

Daowen Wang

List of Publications by Citations

Source: <https://exaly.com/author-pdf/5377788/daowen-wang-publications-by-citations.pdf>

Version: 2024-04-24

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

72
papers

2,603
citations

23
h-index

50
g-index

76
ext. papers

3,652
ext. citations

9.1
avg, IF

5.04
L-index

#	Paper	IF	Citations
72	Precise base editing in rice, wheat and maize with a Cas9-cytidine deaminase fusion. <i>Nature Biotechnology</i> , 2017 , 35, 438-440	44.5	508
71	Cytosine, but not adenine, base editors induce genome-wide off-target mutations in rice. <i>Science</i> , 2019 , 364, 292-295	33.3	324
70	Genome sequence of the progenitor of wheat A subgenome <i>Triticum urartu</i> . <i>Nature</i> , 2018 , 557, 424-428	50.4	205
69	Genome editing of upstream open reading frames enables translational control in plants. <i>Nature Biotechnology</i> , 2018 , 36, 894-898	44.5	128
68	Analysis of the functions of TaGW2 homoeologs in wheat grain weight and protein content traits. <i>Plant Journal</i> , 2018 , 94, 857-866	6.9	123
67	GDP-mannose pyrophosphorylase is a genetic determinant of ammonium sensitivity in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 18308-18313	11.5	92
66	Molecular and functional analysis of phosphomannomutase (PMM) from higher plants and genetic evidence for the involvement of PMM in ascorbic acid biosynthesis in <i>Arabidopsis</i> and <i>Nicotiana benthamiana</i> . <i>Plant Journal</i> , 2007 , 49, 399-413	6.9	84
65	Single-molecule real-time transcript sequencing facilitates common wheat genome annotation and grain transcriptome research. <i>BMC Genomics</i> , 2015 , 16, 1039	4.5	81
64	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. <i>New Phytologist</i> , 2011 , 191, 418-431	9.8	73
63	New insights into the organization, recombination, expression and functional mechanism of low molecular weight glutenin subunit genes in bread wheat. <i>PLoS ONE</i> , 2010 , 5, e13548	3.7	60
62	Pandemonium Breaks Out: Disruption of Salicylic Acid-Mediated Defense by Plant Pathogens. <i>Molecular Plant</i> , 2018 , 11, 1427-1439	14.4	57
61	Natural variation of TaGASR7-A1 affects grain length in common wheat under multiple cultivation conditions. <i>Molecular Breeding</i> , 2014 , 34, 937-947	3.4	53
60	Transcriptome analysis reveals differentially expressed storage protein transcripts in seeds of <i>Aegilops</i> and wheat. <i>Journal of Cereal Science</i> , 2006 , 44, 75-85	3.8	45
59	NPR1 Promotes Its Own and Target Gene Expression in Plant Defense by Recruiting CDK8. <i>Plant Physiology</i> , 2019 , 181, 289-304	6.6	42
58	Association analysis of genomic loci important for grain weight control in elite common wheat varieties cultivated with variable water and fertiliser supply. <i>PLoS ONE</i> , 2013 , 8, e57853	3.7	42
57	Genome-wide analysis of complex wheat gliadins, the dominant carriers of celiac disease epitopes. <i>Scientific Reports</i> , 2017 , 7, 44609	4.9	41
56	Molecular analysis of lipoxygenase (LOX) genes in common wheat and phylogenetic investigation of LOX proteins from model and crop plants. <i>Journal of Cereal Science</i> , 2010 , 52, 387-394	3.8	41

