

Zhensheng Kang

List of Publications by Year in descending order

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Version: 2024-02-01

212
papers

6,520
citations

71102

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times ranked

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#	ARTICLE	IF	CITATIONS
1	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
2	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
3	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
4	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
5	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
6	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
7	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
8	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
9	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
10	TaBln1, a member of the Blufensin family, negatively regulates wheat resistance to stripe rust by reducing Ca ²⁺ influx. <i>Plant Physiology</i> , 2022, 189, 1380-1396.	4.8	10
11	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
12	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
13	A candidate effector protein PstCFEM1 contributes to virulence of stripe rust fungus and impairs wheat immunity. <i>Stress Biology</i> , 2022, 2, 1.	3.1	5
14	Role of Sexual Reproduction in the Evolution of the Wheat Stripe Rust Fungus Races in China. <i>Phytopathology</i> , 2022, 112, 1063-1071.	2.2	2
15	The wheat ABA receptor gene <i>TaPYL1B</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
16	Sensitivity and Resistance Risk Assessment of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> to Triadimefon in China. <i>Plant Disease</i> , 2022, 106, 1690-1699.	1.4	8
17	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
18	Genome-wide association study revealed <i>TaHXK3A</i> as a candidate gene controlling stomatal index in wheat seedlings. <i>Plant, Cell and Environment</i> , 2022, 45, 2306-2323.	5.7	7

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19	CRISPR-Cas12a-Based Diagnostics of Wheat Fungal Diseases. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 7240-7247.	5.2	19
20	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
21	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
22	Genome Sequence of <i>Magnaporthe oryzae</i> EA18 Virulent to Multiple Widely Used Rice Varieties. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 727-730.	2.6	7
23	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
24	Grasses are able to harbor the overwintering of urediospores and the overwintering of teliospores of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> in China. <i>Phytopathology Research</i> , 2022, 4, .	2.4	1
25	Genome-Wide Mapping of Loci for Adult-Plant Resistance to Stripe Rust in Durum Wheat Svevo Using the 90K SNP Array. <i>Plant Disease</i> , 2021, 105, 879-888.	1.4	4
26	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
27	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
28	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
29	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
30	TaAP2-15, An AP2/ERF Transcription Factor, Is Positively Involved in Wheat Resistance to <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 2080.	4.1	19
31	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
32	Overexpression of the wheat NAC transcription factor TaSNAC4-3A gene confers drought tolerance in transgenic Arabidopsis. <i>Plant Physiology and Biochemistry</i> , 2021, 160, 37-50.	5.8	26
33	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
34	AtSTP8, an endoplasmic reticulum-localised monosaccharide transporter from Arabidopsis, is recruited to the extrahaustorial membrane during powdery mildew infection. <i>New Phytologist</i> , 2021, 230, 2404-2419.	7.3	14
35	Genetics of Resistance to Common Root Rot (Spot Blotch), Fusarium Crown Rot, and Sharp Eyespot in Wheat. <i>Frontiers in Genetics</i> , 2021, 12, 699342.	2.3	25
36	Transcription factor BZR2 activates chitinase <i>Cht20.2</i> transcription to confer resistance to wheat stripe rust. <i>Plant Physiology</i> , 2021, 187, 2749-2762.	4.8	21

