

Longjiang Fan

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9501340/publications.pdf>

Version: 2024-02-01

103
papers

4,780
citations

87888

38
h-index

110387

64
g-index

107
all docs

107
docs citations

107
times ranked

5742
citing authors

#	ARTICLE	IF	CITATIONS
1	Widespread noncoding circular <i>scRNA</i> s in plants. <i>New Phytologist</i> , 2015, 208, 88-95.	7.3	374
2	A diverse set of microRNAs and microRNA-like small RNAs in developing rice grains. <i>Genome Research</i> , 2008, 18, 1456-1465.	5.5	332
3	Construction of the third-generation <i>Zea mays</i> haplotype map. <i>GigaScience</i> , 2018, 7, 1-12.	6.4	191
4	miR482 Regulation of NBS-LRR Defense Genes during Fungal Pathogen Infection in Cotton. <i>PLoS ONE</i> , 2013, 8, e84390.	2.5	163
5	<i>Echinochloa crus-galli</i> genome analysis provides insight into its adaptation and invasiveness as a weed. <i>Nature Communications</i> , 2017, 8, 1031.	12.8	138
6	Genomic variation associated with local adaptation of weedy rice during de-domestication. <i>Nature Communications</i> , 2017, 8, 15323.	12.8	132
7	PlantcircBase: A Database for Plant Circular RNAs. <i>Molecular Plant</i> , 2017, 10, 1126-1128.	8.3	131
8	Twenty years of plant genome sequencing: achievements and challenges. <i>Trends in Plant Science</i> , 2022, 27, 391-401.	8.8	125
9	Characterization of the defense transcriptome responsive to <i>Fusarium oxysporum</i> -infection in <i>Arabidopsis</i> using RNA-seq. <i>Gene</i> , 2013, 512, 259-266.	2.2	120
10	Full-length sequence assembly reveals circular RNAs with diverse non-GT/AG splicing signals in rice. <i>RNA Biology</i> , 2017, 14, 1055-1063.	3.1	113
11	Aldo-keto Reductase Metabolizes Glyphosate and Confers Glyphosate Resistance in <i>Echinochloa colona</i> . <i>Plant Physiology</i> , 2019, 181, 1519-1534.	4.8	97
12	Regulation of Nicotine Biosynthesis by an Endogenous Target Mimicry of MicroRNA in Tobacco. <i>Plant Physiology</i> , 2015, 169, 1062-1071.	4.8	96
13	Analysis of transcriptional and epigenetic changes in hybrid vigor of allopolyploid <i>Brassica napus</i> uncovers key roles for small <i>scRNA</i> s. <i>Plant Journal</i> , 2017, 91, 874-893.	5.7	95
14	A Tourist-like MITE insertion in the upstream region of the <i>BnFLC.A10</i> gene is associated with vernalization requirement in rapeseed (<i>Brassica napus</i> L.). <i>BMC Plant Biology</i> , 2012, 12, 238.	3.6	94
15	An ABC-type transporter endowing glyphosate resistance in plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	85
16	Characterization of Small Interfering RNAs Derived from the Geminivirus/Betasatellite Complex Using Deep Sequencing. <i>PLoS ONE</i> , 2011, 6, e16928.	2.5	81
17	Identification and characterization of micro <i>scRNA</i> s in oilseed rape (<i>Brassica napus</i>) responsive to infection with the pathogenic fungus <i>Verticillium longisporum</i> using <i>Brassica</i> <i>scAA</i> (<i>Brassica Arapa</i>) and <i>scCC</i> (<i>Brassica Aoleracea</i>) as reference genomes. <i>New Phytologist</i> , 2014, 204, 577-594.	7.3	79
18	The power and potential of genomics in weed biology and management. <i>Pest Management Science</i> , 2018, 74, 2216-2225.	3.4	76

