

Laurence Yang

List of Publications by Year in descending order

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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	The Escherichia coli transcriptome mostly consists of independently regulated modules. Nature Communications, 2019, 10, 5536.	12.8	161
2	Machine learning and structural analysis of Mycobacterium tuberculosis pan-genome identifies genetic signatures of antibiotic resistance. Nature Communications, 2018, 9, 4306.	12.8	126
3	COBRAme: A computational framework for genome-scale models of metabolism and gene expression. PLoS Computational Biology, 2018, 14, e1006302.	3.2	123
4	EMILIO: A fast algorithm for genome-scale strain design. Metabolic Engineering, 2011, 13, 272-281.	7.0	112
5	Global transcriptional regulatory network for Escherichia coli 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
6	BOFdat: Generating biomass objective functions for genome-scale metabolic models from experimental data. PLoS Computational Biology, 2019, 15, e1006971.	3.2	83
7	Thermosensitivity of growth is determined by chaperone-mediated proteome reallocation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 11548-11553.	7.1	79
8	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
9	Characterizing Strain Variation in Engineered E. coli Using a Multi-Omics-Based Workflow. Cell Systems, 2016, 2, 335-346.	6.2	73
10	Systematic discovery of uncharacterized transcription factors in Escherichia coli K-12 MG1655. Nucleic Acids Research, 2018, 46, 10682-10696.	14.5	65
11	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
12	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
13	A biochemically-interpretable machine learning classifier for microbial GWAS. Nature Communications, 2020, 11, 2580.	12.8	51
14	Dynamic strain scanning optimization: an efficient strain design strategy for balanced yield, titer, and productivity. DySScO strategy for strain design. BMC Biotechnology, 2013, 13, 8.	3.3	50
15	Modeling the multi-scale mechanisms of macromolecular resource allocation. Current Opinion in Microbiology, 2018, 45, 8-15.	5.1	46
16	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
17	DynamicME: dynamic simulation and refinement of integrated models of metabolism and protein expression. BMC Systems Biology, 2019, 13, 2.	3.0	45
18	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

#	ARTICLE	IF	CITATIONS
19	solveME: fast and reliable solution of nonlinear ME models. BMC Bioinformatics, 2016, 17, 391.	2.6	39
20	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
21	Genome-scale model of metabolism and gene expression provides a multi-scale description of acid stress responses in Escherichia coli. PLoS Computational Biology, 2019, 15, e1007525.	3.2	37
22	Principles of proteome allocation are revealed using proteomic data and genome-scale models. Scientific Reports, 2016, 6, 36734.	3.3	31
23	Reliable and efficient solution of genome-scale models of Metabolism and macromolecular Expression. Scientific Reports, 2017, 7, 40863.	3.3	30
24	Synthesizing Systems Biology Knowledge from Omics Using Genome-scale Models. Proteomics, 2020, 20, e1900282.	2.2	22
25	Pseudogene repair driven by selection pressure applied in experimental evolution. Nature Microbiology, 2019, 4, 386-389.	13.3	21
26	Characterizing metabolic pathway diversification in the context of perturbation size. Metabolic Engineering, 2015, 28, 114-122.	7.0	20
27	A bilevel optimization algorithm to identify enzymatic capacity constraints in metabolic networks. Computers and Chemical Engineering, 2008, 32, 2072-2085.	3.8	15
28	Thermodynamic analysis of regulation in metabolic networks using constraint-based modeling. BMC Research Notes, 2010, 3, 125.	1.4	13
29	Visualizing metabolic network dynamics through time-series metabolomic data. BMC Bioinformatics, 2020, 21, 130.	2.6	13
30	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
31	Biomarkers are used to predict quantitative metabolite concentration profiles in human red blood cells. PLoS Computational Biology, 2017, 13, e1005424.	3.2	12
32	Basics of genome-scale metabolic modeling and applications on C1-utilization. FEMS Microbiology Letters, 2018, 365, .	1.8	11
33	Genome-scale Modeling of Metabolism and Macromolecular Expression and Their Applications. Biotechnology and Bioprocess Engineering, 2020, 25, 931-943.	2.6	8
34	Adaptations of Escherichia coli strains to oxidative stress are reflected in properties of their structural proteomes. BMC Bioinformatics, 2020, 21, 162.	2.6	5
35	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
36	Metabolic Model Refinement Using Phenotypic Microarray Data. Methods in Molecular Biology, 2013, 985, 47-59.	0.9	2

#	ARTICLE	IF	CITATIONS
37	Utilizing biomarkers to forecast quantitative metabolite concentration profiles in human red blood cells. , 2017, , .		2
38	Estimating Cellular Goals from High-Dimensional Biological Data. , 2019, , .		2
39	Recent advances in genome-scale modeling of proteome allocation. Current Opinion in Systems Biology, 2021, 26, 39-45.	2.6	2
40	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
41	A dynamic metabolic map for diabetes. Nature Computational Science, 2021, 1, 309-310.	8.0	0
42	What differentiates a stress response from responsiveness in general?. Cell Systems, 2022, 13, 195-200.	6.2	0
43	Title is missing!. , 2019, 15, e1007525.		0
44	Title is missing!. , 2019, 15, e1007525.		0
45	Title is missing!. , 2019, 15, e1007525.		0
46	Title is missing!. , 2019, 15, e1007525.		0