Jonathan M Monk

List of Publications by Year
in descending order

72 papers	5,430 citations	201674 27 h-index	98798 67 g-index
84 all docs	84 docs citations	84 times ranked	6645 citing authors

#	Article	IF	Citations
1	Comparative pangenomics: analysis of 12 microbial pathogen pangenomes reveals conserved global structures of genetic and functional diversity. BMC Genomics, 2022, 23, 7.	2.8	22
2	A curated collection of <i>Klebsiella</i> metabolic models reveals variable substrate usage and gene essentiality. Genome Research, 2022, , .	5.5	10
3	Mathematical models to study the biology of pathogens and the infectious diseases they cause. IScience, 2022, 25, 104079.	4.1	8
4	Systems biology approach to functionally assess the <i>Clostridioides difficile</i> pangenome reveals genetic diversity with discriminatory power. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2119396119.	7.1	5
5	A systems approach discovers the role and characteristics of seven LysR type transcription factors in Escherichia coli. Scientific Reports, 2022, 12, 7274.	3.3	5
6	Pangenome analysis of Enterobacteria reveals richness of secondary metabolite gene clusters and their associated gene sets. Synthetic and Systems Biotechnology, 2022, 7, 900-910.	3.7	9
7	Transmission of <i>Klebsiella</i> strains and plasmids within and between greyâ€headed flying fox colonies. Environmental Microbiology, 2022, 24, 4425-4436.	3.8	3
8	Identifying the effect of vancomycin on health careâ€"associated methicillin-resistant <i>Staphylococcus aureus</i> strains using bacteriological and physiological media. GigaScience, 2021, 10, .	6.4	5
9	Pangenome Analytics Reveal Two-Component Systems as Conserved Targets in ESKAPEE Pathogens. MSystems, 2021, 6, .	3.8	24
10	Experimentally Validated Reconstruction and Analysis of a Genome-Scale Metabolic Model of an Anaerobic Neocallimastigomycota Fungus. MSystems, 2021, 6, .	3.8	33
11	Computation of condition-dependent proteome allocation reveals variability in the macro and micro nutrient requirements for growth. PLoS Computational Biology, 2021, 17, e1007817.	3.2	3
12	Genomeâ€scale metabolic modeling reveals key features of a minimal gene set. Molecular Systems Biology, 2021, 17, e10099.	7.2	15
13	Rapid resistance development to three antistaphylococcal therapies in antibiotic-tolerant staphylococcus aureus bacteremia. PLoS ONE, 2021, 16, e0258592.	2.5	5
14	Highâ€quality genomeâ€scale metabolic modelling of <i>Pseudomonas putida</i> highlights its broad metabolic capabilities. Environmental Microbiology, 2020, 22, 255-269.	3.8	127
15	Reduced Production of Bacterial Membrane Vesicles Predicts Mortality in ST45/USA600 Methicillin-Resistant Staphylococcus aureus Bacteremia. Antibiotics, 2020, 9, 2.	3.7	11
16	A workflow for generating multi-strain genome-scale metabolic models of prokaryotes. Nature Protocols, 2020, 15, 1-14.	12.0	62
17	High-Quality Genome-Scale Models From Error-Prone, Long-Read Assemblies. Frontiers in Microbiology, 2020, 11, 596626.	3.5	3
18	Systems biology analysis of the Clostridioides difficile core-genome contextualizes microenvironmental evolutionary pressures leading to genotypic and phenotypic divergence. Npj Systems Biology and Applications, 2020, 6, 31.	3.0	15

