

Eivind Almaas

List of Publications by Year in descending order

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Version: 2024-02-01

68
papers

2,699
citations

304602

22
h-index

197736

49
g-index

86
all docs

86
docs citations

86
times ranked

3368
citing authors

#	ARTICLE	IF	CITATIONS
1	Complex Network Analysis in Microbial Systems: Theory and Examples. <i>Methods in Molecular Biology</i> , 2022, 2349, 167-191.	0.4	1
2	Experimental determination of <i>Escherichia coli</i> biomass composition for constraint-based metabolic modeling. <i>PLoS ONE</i> , 2022, 17, e0262450.	1.1	8
3	Comparing the impact of vaccination strategies on the spread of COVID-19, including a novel household-targeted vaccination strategy. <i>PLoS ONE</i> , 2022, 17, e0263155.	1.1	8
4	csdR, an R package for differential co-expression analysis. <i>BMC Bioinformatics</i> , 2022, 23, 79.	1.2	2
5	NRF2 drives an oxidative stress response predictive of breast cancer. <i>Free Radical Biology and Medicine</i> , 2022, 184, 170-184.	1.3	8
6	Dynamic Allocation of Carbon Storage and Nutrient-Dependent Exudation in a Revised Genome-Scale Model of <i>Prochlorococcus</i> . <i>Frontiers in Genetics</i> , 2021, 12, 586293.	1.1	15
7	Automatic reconstruction of metabolic pathways from identified biosynthetic gene clusters. <i>BMC Bioinformatics</i> , 2021, 22, 81.	1.2	9
8	Addressing uncertainty in genome-scale metabolic model reconstruction and analysis. <i>Genome Biology</i> , 2021, 22, 64.	3.8	73
9	High-quality genome-scale metabolic model of <i>Aurantiochytrium</i> sp. T66. <i>Biotechnology and Bioengineering</i> , 2021, 118, 2105-2117.	1.7	9
10	Genome-scale metabolic modelling when changes in environmental conditions affect biomass composition. <i>PLoS Computational Biology</i> , 2021, 17, e1008528.	1.5	17
11	Containing pandemics through targeted testing of households. <i>BMC Infectious Diseases</i> , 2021, 21, 548.	1.3	4
12	Transcriptomic Response Analysis of <i>Escherichia coli</i> to Palladium Stress. <i>Frontiers in Microbiology</i> , 2021, 12, 741836.	1.5	6
13	Robust bacterial co-occurrence community structures are independent of r- and K-selection history. <i>Scientific Reports</i> , 2021, 11, 23497.	1.6	3
14	Whole transcriptomic network analysis using Co-expression Differential Network Analysis (CoDiNA). <i>PLoS ONE</i> , 2020, 15, e0240523.	1.1	13
15	An adjustable algal chloroplast plug-and-play model for genome-scale metabolic models. <i>PLoS ONE</i> , 2020, 15, e0229408.	1.1	5
16	Enzyme-Constrained Models and Omics Analysis of <i>Streptomyces coelicolor</i> Reveal Metabolic Changes that Enhance Heterologous Production. <i>IScience</i> , 2020, 23, 101525.	1.9	30
17	Genome-scale reconstructions to assess metabolic phylogeny and organism clustering. <i>PLoS ONE</i> , 2020, 15, e0240953.	1.1	7
18	Identification of key proteins involved in stickleback environmental adaptation with system-level analysis. <i>Physiological Genomics</i> , 2020, 52, 531-548.	1.0	2

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19	An adjustable algal chloroplast plug-and-play model for genome-scale metabolic models. , 2020, 15, e0229408.		0
20	An adjustable algal chloroplast plug-and-play model for genome-scale metabolic models. , 2020, 15, e0229408.		0
21	An adjustable algal chloroplast plug-and-play model for genome-scale metabolic models. , 2020, 15, e0229408.		0
22	An adjustable algal chloroplast plug-and-play model for genome-scale metabolic models. , 2020, 15, e0229408.		0
23	ErrorTracer: an algorithm for identifying the origins of inconsistencies in genome-scale metabolic models. <i>Bioinformatics</i> , 2019, 36, 1644-1646.	1.8	1
24	GREM1 is associated with metastasis and predicts poor prognosis in ER-negative breast cancer patients. <i>Cell Communication and Signaling</i> , 2019, 17, 140.	2.7	32
25	Assessment of weighted topological overlap (wTO) to improve fidelity of gene co-expression networks. <i>BMC Bioinformatics</i> , 2019, 20, 58.	1.2	8
26	Predicting Strain Engineering Strategies Using iKS1317: A Genome-scale Metabolic Model of <i>Streptomyces coelicolor</i> . <i>Biotechnology Journal</i> , 2019, 14, e1800180.	1.8	21
27	ModelExplorer - software for visual inspection and inconsistency correction of genome-scale metabolic reconstructions. <i>BMC Bioinformatics</i> , 2019, 20, 56.	1.2	10
28	Automated generation of genome-scale metabolic draft reconstructions based on KEGG. <i>BMC Bioinformatics</i> , 2018, 19, 467.	1.2	65
29	wTO: an R package for computing weighted topological overlap and a consensus network with integrated visualization tool. <i>BMC Bioinformatics</i> , 2018, 19, 392.	1.2	44
30	The role of PCNA as a scaffold protein in cellular signaling is functionally conserved between yeast and humans. <i>FEBS Open Bio</i> , 2018, 8, 1135-1145.	1.0	23
31	Robust Analysis of Fluxes in Genome-Scale Metabolic Pathways. <i>Scientific Reports</i> , 2017, 7, 268.	1.6	16
32	Comparative analysis of weighted gene co-expression networks in human and mouse. <i>PLoS ONE</i> , 2017, 12, e0187611.	1.1	10
33	A composite network of conserved and tissue specific gene interactions reveals possible genetic interactions in glioma. <i>PLoS Computational Biology</i> , 2017, 13, e1005739.	1.5	15
34	Hypothetical biomolecular probe based on a genetic switch with tunable symmetry and stability. <i>BMC Systems Biology</i> , 2016, 10, 39.	3.0	1
35	Strategies for structuring interdisciplinary education in Systems Biology: an European perspective. <i>Npj Systems Biology and Applications</i> , 2016, 2, 16011.	1.4	21
36	Alginate Biosynthesis Factories in <i>Pseudomonas fluorescens</i> : Localization and Correlation with Alginate Production Level. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1227-1236.	1.4	26

