Johann M Rohwer

List of Publications by Year in descending order

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Version: 2024-02-01

81 papers 2,846 citations

27 h-index

201575

51 g-index

84 all docs

84 docs citations

84 times ranked 3789 citing authors

#	Article	IF	CITATIONS
1	Ribosome and transcript copy numbers, polysome occupancy and enzyme dynamics in <i>Arabidopsis</i> . Molecular Systems Biology, 2009, 5, 314.	3.2	276
2	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	3.2	178
3	Deoxyxylulose 5-Phosphate Synthase Controls Flux through the Methylerythritol 4-Phosphate Pathway in Arabidopsis. Plant Physiology, 2014, 165, 1488-1504.	2.3	154
4	Modelling cellular systems with PySCeS. Bioinformatics, 2005, 21, 560-561.	1.8	152
5	Analysis of sucrose accumulation in the sugar cane culm on the basis of in vitro kinetic data. Biochemical Journal, 2001, 358, 437-445.	1.7	132
6	Network Analysis of Enzyme Activities and Metabolite Levels and Their Relationship to Biomass in a Large Panel of <i>Arabidopsis </i> Accessions Â. Plant Cell, 2010, 22, 2872-2893.	3.1	131
7	Understanding Glucose Transport by the Bacterial Phosphoenolpyruvate: Glycose Phosphotransferase System on the Basis of Kinetic Measurements in Vitro. Journal of Biological Chemistry, 2000, 275, 34909-34921.	1.6	115
8	Metabolic Control Analysis of Glycerol Synthesis in Saccharomyces cerevisiae. Applied and Environmental Microbiology, 2002, 68, 4448-4456.	1.4	107
9	Kinetic model of sucrose accumulation in maturing sugarcane culm tissue. Phytochemistry, 2007, 68, 2375-2392.	1.4	103
10	Implications of macromolecular crowding for signal transduction and metabolite channeling. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 10547-10552.	3.3	102
11	Analysis of sucrose accumulation in the sugar cane culm on the basis of in vitro kinetic data. Biochemical Journal, 2001, 358, 437.	1.7	89
12	Kinetic modelling of plant metabolic pathways. Journal of Experimental Botany, 2012, 63, 2275-2292.	2.4	87
13	Taking enzyme kinetics out of control; putting control into regulation. FEBS Journal, 1993, 212, 833-837.	0.2	80
14	Standards for Reporting Enzyme Data: The STRENDA Consortium: What it aims to do and why it should be helpful. Perspectives in Science, 2014, 1, 131-137.	0.6	65
15	How to Recognize Monofunctional Units in a Metabolic System. Journal of Theoretical Biology, 1996, 179, 213-228.	0.8	58
16	Potency of progestogens used in hormonal therapy: Toward understanding differential actions. Journal of Steroid Biochemistry and Molecular Biology, 2014, 142, 39-47.	1.2	54
17	Impact of Glucocorticoid Receptor Density on Ligand-Independent Dimerization, Cooperative Ligand-Binding and Basal Priming of Transactivation: A Cell Culture Model. PLoS ONE, 2013, 8, e64831.	1.1	43
18	Investigation of the methylerythritol 4-phosphate pathway for microbial terpenoid production through metabolic control analysis. Microbial Cell Factories, 2019, 18, 192.	1.9	42

