

# Adrian M Altenhoff

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Linkage of atmospheric blocks and synoptic-scale Rossby waves: a climatological analysis. <i>Tellus, Series A: Dynamic Meteorology and Oceanography</i> , 2022, 60, 1053.	1.7	77
2	OMAMO: orthology-based alternative model organism selection. <i>Bioinformatics</i> , 2022, 38, 2965-2966.	4.1	1
3	The Quest for Orthologs orthology benchmark service in 2022. <i>Nucleic Acids Research</i> , 2022, 50, W623-W632.	14.5	29
4	OMA orthology in 2021: website overhaul, conserved isoforms, ancestral gene order and more. <i>Nucleic Acids Research</i> , 2021, 49, D373-D379.	14.5	137
5	The Quest for Orthologs benchmark service and consensus calls in 2020. <i>Nucleic Acids Research</i> , 2020, 48, W538-W545.	14.5	41
6	Parallel and Scalable Precise Clustering. , 2020, , .		0
7	OMA standalone: orthology inference among public and custom genomes and transcriptomes. <i>Genome Research</i> , 2019, 29, 1152-1163.	5.5	111
8	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	8.8	261
9	Phylogenetic approaches to identifying fragments of the same gene, with application to the wheat genome. <i>Bioinformatics</i> , 2019, 35, 1159-1166.	4.1	1
10	iHam and pyHam: visualizing and processing hierarchical orthologous groups. <i>Bioinformatics</i> , 2019, 35, 2504-2506.	4.1	22
11	Inferring Orthology and Paralogy. <i>Methods in Molecular Biology</i> , 2019, 1910, 149-175.	0.9	84
12	Expanding the Orthologous Matrix (OMA) programmatic interfaces: REST API and the OmaDB packages for R and Python. <i>F1000Research</i> , 2019, 8, 42.	1.6	11
13	Assigning confidence scores to homoeologs using fuzzy logic. <i>PeerJ</i> , 2019, 6, e6231.	2.0	6
14	Expanding the Orthologous Matrix (OMA) programmatic interfaces: REST API and the OmaDB packages for R and Python. <i>F1000Research</i> , 2019, 8, 42.	1.6	9
15	The OMA orthology database in 2018: retrieving evolutionary relationships among all domains of life through richer web and programmatic interfaces. <i>Nucleic Acids Research</i> , 2018, 46, D477-D485.	14.5	231
16	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018, 34, 323-329.	4.1	36
17	Orthologous Matrix (OMA) algorithm 2.0: more robust to asymmetric evolutionary rates and more scalable hierarchical orthologous group inference. <i>Bioinformatics</i> , 2017, 33, i75-i82.	4.1	82
18	Standardized benchmarking in the quest for orthologs. <i>Nature Methods</i> , 2016, 13, 425-430.	19.0	198

#	ARTICLE	IF	CITATIONS
19	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	8.8	308
20	The SIB Swiss Institute of Bioinformaticsâ€™™ resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016, 44, D27-D37.	14.5	64
21	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.	14.5	201
22	Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. <i>Nucleic Acids Research</i> , 2014, 42, W436-W441.	14.5	13
23	Distinct evolutionary strategies in the GGPPS family from plants. <i>Frontiers in Plant Science</i> , 2014, 5, 230.	3.6	45
24	Speeding up all-against-all protein comparisons while maintaining sensitivity by considering subsequence-level homology. <i>PeerJ</i> , 2014, 2, e607.	2.0	7
25	The Impact of Gene Duplication, Insertion, Deletion, Lateral Gene Transfer and Sequencing Error on Orthology Inference: A Simulation Study. <i>PLoS ONE</i> , 2013, 8, e56925.	2.5	34
26	Inferring Hierarchical Orthologous Groups from Orthologous Gene Pairs. <i>PLoS ONE</i> , 2013, 8, e53786.	2.5	152
27	Quality of Computationally Inferred Gene Ontology Annotations. <i>PLoS Computational Biology</i> , 2012, 8, e1002533.	3.2	103
28	Resolving the Ortholog Conjecture: Orthologs Tend to Be Weakly, but Significantly, More Similar in Function than Paralogs. <i>PLoS Computational Biology</i> , 2012, 8, e1002514.	3.2	217
29	Inferring Orthology and Paralogy. <i>Methods in Molecular Biology</i> , 2012, 855, 259-279.	0.9	87
30	OMA 2011: orthology inference among 1000 complete genomes. <i>Nucleic Acids Research</i> , 2011, 39, D289-D294.	14.5	185
31	A gridded hourly precipitation dataset for Switzerland using rainâ€™gauge analysis and radarâ€™based disaggregation. <i>International Journal of Climatology</i> , 2010, 30, 1764-1775.	3.5	87
32	Phylogenetic and Functional Assessment of Orthologs Inference Projects and Methods. <i>PLoS Computational Biology</i> , 2009, 5, e1000262.	3.2	341
33	Linkage of atmospheric blocks and synoptic-scale Rossby waves: a climatological analysis. <i>Tellus, Series A: Dynamic Meteorology and Oceanography</i> , 2008, , .	1.7	0
34	A stochastic boundary forcing for dissipative particle dynamics. <i>Journal of Computational Physics</i> , 2007, 225, 1125-1136.	3.8	32
35	How to build phylogenetic species trees with OMA. <i>F1000Research</i> , 0, 9, 511.	1.6	8
36	How to build phylogenetic species trees with OMA. <i>F1000Research</i> , 0, 9, 511.	1.6	3