

Chris D Greenman

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

21
papers

5,617
citations

13
h-index

21
g-index

21
ext. papers

6,313
ext. citations

16.1
avg, IF

4.27
L-index

#	Paper	IF	Citations
21	Time Series Path Integral Expansions for Stochastic Processes. <i>Journal of Statistical Physics</i> , 2022 , 187, 1	1.5	
20	PDE MODELS OF ADDER MECHANISMS IN CELLULAR PROLIFERATION.. <i>SIAM Journal on Applied Mathematics</i> , 2020 , 80, 1307-1335	1.8	7
19	Duality relations between spatial birth-death processes and diffusions in Hilbert space. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2020 , 53, 445002	2	1
18	The complexity of genome rearrangement combinatorics under the infinite sites model. <i>Journal of Theoretical Biology</i> , 2020 , 501, 110335	2.3	
17	Doi-Peliti path integral methods for stochastic systems with partial exclusion. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2018 , 505, 211-221	3.3	2
16	A path integral approach to age dependent branching processes. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2017 , 2017, 033101	1.9	10
15	Kinetic theory of age-structured stochastic birth-death processes. <i>Physical Review E</i> , 2016 , 93, 012112	2.4	18
14	A Hierarchical Kinetic Theory of Birth, Death and Fission in Age-Structured Interacting Populations. <i>Journal of Statistical Physics</i> , 2016 , 164, 49-76	1.5	24
13	Computational Cancer Biology: An Evolutionary Perspective. <i>PLoS Computational Biology</i> , 2016 , 12, e1004717	4.17	40
12	Inferring the Clonal Structure of Viral Populations from Time Series Sequencing. <i>PLoS Computational Biology</i> , 2015 , 11, e1004344	5	
11	The relative timing of mutations in a breast cancer genome. <i>PLoS ONE</i> , 2013 , 8, e64991	3.7	17
10	Estimation of rearrangement phylogeny for cancer genomes. <i>Genome Research</i> , 2012 , 22, 346-61	9.7	94
9	Tandem duplication of chromosomal segments is common in ovarian and breast cancer genomes. <i>Journal of Pathology</i> , 2012 , 227, 446-55	9.4	72
8	Cancer. Haploinsufficient gene selection in cancer. <i>Science</i> , 2012 , 337, 47-8	33.3	11
7	Massive genomic rearrangement acquired in a single catastrophic event during cancer development. <i>Cell</i> , 2011 , 144, 27-40	56.2	1628
6	A small-cell lung cancer genome with complex signatures of tobacco exposure. <i>Nature</i> , 2010 , 463, 184-90	30.4	852
5	A comprehensive catalogue of somatic mutations from a human cancer genome. <i>Nature</i> , 2010 , 463, 191-6	30.4	1303

4	Signatures of mutation and selection in the cancer genome. <i>Nature</i> , 2010 , 463, 893-8	50.4	538
3	PICNIC: an algorithm to predict absolute allelic copy number variation with microarray cancer data. <i>Biostatistics</i> , 2010 , 11, 164-75	3.7	164
2	Complex landscapes of somatic rearrangement in human breast cancer genomes. <i>Nature</i> , 2009 , 462, 1005-10	50.4	684
1	Architectures of somatic genomic rearrangement in human cancer amplicons at sequence-level resolution. <i>Genome Research</i> , 2007 , 17, 1296-303	9.7	152