

Zhensheng Kang

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/275029/zhensheng-kang-publications-by-year.pdf>

Version: 2024-04-25

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.

196
papers

3,216
citations

30
h-index

45
g-index

228
ext. papers

5,215
ext. citations

5.2
avg, IF

5.36
L-index

#	Paper	IF	Citations
196	Transcriptional Repression of TaNOX10 by TaWRKY19 Compromises ROS Generation and Enhances Wheat Susceptibility to Stripe Rust.. <i>Plant Cell</i> , 2022 ,	11.6	4
195	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	6.8	1
194	Mechanisms in Growth-Promoting of Cucumber by the Endophytic Fungus Strain ND35.. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022 , 8,	5.6	3
193	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	3.6	2
192	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	5.3	1
191	Prevalent Pest Management Strategies for Grain Aphids: Opportunities and Challenges.. <i>Frontiers in Plant Science</i> , 2021 , 12, 790919	6.2	3
190	TaMYB29: A Novel R2R3-MYB Transcription Factor Involved in Wheat Defense Against Stripe Rust.. <i>Frontiers in Plant Science</i> , 2021 , 12, 783388	6.2	1
189	Variation in cis-Regulation of a NAC Transcription Factor Contributes to Drought Tolerance in Wheat. <i>Molecular Plant</i> , 2021 ,	14.4	6
188	Enhanced stripe rust resistance obtained by combining Yr30 with a widely dispersed, consistent QTL on chromosome arm 4BL. <i>Theoretical and Applied Genetics</i> , 2021 , 1	6	1
187	WheatOmics: A platform combining multiple omics data to accelerate functional genomics studies in wheat. <i>Molecular Plant</i> , 2021 , 14, 1965-1968	14.4	14
186	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	6	1
185	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	5.4	6
184	Evidence of Occurrence of Crown Rust of Barley Caused by var. and Sexual Reproduction of the Pathogen Under Field Conditions in China. <i>Plant Disease</i> , 2021 , PDIS09202029RE	1.5	
183	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	9.8	2
182	Genetics of Resistance to Common Root Rot (Spot Blotch), Crown Rot, and Sharp Eyespot in Wheat. <i>Frontiers in Genetics</i> , 2021 , 12, 699342	4.5	4
181	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	1.5	1
180	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	11.6	17

179	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	3.6	2
178	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	1.5	3
177	RNAi-mediated stable silencing of TaCSN5 confers broad-spectrum resistance to Puccinia striiformis f. sp. tritici. <i>Molecular Plant Pathology</i> , 2021 , 22, 410-421	5.7	5
176	, An AP2/ERF Transcription Factor, Is Positively Involved in Wheat Resistance to f. sp.. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	4
175	Transcription factor BZR2 activates chitinase Cht20.2 transcription to confer resistance to wheat stripe rust. <i>Plant Physiology</i> , 2021 , 187, 2749-2762	6.6	2
174	Wheat- Interactions Under Influence: From Nutrients and Hormone Signals. <i>Frontiers in Nutrition</i> , 2021 , 8, 703293	6.2	2
173	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	6.6	2
172	Field Production, Germinability, and Survival of f. sp. Teliospores in China. <i>Plant Disease</i> , 2021 , 105, 2122-2128	6.5	2
171	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	2.7	2
170	Sensitivity and Resistance Risk Assessment of f. sp. to Triadimefon in China.. <i>Plant Disease</i> , 2021 ,	1.5	3
169	A secreted catalase contributes to Puccinia striiformis resistance to host-derived oxidative stress. <i>Stress Biology</i> , 2021 , 1, 1		1
168	Phenotyping and Genotyping Analyses Reveal the Spread of f. sp. Aeciospores From Susceptible Barberry to Wheat in Qinghai of China.. <i>Frontiers in Plant Science</i> , 2021 , 12, 764304	6.2	0
167	TaClpS1, negatively regulates wheat resistance against Puccinia striiformis f. sp. tritici. <i>BMC Plant Biology</i> , 2020 , 20, 555	5.3	1
166	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	5.3	4
165	, a Yellow Stripe-Like Transporter Gene, Is Required for Wheat Resistance to f. sp.. <i>Genes</i> , 2020 , 11,	4.2	2
164	Hexose transporter PshXT1-mediated sugar uptake is required for pathogenicity of wheat stripe rust. <i>Plant Biotechnology Journal</i> , 2020 , 18, 2367-2369	11.6	7
163	Genome-Wide Identification of Effector Candidates With Conserved Motifs From the Wheat Leaf Rust Fungus. <i>Frontiers in Microbiology</i> , 2020 , 11, 1188	5.7	6
162	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	9.8	3

