Johann M Rohwer

List of Publications by Year
in descending order

81 papers	2,846 citations	201674 27 h-index	182427 51 g-index
84 all docs	84 docs citations	84 times ranked	3789 citing authors

#	Article	IF	Citations
1	BioSimulators: a central registry of simulation engines and services for recommending specific tools. Nucleic Acids Research, 2022, 50, W108-W114.	14.5	11
2	Coupling kinetic models and advectionâ€“diffusion equations. 1. Framework development and application to sucrose translocation and metabolism in sugarcane. In Silico Plants, 2021, 3, .	1.9	5
3	Coupling kinetic models and advectionâ€“diffusion equations. 2. Sensitivity analysis of an advectionâ€“diffusionâ€“reaction model. In Silico Plants, 2021, 3, .	1.9	2
4	Functional Characterisation of Three Glycine N-Acyltransferase Variants and the Effect on Glycine Conjugation to Benzoylâ€“CoA. International Journal of Molecular Sciences, 2021, 22, 3129.	4.1	4
5	Manganese privation induced transcriptional upregulation of the class IIa bacteriocin plantaricin 423 in Lactobacillus plantarum 423. Applied and Environmental Microbiology, 2021, 87, e0097621.	3.1	4
6	The thioredoxin redox potential and redox charge are surrogate measures for flux in the thioredoxin system. Archives of Biochemistry and Biophysics, 2020, 680, 108231.	3.0	7
7	Effect of Drought on the Methylerythritol 4-Phosphate (MEP) Pathway in the Isoprene Emitting Conifer Picea glauca. Frontiers in Plant Science, 2020, 11, 546295.	3.6	27
8	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	7.2	178
9	Workflow for Data Analysis in Experimental and Computational Systems Biology: Using Python as â€˜Glueâ€™. Processes, 2019, 7, 460.	2.8	6
10	Investigation of the methylerythritol 4-phosphate pathway for microbial terpenoid production through metabolic control analysis. Microbial Cell Factories, 2019, 18, 192.	4.0	42
11	STRENDA DB: enabling the validation and sharing of enzyme kinetics data. FEBS Journal, 2018, 285, 2193-2204.	4.7	38
12	PySCeSToolbox: a collection of metabolic pathway analysis tools. Bioinformatics, 2018, 34, 124-125.	4.1	20
13	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.	2.5	2
14	An empirical analysis of enzyme function reporting for experimental reproducibility: Missing/incomplete information in published papers. Biophysical Chemistry, 2018, 242, 22-27.	2.8	19
15	Quantitative measures for redox signaling. Free Radical Biology and Medicine, 2016, 96, 290-303.	2.9	28
16	Identifying the conditions necessary for the thioredoxin ultrasensitive response. Perspectives in Science, 2016, 9, 53-59.	0.6	8
17	An Annual and Seasonal Characterisation of Winery Effluent in South Africa. South African Journal of Enology and Viticulture, 2016, 32, .	0.4	6
18	Tracing regulatory routes in metabolism using generalised supply-demand analysis. BMC Systems Biology, 2015, 9, 89.	3.0	10

