Paul D Thomas

List of Publications by Year
in descending order

72 papers	46,195 citations	61984 43 h-index	95266 68 g-index
76 all docs	76 docs citations	76 times ranked	66760 citing authors

#	Article	IF	Citations
1	\<scp\>PANTHER\</scp\>: Making genome‐scale phylogenetics accessible to all. Protein Science, 2022, 31, 8-22.	7.6	467
2	Harmonizing model organism data in the Alliance of Genome Resources. Genetics, 2022, 220, .	2.9	52
3	The Quest for Orthologs orthology benchmark service in 2022. Nucleic Acids Research, 2022, 50, W623-W632.	14.5	29
4	The Minimum Information about a Molecular Interaction CAusal STatement (MI2CAST). Bioinformatics, 2021, 36, 5712-5718.	4.1	14
5	The InterPro protein families and domains database: 20 years on. Nucleic Acids Research, 2021, 49, D344-D354.	14.5	1,385
6	Bayesian parameter estimation for automatic annotation of gene functions using observational data and phylogenetic trees. PLoS Computational Biology, 2021, 17, e1007948.	3.2	0
7	Reactome and the Gene Ontology: digital convergence of data resources. Bioinformatics, 2021, 37, 3343-3348.	4.1	19
8	Gene Ontology representation for transcription factor functions. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2021, 1864, 194752.	1.9	17
9	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
10	The Gene Ontology resource: enriching a GOld mine. Nucleic Acids Research, 2021, 49, D325-D334.	14.5	2,416
11	Alliance of Genome Resources Portal: unified model organism research platform. Nucleic Acids Research, 2020, 48, D650-D658.	14.5	145
12	The Quest for Orthologs benchmark service and consensus calls in 2020. Nucleic Acids Research, 2020, 48, W538-W545.	14.5	41
13	PhyloGenes: An online phylogenetics and functional genomics resource for plant gene function inference. Plant Direct, 2020, 4, e00293.	1.9	23
14	PEREGRINE: A genome-wide prediction of enhancer to gene relationships supported by experimental evidence. PLoS ONE, 2020, 15, e0243791.	2.5	12
15	Title is missing!. , 2020, 15, e0243791.		0
16	Title is missing!. , 2020, 15, e0243791.		0
17	Title is missing!. , 2020, 15, e0243791.		0
18	Title is missing!. , 2020, 15, e0243791.		0

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19	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.	21.4	76
20	SynGO: An Evidence-Based, Expert-Curated Knowledge Base for the Synapse. Neuron, 2019, 103, 217-234.e4.	8.1	518
21	GO functional similarity clustering depends on similarity measure, clustering method, and annotation completeness. BMC Bioinformatics, 2019, 20, 155.	2.6	19
22	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
23	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
24	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. Nucleic Acids Research, 2019, 47, D351-D360.	14.5	1,291
25	Ancestral Genomes: a resource for reconstructed ancestral genes and genomes across the tree of life. Nucleic Acids Research, 2019, 47, D271-D279.	14.5	17
26	TreeGrafter: phylogenetic tree-based annotation of proteins with Gene Ontology terms and other annotations. Bioinformatics, 2019, 35, 518-520.	4.1	22
27	The MEROPS database of proteolytic enzymes, their substrates and inhibitors in 2017 and a comparison with peptidases in the PANTHER database. Nucleic Acids Research, 2018, 46, D624-D632.	14.5	1,234
28	InterPro in 2017—beyond protein family and domain annotations. Nucleic Acids Research, 2017, 45, D190-D199.	14.5	1,358
29	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
30	The Gene Ontology and the Meaning of Biological Function. Methods in Molecular Biology, 2017, 1446, 15-24.	0.9	156
31	Kat3 coactivators in somatic stem cells and cancer stem cells: biological roles, evolution, and pharmacologic manipulation. Cell Biology and Toxicology, 2016, 32, 61-81.	5.3	42
32	Standardized benchmarking in the quest for orthologs. Nature Methods, 2016, 13, 425-430.	19.0	198
33	PANTHER-PSEP: predicting disease-causing genetic variants using position-specific evolutionary preservation. Bioinformatics, 2016, 32, 2230-2232.	4.1	228
34	Tools for Predicting the Functional Impact of Nonsynonymous Genetic Variation. Genetics, 2016, 203, 635-647.	2.9	84
35	PANTHER version 10: expanded protein families and functions, and analysis tools. Nucleic Acids Research, 2016, 44, D336-D342.	14.5	790
36	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.	3.0	12

