

# Edmund J Crampin

## List of Publications by Year in descending order

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Version: 2024-02-01

87  
papers

3,206  
citations

186254  
28  
h-index

175241  
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. <i>Journal of Controlled Release</i> , 2022, 341, 661-675.	9.9	12
2	A semantics, energy-based approach to automate biomodel composition. <i>PLoS ONE</i> , 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. <i>Genome Research</i> , 2022, 32, 1463-1473.	5.5	5
4	Understanding nano-engineered particle–cell interactions: biological insights from mathematical models. <i>Nanoscale Advances</i> , 2021, 3, 2139-2156.	4.6	17
5	Hierarchical semantic composition of biosimulation models using bond graphs. <i>PLoS Computational Biology</i> , 2021, 17, e1008859.	3.2	15
6	Modular dynamic biomolecular modelling with bond graphs: the unification of stoichiometry, thermodynamics, kinetics and data. <i>Journal of the Royal Society Interface</i> , 2021, 18, 20210478.	3.4	10
7	Bio-nano Science: Better Metrics Would Accelerate Progress. <i>Chemistry of Materials</i> , 2021, 33, 7613-7619.	6.7	4
8	Maintaining the proliferative cell niche in multicellular models of epithelia. <i>Journal of Theoretical Biology</i> , 2021, 527, 110807.	1.7	4
9	Modular assembly of dynamic models in systems biology. <i>PLoS Computational Biology</i> , 2021, 17, e1009513.	3.2	19
10	Analysing and simulating energy-based models in biology using BondGraphTools. <i>European Physical Journal E</i> , 2021, 44, 148.	1.6	13
11	A few clarifications on MIRIBEL. <i>Nature Nanotechnology</i> , 2020, 15, 2-3.	31.5	15
12	Ca <sup>2+</sup> Release via IP <sub>3</sub> Receptors Shapes the Cardiac Ca <sup>2+</sup> Transient for Hypertrophic Signaling. <i>Biophysical Journal</i> , 2020, 119, 1178-1192.	0.5	13
13	Isolating the sources of heterogeneity in nano-engineered particle–cell interactions. <i>Journal of the Royal Society Interface</i> , 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. <i>Frontiers in Physiology</i> , 2020, 11, 587.	2.8	3
15	Physically-plausible modelling of biomolecular systems: A simplified, energy-based model of the mitochondrial electron transport chain. <i>Journal of Theoretical Biology</i> , 2020, 493, 110223.	1.7	16
16	Predicting population extinction in lattice-based birth–death–movement models. <i>Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences</i> , 2020, 476, 20200089.	2.1	5
17	The cardiac Na <sup>+</sup> /K <sup>+</sup> ATPase: An updated, thermodynamically consistent model. <i>Physiome</i> , 2020, , .	0.3	4
18	How Does the Internal Structure of Cardiac Muscle Cells Regulate Cellular Metabolism?. <i>Microscopy and Microanalysis</i> , 2019, 25, 240-241.	0.4	0

