

# Zhensheng Kang

## List of Publications by Year in descending order

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212  
papers

6,520  
citations

71102

41  
h-index

110387

64  
g-index

228  
all docs

228  
docs citations

228  
times ranked

4209  
citing authors

#	ARTICLE	IF	CITATIONS
1	High genome heterozygosity and endemic genetic recombination in the wheat stripe rust fungus. <i>Nature Communications</i> , 2013, 4, 2673.	12.8	238
2	<i>Puccinia striiformis</i> f. sp. <i>tritici</i> miR1 (Pst-miR1), an important pathogenicity factor of <i>Pst</i> , impairs wheat resistance to <i>Pst</i> by suppressing the wheat pathogenesis-related 2 gene. <i>New Phytologist</i> , 2017, 215, 338-350.	7.3	168
3	WheatOmics: A platform combining multiple omics data to accelerate functional genomics studies in wheat. <i>Molecular Plant</i> , 2021, 14, 1965-1968.	8.3	166
4	Genome sequence of <i>Valsa</i> canker pathogens uncovers a potential adaptation of colonization of woody bark. <i>New Phytologist</i> , 2015, 208, 1202-1216.	7.3	158
5	Identification of Eighteen <i>Berberis</i> Species as Alternate Hosts of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> and Virulence Variation in the Pathogen Isolates from Natural Infection of Barberry Plants in China. <i>Phytopathology</i> , 2013, 103, 927-934.	2.2	143
6	The Stripe Rust Resistance Gene Yr10 Encodes an Evolutionary-Conserved and Unique CC-NBS-LRR Sequence in Wheat. <i>Molecular Plant</i> , 2014, 7, 1740-1755.	8.3	132
7	An effector protein of the wheat stripe rust fungus targets chloroplasts and suppresses chloroplast function. <i>Nature Communications</i> , 2019, 10, 5571.	12.8	129
8	Role of Alternate Hosts in Epidemiology and Pathogen Variation of Cereal Rusts. <i>Annual Review of Phytopathology</i> , 2016, 54, 207-228.	7.8	121
9	Host-Induced Gene Silencing: A Powerful Strategy to Control Diseases of Wheat and Barley. <i>International Journal of Molecular Sciences</i> , 2019, 20, 206.	4.1	111
10	Genome-wide A-to-I RNA editing in fungi independent of ADAR enzymes. <i>Genome Research</i> , 2016, 26, 499-509.	5.5	109
11	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.	7.3	108
12	Stripe Rust Effector PstGSRE1 Disrupts Nuclear Localization of ROS-Promoting Transcription Factor TaLOL2 to Defeat ROS-Induced Defense in Wheat. <i>Molecular Plant</i> , 2019, 12, 1624-1638.	8.3	98
13	Delimiting cryptic pathogen species causing apple Valsa canker with multilocus data. <i>Ecology and Evolution</i> , 2014, 4, 1369-1380.	1.9	97
14	Host-induced gene silencing of an important pathogenicity factor <i>Pst</i> CPK1 in <i>Puccinia striiformis</i> f. sp. <i>tritici</i> enhances resistance of wheat to stripe rust. <i>Plant Biotechnology Journal</i> , 2018, 16, 797-807.	8.3	97
15	Transcriptome profiling to identify genes involved in pathogenicity of <i>Valsa mali</i> on apple tree. <i>Fungal Genetics and Biology</i> , 2014, 68, 31-38.	2.1	87
16	SSR and STS markers for wheat stripe rust resistance gene Yr26. <i>Euphytica</i> , 2008, 159, 359-366.	1.2	83
17	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
18	TaADF7, an actin-depolymerizing factor, contributes to wheat resistance against <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>Plant Journal</i> , 2014, 78, 16-30.	5.7	79

