

Jason A Papin

List of Publications by Year in descending order

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139
papers

10,500
citations

41344

49
h-index

37204

96
g-index

168
all docs

168
docs citations

168
times ranked

10966
citing authors

#	ARTICLE	IF	CITATIONS
1	A community-driven global reconstruction of human metabolism. <i>Nature Biotechnology</i> , 2013, 31, 419-425.	17.5	920
2	Applications of genome-scale metabolic reconstructions. <i>Molecular Systems Biology</i> , 2009, 5, 320.	7.2	759
3	Reconstruction of cellular signalling networks and analysis of their properties. <i>Nature Reviews Molecular Cell Biology</i> , 2005, 6, 99-111.	37.0	472
4	Genome-scale microbial in silico models: the constraints-based approach. <i>Trends in Biotechnology</i> , 2003, 21, 162-169.	9.3	365
5	Metabolic pathways in the post-genome era. <i>Trends in Biochemical Sciences</i> , 2003, 28, 250-258.	7.5	347
6	Comparison of network-based pathway analysis methods. <i>Trends in Biotechnology</i> , 2004, 22, 400-405.	9.3	347
7	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	17.5	314
8	Genome-Scale Metabolic Network Analysis of the Opportunistic Pathogen <i>Pseudomonas aeruginosa</i> PAO1. <i>Journal of Bacteriology</i> , 2008, 190, 2790-2803.	2.2	283
9	Functional integration of a metabolic network model and expression data without arbitrary thresholding. <i>Bioinformatics</i> , 2011, 27, 541-547.	4.1	266
10	Metabolic network reconstruction of <i>Chlamydomonas</i> offers insight into light-driven algal metabolism. <i>Molecular Systems Biology</i> , 2011, 7, 518.	7.2	264
11	Genome-Scale Reconstruction and Analysis of the <i>Pseudomonas putida</i> KT2440 Metabolic Network Facilitates Applications in Biotechnology. <i>PLoS Computational Biology</i> , 2008, 4, e1000210.	3.2	237
12	Integration of expression data in genome-scale metabolic network reconstructions. <i>Frontiers in Physiology</i> , 2012, 3, 299.	2.8	235
13	Flux balance analysis in the era of metabolomics. <i>Briefings in Bioinformatics</i> , 2006, 7, 140-150.	6.5	227
14	Hierarchical thinking in network biology: the unbiased modularization of biochemical networks. <i>Trends in Biochemical Sciences</i> , 2004, 29, 641-647.	7.5	189
15	Multiscale Computational Models of Complex Biological Systems. <i>Annual Review of Biomedical Engineering</i> , 2013, 15, 137-154.	12.3	186
16	Dynamic Analysis of Integrated Signaling, Metabolic, and Regulatory Networks. <i>PLoS Computational Biology</i> , 2008, 4, e1000086.	3.2	182
17	Reconciled rat and human metabolic networks for comparative toxicogenomics and biomarker predictions. <i>Nature Communications</i> , 2017, 8, 14250.	12.8	151
18	Systems analysis of metabolism in the pathogenic trypanosomatid <i>Leishmania major</i> . <i>Molecular Systems Biology</i> , 2008, 4, 177.	7.2	145