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19	Revisiting cell-particle association in vitro: A quantitative method to compare particle performance. <i>Journal of Controlled Release</i> , 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. <i>ACS Nano</i> , 2019, 13, 4980-4991.	14.6	53
21	Data-Driven Modelling of the Inositol Trisphosphate Receptor (IP <sub>3</sub> R) and its Role in Calcium-Induced Calcium Release (CICR). <i>Springer Series in Computational Neuroscience</i> , 2019, , 39-68.	0.3	2
22	Corrected pair correlation functions for environments with obstacles. <i>Physical Review E</i> , 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. <i>Scientific Reports</i> , 2019, 9, 3936.	3.3	4
24	Quantifying the Influence of Nanoparticle Polydispersity on Cellular Delivered Dose. <i>Biophysical Journal</i> , 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. <i>Frontiers in Physiology</i> , 2019, 10, 1263.	2.8	8
26	A thermodynamic framework for modelling membrane transporters. <i>Journal of Theoretical Biology</i> , 2019, 481, 10-23.	1.7	24
27	DiSNE Movie Visualization and Assessment of Clonal Kinetics Reveal Multiple Trajectories of Dendritic Cell Development. <i>Cell Reports</i> , 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. <i>Biophysical Journal</i> , 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. <i>PLoS Computational Biology</i> , 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. <i>Journal of Visualized Experiments</i> , 2018, , .	0.3	3
31	Bond Graph Representation of Chemical Reaction Networks. <i>IEEE Transactions on Nanobioscience</i> , 2018, 17, 449-455.	3.3	14
32	Minimum information reporting in bio-nano experimental literature. <i>Nature Nanotechnology</i> , 2018, 13, 777-785.	31.5	455
33	Bond graph modelling of the cardiac action potential: implications for drift and non-unique steady states. <i>Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences</i> , 2018, 474, 20180106.	2.1	19
34	An analytical approach for quantifying the influence of nanoparticle polydispersity on cellular delivered dose. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20180364.	3.4	33
35	Combinatorial Targeting by MicroRNAs Co-ordinates Post-transcriptional Control of EMT. <i>Cell Systems</i> , 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. <i>American Journal of Physiology - Cell Physiology</i> , 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. <i>ACS Macro Letters</i> , 2017, 6, 586-592.	4.8	27
38	Bond graph modelling of chemoelectrical energy transduction. <i>IET Systems Biology</i> , 2017, 11, 127-138.	1.5	18
39	Energy-based analysis of biomolecular pathways. <i>Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences</i> , 2017, 473, 20160825.	2.1	20
40	Distributed gene expression modelling for exploring variability in epigenetic function. <i>BMC Bioinformatics</i> , 2016, 17, 446.	2.6	0
41	A Framework to Account for Sedimentation and Diffusion in Particle-Cell Interactions. <i>Langmuir</i> , 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. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2016, 311, H563-H571.	3.2	11
43	Modular bond graph modelling and analysis of biomolecular systems. <i>IET Systems Biology</i> , 2016, 10, 187-201.	1.5	35
44	Modelling modal gating of ion channels with hierarchical Markov models. <i>Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences</i> , 2016, 472, 20160122.	2.1	14
45	Systems analysis identifies miR-29b regulation of invasiveness in melanoma. <i>Molecular Cancer</i> , 2016, 15, 72.	19.2	21
46	Information theoretic approaches for inference of biological networks from continuous-valued data. <i>BMC Systems Biology</i> , 2016, 10, 89.	3.0	13
47	Regulation of cardiac cellular bioenergetics: mechanisms and consequences. <i>Physiological Reports</i> , 2015, 3, e12464.	1.7	17
48	Network analysis of an in vitro model of androgen-resistance in prostate cancer. <i>BMC Cancer</i> , 2015, 15, 883.	2.6	3
49	Spatially transformed fluorescence image data for ERK-MAPK and selected proteins within human epidermis. <i>GigaScience</i> , 2015, 4, 63.	6.4	6
50	Examination of the Effects of Heterogeneous Organization of RyR Clusters, Myofibrils and Mitochondria on Ca <sup>2+</sup> Release Patterns in Cardiomyocytes. <i>PLoS Computational Biology</i> , 2015, 11, e1004417.	3.2	46
51	Semantics-Based Composition of Integrated Cardiomyocyte Models Motivated by Real-World Use Cases. <i>PLoS ONE</i> , 2015, 10, e0145621.	2.5	29
52	Hierarchical bond graph modelling of biochemical networks. <i>Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences</i> , 2015, 471, 20150642.	2.1	41
53	A spatial model of fluid recycling in the airways of the lung. <i>Journal of Theoretical Biology</i> , 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. <i>Cell Communication and Signaling</i> , 2015, 13, 26.	6.5	47