161	Alternate Hosts of f. sp. and Their Role. <i>Pathogens</i> , 2020 , 9,	4.5	3
160	Association Analysis Identifies New Loci for Resistance to Chinese -Virulent Races of the Stripe Rust Pathogen in a Diverse Panel of Wheat Germplasm. <i>Plant Disease</i> , 2020 , 104, 1751-1762	1.5	11
159	Study of Inheritance and Linkage of Virulence Genes in a Selfing Population of a Pakistani Dominant Race of f. sp.. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	4
158	Is a Potential Susceptibility Factor by Regulating the ROS Burst Negatively in the Wheat- f. sp. Interaction. <i>Frontiers in Plant Science</i> , 2020 , 11, 716	6.2	3
157	Identification of a Hyperparasitic Strain Affecting the Infection Dynamics of f. sp. on Wheat. <i>Frontiers in Microbiology</i> , 2020 , 11, 1277	5.7	0
156	Identification of spp. as Alternate Hosts for Under Controlled Conditions and Morphologic Observations of Sexual Stage Development of the Rust Fungus. <i>Frontiers in Microbiology</i> , 2020 , 11, 1278	5.7	1
155	Molecular Characterization of a Novel Ourmia-Like Virus Infecting. <i>Viruses</i> , 2020 , 12,	6.2	6
154	A novel narnavirus isolated from the wheat stripe rust fungus <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>Archives of Virology</i> , 2020 , 165, 1011-1014	2.6	1
153	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	11.6	12
152	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	5.3	10
151	Introgression of Two Quantitative Trait Loci for Stripe Rust Resistance into Three Chinese Wheat Cultivars. <i>Agronomy</i> , 2020 , 10, 483	3.6	3
150	TaSTP13 contributes to wheat susceptibility to stripe rust possibly by increasing cytoplasmic hexose concentration. <i>BMC Plant Biology</i> , 2020 , 20, 49	5.3	9
149	First Report of a <i>Puccinia striiformis</i> f. sp. <i>tritici</i> Race Virulent to Wheat Stripe Rust Resistance Gene Yr5 in China. <i>Plant Disease</i> , 2020 , 104, 284	1.5	6
148	A stripe rust effector Pst18363 targets and stabilises TaNUDX23 that promotes stripe rust disease. <i>New Phytologist</i> , 2020 , 225, 880-895	9.8	19
147	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	11.6	3
146	Stripe rust resistance genes in a set of Ethiopian bread wheat cultivars and breeding lines. <i>Euphytica</i> , 2020 , 216, 1	2.1	3
145	Transcription Factors Shared by BTH-Induced Resistance and -Mediated Acquired Resistance Improve Broad-Spectrum Disease Resistance in Wheat. <i>Molecular Plant-Microbe Interactions</i> , 2020 , 33, 433-443	3.6	12
144	Haustoria - 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	5.7	10

