Kar-Chun Tan

List of Publications by Year
in descending order

50 papers	2,462 citations	186265 28 h-index	214800 47 g-index
57 all docs	57 docs citations	57 times ranked	2218 citing authors

#	Article	IF	Citations
1	Variability in an effector gene promoter of a necrotrophic fungal pathogen dictates epistasis and effector-triggered susceptibility in wheat. PLoS Pathogens, 2022, 18, e1010149.	4.7	9
2	Transcription factor lineages in plant-pathogenic fungi, connecting diversity with fungal virulence. Fungal Genetics and Biology, 2022, 161, 103712.	2.1	4
3	Septoria Nodorum Blotch of Wheat: Disease Management and Resistance Breeding in the Face of Shifting Disease Dynamics and a Changing Environment. Phytopathology, 2021, 111, 906-920.	2.2	24
4	Identification and cross-validation of genetic loci conferring resistance to Septoria nodorum blotch using a German multi-founder winter wheat population. Theoretical and Applied Genetics, 2021, 134, 125-142.	3.6	11
5	Hidden in plain sight: a molecular field survey of three wheat leaf blotch fungal diseases in North-Western Europe shows co-infection is widespread. European Journal of Plant Pathology, 2021, 160, 949-962.	1.7	9
6	Transcription factor control of virulence in phytopathogenic fungi. Molecular Plant Pathology, 2021, 22, 858-881.	4.2	50
7	GWAS analysis reveals distinct pathogenicity profiles of Australian Parastagonospora nodorum isolates and identification of marker-trait-associations to septoria nodorum blotch. Scientific Reports, 2021, 11, 10085.	3.3	7
8	An optimized sporulation method for the wheat fungal pathogen Pyrenophora tritici-repentis. Plant Methods, 2021, 17, 52.	4.3	2
9	Chromosome-level genome assembly and manually-curated proteome of model necrotroph Parastagonospora nodorum Sn15 reveals a genome-wide trove of candidate effector homologs, and redundancy of virulence-related functions within an accessory chromosome. BMC Genomics, 2021, 22, 382.	2.8	12
10	Gene Validation and Remodelling Using Proteogenomics of Phytophthora cinnamomi, the Causal Agent of Dieback. Frontiers in Microbiology, 2021, 12, 665396.	3.5	3
11	Genetic mapping using a wheat multi-founder population reveals a locus on chromosome 2A controlling resistance to both leaf and glume blotch caused by the necrotrophic fungal pathogen Parastagonospora nodorum. Theoretical and Applied Genetics, 2020, 133, 785-808.	3.6	48
12	A specific fungal transcription factor controls effector gene expression and orchestrates the establishment of the necrotrophic pathogen lifestyle on wheat. Scientific Reports, 2019, 9, 15884.	3.3	34
13	Genomeâ€Wide Association Mapping of Resistance to Septoria Nodorum Leaf Blotch in a Nordic Spring Wheat Collection. Plant Genome, 2019, 12, 180105.	2.8	22
14	Low Amplitude Boom-and-Bust Cycles Define the Septoria Nodorum Blotch Interaction. Frontiers in Plant Science, 2019, 10, 1785.	3.6	16
15	Novel sources of resistance to Septoria nodorum blotch in the Vavilov wheat collection identified by genome-wide association studies. Theoretical and Applied Genetics, 2018, 131, 1223-1238.	3.6	53
16	Accessories Make the Outfit: Accessory Chromosomes and Other Dispensable DNA Regions in Plant-Pathogenic Fungi. Molecular Plant-Microbe Interactions, 2018, 31, 779-788.	2.6	93
17	Vavilov wheat accessions provide useful sources of resistance to tan spot (syn. yellow spot) of wheat. Plant Pathology, 2018, 67, 1076-1087.	2.4	15
18	Pan-Parastagonospora Comparative Genome Analysisâ€"Effector Prediction and Genome Evolution. Genome Biology and Evolution, 2018, 10, 2443-2457.	2.5	43

