

Jeremy S Edwards

List of Publications by Year in descending order

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77
papers

6,988
citations

159358

30
h-index

85405

71
g-index

81
all docs

81
docs citations

81
times ranked

6097
citing authors

#	ARTICLE	IF	CITATIONS
1	In silico predictions of Escherichia coli metabolic capabilities are consistent with experimental data. Nature Biotechnology, 2001, 19, 125-130.	9.4	877
2	Dynamic Flux Balance Analysis of Diauxic Growth in Escherichia coli. Biophysical Journal, 2002, 83, 1331-1340.	0.2	806
3	Escherichia coli K-12 undergoes adaptive evolution to achieve in silico predicted optimal growth. Nature, 2002, 420, 186-189.	13.7	797
4	Advances in flux balance analysis. Current Opinion in Biotechnology, 2003, 14, 491-496.	3.3	694
5	Metabolic modelling of microbes: the flux-balance approach. Environmental Microbiology, 2002, 4, 133-140.	1.8	335
6	Systems Properties of the Haemophilus influenzae Rd Metabolic Genotype. Journal of Biological Chemistry, 1999, 274, 17410-17416.	1.6	333
7	Genome-Scale Metabolic Model of Helicobacter pylori 26695. Journal of Bacteriology, 2002, 184, 4582-4593.	1.0	317
8	Metabolic modeling of microbial strains in silico. Trends in Biochemical Sciences, 2001, 26, 179-186.	3.7	291
9	Minke whale genome and aquatic adaptation in cetaceans. Nature Genetics, 2014, 46, 88-92.	9.4	227
10	Metabolic flux balance analysis and the in silico analysis of Escherichia coli K-12 gene deletions. BMC Bioinformatics, 2000, 1, 1.	1.2	221
11	Robustness Analysis of the Escherichia coli Metabolic Network. Biotechnology Progress, 2000, 16, 927-939.	1.3	179
12	Toward Metabolic Phenomics: Analysis of Genomic Data Using Flux Balances. Biotechnology Progress, 1999, 15, 288-295.	1.3	166
13	Characterizing the metabolic phenotype: A phenotype phase plane analysis. Biotechnology and Bioengineering, 2002, 77, 27-36.	1.7	166
14	Selection analyses of insertional mutants using subgenomic-resolution arrays. Nature Biotechnology, 2001, 19, 1060-1065.	9.4	140
15	The Genome-Scale Metabolic Extreme Pathway Structure in Haemophilus influenzae Shows Significant Network Redundancy. Journal of Theoretical Biology, 2002, 215, 67-82.	0.8	115
16	Comparison of carnivore, omnivore, and herbivore mammalian genomes with a new leopard assembly. Genome Biology, 2016, 17, 211.	3.8	101
17	Korean Genome Project: 1094 Korean personal genomes with clinical information. Science Advances, 2020, 6, eaaz7835.	4.7	75
18	Estimating optimal profiles of genetic alterations using constraint-based models. Biotechnology and Bioengineering, 2005, 89, 243-251.	1.7	72