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19	Simple: A Sequential Immunoperoxidase Labeling and Erasing Method. <i>Journal of Histochemistry and Cytochemistry</i> , 2009, 57, 899-905.	2.5	135
20	Metabolic Network Analysis of <i>Pseudomonas aeruginosa</i> during Chronic Cystic Fibrosis Lung Infection. <i>Journal of Bacteriology</i> , 2010, 192, 5534-5548.	2.2	133
21	Extreme Pathway Lengths and Reaction Participation in Genome-Scale Metabolic Networks. <i>Genome Research</i> , 2002, 12, 1889-1900.	5.5	125
22	The JAK-STAT Signaling Network in the Human B-Cell: An Extreme Signaling Pathway Analysis. <i>Biophysical Journal</i> , 2004, 87, 37-46.	0.5	117
23	The application of flux balance analysis in systems biology. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 372-382.	6.6	116
24	Reconstruction of the metabolic network of <i>Pseudomonas aeruginosa</i> to interrogate virulence factor synthesis. <i>Nature Communications</i> , 2017, 8, 14631.	12.8	116
25	The Genome-Scale Metabolic Extreme Pathway Structure in <i>Haemophilus influenzae</i> Shows Significant Network Redundancy. <i>Journal of Theoretical Biology</i> , 2002, 215, 67-82.	1.7	115
26	Reconciliation of Genome-Scale Metabolic Reconstructions for Comparative Systems Analysis. <i>PLoS Computational Biology</i> , 2011, 7, e1001116.	3.2	111
27	Determination of Redundancy and Systems Properties of the Metabolic Network of <i>Helicobacter pylori</i> Using Genome-Scale Extreme Pathway Analysis. <i>Genome Research</i> , 2002, 12, 760-769.	5.5	106
28	Inference of Network Dynamics and Metabolic Interactions in the Gut Microbiome. <i>PLoS Computational Biology</i> , 2015, 11, e1004338.	3.2	106
29	TIGER: Toolbox for integrating genome-scale metabolic models, expression data, and transcriptional regulatory networks. <i>BMC Systems Biology</i> , 2011, 5, 147.	3.0	104
30	Topological analysis of mass-balanced signaling networks: a framework to obtain network properties including crosstalk. <i>Journal of Theoretical Biology</i> , 2004, 227, 283-297.	1.7	97
31	Metabolic network modeling of microbial communities. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2015, 7, 317-334.	6.6	95
32	Characterizing emergent properties of immunological systems with multi-cellular rule-based computational modeling. <i>Trends in Immunology</i> , 2008, 29, 589-599.	6.8	94
33	A metabolic network approach for the identification and prioritization of antimicrobial drug targets. <i>Trends in Microbiology</i> , 2012, 20, 113-123.	7.7	94
34	Metabolic reconstruction, constraint-based analysis and game theory to probe genome-scale metabolic networks. <i>Current Opinion in Biotechnology</i> , 2010, 21, 502-510.	6.6	91
35	History of antibiotic adaptation influences microbial evolutionary dynamics during subsequent treatment. <i>PLoS Biology</i> , 2017, 15, e2001586.	5.6	90
36	Predicting biological system objectives de novo from internal state measurements. <i>BMC Bioinformatics</i> , 2008, 9, 43.	2.6	89

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37	Inferring Metabolic Mechanisms of Interaction within a Defined Gut Microbiota. <i>Cell Systems</i> , 2018, 7, 245-257.e7.	6.2	89
38	Matrix Formalism to Describe Functional States of Transcriptional Regulatory Systems. <i>PLoS Computational Biology</i> , 2006, 2, e101.	3.2	84
39	Metabolic network analysis integrated with transcript verification for sequenced genomes. <i>Nature Methods</i> , 2009, 6, 589-592.	19.0	83
40	Protein- and zinc-deficient diets modulate the murine microbiome and metabolic phenotype. <i>American Journal of Clinical Nutrition</i> , 2016, 104, 1253-1262.	4.7	83
41	Analysis of Metabolic Capabilities Using Singular Value Decomposition of Extreme Pathway Matrices. <i>Biophysical Journal</i> , 2003, 84, 794-804.	0.5	73
42	Do genome-scale models need exact solvers or clearer standards?. <i>Molecular Systems Biology</i> , 2015, 11, 831.	7.2	68
43	Cross-modulation of pathogen-specific pathways enhances malnutrition during enteric co-infection with <i>Giardia lamblia</i> and enteroaggregative <i>Escherichia coli</i> . <i>PLoS Pathogens</i> , 2017, 13, e1006471.	4.7	68
44	Flux Balance Analysis: Interrogating Genome-Scale Metabolic Networks. <i>Methods in Molecular Biology</i> , 2009, 500, 61-80.	0.9	68
45	Matrix Rigidity Regulates Cancer Cell Growth by Modulating Cellular Metabolism and Protein Synthesis. <i>PLoS ONE</i> , 2012, 7, e37231.	2.5	65
46	Network-based analysis of metabolic regulation in the human red blood cell. <i>Journal of Theoretical Biology</i> , 2003, 225, 185-194.	1.7	64
47	Clinical, Molecular and Genetic Validation of a Murine Orthotopic Xenograft Model of Pancreatic Adenocarcinoma Using Fresh Human Specimens. <i>PLoS ONE</i> , 2013, 8, e77065.	2.5	62
48	Systems-level metabolism of the altered Schaedler flora, a complete gut microbiota. <i>ISME Journal</i> , 2017, 11, 426-438.	9.8	60
49	Novel Multiscale Modeling Tool Applied to <i>Pseudomonas aeruginosa</i> Biofilm Formation. <i>PLoS ONE</i> , 2013, 8, e78011.	2.5	58
50	Integrated Experimental and Computational Analyses Reveal Differential Metabolic Functionality in Antibiotic-Resistant <i>Pseudomonas aeruginosa</i> . <i>Cell Systems</i> , 2019, 8, 3-14.e3.	6.2	56
51	Transcriptome-guided parsimonious flux analysis improves predictions with metabolic networks in complex environments. <i>PLoS Computational Biology</i> , 2020, 16, e1007099.	3.2	55
52	Managing uncertainty in metabolic network structure and improving predictions using EnsembleFBA. <i>PLoS Computational Biology</i> , 2017, 13, e1005413.	3.2	55
53	Development of network-based pathway definitions: the need to analyze real metabolic networks. <i>Trends in Biotechnology</i> , 2003, 21, 195-198.	9.3	51
54	Mechanistic systems modeling to guide drug discovery and development. <i>Drug Discovery Today</i> , 2013, 18, 116-127.	6.4	47

