

Xiaojun Nie

List of Publications by Year in descending order

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64
papers

5,638
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201674

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61
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72
times ranked

5867
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-Wide Identification and Characterization of RNA/DNA Differences Associated with Drought Response in Wheat. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1405.	4.1	4
2	The Landscape of Autophagy-Related (ATG) Genes and Functional Characterization of TaVAMP727 to Autophagy in Wheat. <i>International Journal of Molecular Sciences</i> , 2022, 23, 891.	4.1	2
3	Integrate Small RNA and Degradome Sequencing to Reveal Drought Memory Response in Wheat (<i>Triticum aestivum</i> L.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 5917.	4.1	11
4	A large-scale genomic association analysis identifies the candidate causal genes conferring stripe rust resistance under multiple field environments. <i>Plant Biotechnology Journal</i> , 2021, 19, 177-191.	8.3	54
5	Genome-wide identification of PYL gene family in wheat: Evolution, expression and 3D structure analysis. <i>Genomics</i> , 2021, 113, 854-866.	2.9	37
6	Genome-wide identification and expression analysis of U-box gene family in wild emmer wheat (<i>Triticum turgidum</i> L. ssp. <i>dicoccoides</i>). <i>Gene</i> , 2021, 799, 145840.	2.2	6
7	Genome-Wide Investigation of Spliceosomal SM/LSM Genes in Wheat (<i>Triticum aestivum</i> L.) and Its Progenitors. <i>Agronomy</i> , 2021, 11, 1429.	3.0	0
8	Genome-wide identification and characterization of caffeoyl-coenzyme A O-methyltransferase genes related to the Fusarium head blight response in wheat. <i>BMC Genomics</i> , 2021, 22, 504.	2.8	12
9	Genome-Wide Identification, Evolution, and Expression Analysis of LBD Transcription Factor Family in Bread Wheat (<i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 721253.	3.6	13
10	Genome-Wide Identification of Wheat ZIP Gene Family and Functional Characterization of the TaZIP13-B in Plants. <i>Frontiers in Plant Science</i> , 2021, 12, 748146.	3.6	6
11	The improved assembly of 7DL chromosome provides insight into the structure and evolution of bread wheat. <i>Plant Biotechnology Journal</i> , 2020, 18, 732-742.	8.3	6
12	Genomic and Phenotypic Divergence in Wild Barley Driven by Microgeographic Adaptation. <i>Advanced Science</i> , 2020, 7, 2000709.	11.2	8
13	Co-Regulation of Long Non-Coding RNAs with Allele-Specific Genes in Wheat Responding to Powdery Mildew Infection. <i>Agronomy</i> , 2020, 10, 896.	3.0	5
14	GENOME-WIDE IDENTIFICATION AND ANALYSIS OF THE CSLF GENE FAMILY IN BARLEY (<i>HORDEUM VULGARE</i>) Tj ETQg 0 0 0 rgBT /Overlo	0.8	1
15	Genome-wide Identification, Evolution and Expression Analysis of Basic Helix-loop-helix (bHLH) Gene Family in Barley (<i>Hordeum vulgare</i> L.). <i>Current Genomics</i> , 2020, 21, 624-644.	1.6	14
16	Characteristics and Expression Pattern of MYC Genes in <i>Triticum aestivum</i> , <i>Oryza sativa</i> , and <i>Brachypodium distachyon</i> . <i>Plants</i> , 2019, 8, 274.	3.5	25
17	Frequent intra- and inter-species introgression shapes the landscape of genetic variation in bread wheat. <i>Genome Biology</i> , 2019, 20, 136.	8.8	148
18	Genome-wide identification, expression profiles and regulatory network of MAPK cascade gene family in barley. <i>BMC Genomics</i> , 2019, 20, 750.	2.8	45