55	Gene Duplication and Evolution Dynamics in the Homeologous Regions Harboring Multiple Prolamin and Resistance Gene Families in Hexaploid Wheat. <i>Frontiers in Plant Science</i> , 2018 , 9, 673	6.2	39
54	Heat stress-induced transposon activation correlates with 3D chromatin organization rearrangement in Arabidopsis. <i>Nature Communications</i> , 2020 , 11, 1886	17.4	31
53	A high-quality genome assembly highlights rye genomic characteristics and agronomically important genes. <i>Nature Genetics</i> , 2021 , 53, 574-584	36.3	31
52	Contrasting patterns in the spread of two seed-borne viruses in pea embryos. <i>Plant Journal</i> , 1997 , 11, 1333-1340	6.9	28
51	Genomic and functional genomics analyses of gluten proteins and prospect for simultaneous improvement of end-use and health-related traits in wheat. <i>Theoretical and Applied Genetics</i> , 2020 , 133, 1521-1539	6	25
50	Coexpression network analysis of the genes regulated by two types of resistance responses to powdery mildew in wheat. <i>Scientific Reports</i> , 2016 , 6, 23805	4.9	25
49	Further genetic analysis of a major quantitative trait locus controlling root length and related traits in common wheat. <i>Molecular Breeding</i> , 2014 , 33, 975-985	3.4	23
48	Efficient and fine mapping of RMES1 conferring resistance to sorghum aphid <i>Melanaphis sacchari</i> . <i>Molecular Breeding</i> , 2013 , 31, 777-784	3.4	22
47	New insight into the function of wheat glutenin proteins as investigated with two series of genetic mutants. <i>Scientific Reports</i> , 2017 , 7, 3428	4.9	22
46	Dissecting and enhancing the contributions of high-molecular-weight glutenin subunits to dough functionality and bread quality. <i>Molecular Plant</i> , 2015 , 8, 332-4	14.4	20
45	A transgenic wheat with a stilbene synthase gene resistant to powdery mildew obtained by biolistic method. <i>Science Bulletin</i> , 2000 , 45, 634-638		19
44	Rapid evolutionary dynamics in a 2.8-Mb chromosomal region containing multiple prolamin and resistance gene families in <i>Aegilops tauschii</i> . <i>Plant Journal</i> , 2016 , 87, 495-506	6.9	19
43	New insights into structural organization and gene duplication in a 1.75-Mb genomic region harboring the <i>E</i> gliadin gene family in <i>Aegilops tauschii</i> , the source of wheat D genome. <i>Plant Journal</i> , 2017 , 92, 571-583	6.9	18
42	Reprogramming and remodeling: transcriptional and epigenetic regulation of salicylic acid-mediated plant defense. <i>Journal of Experimental Botany</i> , 2020 , 71, 5256-5268	7	17
41	ThMYC4E, candidate Blue aleurone 1 gene controlling the associated trait in <i>Triticum aestivum</i> . <i>PLoS ONE</i> , 2017 , 12, e0181116	3.7	17
40	High-throughput mining of E-genome-specific SNPs for characterizing <i>Thinopyrum elongatum</i> introgressions in common wheat. <i>Molecular Ecology Resources</i> , 2017 , 17, 1318-1329	8.4	14
39	The TuMYB46L-TuACO3 module regulates ethylene biosynthesis in einkorn wheat defense to powdery mildew. <i>New Phytologist</i> , 2020 , 225, 2526-2541	9.8	14
38	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. <i>BMC Plant Biology</i> , 2010 , 10, 214	5.3	13

37	Analysis of the Gli-D2 locus identifies a genetic target for simultaneously improving the breadmaking and health-related traits of common wheat. <i>Plant Journal</i> , 2018 , 95, 414-426	6.9	12
36	Haplotype variation of Glu-D1 locus and the origin of Glu-D1d allele conferring superior end-use qualities in common wheat. <i>PLoS ONE</i> , 2013 , 8, e74859	3.7	12
35	Interaction between the movement protein of barley yellow dwarf virus and the cell nuclear envelope: role of a putative amphiphilic alpha-helix at the N-terminus of the movement protein. <i>Biopolymers</i> , 2005 , 79, 86-96	2.2	12
34	Achieving Plant Genome Editing While Bypassing Tissue Culture. <i>Trends in Plant Science</i> , 2020 , 25, 427-429	3.1	11
33	Molecular characterization of a novel type of lipoxygenase (LOX) gene from common wheat (<i>Triticum aestivum</i> L.). <i>Molecular Breeding</i> , 2012 , 30, 113-124	3.4	11
32	Homology-mediated inter-chromosomal interactions in hexaploid wheat lead to specific subgenome territories following polyploidization and introgression. <i>Genome Biology</i> , 2021 , 22, 26	18.3	11
31	Grain-specific reduction in lipoxygenase activity improves flour color quality and seed longevity in common wheat. <i>Molecular Breeding</i> , 2015 , 35, 1	3.4	10
30	Identification and characterization of high-molecular-weight glutenin subunits from <i>Agropyron intermedium</i> . <i>PLoS ONE</i> , 2014 , 9, e87477	3.7	10
29	Molecular and Functional Characterization of Sphingosine-1-Phosphate Lyase Homolog from Higher Plants. <i>Journal of Integrative Plant Biology</i> , 2007 , 49, 323-335	8.3	10
28	CRISPR editing-mediated antiviral immunity: a versatile source of resistance to combat plant virus infections. <i>Science China Life Sciences</i> , 2019 , 62, 1246-1249	8.5	9
27	SnRK1 Phosphorylates and Destabilizes WRKY3 to Enhance Barley Immunity to Powdery Mildew. <i>Plant Communications</i> , 2020 , 1, 100083	9	8
26	Wide hybridization: engineering the next leap in wheat yield. <i>Journal of Genetics and Genomics</i> , 2009 , 36, 509-10	4	8
25	Molecular and functional analysis of hypoxanthine-guanine phosphoribosyltransferase from <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2007 , 175, 448-461	9.8	8
24	Development and characterization of marker-free and transgene insertion site-defined transgenic wheat with improved grain storability and fatty acid content. <i>Plant Biotechnology Journal</i> , 2020 , 18, 129-140	11.6	7
23	Wheat heat tolerance is impaired by heightened deletions in the distal end of 4AL chromosomal arm. <i>Plant Biotechnology Journal</i> , 2021 , 19, 1038-1051	11.6	7
22	A novel allele of L-galactono-1,4-lactone dehydrogenase is associated with enhanced drought tolerance through affecting stomatal aperture in common wheat. <i>Scientific Reports</i> , 2016 , 6, 30177	4.9	6
21	Assessment of the individual and combined effects of Rht8 and Ppd-D1a on plant height, time to heading and yield traits in common wheat. <i>Crop Journal</i> , 2019 , 7, 845-856	4.6	6
20	Development of a new set of molecular markers for examining Glu-A1 variants in common wheat and ancestral species. <i>PLoS ONE</i> , 2017 , 12, e0180766	3.7	5

