

Dejun Han

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4734638/publications.pdf>

Version: 2024-02-01

44
papers

1,110
citations

430874

18
h-index

454955

30
g-index

47
all docs

47
docs citations

47
times ranked

817
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Rapid identification of an adult plant stripe rust resistance gene in hexaploid wheat by high-throughput SNP array genotyping of pooled extremes. <i>Theoretical and Applied Genetics</i> , 2018, 131, 43-58.	3.6	80
3	Wheat stripe rust resistance gene Yr24/Yr26: A retrospective review. <i>Crop Journal</i> , 2018, 6, 321-329.	5.2	62
4	Wheat Stripe Rust Grading by Deep Learning With Attention Mechanism and Images From Mobile Devices. <i>Frontiers in Plant Science</i> , 2020, 11, 558126.	3.6	62
5	SNP-based pool genotyping and haplotype analysis accelerate fine-mapping of the wheat genomic region containing stripe rust resistance gene Yr26. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1481-1496.	3.6	61
6	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
7	Development and Validation of KASP-SNP Markers for QTL Underlying Resistance to Stripe Rust in Common Wheat Cultivar P10057. <i>Plant Disease</i> , 2017, 101, 2079-2087.	1.4	46
8	Utilization of the Genomewide Wheat 55K SNP Array for Genetic Analysis of Stripe Rust Resistance in Common Wheat Line P9936. <i>Phytopathology</i> , 2019, 109, 819-827.	2.2	41
9	Genome-wide Mapping for Stripe Rust Resistance Loci in Common Wheat Cultivar Qinnong 142. <i>Plant Disease</i> , 2019, 103, 439-447.	1.4	38
10	Haplotype variations in QTL for salt tolerance in Chinese wheat accessions identified by marker-based and pedigree-based kinship analyses. <i>Crop Journal</i> , 2020, 8, 1011-1024.	5.2	36
11	Saturation Mapping of a Major Effect QTL for Stripe Rust Resistance on Wheat Chromosome 2B in Cultivar Napo 63 Using SNP Genotyping Arrays. <i>Frontiers in Plant Science</i> , 2017, 8, 653.	3.6	34
12	Genome-Wide Association Study and Gene Specific Markers Identified 51 Genes or QTL for Resistance to Stripe Rust in U.S. Winter Wheat Cultivars and Breeding Lines. <i>Frontiers in Plant Science</i> , 2020, 11, 998.	3.6	33
13	Genetic architecture of wheat stripe rust resistance revealed by combining QTL mapping using SNP-based genetic maps and bulked segregant analysis. <i>Theoretical and Applied Genetics</i> , 2019, 132, 443-455.	3.6	31
14	Comparative genome-wide mapping versus extreme pool-genotyping and development of diagnostic SNP markers linked to QTL for adult plant resistance to stripe rust in common wheat. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1777-1792.	3.6	29
15	Combining Single Nucleotide Polymorphism Genotyping Array with Bulk Segregant Analysis to Map a Gene Controlling Adult Plant Resistance to Stripe Rust in Wheat Line O3031-1-5 H62. <i>Phytopathology</i> , 2018, 108, 103-113.	2.2	27
16	Genome-Wide Linkage Mapping Reveals Stripe Rust Resistance in Common Wheat (<i>Triticum aestivum</i>) Xinong1376. <i>Plant Disease</i> , 2019, 103, 2742-2750.	1.4	27
17	Systematic study of the stress-responsive Rboh gene family in <i>Nicotiana tabacum</i> : Genome-wide identification, evolution and role in disease resistance. <i>Genomics</i> , 2020, 112, 1404-1418.	2.9	25
18	Association Analysis Identifies New Loci for Resistance to Chinese <i>Yr26</i> -Virulent Races of the Stripe Rust Pathogen in a Diverse Panel of Wheat Germplasm. <i>Plant Disease</i> , 2020, 104, 1751-1762.	1.4	23

