

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

388640

36
g-index

44
all docs

44
docs citations

44
times ranked

67276
citing authors

#	ARTICLE	IF	CITATIONS
1	<scp>PANTHER</scp>: Making genome-scale phylogenetics accessible to all. Protein Science, 2022, 31, 8-22.	3.1	467
2	The InterPro protein families and domains database: 20 years on. Nucleic Acids Research, 2021, 49, D344-D354.	6.5	1,385
3	Bayesian parameter estimation for automatic annotation of gene functions using observational data and phylogenetic trees. PLoS Computational Biology, 2021, 17, e1007948.	1.5	0
4	Reactome and the Gene Ontology: digital convergence of data resources. Bioinformatics, 2021, 37, 3343-3348.	1.8	19
5	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
6	The Gene Ontology resource: enriching a GOld mine. Nucleic Acids Research, 2021, 49, D325-D334.	6.5	2,416
7	PhyloGenes: An online phylogenetics and functional genomics resource for plant gene function inference. Plant Direct, 2020, 4, e00293.	0.8	23
8	PEREGRINE: A genome-wide prediction of enhancer to gene relationships supported by experimental evidence. PLoS ONE, 2020, 15, e0243791.	1.1	12
9	<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
10	Title is missing!. , 2020, 15, e0243791.		0
11	Title is missing!. , 2020, 15, e0243791.		0
12	Title is missing!. , 2020, 15, e0243791.		0
13	Title is missing!. , 2020, 15, e0243791.		0
14	Systems Biology Graphical Notation: Process Description language Level 1 Version 2.0. Journal of Integrative Bioinformatics, 2019, 16, .	1.0	43
15	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
16	SynGO: An Evidence-Based, Expert-Curated Knowledge Base for the Synapse. Neuron, 2019, 103, 217-234.e4.	3.8	518
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. <i>Nucleic Acids Research</i> , 2019, 47, D351-D360.	6.5	1,291
20	InterPro in 2017â€”beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017, 45, D190-D199.	6.5	1,358
21	PANTHER version 11: expanded annotation data from Gene Ontology and Reactome pathways, and data analysis tool enhancements. <i>Nucleic Acids Research</i> , 2017, 45, D183-D189.	6.5	2,113
22	PANTHER version 10: expanded protein families and functions, and analysis tools. <i>Nucleic Acids Research</i> , 2016, 44, D336-D342.	6.5	790
23	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.	1.4	12
24	The InterPro protein families database: the classification resource after 15 years. <i>Nucleic Acids Research</i> , 2015, 43, D213-D221.	6.5	1,205
25	Large-scale gene function analysis with the PANTHER classification system. <i>Nature Protocols</i> , 2013, 8, 1551-1566.	5.5	2,276
26	PANTHER in 2013: modeling the evolution of gene function, and other gene attributes, in the context of phylogenetic trees. <i>Nucleic Acids Research</i> , 2012, 41, D377-D386.	6.5	1,536
27	BioPAX support in CellDesigner. <i>Bioinformatics</i> , 2011, 27, 3437-3438.	1.8	18
28	Ontologies and Standards in Bioscience Research: For Machine or for Human. <i>Frontiers in Physiology</i> , 2011, 2, 5.	1.3	7
29	PharmGKB summary. <i>Pharmacogenetics and Genomics</i> , 2011, 21, 350-356.	0.7	13
30	The BioPAX community standard for pathway data sharing. <i>Nature Biotechnology</i> , 2010, 28, 935-942.	9.4	613
31	PANTHER version 7: improved phylogenetic trees, orthologs and collaboration with the Gene Ontology Consortium. <i>Nucleic Acids Research</i> , 2010, 38, D204-D210.	6.5	553
32	The Systems Biology Graphical Notation. <i>Nature Biotechnology</i> , 2009, 27, 735-741.	9.4	828
33	PANTHER Pathway: An Ontology-Based Pathway Database Coupled with Data Analysis Tools. <i>Methods in Molecular Biology</i> , 2009, 563, 123-140.	0.4	575
34	PANTHER version 6: protein sequence and function evolution data with expanded representation of biological pathways. <i>Nucleic Acids Research</i> , 2007, 35, D247-D252.	6.5	333
35	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.	6.5	487
36	The PANTHER database of protein families, subfamilies, functions and pathways. <i>Nucleic Acids Research</i> , 2004, 33, D284-D288.	6.5	686

#	ARTICLE	IF	CITATIONS
37	PANTHER: a browsable database of gene products organized by biological function, using curated protein family and subfamily classification. <i>Nucleic Acids Research</i> , 2003, 31, 334-341.	6.5	578
38	PANTHER: A Library of Protein Families and Subfamilies Indexed by Function. <i>Genome Research</i> , 2003, 13, 2129-2141.	2.4	2,703
39	Assessment of Genome-Wide Protein Function Classification for <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2003, 13, 2118-2128.	2.4	40
40	The Sequence of the Human Genome. <i>Science</i> , 2001, 291, 1304-1351.	6.0	12,623