

Oliver EbenhÄjh

List of Publications by Year in descending order

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Version: 2024-02-01

83
papers

2,346
citations

218381

26
h-index

253896

43
g-index

110
all docs

110
docs citations

110
times ranked

3332
citing authors

#	ARTICLE	IF	CITATIONS
1	Assembly of an Interactive Correlation Network for the Arabidopsis Genome Using a Novel Heuristic Clustering Algorithm. <i>Plant Physiology</i> , 2009, 152, 29-43.	2.3	174
2	Expanding Metabolic Networks: Scopes of Compounds, Robustness, and Evolution. <i>Journal of Molecular Evolution</i> , 2005, 61, 498-512.	0.8	167
3	Metabolomics- and Proteomics-Assisted Genome Annotation and Analysis of the Draft Metabolic Network of <i>Chlamydomonas reinhardtii</i> . <i>Genetics</i> , 2008, 179, 157-166.	1.2	141
4	Taxonomic database and cut-off value for processing mcrA gene 454 pyrosequencing data by MOTHUR. <i>Journal of Microbiological Methods</i> , 2014, 103, 3-5.	0.7	93
5	Mathematical modelling of the diurnal regulation of the <i>MEP</i> pathway in <i>Arabidopsis</i> . <i>New Phytologist</i> , 2015, 206, 1075-1085.	3.5	78
6	Emergent Subpopulation Behavior Uncovered with a Community Dynamic Metabolic Model of <i>Escherichia coli</i> Diauxic Growth. <i>MSystems</i> , 2019, 4, .	1.7	77
7	Alternate wetting and drying irrigation for rice in Bangladesh: Is it sustainable and has plant breeding something to offer?. <i>Food and Energy Security</i> , 2013, 2, 120-129.	2.0	74
8	An integrative approach towards completing genome-scale metabolic networks. <i>Molecular BioSystems</i> , 2009, 5, 1889.	2.9	67
9	Evolutionary Optimization of Metabolic Pathways. Theoretical Reconstruction of the Stoichiometry of ATP and NADH Producing Systems. <i>Bulletin of Mathematical Biology</i> , 2001, 63, 21-55.	0.9	65
10	Evaluating potential of green alga <i>Chlorella vulgaris</i> to accumulate phosphorus and to fertilize nutrient-poor soil substrates for crop plants. <i>Journal of Applied Phycology</i> , 2018, 30, 2827-2836.	1.5	60
11	Adjustment of carbon fluxes to light conditions regulates the daily turnover of starch in plants: a computational model. <i>Molecular BioSystems</i> , 2014, 10, 613-627.	2.9	55
12	Short-term acclimation of the photosynthetic electron transfer chain to changing light: a mathematical model. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2014, 369, 20130223.	1.8	55
13	Structural analysis of expanding metabolic networks. <i>Genome Informatics</i> , 2004, 15, 35-45.	0.4	54
14	An environmental perspective on metabolism. <i>Journal of Theoretical Biology</i> , 2008, 252, 530-537.	0.8	51
15	StrigoQuant: A genetically encoded biosensor for quantifying strigolactone activity and specificity. <i>Science Advances</i> , 2016, 2, e1601266.	4.7	51
16	The Metabolic Interplay between Plants and Phytopathogens. <i>Metabolites</i> , 2013, 3, 1-23.	1.3	47
17	A minimal mathematical model of nonphotochemical quenching of chlorophyll fluorescence. <i>BioSystems</i> , 2011, 103, 196-204.	0.9	45
18	The intertwined metabolism during symbiotic nitrogen fixation elucidated by metabolic modelling. <i>Scientific Reports</i> , 2018, 8, 12504.	1.6	45

