

Shaobin Zhong

List of Publications by Year in descending order

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Version: 2024-02-01

75
papers

3,398
citations

236925

25
h-index

155660

55
g-index

75
all docs

75
docs citations

75
times ranked

3873
citing authors

#	ARTICLE	IF	CITATIONS
1	A conserved hypothetical gene is required but not sufficient for <i>Ptr</i> ToxC production in <i>Pyrenophora tritici-repentis</i> . <i>Molecular Plant-Microbe Interactions</i> , 2022, , .	2.6	11
2	Genomic compatibility and inheritance of hexaploidâ€derived <i>Fusarium</i> head blight resistance genes in durum wheat. <i>Plant Genome</i> , 2022, , e20183.	2.8	1
3	Genome Sequence Resources for the Maize Pathogen <i>Fusarium temperatum</i> Isolated in Poland. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 214-217.	2.6	2
4	A lossâ€ofâ€function of the dirigent gene <i>TaDIR1</i> improves resistance to <i>Fusarium</i> crown rot in wheat. <i>Plant Biotechnology Journal</i> , 2021, 19, 866-868.	8.3	28
5	Identification of Fungal Species Associated with Crown and Root Rots of Wheat and Evaluation of Plant Reactions to the Pathogens in North Dakota. <i>Plant Disease</i> , 2021, 105, 3564-3572.	1.4	8
6	Function and evolution of allelic variations of <i>Sr13</i> conferring resistance to stem rust in tetraploid wheat (<i>Triticum turgidum</i> L.). <i>Plant Journal</i> , 2021, 106, 1674-1691.	5.7	15
7	A genome-wide genetic linkage map and reference quality genome sequence for a new race in the wheat pathogen <i>Pyrenophora tritici-repentis</i> . <i>Fungal Genetics and Biology</i> , 2021, 152, 103571.	2.1	8
8	First Report of <i>Fusarium equiseti</i> Causing Seedling Death on Sugar Beet in Minnesota, U.S.A.. <i>Plant Disease</i> , 2021, 105, 2017.	1.4	5
9	Molecular Mapping of Quantitative Trait Loci for <i>Fusarium</i> Head Blight Resistance in the Brazilian Spring Wheat Cultivar <i>Surpresa</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 778472.	3.6	3
10	Molecular Mapping of Loci Conferring Susceptibility to Spot Blotch and Resistance to Powdery Mildew in Barley Using the Sequencing-Based Genotyping Approach. <i>Phytopathology</i> , 2020, 110, 440-446.	2.2	11
11	First Report of <i>Alternaria</i> Leaf Spot Caused by <i>Alternaria tenuissima</i> on Sugar Beet (<i>Beta</i>) Tj ETQq1 1 0.784314 rgBT /Overlo	1.4	6
12	Clove oil-in-water nanoemulsion: Mitigates growth of <i>Fusarium graminearum</i> and trichothecene mycotoxin production during the malting of <i>Fusarium</i> infected barley. <i>Food Chemistry</i> , 2020, 312, 126120.	8.2	29
13	Genetic Mapping and Prediction Analysis of FHB Resistance in a Hard Red Spring Wheat Breeding Population. <i>Frontiers in Plant Science</i> , 2019, 10, 1007.	3.6	24
14	Enhancement of antifungal and mycotoxin inhibitory activities of food-grade thyme oil nanoemulsions with natural emulsifiers. <i>Food Control</i> , 2019, 106, 106709.	5.5	48
15	Influence of nonionic and ionic surfactants on the antifungal and mycotoxin inhibitory efficacy of cinnamon oil nanoemulsions. <i>Food and Function</i> , 2019, 10, 2817-2827.	4.6	34
16	Physical properties, antifungal and mycotoxin inhibitory activities of five essential oil nanoemulsions: Impact of oil compositions and processing parameters. <i>Food Chemistry</i> , 2019, 291, 199-206.	8.2	123
17	Effect of chitosan coatings on physical stability, antifungal and mycotoxin inhibitory activities of lecithin stabilized cinnamon oil-in-water emulsions. <i>LWT - Food Science and Technology</i> , 2019, 106, 98-104.	5.2	32
18	Fine mapping of a dominant gene conferring resistance to spot blotch caused by a new pathotype of <i>Bipolaris sorokiniana</i> in barley. <i>Theoretical and Applied Genetics</i> , 2019, 132, 41-51.	3.6	11