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37	The InterPro protein families database: the classification resource after 15 years. Nucleic Acids Research, 2015, 43, D213-D221.	14.5	1,205
38	Big data and other challenges in the quest for orthologs. Bioinformatics, 2014, 30, 2993-2998.	4.1	109
39	PortEco: a resource for exploring bacterial biology through high-throughput data and analysis tools. Nucleic Acids Research, 2014, 42, D677-D684.	14.5	25
40	Large-scale gene function analysis with the PANTHER classification system. Nature Protocols, 2013, 8, 1551-1566.	12.0	2,276
41	CAFA and the Open World of protein function predictions. Trends in Genetics, 2013, 29, 609-610.	6.7	47
42	On the Use of Gene Ontology Annotations to Assess Functional Similarity among Orthologs and Paralogs: A Short Report. PLoS Computational Biology, 2012, 8, e1002386.	3.2	91
43	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
44	InterPro in 2011: new developments in the family and domain prediction database. Nucleic Acids Research, 2012, 40, D306-D312.	14.5	921
45	BioPAX support in CellDesigner. Bioinformatics, 2011, 27, 3437-3438.	4.1	18
46	Ontologies and Standards in Bioscience Research: For Machine or for Human. Frontiers in Physiology, 2011, 2, 5.	2.8	7
47	PharmGKB summary. Pharmacogenetics and Genomics, 2011, 21, 350-356.	1.5	13
48	Phylogenetic-based propagation of functional annotations within the Gene Ontology consortium. Briefings in Bioinformatics, 2011, 12, 449-462.	6.5	723
49	GIGA: a simple, efficient algorithm for gene tree inference in the genomic age. BMC Bioinformatics, 2010, 11, 312.	2.6	34
50	PANTHER version 7: improved phylogenetic trees, orthologs and collaboration with the Gene Ontology Consortium. Nucleic Acids Research, 2010, 38, D204-D210.	14.5	553
51	The Use of Orthologous Sequences to Predict the Impact of Amino Acid Substitutions on Protein Function. PLoS Genetics, 2010, 6, e1000968.	3.5	39
52	Genome sequence of the necrotrophic plant pathogen Pythium ultimum reveals original pathogenicity mechanisms and effector repertoire. Genome Biology, 2010, 11, R73.	9.6	391
53	Dopamine Genes and Nicotine Dependence in Treatment-Seeking and Community Smokers. Neuropsychopharmacology, 2009, 34, 2252-2264.	5.4	41
54	A systems biology network model for genetic association studies of nicotine addiction and treatment. Pharmacogenetics and Genomics, 2009, 19, 538-551.	1.5	22

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55	Nicotinic acetylcholine receptor Î²2 subunit gene implicated in a systems-based candidate gene study of smoking cessation. Human Molecular Genetics, 2008, 17, 2834-2848.	2.9	129
56	PANTHER version 6: protein sequence and function evolution data with expanded representation of biological pathways. Nucleic Acids Research, 2007, 35, D247-D252.	14.5	333
57	Ontology annotation: mapping genomic regions to biological function. Current Opinion in Chemical Biology, 2007, 11, 4-11.	6.1	76
58	Applications for protein sequence-function evolution data: mRNA/protein expression analysis and coding SNP scoring tools. Nucleic Acids Research, 2006, 34, W645-W650.	14.5	487
59	PANTHER: Protein families and subfamilies modeled on the divergence of function. , 2006, , .		1
60	On the quality of tree-based protein classification. Bioinformatics, 2005, 21, 1876-1890.	4.1	18
61	Accurate Prediction of the Functional Significance of Single Nucleotide Polymorphisms and Mutations in the ABCA1 Gene. PLoS Genetics, 2005, 1, e83.	3.5	115
62	The PANTHER database of protein families, subfamilies, functions and pathways. Nucleic Acids Research, 2004, 33, D284-D288.	14.5	686
63	Coding single-nucleotide polymorphisms associated with complex vs. Mendelian disease: Evolutionary evidence for differences in molecular effects. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 15398-15403.	7.1	258
64	Inferring Nonneutral Evolution from Human-Chimp-Mouse Orthologous Gene Trios. Science, 2003, 302, 1960-1963.	12.6	626
65	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
66	PANTHER: A Library of Protein Families and Subfamilies Indexed by Function. Genome Research, 2003, 13, 2129-2141.	5.5	2,703
67	Assessment of Genome-Wide Protein Function Classification for Drosophila melanogaster. Genome Research, 2003, 13, 2118-2128.	5.5	40
68	The Sequence of the Human Genome. Science, 2001, 291, 1304-1351.	12.6	12,623
69	Statistical Potentials Extracted From Protein Structures: How Accurate Are They?. Journal of Molecular Biology, 1996, 257, 457-469.	4.2	408
70	A simple protein folding algorithm using a binary code and secondary structure constraints. Protein Engineering, Design and Selection, 1995, 8, 769-778.	2.1	100
71	Principles of protein folding â€" A perspective from simple exact models. Protein Science, 1995, 4, 561-602.	7.6	1,321
72	Local and nonlocal interactions in globular proteins and mechanisms of alcohol denaturation. Protein Science, 1993, 2, 2050-2065.	7.6	280