
84	Crystal Structure of Mycobacterium tuberculosis Polyketide Synthase 11 (PKS11) Reveals Intermediates in the Synthesis of Methyl-branched Alkylpyrones. Journal of Biological Chemistry, 2013, 288, 16484-16494.	3.4	21
85	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
86	Automatic modeling of protein backbones in electron-density mapsviaprediction of CÎ±coordinates. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 2043-2054.	2.5	20
87	Chemicalâ€"genetic interaction mapping links carbon metabolism and cell wall structure to tuberculosis drug efficacy. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2201632119.	7.1	20
88	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
89	Identification of a Mycothiol-Dependent Nitroreductase from <i>Mycobacterium tuberculosis</i>. ACS Infectious Diseases, 2018, 4, 771-787.	3.8	19
90	Mycobacterium smegmatis HtrA Blocks the Toxic Activity of a Putative Cell Wall Amidase. Cell Reports, 2019, 27, 2468-2479.e3.	6.4	16

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91	Synthesis, Structure–Activity Relationship, and Mechanistic Studies of Aminoquinazolinones Displaying Antimycobacterial Activity. ACS Infectious Diseases, 2020, 6, 1951-1964.	3.8	16
92	Developing Synergistic Drug Combinations To Restore Antibiotic Sensitivity in Drug-Resistant Mycobacterium tuberculosis. Antimicrobial Agents and Chemotherapy, 2021, 65, .	3.2	16
93	Transposon mutagenesis in Mycobacterium abscessus identifies an essential penicillin-binding protein involved in septal peptidoglycan synthesis and antibiotic sensitivity. ELife, 0, 11, .	6.0	16
94	Statistical analysis of variability in TnSeq data across conditions using zero-inflated negative binomial regression. BMC Bioinformatics, 2019, 20, 603.	2.6	15
95	Cell-Cycle-Associated Expression Patterns Predict Gene Function in Mycobacteria. Current Biology, 2020, 30, 3961-3971.e6.	3.9	13
96	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
97	PPE51 mediates uptake of trehalose across the mycomembrane of Mycobacterium tuberculosis. Scientific Reports, 2022, 12, 2097.	3.3	12
98	Inhibition of CorA-Dependent Magnesium Homeostasis Is Cidal in Mycobacterium tuberculosis. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	9
99	Structure–Activity Relationships of Pyrazolo[1,5-a]pyrimidin-7(4H)-ones as Antitubercular Agents. ACS Infectious Diseases, 2021, 7, 479-492.	3.8	9
100	First Evaluation of GenoType MTBDR $plus$ 2.0 Performed Directly on Respiratory Specimens in Central America. Journal of Clinical Microbiology, 2016, 54, 2498-2502.	3.9	8
101	3-O-Methyl-Alkylgallates Inhibit Fatty Acid Desaturation in Mycobacterium tuberculosis. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	8
102	Exploiting Homoplasy in Genome-Wide Association Studies to Enhance Identification of Antibiotic-Resistance Mutations in Bacterial Genomes. Evolutionary Bioinformatics, 2020, 16, 117693432094493.	1.2	8
103	Automatic generation of communication and teamwork within multi-agent teams. Applied Artificial Intelligence, 2001, 15, 875-916.	3.2	7
104	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
105	A statistical method to identify recombination in bacterial genomes based on SNP incompatibility. BMC Bioinformatics, 2018, 19, 450.	2.6	7
106	Modeling Site-Specific Nucleotide Biases Affecting Himar1 Transposon Insertion Frequencies in TnSeq Data Sets. MSystems, 2021, 6, e0087621.	3.8	7
107	Analysis of Gene Essentiality from TnSeq Data Using Transit. Methods in Molecular Biology, 2022, 2377, 391-421.	0.9	7
108	Biological Profiling Enables Rapid Mechanistic Classification of Phenotypic Screening Hits and Identification of KatG Activation-Dependent Pyridine Carboxamide Prodrugs With Activity Against Mycobacterium tuberculosis. Frontiers in Cellular and Infection Microbiology, 2020, 10, 582416.	3.9	6

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109	Genetic models of latent tuberculosis in mice reveal differential influence of adaptive immunity. Journal of Experimental Medicine, 2021, 218, .	8.5	6
110	Natural brominated phenoxyphenols kill persistent and biofilm-incorporated cells of MRSA and other pathogenic bacteria. Applied Microbiology and Biotechnology, 2020, 104, 5985-5998.	3.6	5
111	The Conserved Translation Factor LepA Is Required for Optimal Synthesis of a Porin Family in Mycobacterium smegmatis. Journal of Bacteriology, 2021, 203, .	2.2	5
112	Characterization of Drug-Resistant Lipid-Dependent Differentially Detectable Mycobacterium tuberculosis. Journal of Clinical Medicine, 2021, 10, 3249.	2.4	5
113	Resistance of Mycobacterium tuberculosis to indole 4-carboxamides occurs through alterations in drug metabolism and tryptophan biosynthesis. Cell Chemical Biology, 2021, 28, 1180-1191.e20.	5.2	5
114	Functional Genomics Screening Utilizing Mutant Mouse Embryonic Stem Cells Identifies Novel Radiation-Response Genes. PLoS ONE, 2015, 10, e0120534.	2.5	5
115	Multiplexed Strain Phenotyping Defines Consequences of Genetic Diversity in Mycobacterium tuberculosis for Infection and Vaccination Outcomes. MSystems, 2022, 7, e0011022.	3.8	3
116	Database Approaches and Data Representation in Structural Bioinformatics. , 2007, , .		1
117	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
118	Identification of cyclic hexapeptides natural products with inhibitory potency against Mycobacterium tuberculosis. BMC Research Notes, 2018, 11, 416.	1.4	1
119	Deletion of Rv2571c Confers Resistance to Arylamide Compounds in Mycobacterium tuberculosis. Antimicrobial Agents and Chemotherapy, 2021, 65, .	3.2	1
120	An improved statistical method to identify chemical-genetic interactions by exploiting concentration-dependence. PLoS ONE, 2021, 16, e0257911.	2.5	1
121	6-Fluorophenylbenzohydrazides inhibit Mycobacterium tuberculosis growth through alteration of tryptophan biosynthesis. European Journal of Medicinal Chemistry, 2021, 226, 113843.	5.5	1
122	A d-Phenylalanine-Benzoxazole Derivative Reveals the Role of the Essential Enzyme Rv3603c in the Pantothenate Biosynthetic Pathway of Mycobacterium tuberculosis. ACS Infectious Diseases, 2022, 8, 330-342.	3.8	1
123	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
124	Mutations in the anti-sigma H factor RshA confer resistance to econazole and clotrimazole in Mycobacterium smegmatis. Access Microbiology, 2019, 1, e000070.	0.5	0
125	Comprehensive analysis of iron utilization by Mycobacterium tuberculosis. , 2020, 16, e1008337.		0
126	Comprehensive analysis of iron utilization by Mycobacterium tuberculosis. , 2020, 16, e1008337.		0

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127	Comprehensive analysis of iron utilization by Mycobacterium tuberculosis. , 2020, 16, e1008337.		0
128	Comprehensive analysis of iron utilization by Mycobacterium tuberculosis. , 2020, 16, e1008337.		0