19	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. <i>Functional Plant Biology</i> , 2008 , 35, 40-50	2.7	5
18	Efficient expression and function of a receptor-like kinase in wheat powdery mildew defence require an intron-located MYB binding site. <i>Plant Biotechnology Journal</i> , 2021 , 19, 897-909	11.6	5
17	The distribution of cotransformed transgenes in particle bombardment-mediated transformed wheat. <i>Transgenic Research</i> , 2015 , 24, 1055-63	3.3	4
16	Reduction of root flavonoid level and its potential involvement in lateral root emergence in <i>Arabidopsis thaliana</i> grown under low phosphate supply. <i>Functional Plant Biology</i> , 2009 , 36, 564-573	2.7	4
15	Identification of new T1BL.1RS translocation lines derived from wheat (<i>Triticum aestivum</i> L. cultivar Xiaoyan No. 6) and rye hybridization. <i>Acta Physiologiae Plantarum</i> , 2008 , 30, 689-695	2.6	4
14	Genetic analysis of chromosomal loci affecting the content of insoluble glutenin in common wheat. <i>Journal of Genetics and Genomics</i> , 2015 , 42, 495-505	4	3
13	A distinct class of plant and animal viral proteins that disrupt mitosis by directly interrupting the mitotic entry switch Wee1-Cdc25-Cdk1. <i>Science Advances</i> , 2020 , 6, eaba3418	14.3	3
12	Partial suppression of l-galactono-1,4-lactone dehydrogenase causes significant reduction in leaf water loss through decreasing stomatal aperture size in <i>Arabidopsis</i> . <i>Plant Growth Regulation</i> , 2014 , 72, 171-179	3.2	3
11	Two interacting transcriptional coactivators cooperatively control plant immune responses. <i>Science Advances</i> , 2021 , 7, eabl7173	14.3	3
10	TaPHT1;9-4B and its transcriptional regulator TaMYB4-7D contribute to phosphate uptake and plant growth in bread wheat. <i>New Phytologist</i> , 2021 , 231, 1968-1983	9.8	2
9	Connecting the Dots: A New and Complete Salicylic Acid Biosynthesis Pathway. <i>Molecular Plant</i> , 2019 , 12, 1539-1541	14.4	2
8	The BZR1-EDS1 module regulates plant growth-defense coordination. <i>Molecular Plant</i> , 2021 , 14, 2072-2084	14.4	2
7	Helitron and CACTA DNA transposons actively reshape the common bread wheat - AK58 genome.. <i>Genomics</i> , 2022 , 114, 110288	4.3	1
6	The florigen interactor BdES43 represses flowering in the model temperate grass <i>Brachypodium distachyon</i> . <i>Plant Journal</i> , 2020 , 102, 262-275	6.9	1
5	Reactions of <i>Triticum urartu</i> accessions to two races of the wheat yellow rust pathogen. <i>Crop Journal</i> , 2018 , 6, 509-515	4.6	1
4	Transcriptional Coactivators: Driving Force of Plant Immunity.. <i>Frontiers in Plant Science</i> , 2022 , 13, 823936	3.2	0
3	A recent burst of gene duplications in Triticeae.. <i>Plant Communications</i> , 2022 , 3, 100268	9	0
2	Assembling the Rye Genome. <i>Compendium of Plant Genomes</i> , 2021 , 101-116	0.8	0

1 Degradation without ubiquitination: new function of a parasite effector. *Trends in Parasitology*, **2021**, 37, 1024-1026

6.4