

Xiaohui Yuan

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

3,260
citations

236833

25
h-index

265120

42
g-index

45
all docs

45
docs citations

45
times ranked

2650
citing authors

#	ARTICLE	IF	CITATIONS
1	rMVP: A Memory-efficient, Visualization-enhanced, and Parallel-accelerated Tool for Genome-wide Association Study. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 619-628.	3.0	396
2	Genome-wide association studies dissect the genetic networks underlying agronomical traits in soybean. <i>Genome Biology</i> , 2017, 18, 161.	3.8	363
3	Natural variation at the soybean J locus improves adaptation to the tropics and enhances yield. <i>Nature Genetics</i> , 2017, 49, 773-779.	9.4	341
4	Overview of Mollisols in the world: Distribution, land use and management. <i>Canadian Journal of Soil Science</i> , 2012, 92, 383-402.	0.5	239
5	Stepwise selection on homeologous PRR genes controlling flowering and maturity during soybean domestication. <i>Nature Genetics</i> , 2020, 52, 428-436.	9.4	229
6	A New Dominant Gene <i>E9</i> Conditions Early Flowering and Maturity in Soybean. <i>Crop Science</i> , 2014, 54, 2529-2535.	0.8	173
7	Factors Affecting the Accuracy of Genomic Selection for Agricultural Economic Traits in Maize, Cattle, and Pig Populations. <i>Frontiers in Genetics</i> , 2019, 10, 189.	1.1	127
8	GmFT2a and GmFT5a Redundantly and Differentially Regulate Flowering through Interaction with and Upregulation of the bZIP Transcription Factor GmFDL19 in Soybean. <i>PLoS ONE</i> , 2014, 9, e97669.	1.1	117
9	GmFT4, a Homolog of FLOWERING LOCUS T, Is Positively Regulated by E1 and Functions as a Flowering Repressor in Soybean. <i>PLoS ONE</i> , 2014, 9, e89030.	1.1	115
10	Allelic Combinations of Soybean Maturity Loci E1, E2, E3 and E4 Result in Diversity of Maturity and Adaptation to Different Latitudes. <i>PLoS ONE</i> , 2014, 9, e106042.	1.1	103
11	Combining structured and unstructured data for predictive models: a deep learning approach. <i>BMC Medical Informatics and Decision Making</i> , 2020, 20, 280.	1.5	99
12	Genetic Variation in Soybean at the Maturity Locus E4 Is Involved in Adaptation to Long Days at High Latitudes. <i>Agronomy</i> , 2013, 3, 117-134.	1.3	86
13	<i>GmCOL1a</i> and <i>GmCOL1b</i> Function as Flowering Repressors in Soybean Under Long-Day Conditions. <i>Plant and Cell Physiology</i> , 2015, 56, 2409-2422.	1.5	73
14	Genetic basis and adaptation trajectory of soybean from its temperate origin to tropics. <i>Nature Communications</i> , 2021, 12, 5445.	5.8	64
15	Molecular identification of genes controlling flowering time, maturity, and photoperiod response in soybean. <i>Plant Systematics and Evolution</i> , 2012, 298, 1217-1227.	0.3	61
16	Interpretable deep learning for automatic diagnosis of 12-lead electrocardiogram. <i>IScience</i> , 2021, 24, 102373.	1.9	61
17	Quantitative Trait Locus Mapping of Flowering Time and Maturity in Soybean Using Next-Generation Sequencing-Based Analysis. <i>Frontiers in Plant Science</i> , 2018, 9, 995.	1.7	57
18	A Variational Bayesian Framework for Cluster Analysis in a Complex Network. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2020, 32, 2115-2128.	4.0	54

