# Jonathan M Monk

## List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4261033/publications.pdf

Version: 2024-02-01

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

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1 | Constraint-based models predict metabolic and associated cellular functions. Nature Reviews Genetics, 2014, 15, 107-120. | 16.3 | 714 |
| 2 | Using Genome-scale Models to Predict Biological Capabilities. Cell, 2015, 161, 971-987. | 28.9 | 590 |
| 3 | Wdr5 Mediates Self-Renewal and Reprogramming via the Embryonic Stem Cell Core Transcriptional Network. Cell, 2011, 145, 183-197. | 28.9 | 521 |
| 4 | iML1515, a knowledgebase that computes Escherichia coli traits. Nature Biotechnology, 2017, 35, 904-908. | 17.5 | 425 |
| 5 | MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276. | 17.5 | 314 |
| 6 | 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 |
| 7 | What Makes a Bacterial Species Pathogenic?:Comparative Genomic Analysis of the Genus Leptospira. PLoS Neglected Tropical Diseases, 2016, 10, e0004403. | 3.0 | 253 |
| 8 | 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 |
| 9 | Optimizing genome-scale network reconstructions. Nature Biotechnology, 2014, 32, 447-452. | 17.5 | 185 |
| 10 | 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 |
| 11 | Machine learning and structural analysis of Mycobacterium tuberculosis pan-genome identifies genetic signatures of antibiotic resistance. Nature Communications, 2018, 9, 4306. | 12.8 | 126 |
| 12 | 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 |
| 13 | Genome-scale metabolic reconstructions of multiple Salmonella strains reveal serovar-specific metabolic traits. Nature Communications, 2018, 9, 3771. | 12.8 | 109 |
| 14 | BOFdat: Generating biomass objective functions for genome-scale metabolic models from experimental data. PLoS Computational Biology, 2019, 15, e1006971. | 3.2 | 83 |
| 15 | 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 |
| 16 | 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 |
| 17 | Characterizing Strain Variation in Engineered E.Âcoli Using a Multi-Omics-Based Workflow. Cell Systems, 2016, 2, 335-346. | 6.2 | 73 |
| 18 | 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 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 19 | A workflow for generating multi-strain genome-scale metabolic models of prokaryotes. Nature Protocols, 2020, 15, 1-14. | 12.0 | 62 |
| 20 | A biochemically-interpretable machine learning classifier for microbial GWAS. Nature Communications, 2020, 11, 2580. | 12.8 | 51 |
| 21 | 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 |
| 22 | Systems biology of the structural proteome. BMC Systems Biology, 2016, 10, 26. | 3.0 | 46 |
| 23 | Impact of insertion sequences on convergent evolution of Shigella species. PLoS Genetics, 2020, 16, e1008931. | 3.5 | 43 |
| 24 | 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 |
| 25 | A computational knowledge-base elucidates the response of Staphylococcus aureus to different media types. PLoS Computational Biology, 2019, 15, e1006644. | 3.2 | 41 |
| 26 | iCN718, an Updated and Improved Genome-Scale Metabolic Network Reconstruction of Acinetobacter baumannii AYE. Frontiers in Genetics, 2018, 9, 121. | 2.3 | 40 |
| 27 | 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 |
| 28 | 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 |
| 29 | ssbio: a Python framework for structural systems biology. Bioinformatics, 2018, 34, 2155-2157. | 4.1 | 36 |
| 30 | Predicting microbial growth. Science, 2014, 344, 1448-1449. | 12.6 | 35 |
| 31 | 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 |
| 32 | Experimentally Validated Reconstruction and Analysis of a Genome-Scale Metabolic Model of an Anaerobic Neocallimastigomycota Fungus. MSystems, 2021, 6, . | 3.8 | 33 |
| 33 | 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 |
| 34 | 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 |
| 35 | Systems Biology and Pangenome of <i>Salmonella</i> O-Antigens. MBio, 2019, 10, . | 4.1 | 26 |
| 36 | Pangenome Analytics Reveal Two-Component Systems as Conserved Targets in ESKAPEE Pathogens. MSystems, 2021, 6, . | 3.8 | 24 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 37 | 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 |
| 38 | 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 |
| 39 | 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 |
| 40 | 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 |
| 41 | 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 |
| 42 | Genomeâ€scale metabolic modeling reveals key features of a minimal gene set. Molecular Systems Biology, 2021, 17, e10099. | 7.2 | 15 |
| 43 | Characterization of CA-MRSA TCH1516 exposed to nafcillin in bacteriological and physiological media. Scientific Data, 2019, 6, 43. | 5.3 | 14 |
| 44 | Predicting Antimicrobial Resistance and Associated Genomic Features from Whole-Genome Sequencing. Journal of Clinical Microbiology, 2019, 57, . | 3.9 | 14 |
| 45 | 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 |
| 46 | Reduced Production of Bacterial Membrane Vesicles Predicts Mortality in ST45/USA600 Methicillin-Resistant Staphylococcus aureus Bacteremia. Antibiotics, 2020, 9, 2. | 3.7 | 11 |
| 47 | 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 |
| 48 | A curated collection of <i>Klebsiella</i> metabolic models reveals variable substrate usage and gene essentiality. Genome Research, 2022, , . | 5.5 | 10 |
| 49 | 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 |
| 50 | 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 |
| 51 | Machine learning in computational biology to accelerate high-throughput protein expression. Bioinformatics, 2017, 33, 2487-2495. | 4.1 | 8 |
| 52 | Profiling the effect of nafcillin on HA-MRSA D712 using bacteriological and physiological media. Scientific Data, 2019, 6, 322. | 5.3 | 8 |
| 53 | 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 |
| 54 | Mathematical models to study the biology of pathogens and the infectious diseases they cause. IScience, 2022, 25, 104079. | 4.1 | 8 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 55 | Pangenome Flux Balance Analysis Toward Panphenomes. , 2020, , 219-232. | | 7 |
| 56 | 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 |
| 57 | 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 |
| 58 | Adaptations of Escherichia coli strains to oxidative stress are reflected in properties of their structural proteomes. BMC Bioinformatics, 2020, 21, 162. | 2.6 | 5 |
| 59 | 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 |
| 60 | Rapid resistance development to three antistaphylococcal therapies in antibiotic-tolerant staphylococcus aureus bacteremia. PLoS ONE, 2021, 16, e0258592. | 2.5 | 5 |
| 61 | 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 |
| 62 | 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 |
| 63 | 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 |
| 64 | Gapless, Unambiguous Genome Sequence for Escherichia coli C, a Workhorse of Industrial Biology. Microbiology Resource Announcements, 2018, 7, . | 0.6 | 3 |
| 65 | High-Quality Genome-Scale Models From Error-Prone, Long-Read Assemblies. Frontiers in Microbiology, 2020, 11, 596626. | 3.5 | 3 |
| 66 | 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 |
| 67 | 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 |
| 68 | 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 |
| 69 | Title is missing!. , 2020, 16, e1007608. | | 0 |
| 70 | Title is missing!. , 2020, 16, e1007608. | | 0 |
| 71 | Title is missing!. , 2020, 16, e1007608. | | 0 |
| 72 | Title is missing!. , 2020, 16, e1007608. | | 0 |