

Amanda Clare

List of Publications by Citations

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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.

25
papers

672
citations

9
h-index

25
g-index

33
ext. papers

813
ext. citations

5.3
avg, IF

3.32
L-index

#	Paper	IF	Citations
25	The automation of science. <i>Science</i> , 2009 , 324, 85-9	33.3	324
24	Measuring scientific impact beyond academia: An assessment of existing impact metrics and proposed improvements. <i>PLoS ONE</i> , 2017 , 12, e0173152	3.7	74
23	Towards Robot Scientists for autonomous scientific discovery. <i>Automated Experimentation</i> , 2010 , 2, 1		73
22	An ontology for a Robot Scientist. <i>Bioinformatics</i> , 2006 , 22, e464-71	7.2	44
21	Accurate prediction of protein functional class from sequence in the Mycobacterium tuberculosis and Escherichia coli genomes using data mining. <i>Yeast</i> , 2000 , 17, 283-93	3.4	34
20	The EXACT description of biomedical protocols. <i>Bioinformatics</i> , 2008 , 24, i295-303	7.2	28
19	How well do we understand the clusters found in microarray data?. <i>In Silico Biology</i> , 2002 , 2, 511-22	2	20
18	The Robot Scientist Adam. <i>Computer</i> , 2009 , 42, 46-54	1.6	18
17	Replicating complex agent based models, a formidable task. <i>Environmental Modelling and Software</i> , 2017 , 92, 142-151	5.2	12
16	AutoLabDB: a substantial open source database schema to support a high-throughput automated laboratory. <i>Bioinformatics</i> , 2012 , 28, 1390-7	7.2	7
15	On the complexity of haplotyping a microbial community. <i>Bioinformatics</i> , 2020 ,	7.2	6
14	PD5: a general purpose library for primer design software. <i>PLoS ONE</i> , 2013 , 8, e80156	3.7	5
13	Recovery of gene haplotypes from a metagenome		5
12	No one tool to rule them all: Prokaryotic gene prediction tool annotations are highly dependent on the organism of study. <i>Bioinformatics</i> , 2021 ,	7.2	4
11	Wiki based management of chemometric research projects. <i>Journal of Chemometrics</i> , 2010 , 24, 408-417	1.6	3
10	Evolutionary search techniques for the Lyndon factorization of biosequences 2019 ,		2
9	A natural language system for retrieval of captioned images. <i>Natural Language Engineering</i> , 2001 , 7, 117-142		2

8	Probabilistic recovery of cryptic haplotypes from metagenomic data		2
7	On the complexity of haplotyping a microbial community		2
6	A Tool for Multiple Targeted Genome Deletions that Is Precise, Scar-Free, and Suitable for Automation. <i>PLoS ONE</i> , 2015 , 10, e0142494	3.7	1
5	Inductive Queries for a Drug Designing Robot Scientist 2010 , 425-451		1
4	Enhanced string factoring from alphabet orderings. <i>Information Processing Letters</i> , 2019 , 143, 4-7	0.8	1
3	Goldilocks: a tool for identifying genomic regions that are just right <i>Bioinformatics</i> , 2016 , 32, 2047-9	7.2	0
2	Laboratory automation in a functional programming language. <i>Journal of the Association for Laboratory Automation</i> , 2014 , 19, 569-76		
1	Evaluation of a Permutation-Based Evolutionary Framework for Lyndon Factorizations. <i>Lecture Notes in Computer Science</i> , 2020 , 390-403	0.9	