

# 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	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-W561.	14.5	567
2	Why linked data is not enough for scientists. <i>Future Generation Computer Systems</i> , 2013, 29, 599-611.	7.5	230
3	FAIRDOMHub: a repository and collaboration environment for sharing systems biology research. <i>Nucleic Acids Research</i> , 2017, 45, D404-D407.	14.5	98
4	SEEK: a systems biology data and model management platform. <i>BMC Systems Biology</i> , 2015, 9, 33.	3.0	75
5	RightField: embedding ontology annotation in spreadsheets. <i>Bioinformatics</i> , 2011, 27, 2021-2022.	4.1	69
6	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	7.2	53
7	The SEEK. <i>Methods in Enzymology</i> , 2011, 500, 629-655.	1.0	44
8	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.	2.6	38
9	Why Linked Data is Not Enough for Scientists. , 2010, , .		37
10	The evolution of standards and data management practices in systems biology. <i>Molecular Systems Biology</i> , 2015, 11, 851.	7.2	35
11	Populous: a tool for building OWL ontologies from templates. <i>BMC Bioinformatics</i> , 2012, 13, S5.	2.6	25
12	Ten simple rules for making a software tool workflow-ready. <i>PLoS Computational Biology</i> , 2022, 18, e1009823.	3.2	7
13	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.	1.3	6
14	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> , 2022, 4, 320-341.	1.5	6
15	Stealthy annotation of experimental biology by spreadsheets. <i>Concurrency Computation Practice and Experience</i> , 2013, 25, 467-480.	2.2	3
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.	0.9	3
17	RightField: Semantic enrichment of Systems Biology data using spreadsheets. , 2012, , .		1
18	OneStop:JWS Online's access point to SBML,SBGN and MIRIAM compliant annotation. <i>Nature Precedings</i> , 2011, , .	0.1	0