Patrick X Zhao

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4052538/publications.pdf

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	Distinguishing HapMap Accessions Through Recursive Set Partitioning in Hierarchical Decision Trees. Frontiers in Plant Science, 2021, 12, 628421.	3.6	0
2	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
3	<i>Serendipita</i> Fungi Modulate the Switchgrass Root Transcriptome to Circumvent Host Defenses and Establish a Symbiotic Relationship. Molecular Plant-Microbe Interactions, 2021, 34, 1128-1142.	2.6	6
4	LegumeIP V3: from models to cropsâ€”an integrative gene discovery platform for translational genomics in legumes. Nucleic Acids Research, 2021, 49, D1472-D1479.	14.5	25
5	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
6	<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
7	Ironâ€“Sulfur Cluster Protein NITROGEN FIXATION S-LIKE1 and Its Interactor FRATAXIN Function in Plant Immunity. Plant Physiology, 2020, 184, 1532-1548.	4.8	13
8	MtSSPdb: The <i>Medicago truncatula</i> Small Secreted Peptide Database. Plant Physiology, 2020, 183, 399-413.	4.8	40
9	Insertional mutagenesis of <i>Brachypodium distachyon</i> using the <i>Tnt1</i> retrotransposable element. Plant Journal, 2020, 103, 1924-1936.	5.7	6
10	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
11	Identification and Functional Investigation of Genomeâ€Encoded, Small, Secreted Peptides in Plants. Current Protocols in Plant Biology, 2019, 4, e20098.	2.8	15
12	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
13	The future of legume genetic data resources: Challenges, opportunities, and priorities. , 2019, 1, e16.		30
14	GWASpro: a high-performance genome-wide association analysis server. Bioinformatics, 2019, 35, 2512-2514.	4.1	18
15	psRNATarget: a plant small RNA target analysis server (2017 release). Nucleic Acids Research, 2018, 46, W49-W54.	14.5	942
16	2D association and integrative omics analysis in rice provides systems biology view in trait analysis. Communications Biology, 2018, 1, 153.	4.4	4
17	Genome-Wide Identification of <i>Medicago</i> Peptides Involved in Macronutrient Responses and Nodulation. Plant Physiology, 2017, 175, 1669-1689.	4.8	101
18	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

#	Article	IF	Citations
19	Mining Functional Modules in Heterogeneous Biological Networks Using Multiplex PageRank Approach. Frontiers in Plant Science, 2016, 7, 903.	3.6	18
20	Nitrogen remobilization and conservation, and underlying senescenceâ€associated gene expression in the perennial switchgrass <i>Panicum virgatum</i>. New Phytologist, 2016, 211, 75-89.	7.3	37
21	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
22	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
23	LegumeIP 2.0â€”a platform for the study of gene function and genome evolution in legumes. Nucleic Acids Research, 2016, 44, D1189-D1194.	14.5	23
24	MET-XAlign: A Metabolite Cross-Alignment Tool for LC/MS-Based Comparative Metabolomics. Analytical Chemistry, 2015, 87, 9114-9119.	6.5	32
25	Bioinformatics Tools for Achieving Better Gene Silencing in Plants. Methods in Molecular Biology, 2015, 1287, 43-60.	0.9	13
26	Prediction of Membrane Transport Proteins and Their Substrate Specificities Using Primary Sequence Information. PLoS ONE, 2014, 9, e100278.	2.5	103
27	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
28	GPLEXUS: enabling genome-scale gene association network reconstruction and analysis for very large-scale expression data. Nucleic Acids Research, 2014, 42, e32-e32.	14.5	9
29	MET-COFEA: A Liquid Chromatography/Mass Spectrometry Data Processing Platform for Metabolite Compound Feature Extraction and Annotation. Analytical Chemistry, 2014, 86, 6245-6253.	6.5	54
30	Quality evaluation of extracted ion chromatograms and chromatographic peaks in liquid chromatography/mass spectrometry-based metabolomics data. BMC Bioinformatics, 2014, 15, S5.	2.6	22
31	Systems and Evolutionary Characterization of MicroRNAs and Their Underlying Regulatory Networks in Soybean Cotyledons. PLoS ONE, 2014, 9, e86153.	2.5	37
32	DeGNServer: Deciphering Genome-Scale Gene Networks through High Performance Reverse Engineering Analysis. BioMed Research International, 2013, 2013, 1-10.	1.9	21
33	Identification of Aluminum Tolerance Quantitative Trait Loci in Tetraploid Alfalfa. Crop Science, 2013, 53, 148-163.	1.8	28
34	Global Transcriptome Sequencing Using the Illumina Platform and the Development of EST-SSR Markers in Autotetraploid Alfalfa. PLoS ONE, 2013, 8, e83549.	2.5	70
35	LegumeIP: an integrative database for comparative genomics and transcriptomics of model legumes. Nucleic Acids Research, 2012, 40, D1221-D1229.	14.5	91
36	Differential mRNA Translation in Medicago truncatula Accessions with Contrasting Responses to Ozone-Induced Oxidative Stress. Molecular Plant, 2012, 5, 187-204.	8.3	12

