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List of Publications by Year in descending order

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8,246
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94433

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times ranked

7557
citing authors

#	ARTICLE	IF	CITATIONS
1	Speed dating for enzymes! Finding the perfect phosphopantetheinyl transferase partner for your polyketide synthase. <i>Microbial Cell Factories</i> , 2022, 21, 9.	4.0	2
2	Transcriptome analysis reveals infection strategies employed by <i>Fusarium graminearum</i> as a root pathogen. <i>Microbiological Research</i> , 2022, 256, 126951.	5.3	7
3	Phylogenomic Analysis of a 55.1-kb 19-Gene Dataset Resolves a Monophyletic <i>Fusarium</i> that Includes the <i>Fusarium solani</i> Species Complex. <i>Phytopathology</i> , 2021, 111, 1064-1079.	2.2	107
4	Map-based cloning identifies velvet A as a critical component of virulence in <i>Fusarium pseudograminearum</i> during infection of wheat heads. <i>Fungal Biology</i> , 2021, 125, 191-200.	2.5	5
5	Identification of Putative Virulence Genes by DNA Methylation Studies in the Cereal Pathogen <i>Fusarium graminearum</i> . <i>Cells</i> , 2021, 10, 1192.	4.1	4
6	A conserved Zn2Cys6 transcription factor, identified in a spontaneous mutant from <i>in vitro</i> passaging, is involved in pathogenicity of the blackleg fungus <i>Leptosphaeria maculans</i> . <i>Fungal Biology</i> , 2021, 125, 541-550.	2.5	2
7	Adaptive defence and sensing responses of host plant roots to fungal pathogen attack revealed by transcriptome and metabolome analyses. <i>Plant, Cell and Environment</i> , 2021, 44, 3756-3774.	5.7	10
8	A method for high-throughput image-based antifungal screening. <i>Journal of Microbiological Methods</i> , 2021, 190, 106342.	1.6	2
9	Role of the XylA gene, encoding a cell wall degrading enzyme, during common wheat, durum wheat and barley colonization by <i>Fusarium graminearum</i> . <i>Fungal Genetics and Biology</i> , 2020, 136, 103318.	2.1	9
10	Fusaristatin A production negatively affects the growth and aggressiveness of the wheat pathogen <i>Fusarium pseudograminearum</i> . <i>Fungal Genetics and Biology</i> , 2020, 136, 103314.	2.1	6
11	Fungicides may have differential efficacies towards the main causal agents of <i>Fusarium</i> head blight of wheat. <i>Pest Management Science</i> , 2020, 76, 3738-3748.	3.4	31
12	Regulators of nitric oxide signaling triggered by host perception in a plant pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11147-11157.	7.1	31
13	Ribosome profiling in plants: what is not lost in translation?. <i>Journal of Experimental Botany</i> , 2020, 71, 5323-5332.	4.8	21
14	Can natural gene drives be part of future fungal pathogen control strategies in plants?. <i>New Phytologist</i> , 2020, 228, 1431-1439.	7.3	26
15	Gene technologies in weed management: a technical feasibility analysis. <i>Current Opinion in Insect Science</i> , 2020, 38, 6-14.	4.4	9
16	Heterologous expression of intact biosynthetic gene clusters in <i>Fusarium graminearum</i> . <i>Fungal Genetics and Biology</i> , 2019, 132, 103248.	2.1	15
17	Gene drives in plants: opportunities and challenges for weed control and engineered resilience. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20191515.	2.6	36
18	Comparative analysis of genetic structures and aggressiveness of <i>Fusarium pseudograminearum</i> populations from two surveys undertaken in 2008 and 2015 at two sites in the wheat belt of Western Australia. <i>Plant Pathology</i> , 2019, 68, 1337-1349.	2.4	6