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19	The glutaredoxin mono- and di-thiol mechanisms for deglutathionylation are functionally equivalent: implications for redox systems biology. Bioscience Reports, 2015, 35, .	2.4	24
20	Incorporating covalent and allosteric effects into rate equations: the case of muscle glycogen synthase. Biochemical Journal, 2014, 462, 525-537.	3.7	3
21	Potency of progestogens used in hormonal therapy: Toward understanding differential actions. Journal of Steroid Biochemistry and Molecular Biology, 2014, 142, 39-47.	2.5	54
22	Deoxyxylulose 5-Phosphate Synthase Controls Flux through the Methylerythritol 4-Phosphate Pathway in Arabidopsis. Plant Physiology, 2014, 165, 1488-1504.	4.8	154
23	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
24	Applications of Kinetic Modeling to Plant Metabolism. Methods in Molecular Biology, 2014, 1083, 275-286.	0.9	3
25	From Top-Down to Bottom-Up: Computational Modeling Approaches for Cellular Redoxin Networks. Antioxidants and Redox Signaling, 2013, 18, 2075-2086.	5.4	39
26	A generic rate equation for catalysed, templateâ€directed polymerisation. FEBS Letters, 2013, 587, 2868-2875.	2.8	9
27	Regulation of glycogen synthase from mammalian skeletal muscle â€" a unifying view of allosteric and covalent regulation. FEBS Journal, 2013, 280, 2-27.	4.7	39
28	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.	2.5	43
29	Reuteran and levan as carbohydrate sinks in transgenic sugarcane. Planta, 2012, 236, 1803-1815.	3.2	4
30	Determining Enzyme Kinetics for Systems Biology with Nuclear Magnetic Resonance Spectroscopy. Metabolites, 2012, 2, 818-843.	2.9	20
31	Technical note On modifying the Arrhenius equation to compensate for temperature changes for reactions within biological systems. Water S A, 2012, 38, .	0.4	13
32	Kinetic modelling of plant metabolic pathways. Journal of Experimental Botany, 2012, 63, 2275-2292.	4.8	87
33	From steadyâ€state to synchronized yeast glycolytic oscillations I: model construction. FEBS Journal, 2012, 279, 2810-2822.	4.7	30
34	Supplyâ€"Demand Analysis. Methods in Enzymology, 2011, 500, 533-554.	1.0	21
35	The logic of kinetic regulation in the thioredoxin system. BMC Systems Biology, 2011, 5, 15.	3.0	39
36	Kinetic and Thermodynamic Aspects of Enzyme Control and Regulation. Journal of Physical Chemistry B, 2010, 114, 16280-16289.	2.6	27

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37	A large-scale protein-function database. Nature Chemical Biology, 2010, 6, 785-785.	8.0	22
38	Network Analysis of Enzyme Activities and Metabolite Levels and Their Relationship to Biomass in a Large Panel of<i>Arabidopsis</i>Accessions Â Â. Plant Cell, 2010, 22, 2872-2893.	6.6	131
39	Ribosome and transcript copy numbers, polysome occupancy and enzyme dynamics in <i>Arabidopsis</i>. Molecular Systems Biology, 2009, 5, 314.	7.2	276
40	Control of specific growth rate in Saccharomyces cerevisiae. Microbiology (United Kingdom), 2009, 155, 1699-1707.	1.8	32
41	Enzymes or redox couples? The kinetics of thioredoxin and glutaredoxin reactions in a systems biology context. Biochemical Journal, 2009, 417, 269-277.	3.7	25
42	Identifying and characterising regulatory metabolites with generalised supplyâ€“demand analysis. Journal of Theoretical Biology, 2008, 252, 546-554.	1.7	22
43	Approximations and their consequences for dynamic modelling of signal transduction pathways. Mathematical Biosciences, 2007, 207, 40-57.	1.9	35
44	Kinetic model of sucrose accumulation in maturing sugarcane culm tissue. Phytochemistry, 2007, 68, 2375-2392.	2.9	103
45	Is there an optimal ribosome concentration for maximal protein production?. IET Systems Biology, 2006, 153, 398.	2.0	2
46	Editorial: 12th BTK Meeting: â€˜Systems Biology: redefining BioThermoKineticsâ€™. IET Systems Biology, 2006, 153, 312.	2.0	1
47	Conditions for effective allosteric feedforward and feedback in metabolic pathways. IET Systems Biology, 2006, 153, 327.	2.0	4
48	Comparing the regulatory behaviour of two cooperative, reversible enzyme mechanisms. IET Systems Biology, 2006, 153, 335.	2.0	3
49	Summation theorems for flux and concentration control coefficients of dynamic systems. IET Systems Biology, 2006, 153, 314.	2.0	10
50	Evaluation of a simplified generic bi-substrate rate equation for computational systems biology. IET Systems Biology, 2006, 153, 338.	2.0	23
51	Experimental evidence for allosteric modifier saturation as predicted by the bi-substrate Hill equation. IET Systems Biology, 2006, 153, 342.	2.0	5
52	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
53	Modelling cellular systems with PySCeS. Bioinformatics, 2005, 21, 560-561.	4.1	152
54	Detailed Kinetic Models Using Metabolomics Data Sets. , 2005, , 215-242.		0

