

# Hong Zhang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3951152/publications.pdf>

Version: 2024-02-01

29  
papers

816  
citations

687363

13  
h-index

526287

27  
g-index

33  
all docs

33  
docs citations

33  
times ranked

967  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	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
4	Characterization of a wheat HSP70 gene and its expression in response to stripe rust infection and abiotic stresses. <i>Molecular Biology Reports</i> , 2011, 38, 301-307.	2.3	70
5	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
6	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
7	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
8	Transcriptome-wide alternative splicing modulation during plant-pathogen interactions in wheat. <i>Plant Science</i> , 2019, 288, 110160.	3.6	41
9	Molecular cytogenetic identification of a wheat "Thinopyrum ponticum substitution line with stripe rust resistance. <i>Genome</i> , 2017, 60, 860-867.	2.0	29
10	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
11	Molecular mapping and marker development for the <i>Triticum dicoccoides</i> -derived stripe rust resistance gene YrSM139-1B in bread wheat cv. Shaanmai 139. <i>Theoretical and Applied Genetics</i> , 2016, 129, 369-376.	3.6	24
12	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
13	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
14	Isolation and characterization of a wheat IF2 homolog required for innate immunity to stripe rust. <i>Plant Cell Reports</i> , 2013, 32, 591-600.	5.6	10
15	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
16	A truncated CC-NB-ARC gene TaRPP13L1-3D positively regulates powdery mildew resistance in wheat via the RanGAP-WPP complex-mediated nucleocytoplasmic shuttle. <i>Planta</i> , 2022, 255, 60.	3.2	9
17	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
18	Characterization of Wheat Stripe Rust Resistance Genes in Shaanmai 139. <i>Acta Agronomica Sinica</i> (China), 2010, 36, 109-114.	0.3	8

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	Fine mapping and distribution analysis of hybrid necrosis genes <i>Ne1</i> and <i>Ne2</i> in wheat in China. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1177-1189.	3.6	6
22	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
23	Cytogenetic and marker assisted identification of a wheat "Psathyrostachys huashanica 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
24	A dominant spotted leaf gene <i>TaSpl1</i> 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
25	Development and Molecular Cytogenetic Identification of Two Wheat-Aegilops geniculata 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
26	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
27	An alternative splicing isoform of wheat <i>TaYRC1</i> resistance protein activates immunity by interacting with dynamin-related proteins. <i>Journal of Experimental Botany</i> , 2022, 73, 5474-5489.	4.8	2
28	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
29	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, .	0.7	0