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19	Nanoscale enrichment of the cytosolic enzyme trichodiene synthase near reorganized endoplasmic reticulum in <i>Fusarium graminearum</i> . <i>Fungal Genetics and Biology</i> , 2019, 124, 73-77.	2.1	11
20	Regulation of a novel <i>Fusarium</i> cytokinin in <i>Fusarium pseudograminearum</i> . <i>Fungal Biology</i> , 2019, 123, 255-266.	2.5	9
21	There it is! <i>Fusarium pseudograminearum</i> did not lose the fusaristatin gene cluster after all. <i>Fungal Biology</i> , 2019, 123, 10-17.	2.5	12
22	Improved prediction of fungal effector proteins from secretomes with EffectorP 2.0. <i>Molecular Plant Pathology</i> , 2018, 19, 2094-2110.	4.2	350
23	Development of three <i>Fusarium</i> crown rot causal agents and systemic translocation of deoxynivalenol following stem base infection of soft wheat. <i>Plant Pathology</i> , 2018, 67, 1055-1065.	2.4	16
24	Transcriptomics of cereal- <i>Fusarium graminearum</i> interactions: what we have learned so far. <i>Molecular Plant Pathology</i> , 2018, 19, 764-778.	4.2	104
25	A high-resolution genetic map of the cereal crown rot pathogen <i>Fusarium pseudograminearum</i> provides a near-complete genome assembly. <i>Molecular Plant Pathology</i> , 2018, 19, 217-226.	4.2	35
26	A multiple near isogenic line (multi-NIL) RNA-seq approach to identify candidate genes underpinning QTL. <i>Theoretical and Applied Genetics</i> , 2018, 131, 613-624.	3.6	30
27	Selection is required for efficient Cas9-mediated genome editing in <i>Fusarium graminearum</i> . <i>Fungal Biology</i> , 2018, 122, 131-137.	2.5	41
28	<i>Fusarium</i> crown rot caused by <i>Fusarium pseudograminearum</i> in cereal crops: recent progress and future prospects. <i>Molecular Plant Pathology</i> , 2018, 19, 1547-1562.	4.2	177
29	The cereal pathogen <i>Fusarium pseudograminearum</i> produces a new class of active cytokinins during infection. <i>Molecular Plant Pathology</i> , 2018, 19, 1140-1154.	4.2	37
30	Genome Sequences of Three Isolates of <i>Fusarium verticillioides</i> . <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	7
31	BdACT2a encodes an agmatine coumaroyl transferase required for pathogen defence in <i>Brachypodium distachyon</i> . <i>Physiological and Molecular Plant Pathology</i> , 2018, 104, 69-76.	2.5	5
32	The <i>Fusarium</i> crown rot pathogen <i>Fusarium pseudograminearum</i> triggers a suite of transcriptional and metabolic changes in bread wheat (<i>Triticum aestivum</i> L.). <i>Annals of Botany</i> , 2017, 119, mcw207.	2.9	52
33	A tomatinase-like enzyme acts as a virulence factor in the wheat pathogen <i>Fusarium graminearum</i> . <i>Fungal Genetics and Biology</i> , 2017, 100, 33-41.	2.1	10
34	LOCALIZER: subcellular localization prediction of both plant and effector proteins in the plant cell. <i>Scientific Reports</i> , 2017, 7, 44598.	3.3	340
35	Transcriptome analysis of <i>Brachypodium</i> during fungal pathogen infection reveals both shared and distinct defense responses with wheat. <i>Scientific Reports</i> , 2017, 7, 17212.	3.3	27
36	Chrysogine Biosynthesis Is Mediated by a Two-Module Nonribosomal Peptide Synthetase. <i>Journal of Natural Products</i> , 2017, 80, 2131-2135.	3.0	37