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37	Wheatâ€™Fusarium graminearum Interactions Under Sitobion avenae Influence: From Nutrients and Hormone Signals. <i>Frontiers in Nutrition</i> , 2021, 8, 703293.	3.7	8
38	Two stripe rust effectors impair wheat resistance by suppressing import of host Feâ€™S protein into chloroplasts. <i>Plant Physiology</i> , 2021, 187, 2530-2543.	4.8	28
39	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
40	Field Production, Germinability, and Survival of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> Teliospores in China. <i>Plant Disease</i> , 2021, 105, 2122-2128.	1.4	7
41	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
42	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
43	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
44	Prevalent Pest Management Strategies for Grain Aphids: Opportunities and Challenges. <i>Frontiers in Plant Science</i> , 2021, 12, 790919.	3.6	14
45	A secreted catalase contributes to <i>Puccinia striiformis</i> resistance to host-derived oxidative stress. <i>Stress Biology</i> , 2021, 1, 1.	3.1	3
46	Phenotyping and Genotyping Analyses Reveal the Spread of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> Aeciospores From Susceptible Barberry to Wheat in Qinghai of China. <i>Frontiers in Plant Science</i> , 2021, 12, 764304.	3.6	4
47	Regulatory changes in <i>TaSNAC8â€™6A</i> are associated with drought tolerance in wheat seedlings. <i>Plant Biotechnology Journal</i> , 2020, 18, 1078-1092.	8.3	73
48	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
49	A stripe rust effector Pst18363 targets and stabilises TaNUDX23 that promotes stripe rust disease. <i>New Phytologist</i> , 2020, 225, 880-895.	7.3	60
50	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
51	Stripe rust resistance genes in a set of Ethiopian bread wheat cultivars and breeding lines. <i>Euphytica</i> , 2020, 216, 1.	1.2	9
52	<i>WRKY</i> Transcription Factors Shared by BTH-Induced Resistance and <i>NPR1</i>-Mediated Acquired Resistance Improve Broad-Spectrum Disease Resistance in Wheat. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 433-443.	2.6	27
53	Haustoria â€™ 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
54	A Cuâ€™only superoxide dismutase from stripe rust fungi functions as a virulence factor deployed for counter defense against hostâ€™derived oxidative stress. <i>Environmental Microbiology</i> , 2020, 22, 5309-5326.	3.8	11

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55	Constitutive Expression of Arabidopsis Senescence Associated Gene 101 in Brachypodium distachyon Enhances Resistance to Puccinia brachypodii and Magnaporthe oryzae. <i>Plants</i> , 2020, 9, 1316.	3.5	3
56	WGVD: an integrated web-database for wheat genome variation and selective signatures. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	7
57	Identification and expression analysis of some wheat F-box subfamilies during plant development and infection by Puccinia triticina. <i>Plant Physiology and Biochemistry</i> , 2020, 155, 535-548.	5.8	17
58	TaClpS1, negatively regulates wheat resistance against Puccinia striiformis f. sp. tritici. <i>BMC Plant Biology</i> , 2020, 20, 555.	3.6	5
59	Genome-wide analysis of the AREB/ABF gene lineage in land plants and functional analysis of TaABF3 in Arabidopsis. <i>BMC Plant Biology</i> , 2020, 20, 558.	3.6	11
60	TaYS1A, a Yellow Stripe-Like Transporter Gene, Is Required for Wheat Resistance to Puccinia striiformis f. sp. Tritici. <i>Genes</i> , 2020, 11, 1452.	2.4	7
61	Hexose transporter <i>HXT1</i> -mediated sugar uptake is required for pathogenicity of wheat stripe rust. <i>Plant Biotechnology Journal</i> , 2020, 18, 2367-2369.	8.3	21
62	Genome-Wide Identification of Effector Candidates With Conserved Motifs From the Wheat Leaf Rust Fungus Puccinia triticina. <i>Frontiers in Microbiology</i> , 2020, 11, 1188.	3.5	21
63	A new mode of NPR1 action via an NB-ARC-NPR1 fusion protein negatively regulates the defence response in wheat to stem rust pathogen. <i>New Phytologist</i> , 2020, 228, 959-972.	7.3	19
64	Alternate Hosts of Puccinia striiformis f. sp. tritici and Their Role. <i>Pathogens</i> , 2020, 9, 434.	2.8	8
65	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
66	Study of Inheritance and Linkage of Virulence Genes in a Selfing Population of a Pakistani Dominant Race of Puccinia striiformis f. sp. tritici. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1685.	4.1	8
67	TaRac6 Is a Potential Susceptibility Factor by Regulating the ROS Burst Negatively in the Wheat-Puccinia striiformis f. sp. tritici Interaction. <i>Frontiers in Plant Science</i> , 2020, 11, 716.	3.6	9
68	Identification of a Hyperparasitic <i>Simplicillium obclavatum</i> Strain Affecting the Infection Dynamics of Puccinia striiformis f. sp. tritici on Wheat. <i>Frontiers in Microbiology</i> , 2020, 11, 1277.	3.5	9
69	Identification of Berberis spp. as Alternate Hosts for Puccinia achnatheri-sibirici 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
70	Molecular Characterization of a Novel Ourmia-Like Virus Infecting Phoma matteucciicola. <i>Viruses</i> , 2020, 12, 231.	3.3	14
71	A novel narnavirus isolated from the wheat stripe rust fungus Puccinia striiformis f. sp. tritici. <i>Archives of Virology</i> , 2020, 165, 1011-1014.	2.1	6
72	A polysaccharide deacetylase from <i>Puccinia striiformis</i> f. sp. tritici is an important pathogenicity gene that suppresses plant immunity. <i>Plant Biotechnology Journal</i> , 2020, 18, 1830-1842.	8.3	34