143	A Cu-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	5.2	4
142	Constitutive Expression of Senescence Associated Gene 101 in Enhances Resistance to and. <i>Plants</i> , 2020 , 9,	4.5	1
141	WGVD: an integrated web-database for wheat genome variation and selective signatures. <i>Database: the Journal of Biological Databases and Curation</i> , 2020 , 2020,	5	2
140	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	5.4	8
139	Regulatory changes in TaSNAC8-6A are associated with drought tolerance in wheat seedlings. <i>Plant Biotechnology Journal</i> , 2020 , 18, 1078-1092	11.6	29
138	Genome-Wide Linkage Mapping Reveals Stripe Rust Resistance in Common Wheat () Xinong1376. <i>Plant Disease</i> , 2019 , 103, 2742-2750	1.5	3
137	Wheat AGAMOUS LIKE 6 transcription factors function in stamen development by regulating the expression of. <i>Development (Cambridge)</i> , 2019 , 146,	6.6	7
136	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	5.3	9
135	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	2.6	2
134	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	3.4	2
133	Inheritance of Virulence and Linkages of Virulence Genes in an Ethiopian Isolate of the Wheat Stripe Rust Pathogen (f. sp.) Determined Through Sexual Recombination on. <i>Plant Disease</i> , 2019 , 103, 2451-2459	1.5	3
132	, a 40S Ribosomal Protein Subunit, Regulates the Growth and Pathogenicity of f. sp.. <i>Frontiers in Microbiology</i> , 2019 , 10, 968	5.7	4
131	Identification of sources of resistance in geographically diverse wheat accessions to stripe rust pathogen in China. <i>Crop Protection</i> , 2019 , 122, 1-8	2.7	7
130	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	2.1	5
129	Genome-wide mapping of adult plant stripe rust resistance in wheat cultivar Toni. <i>Theoretical and Applied Genetics</i> , 2019 , 132, 1693-1704	6	4
128	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	6	11
127	MARPLE, a point-of-care, strain-level disease diagnostics and surveillance tool for complex fungal pathogens. <i>BMC Biology</i> , 2019 , 17, 65	7.3	27
126	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	14.4	21

125	Host-Induced Silencing of Genes Enhances the Resistance of to Head Blight. <i>Frontiers in Plant Science</i> , 2019 , 10, 1362	6.2	9
124	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	14.4	31
123	ABA-Induced Sugar Transporter TaSTP6 Promotes Wheat Susceptibility to Stripe Rust. <i>Plant Physiology</i> , 2019 , 181, 1328-1343	6.6	21
122	Trade-Off Between Triadimefon Sensitivity and Pathogenicity in a Selfed Sexual Population of f. sp.. <i>Frontiers in Microbiology</i> , 2019 , 10, 2729	5.7	5
121	An effector protein of the wheat stripe rust fungus targets chloroplasts and suppresses chloroplast function. <i>Nature Communications</i> , 2019 , 10, 5571	17.4	46
120	Identification of Berberis 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	1.5	6
119	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	2.6	7
118	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	6	16
117	TaCIPK10 interacts with and phosphorylates TaNH2 to activate wheat defense responses to stripe rust. <i>Plant Biotechnology Journal</i> , 2019 , 17, 956-968	11.6	20
116	Host-Induced Gene Silencing: A Powerful Strategy to Control Diseases of Wheat and Barley. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	63
115	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	3.8	14
114	Genome-wide Mapping for Stripe Rust Resistance Loci in Common Wheat Cultivar Qinnong 142. <i>Plant Disease</i> , 2019 , 103, 439-447	1.5	6
113	Wheat stripe rust resistance gene Yr24/Yr26: A retrospective review. <i>Crop Journal</i> , 2018 , 6, 321-329	4.6	27
112	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	6	36
111	A novel MADS-box transcription factor PstMCM1-1 is responsible for full virulence of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>Environmental Microbiology</i> , 2018 , 20, 1452-1463	5.2	6
110	TaNTF2, a contributor for wheat resistance to the stripe rust pathogen. <i>Plant Physiology and Biochemistry</i> , 2018 , 123, 260-267	5.4	8
109	A novel wheat NAC transcription factor, TaNAC30, negatively regulates resistance of wheat to stripe rust. <i>Journal of Integrative Plant Biology</i> , 2018 , 60, 432-443	8.3	31
108	Histological and cytological studies of plant infection by <i>Erysiphe euonymi-japonici</i> . <i>Protoplasma</i> , 2018 , 255, 1613-1620	3.4	0

