

Jason Lloyd-Price

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2448074/publications.pdf>

Version: 2024-02-01

47
papers

5,655
citations

331538

21
h-index

265120

42
g-index

49
all docs

49
docs citations

49
times ranked

8987
citing authors

#	ARTICLE	IF	CITATIONS
1	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. <i>Nature</i> , 2019, 569, 655-662.	13.7	1,638
2	The healthy human microbiome. <i>Genome Medicine</i> , 2016, 8, 51.	3.6	1,214
3	Strains, functions and dynamics in the expanded Human Microbiome Project. <i>Nature</i> , 2017, 550, 61-66.	13.7	929
4	Dynamics of metatranscription in the inflammatory bowel disease gut microbiome. <i>Nature Microbiology</i> , 2018, 3, 337-346.	5.9	408
5	Obese Individuals with and without Type 2 Diabetes Show Different Gut Microbial Functional Capacity and Composition. <i>Cell Host and Microbe</i> , 2019, 26, 252-264.e10.	5.1	274
6	Stability of the human faecal microbiome in a cohort of adult men. <i>Nature Microbiology</i> , 2018, 3, 347-355.	5.9	203
7	Metatranscriptome of human faecal microbial communities in a cohort of adult men. <i>Nature Microbiology</i> , 2018, 3, 356-366.	5.9	168
8	Association Between Sulfur-Metabolizing Bacterial Communities in Stool and Risk of Distal Colorectal Cancer in Men. <i>Gastroenterology</i> , 2020, 158, 1313-1325.	0.6	88
9	Mutual information in random Boolean models of regulatory networks. <i>Physical Review E</i> , 2008, 77, 011901.	0.8	77
10	SGN Sim, a Stochastic Genetic Networks Simulator. <i>Bioinformatics</i> , 2007, 23, 777-779.	1.8	60
11	Growth effects of N-acylethanolamines on gut bacteria reflect altered bacterial abundances in inflammatory bowel disease. <i>Nature Microbiology</i> , 2020, 5, 486-497.	5.9	59
12	Dynamics of transcription driven by the tetA promoter, one event at a time, in live <i>Escherichia coli</i> cells. <i>Nucleic Acids Research</i> , 2012, 40, 8472-8483.	6.5	55
13	Structure of the Mucosal and Stool Microbiome in Lynch Syndrome. <i>Cell Host and Microbe</i> , 2020, 27, 585-600.e4.	5.1	40
14	Dissecting the stochastic transcription initiation process in live <i>Escherichia coli</i> . <i>DNA Research</i> , 2016, 23, 203-214.	1.5	36
15	Temperature-Dependent Model of Multi-step Transcription Initiation in <i>Escherichia coli</i> Based on Live Single-Cell Measurements. <i>PLoS Computational Biology</i> , 2016, 12, e1005174.	1.5	33
16	In vivo kinetics of transcription initiation of the <i>lac</i> promoter in <i>Escherichia coli</i> . Evidence for a sequential mechanism with two rate-limiting steps. <i>BMC Systems Biology</i> , 2011, 5, 149.	3.0	32
17	Stochastic sequence-level model of coupled transcription and translation in prokaryotes. <i>BMC Bioinformatics</i> , 2011, 12, 121.	1.2	29
18	In Vivo Kinetics of Segregation and Polar Retention of MS2-GFP-RNA Complexes in <i>Escherichia coli</i> . <i>Biophysical Journal</i> , 2014, 106, 1928-1937.	0.2	28

