

Wanquan Ji

List of Publications by Year in descending order

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53
papers

1,173
citations

430874

18
h-index

434195

31
g-index

59
all docs

59
docs citations

59
times ranked

1245
citing authors

#	ARTICLE	IF	CITATIONS
1	Cytogenetic and marker assisted identification of a wheat– <i>Psathyrostachys huashanica</i> Keng f. ex P.C.Kuo alien substitution line conferring processing quality and resistance to stripe rust. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 687-698.	1.6	5
2	Identification and DNA Marker Development for a Wheat- <i>Leymus mollis</i> 2Ns (2D) Disomic Chromosome Substitution. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2676.	4.1	3
3	Molecular cytogenetics and development of St-chromosome-specific molecular markers of novel stripe rust resistant wheat– <i>Thinopyrum intermedium</i> and wheat– <i>Thinopyrum ponticum</i> substitution lines. <i>BMC Plant Biology</i> , 2022, 22, 111.	3.6	8
4	Identification of Differentially Expressed Genes in Resistant Tetraploid Wheat (<i>Triticum turgidum</i>) under <i>Sitobion avenae</i> (F.) Infestation. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6012.	4.1	1
5	An alternative splicing isoform of wheat TaYRC1 resistance protein activates immunity by interacting with dynamin-related proteins. <i>Journal of Experimental Botany</i> , 2022, 73, 5474-5489.	4.8	2
6	Development and Molecular Cytogenetic Identification of Two Wheat- <i>Aegilops geniculata</i> Roth 7Mg Chromosome Substitution Lines with Resistance to Fusarium Head Blight, Powdery Mildew and Stripe Rust. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7056.	4.1	3
7	Identification and expression analysis of heat–shock proteins in wheat infected with powdery mildew and stripe rust. <i>Plant Genome</i> , 2021, 14, e20092.	2.8	10
8	Chromosome karyotype and stability of new synthetic hexaploid wheat. <i>Molecular Breeding</i> , 2021, 41, 1.	2.1	4
9	A dominant spotted leaf gene TaSpl1 activates endocytosis and defense-related genes causing cell death in the absence of dominant inhibitors. <i>Plant Science</i> , 2021, 310, 110982.	3.6	4
10	Genome-wide identification, evolution, and expression of the <i>SNARE</i> gene family in wheat resistance to powdery mildew. <i>PeerJ</i> , 2021, 9, e10788.	2.0	6
11	Molecular cytogenetics for a wheat– <i>Aegilops geniculata</i> 3Mg alien addition line with resistance to stripe rust and powdery mildew. <i>BMC Plant Biology</i> , 2021, 21, 575.	3.6	4
12	Large-Scale Cloning and Comparative Analysis of TaNAC Genes in Response to Stripe Rust and Powdery Mildew in Wheat (<i>Triticum aestivum</i> L.). <i>Genes</i> , 2020, 11, 1073.	2.4	8
13	Cytogenetic Analysis and Molecular Marker Development for a New Wheat– <i>Thinopyrum ponticum</i> 1Js (1D) Disomic Substitution Line With Resistance to Stripe Rust and Powdery Mildew. <i>Frontiers in Plant Science</i> , 2020, 11, 1282.	3.6	18
14	Gene co-expression network analysis provides a novel insight into the dynamic response of wheat to powdery mildew stress. <i>Journal of Genetics</i> , 2020, 99, 1.	0.7	6
15	Molecular Characterization and Functional Analysis of Wheat TtLOX Gene Involved in Aphid Resistance. <i>Agronomy</i> , 2020, 10, 780.	3.0	1
16	Characterization and Evaluation of Resistance to Powdery Mildew of Wheat– <i>Aegilops geniculata</i> Roth 7Mg (7A) Alien Disomic Substitution Line W16998. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1861.	4.1	12
17	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
18	Identification of wheat DREB genes and functional characterization of TaDREB3 in response to abiotic stresses. <i>Gene</i> , 2020, 740, 144514.	2.2	43