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19	Variation in cis-regulation of a NAC transcription factor contributes to drought tolerance in wheat. <i>Molecular Plant</i> , 2022, 15, 276-292.	8.3	78
20	Host-Induced Gene Silencing of the MAPKK Gene <i>PsFUZ7</i> Confers Stable Resistance to Wheat Stripe Rust. <i>Plant Physiology</i> , 2017, 175, 1853-1863.	4.8	75
21	Regulatory changes in <i>TaSNAC8</i> are associated with drought tolerance in wheat seedlings. <i>Plant Biotechnology Journal</i> , 2020, 18, 1078-1092.	8.3	73
22	Candidate effector proteins of the necrotrophic apple canker pathogen <i>Valsa mali</i> can suppress BAX-induced PCD. <i>Frontiers in Plant Science</i> , 2015, 6, 579.	3.6	71
23	Virulence Variations of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> Isolates Collected from <i>Berberis</i> spp. in China. <i>Plant Disease</i> , 2016, 100, 131-138.	1.4	71
24	A Conserved <i>Puccinia striiformis</i> Protein Interacts with Wheat NPR1 and Reduces Induction of Pathogenesis-Related Genes in Response to Pathogens. <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 977-989.	2.6	69
25	<i>PST</i> ha5a23, a candidate effector from the obligate biotrophic pathogen <i>Puccinia striiformis</i> f. sp. <i>tritici</i> , is involved in plant defense suppression and rust pathogenicity. <i>Environmental Microbiology</i> , 2017, 19, 1717-1729.	3.8	69
26	<i>TaMCA4</i> , a Novel Wheat Metacaspase Gene Functions in Programmed Cell Death Induced by the Fungal Pathogen <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 755-764.	2.6	67
27	Identification of expressed genes during compatible interaction between stripe rust ( <i>Puccinia</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10	2.8	63
28	Wheat stripe rust resistance gene Yr24/Yr26: A retrospective review. <i>Crop Journal</i> , 2018, 6, 321-329.	5.2	62
29	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
30	Transcriptome Analysis Provides Insights into the Mechanisms Underlying Wheat Plant Resistance to Stripe Rust at the Adult Plant Stage. <i>PLoS ONE</i> , 2016, 11, e0150717.	2.5	61
31	A stripe rust effector <i>Pst18363</i> targets and stabilises <i>TaNUDX23</i> that promotes stripe rust disease. <i>New Phytologist</i> , 2020, 225, 880-895.	7.3	60
32	MARPLE, a point-of-care, strain-level disease diagnostics and surveillance tool for complex fungal pathogens. <i>BMC Biology</i> , 2019, 17, 65.	3.8	56
33	Monodehydroascorbate reductase gene, regulated by the wheat PN-2013 miRNA, contributes to adult wheat plant resistance to stripe rust through ROS metabolism. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 1-12.	1.9	55
34	The wheat ABA receptor gene <i>TaPYL1</i> contributes to drought tolerance and grain yield by increasing water-use efficiency. <i>Plant Biotechnology Journal</i> , 2022, 20, 846-861.	8.3	55
35	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
36	A novel wheat NAC transcription factor, <i>Ta</i> NAC30, negatively regulates resistance of wheat to stripe rust. <i>Journal of Integrative Plant Biology</i> , 2018, 60, 432-443.	8.5	51

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37	Down-regulation of a wheat alkaline/neutral invertase correlates with reduced host susceptibility to wheat stripe rust caused by <i>Puccinia striiformis</i> . <i>Journal of Experimental Botany</i> , 2015, 66, 7325-7338.	4.8	49
38	The calcium sensor TaCBL4 and its interacting protein TaCIPK5 are required for wheat resistance to stripe rust fungus. <i>Journal of Experimental Botany</i> , 2018, 69, 4443-4457.	4.8	49
39	YR36/WKS1-Mediated Phosphorylation of PsbO, an Extrinsic Member of Photosystem II, Inhibits Photosynthesis and Confers Stripe Rust Resistance in Wheat. <i>Molecular Plant</i> , 2019, 12, 1639-1650.	8.3	49
40	Characterization of protein kinase <i>PsrSRPKL</i> , a novel pathogenicity factor in the wheat stripe rust fungus. <i>Environmental Microbiology</i> , 2015, 17, 2601-2617.	3.8	48
41	Virulence and Simple Sequence Repeat Marker Segregation in a <i>Puccinia striiformis</i> f. sp. <i>tritici</i> Population Produced by Selfing a Chinese Isolate on <i>Berberis shensiana</i> . <i>Phytopathology</i> , 2016, 106, 185-191.	2.2	48
42	ABA-Induced Sugar Transporter TaSTP6 Promotes Wheat Susceptibility to Stripe Rust. <i>Plant Physiology</i> , 2019, 181, 1328-1343.	4.8	48
43	A unique invertase is important for sugar absorption of an obligate biotrophic pathogen during infection. <i>New Phytologist</i> , 2017, 215, 1548-1561.	7.3	47
44	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
45	Candidate Effector Pst_8713 Impairs the Plant Immunity and Contributes to Virulence of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1294.	3.6	45
46	An extracellular Zn <sup>2+</sup> -only superoxide dismutase from <i>Puccinia striiformis</i> confers enhanced resistance to host-derived oxidative stress. <i>Environmental Microbiology</i> , 2016, 18, 4118-4135.	3.8	44
47	Genome-Wide Identification of Cyclic Nucleotide-Gated Ion Channel Gene Family in Wheat and Functional Analyses of TaCNGC14 and TaCNGC16. <i>Frontiers in Plant Science</i> , 2018, 9, 18.	3.6	44
48	Ultrastructural and cytochemical studies on the infection process of <i>Sclerotinia sclerotiorum</i> in oilseed rape. <i>Journal of Plant Diseases and Protection</i> , 2008, 115, 9-16.	2.9	41
49	TaADF3, an Actin-Depolymerizing Factor, Negatively Modulates Wheat Resistance Against <i>Puccinia striiformis</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 1214.	3.6	41
50	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
51	Wheat hypersensitive-induced reaction genes TaHIR1 and TaHIR3 are involved in response to stripe rust fungus infection and abiotic stresses. <i>Plant Cell Reports</i> , 2013, 32, 273-283.	5.6	40
52	TaCIPK10 interacts with and phosphorylates TaNH2 to activate wheat defense responses to stripe rust. <i>Plant Biotechnology Journal</i> , 2019, 17, 956-968.	8.3	40
53	Overexpression of a Wheat CCaMK Gene Reduces ABA Sensitivity of <i>Arabidopsis thaliana</i> During Seed Germination and Seedling Growth. <i>Plant Molecular Biology Reporter</i> , 2011, 29, 681-692.	1.8	39
54	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

