Eivind Almaas

List of Publications by Year
in descending order

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	Global organization of metabolic fluxes in the bacterium Escherichia coli. Nature, 2004, 427, 839-843.	13.7	607
2	Peeling the yeast protein network. Proteomics, 2005, 5, 444-449.	1.3	204
3	Comparative Genome-Scale Metabolic Reconstruction and Flux Balance Analysis of Multiple <i>Staphylococcus aureus</i> Genomes Identify Novel Antimicrobial Drug Targets. Journal of Bacteriology, 2009, 191, 4015-4024.	1.0	148
4	Differences in human and chimpanzee gene expression patterns define an evolving network of transcription factors in brain. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 22358-22363.	3.3	142
5	Biological impacts and context of network theory. Journal of Experimental Biology, 2007, 210, 1548-1558.	0.8	126
6	Predicting synthetic rescues in metabolic networks. Molecular Systems Biology, 2008, 4, 168.	3.2	123
7	The Activity Reaction Core and Plasticity of Metabolic Networks. PLoS Computational Biology, 2005, 1, e68.	1.5	121
8	Minimum spanning trees of weighted scale-free networks. Europhysics Letters, 2005, 72, 308-314.	0.7	106
9	Evolutionary cores of domain co-occurrence networks. BMC Evolutionary Biology, 2005, 5, 24.	3.2	90
10	Addressing uncertainty in genome-scale metabolic model reconstruction and analysis. Genome Biology, 2021, 22, 64.	3.8	73
11	<mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML"><mml:mi>s</mml:mi></mml:math>-core network decomposition: A generalization of<mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML"><mml:mi>k</mml:mi></mml:math>-core analysis to weighted networks. Physical Review E, 2013, 88, 062819.	0.8	72
12	Genome-level transcription data of Yersinia pestis analyzed with a New metabolic constraint-based approach. BMC Systems Biology, 2012, 6, 150.	3.0	68
13	Do genomeâ€scale models need exact solvers or clearer standards?. Molecular Systems Biology, 2015, 11, 831.	3.2	68
14	Automated generation of genome-scale metabolic draft reconstructions based on KEGG. BMC Bioinformatics, 2018, 19, 467.	1.2	65
15	Possible sorting mechanism for microparticles in an evanescent field. Physical Review A, 2013, 87, .	1.0	45
16	wTO: an R package for computing weighted topological overlap and a consensus network with integrated visualization tool. BMC Bioinformatics, 2018, 19, 392.	1.2	44
17	Genome-scale reconstruction of the metabolic network in Yersinia pestis, strain 91001. Molecular BioSystems, 2009, 5, 368.	2.9	42
18	Trend Motif: A Graph Mining Approach for Analysis of Dynamic Complex Networks. , 2007, , .		39

#	Article	IF	Citations
19	Exact results and scaling properties of small-world networks. Physical Review E, 2000, 61, 4268-4271.	0.8	36
20	GREM1 is associated with metastasis and predicts poor prognosis in ER-negative breast cancer patients. Cell Communication and Signaling, 2019, 17, 140.	2.7	32
21	Enzyme-Constrained Models and Omics Analysis of Streptomyces coelicolor Reveal Metabolic Changes that Enhance Heterologous Production. IScience, 2020, 23, 101525.	1.9	30
22	Genetic noise control via protein oligomerization. BMC Systems Biology, 2008, 2, 94.	3.0	28
23	Alginate Biosynthesis Factories in Pseudomonas fluorescens: Localization and Correlation with Alginate Production Level. Applied and Environmental Microbiology, 2016, 82, 1227-1236.	1.4	26
24	The role of <scp>PCNA</scp> as a scaffold protein in cellular signaling is functionally conserved between yeast and humans. FEBS Open Bio, 2018, 8, 1135-1145.	1.0	23
25	Two-Component Genetic Switch as a Synthetic Module with Tunable Stability. Physical Review Letters, 2009, 103, 028101.	2.9	22
26	Strategies for structuring interdisciplinary education in Systems Biology: an European perspective. Npj Systems Biology and Applications, 2016, 2, 16011.	1.4	21
27	Predicting Strain Engineering Strategies Using iKS1317: A Genome€Scale Metabolic Model of <i>Streptomyces coelicolor</i>. Biotechnology Journal, 2019, 14, e1800180.	1.8	21
28	Genome-scale metabolic modelling when changes in environmental conditions affect biomass composition. PLoS Computational Biology, 2021, 17, e1008528.	1.5	17
29	Robust Analysis of Fluxes in Genome-Scale Metabolic Pathways. Scientific Reports, 2017, 7, 268.	1.6	16
30	Power Laws in Biological Networks. , 2006, , 1-11.		15
31	A composite network of conserved and tissue specific gene interactions reveals possible genetic interactions in glioma. PLoS Computational Biology, 2017, 13, e1005739.	1.5	15
32	Dynamic Allocation of Carbon Storage and Nutrient-Dependent Exudation in a Revised Genome-Scale Model of Prochlorococcus. Frontiers in Genetics, 2021, 12, 586293.	1.1	15
33	IDENTIFYING DYNAMIC NETWORK MODULES WITH TEMPORAL AND SPATIAL CONSTRAINTS. , 2008, , .		14
34	Population-specific renal proteomes of marine and freshwater three-spined sticklebacks. Journal of Proteomics, 2016, 135, 112-131.	1.2	14
35	Investigating the relationship between k-core and s-core network decompositions. Physica A: Statistical Mechanics and Its Applications, 2016, 449, 111-125.	1.2	13
36	Whole transcriptomic network analysis using Co-expression Differential Network Analysis (CoDiNA). PLoS ONE, 2020, 15, e0240523.	1.1	13

