Xinbin Dai

List of Publications by Year
in descending order

32 papers	6,743 citations	361413 20 h-index	414414 32 g-index
32 all docs	32 docs citations	32 times ranked	9097 citing authors

#	Article	IF	Citations
1	psRNATarget: a plant small RNA target analysis server. Nucleic Acids Research, 2011, 39, W155-W159.	14.5	1,662
2	The Medicago genome provides insight into the evolution of rhizobial symbioses. Nature, 2011, 480, 520-524.	27.8	1,166
3	psRNATarget: a plant small RNA target analysis server (2017 release). Nucleic Acids Research, 2018, 46, W49-W54.	14.5	942
4	iTAK: A Program for Genome-wide Prediction andÂClassification of Plant Transcription Factors, Transcriptional Regulators, and Protein Kinases. Molecular Plant, 2016, 9, 1667-1670.	8.3	735
5	A gene expression atlas of the model legume <i>Medicago truncatula</i>. Plant Journal, 2008, 55, 504-513.	5.7	668
6	Genomeâ€wide analysis of phenylpropanoid defence pathways. Molecular Plant Pathology, 2010, 11, 829-846.	4.2	332
7	Transcript and proteomic analysis of developing white lupin (Lupinus albus L.) roots. BMC Plant Biology, 2009, 9, 1.	3.6	182
8	Terpene Biosynthesis in Glandular Trichomes of Hop Â Â. Plant Physiology, 2008, 148, 1254-1266.	4.8	180
9	Computational analysis of miRNA targets in plants: current status and challenges. Briefings in Bioinformatics, 2011, 12, 115-121.	6.5	116
10	Genome-Wide Identification of <i>Medicago</i> Peptides Involved in Macronutrient Responses and Nodulation. Plant Physiology, 2017, 175, 1669-1689.	4.8	101
11	TrichOME: A Comparative Omics Database for Plant Trichomes Â Â Â. Plant Physiology, 2009, 152, 44-54.	4.8	98
12	LegumeIP: an integrative database for comparative genomics and transcriptomics of model legumes. Nucleic Acids Research, 2012, 40, D1221-D1229.	14.5	91
13	Genomic Inventory and Transcriptional Analysis of <i>Medicago truncatula</i> Transporters. Plant Physiology, 2010, 152, 1716-1730.	4.8	73
14	<i>pssRNAit</i>: A Web Server for Designing Effective and Specific Plant siRNAs with Genome-Wide Off-Target Assessment. Plant Physiology, 2020, 184, 65-81.	4.8	54
15	Comprehensive analysis of small RNA-seq data reveals that combination of miRNA with its isomiRs increase the accuracy of target prediction in <i>Arabidopsis thaliana</i>. RNA Biology, 2014, 11, 1414-1429.	3.1	46
16	MtSSPdb: The <i>Medicago truncatula</i> Small Secreted Peptide Database. Plant Physiology, 2020, 183, 399-413.	4.8	40
17	The CLE53â€"SUNN genetic pathway negatively regulates arbuscular mycorrhiza root colonization in Medicago truncatula. Journal of Experimental Botany, 2020, 71, 4972-4984.	4.8	36
18	A legume specific protein database (LegProt) improves the number of identified peptides, confidence scores and overall protein identification success rates for legume proteomics. Phytochemistry, 2011, 72, 1020-1027.	2.9	29

#	Article	IF	Citations
19	LegumeIP V3: from models to crops—an integrative gene discovery platform for translational genomics in legumes. Nucleic Acids Research, 2021, 49, D1472-D1479.	14.5	25
20	PEPIS: A Pipeline for Estimating Epistatic Effects in Quantitative Trait Locus Mapping and Genome-Wide Association Studies. PLoS Computational Biology, 2016, 12, e1004925.	3.2	23
21	LegumeIP 2.0—a platform for the study of gene function and genome evolution in legumes. Nucleic Acids Research, 2016, 44, D1189-D1194.	14.5	23
22	Regulation of a Virus-Induced Lethal Disease in Tomato Revealed by LongSAGE Analysis. Molecular Plant-Microbe Interactions, 2007, 20, 1477-1488.	2.6	21
23	HRGRN: A Graph Search-Empowered Integrative Database of Arabidopsis Signaling Transduction, Metabolism and Gene Regulation Networks. Plant and Cell Physiology, 2016, 57, e12-e12.	3.1	20
24	A new systematic computational approach to predicting target genes of transcription factors. Nucleic Acids Research, 2007, 35, 4433-4440.	14.5	17
25	Identification and Functional Investigation of Genome‐Encoded, Small, Secreted Peptides in Plants. Current Protocols in Plant Biology, 2019, 4, e20098.	2.8	15
26	Bioinformatics Tools for Achieving Better Gene Silencing in Plants. Methods in Molecular Biology, 2015, 1287, 43-60.	0.9	13
27	Functional genomics of plant transporters in legume nodules. Functional Plant Biology, 2006, 33, 731.	2.1	12
28	A microRNA biogenesis-like pathway for producing phased small interfering RNA from a long non-coding RNA in rice. Journal of Experimental Botany, 2019, 70, 1767-1774.	4.8	8
29	Draft Genome Sequence Resource of Switchgrass Rust Pathogen, *Puccinia novopanici* Isolate Ard-01. Phytopathology, 2019, 109, 1513-1515.	2.2	6
30	Insertional mutagenesis of *Brachypodium distachyon* using the *Tnt1* retrotransposable element. Plant Journal, 2020, 103, 1924-1936.	5.7	6
31	GPU empowered pipelines for calculating genome-wide kinship matrices with ultra-high dimensional genetic variants and facilitating 1D and 2D GWAS. NAR Genomics and Bioinformatics, 2020, 2, lqz009.	3.2	2
32	PIP-SNP: a pipeline for processing SNP data featured as linkage disequilibrium bin mapping, genotype imputing and marker synthesizing. NAR Genomics and Bioinformatics, 2021, 3, lqab060.	3.2	1