David P Hill

List of Publications by Year in descending order

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Ολνίο Ρ.Η.Ι.ι

#	Article	IF	CITATIONS
1	Gene Ontology: tool for the unification of biology. Nature Genetics, 2000, 25, 25-29.	21.4	34,499
2	The Gene Ontology resource: enriching a GOld mine. Nucleic Acids Research, 2021, 49, D325-D334.	14.5	2,416
3	Gene Ontology annotations: what they mean and where they come from. BMC Bioinformatics, 2008, 9, S2.	2.6	124
4	Cross-product extensions of the Gene Ontology. Journal of Biomedical Informatics, 2011, 44, 80-86.	4.3	96
5	A method for increasing expressivity of Gene Ontology annotations using a compositional approach. BMC Bioinformatics, 2014, 15, 155.	2.6	78
6	Cisplatin-resistant triple-negative breast cancer subtypes: multiple mechanisms of resistance. BMC Cancer, 2019, 19, 1039.	2.6	77
7	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
8	Exploring autophagy with Gene Ontology. Autophagy, 2018, 14, 419-436.	9.1	64
9	Harmonizing model organism data in the Alliance of Genome Resources. Genetics, 2022, 220, .	2.9	52
10	PROGRAM DESCRIPTION. Genomics, 2001, 74, 121-128.	2.9	47
11	Dovetailing biology and chemistry: integrating the Gene Ontology with the ChEBI chemical ontology. BMC Genomics, 2013, 14, 513.	2.8	45
12	TermGenie – a web-application for pattern-based ontology class generation. Journal of Biomedical Semantics, 2014, 5, 48.	1.6	30
13	Improving Interpretation of Cardiac Phenotypes and Enhancing Discovery With Expanded Knowledge in the Gene Ontology. Circulation Genomic and Precision Medicine, 2018, 11, e001813.	3.6	24
14	Reactome and the Gene Ontology: digital convergence of data resources. Bioinformatics, 2021, 37, 3343-3348.	4.1	19
15	Modeling biochemical pathways in the gene ontology. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw126.	3.0	11
16	Term Matrix: a novel Gene Ontology annotation quality control system based on ontology term co-annotation patterns. Open Biology, 2020, 10, 200149.	3.6	7
17	Methodology for the inference of gene function from phenotype data. BMC Bioinformatics, 2014, 15, 405.	2.6	5