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55	<i>TaDAD2</i> , a Negative Regulator of Programmed Cell Death, Is Important for the Interaction Between Wheat and the Stripe Rust Fungus. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 79-90.	2.6	37
56	Transcriptional repression of <i>TaNOX10</i> by <i>TaWRKY19</i> compromises ROS generation and enhances wheat susceptibility to stripe rust. <i>Plant Cell</i> , 2022, 34, 1784-1803.	6.6	37
57	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
58	Haustroria "arsenals during the interaction between wheat and <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>Molecular Plant Pathology</i> , 2020, 21, 83-94.	4.2	34
59	A polysaccharide deacetylase from <i>Puccinia striiformis</i> f. sp. <i>tritici</i> is an important pathogenicity gene that suppresses plant immunity. <i>Plant Biotechnology Journal</i> , 2020, 18, 1830-1842.	8.3	34
60	Determining the basis of nonhost resistance in rice to cereal rusts. <i>Euphytica</i> , 2011, 179, 33-40.	1.2	33
61	<i>TaEIL1</i> , a wheat homologue of <i>AtEIN3</i> , acts as a negative regulator in the wheat-stripe rust fungus interaction. <i>Molecular Plant Pathology</i> , 2013, 14, 728-739.	4.2	32
62	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
63	The development of a PCR-based method for detecting <i>Puccinia striiformis</i> latent infections in wheat leaves. <i>European Journal of Plant Pathology</i> , 2008, 120, 241-247.	1.7	30
64	Biological control of oilseed rape <i>Sclerotinia</i> stem rot by <i>Bacillus subtilis</i> strain Em7. <i>Biocontrol Science and Technology</i> , 2014, 24, 39-52.	1.3	30
65	Histological and molecular studies of the non-host interaction between wheat and <i>Uromyces fabae</i> . <i>Planta</i> , 2011, 234, 979-991.	3.2	29
66	A Novel Fungal Hyperparasite of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> , the Causal Agent of Wheat Stripe Rust. <i>PLoS ONE</i> , 2014, 9, e111484.	2.5	29
67	Wheat <i>TaNPSN</i> SNARE homologues are involved in vesicle-mediated resistance to stripe rust ( <i>Puccinia</i> ) Tj ETQq1 1 0.784314 rgBT /Ov 4.8 29	4.8	29
68	Exploration of microRNAs and their targets engaging in the resistance interaction between wheat and stripe rust. <i>Frontiers in Plant Science</i> , 2015, 6, 469.	3.6	29
69	<i>TaDIR1-2</i> , a Wheat Ortholog of Lipid Transfer Protein <i>AtDIR1</i> Contributes to Negative Regulation of Wheat Resistance against <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 521.	3.6	29
70	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
71	First Report of a <i>Puccinia striiformis</i> f. sp. <i>tritici</i> Race Virulent to Wheat Stripe Rust Resistance Gene <i>Yr5</i> in China. <i>Plant Disease</i> , 2020, 104, 284.	1.4	29
72	A rust fungus effector directly binds plant pre-mRNA splice site to reprogram alternative splicing and suppress host immunity. <i>Plant Biotechnology Journal</i> , 2022, 20, 1167-1181.	8.3	29