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19	Genome-wide microsatellite characterisation and marker development in <i>Chenopodium quinoa</i> . <i>Annals of Applied Biology</i> , 2019, 175, 415-423.	2.5	7
20	N ⁶ -methyladenosine regulatory machinery in plants: composition, function and evolution. <i>Plant Biotechnology Journal</i> , 2019, 17, 1194-1208.	8.3	140
21	Hybrid sequencing reveals insight into heat sensing and signaling of bread wheat. <i>Plant Journal</i> , 2019, 98, 1015-1032.	5.7	73
22	Transcriptional Dynamics of Grain Development in Barley (<i>Hordeum vulgare</i> L.). <i>International Journal of Molecular Sciences</i> , 2019, 20, 962.	4.1	29
23	Evolution and Identification of the WRKY Gene Family in Quinoa (<i>Chenopodium quinoa</i>). <i>Genes</i> , 2019, 10, 131.	2.4	22
24	Melatonin: A Small Molecule but Important for Salt Stress Tolerance in Plants. <i>International Journal of Molecular Sciences</i> , 2019, 20, 709.	4.1	140
25	The TIFY Gene Family in Wheat and its Progenitors: Genome-wide Identification, Evolution and Expression Analysis. <i>Current Genomics</i> , 2019, 20, 371-388.	1.6	7
26	Identification and characterisation of RNA editing sites in chloroplast transcripts of einkorn wheat (<i>Triticum monococcum</i>). <i>Annals of Applied Biology</i> , 2018, 172, 197-207.	2.5	16
27	Comprehensive evaluating of wild and cultivated emmer wheat (<i>Triticum turgidum</i> L.) genotypes response to salt stress. <i>Plant Growth Regulation</i> , 2018, 84, 261-273.	3.4	17
28	Conservation analysis of long non-coding RNAs in plants. <i>Science China Life Sciences</i> , 2018, 61, 190-198.	4.9	83
29	Comparative Analysis of the Transcriptional Response of Tolerant and Sensitive Wheat Genotypes to Drought Stress in Field Conditions. <i>Agronomy</i> , 2018, 8, 247.	3.0	15
30	Direct comparison of β -glucan content in wild and cultivated barley. <i>International Journal of Food Properties</i> , 2018, 21, 2218-2228.	3.0	24
31	Complete Chloroplast Genome Sequence of Broomcorn Millet (<i>Panicum miliaceum</i> L.) and Comparative Analysis with Other Panicoideae Species. <i>Agronomy</i> , 2018, 8, 159.	3.0	14
32	Genome-Wide Identification and Expression Analysis of Heat Shock Transcription Factor Family in <i>Chenopodium quinoa</i> Willd. <i>Agronomy</i> , 2018, 8, 103.	3.0	13
33	Genome-Wide Identification and Expression Analysis of the HD-Zip Gene Family in Wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	2.4	41
34	Genome-wide sequence and expressional analysis of autophagy Gene family in bread wheat (<i>Triticum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	3.5	28
35	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018, 361, .	12.6	768
36	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	12.6	2,424

