

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	COBREXAJL: constraint-based reconstruction and exascale analysis. <i>Bioinformatics</i> , 2022, 38, 1171-1172.	1.8	2
2	Network Reconstruction and Modelling Made Reproducible with moped. <i>Metabolites</i> , 2022, 12, 275.	1.3	8
3	Constructing and analysing dynamic models with modelbase v1.2.3: a software update. <i>BMC Bioinformatics</i> , 2021, 22, 203.	1.2	8
4	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
5	Computational Analysis of Alternative Photosynthetic Electron Flows Linked With Oxidative Stress. <i>Frontiers in Plant Science</i> , 2021, 12, 750580.	1.7	9
6	Thermodynamic Limits and Optimality of Microbial Growth. <i>Entropy</i> , 2020, 22, 277.	1.1	23
7	Theoretical and experimental approaches to understand the biosynthesis of starch granules in a physiological context. <i>Photosynthesis Research</i> , 2020, 145, 55-70.	1.6	13
8	From sequence to information. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190448.	1.8	5
9	Balancing energy supply during photosynthesis – a theoretical perspective. <i>Physiologia Plantarum</i> , 2019, 166, 392-402.	2.6	32
10	A single-input binary counting module based on serine integrase site-specific recombination. <i>Nucleic Acids Research</i> , 2019, 47, 4896-4909.	6.5	11
11	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
12	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
13	Modelling phosphorus uptake in microalgae. <i>Biochemical Society Transactions</i> , 2018, 46, 483-490.	1.6	32
14	The importance of the photosynthetic Gibbs effect in the elucidation of the Calvin–Benson–Bascham cycle. <i>Biochemical Society Transactions</i> , 2018, 46, 131-140.	1.6	12
15	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
16	Review and perspective on mathematical modeling of microbial ecosystems. <i>Biochemical Society Transactions</i> , 2018, 46, 403-412.	1.6	43
17	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
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	Mathematical model of a serine integrase-controlled toggle switch with a single input. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20180160.	1.5	11
20	Building Mathematical Models of Biological Systems with <i>modelbase</i> . <i>Journal of Open Research Software</i> , 2018, 6, 24.	2.7	8
21	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
22	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
23	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
24	Design starch: stochastic modeling of starch granule biogenesis. <i>Biochemical Society Transactions</i> , 2017, 45, 885-893.	1.6	6
25	Dynamics of the Bacterial Community Associated with <i>Phaeodactylum tricornutum</i> Cultures. <i>Processes</i> , 2017, 5, 77.	1.3	25
26	The mechanism of Φ C31 integrase directionality: experimental analysis and computational modelling. <i>Nucleic Acids Research</i> , 2016, 44, gkw616.	6.5	20
27	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
28	StrigoQuant: A genetically encoded biosensor for quantifying strigolactone activity and specificity. <i>Science Advances</i> , 2016, 2, e1601266.	4.7	51
29	Modelling Robust Feedback Control Mechanisms That Ensure Reliable Coordination of Histone Gene Expression with DNA Replication. <i>PLoS ONE</i> , 2016, 11, e0165848.	1.1	3
30	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
31	Insight into metabolic pathways of the potential biofuel producer, <i>Paenibacillus polymyxa</i> ICGEB2008. <i>Biotechnology for Biofuels</i> , 2015, 8, 159.	6.2	17
32	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
33	Mathematical modelling of diurnal regulation of carbohydrate allocation by osmo-related processes in plants. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20141357.	1.5	16
34	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
35	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
36	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

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37	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
38	Mesoscopic behavior from microscopic Markov dynamics and its application to calcium release channels. <i>Journal of Theoretical Biology</i> , 2014, 343, 102-112.	0.8	3
39	A generic rate law for surface-active enzymes. <i>FEBS Letters</i> , 2013, 587, 2882-2890.	1.3	20
40	Modelling a molecular calendar: The seasonal photoperiodic response in mammals. <i>Chaos, Solitons and Fractals</i> , 2013, 50, 39-47.	2.5	11
41	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
42	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
43	The Metabolic Interplay between Plants and Phytopathogens. <i>Metabolites</i> , 2013, 3, 1-23.	1.3	47
44	Genome-Scale Metabolic Network Inference. , 2013, , 832-833.		1
45	Evolutionary significance of metabolic network properties. <i>Journal of the Royal Society Interface</i> , 2012, 9, 1168-1176.	1.5	19
46	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
47	Carbohydrate-active enzymes exemplify entropic principles in metabolism. <i>Molecular Systems Biology</i> , 2011, 7, 542.	3.2	32
48	A minimal mathematical model of nonphotochemical quenching of chlorophyll fluorescence. <i>BioSystems</i> , 2011, 103, 196-204.	0.9	45
49	Systems approaches to modelling pathways and networks. <i>Briefings in Functional Genomics</i> , 2011, 10, 266-279.	1.3	21
50	Mass-balanced randomization of metabolic networks. <i>Bioinformatics</i> , 2011, 27, 1397-1403.	1.8	25
51	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
52	CO-EVOLUTION OF METABOLISM AND PROTEIN SEQUENCES. , 2010, , .		4
53	Slow deactivation of ribulose 1,5-bisphosphate carboxylase/oxygenase elucidated by mathematical models. <i>FEBS Journal</i> , 2010, 277, 931-950.	2.2	11
54	Introduction to Focus Issue: Dynamics in Systems Biology. <i>Chaos</i> , 2010, 20, 045101.	1.0	10