#	ARTICLE	IF	CITATIONS
19	Assessing European Wheat Sensitivities to Parastagonospora nodorum Necrotrophic Effectors and Fine-Mapping the Snn3-B1 Locus Conferring Sensitivity to the Effector SnTox3. Frontiers in Plant Science, 2018, 9, 881.	3.6	48
20	Analysis of Reproducibility of Proteome Coverage and Quantitation Using Isobaric Mass Tags (iTRAQ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	3.7	28
21	A functionally conserved Zn₂Cys₆ binuclear cluster transcription factor class regulates necrotrophic effector gene expression and hostâ€specific virulence of two major Pleosporales fungal pathogens of wheat. Molecular Plant Pathology, 2017, 18, 420-434.	4.2	69
22	Regulation of proteinaceous effector expression in phytopathogenic fungi. PLoS Pathogens, 2017, 13, e1006241.	4.7	75
23	Necrotrophic Pathogens of Wheat. , 2016, , 273-278.		11
24	Comprehensive Annotation of the Parastagonospora nodorum Reference Genome Using Next-Generation Genomics, Transcriptomics and Proteogenomics. PLoS ONE, 2016, 11, e0147221.	2.5	47
25	Differential effector gene expression underpins epistasis in a plant fungal disease. Plant Journal, 2016, 87, 343-354.	5.7	75
26	Dissecting the role of histidine kinase and HOG1 mitogen-activated protein kinase signalling in stress tolerance and pathogenicity of Parastagonospora nodorum on wheat. Microbiology (United) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 457 T	1.8	9
27	Functional redundancy of necrotrophic effectors â€" consequences for exploitation for breeding. Frontiers in Plant Science, 2015, 6, 501.	3.6	33
28	Fine-Mapping the Wheat <i>Snn1</i> Locus Conferring Sensitivity to the <i>Parastagonospora nodorum</i> Necrotrophic Effector SnTox1 Using an Eight Founder Multiparent Advanced Generation Inter-Cross Population. G3: Genes, Genomes, Genetics, 2015, 5, 2257-2266.	1.8	38
29	Development of genetic <scp>SSR</scp> markers in <i>Blumeria graminis</i> f. sp. <i>hordei</i> and application to isolates from Australia. Plant Pathology, 2015, 64, 337-343.	2.4	16
30	Sensitivity to three Parastagonospora nodorum necrotrophic effectors in current Australian wheat cultivars and the presence of further fungal effectors. Crop and Pasture Science, 2014, 65, 150.	1.5	37
31	Absence of detectable yield penalty associated with insensitivity to <scp>P</scp>leosporales necrotrophic effectors in wheat grown in the <scp>W</scp>est <scp>A</scp>ustralian wheat belt. Plant Pathology, 2014, 63, 1027-1032.	2.4	20
32	12 Metabolomics and Proteomics to Dissect Fungal Phytopathogenicity. , 2014, , 301-319.		1
33	Proteomic Techniques for Plantâ€"Fungal Interactions. Methods in Molecular Biology, 2012, 835, 75-96.	0.9	4
34	Quantitative Variation in Effector Activity of ToxA Isoforms from <i>Stagonospora nodorum</i> and <i>Pyrenophora tritici-repentis</i>. Molecular Plant-Microbe Interactions, 2012, 25, 515-522.	2.6	70
35	Quantitative proteomic analysis of Gâ€protein signalling in <i>Stagonospora nodorum</i> using isobaric tags for relative and absolute quantification. Proteomics, 2010, 10, 38-47.	2.2	25
36	The Transcription Factor StuA Regulates Central Carbon Metabolism, Mycotoxin Production, and Effector Gene Expression in the Wheat Pathogen Stagonospora nodorum. Eukaryotic Cell, 2010, 9, 1100-1108.	3.4	63

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37	Proteinaceous necrotrophic effectors in fungal virulence. Functional Plant Biology, 2010, 37, 907.	2.1	80
38	SnTox3 Acts in Effector Triggered Susceptibility to Induce Disease on Wheat Carrying the Snn3 Gene. PLoS Pathogens, 2009, 5, e1000581.	4.7	175
39	Proteomic identification of extracellular proteins regulated by the Gna1 GÎ± subunit in Stagonospora nodorum. Mycological Research, 2009, 113, 523-531.	2.5	24
40	Deep proteogenomics; high throughput gene validation by multidimensional liquid chromatography and mass spectrometry of proteins from the fungal wheat pathogen Stagonospora nodorum. BMC Bioinformatics, 2009, 10, 301.	2.6	33
41	Metabolite profiling identifies the mycotoxin alternariol in the pathogen Stagonospora nodorum. Metabolomics, 2009, 5, 330-335.	3.0	48
42	Assessing the impact of transcriptomics, proteomics and metabolomics on fungal phytopathology. Molecular Plant Pathology, 2009, 10, 703-715.	4.2	121
43	A Signaling-Regulated, Short-Chain Dehydrogenase of <i>Stagonospora nodorum</i> Regulates Asexual Development. Eukaryotic Cell, 2008, 7, 1916-1929.	3.4	45
44	A quantitative PCR approach to determine gene copy number. Fungal Genetics Reports, 2008, 55, 5-8.	0.6	53
45	Dothideomyceteâ€"Plant Interactions Illuminated by Genome Sequencing and EST Analysis of the Wheat Pathogen <i>Stagonospora nodorum</i>. Plant Cell, 2007, 19, 3347-3368.	6.6	235
46	Stagonospora nodorum: cause of stagonospora nodorum blotch of wheat. Molecular Plant Pathology, 2006, 7, 147-156.	4.2	153
47	Mannitol 1-Phosphate Metabolism Is Required for Sporulation in Planta of the Wheat Pathogen Stagonospora nodorum. Molecular Plant-Microbe Interactions, 2005, 18, 110-115.	2.6	53
48	Spatial and temporal coordination of expression of immune response genes during Pseudomonas infection of horseshoe crab, Carcinoscorpius rotundicauda. Genes and Immunity, 2005, 6, 557-574.	4.1	34
49	The Disruption of a GÎ± Subunit Sheds New Light on the Pathogenicity of Stagonospora nodorum on Wheat. Molecular Plant-Microbe Interactions, 2004, 17, 456-466.	2.6	83
50	The nutrient supply of pathogenic fungi; a fertile field for study. Molecular Plant Pathology, 2003, 4, 203-210.	4.2	195