

Wolfram Liebermeister

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

7,126
citations

136950

32
h-index

182427

51
g-index

59
all docs

59
docs citations

59
times ranked

8955
citing authors

#	ARTICLE	IF	CITATIONS
1	BioSimulators: a central registry of simulation engines and services for recommending specific tools. <i>Nucleic Acids Research</i> , 2022, 50, W108-W114.	14.5	11
2	Structural Thermokinetic Modelling. <i>Metabolites</i> , 2022, 12, 434.	2.9	2
3	Model Balancing: A Search for In-Vivo Kinetic Constants and Consistent Metabolic States. <i>Metabolites</i> , 2021, 11, 749.	2.9	3
4	Clb3-centered regulations are recurrent across distinct parameter regions in minimal autonomous cell cycle oscillator designs. <i>Npj Systems Biology and Applications</i> , 2020, 6, 8.	3.0	9
5	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	7.2	178
6	Automated generation of bacterial resource allocation models. <i>Metabolic Engineering</i> , 2019, 55, 12-22.	7.0	41
7	Parameter balancing: consistent parameter sets for kinetic metabolic models. <i>Bioinformatics</i> , 2019, 35, 3857-3858.	4.1	9
8	Notions of similarity for systems biology models. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw090.	6.5	17
9	Metabolic enzyme cost explains variable trade-offs between microbial growth rate and yield. <i>PLoS Computational Biology</i> , 2018, 14, e1006010.	3.2	76
10	Metabolite-Enzyme Coevolution: From Single Enzymes to Metabolic Pathways and Networks. <i>Annual Review of Biochemistry</i> , 2018, 87, 187-216.	11.1	106
11	Toward Community Standards and Software for Whole-Cell Modeling. <i>IEEE Transactions on Biomedical Engineering</i> , 2016, 63, 2007-2014.	4.2	51
12	SBtab: a flexible table format for data exchange in systems biology. <i>Bioinformatics</i> , 2016, 32, 2559-2561.	4.1	31
13	Global characterization of in vivo enzyme catalytic rates and their correspondence to in vitro <i>k_{cat}</i> measurements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3401-3406.	7.1	212
14	The Protein Cost of Metabolic Fluxes: Prediction from Enzymatic Rate Laws and Cost Minimization. <i>PLoS Computational Biology</i> , 2016, 12, e1005167.	3.2	144
15	SBML Level 3 package: Hierarchical Model Composition, Version 1 Release 3. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 603-659.	1.5	39
16	SBML Level 3 package: Hierarchical Model Composition, Version 1 Release 3. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 268.	1.5	31
17	Pathway Thermodynamics Highlights Kinetic Obstacles in Central Metabolism. <i>PLoS Computational Biology</i> , 2014, 10, e1003483.	3.2	249
18	Visual account of protein investment in cellular functions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8488-8493.	7.1	304