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55	Guiding the Refinement of Biochemical Knowledgebases with Ensembles of Metabolic Networks and Machine Learning. <i>Cell Systems</i> , 2020, 10, 109-119.e3.	6.2	46
56	Ten simple rules for biologists learning to program. <i>PLoS Computational Biology</i> , 2018, 14, e1005871.	3.2	45
57	Comparative Metabolic Systems Analysis of Pathogenic <i>Burkholderia</i> . <i>Journal of Bacteriology</i> , 2014, 196, 210-226.	2.2	43
58	Proteomic and network analysis characterize stage-specific metabolism in <i>Trypanosoma cruzi</i> . <i>BMC Systems Biology</i> , 2009, 3, 52.	3.0	42
59	Metabolic network analysis predicts efficacy of FDA-approved drugs targeting the causative agent of a neglected tropical disease. <i>BMC Systems Biology</i> , 2012, 6, 27.	3.0	41
60	Core Competencies for Undergraduates in Bioengineering and Biomedical Engineering: Findings, Consequences, and Recommendations. <i>Annals of Biomedical Engineering</i> , 2020, 48, 905-912.	2.5	37
61	Community standards to facilitate development and address challenges in metabolic modeling. <i>Molecular Systems Biology</i> , 2020, 16, e9235.	7.2	37
62	Novel <i>Plasmodium falciparum</i> metabolic network reconstruction identifies shifts associated with clinical antimalarial resistance. <i>BMC Genomics</i> , 2017, 18, 543.	2.8	36
63	Functional States of the Genome-Scale <i>Escherichia Coli</i> Transcriptional Regulatory System. <i>PLoS Computational Biology</i> , 2009, 5, e1000403.	3.2	34
64	Whole-Genome Metabolic Network Reconstruction and Constraint-Based Modeling. <i>Methods in Enzymology</i> , 2011, 500, 411-433.	1.0	33
65	<i>Megasphaera</i> in the Stool Microbiota Is Negatively Associated With Diarrheal Cryptosporidiosis. <i>Clinical Infectious Diseases</i> , 2021, 73, e1242-e1251.	5.8	33
66	Comprehensive analysis of receptor tyrosine kinase activation in human melanomas reveals autocrine signaling through IGF-1R. <i>Melanoma Research</i> , 2011, 21, 274-284.	1.2	32
67	Mechanistic identification of biofluid metabolite changes as markers of acetaminophen-induced liver toxicity in rats. <i>Toxicology and Applied Pharmacology</i> , 2019, 372, 19-32.	2.8	32
68	<i>In Vivo</i> Physiological and Transcriptional Profiling Reveals Host Responses to <i>Clostridium difficile</i> Toxin A and Toxin B. <i>Infection and Immunity</i> , 2013, 81, 3814-3824.	2.2	31
69	A Thirteen-Gene Expression Signature Predicts Survival of Patients with Pancreatic Cancer and Identifies New Genes of Interest. <i>PLoS ONE</i> , 2014, 9, e105631.	2.5	31
70	Genotypic and phenotypic analyses of a <i>Pseudomonas aeruginosa</i> chronic bronchiectasis isolate reveal differences from cystic fibrosis and laboratory strains. <i>BMC Genomics</i> , 2015, 16, 883.	2.8	30
71	Biomedical applications of genome-scale metabolic network reconstructions of human pathogens. <i>Current Opinion in Biotechnology</i> , 2018, 51, 70-79.	6.6	30
72	Bioinformatics and cellular signaling. <i>Current Opinion in Biotechnology</i> , 2004, 15, 78-81.	6.6	29

