

Paul D Thomas

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

70
papers

31,776
citations

40
h-index

76
g-index

76
ext. papers

40,896
ext. citations

12.4
avg, IF

7.12
L-index

#	Paper	IF	Citations
70	The sequence of the human genome. <i>Science</i> , 2001 , 291, 1304-51	33.3	10609
69	PANTHER: a library of protein families and subfamilies indexed by function. <i>Genome Research</i> , 2003 , 13, 2129-41	9.7	2102
68	Large-scale gene function analysis with the PANTHER classification system. <i>Nature Protocols</i> , 2013 , 8, 1551-66	18.8	1648
67	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	20.1	1470
66	PANTHER version 14: more genomes, a new PANTHER GO-slim and improvements in enrichment analysis tools. <i>Nucleic Acids Research</i> , 2019 , 47, D419-D426	20.1	1256
65	PANTHER in 2013: modeling the evolution of gene function, and other gene attributes, in the context of phylogenetic trees. <i>Nucleic Acids Research</i> , 2013 , 41, D377-86	20.1	1204
64	Principles of protein folding--a perspective from simple exact models. <i>Protein Science</i> , 1995 , 4, 561-602	6.3	1159
63	InterPro in 2017-beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017 , 45, D190-D199	20.1	970
62	The InterPro protein families database: the classification resource after 15 years. <i>Nucleic Acids Research</i> , 2015 , 43, D213-21	20.1	954
61	InterPro in 2011: new developments in the family and domain prediction database. <i>Nucleic Acids Research</i> , 2012 , 40, D306-12	20.1	844
60	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. <i>Nucleic Acids Research</i> , 2019 , 47, D351-D360	20.1	835
59	PANTHER version 10: expanded protein families and functions, and analysis tools. <i>Nucleic Acids Research</i> , 2016 , 44, D336-42	20.1	656
58	The MEROPS database of proteolytic enzymes, their substrates and inhibitors in 2017 and a comparison with peptidases in the PANTHER database. <i>Nucleic Acids Research</i> , 2018 , 46, D624-D632	20.1	643
57	The PANTHER database of protein families, subfamilies, functions and pathways. <i>Nucleic Acids Research</i> , 2005 , 33, D284-8	20.1	589
56	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios. <i>Science</i> , 2003 , 302, 1960-3	33.3	517
55	The Gene Ontology resource: enriching a GOLD mine. <i>Nucleic Acids Research</i> , 2021 , 49, D325-D334	20.1	494
54	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, 334-41	20.1	486

53	Protocol Update for large-scale genome and gene function analysis with the PANTHER classification system (v.14.0). <i>Nature Protocols</i> , 2019 , 14, 703-721	18.8	462
52	PANTHER version 7: improved phylogenetic trees, orthologs and collaboration with the Gene Ontology Consortium. <i>Nucleic Acids Research</i> , 2010 , 38, D204-10	20.1	451
51	Applications for protein sequence-function evolution data: mRNA/protein expression analysis and coding SNP scoring tools. <i>Nucleic Acids Research</i> , 2006 , 34, W645-50	20.1	386
50	Statistical potentials extracted from protein structures: how accurate are they?. <i>Journal of Molecular Biology</i> , 1996 , 257, 457-69	6.5	372
49	Phylogenetic-based propagation of functional annotations within the Gene Ontology consortium. <i>Briefings in Bioinformatics</i> , 2011 , 12, 449-62	13.4	371
48	The InterPro protein families and domains database: 20 years on. <i>Nucleic Acids Research</i> , 2021 , 49, D344-D354	13.4	358
47	PANTHER version 6: protein sequence and function evolution data with expanded representation of biological pathways. <i>Nucleic Acids Research</i> , 2007 , 35, D247-52	20.1	295
46	Genome sequence of the necrotrophic plant pathogen <i>Pythium ultimum</i> reveals original pathogenicity mechanisms and effector repertoire. <i>Genome Biology</i> , 2010 , 11, R73	18.3	280
45	Local and nonlocal interactions in globular proteins and mechanisms of alcohol denaturation. <i>Protein Science</i> , 1993 , 2, 2050-65	6.3	256
44	PANTHER version 16: a revised family classification, tree-based classification tool, enhancer regions and extensive API. <i>Nucleic Acids Research</i> , 2021 , 49, D394-D403	20.1	248
43	Coding single-nucleotide polymorphisms associated with complex vs. Mendelian disease: evolutionary evidence for differences in molecular effects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 15398-403	11.5	221
42	SynGO: An Evidence-Based, Expert-Curated Knowledge Base for the Synapse. <i>Neuron</i> , 2019 , 103, 217-234	13.9	147
41	PANTHER-PSEP: predicting disease-causing genetic variants using position-specific evolutionary preservation. <i>Bioinformatics</i> , 2016 , 32, 2230-2	7.2	136
40	Standardized benchmarking in the quest for orthologs. <i>Nature Methods</i> , 2016 , 13, 425-30	21.6	133
39	Nicotinic acetylcholine receptor beta2 subunit gene implicated in a systems-based candidate gene study of smoking cessation. <i>Human Molecular Genetics</i> , 2008 , 17, 2834-48	5.6	118
38	Accurate prediction of the functional significance of single nucleotide polymorphisms and mutations in the ABCA1 gene. <i>PLoS Genetics</i> , 2005 , 1, e83	6	107
37	A simple protein folding algorithm using a binary code and secondary structure constraints. <i>Protein Engineering, Design and Selection</i> , 1995 , 8, 769-78	1.9	92
36	The Gene Ontology and the Meaning of Biological Function. <i>Methods in Molecular Biology</i> , 2017 , 1446, 15-24	1.4	78