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19	Description and Analysis of Metabolic Connectivity and Dynamics in the Human Red Blood Cell. <i>Biophysical Journal</i> , 2002, 83, 646-662.	0.2	63
20	An ethnically relevant consensus Korean reference genome is a step towards personal reference genomes. <i>Nature Communications</i> , 2016, 7, 13637.	5.8	58
21	Time accelerated Monte Carlo simulations of biological networks using the binomial Å-leap method. <i>Bioinformatics</i> , 2005, 21, 2136-2137.	1.8	56
22	Predicting chemical impacts on vertebrate endocrine systems. <i>Environmental Toxicology and Chemistry</i> , 2011, 30, 39-51.	2.2	44
23	Characterization of mutations and loss of heterozygosity of p53 and K-ras2 in pancreatic cancer cell lines by immobilized polymerase chain reaction. <i>BMC Biotechnology</i> , 2003, 3, 11.	1.7	42
24	The first whole genome and transcriptome of the cinereous vulture reveals adaptation in the gastric and immune defense systems and possible convergent evolution between the Old and New World vultures. <i>Genome Biology</i> , 2015, 16, 215.	3.8	41
25	Spatial modeling of dimerization reaction dynamics in the plasma membrane: Monte Carlo vs. continuum differential equations. <i>Biophysical Chemistry</i> , 2006, 121, 194-208.	1.5	40
26	MAPK Cascade Possesses Decoupled Controllability of Signal Amplification and Duration. <i>Biophysical Journal</i> , 2004, 87, L01-L02.	0.2	39
27	KoVariome: Korean National Standard Reference Variome database of whole genomes with comprehensive SNV, indel, CNV, and SV analyses. <i>Scientific Reports</i> , 2018, 8, 5677.	1.6	39
28	The genome of the giant Nomura's jellyfish sheds light on the early evolution of active predation. <i>BMC Biology</i> , 2019, 17, 28.	1.7	38
29	Computational modeling reveals molecular details of epidermal growth factor binding. <i>BMC Cell Biology</i> , 2005, 6, 41.	3.0	35
30	Quantitative understanding of cell signaling: the importance of membrane organization. <i>Current Opinion in Biotechnology</i> , 2010, 21, 677-682.	3.3	35
31	Heterogeneities in EGF receptor density at the cell surface can lead to concave up scatchard plot of EGF binding. <i>FEBS Letters</i> , 2005, 579, 3043-3047.	1.3	33
32	The whale shark genome reveals how genomic and physiological properties scale with body size. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20662-20671.	3.3	32
33	Microscopic Simulation of Membrane Molecule Diffusion on Corralled Membrane Surfaces. <i>Biophysical Journal</i> , 2008, 94, 1551-1564.	0.2	26
34	Advancing Pan-cancer Gene Expression Survival Analysis by Inclusion of Non-coding RNA. <i>RNA Biology</i> , 2020, 17, 1666-1673.	1.5	26
35	Coupled Stochastic Spatial and Non-Spatial Simulations of ErbB1 Signaling Pathways Demonstrate the Importance of Spatial Organization in Signal Transduction. <i>PLoS ONE</i> , 2009, 4, e6316.	1.1	26
36	Digital quantitative measurements of gene expression. <i>Biotechnology and Bioengineering</i> , 2004, 86, 117-124.	1.7	22

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37	Mathematical Simulation of Membrane Protein Clustering for Efficient Signal Transduction. <i>Annals of Biomedical Engineering</i> , 2012, 40, 2307-2318.	1.3	22
38	Orchestration of ErbB3 signaling through heterointeractions and homointeractions. <i>Molecular Biology of the Cell</i> , 2015, 26, 4109-4123.	0.9	22
39	Detecting Changes in the Relative Expression of KRAS2 Splice Variants Using Polymerase Colonies. <i>Biotechnology Progress</i> , 2004, 20, 1836-1839.	1.3	21
40	Detection of allelic variations of human gene expression by polymerase colonies. <i>BMC Genetics</i> , 2004, 5, 3.	2.7	21
41	Monte Carlo simulations of plasma membrane corral-induced EGFR clustering. <i>Journal of Biotechnology</i> , 2011, 151, 261-270.	1.9	19
42	Parallel competition analysis of <i>Saccharomyces cerevisiae</i> strains differing by a single base using polymerase colonies. <i>Nucleic Acids Research</i> , 2003, 31, 84e-84.	6.5	17
43	Autoregulation of regulatory proteins is key for dynamic operation of GALswitch in <i>Saccharomyces cerevisiae</i> . <i>FEBS Letters</i> , 2004, 576, 119-126.	1.3	16
44	Robust global sensitivity in multiple enzyme cascade system explains how the downstream cascade structure may remain unaffected by cross-talk. <i>FEBS Letters</i> , 2004, 558, 79-84.	1.3	15
45	Dynamic Transition States of ErbB1 Phosphorylation Predicted by Spatial Stochastic Modeling. <i>Biophysical Journal</i> , 2013, 105, 1533-1543.	0.2	15
46	Enzymatic Synthesis of Designer DNA Using Cyclic Reversible Termination and a Universal Template. <i>ACS Synthetic Biology</i> , 2020, 9, 283-293.	1.9	15
47	Single Molecule Analysis of <i>c-myc</i> Alternative Splicing Reveals Novel Classifiers for Precursor B-ALL. <i>PLoS ONE</i> , 2011, 6, e22880.	1.1	15
48	ChIP-Seq analysis of the adult male mouse brain after developmental exposure to arsenic. <i>Data in Brief</i> , 2015, 5, 248-254.	0.5	14
49	Using DNA microarray data to understand the ionizing radiation resistance of <i>Deinococcus radiodurans</i> . <i>Trends in Biotechnology</i> , 2003, 21, 381-382.	4.9	13
50	Parallel analysis of mutant human glucose 6-phosphate dehydrogenase in yeast using PCR colonies. <i>Biotechnology and Bioengineering</i> , 2005, 92, 519-531.	1.7	12
51	Analytical Solution of Steady-State Equations for Chemical Reaction Networks with Bilinear Rate Laws. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 957-969.	1.9	11
52	Sequential super-resolution imaging using DNA strand displacement. <i>PLoS ONE</i> , 2018, 13, e0203291.	1.1	11
53	Raptor genomes reveal evolutionary signatures of predatory and nocturnal lifestyles. <i>Genome Biology</i> , 2019, 20, 181.	3.8	11
54	Highly Accurate Chip-Based Resequencing of SARS-CoV-2 Clinical Samples. <i>Langmuir</i> , 2021, 37, 4763-4771.	1.6	10

