Adrian M Altenhoff

List of Publications by Year
in descending order

36 papers	3,268 citations	304743 22 h-index	395702 33 g-index
46 all docs	46 docs citations	46 times ranked	4816 citing authors

#	Article	IF	Citations
1	Phylogenetic and Functional Assessment of Orthologs Inference Projects and Methods. PLoS Computational Biology, 2009, 5, e1000262.	3.2	341
2	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
3	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261
4	The OMA orthology database in 2018: retrieving evolutionary relationships among all domains of life through richer web and programmatic interfaces. Nucleic Acids Research, 2018, 46, D477-D485.	14.5	231
5	Resolving the Ortholog Conjecture: Orthologs Tend to Be Weakly, but Significantly, More Similar in Function than Paralogs. PLoS Computational Biology, 2012, 8, e1002514.	3.2	217
6	The OMA orthology database in 2015: function predictions, better plant support, synteny view and other improvements. Nucleic Acids Research, 2015, 43, D240-D249.	14.5	201
7	Standardized benchmarking in the quest for orthologs. Nature Methods, 2016, 13, 425-430.	19.0	198
8	OMA 2011: orthology inference among 1000 complete genomes. Nucleic Acids Research, 2011, 39, D289-D294.	14.5	185
9	Inferring Hierarchical Orthologous Groups from Orthologous Gene Pairs. PLoS ONE, 2013, 8, e53786.	2.5	152
10	OMA orthology in 2021: website overhaul, conserved isoforms, ancestral gene order and more. Nucleic Acids Research, 2021, 49, D373-D379.	14.5	137
11	OMA standalone: orthology inference among public and custom genomes and transcriptomes. Genome Research, 2019, 29, 1152-1163.	5.5	111
12	Quality of Computationally Inferred Gene Ontology Annotations. PLoS Computational Biology, 2012, 8, e1002533.	3.2	103
13	A gridded hourly precipitation dataset for Switzerland using rain€gauge analysis and radar€based disaggregation. International Journal of Climatology, 2010, 30, 1764-1775.	3.5	87
14	Inferring Orthology and Paralogy. Methods in Molecular Biology, 2012, 855, 259-279.	0.9	87
15	Inferring Orthology and Paralogy. Methods in Molecular Biology, 2019, 1910, 149-175.	0.9	84
16	Orthologous Matrix (OMA) algorithm 2.0: more robust to asymmetric evolutionary rates and more scalable hierarchical orthologous group inference. Bioinformatics, 2017, 33, i75-i82.	4.1	82
17	Linkage of atmospheric blocks and synoptic-scale Rossby waves: a climatological analysis. Tellus, Series A: Dynamic Meteorology and Oceanography, 2022, 60, 1053.	1.7	77
18	The SIB Swiss Institute of Bioinformatics€™ resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-D37.	14.5	64

#	Article	IF	Citations
19	Distinct evolutionary strategies in the GGPPS family from plants. Frontiers in Plant Science, 2014, 5, 230.	3.6	45
20	The Quest for Orthologs benchmark service and consensus calls in 2020. Nucleic Acids Research, 2020, 48, W538-W545.	14.5	41
21	Gearing up to handle the mosaic nature of life in the quest for orthologs. Bioinformatics, 2018, 34, 323-329.	4.1	36
22	The Impact of Gene Duplication, Insertion, Deletion, Lateral Gene Transfer and Sequencing Error on Orthology Inference: A Simulation Study. PLoS ONE, 2013, 8, e56925.	2.5	34
23	A stochastic boundary forcing for dissipative particle dynamics. Journal of Computational Physics, 2007, 225, 1125-1136.	3.8	32
24	The Quest for Orthologs orthology benchmark service in 2022. Nucleic Acids Research, 2022, 50, W623-W632.	14.5	29
25	iHam and pyHam: visualizing and processing hierarchical orthologous groups. Bioinformatics, 2019, 35, 2504-2506.	4.1	22
26	Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. Nucleic Acids Research, 2014, 42, W436-W441.	14.5	13
27	Expanding the Orthologous Matrix (OMA) programmatic interfaces: REST API and the OmaDB packages for R and Python. F1000Research, 2019, 8, 42.	1.6	11
28	Expanding the Orthologous Matrix (OMA) programmatic interfaces: REST API and the OmaDB packages for R and Python. F1000Research, 2019, 8, 42.	1.6	9
29	How to build phylogenetic species trees with OMA. F1000Research, 0, 9, 511.	1.6	8
30	Speeding up all-against-all protein comparisons while maintaining sensitivity by considering subsequence-level homology. PeerJ, 2014, 2, e607.	2.0	7
31	Assigning confidence scores to homoeologs using fuzzy logic. PeerJ, 2019, 6, e6231.	2.0	6
32	How to build phylogenetic species trees with OMA. F1000Research, 0, 9, 511.	1.6	3
33	Phylogenetic approaches to identifying fragments of the same gene, with application to the wheat genome. Bioinformatics, 2019, 35, 1159-1166.	4.1	1
34	OMAMO: orthology-based alternative model organism selection. Bioinformatics, 2022, 38, 2965-2966.	4.1	1
35	Linkage of atmospheric blocks and synoptic-scale Rossby waves: a climatological analysis. Tellus, Series A: Dynamic Meteorology and Oceanography, 2008, , .	1.7	0
36	Parallel and Scalable Precise Clustering. , 2020, , .		0