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19	SCNS2: a compartmentalized stochastic chemical kinetics simulator for dynamic cell populations. <i>Bioinformatics</i> , 2012, 28, 3004-3005.	1.8	27
20	In vivo single-molecule kinetics of activation and subsequent activity of the arabinose promoter. <i>Nucleic Acids Research</i> , 2013, 41, 6544-6552.	6.5	26
21	Asymmetric Disposal of Individual Protein Aggregates in <i>Escherichia coli</i> , One Aggregate at a Time. <i>Journal of Bacteriology</i> , 2012, 194, 1747-1752.	1.0	24
22	Increased cytoplasm viscosity hampers aggregate polar segregation in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2016, 99, 686-699.	1.2	21
23	Effects of the promoter open complex formation on gene expression dynamics. <i>Physical Review E</i> , 2010, 81, 011912.	0.8	20
24	Regulation of mean and noise of the in vivo kinetics of transcription under the control of the <i>lac/ara</i> promoter. <i>FEBS Letters</i> , 2012, 586, 3870-3875.	1.3	20
25	Dynamics of small genetic circuits subject to stochastic partitioning in cell division. <i>Journal of Theoretical Biology</i> , 2014, 356, 11-19.	0.8	20
26	High-sensitivity pattern discovery in large, paired multiomic datasets. <i>Bioinformatics</i> , 2022, 38, i378-i385.	1.8	18
27	Probabilistic RNA partitioning generates transient increases in the normalized variance of RNA numbers in synchronized populations of <i>Escherichia coli</i> . <i>Molecular BioSystems</i> , 2012, 8, 565-571.	2.9	16
28	Information propagation within the Genetic Network of <i>Saccharomyces cerevisiae</i> . <i>BMC Systems Biology</i> , 2010, 4, 143.	3.0	12
29	Robustness and Information Propagation in Attractors of Random Boolean Networks. <i>PLoS ONE</i> , 2012, 7, e42018.	1.1	12
30	Robustness of the division symmetry in <i>Escherichia coli</i> and functional consequences of symmetry breaking. <i>Physical Biology</i> , 2014, 11, 066005.	0.8	10
31	Dynamic Agent-Based Model of Hand-Preference Behavior Patterns in the Mouse. <i>Adaptive Behavior</i> , 2010, 18, 116-131.	1.1	9
32	sgnesR: An R package for simulating gene expression data from an underlying real gene network structure considering delay parameters. <i>BMC Bioinformatics</i> , 2017, 18, 325.	1.2	9
33	CellLine, a stochastic cell lineage simulator. <i>Bioinformatics</i> , 2007, 23, 3409-3411.	1.8	8
34	Quantifying local structure effects in network dynamics. <i>Physical Review E</i> , 2008, 78, 056108.	0.8	6
35	Dynamics of a genetic toggle switch at the nucleotide and codon levels. <i>Physical Review E</i> , 2011, 84, 031903.	0.8	4
36	In silico analysis of division times of <i>Escherichia coli</i> populations as a function of the partitioning scheme of non-functional proteins. <i>In Silico Biology</i> , 2015, 12, 9-21.	0.4	4

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37	Chromosome and plasmid-borne PLacO3O1 promoters differ in sensitivity to critically low temperatures. <i>Scientific Reports</i> , 2019, 9, 4486.	1.6	4
38	Diversity of temporal correlations between genes in models of noisy and noiseless gene networks. <i>BioSystems</i> , 2011, 104, 136-144.	0.9	3
39	Effects of gene length on the dynamics of gene expression. <i>Computational Biology and Chemistry</i> , 2012, 41, 1-9.	1.1	3
40	Bistability in a stochastic RNA-mediated gene network. <i>Physical Review E</i> , 2013, 88, 032714.	0.8	2
41	Predictability and randomness of paw choices are critical elements in the behavioural plasticity of mouse paw preference. <i>Animal Behaviour</i> , 2014, 98, 167-176.	0.8	2
42	The transcription factor network of <i>E. coli</i> steers global responses to shifts in RNAP concentration. <i>Nucleic Acids Research</i> , 0, , .	6.5	2
43	iCellFusion. <i>Advances in Bioinformatics and Biomedical Engineering Book Series</i> , 2016, , 71-99.	0.2	1
44	Parameter Estimation and Tuning of Firefly Luciferase Pathway Model. , 2007, , .		0
45	Information Propagation in the Long-Term Behavior of Gene Regulatory Networks. <i>Intelligent Systems Reference Library</i> , 2011, , 195-217.	1.0	0
46	Modelling Polar Retention of Complexes in Escherichia coli. <i>Lecture Notes in Computer Science</i> , 2014, , 239-243.	1.0	0
47	iCellFusion. , 2017, , 806-834.		0