Daowen Wang

List of Publications by Year
in descending order

75 papers	4,368 citations	172207 29 h-index	114278 63 g-index
76 all docs	76 docs citations	76 times ranked	5384 citing authors

#	Article	IF	Citations
1	Precise base editing in rice, wheat and maize with a Cas9-cytidine deaminase fusion. Nature Biotechnology, 2017, 35, 438-440.	9.4	690
2	Cytosine, but not adenine, base editors induce genome-wide off-target mutations in rice. Science, 2019, 364, 292-295.	6.0	491
3	Genome sequence of the progenitor of wheat A subgenome Triticum urartu. Nature, 2018, 557, 424-428.	13.7	354
4	Genome editing of upstream open reading frames enables translational control in plants. Nature Biotechnology, 2018, 36, 894-898.	9.4	244
5	Analysis of the functions of <i>Ta<scp>GW</scp>2</i> homoeologs in wheat grain weight and protein content traits. Plant Journal, 2018, 94, 857-866.	2.8	211
6	A high-quality genome assembly highlights rye genomic characteristics and agronomically important genes. Nature Genetics, 2021, 53, 574-584.	9.4	164
7	Single-molecule real-time transcript sequencing facilitates common wheat genome annotation and grain transcriptome research. BMC Genomics, 2015, 16, 1039.	1.2	124
8	GDP-mannose pyrophosphorylase is a genetic determinant of ammonium sensitivity in <i>Arabidopsis thaliana</i>. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 18308-18313.	3.3	116
9	Molecular analysis of common wheat genes encoding three types of cytosolic heat shock protein 90 (Hsp90): functional involvement of cytosolic Hsp90s in the control of wheat seedling growth and disease resistance. New Phytologist, 2011, 191, 418-431.	3.5	108
10	Association Analysis of Genomic Loci Important for Grain Weight Control in Elite Common Wheat Varieties Cultivated with Variable Water and Fertiliser Supply. PLoS ONE, 2013, 8, e57853.	1.1	104
11	Natural variation of TaGASR7-A1 affects grain length in common wheat under multiple cultivation conditions. Molecular Breeding, 2014, 34, 937-947.	1.0	102
12	Heat stress-induced transposon activation correlates with 3D chromatin organization rearrangement in Arabidopsis. Nature Communications, 2020, 11, 1886.	5.8	102
13	Pandemonium Breaks Out: Disruption of Salicylic Acid-Mediated Defense by Plant Pathogens. Molecular Plant, 2018, 11, 1427-1439.	3.9	101
14	Molecular and functional analysis of phosphomannomutase (PMM) from higher plants and genetic evidence for the involvement of PMM in ascorbic acid biosynthesis in Arabidopsis and Nicotiana benthamiana. Plant Journal, 2007, 49, 399-413.	2.8	99
15	Gene Duplication and Evolution Dynamics in the Homeologous Regions Harboring Multiple Prolamin and Resistance Gene Families in Hexaploid Wheat. Frontiers in Plant Science, 2018, 9, 673.	1.7	84
16	NPR1 Promotes Its Own and Target Gene Expression in Plant Defense by Recruiting CDK8. Plant Physiology, 2019, 181, 289-304.	2.3	84
17	New Insights into the Organization, Recombination, Expression and Functional Mechanism of Low Molecular Weight Glutenin Subunit Genes in Bread Wheat. PLoS ONE, 2010, 5, e13548.	1.1	74
18	Genome-wide analysis of complex wheat gliadins, the dominant carriers of celiac disease epitopes. Scientific Reports, 2017, 7, 44609.	1.6	71

