Jason Lloyd-Price

List of Publications by Year
in descending order

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		331538	265120
47	5,655	21	42
papers	citations	h-index	g-index

49	49	49	8987
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	High-sensitivity pattern discovery in large, paired multiomic datasets. Bioinformatics, 2022, 38, i378-i385.	1.8	18
2	Growth effects of N-acylethanolamines on gut bacteria reflect altered bacterial abundances in inflammatory bowel disease. Nature Microbiology, 2020, 5, 486-497.	5.9	59
3	Association Between Sulfur-Metabolizing Bacterial Communities in Stool and Risk of Distal Colorectal Cancer in Men. Gastroenterology, 2020, 158, 1313-1325.	0.6	88
4	Structure of the Mucosal and Stool Microbiome in Lynch Syndrome. Cell Host and Microbe, 2020, 27, 585-600.e4.	5.1	40
5	Obese Individuals with and without Type 2 Diabetes Show Different Gut Microbial Functional Capacity and Composition. Cell Host and Microbe, 2019, 26, 252-264.e10.	5.1	274
6	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. Nature, 2019, 569, 655-662.	13.7	1,638
7	Chromosome and plasmid-borne PLacO3O1 promoters differ in sensitivity to critically low temperatures. Scientific Reports, 2019, 9, 4486.	1.6	4
8	Metatranscriptome of human faecal microbial communities in a cohort of adult men. Nature Microbiology, 2018, 3, 356-366.	5.9	168
9	Stability of the human faecal microbiome in a cohort of adult men. Nature Microbiology, 2018, 3, 347-355.	5.9	203
10	Dynamics of metatranscription in the inflammatory bowel disease gut microbiome. Nature Microbiology, 2018, 3, 337-346.	5.9	408
11	Strains, functions and dynamics in the expanded Human Microbiome Project. Nature, 2017, 550, 61-66.	13.7	929
12	sgnesR: An R package for simulating gene expression data from an underlying real gene network structure considering delay parameters. BMC Bioinformatics, 2017, 18, 325.	1.2	9
13	iCellFusion. , 2017, , 806-834.		0
14	Dissecting the stochastic transcription initiation process in liveEscherichia coli. DNA Research, 2016, 23, 203-214.	1.5	36
15	The healthy human microbiome. Genome Medicine, 2016, 8, 51.	3.6	1,214
16	Increased cytoplasm viscosity hampers aggregate polar segregation in <i>Escherichia coli</i>. Molecular Microbiology, 2016, 99, 686-699.	1.2	21
17	Temperature-Dependent Model of Multi-step Transcription Initiation in Escherichia coli Based on Live Single-Cell Measurements. PLoS Computational Biology, 2016, 12, e1005174.	1.5	33
18	iCellFusion. Advances in Bioinformatics and Biomedical Engineering Book Series, 2016, , 71-99.	0.2	1

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19	In silico analysis of division times of Escherichia coli populations as a function of the partitioning scheme of non-functional proteins. In Silico Biology, 2015, 12, 9-21.	0.4	4
20	Robustness of the division symmetry in<i>Escherichia coli</i>and functional consequences of symmetry breaking. Physical Biology, 2014, 11, 066005.	0.8	10
21	Predictability and randomness of paw choices are critical elements in the behavioural plasticity of mouse paw preference. Animal Behaviour, 2014, 98, 167-176.	0.8	2
22	Dynamics of small genetic circuits subject to stochastic partitioning in cell division. Journal of Theoretical Biology, 2014, 356, 11-19.	0.8	20
23	InÂVivo Kinetics of Segregation and Polar Retention of MS2-GFP-RNA Complexes in Escherichia coli. Biophysical Journal, 2014, 106, 1928-1937.	0.2	28
24	Modelling Polar Retention of Complexes in Escherichia coli. Lecture Notes in Computer Science, 2014, , 239-243.	1.0	0
25	In vivo single-molecule kinetics of activation and subsequent activity of the arabinose promoter. Nucleic Acids Research, 2013, 41, 6544-6552.	6.5	26
26	Bistability in a stochastic RNA-mediated gene network. Physical Review E, 2013, 88, 032714.	0.8	2
27	SGNS2: a compartmentalized stochastic chemical kinetics simulator for dynamic cell populations. Bioinformatics, 2012, 28, 3004-3005.	1.8	27
28	Dynamics of transcription driven by the tetA promoter, one event at a time, in live Escherichia coli cells. Nucleic Acids Research, 2012, 40, 8472-8483.	6.5	55
29	Asymmetric Disposal of Individual Protein Aggregates in Escherichia coli, One Aggregate at a Time. Journal of Bacteriology, 2012, 194, 1747-1752.	1.0	24
30	Effects of gene length on the dynamics of gene expression. Computational Biology and Chemistry, 2012, 41, 1-9.	1.1	3
31	Regulation of mean and noise of the in vivo kinetics of transcription under the control of the <i>lac/araâ€•1</i> promoter. FEBS Letters, 2012, 586, 3870-3875.	1.3	20
32	Probabilistic RNA partitioning generates transient increases in the normalized variance of RNA numbers in synchronized populations of Escherichia coli. Molecular BioSystems, 2012, 8, 565-571.	2.9	16
33	Robustness and Information Propagation in Attractors of Random Boolean Networks. PLoS ONE, 2012, 7, e42018.	1.1	12
34	In vivo kinetics of transcription initiation of the lar promoter in Escherichia coli. Evidence for a sequential mechanism with two rate-limiting steps. BMC Systems Biology, 2011, 5, 149.	3.0	32
35	Stochastic sequence-level model of coupled transcription and translation in prokaryotes. BMC Bioinformatics, 2011, 12, 121.	1.2	29
36	Diversity of temporal correlations between genes in models of noisy and noiseless gene networks. BioSystems, 2011, 104, 136-144.	0.9	3

#	ARTICLE	IF	CITATIONS
37	Dynamics of a genetic toggle switch at the nucleotide and codon levels. Physical Review E, 2011, 84, 031903.	0.8	4
38	Information Propagation in the Long-Term Behavior of Gene Regulatory Networks. Intelligent Systems Reference Library, 2011, , 195-217.	1.0	0
39	Information propagation within the Genetic Network of Saccharomyces cerevisiae. BMC Systems Biology, 2010, 4, 143.	3.0	12
40	Dynamic Agent-Based Model of Hand-Preference Behavior Patterns in the Mouse. Adaptive Behavior, 2010, 18, 116-131.	1.1	9
41	Effects of the promoter open complex formation on gene expression dynamics. Physical Review E, 2010, 81, 011912.	0.8	20
42	Quantifying local structure effects in network dynamics. Physical Review E, 2008, 78, 056108.	0.8	6
43	Mutual information in random Boolean models of regulatory networks. Physical Review E, 2008, 77, 011901.	0.8	77
44	SGN Sim, a Stochastic Genetic Networks Simulator. Bioinformatics, 2007, 23, 777-779.	1.8	60
45	CellLine, a stochastic cell lineage simulator. Bioinformatics, 2007, 23, 3409-3411.	1.8	8
46	Parameter Estimation and Tuning of Firefly Luciferase Pathway Model. , 2007, , .		0
47	The transcription factor network of <i>E. coli</i> steers global responses to shifts in RNAP concentration. Nucleic Acids Research, 0, , .	6.5	2