#	ARTICLE	IF	CITATIONS
19	Genomic evidence for convergent evolution of gene clusters for momilactone biosynthesis in land plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12472-12480.	7.1	73
20	Identification of wounding and topping responsive small RNAs in tobacco (<i>Nicotiana tabacum</i>). <i>BMC Plant Biology</i> , 2012, 12, 28.	3.6	68
21	A host plant genome (<i>Zizania latifolia</i>) after a century-long endophyte infection. <i>Plant Journal</i> , 2015, 83, 600-609.	5.7	67
22	PcircRNA_finder: a software for circRNA prediction in plants. <i>Bioinformatics</i> , 2016, 32, 3528-3529.	4.1	60
23	Comparative whole-genome analysis reveals artificial selection effects on <i>Ustilago esculenta</i> genome. <i>DNA Research</i> , 2017, 24, 635-648.	3.4	58
24	Genome Sequence of the Tobacco Bacterial Wilt Pathogen <i>Ralstonia solanacearum</i> . <i>Journal of Bacteriology</i> , 2011, 193, 6088-6089.	2.2	57
25	The Circular RNA Profiles of Colorectal Tumor Metastatic Cells. <i>Frontiers in Genetics</i> , 2018, 9, 34.	2.3	55
26	Diverse genetic mechanisms underlie worldwide convergent rice feralization. <i>Genome Biology</i> , 2020, 21, 70.	8.8	55
27	Genome-wide selection footprints and deleterious variations in young Asian allotetraploid rapeseed. <i>Plant Biotechnology Journal</i> , 2019, 17, 1998-2010.	8.3	54
28	Genome-wide identification of non-coding RNAs interacted with microRNAs in soybean. <i>Frontiers in Plant Science</i> , 2014, 5, 743.	3.6	53
29	Molecular evidence for post-domestication selection in the Waxy gene of Chinese waxy maize. <i>Molecular Breeding</i> , 2008, 22, 329-338.	2.1	49
30	The Absence of TIR-Type Resistance Gene Analogues in the Sugar Beet (<i>Beta vulgaris</i> L.) Genome. <i>Journal of Molecular Evolution</i> , 2004, 58, 40-53.	1.8	48
31	Bi-directional Selection in Upland Rice Leads to Its Adaptive Differentiation from Lowland Rice in Drought Resistance and Productivity. <i>Molecular Plant</i> , 2019, 12, 170-184.	8.3	48
32	Orphan Crops and their Wild Relatives in the Genomic Era. <i>Molecular Plant</i> , 2021, 14, 27-39.	8.3	48
33	PlantscRNAdb: A database for plant single-cell RNA analysis. <i>Molecular Plant</i> , 2021, 14, 855-857.	8.3	48
34	Echinochloa Chloroplast Genomes: Insights into the Evolution and Taxonomic Identification of Two Weedy Species. <i>PLoS ONE</i> , 2014, 9, e113657.	2.5	47
35	Genome re-sequencing suggested a weedy rice origin from domesticated indica-japonica hybridization: a case study from southern China. <i>Planta</i> , 2014, 240, 1353-1363.	3.2	47
36	The Genomes of the Allohexaploid <i>Echinochloa crus-galli</i> and Its Progenitors Provide Insights into Polyploidization-Driven Adaptation. <i>Molecular Plant</i> , 2020, 13, 1298-1310.	8.3	47

