

Xinbin Dai

List of Publications by Year in descending order

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Version: 2024-02-01

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	PIP-SNP: a pipeline for processing SNP data featured as linkage disequilibrium bin mapping, genotype imputing and marker synthesizing. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab060.	3.2	1
2	LegumelP V3: from models to cropsâ€”an integrative gene discovery platform for translational genomics in legumes. <i>Nucleic Acids Research</i> , 2021, 49, D1472-D1479.	14.5	25
3	GPU empowered pipelines for calculating genome-wide kinship matrices with ultra-high dimensional genetic variants and facilitating 1D and 2D GWAS. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqz009.	3.2	2
4	<i>pssRNAit</i> : A Web Server for Designing Effective and Specific Plant siRNAs with Genome-Wide Off-Target Assessment. <i>Plant Physiology</i> , 2020, 184, 65-81.	4.8	54
5	MtSSPdb: The <i>Medicago truncatula</i> Small Secreted Peptide Database. <i>Plant Physiology</i> , 2020, 183, 399-413.	4.8	40
6	Insertional mutagenesis of <i>Brachypodium distachyon</i> using the <i>Tnt1</i> retrotransposable element. <i>Plant Journal</i> , 2020, 103, 1924-1936.	5.7	6
7	The CLE53â€”SUNN genetic pathway negatively regulates arbuscular mycorrhiza root colonization in <i>Medicago truncatula</i> . <i>Journal of Experimental Botany</i> , 2020, 71, 4972-4984.	4.8	36
8	Identification and Functional Investigation of Genome-Encoded, Small, Secreted Peptides in Plants. <i>Current Protocols in Plant Biology</i> , 2019, 4, e20098.	2.8	15
9	Draft Genome Sequence Resource of Switchgrass Rust Pathogen, <i>Puccinia novopanici</i> Isolate Ard-01. <i>Phytopathology</i> , 2019, 109, 1513-1515.	2.2	6
10	A microRNA biogenesis-like pathway for producing phased small interfering RNA from a long non-coding RNA in rice. <i>Journal of Experimental Botany</i> , 2019, 70, 1767-1774.	4.8	8
11	psRNATarget: a plant small RNA target analysis server (2017 release). <i>Nucleic Acids Research</i> , 2018, 46, W49-W54.	14.5	942
12	Genome-Wide Identification of <i>Medicago</i> Peptides Involved in Macronutrient Responses and Nodulation. <i>Plant Physiology</i> , 2017, 175, 1669-1689.	4.8	101
13	PEPIS: A Pipeline for Estimating Epistatic Effects in Quantitative Trait Locus Mapping and Genome-Wide Association Studies. <i>PLoS Computational Biology</i> , 2016, 12, e1004925.	3.2	23
14	iTAK: A Program for Genome-wide Prediction and Classification of Plant Transcription Factors, Transcriptional Regulators, and Protein Kinases. <i>Molecular Plant</i> , 2016, 9, 1667-1670.	8.3	735
15	HRGRN: A Graph Search-Empowered Integrative Database of Arabidopsis Signaling Transduction, Metabolism and Gene Regulation Networks. <i>Plant and Cell Physiology</i> , 2016, 57, e12-e12.	3.1	20
16	LegumelP 2.0â€”a platform for the study of gene function and genome evolution in legumes. <i>Nucleic Acids Research</i> , 2016, 44, D1189-D1194.	14.5	23
17	Bioinformatics Tools for Achieving Better Gene Silencing in Plants. <i>Methods in Molecular Biology</i> , 2015, 1287, 43-60.	0.9	13
18	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> . <i>RNA Biology</i> , 2014, 11, 1414-1429.	3.1	46

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19	LegumelP: an integrative database for comparative genomics and transcriptomics of model legumes. <i>Nucleic Acids Research</i> , 2012, 40, D1221-D1229.	14.5	91
20	The <i>Medicago</i> genome provides insight into the evolution of rhizobial symbioses. <i>Nature</i> , 2011, 480, 520-524.	27.8	1,166
21	Computational analysis of miRNA targets in plants: current status and challenges. <i>Briefings in Bioinformatics</i> , 2011, 12, 115-121.	6.5	116
22	A legume specific protein database (LegProt) improves the number of identified peptides, confidence scores and overall protein identification success rates for legume proteomics. <i>Phytochemistry</i> , 2011, 72, 1020-1027.	2.9	29
23	psRNATarget: a plant small RNA target analysis server. <i>Nucleic Acids Research</i> , 2011, 39, W155-W159.	14.5	1,662
24	Genome-wide analysis of phenylpropanoid defence pathways. <i>Molecular Plant Pathology</i> , 2010, 11, 829-846.	4.2	332
25	Genomic Inventory and Transcriptional Analysis of <i>Medicago truncatula</i> Transporters. <i>Plant Physiology</i> , 2010, 152, 1716-1730.	4.8	73
26	TrichOME: A Comparative Omics Database for Plant Trichomes. <i>Plant Physiology</i> , 2009, 152, 44-54.	4.8	98
27	Transcript and proteomic analysis of developing white lupin (<i>Lupinus albus</i> L.) roots. <i>BMC Plant Biology</i> , 2009, 9, 1.	3.6	182
28	A gene expression atlas of the model legume <i>Medicago truncatula</i> . <i>Plant Journal</i> , 2008, 55, 504-513.	5.7	668
29	Terpene Biosynthesis in Glandular Trichomes of Hop. <i>Plant Physiology</i> , 2008, 148, 1254-1266.	4.8	180
30	Regulation of a Virus-Induced Lethal Disease in Tomato Revealed by LongSAGE Analysis. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 1477-1488.	2.6	21
31	A new systematic computational approach to predicting target genes of transcription factors. <i>Nucleic Acids Research</i> , 2007, 35, 4433-4440.	14.5	17
32	Functional genomics of plant transporters in legume nodules. <i>Functional Plant Biology</i> , 2006, 33, 731.	2.1	12