

Jeremy S Edwards

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8949664/publications.pdf>

Version: 2024-02-01

77
papers

6,988
citations

159585

30
h-index

85541

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.	17.5	877
2	Dynamic Flux Balance Analysis of Diauxic Growth in Escherichia coli. Biophysical Journal, 2002, 83, 1331-1340.	0.5	806
3	Escherichia coli K-12 undergoes adaptive evolution to achieve in silico predicted optimal growth. Nature, 2002, 420, 186-189.	27.8	797
4	Advances in flux balance analysis. Current Opinion in Biotechnology, 2003, 14, 491-496.	6.6	694
5	Metabolic modelling of microbes: the flux-balance approach. Environmental Microbiology, 2002, 4, 133-140.	3.8	335
6	Systems Properties of the Haemophilus influenzae Rd Metabolic Genotype. Journal of Biological Chemistry, 1999, 274, 17410-17416.	3.4	333
7	Genome-Scale Metabolic Model of Helicobacter pylori 26695. Journal of Bacteriology, 2002, 184, 4582-4593.	2.2	317
8	Metabolic modeling of microbial strains in silico. Trends in Biochemical Sciences, 2001, 26, 179-186.	7.5	291
9	Minke whale genome and aquatic adaptation in cetaceans. Nature Genetics, 2014, 46, 88-92.	21.4	227
10	Metabolic flux balance analysis and the in silico analysis of Escherichia coli K-12 gene deletions. BMC Bioinformatics, 2000, 1, 1.	2.6	221
11	Robustness Analysis of the Escherichia coli Metabolic Network. Biotechnology Progress, 2000, 16, 927-939.	2.6	179
12	Toward Metabolic Phenomics: Analysis of Genomic Data Using Flux Balances. Biotechnology Progress, 1999, 15, 288-295.	2.6	166
13	Characterizing the metabolic phenotype: A phenotype phase plane analysis. Biotechnology and Bioengineering, 2002, 77, 27-36.	3.3	166
14	Selection analyses of insertional mutants using subgenomic-resolution arrays. Nature Biotechnology, 2001, 19, 1060-1065.	17.5	140
15	The Genome-Scale Metabolic Extreme Pathway Structure in Haemophilus influenzae Shows Significant Network Redundancy. Journal of Theoretical Biology, 2002, 215, 67-82.	1.7	115
16	Comparison of carnivore, omnivore, and herbivore mammalian genomes with a new leopard assembly. Genome Biology, 2016, 17, 211.	8.8	101
17	Korean Genome Project: 1094 Korean personal genomes with clinical information. Science Advances, 2020, 6, eaaz7835.	10.3	75
18	Estimating optimal profiles of genetic alterations using constraint-based models. Biotechnology and Bioengineering, 2005, 89, 243-251.	3.3	72

#	ARTICLE	IF	CITATIONS
19	Description and Analysis of Metabolic Connectivity and Dynamics in the Human Red Blood Cell. Biophysical Journal, 2002, 83, 646-662.	0.5	63
20	An ethnically relevant consensus Korean reference genome is a step towards personal reference genomes. Nature Communications, 2016, 7, 13637.	12.8	58
21	Time accelerated Monte Carlo simulations of biological networks using the binomial Å-leap method. Bioinformatics, 2005, 21, 2136-2137.	4.1	56
22	Predicting chemical impacts on vertebrate endocrine systems. Environmental Toxicology and Chemistry, 2011, 30, 39-51.	4.3	44
23	Characterization of mutations and loss of heterozygosity of p53 and K-ras2 in pancreatic cancer cell lines by immobilized polymerase chain reaction. BMC Biotechnology, 2003, 3, 11.	3.3	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. Genome Biology, 2015, 16, 215.	8.8	41
25	Spatial modeling of dimerization reaction dynamics in the plasma membrane: Monte Carlo vs. continuum differential equations. Biophysical Chemistry, 2006, 121, 194-208.	2.8	40
26	MAPK Cascade Possesses Decoupled Controllability of Signal Amplification and Duration. Biophysical Journal, 2004, 87, L01-L02.	0.5	39
27	KoVariome: Korean National Standard Reference Variome database of whole genomes with comprehensive SNV, indel, CNV, and SV analyses. Scientific Reports, 2018, 8, 5677.	3.3	39
28	The genome of the giant Nomura jellyfish sheds light on the early evolution of active predation. BMC Biology, 2019, 17, 28.	3.8	38
29	Computational modeling reveals molecular details of epidermal growth factor binding. BMC Cell Biology, 2005, 6, 41.	3.0	35
30	Quantitative understanding of cell signaling: the importance of membrane organization. Current Opinion in Biotechnology, 2010, 21, 677-682.	6.6	35
31	Heterogeneities in EGF receptor density at the cell surface can lead to concave up scatchard plot of EGF binding. FEBS Letters, 2005, 579, 3043-3047.	2.8	33
32	The whale shark genome reveals how genomic and physiological properties scale with body size. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 20662-20671.	7.1	32
33	Microscopic Simulation of Membrane Molecule Diffusion on Corralled Membrane Surfaces. Biophysical Journal, 2008, 94, 1551-1564.	0.5	26
34	Advancing Pan-cancer Gene Expression Survival Analysis by Inclusion of Non-coding RNA. RNA Biology, 2020, 17, 1666-1673.	3.1	26
35	Coupled Stochastic Spatial and Non-Spatial Simulations of ErbB1 Signaling Pathways Demonstrate the Importance of Spatial Organization in Signal Transduction. PLoS ONE, 2009, 4, e6316.	2.5	26
36	Digital quantitative measurements of gene expression. Biotechnology and Bioengineering, 2004, 86, 117-124.	3.3	22

