

Pietuooeo G Schofield

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

1,974
citations

759233

12
h-index

888059

17
g-index

18
all docs

18
docs citations

18
times ranked

3903
citing authors

#	ARTICLE	IF	CITATIONS
1	Profiling of Circulating Free DNA Using Targeted and Genome-wide Sequencing in Patients with SCLC. <i>Journal of Thoracic Oncology</i> , 2020, 15, 216-230.	1.1	49
2	Hypoxia induces rapid changes to histone methylation and reprograms chromatin. <i>Science</i> , 2019, 363, 1222-1226.	12.6	266
3	Mutational signatures of DNA mismatch repair deficiency in <i>C. elegans</i> and human cancers. <i>Genome Research</i> , 2018, 28, 666-675.	5.5	112
4	Examining the role of individual movement in promoting coexistence in a spatially explicit prisoner's dilemma. <i>Journal of Theoretical Biology</i> , 2017, 419, 323-332.	1.7	8
5	How many biological replicates are needed in an RNA-seq experiment and which differential expression tool should you use?. <i>Rna</i> , 2016, 22, 839-851.	3.5	622
6	Dynamical Patterns of Coexisting Strategies in a Hybrid Discrete-continuum Spatial Evolutionary Game Model. <i>Mathematical Modelling of Natural Phenomena</i> , 2016, 11, 49-64.	2.4	13
7	What's in a name? Word inflation, punctuation, abbreviation and cloud formation. <i>Medical Education</i> , 2016, 50, 1264-1268.	2.1	6
8	The Chromatin Remodelling Enzymes SNF2H and SNF2L Position Nucleosomes adjacent to CTCF and Other Transcription Factors. <i>PLoS Genetics</i> , 2016, 12, e1005940.	3.5	96
9	Statistical models for RNA-seq data derived from a two-condition 48-replicate experiment. <i>Bioinformatics</i> , 2015, 31, 3625-3630.	4.1	76
10	Proteotoxic stress reprograms the chromatin landscape of SUMO modification. <i>Science Signaling</i> , 2015, 8, rs7.	3.6	81
11	Directed terminal restriction analysis tool (DRAT): an aid to enzyme selection for directed terminal restriction fragment length polymorphisms. <i>Methods in Ecology and Evolution</i> , 2012, 3, 24-28.	5.2	5
12	A Role for Snf2-Related Nucleosome-Spacing Enzymes in Genome-Wide Nucleosome Organization. <i>Science</i> , 2011, 333, 1758-1760.	12.6	260
13	Modelling contact spread of infection in host-parasitoid systems: Vertical transmission of pathogens can cause chaos. <i>Journal of Theoretical Biology</i> , 2010, 262, 441-451.	1.7	6
14	High-Resolution Whole-Genome Sequencing Reveals That Specific Chromatin Domains from Most Human Chromosomes Associate with Nucleoli. <i>Molecular Biology of the Cell</i> , 2010, 21, 3735-3748.	2.1	274
15	Disease induced dynamics in host-parasitoid systems: chaos and coexistence. <i>Journal of the Royal Society Interface</i> , 2007, 4, 463-471.	3.4	18
16	Chemotaxis-induced spatio-temporal heterogeneity in multi-species host-parasitoid systems. <i>Journal of Mathematical Biology</i> , 2007, 55, 365-388.	1.9	27
17	Spatially Explicit Models of Turelli-Hoffmann Wolbachia Invasive Wave Fronts. <i>Journal of Theoretical Biology</i> , 2002, 215, 121-131.	1.7	54