

Jonathan M Monk

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

74
papers

3,422
citations

25
h-index

58
g-index

84
ext. papers

4,649
ext. citations

10.6
avg, IF

5.57
L-index

#	Paper	IF	Citations
74	Constraint-based models predict metabolic and associated cellular functions. <i>Nature Reviews Genetics</i> , 2014 , 15, 107-20	30.1	552
73	Using Genome-scale Models to Predict Biological Capabilities. <i>Cell</i> , 2015 , 161, 971-987	56.2	433
72	Wdr5 mediates self-renewal and reprogramming via the embryonic stem cell core transcriptional network. <i>Cell</i> , 2011 , 145, 183-97	56.2	433
71	iML1515, a knowledgebase that computes Escherichia coli traits. <i>Nature Biotechnology</i> , 2017 , 35, 904-908	44.5	212
70	Genome-scale metabolic reconstructions of multiple Escherichia coli strains highlight strain-specific adaptations to nutritional environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 20338-43	11.5	176
69	What Makes a Bacterial Species Pathogenic?:Comparative Genomic Analysis of the Genus Leptospira. <i>PLoS Neglected Tropical Diseases</i> , 2016 , 10, e0004403	4.8	170
68	Optimizing genome-scale network reconstructions. <i>Nature Biotechnology</i> , 2014 , 32, 447-52	44.5	152
67	Comparative genome-scale modelling of Staphylococcus aureus strains identifies strain-specific metabolic capabilities linked to pathogenicity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E3801-9	11.5	145
66	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020 , 38, 272-276	47.5	121
65	Machine learning and structural analysis of Mycobacterium tuberculosis pan-genome identifies genetic signatures of antibiotic resistance. <i>Nature Communications</i> , 2018 , 9, 4306	17.4	73
64	Multi-omics Quantification of Species Variation of Escherichia coli Links Molecular Features with Strain Phenotypes. <i>Cell Systems</i> , 2016 , 3, 238-251.e12	10.6	67
63	Model-driven discovery of underground metabolic functions in Escherichia coli. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 929-34	11.5	63
62	High-quality genome-scale metabolic modelling of Pseudomonas putida highlights its broad metabolic capabilities. <i>Environmental Microbiology</i> , 2020 , 22, 255-269	5.2	61
61	Characterizing Strain Variation in Engineered E. coli Using a Multi-Omics-Based Workflow. <i>Cell Systems</i> , 2016 , 2, 335-46	10.6	59
60	Genome-scale metabolic reconstructions of multiple Salmonella strains reveal serovar-specific metabolic traits. <i>Nature Communications</i> , 2018 , 9, 3771	17.4	52
59	Cellular responses to reactive oxygen species are predicted from molecular mechanisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 14368-14373	11.5	46
58	BOFdat: Generating biomass objective functions for genome-scale metabolic models from experimental data. <i>PLoS Computational Biology</i> , 2019 , 15, e1006971	5	39