#	ARTICLE	IF	CITATIONS
37	Selection and mutation on microRNA target sequences during rice evolution. <i>BMC Genomics</i> , 2008, 9, 454.	2.8	45
38	Identification, evolution, and expression partitioning of miRNAs in allopolyploid <i>Brassica napus</i> . <i>Journal of Experimental Botany</i> , 2015, 66, 7241-7253.	4.8	44
39	Genomic Clues for Crop-Weed Interactions and Evolution. <i>Trends in Plant Science</i> , 2018, 23, 1102-1115.	8.8	44
40	Assessment of codivergence of Mastreviruses with their plant hosts. <i>BMC Evolutionary Biology</i> , 2008, 8, 335.	3.2	43
41	Evidence of selectively driven codon usage in rice: Implications for GC content evolution of Gramineae genes. <i>FEBS Letters</i> , 2007, 581, 1015-1021.	2.8	42
42	Genome size and sequence composition of moso bamboo: A comparative study. <i>Science in China Series C: Life Sciences</i> , 2007, 50, 700-705.	1.3	42
43	De-Domestication: An Extension of Crop Evolution. <i>Trends in Plant Science</i> , 2021, 26, 560-574.	8.8	40
44	Identification of phasiRNAs in wild rice (<i>Oryza rufipogon</i>). <i>Plant Signaling and Behavior</i> , 2013, 8, e25079.	2.4	38
45	Genome-wide identification of oil biosynthesis-related long non-coding RNAs in allopolyploid <i>Brassica napus</i> . <i>BMC Genomics</i> , 2018, 19, 745.	2.8	38
46	Genomic evidence of human selection on Vavilovian mimicry. <i>Nature Ecology and Evolution</i> , 2019, 3, 1474-1482.	7.8	38
47	Molecular evolution and selection of a gene encoding two tandem microRNAs in rice. <i>FEBS Letters</i> , 2007, 581, 4789-4793.	2.8	37
48	Analysis of genetic variation and diversity of Rice stripe virus populations through high-throughput sequencing. <i>Frontiers in Plant Science</i> , 2015, 6, 176.	3.6	37
49	Characteristics of plant circular RNAs. <i>Briefings in Bioinformatics</i> , 2018, , .	6.5	37
50	Genomic dissection of small sRNA in wild rice (<i>Oryza rufipogon</i>): lessons for rice domestication. <i>New Phytologist</i> , 2012, 196, 914-925.	7.3	33
51	Sequence variation and selection of small RNAs in domesticated rice. <i>BMC Evolutionary Biology</i> , 2010, 10, 119.	3.2	32
52	Post-Domestication Selection in the Maize Starch Pathway. <i>PLoS ONE</i> , 2009, 4, e7612.	2.5	32
53	Chloroplast DNA insertions into the nuclear genome of rice: the genes, sites and ages of insertion involved. <i>Functional and Integrative Genomics</i> , 2008, 8, 101-108.	3.5	29
54	Genome Re-Sequencing of Semi-Wild Soybean Reveals a Complex Soja Population Structure and Deep Introgression. <i>PLoS ONE</i> , 2014, 9, e108479.	2.5	26