#	ARTICLE	IF	CITATIONS
19	Identification of New Sources of Resistance to Crown Rot and Fusarium Head Blight in Wheat. <i>Plant Disease</i> , 2020, 104, 1979-1985.	1.4	22
20	CRISPR-Cas12a-Based Diagnostics of Wheat Fungal Diseases. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 7240-7247.	5.2	19
21	A major QTL co-localized on chromosome 6BL and its epistatic interaction for enhanced wheat stripe rust resistance. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1409-1424.	3.6	17
22	Stripe rust resistance to a burgeoning <i>Puccinia striiformis</i> f. sp. <i>tritici</i> race CYR34 in current Chinese wheat cultivars for breeding and research. <i>Euphytica</i> , 2019, 215, 1.	1.2	16
23	Genome-Scale Analysis of Homologous Genes among Subgenomes of Bread Wheat (<i>Triticum aestivum</i>) Tj ETQq1 1.0, 784314, rgBT /Ome	4.1	14
24	Genome-Wide Wheat 55K SNP-Based Mapping of Stripe Rust Resistance Loci in Wheat Cultivar Shaannong 33 and Their Alleles Frequencies in Current Chinese Wheat Cultivars and Breeding Lines. <i>Plant Disease</i> , 2021, 105, 1048-1056.	1.4	14
25	Utilization of a Wheat50K SNP Microarray-Derived High-Density Genetic Map for QTL Mapping of Plant Height and Grain Traits in Wheat. <i>Plants</i> , 2021, 10, 1167.	3.5	13
26	Enhanced stripe rust resistance obtained by combining Yr30 with a widely dispersed, consistent QTL on chromosome arm 4BL. <i>Theoretical and Applied Genetics</i> , 2022, 135, 351-365.	3.6	12
27	Genome-Wide Association Study on Root System Architecture and Identification of Candidate Genes in Wheat (<i>Triticum aestivum</i> L.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 1843.	4.1	11
28	A Comparison of UAV RGB and Multispectral Imaging in Phenotyping for Stay Green of Wheat Population. <i>Remote Sensing</i> , 2021, 13, 5173.	4.0	11
29	Epistatic interaction effect between chromosome 1BL (Yr29) and a novel locus on 2AL facilitating resistance to stripe rust in Chinese wheat Changwu 357-9. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2501-2513.	3.6	11
30	Identification of sources of resistance in geographically diverse wheat accessions to stripe rust pathogen in China. <i>Crop Protection</i> , 2019, 122, 1-8.	2.1	10
31	Wheat-root associated prokaryotic community: interplay between plant selection and location. <i>Plant and Soil</i> , 2021, 464, 183.	3.7	10
32	Genome-wide mapping of adult plant stripe rust resistance in wheat cultivar Toni. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1693-1704.	3.6	9
33	Stripe rust resistance genes in a set of Ethiopian bread wheat cultivars and breeding lines. <i>Euphytica</i> , 2020, 216, 1.	1.2	9
34	Refined mapping of stripe rust resistance gene YrP10090 within a desirable haplotype for wheat improvement on chromosome 6A. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2005-2021.	3.6	9
35	The assembly of wheat-associated fungal community differs across growth stages. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 7427-7438.	3.6	8
36	Rapid identification of a major effect QTL conferring adult plant resistance to stripe rust in wheat cultivar Yacoâ€œSâ€œ. <i>Euphytica</i> , 2017, 213, 1.	1.2	7

#	ARTICLE	IF	CITATIONS
37	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
38	A genome-wide association study revealed the genetic variation and candidate genes for grain copper content in bread wheat (<i>Triticum aestivum</i> L.). <i>Food and Function</i> , 2022, 13, 5177-5188.	4.6	6
39	Combined linkage and association mapping reveals two major QTL for stripe rust adult plant resistance in Shaanmai 155 and their haplotype variation in common wheat germplasm. <i>Crop Journal</i> , 2022, 10, 783-792.	5.2	5
40	Analyzing the performance of corn in China using a factor-analytic variance-covariance structure with multiple factors. <i>Crop Science</i> , 2020, 60, 190-201.	1.8	4
41	Construction and Characterization of a Bacterial Artificial Chromosome Library for the Hexaploid Wheat Line 92R137. <i>BioMed Research International</i> , 2014, 2014, 1-9.	1.9	3
42	Evaluation of resistance of current wheat cultivars and breeding lines to stripe rust from three Gorges reservoir area. <i>Journal of General Plant Pathology</i> , 2017, 83, 283-290.	1.0	3
43	Combining genome-wide linkage mapping with extreme pool genotyping for stripe rust resistance gene identification in bread wheat. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	2
44	A comparison of factor-analytic and equal diagonal factor-analytic models in multi-location trials analyses. <i>Agronomy Journal</i> , 2020, 112, 2722-2733.	1.8	0