

Jonathan Cooper

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

2,547
citations

279798

23
h-index

276875

41
g-index

54
all docs

54
docs citations

54
times ranked

2746
citing authors

#	ARTICLE	IF	CITATIONS
1	Chaste: An Open Source C++ Library for Computational Physiology and Biology. PLoS Computational Biology, 2013, 9, e1002970.	3.2	375
2	Simulation of multiple ion channel block provides improved early prediction of compoundsâ€™ clinical torsadogenic risk. Cardiovascular Research, 2011, 91, 53-61.	3.8	282
3	Chaste: A test-driven approach to software development for biological modelling. Computer Physics Communications, 2009, 180, 2452-2471.	7.5	207
4	An integrative computational model for intestinal tissue renewal. Cell Proliferation, 2009, 42, 617-636.	5.3	142
5	Minimum Information About a Simulation Experiment (MIASE). PLoS Computational Biology, 2011, 7, e1001122.	3.2	133
6	CellML and associated tools and techniques. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2008, 366, 3017-3043.	3.4	121
7	COMBINE archive and OMEX format: one file to share all information to reproduce a modeling project. BMC Bioinformatics, 2014, 15, 369.	2.6	114
8	A computational study of discrete mechanical tissue models. Physical Biology, 2009, 6, 036001.	1.8	99
9	Computational assessment of drug-induced effects on the electrocardiogram: from ion channel to body surface potentials. British Journal of Pharmacology, 2013, 168, 718-733.	5.4	98
10	Promoting Coordinated Development of Community-Based Information Standards for Modeling in Biology: The COMBINE Initiative. Frontiers in Bioengineering and Biotechnology, 2015, 3, 19.	4.1	72
11	A numerical guide to the solution of the bidomain equations of cardiac electrophysiology. Progress in Biophysics and Molecular Biology, 2010, 102, 136-155.	2.9	71
12	An overview of the CellML API and its implementation. BMC Bioinformatics, 2010, 11, 178.	2.6	67
13	Chaste: using agile programming techniques to develop computational biology software. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2008, 366, 3111-3136.	3.4	61
14	Chaste: Cancer, Heart and Soft Tissue Environment. Journal of Open Source Software, 2020, 5, 1848.	4.6	58
15	The Cardiac Electrophysiology Web Lab. Biophysical Journal, 2016, 110, 292-300.	0.5	49
16	Ten Simple Rules for Effective Computational Research. PLoS Computational Biology, 2014, 10, e1003506.	3.2	47
17	High-throughput functional curation of cellular electrophysiology models. Progress in Biophysics and Molecular Biology, 2011, 107, 11-20.	2.9	46
18	Ten Simple Rules for a Successful Cross-Disciplinary Collaboration. PLoS Computational Biology, 2015, 11, e1004214.	3.2	46

#	ARTICLE	IF	CITATIONS
19	C haste : incorporating a novel multi-scale spatial and temporal algorithm into a large-scale open source library. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2009, 367, 1907-1930.	3.4	36
20	A call for virtual experiments: Accelerating the scientific process. Progress in Biophysics and Molecular Biology, 2015, 117, 99-106.	2.9	31
21	Considerations for the use of cellular electrophysiology models within cardiac tissue simulations. Progress in Biophysics and Molecular Biology, 2011, 107, 74-80.	2.9	28
22	Cellular cardiac electrophysiology modeling with Chaste and CellML. Frontiers in Physiology, 2014, 5, 511.	2.8	27
23	Simulation Experiment Description Markup Language (SED-ML) Level 1 Version 3 (L1V3). Journal of Integrative Bioinformatics, 2018, 15, .	1.5	27
24	Use of Bayesian Inference for Parameter Recovery in DC and AC Voltammetry. ChemElectroChem, 2018, 5, 917-935.	3.4	26
25	Toward a VPH/Physiome ToolKit. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2010, 2, 134-147.	6.6	24
26	CellML 2.0. Journal of Integrative Bioinformatics, 2020, 17, .	1.5	24
27	An integrated approach to quantitative modelling in angiogenesis research. Journal of the Royal Society Interface, 2015, 12, 20150546.	3.4	23
28	Where next for the reproducibility agenda in computational biology?. BMC Systems Biology, 2016, 10, 52.	3.0	23
29	On the application of partial evaluation to the optimisation of cardiac electrophysiological simulations. , 2006, , .		23
30	Hodgkinâ€Huxley revisited: reparametrization and identifiability analysis of the classic action potential model with approximate Bayesian methods. Royal Society Open Science, 2015, 2, 150499.	2.4	22
31	Reproducible model development in the cardiac electrophysiology Web Lab. Progress in Biophysics and Molecular Biology, 2018, 139, 3-14.	2.9	21
32	Comparing two sequential Monte Carlo samplers for exact and approximate Bayesian inference on biological models. Journal of the Royal Society Interface, 2017, 14, 20170340.	3.4	20
33	The Virtual Physiological Human T ool K it. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2010, 368, 3925-3936.	3.4	18
34	Inference-based assessment of parameter identifiability in nonlinear biological models. Journal of the Royal Society Interface, 2018, 15, 20180318.	3.4	18
35	A model-driven approach to automatic conversion of physical units. Software - Practice and Experience, 2008, 38, 337-359.	3.6	16
36	Simulation Experiment Description Markup Language (SED-ML) Level 1 Version 2. Journal of Integrative Bioinformatics, 2015, 12, 119-212.	1.5	10

#	ARTICLE	IF	CITATIONS
37	Connecting Models to Data in Multiscale Multicellular Tissue Simulations. <i>Procedia Computer Science</i> , 2013, 18, 712-721.	2.0	9
38	Simulation Experiment Description Markup Language (SED-ML) Level 1 Version 2. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 262.	1.5	8
39	TumorML: Concept and requirements of an in silico cancer modelling markup language. , 2011, 2011, 441-4.		7
40	Chaste. <i>International Journal of High Performance Computing Applications</i> , 2014, 28, 13-32.	3.7	6
41	Experience report. <i>ACM SIGPLAN Notices</i> , 2007, 42, 247-250.	0.2	2
42	cellmlmanip and chaste_codegen: automatic CellML to C++ code generation with fixes for singularities and automatically generated Jacobians. <i>Wellcome Open Research</i> , 0, 6, 261.	1.8	2
43	A Posteriori Error Analysis for the Use of Lookup Tables in Cardiac Electrophysiology Simulations. <i>SIAM Journal of Scientific Computing</i> , 2010, 32, 2167-2189.	2.8	1
44	chaste_codegen: automatic CellML to C++ code generation with fixes for singularities and automatically generated Jacobians. <i>Wellcome Open Research</i> , 2021, 6, 261.	1.8	1
45	Experience report. , 2007, , .		0
46	Functional Curation: Potential Future Directions for SED-ML. <i>Nature Precedings</i> , 2011, , .	0.1	0
47	CMakeCatchTemplate: A C++ template project. <i>Journal of Open Research Software</i> , 2021, 9, 17.	5.9	0