

Huaiyu Mi

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

40,263
citations

186265
28
h-index

345221
36
g-index

44
all docs

44
docs citations

44
times ranked

60645
citing authors

#	ARTICLE	IF	CITATIONS
1	The Sequence of the Human Genome. Science, 2001, 291, 1304-1351.	12.6	12,623
2	PANTHER: A Library of Protein Families and Subfamilies Indexed by Function. Genome Research, 2003, 13, 2129-2141.	5.5	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.	14.5	2,455
4	The Gene Ontology resource: enriching a GOLD mine. Nucleic Acids Research, 2021, 49, D325-D334.	14.5	2,416
5	Large-scale gene function analysis with the PANTHER classification system. Nature Protocols, 2013, 8, 1551-1566.	12.0	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.	14.5	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.	14.5	1,536
8	The InterPro protein families and domains database: 20 years on. Nucleic Acids Research, 2021, 49, D344-D354.	14.5	1,385
9	InterPro in 2017â€”beyond protein family and domain annotations. Nucleic Acids Research, 2017, 45, D190-D199.	14.5	1,358
10	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. Nucleic Acids Research, 2019, 47, D351-D360.	14.5	1,291
11	The InterPro protein families database: the classification resource after 15 years. Nucleic Acids Research, 2015, 43, D213-D221.	14.5	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.	12.0	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.	14.5	990
14	The Systems Biology Graphical Notation. Nature Biotechnology, 2009, 27, 735-741.	17.5	828
15	PANTHER version 10: expanded protein families and functions, and analysis tools. Nucleic Acids Research, 2016, 44, D336-D342.	14.5	790
16	The PANTHER database of protein families, subfamilies, functions and pathways. Nucleic Acids Research, 2004, 33, D284-D288.	14.5	686
17	The BioPAX community standard for pathway data sharing. Nature Biotechnology, 2010, 28, 935-942.	17.5	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.	14.5	578

#	ARTICLE	IF	CITATIONS
19	PANTHER Pathway: An Ontology-Based Pathway Database Coupled with Data Analysis Tools. <i>Methods in Molecular Biology</i> , 2009, 563, 123-140.	0.9	575
20	PANTHER version 7: improved phylogenetic trees, orthologs and collaboration with the Gene Ontology Consortium. <i>Nucleic Acids Research</i> , 2010, 38, D204-D210.	14.5	553
21	SynGO: An Evidence-Based, Expert-Curated Knowledge Base for the Synapse. <i>Neuron</i> , 2019, 103, 217-234.e4.	8.1	518
22	Applications for protein sequence-function evolution data: mRNA/protein expression analysis and coding SNP scoring tools. <i>Nucleic Acids Research</i> , 2006, 34, W645-W650.	14.5	487
23	<scp>PANTHER</scp>: Making genome-scale phylogenetics accessible to all. <i>Protein Science</i> , 2022, 31, 8-22.	7.6	467
24	PANTHER version 6: protein sequence and function evolution data with expanded representation of biological pathways. <i>Nucleic Acids Research</i> , 2007, 35, D247-D252.	14.5	333
25	<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
26	Gene Ontology Causal Activity Modeling (GO-CAM) moves beyond GO annotations to structured descriptions of biological functions and systems. <i>Nature Genetics</i> , 2019, 51, 1429-1433.	21.4	76
27	Systems Biology Graphical Notation: Process Description language Level 1 Version 2.0. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, .	1.5	43
28	Assessment of Genome-Wide Protein Function Classification for <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2003, 13, 2118-2128.	5.5	40
29	PhyloGenes: An online phylogenetics and functional genomics resource for plant gene function inference. <i>Plant Direct</i> , 2020, 4, e00293.	1.9	23
30	Reactome and the Gene Ontology: digital convergence of data resources. <i>Bioinformatics</i> , 2021, 37, 3343-3348.	4.1	19
31	BioPAX support in CellDesigner. <i>Bioinformatics</i> , 2011, 27, 3437-3438.	4.1	18
32	PharmGKB summary. <i>Pharmacogenetics and Genomics</i> , 2011, 21, 350-356.	1.5	13
33	Large-scale inference of gene function through phylogenetic annotation of Gene Ontology terms: case study of the apoptosis and autophagy cellular processes. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw155.	3.0	12
34	PEREGRINE: A genome-wide prediction of enhancer to gene relationships supported by experimental evidence. <i>PLoS ONE</i> , 2020, 15, e0243791.	2.5	12
35	Ontologies and Standards in Bioscience Research: For Machine or for Human. <i>Frontiers in Physiology</i> , 2011, 2, 5.	2.8	7
36	Bayesian parameter estimation for automatic annotation of gene functions using observational data and phylogenetic trees. <i>PLoS Computational Biology</i> , 2021, 17, e1007948.	3.2	0

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