## Huaiyu Mi

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1783005/publications.pdf

Version: 2024-02-01

40 papers 40,263 citations

212478 28 h-index 36 g-index

44 all docs

44 docs citations

times ranked

44

67276 citing authors

#	Article	IF	CITATIONS
1	The Sequence of the Human Genome. Science, 2001, 291, 1304-1351.	6.0	12,623
2	PANTHER: A Library of Protein Families and Subfamilies Indexed by Function. Genome Research, 2003, 13, 2129-2141.	2.4	2,703
3	PANTHER version 14: more genomes, a new PANTHER GO-slim and improvements in enrichment analysis tools. Nucleic Acids Research, 2019, 47, D419-D426.	6.5	2,455
4	The Gene Ontology resource: enriching a GOld mine. Nucleic Acids Research, 2021, 49, D325-D334.	6.5	2,416
5	Large-scale gene function analysis with the PANTHER classification system. Nature Protocols, 2013, 8, 1551-1566.	5.5	2,276
6	PANTHER version 11: expanded annotation data from Gene Ontology and Reactome pathways, and data analysis tool enhancements. Nucleic Acids Research, 2017, 45, D183-D189.	6.5	2,113
7	PANTHER in 2013: modeling the evolution of gene function, and other gene attributes, in the context of phylogenetic trees. Nucleic Acids Research, 2012, 41, D377-D386.	6.5	1,536
8	The InterPro protein families and domains database: 20 years on. Nucleic Acids Research, 2021, 49, D344-D354.	6.5	1,385
9	InterPro in 2017â€"beyond protein family and domain annotations. Nucleic Acids Research, 2017, 45, D190-D199.	6.5	1,358
10	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. Nucleic Acids Research, 2019, 47, D351-D360.	6.5	1,291
11	The InterPro protein families database: the classification resource after 15 years. Nucleic Acids Research, 2015, 43, D213-D221.	6.5	1,205
12	Protocol Update for large-scale genome and gene function analysis with the PANTHER classification system (v.14.0). Nature Protocols, 2019, 14, 703-721.	5.5	1,041
13	PANTHER version 16: a revised family classification, tree-based classification tool, enhancer regions and extensive API. Nucleic Acids Research, 2021, 49, D394-D403.	6.5	990
14	The Systems Biology Graphical Notation. Nature Biotechnology, 2009, 27, 735-741.	9.4	828
15	PANTHER version 10: expanded protein families and functions, and analysis tools. Nucleic Acids Research, 2016, 44, D336-D342.	6.5	790
16	The PANTHER database of protein families, subfamilies, functions and pathways. Nucleic Acids Research, 2004, 33, D284-D288.	6.5	686
17	The BioPAX community standard for pathway data sharing. Nature Biotechnology, 2010, 28, 935-942.	9.4	613
18	PANTHER: a browsable database of gene products organized by biological function, using curated protein family and subfamily classification. Nucleic Acids Research, 2003, 31, 334-341.	6.5	578

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19	PANTHER Pathway: An Ontology-Based Pathway Database Coupled with Data Analysis Tools. Methods in Molecular Biology, 2009, 563, 123-140.	0.4	575
20	PANTHER version 7: improved phylogenetic trees, orthologs and collaboration with the Gene Ontology Consortium. Nucleic Acids Research, 2010, 38, D204-D210.	6.5	553
21	SynGO: An Evidence-Based, Expert-Curated Knowledge Base for the Synapse. Neuron, 2019, 103, 217-234.e4.	3.8	518
22	Applications for protein sequence-function evolution data: mRNA/protein expression analysis and coding SNP scoring tools. Nucleic Acids Research, 2006, 34, W645-W650.	6.5	487
23	<scp>PANTHER</scp> : Making genomeâ€scale phylogenetics accessible to all. Protein Science, 2022, 31, 8-22.	3.1	467
24	PANTHER version 6: protein sequence and function evolution data with expanded representation of biological pathways. Nucleic Acids Research, 2007, 35, D247-D252.	6.5	333
25	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	3.2	178
26	Gene Ontology Causal Activity Modeling (GO-CAM) moves beyond GO annotations to structured descriptions of biological functions and systems. Nature Genetics, 2019, 51, 1429-1433.	9.4	76
27	Systems Biology Graphical Notation: Process Description language Level 1 Version 2.0. Journal of Integrative Bioinformatics, 2019, 16, .	1.0	43
28	Assessment of Genome-Wide Protein Function Classification for Drosophila melanogaster. Genome Research, 2003, 13, 2118-2128.	2.4	40
29	PhyloGenes: An online phylogenetics and functional genomics resource for plant gene function inference. Plant Direct, 2020, 4, e00293.	0.8	23
30	Reactome and the Gene Ontology: digital convergence of data resources. Bioinformatics, 2021, 37, 3343-3348.	1.8	19
31	BioPAX support in CellDesigner. Bioinformatics, 2011, 27, 3437-3438.	1.8	18
32	PharmGKB summary. Pharmacogenetics and Genomics, 2011, 21, 350-356.	0.7	13
33	Large-scale inference of gene function through phylogenetic annotation of Gene Ontology terms: case study of the apoptosis and autophagy cellular processes. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw155.	1.4	12
34	PEREGRINE: A genome-wide prediction of enhancer to gene relationships supported by experimental evidence. PLoS ONE, 2020, 15, e0243791.	1.1	12
35	Ontologies and Standards in Bioscience Research: For Machine or for Human. Frontiers in Physiology, 2011, 2, 5.	1.3	7
36	Bayesian parameter estimation for automatic annotation of gene functions using observational data and phylogenetic trees. PLoS Computational Biology, 2021, 17, e1007948.	1.5	0

#	Article	IF	CITATIONS
37	Title is missing!. , 2020, 15, e0243791.		O
38	Title is missing!. , 2020, 15, e0243791.		0
39	Title is missing!. , 2020, 15, e0243791.		O
40	Title is missing!. , 2020, 15, e0243791.		0