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19	Transcriptome analysis reveals differentially expressed storage protein transcripts in seeds of Aegilops and wheat. Journal of Cereal Science, 2006, 44, 75-85.	1.8	63
20	Reprogramming and remodeling: transcriptional and epigenetic regulation of salicylic acid-mediated plant defense. Journal of Experimental Botany, 2020, 71, 5256-5268.	2.4	50
21	Genomic and functional genomics analyses of gluten proteins and prospect for simultaneous improvement of end-use and health-related traits in wheat. Theoretical and Applied Genetics, 2020, 133, 1521-1539.	1.8	49
22	Molecular analysis of lipoxygenase (LOX) genes in common wheat and phylogenetic investigation of LOX proteins from model and crop plants. Journal of Cereal Science, 2010, 52, 387-394.	1.8	48
23	Homology-mediated inter-chromosomal interactions in hexaploid wheat lead to specific subgenome territories following polyploidization and introgression. Genome Biology, 2021, 22, 26.	3.8	47
24	SnRK1 Phosphorylates and Destabilizes WRKY3 to Enhance Barley Immunity to Powdery Mildew. Plant Communications, 2020, 1, 100083.	3.6	34
25	Rapid evolutionary dynamics in a 2.8â€Mb chromosomal region containing multiple prolamin and resistance gene families in <i>Aegilops tauschii</i>. Plant Journal, 2016, 87, 495-506.	2.8	33
26	The <i>TuMYB46L</i>â€<i>TuACO3</i> module regulates ethylene biosynthesis in einkorn wheat defense to powdery mildew. New Phytologist, 2020, 225, 2526-2541.	3.5	33
27	Contrasting patterns in the spread of two seed-borne viruses in pea embryos. Plant Journal, 1997, 11, 1333-1340.	2.8	32
28	Dissecting and Enhancing the Contributions of High-Molecular-Weight Glutenin Subunits to Dough Functionality and Bread Quality. Molecular Plant, 2015, 8, 332-334.	3.9	32
29	Further genetic analysis of a major quantitative trait locus controlling root length and related traits in common wheat. Molecular Breeding, 2014, 33, 975-985.	1.0	31
30	Two interacting transcriptional coactivators cooperatively control plant immune responses. Science Advances, 2021, 7, eabl7173.	4.7	31
31	Coexpression network analysis of the genes regulated by two types of resistance responses to powdery mildew in wheat. Scientific Reports, 2016, 6, 23805.	1.6	29
32	New insights into structural organization and gene duplication in a 1.75â€Mb genomic region harboring the Î±â€gliadin gene family in Aegilops tauschii , the source of wheat D genome. Plant Journal, 2017, 92, 571-583.	2.8	29
33	Efficient and fine mapping of RMES1 conferring resistance to sorghum aphid Melanaphis sacchari. Molecular Breeding, 2013, 31, 777-784.	1.0	28
34	New insight into the function of wheat glutenin proteins as investigated with two series of genetic mutants. Scientific Reports, 2017, 7, 3428.	1.6	28
35	ThMYC4E, candidate Blue aleurone 1 gene controlling the associated trait in Triticum aestivum. PLoS ONE, 2017, 12, e0181116.	1.1	28
36	A transgenic wheat with a stilbene synthase gene resistant to powdery mildew obtained by biolistic method. Science Bulletin, 2000, 45, 634-638.	1.7	26

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37	Highâ€throughput mining of Eâ€genomeâ€specific <scp>SNP</scp>s for characterizing <i>Thinopyrum elongatum</i> introgressions in common wheat. Molecular Ecology Resources, 2017, 17, 1318-1329.	2.2	22
38	Achieving Plant Genome Editing While Bypassing Tissue Culture. Trends in Plant Science, 2020, 25, 427-429.	4.3	22
39	Analysis of the <i>Gliâ€D2</i> locus identifies a genetic target for simultaneously improving the breadmaking and healthâ€related traits of common wheat. Plant Journal, 2018, 95, 414-426.	2.8	19
40	Molecular analysis of phosphomannomutase (PMM) genes reveals a unique PMM duplication event in diverse Triticeae species and the main PMM isozymes in bread wheat tissues. BMC Plant Biology, 2010, 10, 214.	1.6	18
41	Molecular characterization of a novel type of lipoxygenase (LOX) gene from common wheat (Triticum) Tj ETQq1 1 0.784314 rgBT /Overl	1.0	18
42	A recent burst of gene duplications in Triticeae. Plant Communications, 2022, 3, 100268.	3.6	18
43	Haplotype Variation of Glu-D1 Locus and the Origin of Glu-D1d Allele Conferring Superior End-Use Qualities in Common Wheat. PLoS ONE, 2013, 8, e74859.	1.1	17
44	TaPHT1;9â€4B and its transcriptional regulator TaMYB4â€7D contribute to phosphate uptake and plant growth in bread wheat. New Phytologist, 2021, 231, 1968-1983.	3.5	17
45	Wheat heat tolerance is impaired by heightened deletions in the distal end of 4AL chromosomal arm. Plant Biotechnology Journal, 2021, 19, 1038-1051.	4.1	16
46	Development and characterization of markerâ€free and transgene insertion siteâ€defined transgenic wheat with improved grain storability and fatty acid content. Plant Biotechnology Journal, 2020, 18, 129-140.	4.1	15
47	Interaction between the movement protein of barley yellow dwarf virus and the cell nuclear envelope: Role of a putative amphiphilic Î±-helix at the N-terminus of the movement protein. Biopolymers, 2005, 79, 86-96.	1.2	13
48	CRISPR editing-mediated antiviral immunity: a versatile source of resistance to combat plant virus infections. Science China Life Sciences, 2019, 62, 1246-1249.	2.3	13
49	Molecular and functional analysis of hypoxanthineâ€guanine phosphoribosyltransferase from Arabidopsis thaliana. New Phytologist, 2007, 175, 448-461.	3.5	12
50	Molecular and Functional Characterization of Sphingosine-1-Phosphate Lyase Homolog from Higher Plants. Journal of Integrative Plant Biology, 2007, 49, 323-335.	4.1	12
51	Helitron and CACTA DNA transposons actively reshape the common wheat - AK58 genome. Genomics, 2022, 114, 110288.	1.3	12
52	Identification and Characterization of High-Molecular-Weight Glutenin Subunits from Agropyron intermedium. PLoS ONE, 2014, 9, e87477.	1.1	11
53	Grain-specific reduction in lipoxygenase activity improves flour color quality and seed longevity in common wheat. Molecular Breeding, 2015, 35, 1.	1.0	11
54	Assessment of the individual and combined effects of Rht8 and Ppd-D1a on plant height, time to heading and yield traits in common wheat. Crop Journal, 2019, 7, 845-856.	2.3	11