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19	The gene conferring susceptibility to spot blotch caused by <i>Cochliobolus sativus</i> is located at the Mla locus in barley cultivar Bowman. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1531-1539.	3.6	21
20	Influence of oil phase composition on the antifungal and mycotoxin inhibitory activity of clove oil nanoemulsions. <i>Food and Function</i> , 2018, 9, 2872-2882.	4.6	51
21	Molecular Mapping of Fusarium Head Blight Resistance in the Spring Wheat Line ND2710. <i>Phytopathology</i> , 2018, 108, 972-979.	2.2	32
22	Population structure, genetic diversity, and sexual state of the rice brown spot pathogen <i>Bipolaris oryzae</i> from three Asian countries. <i>Plant Pathology</i> , 2018, 67, 181-192.	2.4	26
23	Genetic Diversity and Resistance to Fusarium Head Blight in Synthetic Hexaploid Wheat Derived From <i>Aegilops tauschii</i> and Diverse <i>Triticum turgidum</i> Subspecies. <i>Frontiers in Plant Science</i> , 2018, 9, 1829.	3.6	20
24	Chitosan coatings on lecithin stabilized emulsions inhibit mycotoxin production by Fusarium pathogens. <i>Food Control</i> , 2018, 92, 276-285.	5.5	13
25	Molecular mapping of QTL for Fusarium head blight resistance introgressed into durum wheat. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1939-1951.	3.6	57
26	Genome-wide association mapping of spot blotch resistance to three different pathotypes of <i>Cochliobolus sativus</i> in the USDA barley core collection. <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	17
27	Effects of D Genome Chromosomes and Their A/B Genome Homoeologs on Fusarium Head Blight Resistance in Durum Wheat. <i>Crop Science</i> , 2016, 56, 1049-1058.	1.8	8
28	Sources and Genetics of Spot Blotch Resistance to a New Pathotype of <i>Cochliobolus sativus</i> in the USDA National Small Grains Collection. <i>Plant Disease</i> , 2016, 100, 1988-1993.	1.4	33
29	Coordinated and independent functions of velvet-complex genes in fungal development and virulence of the fungal cereal pathogen <i>Cochliobolus sativus</i> . <i>Fungal Biology</i> , 2016, 120, 948-960.	2.5	25
30	Elgin™ Spring Wheat: A Newly Adapted Cultivar to the North-Central Plains of the United States with High Agronomic and Quality Performance. <i>Journal of Plant Registrations</i> , 2016, 10, 130-134.	0.5	4
31	Toward a better understanding of the genomic region harboring Fusarium head blight resistance QTL Qfhs.ndsu-3AS in durum wheat. <i>Theoretical and Applied Genetics</i> , 2016, 129, 31-43.	3.6	24
32	RNA-Seq Revealed Differences in Transcriptomes between 3ADON and 15ADON Populations of <i>Fusarium graminearum</i> In Vitro and In Planta. <i>PLoS ONE</i> , 2016, 11, e0163803.	2.5	25
33	Prevalence of inversion positive and inversion negative mating type (MAT) alleles and MAT heterokaryons in <i>Sclerotinia sclerotiorum</i> in the United States. <i>Botany</i> , 2015, 93, 497-505.	1.0	3
34	The regulatory gene VosA affects conidiogenesis and is involved in virulence of the fungal cereal pathogen <i>Cochliobolus sativus</i> . <i>Fungal Biology</i> , 2015, 119, 884-900.	2.5	13
35	Identification and mapping of Sr46 from <i>Aegilops tauschii</i> accession Clae 25 conferring resistance to race TTKSK (Ug99) of wheat stem rust pathogen. <i>Theoretical and Applied Genetics</i> , 2015, 128, 431-443.	3.6	33
36	Development of a diagnostic co-dominant marker for stem rust resistance gene Sr47 introgressed from <i>Aegilops speltoides</i> into durum wheat. <i>Theoretical and Applied Genetics</i> , 2015, 128, 2367-2374.	3.6	5

