

Nives Skunca

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

7,481
citations

566801

15
h-index

887659

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docs citations

17
times ranked

18054
citing authors

#	ARTICLE	IF	CITATIONS
1	REVIGO Summarizes and Visualizes Long Lists of Gene Ontology Terms. <i>PLoS ONE</i> , 2011, 6, e21800.	1.1	5,347
2	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	9.0	789
3	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	3.8	308
4	The OMA orthology database in 2015: function predictions, better plant support, synteny view and other improvements. <i>Nucleic Acids Research</i> , 2015, 43, D240-D249.	6.5	201
5	A Transcriptomic-Phylogenomic Analysis of the Evolutionary Relationships of Flatworms. <i>Current Biology</i> , 2015, 25, 1347-1353.	1.8	160
6	The what, where, how and why of gene ontology—a primer for bioinformaticians. <i>Briefings in Bioinformatics</i> , 2011, 12, 723-735.	3.2	122
7	The draft genome sequence of the ferret (<i>Mustela putorius furo</i>) facilitates study of human respiratory disease. <i>Nature Biotechnology</i> , 2014, 32, 1250-1255.	9.4	110
8	Quality of Computationally Inferred Gene Ontology Annotations. <i>PLoS Computational Biology</i> , 2012, 8, e1002533.	1.5	103
9	Translational Selection Is Ubiquitous in Prokaryotes. <i>PLoS Genetics</i> , 2010, 6, e1001004.	1.5	76
10	Primer on the Gene Ontology. <i>Methods in Molecular Biology</i> , 2017, 1446, 25-37.	0.4	63
11	CAFA and the Open World of protein function predictions. <i>Trends in Genetics</i> , 2013, 29, 609-610.	2.9	47
12	The Confidence Information Ontology: a step towards a standard for asserting confidence in annotations. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav043-bav043.	1.4	37
13	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018, 34, 323-329.	1.8	36
14	Phylogenetic Profiling: How Much Input Data Is Enough?. <i>PLoS ONE</i> , 2015, 10, e0114701.	1.1	31
15	Phyletic Profiling with Cliques of Orthologs Is Enhanced by Signatures of Paralogy Relationships. <i>PLoS Computational Biology</i> , 2013, 9, e1002852.	1.5	29
16	Visualizing GO Annotations. <i>Methods in Molecular Biology</i> , 2017, 1446, 207-220.	0.4	12
17	Evaluating Computational Gene Ontology Annotations. <i>Methods in Molecular Biology</i> , 2017, 1446, 97-109.	0.4	10