Edmund J Crampin

List of Publications by Year
in descending order

87 papers	3,206 citations	186265 28 h-index	175258 52 g-index
100 all docs	100 docs citations	100 times ranked	4606 citing authors

#	Article	IF	Citations
1	Spatio-temporal analysis of nanoparticles in live tumor spheroids impacted by cell origin and density. Journal of Controlled Release, 2022, 341, 661-675.	9.9	12
2	A semantics, energy-based approach to automate biomodel composition. PLoS ONE, 2022, 17, e0269497.	2.5	4
3	High temporal resolution RNA-seq time course data reveals widespread synchronous activation between mammalian lncRNAs and neighboring protein-coding genes. Genome Research, 2022, 32, 1463-1473.	5.5	5
4	Understanding nano-engineered particleâ€“cell interactions: biological insights from mathematical models. Nanoscale Advances, 2021, 3, 2139-2156.	4.6	17
5	Hierarchical semantic composition of biosimulation models using bond graphs. PLoS Computational Biology, 2021, 17, e1008859.	3.2	15
6	Modular dynamic biomolecular modelling with bond graphs: the unification of stoichiometry, thermodynamics, kinetics and data. Journal of the Royal Society Interface, 2021, 18, 20210478.	3.4	10
7	Bio-nano Science: Better Metrics Would Accelerate Progress. Chemistry of Materials, 2021, 33, 7613-7619.	6.7	4
8	Maintaining the proliferative cell niche in multicellular models of epithelia. Journal of Theoretical Biology, 2021, 527, 110807.	1.7	4
9	Modular assembly of dynamic models in systems biology. PLoS Computational Biology, 2021, 17, e1009513.	3.2	19
10	Analysing and simulating energy-based models in biology using BondGraphTools. European Physical Journal E, 2021, 44, 148.	1.6	13
11	A few clarifications on MIRIBEL. Nature Nanotechnology, 2020, 15, 2-3.	31.5	15
12	Ca2+ Release via IP3 Receptors Shapes the Cardiac Ca2+ Transient for Hypertrophic Signaling. Biophysical Journal, 2020, 119, 1178-1192.	0.5	13
13	Isolating the sources of heterogeneity in nano-engineered particleâ€“cell interactions. Journal of the Royal Society Interface, 2020, 17, 20200221.	3.4	13
14	Insights From Computational Modeling Into the Contribution of Mechano-Calcium Feedback on the Cardiac End-Systolic Force-Length Relationship. Frontiers in Physiology, 2020, 11, 587.	2.8	3
15	Physically-plausible modelling of biomolecular systems: A simplified, energy-based model of the mitochondrial electron transport chain. Journal of Theoretical Biology, 2020, 493, 110223.	1.7	16
16	Predicting population extinction in lattice-based birthâ€“deathâ€“movement models. Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences, 2020, 476, 20200089.	2.1	5
17	The cardiac Na+/K+ ATPase: An updated, thermodynamically consistent model. Physiome, 2020, , .	0.3	4
18	How Does the Internal Structure of Cardiac Muscle Cells Regulate Cellular Metabolism?. Microscopy and Microanalysis, 2019, 25, 240-241.	0.4	0