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73	Systems analyses characterize integrated functions of biochemical networks. <i>Trends in Biochemical Sciences</i> , 2006, 31, 284-291.	7.5	28
74	Metabolic systems analysis to advance algal biotechnology. <i>Biotechnology Journal</i> , 2010, 5, 660-670.	3.5	28
75	Multiscale computational analysis of <i>Xenopus laevis</i> morphogenesis reveals key insights of systems-level behavior. <i>BMC Systems Biology</i> , 2007, 1, 46.	3.0	27
76	MetDraw: automated visualization of genome-scale metabolic network reconstructions and high-throughput data. <i>Bioinformatics</i> , 2014, 30, 1327-1328.	4.1	26
77	MicroRNAs induced in melanoma treated with combination targeted therapy of Temsirolimus and Bevacizumab. <i>Journal of Translational Medicine</i> , 2013, 11, 218.	4.4	22
78	An engineering design approach to systems biology. <i>Integrative Biology (United Kingdom)</i> , 2017, 9, 574-583.	1.3	22
79	Improving reproducibility in computational biology research. <i>PLoS Computational Biology</i> , 2020, 16, e1007881.	3.2	22
80	<i>In Vivo</i> Gene Essentiality and Metabolism in <i>Bordetella pertussis</i> . <i>MSphere</i> , 2019, 4, .	2.9	21
81	A simplified metabolic network reconstruction to promote understanding and development of flux balance analysis tools. <i>Computers in Biology and Medicine</i> , 2019, 105, 64-71.	7.0	21
82	Minimum bactericidal concentration of ciprofloxacin to <i>Pseudomonas aeruginosa</i> determined rapidly based on pyocyanin secretion. <i>Sensors and Actuators B: Chemical</i> , 2020, 312, 127936.	7.8	20
83	Reconciling high-throughput gene essentiality data with metabolic network reconstructions. <i>PLoS Computational Biology</i> , 2019, 15, e1006507.	3.2	19
84	Novel co-culture plate enables growth dynamic-based assessment of contact-independent microbial interactions. <i>PLoS ONE</i> , 2017, 12, e0182163.	2.5	19
85	Miniaturized Plate Readers for Low-Cost, High-Throughput Phenotypic Screening. <i>Journal of the Association for Laboratory Automation</i> , 2015, 20, 51-55.	2.8	18
86	Evaluating the efficacy of an algae-based treatment to mitigate elicitation of antibiotic resistance. <i>Chemosphere</i> , 2019, 237, 124421.	8.2	18
87	Medusa: Software to build and analyze ensembles of genome-scale metabolic network reconstructions. <i>PLoS Computational Biology</i> , 2020, 16, e1007847.	3.2	18
88	Mechanistic models of microbial community metabolism. <i>Molecular Omics</i> , 2021, 17, 365-375.	2.8	18
89	Genome-wide functional annotation and structural verification of metabolic ORFeome of <i>Chlamydomonas reinhardtii</i> . <i>BMC Genomics</i> , 2011, 12, S4.	2.8	17
90	Systems analysis of the transcriptional response of human ileocecal epithelial cells to <i>Clostridium difficile</i> toxins and effects on cell cycle control. <i>BMC Systems Biology</i> , 2012, 6, 2.	3.0	17