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73	Inheritance and Linkage of Virulence Genes in Chinese Predominant Race CYR32 of the Wheat Stripe Rust Pathogen <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 120.	3.6	28
74	Two stripe rust effectors impair wheat resistance by suppressing import of host Fe-S protein into chloroplasts. <i>Plant Physiology</i> , 2021, 187, 2530-2543.	4.8	28
75	FgPrp4 Kinase Is Important for Spliceosome B-Complex Activation and Splicing Efficiency in <i>Fusarium graminearum</i> . <i>PLoS Genetics</i> , 2016, 12, e1005973.	3.5	27
76	Identification of a Novel <i>Alternaria alternata</i> Strain Able to Hyperparasitize <i>Puccinia striiformis</i> f. sp. <i>tritici</i> , the Causal Agent of Wheat Stripe Rust. <i>Frontiers in Microbiology</i> , 2017, 8, 71.	3.5	27
77	Combining Single Nucleotide Polymorphism Genotyping Array with Bulk Segregant Analysis to Map a Gene Controlling Adult Plant Resistance to Stripe Rust in Wheat Line 03031-1-5 H62. <i>Phytopathology</i> , 2018, 108, 103-113.	2.2	27
78	Role of the BUB3 protein in phragmoplast microtubule reorganization during cytokinesis. <i>Nature Plants</i> , 2018, 4, 485-494.	9.3	27
79	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
80	WRKY Transcription Factors Shared by BTH-Induced Resistance and NPR1-Mediated Acquired Resistance Improve Broad-Spectrum Disease Resistance in Wheat. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 433-443.	2.6	27
81	Characterization of wheat homeodomain-leucine zipper family genes and functional analysis of TaHDZ5-6A in drought tolerance in transgenic <i>Arabidopsis</i> . <i>BMC Plant Biology</i> , 2020, 20, 50.	3.6	27
82	TaSTP13 contributes to wheat susceptibility to stripe rust possibly by increasing cytoplasmic hexose concentration. <i>BMC Plant Biology</i> , 2020, 20, 49.	3.6	27
83	Overexpression of the wheat NAC transcription factor TaSNAC4-3A gene confers drought tolerance in transgenic <i>Arabidopsis</i> . <i>Plant Physiology and Biochemistry</i> , 2021, 160, 37-50.	5.8	26
84	Isolation and characterisation of a DNA encoding a wheat heavy metal-associated isoprenylated protein involved in stress responses. <i>Plant Biology</i> , 2015, 17, 1176-1186.	3.8	25
85	Variability of the Stripe Rust Pathogen. , 2017, , 35-154.		25
86	Genetics of Resistance to Common Root Rot (Spot Blotch), <i>Fusarium</i> Crown Rot, and Sharp Eyespot in Wheat. <i>Frontiers in Genetics</i> , 2021, 12, 699342.	2.3	25
87	TaMDHAR4, a monodehydroascorbate reductase gene participates in the interactions between wheat and <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>Plant Physiology and Biochemistry</i> , 2014, 76, 7-16.	5.8	24
88	Genome-Wide Analysis of Simple Sequence Repeats and Efficient Development of Polymorphic SSR Markers Based on Whole Genome Re-Sequencing of Multiple Isolates of the Wheat Stripe Rust Fungus. <i>PLoS ONE</i> , 2015, 10, e0130362.	2.5	24
89	Endophytic <i>Bacillus subtilis</i> Strain E1R-J Is a Promising Biocontrol Agent for Wheat Powdery Mildew. <i>BioMed Research International</i> , 2015, 2015, 1-8.	1.9	24
90	Virulence and Molecular Diversity of the <i>Puccinia striiformis</i> f. sp. <i>tritici</i> Population in Xinjiang in Relation to Other Regions of Western China. <i>Plant Disease</i> , 2016, 100, 99-107.	1.4	24

