Eva Huala

List of Publications by Year in descending order

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172457 254184 11,257 43 29 43 citations h-index g-index papers 43 43 43 15640 all docs docs citations times ranked citing authors

#	Article	IF	CITATIONS
1	The Gene Ontology resource: enriching a GOld mine. Nucleic Acids Research, 2021, 49, D325-D334.	14.5	2,416
2	The Arabidopsis Information Resource (TAIR): improved gene annotation and new tools. Nucleic Acids Research, 2012, 40, D1202-D1210.	14.5	1,972
3	The Arabidopsis Information Resource (TAIR): gene structure and function annotation. Nucleic Acids Research, 2007, 36, D1009-D1014.	14.5	895
4	The arabidopsis information resource: Making and mining the "gold standard―annotated reference plant genome. Genesis, 2015, 53, 474-485.	1.6	884
5	The Arabidopsis Information Resource (TAIR): a model organism database providing a centralized, curated gateway to Arabidopsis biology, research materials and community. Nucleic Acids Research, 2003, 31, 224-228.	14.5	761
6	Arabidopsis NPH1: A Protein Kinase with a Putative Redox-Sensing Domain. Science, 1997, 278, 2120-2123.	12.6	700
7	The Arabidopsis Information Resource (TAIR): a comprehensive database and web-based information retrieval, analysis, and visualization system for a model plant. Nucleic Acids Research, 2001, 29, 102-105.	14.5	497
8	Functional Annotation of the Arabidopsis Genome Using Controlled Vocabularies. Plant Physiology, 2004, 135, 745-755.	4.8	410
9	Blue-Light Photoreceptors in Higher Plants. Annual Review of Cell and Developmental Biology, 1999, 15, 33-62.	9.4	387
10	Prokaryotic Signal Transduction Mediated by Sensor and Regulator Protein Pairs. Annual Review of Genetics, 1989, 23, 311-336.	7. 6	292
11	LEAFY Interacts with Floral Homeotic Genes to Regulate Arabidopsis Floral Development Plant Cell, 1992, 4, 901-913.	6.6	220
12	TAIR: a resource for integrated Arabidopsis data. Functional and Integrative Genomics, 2002, 2, 239-253.	3.5	184
13	Finding Our Way through Phenotypes. PLoS Biology, 2015, 13, e1002033.	5.6	178
14	RNAcentral: a comprehensive database of non-coding RNA sequences. Nucleic Acids Research, 2017, 45, D128-D134.	14.5	174
15	Text mining for the biocuration workflow. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas020-bas020.	3.0	132
16	The Plant Ontology as a Tool for Comparative Plant Anatomy and Genomic Analyses. Plant and Cell Physiology, 2013, 54, e1-e1.	3.1	131
17	The central domain of Rhizobium meliloti NifA is sufficient to activate transcription from the R. meliloti nifH promoter. Journal of Bacteriology, 1989, 171, 3354-3365.	2.2	119
18	The central domain of Rhizobium leguminosarum DctD functions independently to activate transcription. Journal of Bacteriology, 1992, 174, 1428-1431.	2.2	93

#	Article	IF	Citations
19	Accelerating literature curation with text-mining tools: a case study of using PubTator to curate genes in PubMed abstracts. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas041-bas041.	3.0	83
20	LEAFY Interacts with Floral Homeotic Genes to Regulate Arabidopsis Floral Development. Plant Cell, 1992, 4, 901.	6.6	66
21	BioCreative III interactive task: an overview. BMC Bioinformatics, 2011, 12, S4.	2.6	65
22	Determination and Cell Interactions in Reproductive Meristems Plant Cell, 1993, 5, 1157-1165.	6.6	60
23	Recurated protein interaction datasets. Nature Methods, 2009, 6, 860-861.	19.0	58
24	An ontology approach to comparative phenomics in plants. Plant Methods, 2015, 11, 10.	4.3	53
25	Sustaining the Data and Bioresource Commons. Science, 2010, 330, 592-593.	12.6	52
26	Sustainable funding for biocuration: The Arabidopsis Information Resource (TAIR) as a case study of a subscription-based funding model. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw018.	3.0	47
27	Using the <i>Arabidopsis</i> Information Resource (TAIR) to Find Information About <i>Arabidopsis</i> Genes. Current Protocols in Bioinformatics, 2017, 60, 1.11.1-1.11.45.	25.8	44
28	Photobiology of Diagravitropic Maize Roots. Plant Physiology, 1984, 75, 359-363.	4.8	41
29	Text mining in the biocuration workflow: applications for literature curation at WormBase, dictyBase and TAIR. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas040-bas040.	3.0	35
30	Using The <i>Arabidopsis</i> Information Resource (TAIR) to Find Information About <i>Arabidopsis</i> Genes. Current Protocols in Bioinformatics, 2010, 30, Unit1.11.	25.8	27
31	Community-based gene structure annotation. Trends in Plant Science, 2005, 10, 9-14.	8.8	24
32	PhyloGenes: An online phylogenetics and functional genomics resource for plant gene function inference. Plant Direct, 2020, 4, e00293.	1.9	23
33	Building an efficient curation workflow for the Arabidopsis literature corpus. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas047-bas047.	3.0	19
34	Design, Implementation and Maintenance of a Model Organism Database for Arabidopsis thaliana. Comparative and Functional Genomics, 2004, 5, 362-369.	2.0	16
35	Assessment of community-submitted ontology annotations from a novel database-journal partnership. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas030-bas030.	3.0	16
36	Aerobic inactivation of Rhizobium meliloti NifA in Escherichia coli is mediated by lon and two newly identified genes, snoB and snoC. Journal of Bacteriology, 1991, 173, 382-390.	2.2	15

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37	Emerging semantics to link phenotype and environment. PeerJ, 2015, 3, e1470.	2.0	15
38	Arabidopsis bioinformatics resources: The current state, challenges, and priorities for the future. Plant Direct, 2019, 3, e00109.	1.9	14
39	Current status of the multinational Arabidopsis community. Plant Direct, 2020, 4, e00248.	1.9	13
40	Determination and Cell Interactions in Reproductive Meristems. Plant Cell, 1993, 5, 1157.	6.6	12
41	Arabidopsis Database and Stock Resources. Methods in Molecular Biology, 2014, 1062, 65-96.	0.9	10
42	GFam: a platform for automatic annotation of gene families. Nucleic Acids Research, 2012, 40, e152-e152.	14.5	3
43	Phenotype Ontology Research Coordination Network meeting report: creating a community network for comparing and leveraging phenotype-genotype knowledge across species. Standards in Genomic Sciences, 2012, 6, 440-443.	1.5	1