107	The transcription factor PstSTE12 is required for virulence of <i>Puccinia striiformis</i> f. sp. tritici. <i>Molecular Plant Pathology</i> , 2018 , 19, 961-974	5.7	8
106	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	6	35
105	Host-induced gene silencing of an important pathogenicity factor PsCPK1 in <i>Puccinia striiformis</i> f. sp. tritici enhances resistance of wheat to stripe rust. <i>Plant Biotechnology Journal</i> , 2018 , 16, 797-807	11.6	60
104	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	3.8	17
103	Genome-Wide Identification of Cyclic Nucleotide-Gated Ion Channel Gene Family in Wheat and Functional Analyses of and. <i>Frontiers in Plant Science</i> , 2018 , 9, 18	6.2	24
102	Inheritance and Linkage of Virulence Genes in Chinese Predominant Race CYR32 of the Wheat Stripe Rust Pathogen f. sp.. <i>Frontiers in Plant Science</i> , 2018 , 9, 120	6.2	14
101	Acts as a Positive Regulator in Defense of Wheat Stripe-Rust Infection. <i>Frontiers in Plant Science</i> , 2018 , 9, 152	6.2	4
100	Silencing PsKPP4, a MAP kinase kinase kinase gene, reduces pathogenicity of the stripe rust fungus. <i>Molecular Plant Pathology</i> , 2018 , 19, 2590-2602	5.7	5
99	Wheat Gene Contributes to Stripe Rust Resistance. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	5
98	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	7	22
97	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	6	19
96	Candidate Effector Pst_8713 Impairs the Plant Immunity and Contributes to Virulence of f. sp.. <i>Frontiers in Plant Science</i> , 2018 , 9, 1294	6.2	22
95	A novel citrate synthase isoform contributes infection and stress resistance of the stripe rust fungus. <i>Environmental Microbiology</i> , 2018 , 20, 4037-4050	5.2	4
94	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	7	3
93	Role of the BUB3 protein in phragmoplast microtubule reorganization during cytokinesis. <i>Nature Plants</i> , 2018 , 4, 485-494	11.5	9
92	Basidiospores of <i>Puccinia striiformis</i> f. sp. tritici succeed to infect barberry, while Urediniospores are blocked by non-host resistance. <i>Protospasma</i> , 2017 , 254, 2237-2246	3.4	4
91	<i>Puccinia striiformis</i> f. sp. tritici microRNA-like RNA 1 (Pst-milR1), an important pathogenicity factor of Pst, impairs wheat resistance to Pst by suppressing the wheat pathogenesis-related 2 gene. <i>New Phytologist</i> , 2017 , 215, 338-350	9.8	84
90	Rapid identification of a major effect QTL conferring adult plant resistance to stripe rust in wheat cultivar Yaco. <i>Euphytica</i> , 2017 , 213, 1	2.1	4

89	Host-Induced Gene Silencing of the MAPKK Gene Confers Stable Resistance to Wheat Stripe Rust. <i>Plant Physiology</i> , 2017 , 175, 1853-1863	6.6	42
88	GTP-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	3.7	9
87	Overexpression of AtPAD4 in transgenic <i>Brachypodium distachyon</i> enhances resistance to <i>Puccinia brachypodii</i> . <i>Plant Biology</i> , 2017 , 19, 868-874	3.7	6
86	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	1.5	17
85	Variability of the Stripe Rust Pathogen 2017 , 35-154		14
84	A unique invertase is important for sugar absorption of an obligate biotrophic pathogen during infection. <i>New Phytologist</i> , 2017 , 215, 1548-1561	9.8	23
83	Basidiomycete-specific PsCaMKL1 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	5.2	4
82	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	2.1	1
81	PSTha5a23, 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	5.2	37
80	Is Involved in Wheat Defense against Stripe Rust Pathogen Mediated by. <i>Frontiers in Plant Science</i> , 2017 , 8, 156	6.2	13
79	TaDIR1-2, a Wheat Ortholog of Lipid Transfer Protein AtDIR1 Contributes to Negative Regulation of Wheat Resistance against f. sp.. <i>Frontiers in Plant Science</i> , 2017 , 8, 521	6.2	18
78	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	6.2	24
77	Identification of a Novel Strain Able to Hyperparasitize f. sp. , the Causal Agent of Wheat Stripe Rust. <i>Frontiers in Microbiology</i> , 2017 , 8, 71	5.7	12
76	Molecular Characterization of Novel Totivirus-Like Double-Stranded RNAs from f. sp. , the Causal Agent of Wheat Stripe Rust. <i>Frontiers in Microbiology</i> , 2017 , 8, 1960	5.7	9
75	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	1.7	4
74	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	3.4	4
73	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	1.5	39
72	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, 1853-1859	3.8	30