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19	Revisiting cellâ€“particle association in vitro: A quantitative method to compare particle performance. Journal of Controlled Release, 2019, 307, 355-367.	9.9	23
20	Link between Low-Fouling and Stealth: A Whole Blood Biomolecular Corona and Cellular Association Analysis on Nanoengineered Particles. ACS Nano, 2019, 13, 4980-4991.	14.6	53
21	Data-Driven Modelling of the Inositol Trisphosphate ReceptorÂ($$ext {IP}_3ext {R}$$) and its Role in Calcium-Induced Calcium ReleaseÂ(CICR). Springer Series in Computational Neuroscience, 2019, , 39-68.	0.3	2
22	Corrected pair correlation functions for environments with obstacles. Physical Review E, 2019, 99, 032124.	2.1	5
23	Mathematical modelling indicates that lower activity of the haemostatic system in neonates is primarily due to lower prothrombin concentration. Scientific Reports, 2019, 9, 3936.	3.3	4
24	Quantifying the Influence of Nanoparticle Polydispersity on Cellular Delivered Dose. Biophysical Journal, 2019, 116, 33a.	0.5	1
25	Assessing Cardiomyocyte Excitation-Contraction Coupling Site Detection From Live Cell Imaging Using a Structurally-Realistic Computational Model of Calcium Release. Frontiers in Physiology, 2019, 10, 1263.	2.8	8
26	A thermodynamic framework for modelling membrane transporters. Journal of Theoretical Biology, 2019, 481, 10-23.	1.7	24
27	DiSNE Movie Visualization and Assessment of Clonal Kinetics Reveal Multiple Trajectories of Dendritic Cell Development. Cell Reports, 2018, 22, 2557-2566.	6.4	33
28	Creatine-Kinase Shuttle and Rapid Mitochondrial Membrane Potential Conductivity are Needed Simultaneously to Maintain Uniform Metabolite Distributions in the Cardiac Cell Contraction Cycle. Biophysical Journal, 2018, 114, 550a.	0.5	1
29	Insights on the impact of mitochondrial organisation on bioenergetics in high-resolution computational models of cardiac cell architecture. PLoS Computational Biology, 2018, 14, e1006640.	3.2	23
30	Creating a Structurally Realistic Finite Element Geometric Model of a Cardiomyocyte to Study the Role of Cellular Architecture in Cardiomyocyte Systems Biology. Journal of Visualized Experiments, 2018, , .	0.3	3
31	Bond Graph Representation of Chemical Reaction Networks. IEEE Transactions on Nanobioscience, 2018, 17, 449-455.	3.3	14
32	Minimum information reporting in bioâ€“nano experimental literature. Nature Nanotechnology, 2018, 13, 777-785.	31.5	455
33	Bond graph modelling of theÂcardiac action potential: implications for drift and non-unique steady states. Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences, 2018, 474, 20180106.	2.1	19
34	An analytical approach for quantifying the influence of nanoparticle polydispersity on cellular delivered dose. Journal of the Royal Society Interface, 2018, 15, 20180364.	3.4	33
35	Combinatorial Targeting by MicroRNAs Co-ordinates Post-transcriptional Control of EMT. Cell Systems, 2018, 7, 77-91.e7.	6.2	92
36	Changes in mitochondrial morphology and organization can enhance energy supply from mitochondrial oxidative phosphorylation in diabetic cardiomyopathy. American Journal of Physiology - Cell Physiology, 2017, 312, C190-C197.	4.6	33

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37	Charge Has a Marked Influence on Hyperbranched Polymer Nanoparticle Association in Whole Human Blood. ACS Macro Letters, 2017, 6, 586-592.	4.8	27
38	Bond graph modelling of chemoelectrical energy transduction. IET Systems Biology, 2017, 11, 127-138.	1.5	18
39	Energy-based analysis of biomolecular pathways. Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences, 2017, 473, 20160825.	2.1	20
40	Distributed gene expression modelling for exploring variability in epigenetic function. BMC Bioinformatics, 2016, 17, 446.	2.6	0
41	A Framework to Account for Sedimentation and Diffusion in Particleâ€“Cell Interactions. Langmuir, 2016, 32, 12394-12402.	3.5	48
42	Myocardial energetics is not compromised during compensated hypertrophy in the Dahl salt-sensitive rat model of hypertension. American Journal of Physiology - Heart and Circulatory Physiology, 2016, 311, H563-H571.	3.2	11
43	Modular bondâ€graph modelling and analysis of biomolecular systems. IET Systems Biology, 2016, 10, 187-201.	1.5	35
44	Modelling modal gating of ion channels with hierarchical Markov models. Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences, 2016, 472, 20160122.	2.1	14
45	Systems analysis identifies miR-29b regulation of invasiveness in melanoma. Molecular Cancer, 2016, 15, 72.	19.2	21
46	Information theoretic approaches for inference of biological networks from continuous-valued data. BMC Systems Biology, 2016, 10, 89.	3.0	13
47	Regulation of cardiac cellular bioenergetics: mechanisms and consequences. Physiological Reports, 2015, 3, e12464.	1.7	17
48	Network analysis of an in vitro model of androgen-resistance in prostate cancer. BMC Cancer, 2015, 15, 883.	2.6	3
49	Spatially transformed fluorescence image data for ERK-MAPK and selected proteins within human epidermis. GigaScience, 2015, 4, 63.	6.4	6
50	Examination of the Effects of Heterogeneous Organization of RyR Clusters, Myofibrils and Mitochondria on Ca2+ Release Patterns in Cardiomyocytes. PLoS Computational Biology, 2015, 11, e1004417.	3.2	46
51	Semantics-Based Composition of Integrated Cardiomyocyte Models Motivated by Real-World Use Cases. PLoS ONE, 2015, 10, e0145621.	2.5	29
52	Hierarchical bond graph modelling of biochemical networks. Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences, 2015, 471, 20150642.	2.1	41
53	A spatial model of fluid recycling in the airways of the lung. Journal of Theoretical Biology, 2015, 382, 198-215.	1.7	10
54	Stimulus-dependent differences in signalling regulate epithelial-mesenchymal plasticity and change the effects of drugs in breast cancer cell lines. Cell Communication and Signaling, 2015, 13, 26.	6.5	47