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19	The logic of kinetic regulation in the thioredoxin system. BMC Systems Biology, 2011, 5, 15.	3.0	39
20	From Top-Down to Bottom-Up: Computational Modeling Approaches for Cellular Redoxin Networks. Antioxidants and Redox Signaling, 2013, 18, 2075-2086.	2.5	39
21	Regulation of glycogen synthase from mammalian skeletal muscle – a unifying view of allosteric and covalent regulation. FEBS Journal, 2013, 280, 2-27.	2.2	39
22	STRENDA DB: enabling the validation and sharing of enzyme kinetics data. FEBS Journal, 2018, 285, 2193-2204.	2.2	38
23	Approximations and their consequences for dynamic modelling of signal transduction pathways. Mathematical Biosciences, 2007, 207, 40-57.	0.9	35
24	Composite control of cell function: metabolic pathways behaving as single control units. FEBS Letters, 1995, 368, 1-4.	1.3	33
25	Protein-level expression and localization of sucrose synthase in the sugarcane culm. Physiologia Plantarum, 2004, 121, 187-195.	2.6	33
26	Control of specific growth rate in Saccharomyces cerevisiae. Microbiology (United Kingdom), 2009, 155, 1699-1707.	0.7	32
27	From steadyâ€state to synchronized yeast glycolytic oscillations I: model construction. FEBS Journal, 2012, 279, 2810-2822.	2.2	30
28	Quantitative measures for redox signaling. Free Radical Biology and Medicine, 2016, 96, 290-303.	1.3	28
29	Partial purification and characterisation of sucrose synthase in sugarcane. Journal of Plant Physiology, 2005, 162, 11-20.	1.6	27
30	Kinetic and Thermodynamic Aspects of Enzyme Control and Regulation. Journal of Physical Chemistry B, 2010, 114, 16280-16289.	1.2	27
31	Effect of Drought on the Methylerythritol 4-Phosphate (MEP) Pathway in the Isoprene Emitting Conifer Picea glauca. Frontiers in Plant Science, 2020, 11, 546295.	1.7	27
32	Enzymes or redox couples? The kinetics of thioredoxin and glutaredoxin reactions in a systems biology context. Biochemical Journal, 2009, 417, 269-277.	1.7	25
33	The glutaredoxin mono- and di-thiol mechanisms for deglutathionylation are functionally equivalent: implications for redox systems biology. Bioscience Reports, 2015, 35, .	1.1	24
34	Evaluation of a simplified generic bi-substrate rate equation for computational systems biology. IET Systems Biology, 2006, 153, 338.	2.0	23
35	A kinetic study of sugarcane sucrose synthase. FEBS Journal, 2004, 271, 3971-3977.	0.2	22
36	Identifying and characterising regulatory metabolites with generalised supply–demand analysis. Journal of Theoretical Biology, 2008, 252, 546-554.	0.8	22

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37	A large-scale protein-function database. Nature Chemical Biology, 2010, 6, 785-785.	3.9	22
38	Supply–Demand Analysis. Methods in Enzymology, 2011, 500, 533-554.	0.4	21
39	Determining Enzyme Kinetics for Systems Biology with Nuclear Magnetic Resonance Spectroscopy. Metabolites, 2012, 2, 818-843.	1.3	20
40	PySCeSToolbox: a collection of metabolic pathway analysis tools. Bioinformatics, 2018, 34, 124-125.	1.8	20
41	An empirical analysis of enzyme function reporting for experimental reproducibility: Missing/incomplete information in published papers. Biophysical Chemistry, 2018, 242, 22-27.	1.5	19
42	Changes in the Cellular Energy State Affect the Activity of the Bacterial Phosphotransferase System. FEBS Journal, 1996, 235, 225-230.	0.2	18
43	Modelling cellular processes with Python and Scipy. Molecular Biology Reports, 2002, 29, 249-254.	1.0	18
44	Limits to inducer exclusion: inhibition of the bacterial phosphotransferase system by glycerol kinase. Molecular Microbiology, 1998, 29, 641-652.	1.2	15
45	Subtleties in control by metabolic channelling and enzyme organization. Molecular and Cellular Biochemistry, 1998, 184, 311-320.	1.4	14
46	Technical note On modifying the Arrhenius equation to compensate for temperature changes for reactions within biological systems. Water S A, 2012, 38, .	0.2	13
47	Energy, control and DNA structure in the living cell. Biophysical Chemistry, 1995, 55, 153-165.	1.5	12
48	BioSimulators: a central registry of simulation engines and services for recommending specific tools. Nucleic Acids Research, 2022, 50, W108-W114.	6.5	11
49	Summation theorems for flux and concentration control coefficients of dynamic systems. IET Systems Biology, 2006, 153, 314.	2.0	10
50	Tracing regulatory routes in metabolism using generalised supply-demand analysis. BMC Systems Biology, 2015, 9, 89.	3.0	10
51	A generic rate equation for catalysed, templateâ€directed polymerisation. FEBS Letters, 2013, 587, 2868-2875.	1.3	9
52	Experimental supply-demand analysis of anaerobic yeast energy metabolism. Molecular Biology Reports, 2002, 29, 203-209.	1.0	8
53	Identifying the conditions necessary for the thioredoxin ultrasensitive response. Perspectives in Science, 2016, 9, 53-59.	0.6	8
54	The thioredoxin redox potential and redox charge are surrogate measures for flux in the thioredoxin system. Archives of Biochemistry and Biophysics, 2020, 680, 108231.	1.4	7