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55	MicroRNA Analysis of Human Stroke Brain Tissue Resected during Decompressive Craniectomy/Stroke-Ectomy Surgery. <i>Genes</i> , 2021, 12, 1860.	1.0	9
56	A probabilistic framework for microarray data analysis: Fundamental probability models and statistical inference. <i>Journal of Theoretical Biology</i> , 2010, 264, 211-222.	0.8	8
57	Next-generation sequencing library construction on a surface. <i>BMC Genomics</i> , 2018, 19, 416.	1.2	8
58	A highly sensitive ISFET using pH-to-current conversion for real-time DNA sequencing. , 2014, , .		7
59	Starvation-Associated Genome Restructuring Can Lead to Reproductive Isolation in Yeast. <i>PLoS ONE</i> , 2013, 8, e66414.	1.1	6
60	Effect of Spatial Inhomogeneities on the Membrane Surface on Receptor Dimerization and Signal Initiation. <i>Frontiers in Cell and Developmental Biology</i> , 2016, 4, 81.	1.8	6
61	Welfare Genome Project: A Participatory Korean Personal Genome Project With Free Health Check-Up and Genetic Report Followed by Counseling. <i>Frontiers in Genetics</i> , 2021, 12, 633731.	1.1	6
62	Whole Genome Analysis of the Red-Crowned Crane Provides Insight into Avian Longevity. <i>Molecules and Cells</i> , 2020, 43, 86-95.	1.0	6
63	Assaying gene function by growth competition experiment. <i>Metabolic Engineering</i> , 2004, 6, 212-219.	3.6	5
64	RecA mediated initial alignment of homologous DNA molecules displays apparent first order kinetics with little effect of heterology. <i>DNA Repair</i> , 2004, 3, 61-65.	1.3	5
65	Integrated statistical and pathway approach to next-generation sequencing analysis: a family-based study of hypertension. <i>BMC Proceedings</i> , 2014, 8, S104.	1.8	5
66	An integrated mechanistic model for transcription-coupled nucleotide excision repair. <i>DNA Repair</i> , 2004, 3, 343-348.	1.3	4
67	Parallel analysis of tetramerization domain mutants of the human p53 protein using PCR colonies. <i>Genomic Medicine</i> , 2007, 1, 113-124.	0.6	4
68	[INVITED] Electrophoretic plasmonic nanopore biochip genome sequencer. <i>Optics and Laser Technology</i> , 2019, 109, 199-211.	2.2	4
69	Detecting SARS-CoV-2 and its variant strains with a full genome tiling array. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	4
70	The impact of high density receptor clusters on VEGF signaling. <i>Electronic Proceedings in Theoretical Computer Science</i> , EPTCS, 2013, 2013, 37-52.	0.8	3
71	Elevated SARS-CoV-2 in peripheral blood and increased COVID-19 severity in American Indians/Alaska Natives. <i>Experimental Biology and Medicine</i> , 2022, 247, 1253-1263.	1.1	2
72	Polony Sequencing: History, Technology, and Applications. , 0, , 57-76.		1

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73	The role of reaction engineering in cancer biology: Bio-imaging informatics reveals implications of the plasma membrane heterogeneities. <i>Chemical Engineering Science</i> , 2007, 62, 5222-5231.	1.9	0
74	Genomic analysis of <i>Saccharomyces cerevisiae</i> isolates that grow optimally with glucose as the sole carbon source. <i>Electrophoresis</i> , 2012, 33, 3514-3520.	1.3	0
75	The Shuttling Scaffold Model for Prevention of Yeast Pheromone Pathway Misactivation. <i>Bulletin of Mathematical Biology</i> , 2012, 74, 2861-2874.	0.9	0
76	An Adaptive Coarse Graining Method for Signal Transduction in Three Dimensions. <i>Fundamenta Informaticae</i> , 2012, 118, 371-384.	0.3	0
77	LT1, an ONT long-read-based assembly scaffolded with Hi-C data and polished with short reads. <i>GigaByte</i> , 0, 2022, 1-16.	0.0	0