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91	G1± proteins Gvm2 and Gvm3 regulate vegetative growth, asexual development, and pathogenicity on apple in <i>Valsa mali</i> . PLoS ONE, 2017, 12, e0173141.	2.5	24
92	A Nested PCR Assay for Detecting <i>Valsa mali</i> var. <i>mali</i> in Different Tissues of Apple Trees. Plant Disease, 2012, 96, 1645-1652.	1.4	23
93	Genetic and Molecular Mapping of Stripe Rust Resistance Gene in Wheat “ <i>Psathyrostachys huashanica</i> ” Translocation Line H9020-1-6-8-3. Plant Disease, 2012, 96, 1482-1487.	1.4	23
94	Comparative virulence phenotypes and molecular genotypes of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> , the wheat stripe rust pathogen in China and the United States. Fungal Biology, 2012, 116, 643-653.	2.5	23
95	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. Plant Disease, 2020, 104, 1751-1762.	1.4	23
96	PsANT, the adenine nucleotide translocase of <i>Puccinia striiformis</i> , promotes cell death and fungal growth. Scientific Reports, 2015, 5, 11241.	3.3	21
97	Quantitative Proteomics Reveals the Defense Response of Wheat against <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . Scientific Reports, 2016, 6, 34261.	3.3	21
98	Hexose transporter <i>PsHXT1</i> -mediated sugar uptake is required for pathogenicity of wheat stripe rust. Plant Biotechnology Journal, 2020, 18, 2367-2369.	8.3	21
99	Genome-Wide Identification of Effector Candidates With Conserved Motifs From the Wheat Leaf Rust Fungus <i>Puccinia triticina</i> . Frontiers in Microbiology, 2020, 11, 1188.	3.5	21
100	Transcription factor BZR2 activates chitinase <i>Cht20.2</i> transcription to confer resistance to wheat stripe rust. Plant Physiology, 2021, 187, 2749-2762.	4.8	21
101	Spatial genetic diversity and interregional spread of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> in Northwest China. European Journal of Plant Pathology, 2011, 131, 685-693.	1.7	20
102	Nitric Oxide and Reactive Oxygen Species Coordinately Regulate the Germination of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> Urediniospores. Frontiers in Microbiology, 2016, 7, 178.	3.5	20
103	TaRar1 Is Involved in Wheat Defense against Stripe Rust Pathogen Mediated by YrSu. Frontiers in Plant Science, 2017, 8, 156.	3.6	19
104	Host-Induced Silencing of <i>Fusarium graminearum</i> Genes Enhances the Resistance of <i>Brachypodium distachyon</i> to <i>Fusarium</i> Head Blight. Frontiers in Plant Science, 2019, 10, 1362.	3.6	19
105	TaAMT2;3a, a wheat AMT2-type ammonium transporter, facilitates the infection of stripe rust fungus on wheat. BMC Plant Biology, 2019, 19, 239.	3.6	19
106	A new mode of NPR1 action via an NB-ARC-NPR1 fusion protein negatively regulates the defence response in wheat to stem rust pathogen. New Phytologist, 2020, 228, 959-972.	7.3	19
107	TaAP2-15, An AP2/ERF Transcription Factor, Is Positively Involved in Wheat Resistance to <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . International Journal of Molecular Sciences, 2021, 22, 2080.	4.1	19
108	CRISPR-Cas12a-Based Diagnostics of Wheat Fungal Diseases. Journal of Agricultural and Food Chemistry, 2022, 70, 7240-7247.	5.2	19

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109	The transcription factor <i>PstSTE12</i> is required for virulence of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>Molecular Plant Pathology</i> , 2018, 19, 961-974.	4.2	18
110	Mechanisms in Growth-Promoting of Cucumber by the Endophytic Fungus <i>Chaetomium globosum</i> Strain ND35. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 180.	3.5	18
111	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
112	Identification and expression analysis of some wheat F-box subfamilies during plant development and infection by <i>Puccinia triticina</i> . <i>Plant Physiology and Biochemistry</i> , 2020, 155, 535-548.	5.8	17
113	TaMYB29: A Novel R2R3-MYB Transcription Factor Involved in Wheat Defense Against Stripe Rust. <i>Frontiers in Plant Science</i> , 2021, 12, 783388.	3.6	17
114	Genome-wide analysis of trehalose-6-phosphate phosphatases (TPP) gene family in wheat indicates their roles in plant development and stress response. <i>BMC Plant Biology</i> , 2022, 22, 120.	3.6	17
115	Immunolocalization of 1,3- $\beta$ -Glucanases Secreted by <i>Gaeumannomyces graminis</i> var. <i>tritici</i> in Infected Wheat Roots. <i>Journal of Phytopathology</i> , 2010, 158, 344-350.	1.0	16
116	TaSYP71, a Qc-SNARE, Contributes to Wheat Resistance against <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 544.	3.6	16
117	Molecular Characterization of Novel Totivirus-Like Double-Stranded RNAs from <i>Puccinia striiformis</i> f. sp. <i>tritici</i> , the Causal Agent of Wheat Stripe Rust. <i>Frontiers in Microbiology</i> , 2017, 8, 1960.	3.5	16
118	A novel citrate synthase isoform contributes infection and stress resistance of the stripe rust fungus. <i>Environmental Microbiology</i> , 2018, 20, 4037-4050.	3.8	16
119	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
120	The genome of the rice variety LTH provides insight into its universal susceptibility mechanism to worldwide rice blast fungal strains. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1012-1026.	4.1	16
121	<i>scpTaMDAR6</i> acts as a negative regulator of plant cell death and participates indirectly in stomatal regulation during the wheat stripe rust-fungus interaction. <i>Physiologia Plantarum</i> , 2016, 156, 262-277.	5.2	15
122	TaMCA1, a regulator of cell death, is important for the interaction between wheat and <i>Puccinia striiformis</i> . <i>Scientific Reports</i> , 2016, 6, 26946.	3.3	15
123	Identification of <i>Berberis</i> Species Collected from the Himalayan Region of Pakistan Susceptible to <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>Plant Disease</i> , 2019, 103, 461-467.	1.4	15
124	The cloning and characterization of a DEAD-Box RNA helicase from stress-responsive wheat. <i>Physiological and Molecular Plant Pathology</i> , 2014, 88, 36-42.	2.5	14
125	Wheat AGAMOUS LIKE 6 transcription factors function in stamen development by regulating the expression of Ta APETALA3. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	14
126	Complete genome sequence of a novel mitovirus from the wheat stripe rust fungus <i>Puccinia striiformis</i> . <i>Archives of Virology</i> , 2019, 164, 897-901.	2.1	14

