

Paul D Thomas

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6737736/publications.pdf>

Version: 2024-02-01

72
papers

46,195
citations

71004

43
h-index

107981

68
g-index

76
all docs

76
docs citations

76
times ranked

74027
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	Harmonizing model organism data in the Alliance of Genome Resources. Genetics, 2022, 220, .	1.2	52
3	The Quest for Orthologs orthology benchmark service in 2022. Nucleic Acids Research, 2022, 50, W623-W632.	6.5	29
4	The Minimum Information about a Molecular Interaction CAusal STatement (MI2CAST). Bioinformatics, 2021, 36, 5712-5718.	1.8	14
5	The InterPro protein families and domains database: 20 years on. Nucleic Acids Research, 2021, 49, D344-D354.	6.5	1,385
6	Bayesian parameter estimation for automatic annotation of gene functions using observational data and phylogenetic trees. PLoS Computational Biology, 2021, 17, e1007948.	1.5	0
7	Reactome and the Gene Ontology: digital convergence of data resources. Bioinformatics, 2021, 37, 3343-3348.	1.8	19
8	Gene Ontology representation for transcription factor functions. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2021, 1864, 194752.	0.9	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.	6.5	990
10	The Gene Ontology resource: enriching a GOld mine. Nucleic Acids Research, 2021, 49, D325-D334.	6.5	2,416
11	Alliance of Genome Resources Portal: unified model organism research platform. Nucleic Acids Research, 2020, 48, D650-D658.	6.5	145
12	The Quest for Orthologs benchmark service and consensus calls in 2020. Nucleic Acids Research, 2020, 48, W538-W545.	6.5	41
13	PhyloGenes: An online phylogenetics and functional genomics resource for plant gene function inference. Plant Direct, 2020, 4, e00293.	0.8	23
14	PEREGRINE: A genome-wide prediction of enhancer to gene relationships supported by experimental evidence. PLoS ONE, 2020, 15, e0243791.	1.1	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

#	ARTICLE	IF	CITATIONS
19	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.	9.4	76
20	SynGO: An Evidence-Based, Expert-Curated Knowledge Base for the Synapse. <i>Neuron</i> , 2019, 103, 217-234.e4.	3.8	518
21	GO functional similarity clustering depends on similarity measure, clustering method, and annotation completeness. <i>BMC Bioinformatics</i> , 2019, 20, 155.	1.2	19
22	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.	5.5	1,041
23	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.	6.5	2,455
24	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
25	Ancestral Genomes: a resource for reconstructed ancestral genes and genomes across the tree of life. <i>Nucleic Acids Research</i> , 2019, 47, D271-D279.	6.5	17
26	TreeGrafter: phylogenetic tree-based annotation of proteins with Gene Ontology terms and other annotations. <i>Bioinformatics</i> , 2019, 35, 518-520.	1.8	22
27	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.	6.5	1,234
28	InterPro in 2017â€”beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017, 45, D190-D199.	6.5	1,358
29	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
30	The Gene Ontology and the Meaning of Biological Function. <i>Methods in Molecular Biology</i> , 2017, 1446, 15-24.	0.4	156
31	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.	2.4	42
32	Standardized benchmarking in the quest for orthologs. <i>Nature Methods</i> , 2016, 13, 425-430.	9.0	198
33	PANTHER-PSEP: predicting disease-causing genetic variants using position-specific evolutionary preservation. <i>Bioinformatics</i> , 2016, 32, 2230-2232.	1.8	228
34	Tools for Predicting the Functional Impact of Nonsynonymous Genetic Variation. <i>Genetics</i> , 2016, 203, 635-647.	1.2	84
35	PANTHER version 10: expanded protein families and functions, and analysis tools. <i>Nucleic Acids Research</i> , 2016, 44, D336-D342.	6.5	790
36	Large-scale inference of gene function through phylogenetic annotation of Gene Ontology terms: case study of the apoptosis and autophagy cellular processes. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw155.	1.4	12