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19	Review and perspective on mathematical modeling of microbial ecosystems. <i>Biochemical Society Transactions</i> , 2018, 46, 403-412.	1.6	43
20	A mathematical model of non-photochemical quenching to study short-term light memory in plants. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2016, 1857, 1860-1869.	0.5	39
21	A Bacterial Glucanotransferase Can Replace the Complex Maltose Metabolism Required for Starch to Sucrose Conversion in Leaves at Night. <i>Journal of Biological Chemistry</i> , 2013, 288, 28581-28598.	1.6	34
22	A Diverse Community To Study Communities: Integration of Experiments and Mathematical Models To Study Microbial Consortia. <i>Journal of Bacteriology</i> , 2017, 199, .	1.0	33
23	Carbohydrate-active enzymes exemplify entropic principles in metabolism. <i>Molecular Systems Biology</i> , 2011, 7, 542.	3.2	32
24	Modelling phosphorus uptake in microalgae. <i>Biochemical Society Transactions</i> , 2018, 46, 483-490.	1.6	32
25	Balancing energy supply during photosynthesis – a theoretical perspective. <i>Physiologia Plantarum</i> , 2019, 166, 392-402.	2.6	32
26	Regulatory principles and experimental approaches to the circadian control of starch turnover. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20130979.	1.5	29
27	Stoichiometric Design of Metabolic Networks: Multifunctionality, Clusters, Optimization, Weak and Strong Robustness. <i>Bulletin of Mathematical Biology</i> , 2003, 65, 323-357.	0.9	28
28	MetaPath Online: a web server implementation of the network expansion algorithm. <i>Nucleic Acids Research</i> , 2007, 35, W613-W618.	6.5	27
29	A systems-wide understanding of photosynthetic acclimation in algae and higher plants. <i>Journal of Experimental Botany</i> , 2017, 68, 2667-2681.	2.4	26
30	Mass-balanced randomization of metabolic networks. <i>Bioinformatics</i> , 2011, 27, 1397-1403.	1.8	25
31	Dynamics of the Bacterial Community Associated with <i>Phaeodactylum tricornutum</i> Cultures. <i>Processes</i> , 2017, 5, 77.	1.3	25
32	Thermodynamic Limits and Optimality of Microbial Growth. <i>Entropy</i> , 2020, 22, 277.	1.1	23
33	A cross species comparison of metabolic network functions. <i>Genome Informatics</i> , 2005, 16, 203-13.	0.4	22
34	Evolutionary changes of metabolic networks and their biosynthetic capacities. <i>IET Systems Biology</i> , 2006, 153, 354.	2.0	21
35	Systems approaches to modelling pathways and networks. <i>Briefings in Functional Genomics</i> , 2011, 10, 266-279.	1.3	21
36	Biosynthetic Potentials of Metabolites and Their Hierarchical Organization. <i>PLoS Computational Biology</i> , 2008, 4, e1000049.	1.5	20

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37	A generic rate law for surface-active enzymes. FEBS Letters, 2013, 587, 2882-2890.	1.3	20
38	The mechanism of Φ C31 integrase directionality: experimental analysis and computational modelling. Nucleic Acids Research, 2016, 44, gkw616.	6.5	20
39	Metabolic synergy: increasing biosynthetic capabilities by network cooperation. Genome Informatics, 2007, 18, 320-9.	0.4	20
40	Evolutionary significance of metabolic network properties. Journal of the Royal Society Interface, 2012, 9, 1168-1176.	1.5	19
41	MEASURING CORRELATIONS IN METABOLOMIC NETWORKS WITH MUTUAL INFORMATION. , 2008, , .		17
42	Insight into metabolic pathways of the potential biofuel producer, Paenibacillus polymyxa ICGEB2008. Biotechnology for Biofuels, 2015, 8, 159.	6.2	17
43	Mathematical modelling of diurnal regulation of carbohydrate allocation by osmo-related processes in plants. Journal of the Royal Society Interface, 2015, 12, 20141357.	1.5	16
44	Comparing flux balance analysis to network expansion: producibility, sustainability and the scope of compounds. Genome Informatics, 2008, 20, 91-101.	0.4	14
45	Theoretical and experimental approaches to understand the biosynthesis of starch granules in a physiological context. Photosynthesis Research, 2020, 145, 55-70.	1.6	13
46	Functional Classification of Genome-Scale Metabolic Networks. Eurasip Journal on Bioinformatics and Systems Biology, 2009, 2009, 1-13.	1.4	12
47	The importance of the photosynthetic Gibbs effect in the elucidation of the Calvin-Benson-Bassham cycle. Biochemical Society Transactions, 2018, 46, 131-140.	1.6	12
48	METABOLIC SYNERGY: INCREASING BIOSYNTHETIC CAPABILITIES BY NETWORK COOPERATION. , 2007, , .		11
49	Ground State Robustness as an Evolutionary Design Principle in Signaling Networks. PLoS ONE, 2009, 4, e8001.	1.1	11
50	Slow deactivation of ribulose 1,5-bisphosphate carboxylase/oxygenase elucidated by mathematical models. FEBS Journal, 2010, 277, 931-950.	2.2	11
51	Modelling a molecular calendar: The seasonal photoperiodic response in mammals. Chaos, Solitons and Fractals, 2013, 50, 39-47.	2.5	11
52	Mathematical model of a serine integrase-controlled toggle switch with a single input. Journal of the Royal Society Interface, 2018, 15, 20180160.	1.5	11
53	A single-input binary counting module based on serine integrase site-specific recombination. Nucleic Acids Research, 2019, 47, 4896-4909.	6.5	11
54	Introduction to Focus Issue: Dynamics in Systems Biology. Chaos, 2010, 20, 045101.	1.0	10