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55	Modelling the conditional regulatory activity of methylated and bivalent promoters. <i>Epigenetics and Chromatin</i> , 2015, 8, 21.	3.9	6
56	Regulation of ERK-MAPK signaling in human epidermis. <i>BMC Systems Biology</i> , 2015, 9, 41.	3.0	33
57	Virtual Reference Environments: a simple way to make research reproducible. <i>Briefings in Bioinformatics</i> , 2015, 16, 901-903.	6.5	23
58	NAIL, a software toolset for inferring, analyzing and visualizing regulatory networks. <i>Bioinformatics</i> , 2015, 31, 277-278.	4.1	12
59	Predicting expression: the complementary power of histone modification and transcription factor binding data. <i>Epigenetics and Chromatin</i> , 2014, 7, 36.	3.9	32
60	Statistical analysis of modal gating in ion channels. <i>Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences</i> , 2014, 470, 20140030.	2.1	14
61	Energy-based analysis of biochemical cycles using bond graphs. <i>Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences</i> , 2014, 470, 20140459.	2.1	50
62	Multiscale modelling of saliva secretion. <i>Mathematical Biosciences</i> , 2014, 257, 69-79.	1.9	19
63	Integration of Steady-State and Temporal Gene Expression Data for the Inference of Gene Regulatory Networks. <i>PLoS ONE</i> , 2013, 8, e72103.	2.5	15
64	Gene network inference and visualization tools for biologists: application to new human transcriptome datasets. <i>Nucleic Acids Research</i> , 2012, 40, 2377-2398.	14.5	65
65	MCMC Can Detect Nonidentifiable Models. <i>Biophysical Journal</i> , 2012, 103, 2275-2286.	0.5	80
66	A Kinetic Model for Type I and II IP3R Accounting for Mode Changes. <i>Biophysical Journal</i> , 2012, 103, 658-668.	0.5	59
67	MCMC Estimation of Markov Models for Ion Channels. <i>Biophysical Journal</i> , 2011, 100, 1919-1929.	0.5	54
68	A Graphical User Interface for a Method to Infer Kinetics and Network Architecture (MIKANA). <i>PLoS ONE</i> , 2011, 6, e27534.	2.5	6
69	Cardiac cell modelling: Observations from the heart of the cardiac physiome project. <i>Progress in Biophysics and Molecular Biology</i> , 2011, 104, 2-21.	2.9	139
70	Gene Network Analysis and Application. <i>Seibutsu Butsuri</i> , 2011, 51, 182-185.	0.1	1
71	Enzyme catalyzed reactions: From experiment to computational mechanism reconstruction. <i>Computational Biology and Chemistry</i> , 2010, 34, 11-18.	2.3	7
72	Why has reversal of the actin-myosin cross-bridge cycle not been observed experimentally?. <i>Journal of Applied Physiology</i> , 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. <i>Biophysical Journal</i> , 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 Ca <sup>2+</sup> (SERCA) Pump. <i>Biophysical Journal</i> , 2009, 96, 2029-2042.	0.5	76
76	Sensitivity of NFAT Cycling to Cytosolic Calcium Concentration: Implications for Hypertrophic Signals in Cardiac Myocytes. <i>Biophysical Journal</i> , 2009, 96, 2095-2104.	0.5	38
77	Using Physiome standards to couple cellular functions for rat cardiac excitation-contraction. <i>Experimental Physiology</i> , 2008, 93, 919-929.	2.0	46
78	Bioinformatics, multiscale modeling and the IUPS Physiome Project. <i>Briefings in Bioinformatics</i> , 2008, 9, 333-343.	6.5	89
79	Computational biology of cardiac myocytes: proposed standards for the physiome. <i>Journal of Experimental Biology</i> , 2007, 210, 1576-1583.	1.7	45
80	The balance between inactivation and activation of the Na <sup>+</sup> -K <sup>+</sup> pump underlies the triphasic accumulation of extracellular K <sup>+</sup> during myocardial ischemia. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2007, 293, H3036-H3045.	3.2	46
81	Modeling Hypertrophic IP3 Transients in the Cardiac Myocyte. <i>Biophysical Journal</i> , 2007, 93, 3421-3433.	0.5	49
82	Reconstructing biochemical pathways from time course data. <i>Proteomics</i> , 2007, 7, 828-838.	2.2	40
83	A Dynamic Model of Excitation-Contraction Coupling during Acidosis in Cardiac Ventricular Myocytes. <i>Biophysical Journal</i> , 2006, 90, 3074-3090.	0.5	59
84	Acidosis in models of cardiac ventricular myocytes. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2006, 364, 1171-1186.	3.4	41
85	Minimum information requested in the annotation of biochemical models (MIRIAM). <i>Nature Biotechnology</i> , 2005, 23, 1509-1515.	17.5	553
86	Multi-scale modelling and the IUPS physiome project. <i>Journal of Molecular Histology</i> , 2004, 35, 707-714.	2.2	32
87	Extracting Biochemical Reaction Kinetics from Time Series Data. <i>Lecture Notes in Computer Science</i> , 2004, , 329-336.	1.3	3