Todd J Vision

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5331029/publications.pdf

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		172443	149686
61	5,347	29	56
papers	citations	h-index	g-index
81	81	81	8820
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	The Origins of Genomic Duplications in <i>Arabidopsis</i> . Science, 2000, 290, 2114-2117.	12.6	940
2	The iPlant Collaborative: Cyberinfrastructure for Plant Biology. Frontiers in Plant Science, 2011, 2, 34.	3.6	396
3	Insights into evolution of multicellular fungi from the assembled chromosomes of the mushroom <i>Coprinopsis cinerea</i> (<i>Coprinus cinereus</i>). Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 11889-11894.	7.1	389
4	Comparing sequenced segments of the tomato and <i>Arabidopsis</i> genomes: Large-scale duplication followed by selective gene loss creates a network of synteny. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 9121-9126.	7.1	381
5	Data reuse and the open data citation advantage. PeerJ, 2013, 1, e175.	2.0	352
6	The molecular ecologist's guide to expressed sequence tags. Molecular Ecology, 2006, 16, 907-924.	3.9	326
7	Contrasting Modes of Diversification in the Aux/IAA and ARF Gene Families. Plant Physiology, 2004, 135, 1738-1752.	4.8	268
8	Divergence in Expression between Duplicated Genes in Arabidopsis. Molecular Biology and Evolution, 2007, 24, 2298-2309.	8.9	226
9	Identification and Characterization of Aluminum Tolerance Loci in Arabidopsis (Landsberg erecta \tilde{A} —) Tj ETQq1 1 (Plant Physiology, 2003, 132, 936-948.	0.784314 r 4.8	rgBT /Ove <mark>rlo</mark> 147
10	Patterns of Nucleotide Substitution Among Simultaneously Duplicated Gene Pairs in Arabidopsis thaliana. Molecular Biology and Evolution, 2002, 19, 1464-1473.	8.9	117
11	Genome-Scale Phylogenetics: Inferring the Plant Tree of Life from 18,896 Gene Trees. Systematic Biology, 2011, 60, 117-125.	5.6	110
12	A decadal view of biodiversity informatics: challenges and priorities. BMC Ecology, 2013, 13, 16.	3.0	110
13	Selective Mapping: A Strategy for Optimizing the Construction of High-Density Linkage Maps. Genetics, 2000, 155, 407-420.	2.9	108
14	Using ESTs for phylogenomics: can one accurately infer a phylogenetic tree from a gappy alignment?. BMC Evolutionary Biology, 2008, 8, 95.	3.2	106
15	Open Data and the Social Contract of Scientific Publishing. BioScience, 2010, 60, 330-331.	4.9	105
16	Evolutionary Characters, Phenotypes and Ontologies: Curating Data from the Systematic Biology Literature. PLoS ONE, 2010, 5, e10708.	2.5	83
17	Fast identification and statistical evaluation of segmental homologies in comparative maps. Bioinformatics, 2003, 19, i74-i80.	4.1	82
18	A computational system to select candidate genes for complex human traits. Bioinformatics, 2007, 23, 1132-1140.	4.1	79

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19	Phenex: Ontological Annotation of Phenotypic Diversity. PLoS ONE, 2010, 5, e10500.	2.5	78
20	Taking the First Steps towards a Standard for Reporting on Phylogenies: Minimum Information about a Phylogenetic Analysis (MIAPA). OMICS A Journal of Integrative Biology, 2006, 10, 231-237.	2.0	76
21	The Teleost Anatomy Ontology: Anatomical Representation for the Genomics Age. Systematic Biology, 2010, 59, 369-383.	5.6	76
22	Data archiving is a good investment. Nature, 2011, 473, 285-285.	27.8	72
23	500,000 fish phenotypes: The new informatics landscape for evolutionary and developmental biology of the vertebrate skeleton. Journal of Applied Ichthyology, 2012, 28, 300-305.	0.7	52
24	Improving Quantitative Trait Loci Mapping Resolution in Experimental Crosses by the Use of Genotypically Selected Samples. Genetics, 2005, 170, 401-408.	2.9	50
25	DataONE: Data Observation Network for Earth $\hat{A}-$ Preserving Data and Enabling Innovation in the Biological and Environmental Sciences. D-Lib Magazine, 2011, 17, .	0.5	46
26	Fine mapping a QTL for carbon isotope composition in tomato. Theoretical and Applied Genetics, 2008, 117, 221-233.	3.6	43
27	The Standing Pool of Genomic Structural Variation in a Natural Population of Mimulus guttatus. Genome Biology and Evolution, 2014, 6, 53-64.	2.5	42
28	Tracking the evolution of alternatively spliced exons within the Dscam family. BMC Evolutionary Biology, 2006, 6, 16.	3.2	41
29	The vertebrate taxonomy ontology: a framework for reasoning across model organism and species phenotypes. Journal of Biomedical Semantics, 2013, 4, 34.	1.6	39
30	Phenoscape: Identifying Candidate Genes for Evolutionary Phenotypes. Molecular Biology and Evolution, 2016, 33, 13-24.	8.9	37
31	Phytome: a platform for plant comparative genomics. Nucleic Acids Research, 2006, 34, D724-D730.	14.5	35
32	Science Incubators: Synthesis Centers and Their Role in the Research Ecosystem. PLoS Biology, 2013, 11, e1001468.	5.6	32
33	The effects of resource availability and environmental conditions on genetic rankings for carbon isotope discrimination during growth in tomato and rice. Functional Plant Biology, 2005, 32, 1089.	2.1	27
34	Pathogen-induced systemic resistance in Ipomoea purpurea. Oecologia, 1995, 102, 494-500.	2.0	23
35	Using the phenoscape knowledgebase to relate genetic perturbations to phenotypic evolution. Genesis, 2015, 53, 561-571.	1.6	19
36	Annotation of phenotypes using ontologies: a gold standard for the training and evaluation of natural language processing systems. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	19

