

# James T Yurkovich

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Is the kinetome conserved?. <i>Molecular Systems Biology</i> , 2022, 18, e10782.	7.2	6
2	MASSpy: Building, simulating, and visualizing dynamic biological models in Python using mass action kinetics. <i>PLoS Computational Biology</i> , 2021, 17, e1008208.	3.2	20
3	Gut microbiome pattern reflects healthy ageing and predicts survival in humans. <i>Nature Metabolism</i> , 2021, 3, 274-286.	11.9	278
4	The quantitative metabolome is shaped by abiotic constraints. <i>Nature Communications</i> , 2021, 12, 3178.	12.8	15
5	Analyzing Metabolic States of Adipogenic and Osteogenic Differentiation in Human Mesenchymal Stem Cells via Genome Scale Metabolic Model Reconstruction. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 642681.	3.7	5
6	Unraveling the functions of uncharacterized transcription factors in <i>Escherichia coli</i> using CHIP-exo. <i>Nucleic Acids Research</i> , 2021, 49, 9696-9710.	14.5	30
7	Poliovirus Vaccination Induces a Humoral Immune Response That Cross Reacts With SARS-CoV-2. <i>Frontiers in Medicine</i> , 2021, 8, 710010.	2.6	13
8	<i>Escherichia coli</i> Data-Driven Strain Design Using Aggregated Adaptive Laboratory Evolution Mutational Data. <i>ACS Synthetic Biology</i> , 2021, 10, 3379-3395.	3.8	5
9	Metabolic and Transcriptional Changes across Osteogenic Differentiation of Mesenchymal Stromal Cells. <i>Bioengineering</i> , 2021, 8, 208.	3.5	6
10	BiGG Models 2020: multi-strain genome-scale models and expansion across the phylogenetic tree. <i>Nucleic Acids Research</i> , 2020, 48, D402-D406.	14.5	130
11	A systems approach to clinical oncology uses deep phenotyping to deliver personalized care. <i>Nature Reviews Clinical Oncology</i> , 2020, 17, 183-194.	27.6	41
12	Metabolic Network Analysis Reveals Altered Bile Acid Synthesis and Metabolism in Alzheimer's Disease. <i>Cell Reports Medicine</i> , 2020, 1, 100138.	6.5	102
13	Causal mutations from adaptive laboratory evolution are outlined by multiple scales of genome annotations and condition-specificity. <i>BMC Genomics</i> , 2020, 21, 514.	2.8	23
14	Intricate Genetic Programs Controlling Dormancy in <i>Mycobacterium tuberculosis</i> . <i>Cell Reports</i> , 2020, 31, 107577.	6.4	31
15	Visualizing metabolic network dynamics through time-series metabolomic data. <i>BMC Bioinformatics</i> , 2020, 21, 130.	2.6	13
16	Synthesizing Systems Biology Knowledge from Omics Using Genome-Scale Models. <i>Proteomics</i> , 2020, 20, e1900282.	2.2	22
17	Current Status and Future Prospects of Genome-Scale Metabolic Modeling to Optimize the Use of Mesenchymal Stem Cells in Regenerative Medicine. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 239.	4.1	12
18	Community standards to facilitate development and address challenges in metabolic modeling. <i>Molecular Systems Biology</i> , 2020, 16, e9235.	7.2	37

