

Allyson L Lister

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6081571/publications.pdf>

Version: 2024-02-01

17
papers

3,016
citations

759233

12
h-index

794594

19
g-index

21
all docs

21
docs citations

21
times ranked

5744
citing authors

#	ARTICLE	IF	CITATIONS
1	Helping the Consumers and Producers of Standards, Repositories and Policies to Enable FAIR Data. <i>Data Intelligence</i> , 2020, 2, 151-157.	1.5	10
2	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	7.2	178
3	FAIRsharing as a community approach to standards, repositories and policies. <i>Nature Biotechnology</i> , 2019, 37, 358-367.	17.5	228
4	The Ontology for Biomedical Investigations. <i>PLoS ONE</i> , 2016, 11, e0154556.	2.5	217
5	The Software Ontology (SWO): a resource for reproducibility in biomedical data analysis, curation and digital preservation. <i>Journal of Biomedical Semantics</i> , 2014, 5, 25.	1.6	56
6	MIREOT: The minimum information to reference an external ontology term. <i>Applied Ontology</i> , 2011, 6, 23-33.	2.0	78
7	Controlled vocabularies and semantics in systems biology. <i>Molecular Systems Biology</i> , 2011, 7, 543.	7.2	246
8	Quantitative Fitness Analysis Shows That NMD Proteins and Many Other Protein Complexes Suppress or Enhance Distinct Telomere Cap Defects. <i>PLoS Genetics</i> , 2011, 7, e1001362.	3.5	65
9	Annotation of SBML models through rule-based semantic integration. <i>Journal of Biomedical Semantics</i> , 2010, 1, S3.	1.6	16
10	Live Coverage of Scientific Conferences Using Web Technologies. <i>PLoS Computational Biology</i> , 2010, 6, e1000563.	3.2	8
11	Live Coverage of Intelligent Systems for Molecular Biology/European Conference on Computational Biology (ISMB/ECCB) 2009. <i>PLoS Computational Biology</i> , 2010, 6, e1000640.	3.2	4
12	Managing Experimental Data Using FuGE. <i>Methods in Molecular Biology</i> , 2010, 604, 333-343.	0.9	4
13	Modeling and Managing Experimental Data Using FuGE. <i>OMICS A Journal of Integrative Biology</i> , 2009, 13, 239-251.	2.0	8
14	Saint: a lightweight integration environment for model annotation. <i>Bioinformatics</i> , 2009, 25, 3026-3027.	4.1	25
15	The minimum information about a genome sequence (MIGS) specification. <i>Nature Biotechnology</i> , 2008, 26, 541-547.	17.5	1,069
16	eGenomics: Cataloguing Our Complete Genome Collection III. <i>Comparative and Functional Genomics</i> , 2007, 2007, 1-7.	2.0	4
17	The International Protein Index: An integrated database for proteomics experiments. <i>Proteomics</i> , 2004, 4, 1985-1988.	2.2	685