James T Yurkovich

List of Publications by Year
in descending order

51 papers	2,788 citations	304743 22 h-index	214800 47 g-index
71 all docs	71 docs citations	71 times ranked	3973 citing authors

#	Article	IF	Citations
1	Creation and analysis of biochemical constraint-based models using the COBRA Toolbox v.3.0. Nature Protocols, 2019, 14, 639-702.	12.0	833
2	Gut microbiome pattern reflects healthy ageing and predicts survival in humans. Nature Metabolism, 2021, 3, 274-286.	11.9	278
3	BiGG Models 2020: multi-strain genome-scale models and expansion across the phylogenetic tree. Nucleic Acids Research, 2020, 48, D402-D406.	14.5	130
4	Machine learning and structural analysis of Mycobacterium tuberculosis pan-genome identifies genetic signatures of antibiotic resistance. Nature Communications, 2018, 9, 4306.	12.8	126
5	Elucidating dynamic metabolic physiology through network integration of quantitative time-course metabolomics. Scientific Reports, 2017, 7, 46249.	3.3	121
6	Genome-scale metabolic reconstructions of multiple Salmonella strains reveal serovar-specific metabolic traits. Nature Communications, 2018, 9, 3771.	12.8	109
7	Metabolic Network Analysis Reveals Altered Bile Acid Synthesis and Metabolism in Alzheimer's Disease. Cell Reports Medicine, 2020, 1, 100138.	6.5	102
8	Global transcriptional regulatory network for <i>Escherichia coli</i> robustly connects gene expression to transcription factor activities. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 10286-10291.	7.1	89
9	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
10	Systematic discovery of uncharacterized transcription factors in Escherichia coli K-12 MG1655. Nucleic Acids Research, 2018, 46, 10682-10696.	14.5	65
11	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
12	Toward Community Standards and Software for Whole-Cell Modeling. IEEE Transactions on Biomedical Engineering, 2016, 63, 2007-2014.	4.2	51
13	Modeling the multi-scale mechanisms of macromolecular resource allocation. Current Opinion in Microbiology, 2018, 45, 8-15.	5.1	46
14	Quantitative time-course metabolomics in human red blood cells reveal the temperature dependence of human metabolic networks. Journal of Biological Chemistry, 2017, 292, 19556-19564.	3.4	45
15	Characterizing posttranslational modifications in prokaryotic metabolism using a multiscale workflow. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 11096-11101.	7.1	44
16	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
17	A systems approach to clinical oncology uses deep phenotyping to deliver personalized care. Nature Reviews Clinical Oncology, 2020, 17, 183-194.	27.6	41
18	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

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19	Community standards to facilitate development and address challenges in metabolic modeling. Molecular Systems Biology, 2020, 16, e9235.	7.2	37
20	Temperature-Dependent Estimation of Gibbs Energies Using an Updated Group-Contribution Method. Biophysical Journal, 2018, 114, 2691-2702.	0.5	36
21	Principles of proteome allocation are revealed using proteomic data and genome-scale models. Scientific Reports, 2016, 6, 36734.	3.3	31
22	Intricate Genetic Programs Controlling Dormancy in Mycobacterium tuberculosis. Cell Reports, 2020, 31, 107577.	6.4	31
23	Unraveling the functions of uncharacterized transcription factors in <i>Escherichia coli</i> using ChIP-exo. Nucleic Acids Research, 2021, 49, 9696-9710.	14.5	30
24	Quantitative -omic data empowers bottom-up systems biology. Current Opinion in Biotechnology, 2018, 51, 130-136.	6.6	28
25	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
26	Causal mutations from adaptive laboratory evolution are outlined by multiple scales of genome annotations and condition-specificity. BMC Genomics, 2020, 21, 514.	2.8	23
27	Synthesizing Systems Biology Knowledge from Omics Using Genomeâ€Scale Models. Proteomics, 2020, 20, e1900282.	2.2	22
28	MASSpy: Building, simulating, and visualizing dynamic biological models in Python using mass action kinetics. PLoS Computational Biology, 2021, 17, e1008208.	3.2	20
29	Solving Puzzles With Missing Pieces: The Power of Systems Biology. Proceedings of the IEEE, 2016, 104, 2-7.	21.3	17
30	The quantitative metabolome is shaped by abiotic constraints. Nature Communications, 2021, 12, 3178.	12.8	15
31	A Padawan Programmerâ€™s Guide to Developing Software Libraries. Cell Systems, 2017, 5, 431-437.	6.2	14
32	Blood Is a Window into Health and Disease. Clinical Chemistry, 2019, 65, 1204-1206.	3.2	13
33	Visualizing metabolic network dynamics through time-series metabolomic data. BMC Bioinformatics, 2020, 21, 130.	2.6	13
34	Poliovirus Vaccination Induces a Humoral Immune Response That Cross Reacts With SARS-CoV-2. Frontiers in Medicine, 2021, 8, 710010.	2.6	13
35	Biomarkers are used to predict quantitative metabolite concentration profiles in human red blood cells. PLoS Computational Biology, 2017, 13, e1005424.	3.2	12
36	Systems biology as an emerging paradigm in transfusion medicine. BMC Systems Biology, 2018, 12, 31.	3.0	12