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19	Genome-Scale Metabolic Model of Xanthomonas phaseoli pv. manihotis: An Approach to Elucidate Pathogenicity at the Metabolic Level. Frontiers in Genetics, 2020, 11, 837.	2.3	5
20	Genome Sequence Comparison of Staphylococcus aureus TX0117 and a Beta-Lactamase-Cured Derivative Shows Increased Cationic Peptide Resistance Accompanying Mutations in <i>relA</i> and <i>mnaA</i>. Microbiology Resource Announcements, 2020, 9, .	0.6	2
21	Reconstruction and Validation of a Genome-Scale Metabolic Model of Streptococcus oralis (iCJ415), a Human Commensal and Opportunistic Pathogen. Frontiers in Genetics, 2020, 11, 116.	2.3	11
22	Machine learning with random subspace ensembles identifies antimicrobial resistance determinants from pan-genomes of three pathogens. PLoS Computational Biology, 2020, 16, e1007608.	3.2	49
23	Impact of insertion sequences on convergent evolution of Shigella species. PLoS Genetics, 2020, 16, e1008931.	3.5	43
24	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	17.5	314
25	Distinct Subpopulations of Intravalvular Methicillin-Resistant Staphylococcus aureus with Variable Susceptibility to Daptomycin in Tricuspid Valve Endocarditis. Antimicrobial Agents and Chemotherapy, 2020, 64, .	3.2	8
26	Adaptations of Escherichia coli strains to oxidative stress are reflected in properties of their structural proteomes. BMC Bioinformatics, 2020, 21, 162.	2.6	5
27	Pangenome Flux Balance Analysis Toward Panphenomes. , 2020, , 219-232.		7
28	A biochemically-interpretable machine learning classifier for microbial GWAS. Nature Communications, 2020, 11, 2580.	12.8	51
29	Title is missing!. , 2020, 16, e1007608.		0
30	Title is missing!. , 2020, 16, e1007608.		0
31	Title is missing!. , 2020, 16, e1007608.		0
32	Title is missing!. , 2020, 16, e1007608.		0
33	Cellular responses to reactive oxygen species are predicted from molecular mechanisms. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14368-14373.	7.1	79
34	Systems Biology and Pangenome of <i>Salmonella</i> O-Antigens. MBio, 2019, 10, .	4.1	26
35	Strain-Specific Metabolic Requirements Revealed by a Defined Minimal Medium for Systems Analyses of <i>Staphylococcus aureus</i>. Applied and Environmental Microbiology, 2019, 85, .	3.1	21
36	A computational knowledge-base elucidates the response of Staphylococcus aureus to different media types. PLoS Computational Biology, 2019, 15, e1006644.	3.2	41

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37	Comparative Genome-Scale Metabolic Modeling of Metallo-Beta-Lactamaseâ€"Producing Multidrug-Resistant Klebsiella pneumoniae Clinical Isolates. Frontiers in Cellular and Infection Microbiology, 2019, 9, 161.	3.9	33
38	BOFdat: Generating biomass objective functions for genome-scale metabolic models from experimental data. PLoS Computational Biology, 2019, 15, e1006971.	3.2	83
39	Characterization of CA-MRSA TCH1516 exposed to nafcillin in bacteriological and physiological media. Scientific Data, 2019, 6, 43.	5.3	14
40	Draft Genome Sequences of Four Metallo-Beta-Lactamase-Producing Multidrug-Resistant Klebsiella pneumoniae Clinical Isolates, Including Two Colistin-Resistant Strains, from Cairo, Egypt. Microbiology Resource Announcements, 2019, 8, .	0.6	23
41	Systems-level analysis of NalD mutation, a recurrent driver of rapid drug resistance in acute Pseudomonas aeruginosa infection. PLoS Computational Biology, 2019, 15, e1007562.	3.2	11
42	Profiling the effect of nafcillin on HA-MRSA D712 using bacteriological and physiological media. Scientific Data, 2019, 6, 322.	5.3	8
43	Predicting Antimicrobial Resistance and Associated Genomic Features from Whole-Genome Sequencing. Journal of Clinical Microbiology, 2019, 57, .	3.9	14
44	ssbio: a Python framework for structural systems biology. Bioinformatics, 2018, 34, 2155-2157.	4.1	36
45	Updated and standardized genome-scale reconstruction of Mycobacterium tuberculosis H37Rv, iEK1011, simulates flux states indicative of physiological conditions. BMC Systems Biology, 2018, 12, 25.	3.0	63
46	Integration of Comparative Genomics with Genome-Scale Metabolic Modeling to Investigate Strain-Specific Phenotypical Differences. Methods in Molecular Biology, 2018, 1716, 151-175.	0.9	4
47	Metagenomics-Based, Strain-Level Analysis of Escherichia coli From a Time-Series of Microbiome Samples From a Crohn's Disease Patient. Frontiers in Microbiology, 2018, 9, 2559.	3.5	37
48	Thermodynamic favorability and pathway yield as evolutionary tradeoffs in biosynthetic pathway choice. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 11339-11344.	7.1	30
49	Machine learning and structural analysis of Mycobacterium tuberculosis pan-genome identifies genetic signatures of antibiotic resistance. Nature Communications, 2018, 9, 4306.	12.8	126
50	Gapless, Unambiguous Genome Sequence for Escherichia coli C, a Workhorse of Industrial Biology. Microbiology Resource Announcements, 2018, 7, .	0.6	3
51	Genome-scale metabolic reconstructions of multiple Salmonella strains reveal serovar-specific metabolic traits. Nature Communications, 2018, 9, 3771.	12.8	109
52	Escherichia coli B2 strains prevalent in inflammatory bowel disease patients have distinct metabolic capabilities that enable colonization of intestinal mucosa. BMC Systems Biology, 2018, 12, 66.	3.0	39
53	iCN718, an Updated and Improved Genome-Scale Metabolic Network Reconstruction of Acinetobacter baumannii AYE. Frontiers in Genetics, 2018, 9, 121.	2.3	40
54	The Staphylococcus aureus Two-Component System AgrAC Displays Four Distinct Genomic Arrangements That Delineate Genomic Virulence Factor Signatures. Frontiers in Microbiology, 2018, 9, 1082.	3.5	26