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37	Compensatory Evolution in RNA Secondary Structures Increases Substitution Rate Variation among Sites. Molecular Biology and Evolution, 2008, 25, 1778-1787.	8.9	18
38	Journal data policies: Exploring how the understanding of editors and authors corresponds to the policies themselves. PLoS ONE, 2020, 15, e0230281.	2.5	18
39	Annotation of phenotypic diversity: decoupling data curation and ontology curation using Phenex. Journal of Biomedical Semantics, 2014, 5, 45.	1.6	16
40	Comparison of fullâ€text searching to metadata searching for genes in two biomedical literature cohorts. Journal of the Association for Information Science and Technology, 2007, 58, 2341-2352.	2.6	14
41	Gene order in plants: a slow but sure shuffle. New Phytologist, 2005, 168, 51-60.	7. 3	13
42	Beginning to track 1000 datasets from public repositories into the published literature. Proceedings of the American Society for Information Science and Technology, 2011, 48, 1-4.	0.2	13
43	Do synthesis centers synthesize? A semantic analysis of topical diversity in research. Research Policy, 2021, 50, 104069.	6.4	13
44	Assessing the Significance of Quantitative Trait Loci in Replicable Mapping Populations. Genetics, 2006, 174, 1063-1068.	2.9	12
45	A Logical Model of Homology for Comparative Biology. Systematic Biology, 2020, 69, 345-362.	5.6	11
46	Evaluating data citation and sharing policies in the environmental sciences. Proceedings of the American Society for Information Science and Technology, 2010, 47, 1-2.	0.2	7
47	Inferring species trees from gene duplication episodes. , 2010, , .		7
48	Systematic Identification of Balanced Transposition Polymorphisms in Saccharomyces cerevisiae. PLoS Genetics, 2009, 5, e1000502.	3.5	6
49	Assessing Bayesian Phylogenetic Information Content of Morphological Data Using Knowledge From Anatomy Ontologies. Systematic Biology, 2022, 71, 1290-1306.	5.6	6
50	Genetic architecture influences when and how hybridization contributes to colonization. Evolution; International Journal of Organic Evolution, 2020, 74, 1590-1602.	2.3	5
51	A hierarchical model for incomplete alignments in phylogenetic inference. Bioinformatics, 2009, 25, 592-598.	4.1	4
52	What Factors Influence Where Researchers Deposit their Data? A Survey of Researchers Submitting to Data Repositories. International Journal of Digital Curation, 2015, 10, 68-81.	0.2	4
53	ODIN: the ORCID and DataCite interoperability network. International Journal of Knowledge and Learning, 2014, 9, 305.	0.2	3
54	Open data for evolutionary synthesis: an introduction to the NESCent collection. Scientific Data, 2014, 1, 140030.	5.3	2

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55	INVESTIGATING THE IMPORTANCE OF ANATOMICAL HOMOLOGY FOR CROSS-SPECIES PHENOTYPE COMPARISONS USING SEMANTIC SIMILARITY. , 2016, , .		2
56	Avoiding "conflicts of interest†a computational approach to scheduling parallel conference tracks and its human evaluation. PeerJ Computer Science, 2019, 5, e234.	4. 5	2
57	Computational Tools and Resources in Plant Genome Informatics. , 0, , .		1
58	Complete plastome sequences of two Psidium species from the Gal \tilde{A}_i pagos Islands. F1000Research, 2018, 7, 1361.	1.6	1
59	Phenex: Ontological Annotation of Phenotypic Diversity. Nature Precedings, 2009, , .	0.1	O
60	Linking Evolution, Ecology, and Health: TriCEM. BioScience, 2015, 65, 748-749.	4.9	0
61	Evolution of anatomical concept usage over time. , 2017, , .		0