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37	The defence-associated transcriptome of hexaploid wheat displays homoeolog expression and induction bias. <i>Plant Biotechnology Journal</i> , 2017, 15, 533-543.	8.3	110
38	Targeting pathogen sterols: Defence and counterdefence?. <i>PLoS Pathogens</i> , 2017, 13, e1006297.	4.7	24
39	Mycotoxigenic Potentials of <i>Fusarium</i> Species in Various Culture Matrices Revealed by Mycotoxin Profiling. <i>Toxins</i> , 2017, 9, 6.	3.4	56
40	High-throughput FACS-based mutant screen identifies a gain-of-function allele of the <i>Fusarium graminearum</i> adenylyl cyclase causing deoxynivalenol over-production. <i>Fungal Genetics and Biology</i> , 2016, 90, 1-11.	2.1	20
41	Enzyme-driven metabolomic screening: a proof-of-principle method for discovery of plant defence compounds targeted by pathogens. <i>New Phytologist</i> , 2016, 212, 770-779.	7.3	10
42	EffectorP: predicting fungal effector proteins from secretomes using machine learning. <i>New Phytologist</i> , 2016, 210, 743-761.	7.3	438
43	The Fdb3 transcription factor of the <i>Fusarium</i> Detoxification of Benzoxazolinone gene cluster is required for MBOA but not BOA degradation in <i>Fusarium pseudograminearum</i> . <i>Fungal Genetics and Biology</i> , 2016, 88, 44-53.	2.1	8
44	Degradation of the benzoxazolinone class of phytoalexins is important for virulence of <i>Fusarium pseudograminearum</i> towards wheat. <i>Molecular Plant Pathology</i> , 2015, 16, 946-962.	4.2	51
45	Genome-Wide Analysis in Three <i>Fusarium</i> Pathogens Identifies Rapidly Evolving Chromosomes and Genes Associated with Pathogenicity. <i>Genome Biology and Evolution</i> , 2015, 7, 1613-1627.	2.5	77
46	An update to polyketide synthase and non-ribosomal synthetase genes and nomenclature in <i>Fusarium</i> . <i>Fungal Genetics and Biology</i> , 2015, 75, 20-29.	2.1	123
47	Advances and Challenges in Computational Prediction of Effectors from Plant Pathogenic Fungi. <i>PLoS Pathogens</i> , 2015, 11, e1004806.	4.7	197
48	Brachypodium as an emerging model for cereal-pathogen interactions. <i>Annals of Botany</i> , 2015, 115, 717-731.	2.9	60
49	A β -lactamase from cereal infecting <i>Fusarium</i> spp. catalyses the first step in the degradation of the benzoxazolinone class of phytoalexins. <i>Fungal Genetics and Biology</i> , 2015, 83, 1-9.	2.1	23
50	Genomic Analysis of <i>Xanthomonas translucens</i> Pathogenic on Wheat and Barley Reveals Cross-Kingdom Gene Transfer Events and Diverse Protein Delivery Systems. <i>PLoS ONE</i> , 2014, 9, e84995.	2.5	39
51	Genome Sequence of <i>Fusarium graminearum</i> Isolate CS3005. <i>Genome Announcements</i> , 2014, 2, .	0.8	32
52	Diversifying selection in the wheat stem rust fungus acts predominantly on pathogen-associated gene families and reveals candidate effectors. <i>Frontiers in Plant Science</i> , 2014, 5, 372.	3.6	45
53	11 Application of Genomics to the Study of Pathogenicity and Development in <i>Fusarium</i> . , 2014, , 267-300.		9
54	Identification of the Biosynthetic Gene Clusters for the Lipopeptides Fusaristatin A and W493 B in <i>Fusarium graminearum</i> and <i>F. pseudograminearum</i> . <i>Journal of Natural Products</i> , 2014, 77, 2619-2625.	3.0	55

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55	Transcriptome and Allele Specificity Associated with a 3BL Locus for Fusarium Crown Rot Resistance in Bread Wheat. PLoS ONE, 2014, 9, e113309.	2.5	42
56	Cross-kingdom gene transfer facilitates the evolution of virulence in fungal pathogens. Plant Science, 2013, 210, 151-158.	3.6	38
57	4 Fungal Toxins of Agricultural Importance. , 2013, , 75-113.		1
58	<i>Fusarium</i> Pathogenomics. Annual Review of Microbiology, 2013, 67, 399-416.	7.3	475
59	An ABC pleiotropic drug resistance transporter of <i>Fusarium graminearum</i> with a role in crown and root diseases of wheat. FEMS Microbiology Letters, 2013, 348, 36-45.	1.8	55
60	Coverage and Consistency: Bioinformatics Aspects of the Analysis of Multirun iTRAQ Experiments with Wheat Leaves. Journal of Proteome Research, 2013, 12, 4870-4881.	3.7	14
61	Genome Sequences of Six Wheat-Infecting <i>Fusarium</i> Species Isolates. Genome Announcements, 2013, 1, .	0.8	38
62	A comparative hidden Markov model analysis pipeline identifies proteins characteristic of cereal-infecting fungi. BMC Genomics, 2013, 14, 807.	2.8	26
63	Genome Sequences of Pseudomonas spp. Isolated from Cereal Crops. Genome Announcements, 2013, 1, .	0.8	12
64	Fusarium Virulence Assay on Wheat and Barley Seedlings. Bio-protocol, 2013, 3, .	0.4	8
65	A Highly Conserved Effector in <i>Fusarium oxysporum</i> Is Required for Full Virulence on <i>Arabidopsis</i>. Molecular Plant-Microbe Interactions, 2012, 25, 180-190.	2.6	156
66	Comparative Pathogenomics Reveals Horizontally Acquired Novel Virulence Genes in Fungi Infecting Cereal Hosts. PLoS Pathogens, 2012, 8, e1002952.	4.7	176
67	On the trail of a cereal killer: recent advances in <i>Fusarium graminearum</i> pathogenomics and host resistance. Molecular Plant Pathology, 2012, 13, 399-413.	4.2	229
68	Auxin Signaling and Transport Promote Susceptibility to the Root-Infecting Fungal Pathogen <i>Fusarium oxysporum</i> in <i>Arabidopsis</i>. Molecular Plant-Microbe Interactions, 2011, 24, 733-748.	2.6	146
69	Early activation of wheat polyamine biosynthesis during Fusarium head blight implicates putrescine as an inducer of trichothecene mycotoxin production. BMC Plant Biology, 2010, 10, 289.	3.6	107
70	Comparative genomics reveals mobile pathogenicity chromosomes in Fusarium. Nature, 2010, 464, 367-373.	27.8	1,442
71	Low pH regulates the production of deoxynivalenol by Fusarium graminearum. Microbiology (United Kingdom) 151, 112-119. doi:10.1099/mic/0/000000.0	1.8	112
72	Nutrient profiling reveals potent inducers of trichothecene biosynthesis in Fusarium graminearum. Fungal Genetics and Biology, 2009, 46, 604-613.	2.1	247