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128	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
129	RNAi-mediated stable silencing of <i>TaCSN5</i> confers broad-spectrum resistance to <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>Molecular Plant Pathology</i> , 2021, 22, 410-421.	4.2	14
130	AtSTP8, an endoplasmic reticulum-localised monosaccharide transporter from <i>Arabidopsis</i> , is recruited to the extrahaustorial membrane during powdery mildew infection. <i>New Phytologist</i> , 2021, 230, 2404-2419.	7.3	14
131	Prevalent Pest Management Strategies for Grain Aphids: Opportunities and Challenges. <i>Frontiers in Plant Science</i> , 2021, 12, 790919.	3.6	14
132	Sugar transporter <i>TaSTP3</i> activation by <i>TaWRKY19</i> /61/82 enhances stripe rust susceptibility in wheat. <i>New Phytologist</i> , 2022, 236, 266-282.	7.3	14
133	TaAbc1, a Member of Abc1-Like Family Involved in Hypersensitive Response against the Stripe Rust Fungal Pathogen in Wheat. <i>PLoS ONE</i> , 2013, 8, e58969.	2.5	13
134	Overexpression of <i>AtPAD4</i> in transgenic <i>Brachypodium distachyon</i> enhances resistance to <i>Puccinia brachypodii</i> . <i>Plant Biology</i> , 2017, 19, 868-874.	3.8	13
135	TaMAPK4 Acts as a Positive Regulator in Defense of Wheat Stripe-Rust Infection. <i>Frontiers in Plant Science</i> , 2018, 9, 152.	3.6	13
136	Determination of heterozygosity for avirulence/virulence loci through sexual hybridization of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>Frontiers of Agricultural Science and Engineering</i> , 2017, 4, 48.	1.4	13
137	A serine-rich effector from the stripe rust pathogen targets a Raf-like kinase to suppress host immunity. <i>Plant Physiology</i> , 2022, 190, 762-778.	4.8	13
138	Race Composition of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> in Tibet, China. <i>Plant Disease</i> , 2012, 96, 1615-1620.	1.4	12
139	TaTypA, a Ribosome-Binding GTPase Protein, Positively Regulates Wheat Resistance to the Stripe Rust Fungus. <i>Frontiers in Plant Science</i> , 2016, 7, 873.	3.6	12
140	Identification of <i>microRNAs</i> and their corresponding targets involved in the susceptibility interaction of wheat response to <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>Physiologia Plantarum</i> , 2016, 157, 95-107.	5.2	12
141	A novel MADS-box transcription factor <i>PstMCM1</i> is responsible for full virulence of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>Environmental Microbiology</i> , 2018, 20, 1452-1463.	3.8	12
142	TaNTF2, a contributor for wheat resistance to the stripe rust pathogen. <i>Plant Physiology and Biochemistry</i> , 2018, 123, 260-267.	5.8	12
143	Wheat Gene TaATG8j Contributes to Stripe Rust Resistance. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1666.	4.1	12
144	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