35	On the Use of Gene Ontology Annotations to Assess Functional Similarity among Orthologs and Paralogs: A Short Report. <i>PLoS Computational Biology</i> , 2012 , 8, e1002386	5	75
34	Alliance of Genome Resources Portal: unified model organism research platform. <i>Nucleic Acids Research</i> , 2020 , 48, D650-D658	20.1	71
33	Tools for Predicting the Functional Impact of Nonsynonymous Genetic Variation. <i>Genetics</i> , 2016 , 203, 635-47	4	66
32	Ontology annotation: mapping genomic regions to biological function. <i>Current Opinion in Chemical Biology</i> , 2007 , 11, 4-11	9.7	66
31	Dopamine genes and nicotine dependence in treatment-seeking and community smokers. <i>Neuropsychopharmacology</i> , 2009 , 34, 2252-64	8.7	38
30	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	36.3	37
29	Assessment of genome-wide protein function classification for <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2003 , 13, 2118-28	9.7	35
28	CAFA and the open world of protein function predictions. <i>Trends in Genetics</i> , 2013 , 29, 609-10	8.5	34
27	The use of orthologous sequences to predict the impact of amino acid substitutions on protein function. <i>PLoS Genetics</i> , 2010 , 6, e1000968	6	34
26	Kat3 coactivators in somatic stem cells and cancer stem cells: biological roles, evolution, and pharmacologic manipulation. <i>Cell Biology and Toxicology</i> , 2016 , 32, 61-81	7.4	32
25	GIGA: a simple, efficient algorithm for gene tree inference in the genomic age. <i>BMC Bioinformatics</i> , 2010 , 11, 312	3.6	29
24	PortEco: a resource for exploring bacterial biology through high-throughput data and analysis tools. <i>Nucleic Acids Research</i> , 2014 , 42, D677-84	20.1	25
23	A systems biology network model for genetic association studies of nicotine addiction and treatment. <i>Pharmacogenetics and Genomics</i> , 2009 , 19, 538-51	1.9	20
22	On the quality of tree-based protein classification. <i>Bioinformatics</i> , 2005 , 21, 1876-90	7.2	18
21	The Quest for Orthologs benchmark service and consensus calls in 2020. <i>Nucleic Acids Research</i> , 2020 , 48, W538-W545	20.1	17
20	BioPAX support in CellDesigner. <i>Bioinformatics</i> , 2011 , 27, 3437-8	7.2	15
19	GO functional similarity clustering depends on similarity measure, clustering method, and annotation completeness. <i>BMC Bioinformatics</i> , 2019 , 20, 155	3.6	12
18	PANTHER: Making genome-scale phylogenetics accessible to all. <i>Protein Science</i> , 2021 ,	6.3	12

17	TreeGrafter: phylogenetic tree-based annotation of proteins with Gene Ontology terms and other annotations. <i>Bioinformatics</i> , 2019 , 35, 518-520	7.2	12
16	PharmGKB summary: dopamine receptor D2. <i>Pharmacogenetics and Genomics</i> , 2011 , 21, 350-6	1.9	11
15	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,	5	10
14	PhyloGenes: An online phylogenetics and functional genomics resource for plant gene function inference. <i>Plant Direct</i> , 2020 , 4, e00293	3.3	8
13	Ontologies and standards in bioscience research: for machine or for human. <i>Frontiers in Physiology</i> , 2011 , 2, 5	4.6	6
12	Ancestral Genomes: a resource for reconstructed ancestral genes and genomes across the tree of life. <i>Nucleic Acids Research</i> , 2019 , 47, D271-D279	20.1	5
11	The Minimum Information about a Molecular Interaction CAusal STatement (MI2CAST). <i>Bioinformatics</i> , 2021 , 36, 5712-5718	7.2	5
10	PEREGRINE: A genome-wide prediction of enhancer to gene relationships supported by experimental evidence. <i>PLoS ONE</i> , 2020 , 15, e0243791	3.7	3
9	Reactome and the Gene Ontology: Digital convergence of data resources. <i>Bioinformatics</i> , 2021 ,	7.2	3
8	Gene Ontology representation for transcription factor functions. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021 , 1864, 194752	6	2
7	PANTHER: Protein families and subfamilies modeled on the divergence of function 2006 ,		1
6	Single Nucleotide Polymorphisms in Human Disease and Evolution: Phylogenies and Genealogies		1
5	Bayesian parameter estimation for automatic annotation of gene functions using observational data and phylogenetic trees. <i>PLoS Computational Biology</i> , 2021 , 17, e1007948	5	
4	PEREGRINE: A genome-wide prediction of enhancer to gene relationships supported by experimental evidence 2020 , 15, e0243791		
3	PEREGRINE: A genome-wide prediction of enhancer to gene relationships supported by experimental evidence 2020 , 15, e0243791		
2	PEREGRINE: A genome-wide prediction of enhancer to gene relationships supported by experimental evidence 2020 , 15, e0243791		
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