#	ARTICLE	IF	CITATIONS
19	A note on the kinetics of enzyme action: A decomposition that highlights thermodynamic effects. FEBS Letters, 2013, 587, 2772-2777.	2.8	108
20	Spanning high-dimensional expression space using ribosome-binding site combinatorics. Nucleic Acids Research, 2013, 41, e98-e98.	14.5	165
21	Glycolytic strategy as a tradeoff between energy yield and protein cost. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 10039-10044.	7.1	446
22	Steady-State Metabolite Concentrations Reflect a Balance between Maximizing Enzyme Efficiency and Minimizing Total Metabolite Load. PLoS ONE, 2013, 8, e75370.	2.5	67
23	Systematic Construction of Kinetic Models from Genome-Scale Metabolic Networks. PLoS ONE, 2013, 8, e79195.	2.5	102
24	Global Network Reorganization During Dynamic Adaptations of <i>Bacillus subtilis</i> Metabolism. Science, 2012, 335, 1099-1103.	12.6	255
25	Propagating semantic information in biochemical network models. BMC Bioinformatics, 2012, 13, 18.	2.6	11
26	Condition-Dependent Transcriptome Reveals High-Level Regulatory Architecture in <i>Bacillus subtilis</i> . Science, 2012, 335, 1103-1106.	12.6	809
27	The Moderately Efficient Enzyme: Evolutionary and Physicochemical Trends Shaping Enzyme Parameters. Biochemistry, 2011, 50, 4402-4410.	2.5	810
28	Sustainable Model Building. Methods in Enzymology, 2011, 500, 371-395.	1.0	11
29	Retrieval, alignment, and clustering of computational models based on semantic annotations. Molecular Systems Biology, 2011, 7, 512.	7.2	32
30	Modular rate laws for enzymatic reactions: thermodynamics, elasticities and implementation. Bioinformatics, 2010, 26, 1528-1534.	4.1	110
31	Annotation and merging of SBML models with semanticSBML. Bioinformatics, 2010, 26, 421-422.	4.1	88
32	Parameter Balancing in Kinetic Models of Cell Metabolism. Journal of Physical Chemistry B, 2010, 114, 16298-16303.	2.6	43
33	Integrating quantitative proteomics and metabolomics with a genome-scale metabolic network model. Bioinformatics, 2010, 26, i255-i260.	4.1	219
34	A Quantitative Study of the Hog1 MAPK Response to Fluctuating Osmotic Stress in <i>Saccharomyces cerevisiae</i> . PLoS ONE, 2010, 5, e9522.	2.5	64
35	Nested uncertainties in biochemical models. IET Systems Biology, 2009, 3, 1-9.	1.5	35
36	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. Nature Biotechnology, 2008, 26, 1155-1160.	17.5	530

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37	EXPLORING THE EFFECT OF VARIABLE ENZYME CONCENTRATIONS IN A KINETIC MODEL OF YEAST GLYCOLYSIS. , 2008, , .		7
38	Systems biology standardsâ€”the community speaks. Nature Biotechnology, 2007, 25, 390-391.	17.5	87
39	AUTOMATICALLY GENERATED MODEL OF A METABOLIC NETWORK. , 2007, , .		5
40	Bringing metabolic networks to life: convenience rate law and thermodynamic constraints. Theoretical Biology and Medical Modelling, 2006, 3, 41.	2.1	191
41	Bringing metabolic networks to life: integration of kinetic, metabolic, and proteomic data. Theoretical Biology and Medical Modelling, 2006, 3, 42.	2.1	61
42	A comprehensive library of fluorescent transcriptional reporters for Escherichia coli. Nature Methods, 2006, 3, 623-628.	19.0	680
43	Mathematical modeling of intracellular signaling pathways. BMC Neuroscience, 2006, 7, S10.	1.9	119
44	SBMLmerge, a system for combining biochemical network models. Genome Informatics, 2006, 17, 62-71.	0.4	21
45	Response to temporal parameter fluctuations in biochemical networks. Journal of Theoretical Biology, 2005, 234, 423-438.	1.7	11
46	Biochemical network models simplified by balanced truncation. FEBS Journal, 2005, 272, 4034-4043.	4.7	51
47	Biochemical networks with uncertain parameters. IET Systems Biology, 2005, 152, 97.	2.0	47
48	Predicting Physiological Concentrations of Metabolites from Their Molecular Structure. Journal of Computational Biology, 2005, 12, 1307-1315.	1.6	9
49	A theory of optimal differential gene expression. BioSystems, 2004, 76, 261-278.	2.0	21
50	Inferring dynamic properties of biochemical reaction networks from structural knowledge. Genome Informatics, 2004, 15, 125-37.	0.4	12
51	Does mapping reveal correlation between gene expression and proteinâ€”protein interaction?. Nature Genetics, 2003, 33, 15-16.	21.4	20
52	Linear modes of gene expression determined by independent component analysis. Bioinformatics, 2002, 18, 51-60.	4.1	303
53	Ratcheting in post-translational protein translocation: a mathematical model ¹¹ Edited by G. von Heijne. Journal of Molecular Biology, 2001, 305, 643-656.	4.2	50