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19	The Emerging Role of Long Non-Coding RNAs in Plant Defense Against Fungal Stress. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2659.	4.1	25
20	Genome-wide identification of GRAS genes in <i>Brachypodium distachyon</i> and functional characterization of BdSLR1 and BdSLRL1. <i>BMC Genomics</i> , 2019, 20, 635.	2.8	24
21	Molecular cytogenetic identification of two wheat– <i>Thinopyrum ponticum</i> substitution lines conferring stripe rust resistance. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	19
22	Transcriptome-wide alternative splicing modulation during plant-pathogen interactions in wheat. <i>Plant Science</i> , 2019, 288, 110160.	3.6	41
23	Transcriptome and Proteome-Based Network Analysis Reveals a Model of Gene Activation in Wheat Resistance to Stripe Rust. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1106.	4.1	24
24	Cloning, prokaryotic expression, and subcellular localisation of the <i>TaMAPK10-like</i> gene in common wheat. <i>Canadian Journal of Plant Science</i> , 2019, 99, 460-466.	0.9	1
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	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
27	Molecular cytogenetics identification of a wheat – <i>Leymus mollis</i> double disomic addition line with stripe rust resistance. <i>Genome</i> , 2017, 60, 375-383.	2.0	10
28	Molecular cytogenetic identification of a wheat – <i>Thinopyrum ponticum</i> substitution line with stripe rust resistance. <i>Genome</i> , 2017, 60, 860-867.	2.0	29
29	Isolation and molecular cytogenetic characterization of a wheat – <i>Leymus mollis</i> double monosomic addition line and its progenies with resistance to stripe rust. <i>Genome</i> , 2017, 60, 1029-1036.	2.0	7
30	Introgression of the <i>Aegilops speltoides</i> Su1-Ph1 Suppressor into Wheat. <i>Frontiers in Plant Science</i> , 2017, 8, 2163.	3.6	45
31	Development and molecular cytogenetic identification of a new wheat – <i>Leymus mollis</i> Lm#6Ns disomic addition line. <i>Plant Breeding</i> , 2016, 135, 654-662.	1.9	0
32	Chromosomal structural changes and microsatellite variations in newly synthesized hexaploid wheat mediated by unreduced gametes. <i>Journal of Genetics</i> , 2016, 95, 819-830.	0.7	8
33	Molecular cytogenetic identification of a wheat – <i>Aegilops geniculata</i> Roth 7Mg disomic addition line with powdery mildew resistance. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	28
34	Molecular cytogenetic identification of a wheat –rye 1R addition line with multiple spikelets and resistance to powdery mildew. <i>Genome</i> , 2016, 59, 277-288.	2.0	25
35	Genome-wide identification and functional prediction of novel and fungi-responsive lincRNAs in <i>Triticum aestivum</i> . <i>BMC Genomics</i> , 2016, 17, 238.	2.8	74
36	Identification and mapping of PmSE5785, a new recessive powdery mildew resistance locus, in synthetic hexaploid wheat. <i>Euphytica</i> , 2016, 207, 619-626.	1.2	14

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37	Quantitative proteomics reveals the central changes of wheat in response to powdery mildew. <i>Journal of Proteomics</i> , 2016, 130, 108-119.	2.4	45
38	Spontaneous and Divergent Hexaploid Triticales Derived from Common Wheat \bar{A} -Rye by Complete Elimination of D-Genome Chromosomes. <i>PLoS ONE</i> , 2015, 10, e0120421.	2.5	26
39	Global Identification of MicroRNAs and Their Targets in Barley under Salinity Stress. <i>PLoS ONE</i> , 2015, 10, e0137990.	2.5	71
40	Identification and evaluation of disease resistance and HMW-GS composition of <i>Aegilops geniculata</i> Roth. <i>Genetic Resources and Crop Evolution</i> , 2015, 62, 1085-1093.	1.6	5
41	Wheat NAC transcription factor TaNAC29 is involved in response to salt stress. <i>Plant Physiology and Biochemistry</i> , 2015, 96, 356-363.	5.8	75
42	Genetic effect of locus B2 inhibiting awning in double-ditelosomic 6B of <i>Triticum durum</i> DR147. <i>Genetic Resources and Crop Evolution</i> , 2015, 62, 407-418.	1.6	7
43	Development and Molecular Cytogenetic Identification of a Novel Wheat \bar{A} – <i>Leymus mollis</i> Lm#7Ns (7D) Disomic Substitution Line with Stripe Rust Resistance. <i>PLoS ONE</i> , 2015, 10, e0140227.	2.5	22
44	Development and discrimination of 12 double ditelosomics in tetraploid wheat cultivar DR147. <i>Genome</i> , 2014, 57, 89-95.	2.0	9
45	Large-scale transcriptome comparison reveals distinct gene activations in wheat responding to stripe rust and powdery mildew. <i>BMC Genomics</i> , 2014, 15, 898.	2.8	178
46	Proteomic Analysis of the Defense Response of Wheat to the Powdery Mildew Fungus, <i>Blumeria graminis</i> f. sp. <i>tritici</i> . <i>Protein Journal</i> , 2014, 33, 513-524.	1.6	18
47	Long non-coding genes implicated in response to stripe rust pathogen stress in wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	2.3	70
48	Molecular characterisation and expression of a pathogen-induced senescence-associated gene in wheat (<i>Triticum aestivum</i>). <i>Australasian Plant Pathology</i> , 2013, 42, 53-61.	1.0	2
49	Genetic analysis of wheat (<i>Triticum aestivum</i> L.) and related species with SSR markers. <i>Genetic Resources and Crop Evolution</i> , 2013, 60, 1105-1117.	1.6	19
50	High-density mapping and marker development for the powdery mildew resistance gene PmAS846 derived from wild emmer wheat (<i>Triticum turgidum</i> var. <i>dicoccoides</i>). <i>Theoretical and Applied Genetics</i> , 2012, 124, 1549-1560.	3.6	54
51	Gene Expression in Wheat Induced by Inoculation with <i>Puccinia striiformis</i> West. <i>Plant Molecular Biology Reporter</i> , 2011, 29, 458-465.	1.8	18
52	Expression of special genes inhibited by powdery mildew (<i>Blumeria graminis</i> f. sp. <i>tritici</i>) in wheat germplasm N9436. <i>Frontiers of Agriculture in China</i> , 2010, 4, 10-17.	0.2	2
53	Comparison of the genetic diversity between <i>Triticum aestivum</i> ssp. <i>tibetanum</i> Shao and Tibetan wheat landraces (<i>Triticum aestivum</i> L.) by using intron-splice junction primers. <i>Genetic Resources and Crop Evolution</i> , 2010, 57, 1141-1150.	1.6	9