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37	Current Status and Future Prospects of Genome-Scale Metabolic Modeling to Optimize the Use of Mesenchymal Stem Cells in Regenerative Medicine. Frontiers in Bioengineering and Biotechnology, 2020, 8, 239.	4.1	12
38	Genome-scale metabolic model of the rat liver predicts effects of diet restriction. Scientific Reports, 2019, 9, 9807.	3.3	10
39	Metabolic Network Analysis Reveals Altered Bile Acid Synthesis and Cholesterol Metabolism in Alzheimer's Disease. SSRN Electronic Journal, 0, , .	0.4	6
40	Is the kinetome conserved?. Molecular Systems Biology, 2022, 18, e10782.	7.2	6
41	Metabolic and Transcriptional Changes across Osteogenic Differentiation of Mesenchymal Stromal Cells. Bioengineering, 2021, 8, 208.	3.5	6
42	Analyzing Metabolic States of Adipogenic and Osteogenic Differentiation in Human Mesenchymal Stem Cells via Genome Scale Metabolic Model Reconstruction. Frontiers in Cell and Developmental Biology, 2021, 9, 642681.	3.7	5
43	<i>Escherichia coli</i> Data-Driven Strain Design Using Aggregated Adaptive Laboratory Evolution Mutational Data. ACS Synthetic Biology, 2021, 10, 3379-3395.	3.8	5
44	Electron impact on N2/CH4 mixtures in He droplets—probing chemistry in Titan's atmosphere. RSC Advances, 2012, 2, 10492.	3.6	4
45	Network-level allosteric effects are elucidated by detailing how ligand-binding events modulate utilization of catalytic potentials. PLoS Computational Biology, 2018, 14, e1006356.	3.2	3
46	Monocarbon cationic cluster yields from N2/CH4 mixtures embedded in He nanodroplets and their calculated binding energies. Journal of Chemical Physics, 2014, 140, 034316.	3.0	2
47	Utilizing biomarkers to forecast quantitative metabolite concentration profiles in human red blood cells. , 2017, , .		2
48	Metabolic Analysis of Red Blood Cells Stored at High Temperature. Blood, 2016, 128, 3848-3848.	1.4	0
49	Systemic Post-Translational Control of Bacterial Metabolism Regulates Adaptation in Dynamic Environments. SSRN Electronic Journal, 0, , .	0.4	0
50	ErythroDB: A multi‑omic visual knowledge base for the human red blood cell. FASEB Journal, 2018, 32, 863.1.	0.5	0
51	Toward a Proteome-Complete Computational Model of the Human Red Blood Cell. Blood, 2018, 132, 4888-4888.	1.4	0