57	Systems biology of the structural proteome. <i>BMC Systems Biology</i> , 2016 , 10, 26	3.5	39
56	Updated and standardized genome-scale reconstruction of Mycobacterium tuberculosis H37Rv, iEK1011, simulates flux states indicative of physiological conditions. <i>BMC Systems Biology</i> , 2018 , 12, 25	3.5	33
55	A biochemically-interpretable machine learning classifier for microbial GWAS. <i>Nature Communications</i> , 2020 , 11, 2580	17.4	32
54	Systems biology definition of the core proteome of metabolism and expression is consistent with high-throughput data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 10810-5	11.5	31
53	Genetics. Predicting microbial growth. <i>Science</i> , 2014 , 344, 1448-9	33.3	29
52	Machine learning with random subspace ensembles identifies antimicrobial resistance determinants from pan-genomes of three pathogens. <i>PLoS Computational Biology</i> , 2020 , 16, e1007608	5	28
51	A workflow for generating multi-strain genome-scale metabolic models of prokaryotes. <i>Nature Protocols</i> , 2020 , 15, 1-14	18.8	28
50	Memote: A community driven effort towards a standardized genome-scale metabolic model test suite		26
49	ssbio: a Python framework for structural systems biology. <i>Bioinformatics</i> , 2018 , 34, 2155-2157	7.2	25
48	Metagenomics-Based, Strain-Level Analysis of From a Time-Series of Microbiome Samples From a Crohn's Disease Patient. <i>Frontiers in Microbiology</i> , 2018 , 9, 2559	5.7	24
47	Escherichia coli B2 strains prevalent in inflammatory bowel disease patients have distinct metabolic capabilities that enable colonization of intestinal mucosa. <i>BMC Systems Biology</i> , 2018 , 12, 66	3.5	22
46	iCN718, an Updated and Improved Genome-Scale Metabolic Network Reconstruction of AYE. <i>Frontiers in Genetics</i> , 2018 , 9, 121	4.5	20
45	Thermodynamic favorability and pathway yield as evolutionary tradeoffs in biosynthetic pathway choice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 11339-11344	11.5	20
44	A computational knowledge-base elucidates the response of Staphylococcus aureus to different media types. <i>PLoS Computational Biology</i> , 2019 , 15, e1006644	5	18
43	Comparative Genome-Scale Metabolic Modeling of Metallo-Beta-Lactamase-Producing Multidrug-Resistant Clinical Isolates. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019 , 9, 161	5.9	16
42	Systems biology-guided identification of synthetic lethal gene pairs and its potential use to discover antibiotic combinations. <i>Scientific Reports</i> , 2015 , 5, 16025	4.9	13
41	Systems Biology and Pangenome of O-Antigens. <i>MBio</i> , 2019 , 10,	7.8	11
40	Impact of insertion sequences on convergent evolution of Shigella species. <i>PLoS Genetics</i> , 2020 , 16, e1008931	10.8	11

39	The Two-Component System AgrAC Displays Four Distinct Genomic Arrangements That Delineate Genomic Virulence Factor Signatures. <i>Frontiers in Microbiology</i> , 2018 , 9, 1082	5.7	10
38	Pangenome Analytics Reveal Two-Component Systems as Conserved Targets in ESKAPEE Pathogens. <i>MSystems</i> , 2021 , 6,	7.6	10
37	Experimentally Validated Reconstruction and Analysis of a Genome-Scale Metabolic Model of an Anaerobic Neocallimastigomycota Fungus. <i>MSystems</i> , 2021 , 6,	7.6	10
36	Systems biology analysis of the <i>Clostridioides difficile</i> core-genome contextualizes microenvironmental evolutionary pressures leading to genotypic and phenotypic divergence. <i>Npj Systems Biology and Applications</i> , 2020 , 6, 31	5	9
35	Predicting Antimicrobial Resistance and Associated Genomic Features from Whole-Genome Sequencing. <i>Journal of Clinical Microbiology</i> , 2019 , 57,	9.7	9
34	Systems-level analysis of NalD mutation, a recurrent driver of rapid drug resistance in acute <i>Pseudomonas aeruginosa</i> infection. <i>PLoS Computational Biology</i> , 2019 , 15, e1007562	5	8
33	BOFdat: generating biomass objective function stoichiometric coefficients from experimental data		7
32	Machine learning in computational biology to accelerate high-throughput protein expression. <i>Bioinformatics</i> , 2017 , 33, 2487-2495	7.2	6
31	Strain-Specific Metabolic Requirements Revealed by a Defined Minimal Medium for Systems Analyses of. <i>Applied and Environmental Microbiology</i> , 2019 , 85,	4.8	6
30	Model-driven discovery of synergistic inhibitors against <i>E. coli</i> and <i>S. enterica</i> serovar Typhimurium targeting a novel synthetic lethal pair, <i>aldA</i> and <i>prpC</i> . <i>Frontiers in Microbiology</i> , 2015 , 6, 958	5.7	6
29	Genome-scale metabolic modeling reveals key features of a minimal gene set. <i>Molecular Systems Biology</i> , 2021 , 17, e10099	12.2	6
28	Draft Genome Sequences of Four Metallo-Beta-Lactamase-Producing Multidrug-Resistant <i>Klebsiella pneumoniae</i> Clinical Isolates, Including Two Colistin-Resistant Strains, from Cairo, Egypt. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	6
27	Characterization of CA-MRSA TCH1516 exposed to nafcillin in bacteriological and physiological media. <i>Scientific Data</i> , 2019 , 6, 43	8.2	4
26	Reconstruction and Validation of a Genome-Scale Metabolic Model of (iCJ415), a Human Commensal and Opportunistic Pathogen. <i>Frontiers in Genetics</i> , 2020 , 11, 116	4.5	4
25	Distinct Subpopulations of Intra-Valvular Methicillin-Resistant <i>Staphylococcus aureus</i> with Variable Susceptibility to Daptomycin in Tricuspid Valve Endocarditis. <i>Antimicrobial Agents and Chemotherapy</i> , 2020 , 64,	5.9	4
24	The aldehyde dehydrogenase, <i>AldA</i> , is essential for L-1,2-propanediol utilization in laboratory-evolved <i>Escherichia coli</i> . <i>Microbiological Research</i> , 2017 , 194, 47-52	5.3	4
23	Reduced Production of Bacterial Membrane Vesicles Predicts Mortality in ST45/USA600 Methicillin-Resistant Bacteremia. <i>Antibiotics</i> , 2019 , 9,	4.9	4
22	Integration of Comparative Genomics with Genome-Scale Metabolic Modeling to Investigate Strain-Specific Phenotypical Differences. <i>Methods in Molecular Biology</i> , 2018 , 1716, 151-175	1.4	4

