

Chris D Greenman

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

6,712
citations

623734

14
h-index

752698

20
g-index

21
all docs

21
docs citations

21
times ranked

10798
citing authors

#	ARTICLE	IF	CITATIONS
1	Time Series Path Integral Expansions for Stochastic Processes. <i>Journal of Statistical Physics</i> , 2022, 187, 1.	1.2	1
2	PDE Models of Adder Mechanisms in Cellular Proliferation. <i>SIAM Journal on Applied Mathematics</i> , 2020, 80, 1307-1335.	1.8	22
3	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	3
4	The complexity of genome rearrangement combinatorics under the infinite sites model. <i>Journal of Theoretical Biology</i> , 2020, 501, 110335.	1.7	1
5	Doi-Peliti path integral methods for stochastic systems with partial exclusion. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2018, 505, 211-221.	2.6	3
6	A path integral approach to age dependent branching processes. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2017, 2017, 033101.	2.3	13
7	Kinetic theory of age-structured stochastic birth-death processes. <i>Physical Review E</i> , 2016, 93, 012112.	2.1	24
8	A Hierarchical Kinetic Theory of Birth, Death and Fission in Age-Structured Interacting Populations. <i>Journal of Statistical Physics</i> , 2016, 164, 49-76.	1.2	38
9	Computational Cancer Biology: An Evolutionary Perspective. <i>PLoS Computational Biology</i> , 2016, 12, e1004717.	3.2	74
10	Inferring the Clonal Structure of Viral Populations from Time Series Sequencing. <i>PLoS Computational Biology</i> , 2015, 11, e1004344.	3.2	0
11	The Relative Timing of Mutations in a Breast Cancer Genome. <i>PLoS ONE</i> , 2013, 8, e64991.	2.5	22
12	Haploinsufficient Gene Selection in Cancer. <i>Science</i> , 2012, 337, 47-48.	12.6	12
13	Estimation of rearrangement phylogeny for cancer genomes. <i>Genome Research</i> , 2012, 22, 346-361.	5.5	108
14	Tandem duplication of chromosomal segments is common in ovarian and breast cancer genomes. <i>Journal of Pathology</i> , 2012, 227, 446-455.	4.5	81
15	Massive Genomic Rearrangement Acquired in a Single Catastrophic Event during Cancer Development. <i>Cell</i> , 2011, 144, 27-40.	28.9	2,020
16	A small-cell lung cancer genome with complex signatures of tobacco exposure. <i>Nature</i> , 2010, 463, 184-190.	27.8	972
17	A comprehensive catalogue of somatic mutations from a human cancer genome. <i>Nature</i> , 2010, 463, 191-196.	27.8	1,519
18	Signatures of mutation and selection in the cancer genome. <i>Nature</i> , 2010, 463, 893-898.	27.8	661

#	ARTICLE	IF	CITATIONS
19	PICNIC: an algorithm to predict absolute allelic copy number variation with microarray cancer data. <i>Biostatistics</i> , 2010, 11, 164-175.	1.5	182
20	Complex landscapes of somatic rearrangement in human breast cancer genomes. <i>Nature</i> , 2009, 462, 1005-1010.	27.8	776
21	Architectures of somatic genomic rearrangement in human cancer amplicons at sequence-level resolution. <i>Genome Research</i> , 2007, 17, 1296-1303.	5.5	180