71	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	1.5	15
70	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	5.2	22
69	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	4.9	13
68	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	4.9	10
67	Role of Alternate Hosts in Epidemiology and Pathogen Variation of Cereal Rusts. <i>Annual Review of Phytopathology</i> , 2016 , 54, 207-28	10.8	67
66	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	4.6	9
65	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	5.2	9
64	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	2.1	3
63	Genome-wide A-to-I RNA editing in fungi independent of ADAR enzymes. <i>Genome Research</i> , 2016 , 26, 499-509	9.7	74
62	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	3.7	35
61	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	5.7	14
60	FgPrp4 Kinase Is Important for Spliceosome B-Complex Activation and Splicing Efficiency in <i>Fusarium graminearum</i> . <i>PLoS Genetics</i> , 2016 , 12, e1005973	6	20
59	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	6.2	10
58	TaTypA, a Ribosome-Binding GTPase Protein, Positively Regulates Wheat Resistance to the Stripe Rust Fungus. <i>Frontiers in Plant Science</i> , 2016 , 7, 873	6.2	9
57	Characterization and Genetic Analysis of Rice Mutant Exhibiting Compromised Non-host Resistance to f. sp. (). <i>Frontiers in Plant Science</i> , 2016 , 7, 1822	6.2	5
56	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	1.8	6
55	TaMDAR6 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, 262-77	4.6	11
54	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	3.6	30

53	Distribution and molecular variability of four tobacco viruses in China. <i>Virologica Sinica</i> , 2016 , 31, 525-527.	7.4	0
52	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	4.9	3
51	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	1.6	4
50	Isolation and characterisation of cDNA encoding a wheat heavy metal-associated isoprenylated protein involved in stress responses. <i>Plant Biology</i> , 2015 , 17, 1176-86	3.7	13
49	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, 7325-38	7	26
48	Characterization of protein kinase PsSRPKL, a novel pathogenicity factor in the wheat stripe rust fungus. <i>Environmental Microbiology</i> , 2015 , 17, 2601-17	5.2	32
47	Genome sequence of <i>Valsa</i> canker pathogens uncovers a potential adaptation of colonization of woody bark. <i>New Phytologist</i> , 2015 , 208, 1202-16	9.8	74
46	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	3.7	19
45	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	6.2	20
44	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	6.2	37
43	Endophytic <i>Bacillus subtilis</i> strain E1R-J is a promising biocontrol agent for wheat powdery mildew. <i>BioMed Research International</i> , 2015 , 2015, 462645	3	15
42	PsANT, the adenine nucleotide translocase of <i>Puccinia striiformis</i> , promotes cell death and fungal growth. <i>Scientific Reports</i> , 2015 , 5, 11241	4.9	13
41	Determination of the Role of <i>Berberis</i> spp. in Wheat Stem Rust in China. <i>Plant Disease</i> , 2015 , 99, 1113-1117	11.7	5
40	TaADF3, an Actin-Depolymerizing Factor, Negatively Modulates Wheat Resistance Against <i>Puccinia striiformis</i> . <i>Frontiers in Plant Science</i> , 2015 , 6, 1214	6.2	23
39	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	6.9	49
38	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	6	35
37	The stripe rust resistance gene Yr10 encodes an evolutionary-conserved and unique CC-NBS-LRR sequence in wheat. <i>Molecular Plant</i> , 2014 , 7, 1740-55	14.4	88
36	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	2.6	6