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73	Characterization of wheat homeodomain-leucine zipper family genes and functional analysis of TaHDZ5-6A in drought tolerance in transgenic Arabidopsis. <i>BMC Plant Biology</i> , 2020, 20, 50.	3.6	27
74	Introgression of Two Quantitative Trait Loci for Stripe Rust Resistance into Three Chinese Wheat Cultivars. <i>Agronomy</i> , 2020, 10, 483.	3.0	8
75	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
76	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
77	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
78	Host-Induced Silencing of <i>Fusarium graminearum</i> Genes Enhances the Resistance of <i>Brachypodium distachyon</i> to <i>Fusarium</i> Head Blight. <i>Frontiers in Plant Science</i> , 2019, 10, 1362.	3.6	19
79	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
80	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
81	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
82	TaAMT2;3a, a wheat AMT2-type ammonium transporter, facilitates the infection of stripe rust fungus on wheat. <i>BMC Plant Biology</i> , 2019, 19, 239.	3.6	19
83	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
84	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
85	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
86	PsRPs26, a 40S Ribosomal Protein Subunit, Regulates the Growth and Pathogenicity of <i>Puccinia striiformis</i> f. sp. <i>Tritici</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 968.	3.5	6
87	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
88	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
89	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
90	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

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91	ABA-Induced Sugar Transporter TaSTP6 Promotes Wheat Susceptibility to Stripe Rust. <i>Plant Physiology</i> , 2019, 181, 1328-1343.	4.8	48
92	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
93	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
94	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
95	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
96	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
97	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
98	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
99	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
100	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
101	Wheat stripe rust resistance gene Yr24/Yr26: A retrospective review. <i>Crop Journal</i> , 2018, 6, 321-329.	5.2	62
102	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
103	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
104	TaNTF2, a contributor for wheat resistance to the stripe rust pathogen. <i>Plant Physiology and Biochemistry</i> , 2018, 123, 260-267.	5.8	12
105	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
106	Histological and cytological studies of plant infection by <i>Erysiphe euonymi-japonici</i> . <i>Protoplasma</i> , 2018, 255, 1613-1620.	2.1	2
107	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
108	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

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109	Host-induced gene silencing of an important pathogenicity factor <i>P_{CPK1}</i> 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
110	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
111	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
112	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
113	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
114	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
115	Role of the BUB3 protein in phragmoplast microtubule reorganization during cytokinesis. <i>Nature Plants</i> , 2018, 4, 485-494.	9.3	27
116	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
117	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
118	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
119	Silencing <i>PsKPP4</i> , a MAP kinase kinase kinase gene, reduces pathogenicity of the stripe rust fungus. <i>Molecular Plant Pathology</i> , 2018, 19, 2590-2602.	4.2	8
120	Wheat Gene TaATG8j Contributes to Stripe Rust Resistance. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1666.	4.1	12
121	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
122	Basidiospores of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> succeed to infect barberry, while Urediniospores are blocked by non-host resistance. <i>Protoplasma</i> , 2017, 254, 2237-2246.	2.1	7
123	<i>Puccinia striiformis</i> f. sp. <i>tritici</i> mi ^{cro} RNA-like ^{RNA} 1 (<i>Pst</i> - <i>milR1</i>), 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
124	Rapid identification of a major effect QTL conferring adult plant resistance to stripe rust in wheat cultivar Yaco ^o S ^e Euphytica, 2017, 213, 1.	1.2	7
125	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
126	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

