

Patrick X Zhao

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

8,173
citations

186265
28
h-index

175258
52
g-index

56
all docs

56
docs citations

56
times ranked

10634
citing authors

#	ARTICLE	IF	CITATIONS
1	psRNATarget: a plant small RNA target analysis server. <i>Nucleic Acids Research</i> , 2011, 39, W155-W159.	14.5	1,662
2	The Medicago genome provides insight into the evolution of rhizobial symbioses. <i>Nature</i> , 2011, 480, 520-524.	27.8	1,166
3	psRNATarget: a plant small RNA target analysis server (2017 release). <i>Nucleic Acids Research</i> , 2018, 46, W49-W54.	14.5	942
4	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
5	A gene expression atlas of the model legume <i>Medicago truncatula</i> . <i>Plant Journal</i> , 2008, 55, 504-513.	5.7	668
6	Large-scale insertional mutagenesis using the <i>Tnt1</i> retrotransposon in the model legume <i>Medicago truncatula</i> . <i>Plant Journal</i> , 2008, 54, 335-347.	5.7	442
7	Genome-wide SNP discovery in tetraploid alfalfa using 454 sequencing and high resolution melting analysis. <i>BMC Genomics</i> , 2011, 12, 1-11.	2.8	353
8	Genome-wide analysis of phenylpropanoid defence pathways. <i>Molecular Plant Pathology</i> , 2010, 11, 829-846.	4.2	332
9	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
10	Terpene Biosynthesis in Glandular Trichomes of Hop <i>H. h.</i> <i>Plant Physiology</i> , 2008, 148, 1254-1266.	4.8	180
11	Computational analysis of miRNA targets in plants: current status and challenges. <i>Briefings in Bioinformatics</i> , 2011, 12, 115-121.	6.5	116
12	Prediction of Membrane Transport Proteins and Their Substrate Specificities Using Primary Sequence Information. <i>PLoS ONE</i> , 2014, 9, e100278.	2.5	103
13	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
14	TrichOME: A Comparative Omics Database for Plant Trichomes <i>H. h.</i> <i>Plant Physiology</i> , 2009, 152, 44-54.	4.8	98
15	LegumelP: an integrative database for comparative genomics and transcriptomics of model legumes. <i>Nucleic Acids Research</i> , 2012, 40, D1221-D1229.	14.5	91
16	Combining Machine Learning and Homology-Based Approaches to Accurately Predict Subcellular Localization in Arabidopsis. <i>Plant Physiology</i> , 2010, 154, 36-54.	4.8	78
17	Genomic Inventory and Transcriptional Analysis of <i>Medicago truncatula</i> Transporters. <i>Plant Physiology</i> , 2010, 152, 1716-1730.	4.8	73
18	Global Transcriptome Sequencing Using the Illumina Platform and the Development of EST-SSR Markers in Autotetraploid Alfalfa. <i>PLoS ONE</i> , 2013, 8, e83549.	2.5	70

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19	MET-COFEA: A Liquid Chromatography/Mass Spectrometry Data Processing Platform for Metabolite Compound Feature Extraction and Annotation. <i>Analytical Chemistry</i> , 2014, 86, 6245-6253.	6.5	54
20	<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
21	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
22	MtSSPdb: The <i>Medicago truncatula</i> Small Secreted Peptide Database. <i>Plant Physiology</i> , 2020, 183, 399-413.	4.8	40
23	Nitrogen remobilization and conservation, and underlying senescence-associated gene expression in the perennial switchgrass <i>Panicum virgatum</i>. <i>New Phytologist</i> , 2016, 211, 75-89.	7.3	37
24	Systems and Evolutionary Characterization of MicroRNAs and Their Underlying Regulatory Networks in Soybean Cotyledons. <i>PLoS ONE</i> , 2014, 9, e86153.	2.5	37
25	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
26	MET-XAlign: A Metabolite Cross-Alignment Tool for LC/MS-Based Comparative Metabolomics. <i>Analytical Chemistry</i> , 2015, 87, 9114-9119.	6.5	32
27	The future of legume genetic data resources: Challenges, opportunities, and priorities. , 2019, 1, e16.		30
28	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
29	Subcellular targeting of an evolutionarily conserved plant defensin <sc>M</sc>t<sc>D</sc>ef4.2 determines the outcome of plantâ€“pathogen interaction in transgenic <sc>A</sc>rabisidopsis. <i>Molecular Plant Pathology</i> , 2012, 13, 1032-1046.	4.2	29
30	Identification of Aluminum Tolerance Quantitative Trait Loci in Tetraploid Alfalfa. <i>Crop Science</i> , 2013, 53, 148-163.	1.8	28
31	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
32	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
33	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
34	Mining Functional Elements in Messenger RNAs: Overview, Challenges, and Perspectives. <i>Frontiers in Plant Science</i> , 2011, 2, 84.	3.6	22
35	Quality evaluation of extracted ion chromatograms and chromatographic peaks in liquid chromatography/mass spectrometry-based metabolomics data. <i>BMC Bioinformatics</i> , 2014, 15, S5.	2.6	22
36	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

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37	DeGNServer: Deciphering Genome-Scale Gene Networks through High Performance Reverse Engineering Analysis. <i>BioMed Research International</i> , 2013, 2013, 1-10.	1.9	21
38	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
39	Mining Functional Modules in Heterogeneous Biological Networks Using Multiplex PageRank Approach. <i>Frontiers in Plant Science</i> , 2016, 7, 903.	3.6	18
40	GWASpro: a high-performance genome-wide association analysis server. <i>Bioinformatics</i> , 2019, 35, 2512-2514.	4.1	18
41	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
42	Inferring large-scale gene regulatory networks using a low-order constraint-based algorithm. <i>Molecular BioSystems</i> , 2010, 6, 988.	2.9	13
43	Iron-Sulfur Cluster Protein NITROGEN FIXATION S-LIKE1 and Its Interactor FRATAXIN Function in Plant Immunity. <i>Plant Physiology</i> , 2020, 184, 1532-1548.	4.8	13
44	Bioinformatics Tools for Achieving Better Gene Silencing in Plants. <i>Methods in Molecular Biology</i> , 2015, 1287, 43-60.	0.9	13
45	Functional genomics of plant transporters in legume nodules. <i>Functional Plant Biology</i> , 2006, 33, 731.	2.1	12
46	Differential mRNA Translation in <i>Medicago truncatula</i> Accessions with Contrasting Responses to Ozone-Induced Oxidative Stress. <i>Molecular Plant</i> , 2012, 5, 187-204.	8.3	12
47	GPLEXUS: enabling genome-scale gene association network reconstruction and analysis for very large-scale expression data. <i>Nucleic Acids Research</i> , 2014, 42, e32-e32.	14.5	9
48	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
49	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
50	<i>Serendipita</i> Fungi Modulate the Switchgrass Root Transcriptome to Circumvent Host Defenses and Establish a Symbiotic Relationship. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1128-1142.	2.6	6
51	2D association and integrative omics analysis in rice provides systems biology view in trait analysis. <i>Communications Biology</i> , 2018, 1, 153.	4.4	4
52	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
53	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
54	Distinguishing HapMap Accessions Through Recursive Set Partitioning in Hierarchical Decision Trees. <i>Frontiers in Plant Science</i> , 2021, 12, 628421.	3.6	0