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55	Modelling the conditional regulatory activity of methylated and bivalent promoters. Epigenetics and Chromatin, 2015, 8, 21.	3.9	6
56	Regulation of ERK-MAPK signaling in human epidermis. BMC Systems Biology, 2015, 9, 41.	3.0	33
57	Virtual Reference Environments: a simple way to make research reproducible. Briefings in Bioinformatics, 2015, 16, 901-903.	6.5	23
58	NAIL, a software toolset for inferring, analyzing and visualizing regulatory networks. Bioinformatics, 2015, 31, 277-278.	4.1	12
59	Predicting expression: the complementary power of histone modification and transcription factor binding data. Epigenetics and Chromatin, 2014, 7, 36.	3.9	32
60	Statistical analysis of modal gating in ion channels. Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences, 2014, 470, 20140030.	2.1	14
61	Energy-based analysis of biochemical cycles using bond graphs. Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences, 2014, 470, 20140459.	2.1	50
62	Multiscale modelling of saliva secretion. Mathematical Biosciences, 2014, 257, 69-79.	1.9	19
63	Integration of Steady-State and Temporal Gene Expression Data for the Inference of Gene Regulatory Networks. PLoS ONE, 2013, 8, e72103.	2.5	15
64	Gene network inference and visualization tools for biologists: application to new human transcriptome datasets. Nucleic Acids Research, 2012, 40, 2377-2398.	14.5	65
65	MCMC Can Detect Nonidentifiable Models. Biophysical Journal, 2012, 103, 2275-2286.	0.5	80
66	A Kinetic Model for Type I and II IP3R Accounting for Mode Changes. Biophysical Journal, 2012, 103, 658-668.	0.5	59
67	MCMC Estimation of Markov Models for Ion Channels. Biophysical Journal, 2011, 100, 1919-1929.	0.5	54
68	A Graphical User Interface for a Method to Infer Kinetics and Network Architecture (MIKANA). PLoS ONE, 2011, 6, e27534.	2.5	6
69	Cardiac cell modelling: Observations from the heart of the cardiac physiome project. Progress in Biophysics and Molecular Biology, 2011, 104, 2-21.	2.9	139
70	Gene Network Analysis and Application. Seibutsu Butsuri, 2011, 51, 182-185.	0.1	1
71	Enzyme catalyzed reactions: From experiment to computational mechanism reconstruction. Computational Biology and Chemistry, 2010, 34, 11-18.	2.3	7
72	Why has reversal of the actin-myosin cross-bridge cycle not been observed experimentally?. Journal of Applied Physiology, 2010, 108, 1465-1471.	2.5	13

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73	A Metabolite-Sensitive, Thermodynamically Constrained Model of Cardiac Cross-Bridge Cycling: Implications for Force Development during Ischemia. Biophysical Journal, 2010, 98, 267-276.	0.5	38
74	Inference of an in situ epidermal intracellular signaling cascade. , 2010, 2010, 799-802.		3
75	A Thermodynamic Model of the Cardiac Sarcoplasmic/Endoplasmic Ca2+ (SERCA) Pump. Biophysical Journal, 2009, 96, 2029-2042.	0.5	76
76	Sensitivity of NFAT Cycling to Cytosolic Calcium Concentration: Implications for Hypertrophic Signals in Cardiac Myocytes. Biophysical Journal, 2009, 96, 2095-2104.	0.5	38
77	Using Physiome standards to couple cellular functions for rat cardiac excitationâ€“contraction. Experimental Physiology, 2008, 93, 919-929.	2.0	46
78	Bioinformatics, multiscale modeling and the IUPS Physiome Project. Briefings in Bioinformatics, 2008, 9, 333-343.	6.5	89
79	Computational biology of cardiac myocytes: proposed standards for the physiome. Journal of Experimental Biology, 2007, 210, 1576-1583.	1.7	45
80	The balance between inactivation and activation of the Na⁺-K⁺pump underlies the triphasic accumulation of extracellular K⁺during myocardial ischemia. American Journal of Physiology - Heart and Circulatory Physiology, 2007, 293, H3036-H3045.	3.2	46
81	Modeling Hypertrophic IP3 Transients in the Cardiac Myocyte. Biophysical Journal, 2007, 93, 3421-3433.	0.5	49
82	Reconstructing biochemical pathways from time course data. Proteomics, 2007, 7, 828-838.	2.2	40
83	A Dynamic Model of Excitation-Contraction Coupling during Acidosis in Cardiac Ventricular Myocytes. Biophysical Journal, 2006, 90, 3074-3090.	0.5	59
84	Acidosis in models of cardiac ventricular myocytes. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2006, 364, 1171-1186.	3.4	41
85	Minimum information requested in the annotation of biochemical models (MIRIAM). Nature Biotechnology, 2005, 23, 1509-1515.	17.5	553
86	Multi-scale modelling and the IUPS physiome project. Journal of Molecular Histology, 2004, 35, 707-714.	2.2	32
87	Extracting Biochemical Reaction Kinetics from Time Series Data. Lecture Notes in Computer Science, 2004, , 329-336.	1.3	3