#	ARTICLE	IF	CITATIONS
19	Genome-scale metabolic model of the rat liver predicts effects of diet restriction. <i>Scientific Reports</i> , 2019, 9, 9807.	3.3	10
20	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.	7.1	79
21	Blood Is a Window into Health and Disease. <i>Clinical Chemistry</i> , 2019, 65, 1204-1206.	3.2	13
22	Creation and analysis of biochemical constraint-based models using the COBRA Toolbox v.3.0. <i>Nature Protocols</i> , 2019, 14, 639-702.	12.0	833
23	Modeling the multi-scale mechanisms of macromolecular resource allocation. <i>Current Opinion in Microbiology</i> , 2018, 45, 8-15.	5.1	46
24	Quantitative -omic data empowers bottom-up systems biology. <i>Current Opinion in Biotechnology</i> , 2018, 51, 130-136.	6.6	28
25	Updated and standardized genome-scale reconstruction of <i>Mycobacterium tuberculosis</i> H37Rv, iEK1011, simulates flux states indicative of physiological conditions. <i>BMC Systems Biology</i> , 2018, 12, 25.	3.0	63
26	Systems biology as an emerging paradigm in transfusion medicine. <i>BMC Systems Biology</i> , 2018, 12, 31.	3.0	12
27	Characterizing posttranslational modifications in prokaryotic metabolism using a multiscale workflow. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 11096-11101.	7.1	44
28	Network-level allosteric effects are elucidated by detailing how ligand-binding events modulate utilization of catalytic potentials. <i>PLoS Computational Biology</i> , 2018, 14, e1006356.	3.2	3
29	Machine learning and structural analysis of <i>Mycobacterium tuberculosis</i> pan-genome identifies genetic signatures of antibiotic resistance. <i>Nature Communications</i> , 2018, 9, 4306.	12.8	126
30	Genome-scale metabolic reconstructions of multiple <i>Salmonella</i> strains reveal serovar-specific metabolic traits. <i>Nature Communications</i> , 2018, 9, 3771.	12.8	109
31	<i>Escherichia coli</i> 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.	3.0	39
32	The <i>Staphylococcus aureus</i> Two-Component System AgrAC Displays Four Distinct Genomic Arrangements That Delineate Genomic Virulence Factor Signatures. <i>Frontiers in Microbiology</i> , 2018, 9, 1082.	3.5	26
33	Systematic discovery of uncharacterized transcription factors in <i>Escherichia coli</i> K-12 MG1655. <i>Nucleic Acids Research</i> , 2018, 46, 10682-10696.	14.5	65
34	Temperature-Dependent Estimation of Gibbs Energies Using an Updated Group-Contribution Method. <i>Biophysical Journal</i> , 2018, 114, 2691-2702.	0.5	36
35	ErythroDB: A multi-omic visual knowledge base for the human red blood cell. <i>FASEB Journal</i> , 2018, 32, 863.1.	0.5	0
36	Toward a Proteome-Complete Computational Model of the Human Red Blood Cell. <i>Blood</i> , 2018, 132, 4888-4888.	1.4	0

#	ARTICLE	IF	CITATIONS
37	Elucidating dynamic metabolic physiology through network integration of quantitative time-course metabolomics. <i>Scientific Reports</i> , 2017, 7, 46249.	3.3	121
38	Quantitative time-course metabolomics in human red blood cells reveal the temperature dependence of human metabolic networks. <i>Journal of Biological Chemistry</i> , 2017, 292, 19556-19564.	3.4	45
39	A Padawan Programmer's Guide to Developing Software Libraries. <i>Cell Systems</i> , 2017, 5, 431-437.	6.2	14
40	Global transcriptional regulatory network for <i>Escherichia coli</i> robustly connects gene expression to transcription factor activities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10286-10291.	7.1	89
41	Biomarkers are used to predict quantitative metabolite concentration profiles in human red blood cells. <i>PLoS Computational Biology</i> , 2017, 13, e1005424.	3.2	12
42	Utilizing biomarkers to forecast quantitative metabolite concentration profiles in human red blood cells. , 2017, , .		2
43	Toward Community Standards and Software for Whole-Cell Modeling. <i>IEEE Transactions on Biomedical Engineering</i> , 2016, 63, 2007-2014.	4.2	51
44	Principles of proteome allocation are revealed using proteomic data and genome-scale models. <i>Scientific Reports</i> , 2016, 6, 36734.	3.3	31
45	Solving Puzzles With Missing Pieces: The Power of Systems Biology. <i>Proceedings of the IEEE</i> , 2016, 104, 2-7.	21.3	17
46	Metabolic Analysis of Red Blood Cells Stored at High Temperature. <i>Blood</i> , 2016, 128, 3848-3848.	1.4	0
47	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, 10810-10815.	7.1	42
48	Monocarbon cationic cluster yields from N <sub>2</sub> /CH <sub>4</sub> mixtures embedded in He nanodroplets and their calculated binding energies. <i>Journal of Chemical Physics</i> , 2014, 140, 034316.	3.0	2
49	Electron impact on N <sub>2</sub> /CH <sub>4</sub> mixtures in He droplets—probing chemistry in Titan's atmosphere. <i>RSC Advances</i> , 2012, 2, 10492.	3.6	4
50	Metabolic Network Analysis Reveals Altered Bile Acid Synthesis and Cholesterol Metabolism in Alzheimer's Disease. <i>SSRN Electronic Journal</i> , 0, , .	0.4	6
51	Systemic Post-Translational Control of Bacterial Metabolism Regulates Adaptation in Dynamic Environments. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0