

Stuart Owen

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.

17
papers

959
citations

10
h-index

20
g-index

20
ext. papers

1,156
ext. citations

6.6
avg, IF

3
L-index

#	Paper	IF	Citations
17	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021 , 17, e10387	12.2	9
16	Data Management in Computational Systems Biology: Exploring Standards, Tools, Databases, and Packaging Best Practices. <i>Methods in Molecular Biology</i> , 2019 , 2049, 285-314	1.4	1
15	FAIRDOMHub: a repository and collaboration environment for sharing systems biology research. <i>Nucleic Acids Research</i> , 2017 , 45, D404-D407	20.1	62
14	SEEK: a systems biology data and model management platform. <i>BMC Systems Biology</i> , 2015 , 9, 33	3.5	53
13	The evolution of standards and data management practices in systems biology. <i>Molecular Systems Biology</i> , 2015 , 11, 851	12.2	29
12	Why linked data is not enough for scientists. <i>Future Generation Computer Systems</i> , 2013 , 29, 599-611	7.5	160
11	The Taverna workflow suite: designing and executing workflows of Web Services on the desktop, web or in the cloud. <i>Nucleic Acids Research</i> , 2013 , 41, W557-61	20.1	457
10	Stealthy annotation of experimental biology by spreadsheets. <i>Concurrency Computation Practice and Experience</i> , 2013 , 25, 467-480	1.4	0
9	Semantic Data and Models Sharing in Systems Biology: The Just Enough Results Model and the SEEK Platform. <i>Lecture Notes in Computer Science</i> , 2013 , 212-227	0.9	4
8	2012 ,		1
7	Populous: a tool for building OWL ontologies from templates. <i>BMC Bioinformatics</i> , 2012 , 13 Suppl 1, S5	3.6	22
6	The SEEK: a platform for sharing data and models in systems biology. <i>Methods in Enzymology</i> , 2011 , 500, 629-55	1.7	36
5	RightField: embedding ontology annotation in spreadsheets. <i>Bioinformatics</i> , 2011 , 27, 2021-2	7.2	57
4	Why Linked Data is Not Enough for Scientists 2010 ,		31
3	Performing statistical analyses on quantitative data in Taverna workflows: an example using R and maxdBrowse to identify differentially-expressed genes from microarray data. <i>BMC Bioinformatics</i> , 2008 , 9, 334	3.6	33
2	COVID-19 Disease Map, a computational knowledge repository of SARS-CoV-2 virus-host interaction mechanisms		4
1	The Specimen Data Refinery: A Canonical Workflow Framework and FAIR Digital Object Approach to Speeding up Digital Mobilisation of Natural History Collections. <i>Data Intelligence</i> , 1-19	3	0

