Jun Guo

List of Publications by Year
in descending order

35 papers	1,433 citations	471509 17 h-index	361022 35 g-index
40 all docs	40 docs citations	40 times ranked	1342 citing authors

#	Article	IF	Citations
1	High genome heterozygosity and endemic genetic recombination in the wheat stripe rust fungus. Nature Communications, 2013, 4, 2673.	12.8	238
2	BES/BZR Transcription Factor TaBZR2 Positively Regulates Drought Responses by Activation of <i>TaGST1</i>. Plant Physiology, 2019, 180, 605-620.	4.8	151
3	Host-Induced Gene Silencing: A Powerful Strategy to Control Diseases of Wheat and Barley. International Journal of Molecular Sciences, 2019, 20, 206.	4.1	111
4	Stripe Rust Effector PstGSRE1 Disrupts Nuclear Localization of ROS-Promoting Transcription Factor TaLOL2 to Defeat ROS-Induced Defense in Wheat. Molecular Plant, 2019, 12, 1624-1638.	8.3	98
5	Hostâ€induced gene silencing of an important pathogenicity factor <i><scp>P</scp>s<scp>CPK</scp>1</i> in <i>Puccinia striiformis</i> f. sp. <i>tritici</i> enhances resistance of wheat to stripe rust. Plant Biotechnology Journal, 2018, 16, 797-807.	8.3	97
6	Host-Induced Gene Silencing of the MAPKK Gene <i>PsFUZ7</i> Confers Stable Resistance to Wheat Stripe Rust. Plant Physiology, 2017, 175, 1853-1863.	4.8	75
7	A stripe rust effector Pst18363 targets and stabilises TaNUDX23 that promotes stripe rust disease. New Phytologist, 2020, 225, 880-895.	7.3	60
8	Genome-Wide Analysis of the GRAS Gene Family and Functional Identification of GmGRAS37 in Drought and Salt Tolerance. Frontiers in Plant Science, 2020, 11, 604690.	3.6	52
9	The calcium sensor TaCBL4 and its interacting protein TaCIPK5 are required for wheat resistance to stripe rust fungus. Journal of Experimental Botany, 2018, 69, 4443-4457.	4.8	49
10	TaARPC3, Contributes to Wheat Resistance against the Stripe Rust Fungus. Frontiers in Plant Science, 2017, 8, 1245.	3.6	46
11	Genome-Wide Identification of Cyclic Nucleotide-Gated Ion Channel Gene Family in Wheat and Functional Analyses of TaCNGC14 and TaCNGC16. Frontiers in Plant Science, 2018, 9, 18.	3.6	44
12	Molecular Characterization of a Fus3/Kss1 Type MAPK from Puccinia striiformis f. sp. tritici, PsMAPK1. PLoS ONE, 2011, 6, e21895.	2.5	41
13	Wheat hypersensitive-induced reaction genes TaHIR1 and TaHIR3 are involved in response to stripe rust fungus infection and abiotic stresses. Plant Cell Reports, 2013, 32, 273-283.	5.6	40
14	TaCIPK10 interacts with and phosphorylates TaNH2 to activate wheat defense responses to stripe rust. Plant Biotechnology Journal, 2019, 17, 956-968.	8.3	40
15	Wheat zinc finger protein TaLSD1, a negative regulator of programmed cell death, is involved in wheat resistance against stripe rust fungus. Plant Physiology and Biochemistry, 2013, 71, 164-172.	5.8	33
16	A Novel Fungal Hyperparasite of Puccinia striiformis f. sp. tritici, the Causal Agent of Wheat Stripe Rust. PLoS ONE, 2014, 9, e111484.	2.5	29
17	TaDIR1-2, a Wheat Ortholog of Lipid Transfer Protein AtDIR1 Contributes to Negative Regulation of Wheat Resistance against Puccinia striiformis f. sp. tritici. Frontiers in Plant Science, 2017, 8, 521.	3.6	29
18	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

#	Article	IF	Citations
19	Host-Induced Silencing of Fusarium graminearum Genes Enhances the Resistance of Brachypodium distachyon to Fusarium Head Blight. Frontiers in Plant Science, 2019, 10, 1362.	3.6	19
20	TaAP2-15, An AP2/ERF Transcription Factor, Is Positively Involved in Wheat Resistance to Puccinia striiformis f. sp. tritici. International Journal of Molecular Sciences, 2021, 22, 2080.	4.1	19
21	Genome-Wide Analysis of the DUF4228 Family in Soybean and Functional Identification of GmDUF4228â€“70 in Response to Drought and Salt Stresses. Frontiers in Plant Science, 2021, 12, 628299.	3.6	19
22	The transcription factor <i>PstSTE12</i> is required for virulence of <i>Puccinia striiformis</i> f. sp. <i>tritici</i>. Molecular Plant Pathology, 2018, 19, 961-974.	4.2	18
23	RNAiâ€mediated stable silencing of <i>TaCSN5</i> confers broadâ€spectrum resistance to <i>Puccinia striiformis</i> f. sp. <i>tritici</i>. Molecular Plant Pathology, 2021, 22, 410-421.	4.2	14
24	A serine-rich effector from the stripe rust pathogen targets a Raf-like kinase to suppress host immunity. Plant Physiology, 2022, 190, 762-778.	4.8	13
25	TaTypA, a Ribosome-Binding GTPase Protein, Positively Regulates Wheat Resistance to the Stripe Rust Fungus. Frontiers in Plant Science, 2016, 7, 873.	3.6	12
26	A novel MADSâ€box transcription factor <i>PstMCM1â€1</i> is responsible for full virulence of <i>Puccinia striiformis</i> f. sp. <i>tritici</i>. Environmental Microbiology, 2018, 20, 1452-1463.	3.8	12
27	Silencing <i>PsKPP4</i>, a MAP kinase kinase kinase gene, reduces pathogenicity of the stripe rust fungus. Molecular Plant Pathology, 2018, 19, 2590-2602.	4.2	8
28	Genome-Wide Analysis of the C2 Domain Family in Soybean and Identification of a Putative Abiotic Stress Response Gene GmC2-148. Frontiers in Plant Science, 2021, 12, 620544.	3.6	8
29	Basidiospores of Puccinia striiformis f. sp. tritici succeed to infect barberry, while Urediniospores are blocked by non-host resistance. Protoplasma, 2017, 254, 2237-2246.	2.1	7
30	Basidiomyceteâ€specific <i>PsCaMKL1</i> encoding a CaMKâ€like protein kinase is required for full virulence of <i>Puccinia striiformis</i> f. sp. <i>tritici</i>. Environmental Microbiology, 2017, 19, 4177-4189.	3.8	7
31	TaYS1A, a Yellow Stripe-Like Transporter Gene, Is Required for Wheat Resistance to Puccinia striiformis f. sp. Tritici. Genes, 2020, 11, 1452.	2.4	7
32	Corrigendum to: The calcium sensor TaCBL4 and its interacting protein TaCIPK5 are required for wheat resistance to stripe rust fungus. Journal of Experimental Botany, 2018, 69, 5309-5309.	4.8	5
33	TaClpS1, negatively regulates wheat resistance against Puccinia striiformis f. sp. tritici. BMC Plant Biology, 2020, 20, 555.	3.6	5
34	A candidate effector protein PstCFEM1 contributes to virulence of stripe rust fungus and impairs wheat immunity. Stress Biology, 2022, 2, 1.	3.1	5
35	A conidiation-related gene is highly expressed at the resting urediospore stage inPuccinia striiformisf. sp.tritici. Journal of Basic Microbiology, 2013, 53, 695-702.	3.3	1