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55	Workflow for Data Analysis in Experimental and Computational Systems Biology: Using Python as â€~Glue'. Processes, 2019, 7, 460.	1.3	6
56	An Annual and Seasonal Characterisation of Winery Effluent in South Africa. South African Journal of Enology and Viticulture, 2016, 32, .	0.8	6
57	HIERARCHIES IN CONTROL. Journal of Biological Systems, 1995, 03, 139-144.	0.5	5
58	Experimental evidence for allosteric modifier saturation as predicted by the bi-substrate Hill equation. IET Systems Biology, 2006, 153, 342.	2.0	5
59	Coupling kinetic models and advection–diffusion equations. 1. Framework development and application to sucrose translocation and metabolism in sugarcane. In Silico Plants, 2021, 3, .	0.8	5
60	How to distinguish between the vacuum cleaner and flippase mechanisms of the lmrA multi-drug transporter in Lactococcus lactis. Molecular Biology Reports, 2002, 29, 107-112.	1.0	4
61	Conditions for effective allosteric feedforward and feedback in metabolic pathways. IET Systems Biology, 2006, 153, 327.	2.0	4
62	Reuteran and levan as carbohydrate sinks in transgenic sugarcane. Planta, 2012, 236, 1803-1815.	1.6	4
63	Functional Characterisation of Three Glycine N-Acyltransferase Variants and the Effect on Glycine Conjugation to Benzoyl–CoA. International Journal of Molecular Sciences, 2021, 22, 3129.	1.8	4
64	Manganese privation induced transcriptional upregulation of the class IIa bacteriocin plantaricin 423 in Lactobacillus plantarum 423. Applied and Environmental Microbiology, 2021, 87, e0097621.	1.4	4
65	Subtleties in control by metabolic channelling and enzyme organization. , 1998, , 311-320.		4
66	ThermoKinetic modelling. Membrane potential as a dependent variable in ion transport processes. Molecular Biology Reports, 2002, 29, 217-225.	1.0	3
67	ECA: control in ecosystems. Molecular Biology Reports, 2002, 29, 113-117.	1.0	3
68	Comparing the regulatory behaviour of two cooperative, reversible enzyme mechanisms. IET Systems Biology, 2006, 153, 335.	2.0	3
69	Incorporating covalent and allosteric effects into rate equations: the case of muscle glycogen synthase. Biochemical Journal, 2014, 462, 525-537.	1.7	3
70	Direct Transfer of Control and Multidrug Resistance. , 1996, , 283-292.		3
71	Applications of Kinetic Modeling to Plant Metabolism. Methods in Molecular Biology, 2014, 1083, 275-286.	0.4	3
72	Is there an optimal ribosome concentration for maximal protein production?. IET Systems Biology, 2006, 153, 398.	2.0	2

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73	Delving deeper: Relating the behaviour of a metabolic system to the properties of its components using symbolic metabolic control analysis. PLoS ONE, 2018, 13, e0207983.	1.1	2
74	Coupling kinetic models and advection–diffusion equations. 2. Sensitivity analysis of an advection–diffusion–reaction model. In Silico Plants, 2021, 3, .	0.8	2
75	An Integrated Approach to the Analysis of the Control and Regulation of Cellular Systems. , 2000, , 73-79.		2
76	Editorial: 12th BTK Meeting: â€~Systems Biology: redefining BioThermoKinetics'. IET Systems Biology, 2006, 153, 312.	2.0	1
77	Software tools that facilitate kinetic modelling with large data sets: an example using growth modelling in sugarcane. IET Systems Biology, 2006, 153, 385.	2.0	1
78	Regulatory design and function in metabolism. Biochemical Society Transactions, 2002, 30, A5-A5.	1.6	0
79	Detailed Kinetic Models Using Metabolomics Data Sets. , 2005, , 215-242.		0
80	Putting the Cart before the Horse: Designing a Metabolic System in order to Understand it. , 2000, , 299-308.		0
81	Moiety Conservation and Flux Enhancement. , 2000, , 27-32.		0