

Stuart Owen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8200698/publications.pdf>

Version: 2024-02-01

18
papers

1,311
citations

933447

10
h-index

940533

16
g-index

20
all docs

20
docs citations

20
times ranked

2760
citing authors

#	ARTICLE	IF	CITATIONS
1	Ten simple rules for making a software tool workflow-ready. PLoS Computational Biology, 2022, 18, e1009823.	3.2	7
2	The Specimen Data Refinery: A Canonical Workflow Framework and FAIR Digital Object Approach to Speeding up Digital Mobilisation of Natural History Collections. Data Intelligence, 2022, 4, 320-341.	1.5	6
3	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	7.2	53
4	Data Management in Computational Systems Biology: Exploring Standards, Tools, Databases, and Packaging Best Practices. Methods in Molecular Biology, 2019, 2049, 285-314.	0.9	3
5	FAIRDOMHub: a repository and collaboration environment for sharing systems biology research. Nucleic Acids Research, 2017, 45, D404-D407.	14.5	98
6	The evolution of standards and data management practices in systems biology. Molecular Systems Biology, 2015, 11, 851.	7.2	35
7	SEEK: a systems biology data and model management platform. BMC Systems Biology, 2015, 9, 33.	3.0	75
8	Why linked data is not enough for scientists. Future Generation Computer Systems, 2013, 29, 599-611.	7.5	230
9	The Taverna workflow suite: designing and executing workflows of Web Services on the desktop, web or in the cloud. Nucleic Acids Research, 2013, 41, W557-W561.	14.5	567
10	Stealthy annotation of experimental biology by spreadsheets. Concurrency Computation Practice and Experience, 2013, 25, 467-480.	2.2	3
11	Semantic Data and Models Sharing in Systems Biology: The Just Enough Results Model and the SEEK Platform. Lecture Notes in Computer Science, 2013, , 212-227.	1.3	6
12	RightField: Semantic enrichment of Systems Biology data using spreadsheets. , 2012, , .		1
13	Populous: a tool for building OWL ontologies from templates. BMC Bioinformatics, 2012, 13, S5.	2.6	25
14	The SEEK. Methods in Enzymology, 2011, 500, 629-655.	1.0	44
15	OneStop:JWS Online's access point to SBML,SBGN and MIRIAM compliant annotation. Nature Precedings, 2011, , .	0.1	0
16	RightField: embedding ontology annotation in spreadsheets. Bioinformatics, 2011, 27, 2021-2022.	4.1	69
17	Why Linked Data is Not Enough for Scientists. , 2010, , .		37
18	Performing statistical analyses on quantitative data in Taverna workflows: An example using R and maxdBrowse to identify differentially-expressed genes from microarray data. BMC Bioinformatics, 2008, 9, 334.	2.6	38