#	ARTICLE	IF	CITATIONS
55	Genomic insights into the evolution of <i>Echinochloa</i> species as weed and orphan crop. <i>Nature Communications</i> , 2022, 13, 689.	12.8	26
56	A complete physical map of a wild beet (<i>Beta procumbens</i>) translocation in sugar beet. <i>Molecular Genetics and Genomics</i> , 2006, 275, 504-511.	2.1	25
57	Nicotine biosynthesis is regulated by two more layers: Small and long non-protein-coding RNAs. <i>Plant Signaling and Behavior</i> , 2016, 11, e1184811.	2.4	25
58	Genome Sequence of <i>Bacillus subtilis</i> subsp. <i>spizizenii</i> gtP20b, Isolated from the Indian Ocean. <i>Journal of Bacteriology</i> , 2011, 193, 1276-1277.	2.2	23
59	Genetic and genotype × environment interaction effects from embryo, endosperm, cytoplasm and maternal plant for rice grain shape traits of indica rice. <i>Field Crops Research</i> , 2000, 68, 191-198.	5.1	22
60	A transcriptomic profile of topping responsive non-coding RNAs in tobacco roots (<i>Nicotiana glauca</i>). <i>Plant Physiology</i> , 2010, 154, 1054-1062.	2.8	22
61	Patterns of selective constraints in noncoding DNA of rice. <i>BMC Evolutionary Biology</i> , 2007, 7, 208.	3.2	20
62	Development of DArT markers for a linkage map of flue-cured tobacco. <i>Science Bulletin</i> , 2013, 58, 641-648.	1.7	20
63	A diverse set of miRNAs responsive to begomovirus-associated betasatellite in <i>Nicotiana benthamiana</i> . <i>BMC Plant Biology</i> , 2014, 14, 60.	3.6	19
64	Population genomic analysis reveals domestication of cultivated rye from weedy rye. <i>Molecular Plant</i> , 2022, 15, 552-561.	8.3	19
65	Molecular phylogeny of miR390-guided trans-acting siRNA genes (TAS3) in the grass family. <i>Plant Systematics and Evolution</i> , 2009, 283, 125-132.	0.9	18
66	Effect of the pollen of transgenic rice line, TT9-3 with a fused cry1Ab/cry1Ac gene from <i>Bacillus thuringiensis</i> Berliner on non-target domestic silkworm, <i>Bombyx mori</i> Linnaeus (Lepidoptera: Bombycidae). <i>Journal of Economic Entomology</i> , 2011, 104, 297-302.	1.7	17
67	Accumulation of high OPDA level correlates with reduced ROS and elevated GSH benefiting white cell survival in variegated leaves. <i>Scientific Reports</i> , 2017, 7, 44158.	3.3	17
68	Gibberellin deficiency is responsible for shy-flowering nature of <i>Epipremnum aureum</i> . <i>Scientific Reports</i> , 2016, 6, 28598.	3.3	16
69	A naive Bayes algorithm for tissue origin diagnosis (TOD-Bayes) of synchronous multifocal tumors in the hepatobiliary and pancreatic system. <i>International Journal of Cancer</i> , 2018, 142, 357-368.	5.1	16
70	Quinclorac resistance in <i>Echinochloa phyllopogon</i> is associated with reduced ethylene synthesis rather than enhanced cyanide detoxification by Î²-cyanoalanine synthase. <i>Pest Management Science</i> , 2020, 76, 1195-1204.	3.4	16
71	Horizontal transfer and evolution of the biosynthetic gene cluster for benzoxazinoids in plants. <i>Plant Communications</i> , 2022, 3, 100320.	7.7	16
72	Draft Genome Sequence of the Marine <i>Streptomyces</i> sp. Strain PP-C42, Isolated from the Baltic Sea. <i>Journal of Bacteriology</i> , 2011, 193, 3691-3692.	2.2	15