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91	Increased Urinary Trimethylamine N-Oxide Following Cryptosporidium Infection and Protein Malnutrition Independent of Microbiome Effects. <i>Journal of Infectious Diseases</i> , 2017, 216, 64-71.	4.0	16
92	Genome-Scale Characterization of Toxicity-Induced Metabolic Alterations in Primary Hepatocytes. <i>Toxicological Sciences</i> , 2019, 172, 279-291.	3.1	15
93	Identifying functional metabolic shifts in heart failure with the integration of omics data and a heart-specific, genome-scale model. <i>Cell Reports</i> , 2021, 34, 108836.	6.4	15
94	Growth-altering microbial interactions are responsive to chemical context. <i>PLoS ONE</i> , 2017, 12, e0164919.	2.5	15
95	Dephosphorylation of β -Arrestin 1 in Glioblastomas. <i>Journal of Neuropathology and Experimental Neurology</i> , 2009, 68, 535-541.	1.7	13
96	Novel Drivers of Virulence in <i>Clostridioides difficile</i> Identified via Context-Specific Metabolic Network Analysis. <i>MSystems</i> , 2021, 6, e0091921.	3.8	13
97	High temporal resolution of glucosyltransferase dependent and independent effects of <i>Clostridium difficile</i> toxins across multiple cell types. <i>BMC Microbiology</i> , 2015, 15, 7.	3.3	12
98	Systems level analysis of the <i>Chlamydomonas reinhardtii</i> metabolic network reveals variability in evolutionary co-conservation. <i>Molecular BioSystems</i> , 2016, 12, 2394-2407.	2.9	12
99	Collaborating with our community to increase code sharing. <i>PLoS Computational Biology</i> , 2021, 17, e1008867.	3.2	12
100	An updated genome-scale metabolic network reconstruction of <i>Pseudomonas aeruginosa</i> PA14 to characterize mucin-driven shifts in bacterial metabolism. <i>Npj Systems Biology and Applications</i> , 2021, 7, 37.	3.0	12
101	Mechanistic Exploration of Phthalimide Neovascular Factor 1 Using Network Analysis Tools. <i>Tissue Engineering</i> , 2007, 13, 2561-2575.	4.6	11
102	Influential Parameters for the Analysis of Intracellular Parasite Metabolomics. <i>MSphere</i> , 2018, 3, .	2.9	11
103	Harnessing Systems Biology Approaches to Engineer Functional Microvascular Networks. <i>Tissue Engineering - Part B: Reviews</i> , 2010, 16, 361-370.	4.8	10
104	Systems Analysis of Small Signaling Modules Relevant to Eight Human Diseases. <i>Annals of Biomedical Engineering</i> , 2011, 39, 621-635.	2.5	10
105	Predicting changes in renal metabolism after compound exposure with a genome-scale metabolic model. <i>Toxicology and Applied Pharmacology</i> , 2021, 412, 115390.	2.8	10
106	Untargeted Metabolomics Reveals Species-Specific Metabolite Production and Shared Nutrient Consumption by <i>Pseudomonas aeruginosa</i> and <i>Staphylococcus aureus</i> . <i>MSystems</i> , 2021, 6, e0048021.	3.8	9
107	Novel pathway compendium analysis elucidates mechanism of pro-angiogenic synthetic small molecule. <i>Bioinformatics</i> , 2008, 24, 2384-2390.	4.1	8
108	Nano-motion Dynamics are Determined by Surface-Tethered Selectin Mechanokinetics and Bond Formation. <i>PLoS Computational Biology</i> , 2009, 5, e1000612.	3.2	8