#	ARTICLE	IF	CITATIONS
37	Optimal flux patterns in cellular metabolic networks. Chaos, 2007, 17, 026107.	1.0	11
38	Comparative analysis of weighted gene co-expression networks in human and mouse. PLoS ONE, 2017, 12, e0187611.	1.1	10
39	ModelExplorer - software for visual inspection and inconsistency correction of genome-scale metabolic reconstructions. BMC Bioinformatics, 2019, 20, 56.	1.2	10
40	Automatic reconstruction of metabolic pathways from identified biosynthetic gene clusters. BMC Bioinformatics, 2021, 22, 81.	1.2	9
41	High€quality genome€scale metabolic model of <i>Aurantiochytrium</i> sp. T66. Biotechnology and Bioengineering, 2021, 118, 2105-2117.	1.7	9
42	Assessment of weighted topological overlap (wTO) to improve fidelity of gene co-expression networks. BMC Bioinformatics, 2019, 20, 58.	1.2	8
43	Experimental determination of Escherichia coli biomass composition for constraint-based metabolic modeling. PLoS ONE, 2022, 17, e0262450.	1.1	8
44	Comparing the impact of vaccination strategies on the spread of COVID-19, including a novel household-targeted vaccination strategy. PLoS ONE, 2022, 17, e0263155.	1.1	8
45	NRF2 drives an oxidative stress response predictive of breast cancer. Free Radical Biology and Medicine, 2022, 184, 170-184.	1.3	8
46	Genome-scale reconstructions to assess metabolic phylogeny and organism clustering. PLoS ONE, 2020, 15, e0240953.	1.1	7
47	SCALE-FREE NETWORKS IN BIOLOGY. Complex Systems and Interdisciplinary Science, 2007, , 1-19.	0.2	6
48	Non-Invasive Analysis of Recombinant mRNA Stability in Escherichia coli by a Combination of Transcriptional Inducer Wash-Out and qRT-PCR. PLoS ONE, 2013, 8, e66429.	1.1	6
49	Transcriptomic Response Analysis of Escherichia coli to Palladium Stress. Frontiers in Microbiology, 2021, 12, 741836.	1.5	6
50	An adjustable algal chloroplast plug-and-play model for genome-scale metabolic models. PLoS ONE, 2020, 15, e0229408.	1.1	5
51	Containing pandemics through targeted testing of households. BMC Infectious Diseases, 2021, 21, 548.	1.3	4
52	Systems Biology of Microbial Communities. Methods in Molecular Biology, 2009, 500, 469-494.	0.4	4
53	Introduction to Systems Biology for Mathematical Programmers. Engineering and Management Innovation, 2008, , .	0.1	3
54	The Activity Reaction Core and Plasticity of Metabolic Networks. PLoS Computational Biology, 2005, preprint, e68.	1.5	3

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55	Robust bacterial co-occurence community structures are independent of r- and K-selection history. Scientific Reports, 2021, 11, 23497.	1.6	3
56	Complex Network Analysis in Microbial Systems: Theory and Examples. Methods in Molecular Biology, 2012, 881, 551-571.	0.4	2
57	THE ARCHITECTURE OF COMPLEXITY: FROM WWW TO CELLULAR METABOLISM. , 2006, , 107-125.		2
58	Identification of key proteins involved in stickleback environmental adaptation with system-level analysis. Physiological Genomics, 2020, 52, 531-548.	1.0	2
59	csdR, an R package for differential co-expression analysis. BMC Bioinformatics, 2022, 23, 79.	1.2	2
60	Hypothetical biomolecular probe based on a genetic switch with tunable symmetry and stability. BMC Systems Biology, 2016, 10, 39.	3.0	1
61	ErrorTracer: an algorithm for identifying the origins of inconsistencies in genome-scale metabolic models. Bioinformatics, 2019, 36, 1644-1646.	1.8	1
62	Complex Network Analysis in Microbial Systems: Theory and Examples. Methods in Molecular Biology, 2022, 2349, 167-191.	0.4	1
63	Metabolic Networks. , 2005, , 243-264.		0
64	Scale-Free Networks in Cell Biology. , 2007, , 1760-1766.		0
65	An adjustable algal chloroplast plug-and-play model for genome-scale metabolic models. , 2020, 15, e0229408.		0
66	An adjustable algal chloroplast plug-and-play model for genome-scale metabolic models. , 2020, 15, e0229408.		0
67	An adjustable algal chloroplast plug-and-play model for genome-scale metabolic models. , 2020, 15, e0229408.		0
68	An adjustable algal chloroplast plug-and-play model for genome-scale metabolic models. , 2020, 15, e0229408.		0