#	ARTICLE	IF	CITATIONS
37	Subcellular targeting of an evolutionarily conserved plant defensin <scp>M</scp>t<scp>D</scp>ef4.2 determines the outcome of plantâ€"pathogen interaction in transgenic <scp>A</scp>rabidopsis. Molecular Plant Pathology, 2012, 13, 1032-1046.	4.2	29
38	The Medicago genome provides insight into the evolution of rhizobial symbioses. Nature, 2011, 480, 520-524.	27.8	1,166
39	Computational analysis of miRNA targets in plants: current status and challenges. Briefings in Bioinformatics, 2011, 12, 115-121.	6.5	116
40	Mining Functional Elements in Messenger RNAs: Overview, Challenges, and Perspectives. Frontiers in Plant Science, 2011, 2, 84.	3.6	22
41	Genome-wide SNP discovery in tetraploid alfalfa using 454 sequencing and high resolution melting analysis. BMC Genomics, 2011, 12, 1-11.	2.8	353
42	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
43	psRNATarget: a plant small RNA target analysis server. Nucleic Acids Research, 2011, 39, W155-W159.	14.5	1,662
44	Genomeâ€wide analysis of phenylpropanoid defence pathways. Molecular Plant Pathology, 2010, 11, 829-846.	4.2	332
45	Genomic Inventory and Transcriptional Analysis of <i>Medicago truncatula</i> Transporters. Plant Physiology, 2010, 152, 1716-1730.	4.8	73
46	Combining Machine Learning and Homology-Based Approaches to Accurately Predict Subcellular Localization in Arabidopsis. Plant Physiology, 2010, 154, 36-54.	4.8	78
47	Inferring large-scale gene regulatory networks using a low-order constraint-based algorithm. Molecular BioSystems, 2010, 6, 988.	2.9	13
48	TrichOME: A Comparative Omics Database for Plant Trichomes Â Â Â. Plant Physiology, 2009, 152, 44-54.	4.8	98
49	Transcript and proteomic analysis of developing white lupin (Lupinus albus L.) roots. BMC Plant Biology, 2009, 9, 1.	3.6	182
50	A gene expression atlas of the model legume <i>Medicago truncatula</i>. Plant Journal, 2008, 55, 504-513.	5.7	668
51	Largeâ€scale insertional mutagenesis using the <i>Tnt1</i> retrotransposon in the model legume <i>Medicago truncatula</i>. Plant Journal, 2008, 54, 335-347.	5.7	442
52	Terpene Biosynthesis in Glandular Trichomes of Hop Â Â. Plant Physiology, 2008, 148, 1254-1266.	4.8	180
53	Regulation of a Virus-Induced Lethal Disease in Tomato Revealed by LongSAGE Analysis. Molecular Plant-Microbe Interactions, 2007, 20, 1477-1488.	2.6	21
54	Functional genomics of plant transporters in legume nodules. Functional Plant Biology, 2006, 33, 731.	2.1	12