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55	Modeling the complex dynamics of enzyme-pathway coevolution. <i>Chaos</i> , 2010, 20, 045115.	1.0	9
56	ANALYZING GENE COEXPRESSION DATA BY AN EVOLUTIONARY MODEL. , 2010, , .		0
57	Compound clustering and consensus scopes of metabolic networks. , 2010, , 211-218.		0
58	ANALYSIS AND PREDICTION OF NUTRITIONAL REQUIREMENTS USING STRUCTURAL PROPERTIES OF METABOLIC NETWORKS AND SUPPORT VECTOR MACHINES. , 2010, , .		0
59	Ground State Robustness as an Evolutionary Design Principle in Signaling Networks. <i>PLoS ONE</i> , 2009, 4, e8001.	1.1	11
60	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
61	Functional Classification of Genome-Scale Metabolic Networks. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2009, 2009, 1-13.	1.4	12
62	An integrative approach towards completing genome-scale metabolic networks. <i>Molecular BioSystems</i> , 2009, 5, 1889.	2.9	67
63	An environmental perspective on metabolism. <i>Journal of Theoretical Biology</i> , 2008, 252, 530-537.	0.8	51
64	Hardness and Approximability of the Inverse Scope Problem. <i>Lecture Notes in Computer Science</i> , 2008, , 99-112.	1.0	5
65	COMPARING FLUX BALANCE ANALYSIS TO NETWORK EXPANSION: PRODUCIBILITY, SUSTAINABILITY AND THE SCOPE OF COMPOUNDS. , 2008, , .		9
66	Biosynthetic Potentials of Metabolites and Their Hierarchical Organization. <i>PLoS Computational Biology</i> , 2008, 4, e1000049.	1.5	20
67	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
68	MEASURING CORRELATIONS IN METABOLOMIC NETWORKS WITH MUTUAL INFORMATION. , 2008, , .		17
69	BIOSYNTHETIC POTENTIALS FROM SPECIES-SPECIFIC METABOLIC NETWORKS. , 2008, , .		3
70	Comparing flux balance analysis to network expansion: producibility, sustainability and the scope of compounds. <i>Genome Informatics</i> , 2008, 20, 91-101.	0.4	14
71	MetaPath Online: a web server implementation of the network expansion algorithm. <i>Nucleic Acids Research</i> , 2007, 35, W613-W618.	6.5	27
72	METABOLIC SYNERGY: INCREASING BIOSYNTHETIC CAPABILITIES BY NETWORK COOPERATION. , 2007, , .		11

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73	Metabolic synergy: increasing biosynthetic capabilities by network cooperation. <i>Genome Informatics</i> , 2007, 18, 320-9.	0.4	20
74	Can biochemical properties serve as selective pressure for gene selection during inter-species and endosymbiotic lateral gene transfer?. <i>IET Systems Biology</i> , 2006, 153, 212.	2.0	3
75	Evolutionary changes of metabolic networks and their biosynthetic capacities. <i>IET Systems Biology</i> , 2006, 153, 354.	2.0	21
76	Hierarchy of metabolic compounds based on their synthesising capacity. <i>IET Systems Biology</i> , 2006, 153, 359.	2.0	8
77	Structural analysis of expressed metabolic subnetworks. <i>Genome Informatics</i> , 2006, 17, 163-72.	0.4	3
78	Patterns of interactions of reaction pairs in metabolic networks. <i>Genome Informatics</i> , 2006, 17, 208-18.	0.4	1
79	Expanding Metabolic Networks: Scopes of Compounds, Robustness, and Evolution. <i>Journal of Molecular Evolution</i> , 2005, 61, 498-512.	0.8	167
80	A cross species comparison of metabolic network functions. <i>Genome Informatics</i> , 2005, 16, 203-13.	0.4	22
81	Structural analysis of expanding metabolic networks. <i>Genome Informatics</i> , 2004, 15, 35-45.	0.4	54
82	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
83	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