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37	Population-specific renal proteomes of marine and freshwater three-spined sticklebacks. <i>Journal of Proteomics</i> , 2016, 135, 112-131.	1.2	14
38	Investigating the relationship between k -core and s -core network decompositions. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2016, 449, 111-125.	1.2	13
39	Do genome-scale models need exact solvers or clearer standards?. <i>Molecular Systems Biology</i> , 2015, 11, 831.	3.2	68
40	s -core network decomposition: A generalization of k -core analysis to weighted networks. <i>Physical Review E</i> , 2013, 88, 062819.	0.8	72
41	Possible sorting mechanism for microparticles in an evanescent field. <i>Physical Review A</i> , 2013, 87, .	1.0	45
42	Non-Invasive Analysis of Recombinant mRNA Stability in <i>Escherichia coli</i> by a Combination of Transcriptional Inducer Wash-Out and qRT-PCR. <i>PLoS ONE</i> , 2013, 8, e66429.	1.1	6
43	Complex Network Analysis in Microbial Systems: Theory and Examples. <i>Methods in Molecular Biology</i> , 2012, 881, 551-571.	0.4	2
44	Genome-level transcription data of <i>Yersinia pestis</i> analyzed with a New metabolic constraint-based approach. <i>BMC Systems Biology</i> , 2012, 6, 150.	3.0	68
45	Comparative Genome-Scale Metabolic Reconstruction and Flux Balance Analysis of Multiple <i>Staphylococcus aureus</i> Genomes Identify Novel Antimicrobial Drug Targets. <i>Journal of Bacteriology</i> , 2009, 191, 4015-4024.	1.0	148
46	Two-Component Genetic Switch as a Synthetic Module with Tunable Stability. <i>Physical Review Letters</i> , 2009, 103, 028101.	2.9	22
47	Differences in human and chimpanzee gene expression patterns define an evolving network of transcription factors in brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 22358-22363.	3.3	142
48	Genome-scale reconstruction of the metabolic network in <i>Yersinia pestis</i> , strain 91001. <i>Molecular BioSystems</i> , 2009, 5, 368.	2.9	42
49	Systems Biology of Microbial Communities. <i>Methods in Molecular Biology</i> , 2009, 500, 469-494.	0.4	4
50	Genetic noise control via protein oligomerization. <i>BMC Systems Biology</i> , 2008, 2, 94.	3.0	28
51	Predicting synthetic rescues in metabolic networks. <i>Molecular Systems Biology</i> , 2008, 4, 168.	3.2	123
52	IDENTIFYING DYNAMIC NETWORK MODULES WITH TEMPORAL AND SPATIAL CONSTRAINTS. , 2008, , .		14
53	Introduction to Systems Biology for Mathematical Programmers. <i>Engineering and Management Innovation</i> , 2008, , .	0.1	3
54	SCALE-FREE NETWORKS IN BIOLOGY. <i>Complex Systems and Interdisciplinary Science</i> , 2007, , 1-19.	0.2	6

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55	Scale-Free Networks in Cell Biology. , 2007, , 1760-1766.		0
56	Biological impacts and context of network theory. Journal of Experimental Biology, 2007, 210, 1548-1558.	0.8	126
57	Trend Motif: A Graph Mining Approach for Analysis of Dynamic Complex Networks. , 2007, , .		39
58	Optimal flux patterns in cellular metabolic networks. Chaos, 2007, 17, 026107.	1.0	11
59	Power Laws in Biological Networks. , 2006, , 1-11.		15
60	THE ARCHITECTURE OF COMPLEXITY: FROM WWW TO CELLULAR METABOLISM. , 2006, , 107-125.		2
61	Minimum spanning trees of weighted scale-free networks. Europhysics Letters, 2005, 72, 308-314.	0.7	106
62	Evolutionary cores of domain co-occurrence networks. BMC Evolutionary Biology, 2005, 5, 24.	3.2	90
63	Peeling the yeast protein network. Proteomics, 2005, 5, 444-449.	1.3	204
64	Metabolic Networks. , 2005, , 243-264.		0
65	The Activity Reaction Core and Plasticity of Metabolic Networks. PLoS Computational Biology, 2005, 1, e68.	1.5	121
66	The Activity Reaction Core and Plasticity of Metabolic Networks. PLoS Computational Biology, 2005, preprint, e68.	1.5	3
67	Global organization of metabolic fluxes in the bacterium Escherichia coli. Nature, 2004, 427, 839-843.	13.7	607
68	Exact results and scaling properties of small-world networks. Physical Review E, 2000, 61, 4268-4271.	0.8	36