

Kieran Smallbone

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

3,827
citations

218381

26
h-index

315357

38
g-index

47
all docs

47
docs citations

47
times ranked

4945
citing authors

#	ARTICLE	IF	CITATIONS
1	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	3.2	178
2	Bicarbonate-rich fluid secretion predicted by a computational model of guinea pig pancreatic duct epithelium. <i>Journal of Physiology</i> , 2017, 595, 1947-1972.	1.3	20
3	Metabolic regulation is sufficient for global and robust coordination of glucose uptake, catabolism, energy production and growth in <i>Escherichia coli</i> . <i>PLoS Computational Biology</i> , 2017, 13, e1005396.	1.5	85
4	Toward Community Standards and Software for Whole-Cell Modeling. <i>IEEE Transactions on Biomedical Engineering</i> , 2016, 63, 2007-2014.	2.5	51
5	Recon 2.2: from reconstruction to model of human metabolism. <i>Metabolomics</i> , 2016, 12, 109.	1.4	243
6	A robust and efficient method for estimating enzyme complex abundance and metabolic flux from expression data. <i>Computational Biology and Chemistry</i> , 2015, 59, 98-112.	1.1	22
7	BioPreDyn-bench: a suite of benchmark problems for dynamic modelling in systems biology. <i>BMC Systems Biology</i> , 2015, 9, 8.	3.0	61
8	Playing off the curve - testing quantitative predictions of skill acquisition theories in development of chess performance. <i>Frontiers in Psychology</i> , 2014, 5, 923.	1.1	17
9	A mathematical model of the colon crypt capturing compositional dynamic interactions between cell types. <i>International Journal of Experimental Pathology</i> , 2014, 95, 1-7.	0.6	12
10	A model of yeast glycolysis based on a consistent kinetic characterisation of all its enzymes. <i>FEBS Letters</i> , 2013, 587, 2832-2841.	1.3	113
11	Kinetic Modeling of Metabolic Pathways: Application to Serine Biosynthesis. <i>Methods in Molecular Biology</i> , 2013, 985, 113-121.	0.4	1
12	A community-driven global reconstruction of human metabolism. <i>Nature Biotechnology</i> , 2013, 31, 419-425.	9.4	920
13	Version 6 of the consensus yeast metabolic network refines biochemical coverage and improves model performance. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat059.	1.4	89
14	Large-Scale Metabolic Models: From Reconstruction to Differential Equations. <i>Industrial Biotechnology</i> , 2013, 9, 179-184.	0.5	58
15	Systematic Construction of Kinetic Models from Genome-Scale Metabolic Networks. <i>PLoS ONE</i> , 2013, 8, e79195.	1.1	102
16	Yeast 5 "an expanded reconstruction of the <i>Saccharomyces cerevisiae</i> metabolic network. <i>BMC Systems Biology</i> , 2012, 6, 55.	3.0	118
17	Improving metabolic flux predictions using absolute gene expression data. <i>BMC Systems Biology</i> , 2012, 6, 73.	3.0	126
18	Mechanistic modelling of cancer: some reflections from software engineering and philosophy of science. <i>Die Naturwissenschaften</i> , 2012, 99, 973-983.	0.6	1

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19	Modelling acidosis and the cell cycle in multicellular tumour spheroids. <i>Journal of Theoretical Biology</i> , 2012, 298, 107-115.	0.8	11
20	Building a Kinetic Model of Trehalose Biosynthesis in <i>Saccharomyces cerevisiae</i> . <i>Methods in Enzymology</i> , 2011, 500, 355-370.	0.4	17
21	The SuBliMinal Toolbox: automating steps in the reconstruction of metabolic networks. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 187-203.	1.0	67
22	A probabilistic approach to identify putative drug targets in biochemical networks. <i>Journal of the Royal Society Interface</i> , 2011, 8, 880-895.	1.5	41
23	Kinetic modelling of large-scale metabolic networks. , 2011, , .		2
24	The SuBliMinal Toolbox: automating steps in the reconstruction of metabolic networks. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 186.	1.0	51
25	Modelling Aspects of Tumour Metabolism. , 2011, , .		0
26	Why does yeast ferment? A flux balance analysis study. <i>Biochemical Society Transactions</i> , 2010, 38, 1225-1229.	1.6	26
27	Episodic, transient systemic acidosis delays evolution of the malignant phenotype: Possible mechanism for cancer prevention by increased physical activity. <i>Biology Direct</i> , 2010, 5, 22.	1.9	21
28	Towards a genome-scale kinetic model of cellular metabolism. <i>BMC Systems Biology</i> , 2010, 4, 6.	3.0	132
29	Enzyme kinetics informatics: from instrument to browser. <i>FEBS Journal</i> , 2010, 277, 3769-3779.	2.2	20
30	Further developments towards a genome-scale metabolic model of yeast. <i>BMC Systems Biology</i> , 2010, 4, 145.	3.0	95
31	Why are (the best) women so good at chess? Participation rates and gender differences in intellectual domains. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2009, 276, 1161-1165.	1.2	38
32	Flux balance analysis: A geometric perspective. <i>Journal of Theoretical Biology</i> , 2009, 258, 311-315.	0.8	66
33	Capturing the essence of a metabolic network: A flux balance analysis approach. <i>Journal of Theoretical Biology</i> , 2009, 260, 445-452.	0.8	31
34	Tumour glycolysis: The many faces of HIF. <i>Journal of Theoretical Biology</i> , 2008, 254, 508-513.	0.8	22
35	Mathematical modelling of tumour acidity. <i>Journal of Theoretical Biology</i> , 2008, 255, 106-112.	0.8	36
36	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. <i>Nature Biotechnology</i> , 2008, 26, 1155-1160.	9.4	530

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37	A MODEL TO INVESTIGATE THE FEASIBILITY OF FDG AS A SURROGATE MARKER OF HYPOXIA. , 2007, , .		1
38	Metabolic changes during carcinogenesis: Potential impact on invasiveness. Journal of Theoretical Biology, 2007, 244, 703-713.	0.8	164
39	Something from nothing~â€fâ~â€fbridging the gap between constraintâ€based and kinetic modelling. FEBS Journal, 2007, 274, 5576-5585.	2.2	84
40	Quiescence as a mechanism for cyclical hypoxia and acidosis. Journal of Mathematical Biology, 2007, 55, 767-779.	0.8	8
41	The role of acidity in solid tumour growth and invasion. Journal of Theoretical Biology, 2005, 235, 476-484.	0.8	140