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73	Novel Genes of <i>Fusarium graminearum</i> That Negatively Regulate Deoxynivalenol Production and Virulence. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 1588-1600.	2.6	103
74	The <i>Fusarium</i> mycotoxin deoxynivalenol elicits hydrogen peroxide production, programmed cell death and defence responses in wheat. <i>Molecular Plant Pathology</i> , 2008, 9, 435-445.	4.2	236
75	Towards defining the nuclear proteome. <i>Genome Biology</i> , 2008, 9, R15.	9.6	29
76	Phases of Infection and Gene Expression of <i>Fusarium graminearum</i> During Crown Rot Disease of Wheat. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 1571-1581.	2.6	98
77	A Zn(II)2Cys6 DNA binding protein regulates the sirodesmin PL biosynthetic gene cluster in <i>Leptosphaeria maculans</i> . <i>Fungal Genetics and Biology</i> , 2008, 45, 671-682.	2.1	42
78	Production of the toxin sirodesmin PL by <i>Leptosphaeria maculans</i> during infection of <i>Brassica napus</i> . <i>Molecular Plant Pathology</i> , 2007, 8, 791-802.	4.2	74
79	Origin and distribution of epipolythiodioxopiperazine (ETP) gene clusters in filamentous ascomycetes. <i>BMC Evolutionary Biology</i> , 2007, 7, 174.	3.2	151
80	The M flax rust resistance pre-mRNA is alternatively spliced and contains a complex upstream untranslated region. <i>Theoretical and Applied Genetics</i> , 2007, 115, 373-382.	3.6	9
81	A role for the mycotoxin deoxynivalenol in stem colonisation during crown rot disease of wheat caused by <i>Fusarium graminearum</i> and <i>Fusarium pseudograminearum</i> . <i>Physiological and Molecular Plant Pathology</i> , 2006, 69, 73-85.	2.5	152
82	Bioinformatic and expression analysis of the putative gliotoxin biosynthetic gene cluster of <i>Aspergillus fumigatus</i> . <i>FEMS Microbiology Letters</i> , 2005, 248, 241-248.	1.8	225
83	The epipolythiodioxopiperazine (ETP) class of fungal toxins: distribution, mode of action, functions and biosynthesis. <i>Microbiology (United Kingdom)</i> , 2005, 151, 1021-1032.	1.8	397
84	The ABC transporter gene in the sirodesmin biosynthetic gene cluster of <i>Leptosphaeria maculans</i> is not essential for sirodesmin production but facilitates self-protection. <i>Fungal Genetics and Biology</i> , 2005, 42, 257-263.	2.1	85
85	The sirodesmin biosynthetic gene cluster of the plant pathogenic fungus <i>Leptosphaeria maculans</i> . <i>Molecular Microbiology</i> , 2004, 53, 1307-1318.	2.5	212
86	Negative selection using thymidine kinase increases the efficiency of recovery of transformants with targeted genes in the filamentous fungus <i>Leptosphaeria maculans</i> . <i>Current Genetics</i> , 2004, 45, 249-255.	1.7	88