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55	Efficient expression and function of a receptorâ€like kinase in wheat powdery mildew defence require an intronâ€located MYB binding site. Plant Biotechnology Journal, 2021, 19, 897-909.	4.1	11
56	The BZR1-EDS1 module regulates plant growth-defense coordination. Molecular Plant, 2021, 14, 2072-2087.	3.9	11
57	The Interplay between Hydrogen Sulfide and Phytohormone Signaling Pathways under Challenging Environments. International Journal of Molecular Sciences, 2022, 23, 4272.	1.8	11
58	A novel allele of L-galactono-1,4-lactone dehydrogenase is associated with enhanced drought tolerance through affecting stomatal aperture in common wheat. Scientific Reports, 2016, 6, 30177.	1.6	10
59	A distinct class of plant and animal viral proteins that disrupt mitosis by directly interrupting the mitotic entry switch Wee1-Cdc25-Cdk1. Science Advances, 2020, 6, eaba3418.	4.7	10
60	A potential nuclear envelope-targeting domain and an arginine-rich RNA binding element identified in the putative movement protein of the GAV strain of Barley yellow dwarf virus. Functional Plant Biology, 2008, 35, 40.	1.1	8
61	Wide hybridization: engineering the next leap in wheat yield. Journal of Genetics and Genomics, 2009, 36, 509-510.	1.7	8
62	Transcriptional Coactivators: Driving Force of Plant Immunity. Frontiers in Plant Science, 2022, 13, 823937.	1.7	7
63	Identification of new T1BL.1RS translocation lines derived from wheat (Triticum aestivum L. cultivar) Tj ETQq1 1 0.784314 rgBT /Overlo	1.0	5
64	Reduction of root flavonoid level and its potential involvement in lateral root emergence in Arabidopsis thaliana grown under low phosphate supply. Functional Plant Biology, 2009, 36, 564.	1.1	5
65	Development of a new set of molecular markers for examining Glu-A1 variants in common wheat and ancestral species. PLoS ONE, 2017, 12, e0180766.	1.1	5
66	The florigen interactor BdES43 represses flowering in the model temperate grass <i>Brachypodium distachyon</i>. Plant Journal, 2020, 102, 262-275.	2.8	5
67	The distribution of cotransformed transgenes in particle bombardment-mediated transformed wheat. Transgenic Research, 2015, 24, 1055-1063.	1.3	4
68	Connecting the Dots: A New and Complete Salicylic Acid Biosynthesis Pathway. Molecular Plant, 2019, 12, 1539-1541.	3.9	4
69	Partial suppression of l-galactono-1,4-lactone dehydrogenase causes significant reduction in leaf water loss through decreasing stomatal aperture size in Arabidopsis. Plant Growth Regulation, 2014, 72, 171-179.	1.8	3
70	Genetic Analysis of Chromosomal Loci Affecting the Content of Insoluble Glutenin in Common Wheat. Journal of Genetics and Genomics, 2015, 42, 495-505.	1.7	3
71	Reactions of Triticum urartu accessions to two races of the wheat yellow rust pathogen. Crop Journal, 2018, 6, 509-515.	2.3	2
72	Dissecting and enhancing the contributions of high-molecular-weight glutenin subunits to dough functionality and bread quality. Molecular Plant, 2014, , .	3.9	1

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73	Degradation without ubiquitination: new function of a parasite effector. Trends in Parasitology, 2021, 37, 1024-1026.	1.5	1
74	Hijacking of host mitochondria by Toxoplasma gondii and SARS-CoV-2. Trends in Parasitology, 2022, 38, 269-271.	1.5	1
75	Assembling the Rye Genome. Compendium of Plant Genomes, 2021, , 101-116.	0.3	0