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37	Identification and Analysis of RNA Editing Sites in the Chloroplast Transcripts of <i>Aegilops tauschii</i> L. Genes, 2017, 8, 13.	2.4	34
38	Genome-Wide Identification and Analysis of MAPK and MAPKK Gene Families in Bread Wheat (<i>Triticum</i>) Tj ETQq0 0.0 rgBT /Overlock 10	2.4	35
39	Genome-Wide Identification and Characterization of Salinity Stress-Responsive miRNAs in Wild Emmer Wheat (<i>Triticum turgidum</i> ssp. <i>dicoccoides</i>). Genes, 2017, 8, 156.	2.4	36
40	Genome-wide identification, phylogeny and expressional profiles of mitogen activated protein kinase kinase kinase (MAPKKK) gene family in bread wheat (<i>Triticum aestivum</i> L.). BMC Genomics, 2016, 17, 668.	2.8	131
41	De novo Assembly and Characterization of the Transcriptome of Broomcorn Millet (<i>Panicum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	3.8	29
42	Genome-Wide Identification, Evolution, and Co-expression Network Analysis of Mitogen-Activated Protein Kinase Kinase Kinases in <i>Brachypodium distachyon</i> . Frontiers in Plant Science, 2016, 7, 1400.	3.6	25
43	Genome-wide characterization of microsatellites in Triticeae species: abundance, distribution and evolution. Scientific Reports, 2016, 6, 32224.	3.3	30
44	Genome-wide identification, phylogeny and expression analysis of AP2/ERF transcription factors family in <i>Brachypodium distachyon</i> . BMC Genomics, 2016, 17, 636.	2.8	59
45	Selection and evaluation of reference genes for quantitative gene expression analysis in broomcorn millet (<i>Panicum miliaceum</i> L.). Journal of Plant Biology, 2016, 59, 435-443.	2.1	8
46	Transcriptome-wide identification and expression profiles of the WRKY transcription factor family in Broomcorn millet (<i>Panicum miliaceum</i> L.). BMC Genomics, 2016, 17, 343.	2.8	58
47	Characterization of microRNAs and their targets in wild barley (<i>Hordeum vulgare</i> subsp.) Tj ETQq1 1 0.784314 rgBT /Overlock 10	2.0	4
48	Global Identification of MicroRNAs and Their Targets in Barley under Salinity Stress. PLoS ONE, 2015, 10, e0137990.	2.5	71
49	Comparative Analysis of Asteraceae Chloroplast Genomes: Structural Organization, RNA Editing and Evolution. Plant Molecular Biology Reporter, 2015, 33, 1526-1538.	1.8	65
50	Construction and Characterization of a Bacterial Artificial Chromosome Library for the Hexaploid Wheat Line 92R137. BioMed Research International, 2014, 2014, 1-9.	1.9	3
51	Comparative analysis of <i>Stowaway</i> -like miniature inverted repeat transposable elements in wheat group 7 chromosomes: Abundance, composition, and evolution. Journal of Systematics and Evolution, 2014, 52, 743-749.	3.1	2
52	Comparative analysis of codon usage patterns in chloroplast genomes of the Asteraceae family. Plant Molecular Biology Reporter, 2014, 32, 828-840.	1.8	61
53	Computational Identification and Comparative Analysis of miRNAs in Wheat Group 7 Chromosomes. Plant Molecular Biology Reporter, 2014, 32, 487-500.	1.8	10
54	Large-scale identification of microsatellites for a major invasive weed, <i>Ageratina adenophora</i> , using the Illumina sequencing technology. Weed Research, 2014, 54, 133-139.	1.7	3

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55	Preparation of High Molecular Weight gDNA and Bacterial Artificial Chromosome (BAC) Libraries in Plants. <i>Methods in Molecular Biology</i> , 2014, 1099, 41-63.	0.9	3
56	Dispersion and domestication shaped the genome of bread wheat. <i>Plant Biotechnology Journal</i> , 2013, 11, 564-571.	8.3	79
57	A 4-gigabase physical map unlocks the structure and evolution of the complex genome of <i>Aegilops tauschii</i> , the wheat D-genome progenitor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7940-7945.	7.1	214
58	Identification and Characterization of MicroRNAs from Barley (<i>Hordeum vulgare</i> L.) by High-Throughput Sequencing. <i>International Journal of Molecular Sciences</i> , 2012, 13, 2973-2984.	4.1	80
59	Development of chromosome-specific microsatellite markers in <i>Triticum aestivum</i> (Poaceae) using NGS technology. <i>American Journal of Botany</i> , 2012, 99, e369-71.	1.7	25
60	Analysis of codon usage patterns of the chloroplast genomes in the Poaceae family. <i>Australian Journal of Botany</i> , 2012, 60, 461.	0.6	36
61	Complete Chloroplast Genome Sequence of a Major Invasive Species, Crofton Weed (<i>Ageratina</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 234	2.5	234
62	Non-gridded library: a new approach for BAC (bacterial artificial chromosome) exploitation in hexaploid wheat (<i>Triticum aestivum</i>). <i>Nucleic Acids Research</i> , 2000, 28, 106e-106.	14.5	37
63	Patterns and impacting factors of gene evolutionary rate between wild and cultivated emmer wheat () Tj ETQq1 1 0.784314 rgBT /Overlock 234	3.1	6
64	Genetic Diversity of Transcription Factor Genes in <i>Triticum</i> and Mining for Promising Haplotypes for Beneficial Agronomic Traits. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	5