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55	Machine learning in computational biology to accelerate high-throughput protein expression. Bioinformatics, 2017, 33, 2487-2495.	4.1	8
56	iML1515, a knowledgebase that computes Escherichia coli traits. Nature Biotechnology, 2017, 35, 904-908.	17.5	425
57	The aldehyde dehydrogenase, AldA, is essential for L-1,2-propanediol utilization in laboratory-evolved Escherichia coli. Microbiological Research, 2017, 194, 47-52.	5.3	5
58	What Makes a Bacterial Species Pathogenic?:Comparative Genomic Analysis of the Genus Leptospira. PLoS Neglected Tropical Diseases, 2016, 10, e0004403.	3.0	253
59	Characterizing Strain Variation in Engineered E.Âcoli Using a Multi-Omics-Based Workflow. Cell Systems, 2016, 2, 335-346.	6.2	73
60	Multi-omics Quantification of Species Variation of Escherichia coli Links Molecular Features with Strain Phenotypes. Cell Systems, 2016, 3, 238-251.e12.	6.2	124
61	Systems biology of the structural proteome. BMC Systems Biology, 2016, 10, 26.	3.0	46
62	Comparative genome-scale modelling of <i>Staphylococcus aureus</i> strains identifies strain-specific metabolic capabilities linked to pathogenicity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3801-9.	7.1	229
63	Systems biology-guided identification of synthetic lethal gene pairs and its potential use to discover antibiotic combinations. Scientific Reports, 2015, 5, 16025.	3.3	19
64	Model-driven discovery of synergistic inhibitors against E. coli and S. enterica serovar Typhimurium targeting a novel synthetic lethal pair, aldA and prpC. Frontiers in Microbiology, 2015, 6, 958.	3.5	8
65	Using Genome-scale Models to Predict Biological Capabilities. Cell, 2015, 161, 971-987.	28.9	590
66	Model-driven discovery of underground metabolic functions in <i>Escherichia coli</i>. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 929-934.	7.1	82
67	Systems biology definition of the core proteome of metabolism and expression is consistent with high-throughput data. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10810-10815.	7.1	42
68	Optimizing genome-scale network reconstructions. Nature Biotechnology, 2014, 32, 447-452.	17.5	185
69	Constraint-based models predict metabolic and associated cellular functions. Nature Reviews Genetics, 2014, 15, 107-120.	16.3	714
70	Predicting microbial growth. Science, 2014, 344, 1448-1449.	12.6	35
71	Genome-scale metabolic reconstructions of multiple <i>Escherichia coli</i> strains highlight strain-specific adaptations to nutritional environments. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20338-20343.	7.1	270
72	Wdr5 Mediates Self-Renewal and Reprogramming via the Embryonic Stem Cell Core Transcriptional Network. Cell, 2011, 145, 183-197.	28.9	521