#	ARTICLE	IF	CITATIONS
37	The InterPro protein families database: the classification resource after 15 years. <i>Nucleic Acids Research</i> , 2015, 43, D213-D221.	6.5	1,205
38	Big data and other challenges in the quest for orthologs. <i>Bioinformatics</i> , 2014, 30, 2993-2998.	1.8	109
39	PortEco: a resource for exploring bacterial biology through high-throughput data and analysis tools. <i>Nucleic Acids Research</i> , 2014, 42, D677-D684.	6.5	25
40	Large-scale gene function analysis with the PANTHER classification system. <i>Nature Protocols</i> , 2013, 8, 1551-1566.	5.5	2,276
41	CAFA and the Open World of protein function predictions. <i>Trends in Genetics</i> , 2013, 29, 609-610.	2.9	47
42	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.	1.5	91
43	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
44	InterPro in 2011: new developments in the family and domain prediction database. <i>Nucleic Acids Research</i> , 2012, 40, D306-D312.	6.5	921
45	BioPAX support in CellDesigner. <i>Bioinformatics</i> , 2011, 27, 3437-3438.	1.8	18
46	Ontologies and Standards in Bioscience Research: For Machine or for Human. <i>Frontiers in Physiology</i> , 2011, 2, 5.	1.3	7
47	PharmGKB summary. <i>Pharmacogenetics and Genomics</i> , 2011, 21, 350-356.	0.7	13
48	Phylogenetic-based propagation of functional annotations within the Gene Ontology consortium. <i>Briefings in Bioinformatics</i> , 2011, 12, 449-462.	3.2	723
49	GIGA: a simple, efficient algorithm for gene tree inference in the genomic age. <i>BMC Bioinformatics</i> , 2010, 11, 312.	1.2	34
50	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
51	The Use of Orthologous Sequences to Predict the Impact of Amino Acid Substitutions on Protein Function. <i>PLoS Genetics</i> , 2010, 6, e1000968.	1.5	39
52	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.	13.9	391
53	Dopamine Genes and Nicotine Dependence in Treatment-Seeking and Community Smokers. <i>Neuropsychopharmacology</i> , 2009, 34, 2252-2264.	2.8	41
54	A systems biology network model for genetic association studies of nicotine addiction and treatment. <i>Pharmacogenetics and Genomics</i> , 2009, 19, 538-551.	0.7	22

#	ARTICLE	IF	CITATIONS
55	Nicotinic acetylcholine receptor $\alpha 2$ subunit gene implicated in a systems-based candidate gene study of smoking cessation. <i>Human Molecular Genetics</i> , 2008, 17, 2834-2848.	1.4	129
56	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
57	Ontology annotation: mapping genomic regions to biological function. <i>Current Opinion in Chemical Biology</i> , 2007, 11, 4-11.	2.8	76
58	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
59	PANTHER: Protein families and subfamilies modeled on the divergence of function. , 2006, , .		1
60	On the quality of tree-based protein classification. <i>Bioinformatics</i> , 2005, 21, 1876-1890.	1.8	18
61	Accurate Prediction of the Functional Significance of Single Nucleotide Polymorphisms and Mutations in the ABCA1 Gene. <i>PLoS Genetics</i> , 2005, 1, e83.	1.5	115
62	The PANTHER database of protein families, subfamilies, functions and pathways. <i>Nucleic Acids Research</i> , 2004, 33, D284-D288.	6.5	686
63	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, 15398-15403.	3.3	258
64	Inferring Nonneutral Evolution from Human-Chimp-Mouse Orthologous Gene Trios. <i>Science</i> , 2003, 302, 1960-1963.	6.0	626
65	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
66	PANTHER: A Library of Protein Families and Subfamilies Indexed by Function. <i>Genome Research</i> , 2003, 13, 2129-2141.	2.4	2,703
67	Assessment of Genome-Wide Protein Function Classification for <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2003, 13, 2118-2128.	2.4	40
68	The Sequence of the Human Genome. <i>Science</i> , 2001, 291, 1304-1351.	6.0	12,623
69	Statistical Potentials Extracted From Protein Structures: How Accurate Are They?. <i>Journal of Molecular Biology</i> , 1996, 257, 457-469.	2.0	408
70	A simple protein folding algorithm using a binary code and secondary structure constraints. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 769-778.	1.0	100
71	Principles of protein folding â€” A perspective from simple exact models. <i>Protein Science</i> , 1995, 4, 561-602.	3.1	1,321
72	Local and nonlocal interactions in globular proteins and mechanisms of alcohol denaturation. <i>Protein Science</i> , 1993, 2, 2050-2065.	3.1	280