## Kieran Smallbone

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8529262/publications.pdf

Version: 2024-02-01

41 papers

3,827 citations

26 h-index 315357 38 g-index

47 all docs

47 docs citations

47 times ranked

4945 citing authors

#	Article	IF	CITATIONS
1	A community-driven global reconstruction of human metabolism. Nature Biotechnology, 2013, 31, 419-425.	9.4	920
2	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. Nature Biotechnology, 2008, 26, 1155-1160.	9.4	530
3	Recon 2.2: from reconstruction to model of human metabolism. Metabolomics, 2016, 12, 109.	1.4	243
4	<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
5	Metabolic changes during carcinogenesis: Potential impact on invasiveness. Journal of Theoretical Biology, 2007, 244, 703-713.	0.8	164
6	The role of acidity in solid tumour growth and invasion. Journal of Theoretical Biology, 2005, 235, 476-484.	0.8	140
7	Towards a genome-scale kinetic model of cellular metabolism. BMC Systems Biology, 2010, 4, 6.	3.0	132
8	Improving metabolic flux predictions using absolute gene expression data. BMC Systems Biology, 2012, 6, 73.	3.0	126
9	Yeast 5 – an expanded reconstruction of the Saccharomyces cerevisiae metabolic network. BMC Systems Biology, 2012, 6, 55.	3.0	118
10	A model of yeast glycolysis based on a consistent kinetic characterisation of all its enzymes. FEBS Letters, 2013, 587, 2832-2841.	1.3	113
11	Systematic Construction of Kinetic Models from Genome-Scale Metabolic Networks. PLoS ONE, 2013, 8, e79195.	1.1	102
12	Further developments towards a genome-scale metabolic model of yeast. BMC Systems Biology, 2010, 4, 145.	3.0	95
13	Version 6 of the consensus yeast metabolic network refines biochemical coverage and improves model performance. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat059.	1.4	89
14	Metabolic regulation is sufficient for global and robust coordination of glucose uptake, catabolism, energy production and growth in Escherichia coli. PLoS Computational Biology, 2017, 13, e1005396.	1.5	85
15	Something from nothing â^' bridging the gap between constraintâ€based and kinetic modelling. FEBS Journal, 2007, 274, 5576-5585.	2.2	84
16	The SuBliMinaL Toolbox: automating steps in the reconstruction of metabolic networks. Journal of Integrative Bioinformatics, 2011, 8, 187-203.	1.0	67
17	Flux balance analysis: A geometric perspective. Journal of Theoretical Biology, 2009, 258, 311-315.	0.8	66
18	BioPreDyn-bench: a suite of benchmark problems for dynamic modelling in systems biology. BMC Systems Biology, 2015, 9, 8.	3.0	61

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19	Large-Scale Metabolic Models: From Reconstruction to Differential Equations. Industrial Biotechnology, 2013, 9, 179-184.	0.5	58
20	Toward Community Standards and Software for Whole-Cell Modeling. IEEE Transactions on Biomedical Engineering, 2016, 63, 2007-2014.	2.5	51
21	The SuBliMinaL Toolbox: automating steps in the reconstruction of metabolic networks. Journal of Integrative Bioinformatics, 2011, 8, 186.	1.0	51
22	A probabilistic approach to identify putative drug targets in biochemical networks. Journal of the Royal Society Interface, 2011, 8, 880-895.	1.5	41
23	Why are (the best) women so good at chess? Participation rates and gender differences in intellectual domains. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 1161-1165.	1.2	38
24	Mathematical modelling of tumour acidity. Journal of Theoretical Biology, 2008, 255, 106-112.	0.8	36
25	Capturing the essence of a metabolic network: A flux balance analysis approach. Journal of Theoretical Biology, 2009, 260, 445-452.	0.8	31
26	Why does yeast ferment? A flux balance analysis study. Biochemical Society Transactions, 2010, 38, 1225-1229.	1.6	26
27	Tumour glycolysis: The many faces of HIF. Journal of Theoretical Biology, 2008, 254, 508-513.	0.8	22
28	A robust and efficient method for estimating enzyme complex abundance and metabolic flux from expression data. Computational Biology and Chemistry, 2015, 59, 98-112.	1.1	22
29	Episodic, transient systemic acidosis delays evolution of the malignant phenotype: Possible mechanism for cancer prevention by increased physical activity. Biology Direct, 2010, 5, 22.	1.9	21
30	Enzyme kinetics informatics: from instrument to browser. FEBS Journal, 2010, 277, 3769-3779.	2.2	20
31	Bicarbonateâ€rich fluid secretion predicted by a computational model of guineaâ€pig pancreatic duct epithelium. Journal of Physiology, 2017, 595, 1947-1972.	1.3	20
32	Building a Kinetic Model of Trehalose Biosynthesis in Saccharomyces cerevisiae. Methods in Enzymology, 2011, 500, 355-370.	0.4	17
33	Playing off the curve - testing quantitative predictions of skill acquisition theories in development of chess performance. Frontiers in Psychology, 2014, 5, 923.	1.1	17
34	A mathematical model of the colon crypt capturing compositional dynamic interactions between cell types. International Journal of Experimental Pathology, 2014, 95, 1-7.	0.6	12
35	Modelling acidosis and the cell cycle in multicellular tumour spheroids. Journal of Theoretical Biology, 2012, 298, 107-115.	0.8	11
36	Quiescence as a mechanism for cyclical hypoxia and acidosis. Journal of Mathematical Biology, 2007, 55, 767-779.	0.8	8

#	Article	IF	CITATIONS
37	Kinetic modelling of large-scale metabolic networks. , 2011, , .		2
38	A MODEL TO INVESTIGATE THE FEASIBILITY OF FDG AS A SURROGATE MARKER OF HYPOXIA. , 2007, , .		1
39	Mechanistic modelling of cancer: some reflections from software engineering and philosophy of science. Die Naturwissenschaften, 2012, 99, 973-983.	0.6	1
40	Kinetic Modeling of Metabolic Pathways: Application to Serine Biosynthesis. Methods in Molecular Biology, 2013, 985, 113-121.	0.4	1
41	Modelling Aspects of Tumour Metabolism. , 2011, , .		0