35	TaMDHAR4, a monodehydroascorbate reductase gene participates in the interactions between wheat and <i>Puccinia striiformis</i> f. sp. tritici. <i>Plant Physiology and Biochemistry</i> , 2014 , 76, 7-16	5.4	18
34	A novel fungal hyperparasite of <i>Puccinia striiformis</i> f. sp. tritici, the causal agent of wheat stripe rust. <i>PLoS ONE</i> , 2014 , 9, e111484	3.7	17
33	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	1.7	21
32	Proteomic analysis of rice nonhost resistance to <i>Puccinia striiformis</i> f. sp. tritici using two-dimensional electrophoresis. <i>International Journal of Molecular Sciences</i> , 2014 , 15, 21644-59	6.3	9
31	Wheat TaNPSN SNARE homologues are involved in vesicle-mediated resistance to stripe rust (<i>Puccinia striiformis</i> f. sp. tritici). <i>Journal of Experimental Botany</i> , 2014 , 65, 4807-20	7	25
30	Delimiting cryptic pathogen species causing apple Valsa canker with multilocus data. <i>Ecology and Evolution</i> , 2014 , 4, 1369-80	2.8	42
29	Construction and characterization of a bacterial artificial chromosome library for the hexaploid wheat line 92R137. <i>BioMed Research International</i> , 2014 , 2014, 845806	3	3
28	Transcriptome profiling to identify genes involved in pathogenicity of <i>Valsa mali</i> on apple tree. <i>Fungal Genetics and Biology</i> , 2014 , 68, 31-8	3.9	40
27	Population genetic diversity of <i>Puccinia striiformis</i> f. sp. tritici on different wheat varieties in Tianshui, Gansu Province. <i>World Journal of Microbiology and Biotechnology</i> , 2013 , 29, 173-81	4.4	5
26	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	2.1	4
25	TaEIL1, a wheat homologue of AtEIN3, acts as a negative regulator in the wheat-stripe rust fungus interaction. <i>Molecular Plant Pathology</i> , 2013 , 14, 728-39	5.7	21
24	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, 273-83	5.1	27
23	Identification of eighteen <i>Berberis</i> species as alternate hosts of <i>Puccinia striiformis</i> f. sp. tritici and virulence variation in the pathogen isolates from natural infection of barberry plants in China. <i>Phytopathology</i> , 2013 , 103, 927-34	3.8	92
22	High genome heterozygosity and endemic genetic recombination in the wheat stripe rust fungus. <i>Nature Communications</i> , 2013 , 4, 2673	17.4	148
21	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	3.7	10
20	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	1.5	18
19	Race Composition of <i>Puccinia striiformis</i> f. sp. tritici in Tibet, China. <i>Plant Disease</i> , 2012 , 96, 1615-1620	1.5	9
18	Genetic and Molecular Mapping of Stripe Rust Resistance Gene in Wheat-Psathyrostachys huashanica Translocation Line H9020-1-6-8-3. <i>Plant Disease</i> , 2012 , 96, 1482-1487	1.5	22

17	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. <i>Fungal Biology</i> , 2012 , 116, 643-53	2.8	18
16	TaMCA4, 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, 755-64	3.6	52
15	TaDAD2, 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	3.6	27
14	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	1.8	5
13	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
12	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	2.1	16
11	Determining the basis of nonhost resistance in rice to cereal rusts. <i>Euphytica</i> , 2011 , 179, 33-40	2.1	30
10	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	1.7	38
9	Histological and molecular studies of the non-host interaction between wheat and <i>Uromyces fabae</i> . <i>Planta</i> , 2011 , 234, 979-91	4.7	26
8	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	2.6	6
7	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	1.8	11
6	Development of Race-Specific SCAR Markers for Detection of Chinese Races CYR32 and CYR33 of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>Plant Disease</i> , 2010 , 94, 221-228	1.5	8
5	Identification of expressed genes during compatible interaction between stripe rust (<i>Puccinia striiformis</i>) and wheat using a cDNA library. <i>BMC Genomics</i> , 2009 , 10, 586	4.5	48
4	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	1.5	25
3	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	2.1	28
2	SSR and STS markers for wheat stripe rust resistance gene <i>Yr26</i> . <i>Euphytica</i> , 2008 , 159, 359-366	2.1	57
1	A candidate effector protein PstCFEM1 contributes to virulence of stripe rust fungus and impairs wheat immunity. <i>Stress Biology</i> , 1		0