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55	Partial purification and characterisation of sucrose synthase in sugarcane. Journal of Plant Physiology, 2005, 162, 11-20.	3.5	27
56	A kinetic study of sugarcane sucrose synthase. FEBS Journal, 2004, 271, 3971-3977.	0.2	22
57	Protein-level expression and localization of sucrose synthase in the sugarcane culm. Physiologia Plantarum, 2004, 121, 187-195.	5.2	33
58	Metabolic Control Analysis of Glycerol Synthesis in Saccharomyces cerevisiae. Applied and Environmental Microbiology, 2002, 68, 4448-4456.	3.1	107
59	Regulatory design and function in metabolism. Biochemical Society Transactions, 2002, 30, A5-A5.	3.4	0
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.	2.3	4
61	Modelling cellular processes with Python and Scipy. Molecular Biology Reports, 2002, 29, 249-254.	2.3	18
62	Experimental supply-demand analysis of anaerobic yeast energy metabolism. Molecular Biology Reports, 2002, 29, 203-209.	2.3	8
63	ThermoKinetic modelling. Membrane potential as a dependent variable in ion transport processes. Molecular Biology Reports, 2002, 29, 217-225.	2.3	3
64	ECA: control in ecosystems. Molecular Biology Reports, 2002, 29, 113-117.	2.3	3
65	Analysis of sucrose accumulation in the sugar cane culm on the basis of in vitro kinetic data. Biochemical Journal, 2001, 358, 437.	3.7	89
66	Analysis of sucrose accumulation in the sugar cane culm on the basis of in vitro kinetic data. Biochemical Journal, 2001, 358, 437-445.	3.7	132
67	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.	3.4	115
68	An Integrated Approach to the Analysis of the Control and Regulation of Cellular Systems. , 2000, , 73-79.		2
69	Putting the Cart before the Horse: Designing a Metabolic System in order to Understand it. , 2000, , 299-308.		0
70	Moiety Conservation and Flux Enhancement. , 2000, , 27-32.		0
71	Subtleties in control by metabolic channelling and enzyme organization. Molecular and Cellular Biochemistry, 1998, 184, 311-320.	3.1	14
72	Limits to inducer exclusion: inhibition of the bacterial phosphotransferase system by glycerol kinase. Molecular Microbiology, 1998, 29, 641-652.	2.5	15

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73	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.	7.1	102
74	Subtleties in control by metabolic channelling and enzyme organization. , 1998, , 311-320.		4
75	Changes in the Cellular Energy State Affect the Activity of the Bacterial Phosphotransferase System. FEBS Journal, 1996, 235, 225-230.	0.2	18
76	How to Recognize Monofunctional Units in a Metabolic System. Journal of Theoretical Biology, 1996, 179, 213-228.	1.7	58
77	Direct Transfer of Control and Multidrug Resistance. , 1996, , 283-292.		3
78	Energy, control and DNA structure in the living cell. Biophysical Chemistry, 1995, 55, 153-165.	2.8	12
79	HIERARCHIES IN CONTROL. Journal of Biological Systems, 1995, 03, 139-144.	1.4	5
80	Composite control of cell function: metabolic pathways behaving as single control units. FEBS Letters, 1995, 368, 1-4.	2.8	33
81	Taking enzyme kinetics out of control; putting control into regulation. FEBS Journal, 1993, 212, 833-837.	0.2	80