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127	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
128	Variability of the Stripe Rust Pathogen. , 2017, , 35-154.		25
129	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
130	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
131	The non-host pathogen <i>Puccinia triticina</i> elicits an active transcriptional response in rice. <i>European Journal of Plant Pathology</i> , 2017, 147, 553-569.	1.7	1
132	<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
133	TaRar1 Is Involved in Wheat Defense against Stripe Rust Pathogen Mediated by YrSu. <i>Frontiers in Plant Science</i> , 2017, 8, 156.	3.6	19
134	TaDIR1-2, a Wheat Ortholog of Lipid Transfer Protein AtDIR1 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
135	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
136	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
137	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
138	G β proteins Gvm2 and Gvm3 regulate vegetative growth, asexual development, and pathogenicity on apple in <i>Valsa mali</i> . <i>PLoS ONE</i> , 2017, 12, e0173141.	2.5	24
139	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
140	Nitric Oxide and Reactive Oxygen Species Coordinately Regulate the Germination of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> Urediniospores. <i>Frontiers in Microbiology</i> , 2016, 7, 178.	3.5	20
141	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
142	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
143	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
144	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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146	<i>TaMDAR6</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
147	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
148	Distribution and molecular variability of four tobacco viruses in China. <i>Virologica Sinica</i> , 2016, 31, 525-527.	3.0	1
149	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
150	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
151	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
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153	An extracellular Zn-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
154	Quantitative Proteomics Reveals the Defense Response of Wheat against <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>Scientific Reports</i> , 2016, 6, 34261.	3.3	21
155	<i>TaMCA1</i> , 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
156	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
157	Identification of microRNAs 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
158	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
159	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
160	Genome-wide A-to-I RNA editing in fungi independent of ADAR enzymes. <i>Genome Research</i> , 2016, 26, 499-509.	5.5	109
161	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
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164	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
165	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
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174	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
175	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
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177	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
178	Wheat TaNPSN SNARE homologues are involved in vesicle-mediated resistance to stripe rust (<i>Puccinia</i>) Tj ETQq0 0 0 IgBT / Overlock 10 T	4.8	29
179	Delimiting cryptic pathogen species causing apple <i>Valsa</i> canker with multilocus data. <i>Ecology and Evolution</i> , 2014, 4, 1369-1380.	1.9	97
180	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

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182	TaADF7, an actinâ€‘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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184	The Stripe Rust Resistance Gene Yr10 Encodes an Evolutionary-Conserved and Unique CCâ€‘NBSâ€‘LRR Sequence in Wheat. <i>Molecular Plant</i> , 2014, 7, 1740-1755.	8.3	132
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189	<i>TaEIL1</i> , a wheat homologue of <i>AtEIN3</i> , acts as a negative regulator in the wheatâ€‘stripe rust fungus interaction. <i>Molecular Plant Pathology</i> , 2013, 14, 728-739.	4.2	32
190	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
191	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
192	High genome heterozygosity and endemic genetic recombination in the wheat stripe rust fungus. <i>Nature Communications</i> , 2013, 4, 2673.	12.8	238
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194	A Nested PCR Assay for Detecting <i>Valsa mali</i> var. <i>mali</i> in Different Tissues of Apple Trees. <i>Plant Disease</i> , 2012, 96, 1645-1652.	1.4	23
195	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
196	Genetic and Molecular Mapping of Stripe Rust Resistance Gene in Wheatâ€‘ <i>Psathyrostachys huashanica</i> Translocation Line H9020-1-6-8-3. <i>Plant Disease</i> , 2012, 96, 1482-1487.	1.4	23
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202	Spatial genetic diversity and interregional spread of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> in Northwest China. <i>European Journal of Plant Pathology</i> , 2011, 131, 685-693.	1.7	20
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208	Immunolocalization of 1,3- β -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
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