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37	<i>Brachypodium distachyon</i> – <i>Cochliobolus sativus</i> Pathosystem is a New Model for Studying Plant–Fungal Interactions in Cereal Crops. <i>Phytopathology</i> , 2015, 105, 482-489.	2.2	13
38	The Role of Mitogen-Activated Protein (MAP) Kinase Signaling Components in the Fungal Development, Stress Response and Virulence of the Fungal Cereal Pathogen <i>Bipolaris sorokiniana</i> . <i>PLoS ONE</i> , 2015, 10, e0128291.	2.5	35
39	Characterization of <i>Thinopyrum</i> Species for Wheat Stem Rust Resistance and Ploidy Level. <i>Crop Science</i> , 2014, 54, 2663-2672.	1.8	12
40	Identification and molecular mapping of quantitative trait loci for Fusarium head blight resistance in emmer and durum wheat using a single nucleotide polymorphism-based linkage map. <i>Molecular Breeding</i> , 2014, 34, 1677-1687.	2.1	55
41	Functional characterization of the gene FoOCH1 encoding a putative Î±-1,6-mannosyltransferase in <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> . <i>Fungal Genetics and Biology</i> , 2014, 65, 1-13.	2.1	40
42	Construction of genetic linkage maps and QTL mapping for X-disease resistance in tetraploid chokecherry (<i>Prunus virginiana</i> L.) using SSR and AFLP markers. <i>Molecular Breeding</i> , 2014, 34, 143-157.	2.1	7
43	Genetic analysis and molecular mapping of crown rust resistance in common wheat. <i>Theoretical and Applied Genetics</i> , 2014, 127, 609-619.	3.6	9
44	“Velva”™ Spring Wheat: An Adapted Cultivar to North-Central Plains of the United States with High Agronomic and Quality Performance. <i>Journal of Plant Registrations</i> , 2014, 8, 32-37.	0.5	5
45	Identification and characterization of <i>Pestalotiopsis</i> spp. causing twig blight disease of bayberry (<i>Myrica rubra</i> Sieb. & Zucc) in China. <i>European Journal of Plant Pathology</i> , 2013, 137, 451-461.	1.7	20
46	Comparative Genome Structure, Secondary Metabolite, and Effector Coding Capacity across <i>Cochliobolus</i> Pathogens. <i>PLoS Genetics</i> , 2013, 9, e1003233.	3.5	232
47	Identification and application of a unique genetic locus in diagnosis of <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> tropical race 4. <i>Canadian Journal of Plant Pathology</i> , 2013, 35, 482-493.	1.4	21
48	“Prosper”™: A High-Yielding Hard Red Spring Wheat Cultivar Adapted to the North Central Plains of the USA. <i>Journal of Plant Registrations</i> , 2013, 7, 75-80.	0.5	18
49	Diverse Lifestyles and Strategies of Plant Pathogenesis Encoded in the Genomes of Eighteen Dothideomycetes Fungi. <i>PLoS Pathogens</i> , 2012, 8, e1003037.	4.7	595
50	Tetraploid Tunisian Wheat Germplasm as a New Source of Fusarium Head Blight Resistance. <i>Crop Science</i> , 2012, 52, 136-145.	1.8	43
51	Genetic structure of <i>Cochliobolus sativus</i> populations sampled from roots and leaves of barley and wheat in North and South Dakota. <i>Journal of Phytopathology</i> , 2012, 160, 637-646.	1.0	6
52	Development and cross-species/genera transferability of microsatellite markers discovered using 454 genome sequencing in chokecherry (<i>Prunus virginiana</i> L.). <i>Plant Cell Reports</i> , 2012, 31, 2047-2055.	5.6	25
53	AFLP, Pathogenicity, and VCG Analyses of <i>Fusarium oxysporum</i> and <i>Fusarium pseudocircinatum</i> from <i>Acacia koa</i> . <i>Plant Disease</i> , 2012, 96, 1111-1117.	1.4	13
54	Construction of Hairpin RNA-Expressing Vectors for RNA-Mediated Gene Silencing in Fungi. <i>Methods in Molecular Biology</i> , 2012, 835, 623-633.	0.9	6