21	Genome-Scale Metabolic Model of pv. : An Approach to Elucidate Pathogenicity at the Metabolic Level. <i>Frontiers in Genetics</i> , 2020 , 11, 837	4.5	3
20	Profiling the effect of nafcillin on HA-MRSA D712 using bacteriological and physiological media. <i>Scientific Data</i> , 2019 , 6, 322	8.2	3
19	Pangenome Flux Balance Analysis Toward Panphenomes 2020 , 219-232		2
18	ssbio: A Python Framework for Structural Systems Biology		2
17	Pangenome Analysis of Enterobacteria Reveals Richness of Secondary Metabolite Gene Clusters and their Associated Gene Sets		2
16	Gapless, Unambiguous Genome Sequence for Escherichia coli C, a Workhorse of Industrial Biology. <i>Microbiology Resource Announcements</i> , 2018 , 7,	1.3	2
15	Genome Sequence Comparison of Staphylococcus aureus TX0117 and a Beta-Lactamase-Cured Derivative Shows Increased Cationic Peptide Resistance Accompanying Mutations in and. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	1
14	Adaptations of Escherichia coli strains to oxidative stress are reflected in properties of their structural proteomes. <i>BMC Bioinformatics</i> , 2020 , 21, 162	3.6	1
13	Comparative pangenomics: analysis of 12 microbial pathogen pangenomes reveals conserved global structures of genetic and functional diversity.. <i>BMC Genomics</i> , 2022 , 23, 7	4.5	1
12	Rapid resistance development to three antistaphylococcal therapies in antibiotic-tolerant staphylococcus aureus bacteremia. <i>PLoS ONE</i> , 2021 , 16, e0258592	3.7	1
11	Computation of condition-dependent proteome allocation reveals variability in the macro and micro nutrient requirements for growth		1
10	Laboratory evolution of multiple E. coli strains reveals unifying principles of adaptation but diversity in driving genotypes		1
9	Computation of condition-dependent proteome allocation reveals variability in the macro and micro nutrient requirements for growth. <i>PLoS Computational Biology</i> , 2021 , 17, e1007817	5	1
8	Systems biology approach to functionally assess the pangenome reveals genetic diversity with discriminatory power.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119, e2119396119	11.5	1
7	High-Quality Genome-Scale Models From Error-Prone, Long-Read Assemblies. <i>Frontiers in Microbiology</i> , 2020 , 11, 596626	5.7	0
6	Mathematical models to study the biology of pathogens and the infectious diseases they cause.. <i>IScience</i> , 2022 , 25, 104079	6.1	0
5	Machine learning with random subspace ensembles identifies antimicrobial resistance determinants from pan-genomes of three pathogens 2020 , 16, e1007608		
4	Machine learning with random subspace ensembles identifies antimicrobial resistance determinants from pan-genomes of three pathogens 2020 , 16, e1007608		

- 3 Machine learning with random subspace ensembles identifies antimicrobial resistance determinants from pan-genomes of three pathogens **2020**, 16, e1007608
- 2 Machine learning with random subspace ensembles identifies antimicrobial resistance determinants from pan-genomes of three pathogens **2020**, 16, e1007608
- 1 A systems approach discovers the role and characteristics of seven LysR type transcription factors in *Escherichia coli*. *Scientific Reports*, **2022**, 12, 7274 4·9