#	ARTICLE	IF	CITATIONS
37	Mathematical Simulation of Membrane Protein Clustering for Efficient Signal Transduction. <i>Annals of Biomedical Engineering</i> , 2012, 40, 2307-2318.	2.5	22
38	Orchestration of ErbB3 signaling through heterointeractions and homointeractions. <i>Molecular Biology of the Cell</i> , 2015, 26, 4109-4123.	2.1	22
39	Detecting Changes in the Relative Expression of KRAS2 Splice Variants Using Polymerase Colonies. <i>Biotechnology Progress</i> , 2004, 20, 1836-1839.	2.6	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.	3.8	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.	14.5	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.	2.8	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.	2.8	15
45	Dynamic Transition States of ErbB1 Phosphorylation Predicted by Spatial Stochastic Modeling. <i>Biophysical Journal</i> , 2013, 105, 1533-1543.	0.5	15
46	Enzymatic Synthesis of Designer DNA Using Cyclic Reversible Termination and a Universal Template. <i>ACS Synthetic Biology</i> , 2020, 9, 283-293.	3.8	15
47	Single Molecule Analysis of c-myc Alternative Splicing Reveals Novel Classifiers for Precursor B-ALL. <i>PLoS ONE</i> , 2011, 6, e22880.	2.5	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.	1.0	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.	9.3	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.	3.3	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.	3.0	11
52	Sequential super-resolution imaging using DNA strand displacement. <i>PLoS ONE</i> , 2018, 13, e0203291.	2.5	11
53	Raptor genomes reveal evolutionary signatures of predatory and nocturnal lifestyles. <i>Genome Biology</i> , 2019, 20, 181.	8.8	11
54	Highly Accurate Chip-Based Resequencing of SARS-CoV-2 Clinical Samples. <i>Langmuir</i> , 2021, 37, 4763-4771.	3.5	10

#	ARTICLE	IF	CITATIONS
55	MicroRNA Analysis of Human Stroke Brain Tissue Resected during Decompressive Craniectomy/Stroke-Ectomy Surgery. <i>Genes</i> , 2021, 12, 1860.	2.4	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.	1.7	8
57	Next-generation sequencing library construction on a surface. <i>BMC Genomics</i> , 2018, 19, 416.	2.8	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.	2.5	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.	3.7	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.	2.3	6
62	Whole Genome Analysis of the Red-Crowned Crane Provides Insight into Avian Longevity. <i>Molecules and Cells</i> , 2020, 43, 86-95.	2.6	6
63	Assaying gene function by growth competition experiment. <i>Metabolic Engineering</i> , 2004, 6, 212-219.	7.0	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.	2.8	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.	1.6	5
66	An integrated mechanistic model for transcription-coupled nucleotide excision repair. <i>DNA Repair</i> , 2004, 3, 343-348.	2.8	4
67	Parallel analysis of tetramerization domain mutants of the human p53 protein using PCR colonies. <i>Genomic Medicine</i> , 2007, 1, 113-124.	0.3	4
68	[INVITED] Electrophoretic plasmonic nanopore biochip genome sequencer. <i>Optics and Laser Technology</i> , 2019, 109, 199-211.	4.6	4
69	Detecting SARS-CoV-2 and its variant strains with a full genome tiling array. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	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.	2.4	2
72	Polony Sequencing: History, Technology, and Applications. , 0, , 57-76.		1

#	ARTICLE	IF	CITATIONS
73	The role of reaction engineering in cancer biology: Bio-imaging informatics reveals implications of the plasma membrane heterogeneities. Chemical Engineering Science, 2007, 62, 5222-5231.	3.8	0
74	Genomic analysis of <i>Saccharomyces cerevisiae</i> isolates that grow optimally with glucose as the sole carbon source. Electrophoresis, 2012, 33, 3514-3520.	2.4	0
75	The Shuttling Scaffold Model for Prevention of Yeast Pheromone Pathway Misactivation. Bulletin of Mathematical Biology, 2012, 74, 2861-2874.	1.9	0
76	An Adaptive Coarse Graining Method for Signal Transduction in Three Dimensions. Fundamenta Informaticae, 2012, 118, 371-384.	0.4	0
77	LT1, an ONT long-read-based assembly scaffolded with Hi-C data and polished with short reads. GigaByte, 0, 2022, 1-16.	0.0	0