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55	Sfpâ€type 4â€phosphopantetheinyl transferase is required for lysine synthesis, tolerance to oxidative stress and virulence in the plant pathogenic fungus <i>Cochliobolus sativus</i>. <i>Molecular Plant Pathology</i> , 2012, 13, 375-387.	4.2	49
56	Obligate biotrophy features unraveled by the genomic analysis of rust fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9166-9171.	7.1	640
57	RNAâ€mediated gene silencing in the cereal fungal pathogen <i>Cochliobolus sativus</i>. <i>Molecular Plant Pathology</i> , 2011, 12, 289-298.	4.2	25
58	Characterization of <i>Puccinia psidii</i> isolates in Hawaii using microsatellite DNA markers. <i>Journal of General Plant Pathology</i> , 2011, 77, 178-181.	1.0	15
59	Identification and molecular mapping of two QTLs with major effects for resistance to Fusarium head blight in wheat. <i>Theoretical and Applied Genetics</i> , 2011, 123, 1107-1119.	3.6	65
60	Molecular characterization of <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> race 1 and 4 isolates from Taiwan and Southern China. <i>Canadian Journal of Plant Pathology</i> , 2011, 33, 168-178.	1.4	19
61	The 3ADON Population of <i>Fusarium graminearum</i> Found in North Dakota Is More Aggressive and Produces a Higher Level of DON than the Prevalent 15ADON Population in Spring Wheat. <i>Phytopathology</i> , 2010, 100, 1007-1014.	2.2	152
62	Molecular and Cytogenetic Characterization of Wheat Introgression Lines Carrying the Stem Rust Resistance Gene Sr39. <i>Crop Science</i> , 2010, 50, 1393-1400.	1.8	14
63	Transcription, Translation, and the Evolution of Specialists and Generalists. <i>Molecular Biology and Evolution</i> , 2009, 26, 2661-2678.	8.9	20
64	Reactions of hard red spring wheat to common root rot under field conditions of Northern United States of America. <i>Euphytica</i> , 2009, 167, 165-172.	1.2	9
65	Development and Characterization of Expressed Sequence Tag-Derived Microsatellite Markers for the Wheat Stem Rust Fungus <i>Puccinia graminis</i> f. sp. <i>tritici</i>. <i>Phytopathology</i> , 2009, 99, 282-289.	2.2	45
66	PERMANENT GENETIC RESOURCES: Development of microsatellite markers for the guava rust fungus, <i>Puccinia psidii</i>. <i>Molecular Ecology Resources</i> , 2008, 8, 348-350.	4.8	23
67	Analysis of Expressed Sequence Tags from the Fungal Banana Pathogen <i>Mycosphaerella fijiensis</i> . <i>The Open Mycology Journal</i> , 2008, 2, 61-73.	0.8	11
68	Molecular karyotyping and chromosome length polymorphism in <i>Cochliobolus sativus</i> . <i>Mycological Research</i> , 2007, 111, 78-86.	2.5	12
69	Molecular Mapping and Marker-Assisted Selection of Genes for Septoria Speckled Leaf Blotch Resistance in Barley. <i>Phytopathology</i> , 2006, 96, 993-999.	2.2	32
70	Evolutionary genomics of ecological specialization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 11719-11724.	7.1	86
71	Molecular Mapping of the Leaf Rust Resistance Gene Rph6 in Barley and Its Linkage Relationships with Rph5 and Rph7. <i>Phytopathology</i> , 2003, 93, 604-609.	2.2	32
72	A Molecular Genetic Map and Electrophoretic Karyotype of the Plant Pathogenic Fungus <i>Cochliobolus sativus</i> . <i>Molecular Plant-Microbe Interactions</i> , 2002, 15, 481-492.	2.6	64

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73	Genetic and molecular characterization of mating type genes in <i>Cochliobolus sativus</i> . <i>Mycologia</i> , 2001, 93, 852-863.	1.9	18
74	Virulence and Molecular Diversity in <i>Cochliobolus sativus</i> . <i>Phytopathology</i> , 2001, 91, 469-476.	2.2	91
75	Genetic and Molecular Characterization of Mating Type Genes in <i>Cochliobolus sativus</i> . <i>Mycologia</i> , 2001, 93, 852.	1.9	12