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19	KAML: improving genomic prediction accuracy of complex traits using machine learning determined parameters. <i>Genome Biology</i> , 2020, 21, 146.	3.8	51
20	GmmiR156b overexpression delays flowering time in soybean. <i>Plant Molecular Biology</i> , 2015, 89, 353-363.	2.0	49
21	Chromosome-scale genome assembly of sweet cherry (<i>Prunus avium</i> L.) cv. Tieton obtained using long-read and Hi-C sequencing. <i>Horticulture Research</i> , 2020, 7, 122.	2.9	44
22	A gene prioritization method based on a swine multi-omics knowledgebase and a deep learning model. <i>Communications Biology</i> , 2020, 3, 502.	2.0	36
23	A gene-phenotype relationship extraction pipeline from the biomedical literature using a representation learning approach. <i>Bioinformatics</i> , 2018, 34, i386-i394.	1.8	35
24	GmLPA1, Encoding an anaphase-promoting complex-like Protein, affects Leaf Petiole Angle. <i>Plant Physiology</i> , 2017, 174, pp.00074.2017.	2.3	33
25	Quantitative Trait Locus Mapping of Soybean Maturity Gene <i>qE6</i> . <i>Crop Science</i> , 2017, 57, 2547-2554.	0.8	29
26	QTL mapping for flowering time in different latitude in soybean. <i>Euphytica</i> , 2015, 206, 725-736.	0.6	27
27	Sequence composition of BAC clones and SSR markers mapped to Upland cotton chromosomes 11 and 21 targeting resistance to soil-borne pathogens. <i>Frontiers in Plant Science</i> , 2015, 6, 791.	1.7	22
28	<i>Pleurotus eryngii</i> Genomes Reveal Evolution and Adaptation to the Gobi Desert Environment. <i>Frontiers in Microbiology</i> , 2019, 10, 2024.	1.5	19
29	High-Throughput Phenotyping of Morphological Seed and Fruit Characteristics Using X-Ray Computed Tomography. <i>Frontiers in Plant Science</i> , 2020, 11, 601475.	1.7	19
30	A Global Analysis of the Polygalacturonase Gene Family in Soybean (<i>Glycine max</i>). <i>PLoS ONE</i> , 2016, 11, e0163012.	1.1	17
31	3D Morphological Processing for Wheat Spike Phenotypes Using Computed Tomography Images. <i>Remote Sensing</i> , 2019, 11, 1110.	1.8	16
32	Rapid identification of consistent novel QTLs underlying long-juvenile trait in soybean by multiple genetic populations and genotyping-by-sequencing. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	16
33	Genomic Analyses Reveal Evidence of Independent Evolution, Demographic History, and Extreme Environment Adaptation of Tibetan Plateau <i>Agaricus bisporus</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1786.	1.5	14
34	Efficiently predicting large-scale protein-protein interactions using MapReduce. <i>Computational Biology and Chemistry</i> , 2017, 69, 202-206.	1.1	13
35	Multiscale Contour Steered Region Integral and Its Application for Cultivar Classification. <i>IEEE Access</i> , 2019, 7, 69087-69100.	2.6	12
36	QTLMiner: QTL database curation by mining tables in literature. <i>Bioinformatics</i> , 2015, 31, 1689-1691.	1.8	8

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37	InDel marker detection by integration of multiple softwares using machine learning techniques. BMC Bioinformatics, 2016, 17, 548.	1.2	8
38	Multiscale Crossing Representation Using Combined Feature of Contour and Venation for Leaf Image Identification. , 2016, , .		8
39	MFCIS: an automatic leaf-based identification pipeline for plant cultivars using deep learning and persistent homology. Horticulture Research, 2021, 8, 172.	2.9	7
40	A Robust and Rapid Candidate Gene Mapping Pipeline Based on M2 Populations. Frontiers in Plant Science, 2021, 12, 681816.	1.7	6
41	Local R-Symmetry Co-Occurrence: Characterising Leaf Image Patterns for Identifying Cultivars. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, PP, 1-1.	1.9	5
42	PopGeV: a web-based large-scale population genome browser: Fig. 1.. Bioinformatics, 2015, 31, 3048-3050.	1.8	3
43	Bar charts detection and analysis in biomedical literature of PubMed Central. AMIA ... Annual Symposium proceedings, 2017, 2017, 859-865.	0.2	3
44	Cascade word embedding to sentence embedding: A class label enhanced approach to phenotype extraction. , 2017, , .		2
45	Identifying overlapping protein complexes in yeast protein interaction network via fuzzy clustering. , 2017, , .		0