#	ARTICLE	IF	CITATIONS
73	Expansion of <i>MIR482/2118</i> by a class II transposable element in cotton. <i>Plant Journal</i> , 2020, 103, 2084-2099.	5.7	15
74	A Suppressor Mutation Partially Reverts the xantha Trait via Lowered Methylation in the Promoter of Genomes Uncoupled 4 in Rice. <i>Frontiers in Plant Science</i> , 2019, 10, 1003.	3.6	14
75	Recent origination of circular RNAs in plants. <i>New Phytologist</i> , 2022, 233, 515-525.	7.3	14
76	Identification of NBS-Type Resistance Gene Homologs in Tobacco Genome. <i>Plant Molecular Biology Reporter</i> , 2010, 28, 152-161.	1.8	13
77	RiceRelativesGD: a genomic database of rice relatives for rice research. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	13
78	Alteration of the Alkaloid Profile in Genetically Modified Tobacco Reveals a Role of Methylene tetrahydrofolate Reductase in Nicotine N-Demethylation. <i>Plant Physiology</i> , 2013, 161, 1049-1060.	4.8	12
79	Elimination of a Retrotransposon for Quenching Genome Instability in Modern Rice. <i>Molecular Plant</i> , 2019, 12, 1395-1407.	8.3	12
80	TOD-CUP: a gene expression rank-based majority vote algorithm for tissue origin diagnosis of cancers of unknown primary. <i>Briefings in Bioinformatics</i> , 2021, 22, 2106-2118.	6.5	12
81	Characterization and evolution of gene clusters for terpenoid phytoalexin biosynthesis in tobacco. <i>Planta</i> , 2019, 250, 1687-1702.	3.2	11
82	iSNAP: a small RNA-based molecular marker technique. <i>Plant Breeding</i> , 2011, 130, 515-520.	1.9	9
83	Impact of Maternal Nicotine Exposure on Expression of Myelin-Related Genes in Zebrafish Larvae. <i>Zebrafish</i> , 2014, 11, 10-16.	1.1	9
84	Identifying the clonal origin of synchronous multifocal tumors in the hepatobiliary and pancreatic system using multi-omic platforms. <i>Oncotarget</i> , 2017, 8, 5016-5025.	1.8	9
85	Gene Modules Co-regulated with Biosynthetic Gene Clusters for Allelopathy between Rice and Barnyardgrass. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3846.	4.1	9
86	Age, Gender and Geographic Differences in Global Health Burden of Cirrhosis and Liver Cancer due to Nonalcoholic Steatohepatitis. <i>Journal of Cancer</i> , 2021, 12, 2855-2865.	2.5	9
87	Rice bioinformatics in the genomic era: Status and perspectives. <i>Crop Journal</i> , 2021, 9, 609-621.	5.2	9
88	miR-377-3p-Mediated EGR1 Downregulation Promotes B[a]P-Induced Lung Tumorigenesis by Wnt/Beta-Catenin Transduction. <i>Frontiers in Oncology</i> , 2021, 11, 699004.	2.8	8
89	Weedy rice, a hidden gold mine in the paddy field. <i>Molecular Plant</i> , 2022, 15, 566-568.	8.3	8
90	PlantcircBase 7.0: Full-length transcripts and conservation of plant circRNAs. <i>Plant Communications</i> , 2022, 3, 100343.	7.7	8

#	ARTICLE	IF	CITATIONS
91	Lateral transfers lead to the birth of momilactone biosynthetic gene clusters in grass. <i>Plant Journal</i> , 2022, 111, 1354-1367.	5.7	8
92	Ancient DNA sequences of rice from the low Yangtze reveal significant genotypic divergence. <i>Science Bulletin</i> , 2011, 56, 3108.	1.7	6
93	Mapping epistasis and environment–QTX interaction based on four -omics genotypes for the detected QTX loci controlling complex traits in tobacco. <i>Crop Journal</i> , 2013, 1, 151-159.	5.2	6
94	Identification and Characterization of γ -Ray-Induced Mutations in Rice Cytoplasmic Genomes by Whole-Genome Sequencing. <i>Cytogenetic and Genome Research</i> , 2020, 160, 100-109.	1.1	6
95	Large-scale identification of extracellular plant miRNAs in mammals implicates their dietary intake. <i>PLoS ONE</i> , 2021, 16, e0257878.	2.5	6
96	Signaling pathway perturbation analysis for assessment of biological impact of cigarette smoke on lung cells. <i>Scientific Reports</i> , 2021, 11, 16715.	3.3	5
97	Multi-omics molecular biomarkers and database of osteoarthritis. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	3.0	5
98	Effects of Sample Size on Plant Single-Cell RNA Profiling. <i>Current Issues in Molecular Biology</i> , 2021, 43, 1685-1697.	2.4	4
99	scDetect: a rank-based ensemble learning algorithm for cell type identification of single-cell RNA sequencing in cancer. <i>Bioinformatics</i> , 2021, 37, 4115-4122.	4.1	3
100	The complete chloroplast genome of <i>Echinochloa haploclada</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3105-3106.	0.4	2
101	The complete chloroplast genome of weedy rice <i>Oryza sativa</i> f. <i>spontanea</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3016-3017.	0.4	1
102	The complete chloroplast genome of <i>Nicotiana plumbaginifolia</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 239-240.	0.4	0
103	The whole chloroplast genome of <i>Secale strictum</i> subsp. <i>kuprijanovii</i> , a wild and perennial kinship to cultivated rye. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 112-114.	0.4	0