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109	Linking Genome-Scale Metabolic Modeling and Genome Annotation. <i>Methods in Molecular Biology</i> , 2013, 985, 61-83.	0.9	8
110	Metabolic network-guided binning of metagenomic sequence fragments. <i>Bioinformatics</i> , 2016, 32, 867-874.	4.1	8
111	Computational Models of Algae Metabolism for Industrial Applications. <i>Industrial Biotechnology</i> , 2013, 9, 185-195.	0.8	7
112	Multiscale Computational Modeling in Vascular Biology: From Molecular Mechanisms to Tissue-Level Structure and Function. <i>Studies in Mechanobiology, Tissue Engineering and Biomaterials</i> , 2013, , 209-240.	1.0	7
113	Phthalimide neovascular factor 1 (PNF1) modulates MT1â€MMP activity in human microvascular endothelial cells. <i>Biotechnology and Bioengineering</i> , 2009, 103, 796-807.	3.3	6
114	Leveraging the effects of chloroquine on resistant malaria parasites for combination therapies. <i>BMC Bioinformatics</i> , 2019, 20, 186.	2.6	6
115	Fecal sphingolipids predict parenteral nutritionâ€associated cholestasis in the neonatal intensive care unit. <i>Journal of Parenteral and Enteral Nutrition</i> , 2022, 46, 1903-1913.	2.6	6
116	Advancing code sharing in the computational biology community. <i>PLoS Computational Biology</i> , 2022, 18, e1010193.	3.2	6
117	Genome-Scale Model-Based Identification of Metabolite Indicators for Early Detection of Kidney Toxicity. <i>Toxicological Sciences</i> , 2020, 173, 293-312.	3.1	5
118	Systems biology approaches help to facilitate interpretation of cross-species comparisons. <i>Current Opinion in Toxicology</i> , 2020, 23-24, 74-79.	5.0	5
119	From â€What Is?â€to â€What Isn't?â€-Computational Biology. <i>PLoS Computational Biology</i> , 2015, 11, e1004318.	3.2	5
120	Determination of Redundancy and Systems Properties of the Metabolic Network of <i>Helicobacter pylori</i> Using Genome-Scale Extreme Pathway Analysis. <i>Genome Research</i> , 2002, 12, 760-769.	5.5	5
121	Comparative analyses of parasites with a comprehensive database of genome-scale metabolic models. <i>PLoS Computational Biology</i> , 2022, 18, e1009870.	3.2	5
122	Gramâ€negative Microbiota Blooms in Premature Twins Discordant for Parenteral Nutritionâ€associated Cholestasis. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2020, 70, 640-644.	1.8	4
123	Metabolic Network Reconstructions to Predict Drug Targets and Off-Target Effects. <i>Methods in Molecular Biology</i> , 2020, 2088, 315-330.	0.9	4
124	One thousand simple rules. <i>PLoS Computational Biology</i> , 2018, 14, e1006670.	3.2	3
125	Multidimensional Clinical Surveillance of <i>Pseudomonas aeruginosa</i> Reveals Complex Relationships between Isolate Source, Morphology, and Antimicrobial Resistance. <i>MSphere</i> , 2021, 6, e0039321.	2.9	3
126	Quantifying cumulative phenotypic and genomic evidence for procedural generation of metabolic network reconstructions. <i>PLoS Computational Biology</i> , 2022, 18, e1009341.	3.2	3

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127	Wisdom of crowds in computational biology. PLoS Computational Biology, 2019, 15, e1007032.	3.2	2
128	Clostridioides difficile: Sometimes It Pays To Be Difficult. Cell Host and Microbe, 2020, 28, 358-359.	11.0	1
129	Conserved Virulence-Linked Metabolic Reprogramming in <i>Clostridioides Difficile</i> Identified Through Genome-Scale Metabolic Network Analysis. SSRN Electronic Journal, 0, , .	0.4	1
130	Application of a novel optimization-based approach to characterize integrated signalling, regulatory, and metabolic biochemical networks. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2008, 41, 11630-11635.	0.4	0
131	A scalable systems analysis approach for regulated metabolic networks. , 2009, 2009, 5464-5.		0
132	Computing Biology. PLoS Computational Biology, 2016, 12, e1005050.	3.2	0
133	Computational approaches to understanding Clostridioides difficile metabolism and virulence. Current Opinion in Microbiology, 2022, 65, 108-115.	5.1	0
134	Medusa: Software to build and analyze ensembles of genome-scale metabolic network reconstructions. , 2020, 16, e1007847.		0
135	Medusa: Software to build and analyze ensembles of genome-scale metabolic network reconstructions. , 2020, 16, e1007847.		0
136	Medusa: Software to build and analyze ensembles of genome-scale metabolic network reconstructions. , 2020, 16, e1007847.		0
137	Medusa: Software to build and analyze ensembles of genome-scale metabolic network reconstructions. , 2020, 16, e1007847.		0
138	Medusa: Software to build and analyze ensembles of genome-scale metabolic network reconstructions. , 2020, 16, e1007847.		0
139	Medusa: Software to build and analyze ensembles of genome-scale metabolic network reconstructions. , 2020, 16, e1007847.		0