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55	Integration of Proteomic and Metabolomic Profiling as well as Metabolic Modeling for the Functional Analysis of Metabolic Networks. <i>Methods in Molecular Biology</i> , 2011, 694, 341-363.	0.4	10
56	COMPARING FLUX BALANCE ANALYSIS TO NETWORK EXPANSION: PRODUCIBILITY, SUSTAINABILITY AND THE SCOPE OF COMPOUNDS. , 2008, , .		9
57	Modeling the complex dynamics of enzyme-pathway coevolution. <i>Chaos</i> , 2010, 20, 045115.	1.0	9
58	Modeling temperature entrainment of circadian clocks using the Arrhenius equation and a reconstructed model from <i>Chlamydomonas reinhardtii</i> . <i>Journal of Biological Physics</i> , 2012, 38, 449-464.	0.7	9
59	Computational Analysis of Alternative Photosynthetic Electron Flows Linked With Oxidative Stress. <i>Frontiers in Plant Science</i> , 2021, 12, 750580.	1.7	9
60	Hierarchy of metabolic compounds based on their synthesising capacity. <i>IET Systems Biology</i> , 2006, 153, 359.	2.0	8
61	A reductionist approach to model photosynthetic self-regulation in eukaryotes in response to light. <i>Biochemical Society Transactions</i> , 2015, 43, 1133-1139.	1.6	8
62	A simplified mathematical model of directional DNA site-specific recombination by serine integrases. <i>Journal of the Royal Society Interface</i> , 2017, 14, 20160618.	1.5	8
63	Data-driven dynamical model indicates that the heat shock response in <i>Chlamydomonas reinhardtii</i> is tailored to handle natural temperature variation. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20170965.	1.5	8
64	Constructing and analysing dynamic models with modelbase v1.2.3: a software update. <i>BMC Bioinformatics</i> , 2021, 22, 203.	1.2	8
65	Building Mathematical Models of Biological Systems with <tt>modelbase</tt>. <i>Journal of Open Research Software</i> , 2018, 6, 24.	2.7	8
66	Network Reconstruction and Modelling Made Reproducible with moped. <i>Metabolites</i> , 2022, 12, 275.	1.3	8
67	Optimal efficiency of the Q-cycle mechanism around physiological temperatures from an open quantum systems approach. <i>Scientific Reports</i> , 2019, 9, 16657.	1.6	7
68	Design starch: stochastic modeling of starch granule biogenesis. <i>Biochemical Society Transactions</i> , 2017, 45, 885-893.	1.6	6
69	Hardness and Approximability of the Inverse Scope Problem. <i>Lecture Notes in Computer Science</i> , 2008, , 99-112.	1.0	5
70	The view of microbes as energy converters illustrates the trade-off between growth rate and yield. <i>Biochemical Society Transactions</i> , 2021, 49, 1663-1674.	1.6	5
71	From sequence to information. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190448.	1.8	5
72	CO-EVOLUTION OF METABOLISM AND PROTEIN SEQUENCES. , 2010, , .		4

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73	Can biochemical properties serve as selective pressure for gene selection during inter-species and endosymbiotic lateral gene transfer?. IET Systems Biology, 2006, 153, 212.	2.0	3
74	Mesoscopic behavior from microscopic Markov dynamics and its application to calcium release channels. Journal of Theoretical Biology, 2014, 343, 102-112.	0.8	3
75	BIOSYNTHETIC POTENTIALS FROM SPECIES-SPECIFIC METABOLIC NETWORKS. , 2008, , .		3
76	Modelling Robust Feedback Control Mechanisms That Ensure Reliable Coordination of Histone Gene Expression with DNA Replication. PLoS ONE, 2016, 11, e0165848.	1.1	3
77	Structural analysis of expressed metabolic subnetworks. Genome Informatics, 2006, 17, 163-72.	0.4	3
78	COBREXA.jl: constraint-based reconstruction and exascale analysis. Bioinformatics, 2022, 38, 1171-1172.	1.8	2
79	Genome-Scale Metabolic Network Inference. , 2013, , 832-833.		1
80	Patterns of interactions of reaction pairs in metabolic networks. Genome Informatics, 2006, 17, 208-18.	0.4	1
81	ANALYZING GENE COEXPRESSION DATA BY AN EVOLUTIONARY MODEL. , 2010, , .		0
82	Compound clustering and consensus scopes of metabolic networks. , 2010, , 211-218.		0
83	ANALYSIS AND PREDICTION OF NUTRITIONAL REQUIREMENTS USING STRUCTURAL PROPERTIES OF METABOLIC NETWORKS AND SUPPORT VECTOR MACHINES. , 2010, , .		0