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146	A Cu <sup>2+</sup> -only superoxide dismutase from stripe rust fungi functions as a virulence factor deployed for counter defense against host-derived oxidative stress. <i>Environmental Microbiology</i> , 2020, 22, 5309-5326.	3.8	11
147	Genome-wide analysis of the AREB/ABF gene lineage in land plants and functional analysis of TaABF3 in <i>Arabidopsis</i> . <i>BMC Plant Biology</i> , 2020, 20, 558.	3.6	11
148	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
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150	Proteomic Analysis of Rice Nonhost Resistance to <i>Puccinia striiformis</i> f. sp. <i>tritici</i> Using Two-Dimensional Electrophoresis. <i>International Journal of Molecular Sciences</i> , 2014, 15, 21644-21659.	4.1	10
151	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
152	TaBln1, a member of the Blufensin family, negatively regulates wheat resistance to stripe rust by reducing Ca <sup>2+</sup> influx. <i>Plant Physiology</i> , 2022, 189, 1380-1396.	4.8	10
153	Identification of wheat proteins with altered expression levels in leaves infected by the stripe rust pathogen. <i>Acta Physiologiae Plantarum</i> , 2011, 33, 2423-2435.	2.1	9
154	Determination of the Role of <i>Berberis</i> spp. in Wheat Stem Rust in China. <i>Plant Disease</i> , 2015, 99, 1113-1117.	1.4	9
155	Genetic Analysis and Molecular Mapping of a Stripe Rust Resistance Gene in Chinese Wheat Differential Guinong 22. <i>Journal of Phytopathology</i> , 2016, 164, 476-484.	1.0	9
156	Two distinct Ras genes from <i>Puccinia striiformis</i> exhibit differential roles in rust pathogenicity and cell death. <i>Environmental Microbiology</i> , 2016, 18, 3910-3922.	3.8	9
157	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
158	Stripe rust resistance genes in a set of Ethiopian bread wheat cultivars and breeding lines. <i>Euphytica</i> , 2020, 216, 1.	1.2	9
159	TaRac6 Is a Potential Susceptibility Factor by Regulating the ROS Burst Negatively in the Wheat- <i>Puccinia striiformis</i> f. sp. <i>tritici</i> Interaction. <i>Frontiers in Plant Science</i> , 2020, 11, 716.	3.6	9
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161	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
162	Characterization and Genetic Analysis of Rice Mutant <i>crr1</i> Exhibiting Compromised Non-host Resistance to <i>Puccinia striiformis</i> f. sp. <i>tritici</i> (Pst). <i>Frontiers in Plant Science</i> , 2016, 7, 1822.	3.6	8

