

# Laurence Yang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/796215/publications.pdf>

Version: 2024-02-01

46  
papers

1,751  
citations

304743

22  
h-index

330143

37  
g-index

56  
all docs

56  
docs citations

56  
times ranked

1967  
citing authors

#	ARTICLE	IF	CITATIONS
1	What differentiates a stress response from responsiveness in general?. Cell Systems, 2022, 13, 195-200.	6.2	0
2	Restoration of fitness lost due to dysregulation of the pyruvate dehydrogenase complex is triggered by ribosomal binding site modifications. Cell Reports, 2021, 35, 108961.	6.4	13
3	A dynamic metabolic map for diabetes. Nature Computational Science, 2021, 1, 309-310.	8.0	0
4	Recent advances in genome-scale modeling of proteome allocation. Current Opinion in Systems Biology, 2021, 26, 39-45.	2.6	2
5	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
6	OxyR Is a Convergent Target for Mutations Acquired during Adaptation to Oxidative Stress-Prone Metabolic States. Molecular Biology and Evolution, 2020, 37, 660-667.	8.9	52
7	Metabolic and genetic basis for auxotrophies in Gram-negative species. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 6264-6273.	7.1	39
8	Visualizing metabolic network dynamics through time-series metabolomic data. BMC Bioinformatics, 2020, 21, 130.	2.6	13
9	Synthesizing Systems Biology Knowledge from Omics Using Genome-Scale Models. Proteomics, 2020, 20, e1900282.	2.2	22
10	Adaptations of Escherichia coli strains to oxidative stress are reflected in properties of their structural proteomes. BMC Bioinformatics, 2020, 21, 162.	2.6	5
11	Genome-scale Modeling of Metabolism and Macromolecular Expression and Their Applications. Biotechnology and Bioprocess Engineering, 2020, 25, 931-943.	2.6	8
12	A biochemically-interpretable machine learning classifier for microbial GWAS. Nature Communications, 2020, 11, 2580.	12.8	51
13	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
14	Estimating Cellular Goals from High-Dimensional Biological Data. , 2019, , .		2
15	Pseudogene repair driven by selection pressure applied in experimental evolution. Nature Microbiology, 2019, 4, 386-389.	13.3	21
16	DynamicME: dynamic simulation and refinement of integrated models of metabolism and protein expression. BMC Systems Biology, 2019, 13, 2.	3.0	45
17	BOFdat: Generating biomass objective functions for genome-scale metabolic models from experimental data. PLoS Computational Biology, 2019, 15, e1006971.	3.2	83
18	Adaptive evolution reveals a tradeoff between growth rate and oxidative stress during naphthoquinone-based aerobic respiration. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25287-25292.	7.1	56

#	ARTICLE	IF	CITATIONS
19	Genome-scale model of metabolism and gene expression provides a multi-scale description of acid stress responses in <i>Escherichia coli</i> . <i>PLoS Computational Biology</i> , 2019, 15, e1007525.	3.2	37
20	The <i>Escherichia coli</i> transcriptome mostly consists of independently regulated modules. <i>Nature Communications</i> , 2019, 10, 5536.	12.8	161
21	Title is missing!. , 2019, 15, e1007525.		0
22	Title is missing!. , 2019, 15, e1007525.		0
23	Title is missing!. , 2019, 15, e1007525.		0
24	Title is missing!. , 2019, 15, e1007525.		0
25	Modeling the multi-scale mechanisms of macromolecular resource allocation. <i>Current Opinion in Microbiology</i> , 2018, 45, 8-15.	5.1	46
26	Basics of genome-scale metabolic modeling and applications on C1-utilization. <i>FEMS Microbiology Letters</i> , 2018, 365, .	1.8	11
27	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
28	COBRAME: A computational framework for genome-scale models of metabolism and gene expression. <i>PLoS Computational Biology</i> , 2018, 14, e1006302.	3.2	123
29	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
30	Reliable and efficient solution of genome-scale models of Metabolism and macromolecular Expression. <i>Scientific Reports</i> , 2017, 7, 40863.	3.3	30
31	Thermosensitivity of growth is determined by chaperone-mediated proteome reallocation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11548-11553.	7.1	79
32	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
33	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
34	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
35	Utilizing biomarkers to forecast quantitative metabolite concentration profiles in human red blood cells. , 2017, , .		2
36	solveME: fast and reliable solution of nonlinear ME models. <i>BMC Bioinformatics</i> , 2016, 17, 391.	2.6	39

#	ARTICLE	IF	CITATIONS
37	Principles of proteome allocation are revealed using proteomic data and genome-scale models. <i>Scientific Reports</i> , 2016, 6, 36734.	3.3	31
38	Characterizing Strain Variation in Engineered E.Âcoli Using a Multi-Omics-Based Workflow. <i>Cell Systems</i> , 2016, 2, 335-346.	6.2	73
39	Characterizing metabolic pathway diversification in the context of perturbation size. <i>Metabolic Engineering</i> , 2015, 28, 114-122.	7.0	20
40	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
41	Metabolic Model Refinement Using Phenotypic Microarray Data. <i>Methods in Molecular Biology</i> , 2013, 985, 47-59.	0.9	2
42	Dynamic strain scanning optimization: an efficient strain design strategy for balanced yield, titer, and productivity. DySScO strategy for strain design. <i>BMC Biotechnology</i> , 2013, 13, 8.	3.3	50
43	EMLiO: A fast algorithm for genome-scale strain design. <i>Metabolic Engineering</i> , 2011, 13, 272-281.	7.0	112
44	Rapid design of system-wide metabolic network modifications using iterative linear programming. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2010, 43, 391-396.	0.4	1
45	Thermodynamic analysis of regulation in metabolic networks using constraint-based modeling. <i>BMC Research Notes</i> , 2010, 3, 125.	1.4	13
46	A bilevel optimization algorithm to identify enzymatic capacity constraints in metabolic networks. <i>Computers and Chemical Engineering</i> , 2008, 32, 2072-2085.	3.8	15