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164	Trade-Off Between Triadimefon Sensitivity and Pathogenicity in a Selfed Sexual Population of <i>Puccinia striiformis</i> f. sp. <i>Tritici</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2729.	3.5	8
165	Alternate Hosts of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> and Their Role. <i>Pathogens</i> , 2020, 9, 434.	2.8	8
166	Study of Inheritance and Linkage of Virulence Genes in a Selfing Population of a Pakistani Dominant Race of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 1685.	4.1	8
167	Introgression of Two Quantitative Trait Loci for Stripe Rust Resistance into Three Chinese Wheat Cultivars. <i>Agronomy</i> , 2020, 10, 483.	3.0	8
168	Distinct Transcriptomic Reprogramming in the Wheat Stripe Rust Fungus During the Initial Infection of Wheat and Barberry. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 198-209.	2.6	8
169	Wheat-Fusarium graminearum Interactions Under Sitobion avenae Influence: From Nutrients and Hormone Signals. <i>Frontiers in Nutrition</i> , 2021, 8, 703293.	3.7	8
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171	Microarray-based identification of conserved microRNA from wheat and their expression profiles response to <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>Canadian Journal of Plant Pathology</i> , 2015, 37, 82-91.	1.4	7
172	Proteomic analysis of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> (Pst) during uredospore germination. <i>European Journal of Plant Pathology</i> , 2016, 144, 121-132.	1.7	7
173	Basidiospores of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> succeed to infect barberry, while Urediniospores are blocked by non-host resistance. <i>Protospasma</i> , 2017, 254, 2237-2246.	2.1	7
174	Rapid identification of a major effect QTL conferring adult plant resistance to stripe rust in wheat cultivar Yaco. <i>Euphytica</i> , 2017, 213, 1.	1.2	7
175	Basidiomycete-specific <i>PsCaMKL1</i> encoding a CaMK-like protein kinase is required for full virulence of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>Environmental Microbiology</i> , 2017, 19, 4177-4189.	3.8	7
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177	TaYS1A, a Yellow Stripe-Like Transporter Gene, Is Required for Wheat Resistance to <i>Puccinia striiformis</i> f. sp. <i>Tritici</i> . <i>Genes</i> , 2020, 11, 1452.	2.4	7
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179	Evaluation of the Potential Risk of the Emerging <i>Yr5</i> -Virulent Races of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> to 165 Chinese Wheat Cultivars. <i>Plant Disease</i> , 2022, 106, 1867-1874.	1.4	7
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182	Light and Electron Microscopy Studies on the Infection of a Wild-type and Metalaxyl-resistant Isolate of <i>Phytophthora sojae</i> in Soybean Hypocotyls. <i>Journal of Phytopathology</i> , 2011, 159, 368-376.	1.0	6
183	Complete genomic sequence and organization of a novel mycovirus from <i>Phoma matteuccicola</i> strain LG915. <i>Archives of Virology</i> , 2019, 164, 2209-2213.	2.1	6
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185	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
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187	Functional Characterization of the Wheat Macrophage Migration Inhibitory Factor TaMIF1 in Wheat-Stripe Rust ( <i>Puccinia striiformis</i> ) Interaction. <i>Biology</i> , 2021, 10, 878.	2.8	6
188	Combination of Marker-Assisted Backcross Selection of Yr59 and Phenotypic Selection to Improve Stripe Rust Resistance and Agronomic Performance in Four Elite Wheat Cultivars. <i>Agronomy</i> , 2022, 12, 497.	3.0	6
189	Characterization of a Ran gene from <i>Puccinia striiformis</i> f. sp. <i>tritici</i> involved in fungal growth and anti-cell death. <i>Scientific Reports</i> , 2016, 6, 35248.	3.3	5
190	Comparison of cell death and accumulation of reactive oxygen species in wheat lines with or without Yr36 responding to <i>Puccinia striiformis</i> f. sp. <i>tritici</i> under low and high temperatures at seedling and adult-plant stages. <i>Protoplasma</i> , 2016, 253, 787-802.	2.1	5
191	Corrigendum to: The calcium sensor TaCBL4 and its interacting protein TaCIPK5 are required for wheat resistance to stripe rust fungus. <i>Journal of Experimental Botany</i> , 2018, 69, 5309-5309.	4.8	5
192	TaClpS1, negatively regulates wheat resistance against <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>BMC Plant Biology</i> , 2020, 20, 555.	3.6	5
193	Improving stripe rust resistance and agronomic performance in three elite wheat cultivars using a combination of phenotypic selection and marker detection of Yr48. <i>Crop Protection</i> , 2021, 148, 105752.	2.1	5
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195	Investigation of Host Responses of Different Potato Genotypes at Tissue, Cellular and Subcellular Levels After Infection with <i>Phytophthora infestans</i> . <i>American Journal of Potato Research</i> , 2013, 90, 524-532.	0.9	4
196	Inheritance of Virulence and Linkages of Virulence Genes in an Ethiopian Isolate of the Wheat Stripe Rust Pathogen ( <i>Puccinia striiformis</i> f. sp. <i>tritici</i> ) Determined Through Sexual Recombination on <i>Berberis holstii</i> (Retracted). <i>Plant Disease</i> , 2019, 103, 2451-2459.	1.4	4
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198	A novel hexa-segmented dsRNA mycovirus confers hypovirulence in the phytopathogenic fungus <i>Diaporthe pseudophoenicicola</i> . <i>Environmental Microbiology</i> , 2022, 24, 4274-4284.	3.8	4

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201	Constitutive Expression of Arabidopsis Senescence Associated Gene 101 in <i>Brachypodium distachyon</i> Enhances Resistance to <i>Puccinia brachypodii</i> and <i>Magnaporthe oryzae</i> . <i>Plants</i> , 2020, 9, 1316.	3.5	3
202	Identification of <i>Berberis</i> spp. as Alternate Hosts for <i>Puccinia achnatheri-sibirici</i> Under Controlled Conditions and Morphologic Observations of Sexual Stage Development of the Rust Fungus. <i>Frontiers in Microbiology</i> , 2020, 11, 1278.	3.5	3
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205	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
206	Identification of <i>Mahonia</i> Species as Alternate Hosts for <i>Puccinia striiformis</i> f. sp. <i>tritici</i> and Determination of Existence of Sexual Propagation of the Rust Pathogen on <i>Mahonia</i> Under Natural Conditions in China. <i>Phytopathology</i> , 2022, 112, 1422-1430.	2.2	2
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208	An alternative splicing isoform of wheat TaYRG1 resistance protein activates immunity by interacting with dynamin-related proteins. <i>Journal of Experimental Botany</i> , 2022, 73, 5474-5489.	4.8	2
209	Distribution and molecular variability of four tobacco viruses in China. <i>Virologica Sinica</i> , 2016, 31, 525-527.	3.0	1
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211	Evidence of occurrence of Crown Rust of Barley Caused by <i>Puccinia coronata</i> var. <i>hordei</i> and sexual reproduction of the pathogen under field conditions in China. <i>Plant Disease</i> , 2021, , PDIS09202029RE.	1.4	1
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