

Donald M Gardiner

List of Publications by Year in descending order

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86
papers

8,246
citations

94433

37
h-index

54911

84
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all docs

95
docs citations

95
times ranked

7557
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010, 464, 367-373.	27.8	1,442
2	<i>Fusarium</i> Pathogenomics. <i>Annual Review of Microbiology</i> , 2013, 67, 399-416.	7.3	475
3	EffectorP: predicting fungal effector proteins from secretomes using machine learning. <i>New Phytologist</i> , 2016, 210, 743-761.	7.3	438
4	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
5	Improved prediction of fungal effector proteins from secretomes with EffectorP 2.0. <i>Molecular Plant Pathology</i> , 2018, 19, 2094-2110.	4.2	350
6	LOCALIZER: subcellular localization prediction of both plant and effector proteins in the plant cell. <i>Scientific Reports</i> , 2017, 7, 44598.	3.3	340
7	Nutrient profiling reveals potent inducers of trichothecene biosynthesis in <i>Fusarium graminearum</i> . <i>Fungal Genetics and Biology</i> , 2009, 46, 604-613.	2.1	247
8	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
9	On the trail of a cereal killer: recent advances in <i>Fusarium graminearum</i> pathogenomics and host resistance. <i>Molecular Plant Pathology</i> , 2012, 13, 399-413.	4.2	229
10	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
11	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
12	Advances and Challenges in Computational Prediction of Effectors from Plant Pathogenic Fungi. <i>PLoS Pathogens</i> , 2015, 11, e1004806.	4.7	197
13	<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
14	Comparative Pathogenomics Reveals Horizontally Acquired Novel Virulence Genes in Fungi Infecting Cereal Hosts. <i>PLoS Pathogens</i> , 2012, 8, e1002952.	4.7	176
15	A Highly Conserved Effector in <i>Fusarium oxysporum</i> Is Required for Full Virulence on <i>Arabidopsis</i> . <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 180-190.	2.6	156
16	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
17	Origin and distribution of epipolythiodioxopiperazine (ETP) gene clusters in filamentous ascomycetes. <i>BMC Evolutionary Biology</i> , 2007, 7, 174.	3.2	151
18	Auxin Signaling and Transport Promote Susceptibility to the Root-Infecting Fungal Pathogen <i>Fusarium oxysporum</i> in <i>Arabidopsis</i> . <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 733-748.	2.6	146

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19	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
20	Low pH regulates the production of deoxynivalenol by <i>Fusarium graminearum</i> . <i>Microbiology (United Kingdom)</i> , 2015, 155, 118-122.	1.8	112
21	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
22	Early activation of wheat polyamine biosynthesis during <i>Fusarium</i> head blight implicates putrescine as an inducer of trichothecene mycotoxin production. <i>BMC Plant Biology</i> , 2010, 10, 289.	3.6	107
23	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
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	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
26	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
27	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
28	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
29	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
30	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
31	<i>Brachypodium</i> as an emerging model for cereal-pathogen interactions. <i>Annals of Botany</i> , 2015, 115, 717-731.	2.9	60
32	Mycotoxigenic Potentials of <i>Fusarium</i> Species in Various Culture Matrices Revealed by Mycotoxin Profiling. <i>Toxins</i> , 2017, 9, 6.	3.4	56
33	An ABC pleiotropic drug resistance transporter of <i>Fusarium graminearum</i> with a role in crown and root diseases of wheat. <i>FEMS Microbiology Letters</i> , 2013, 348, 36-45.	1.8	55
34	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
35	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
36	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

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37	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
38	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
39	Transcriptome and Allele Specificity Associated with a 3BL Locus for Fusarium Crown Rot Resistance in Bread Wheat. <i>PLoS ONE</i> , 2014, 9, e113309.	2.5	42
40	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
41	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
42	Cross-kingdom gene transfer facilitates the evolution of virulence in fungal pathogens. <i>Plant Science</i> , 2013, 210, 151-158.	3.6	38
43	Genome Sequences of Six Wheat-Infecting <i>Fusarium</i> Species Isolates. <i>Genome Announcements</i> , 2013, 1, .	0.8	38
44	Chrysozine Biosynthesis Is Mediated by a Two-Module Nonribosomal Peptide Synthetase. <i>Journal of Natural Products</i> , 2017, 80, 2131-2135.	3.0	37
45	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
46	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
47	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
48	Genome Sequence of <i>Fusarium graminearum</i> Isolate CS3005. <i>Genome Announcements</i> , 2014, 2, .	0.8	32
49	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
50	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
51	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
52	Towards defining the nuclear proteome. <i>Genome Biology</i> , 2008, 9, R15.	9.6	29
53	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
54	A comparative hidden Markov model analysis pipeline identifies proteins characteristic of cereal-infecting fungi. <i>BMC Genomics</i> , 2013, 14, 807.	2.8	26

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55	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
56	Targeting pathogen sterols: Defence and counterdefence?. <i>PLoS Pathogens</i> , 2017, 13, e1006297.	4.7	24
57	A β -lactamase from cereal infecting <i>Fusarium</i> spp. catalyses the first step in the degradation of the benzoxazinone class of phytoalexins. <i>Fungal Genetics and Biology</i> , 2015, 83, 1-9.	2.1	23
58	Ribosome profiling in plants: what is not lost in translation?. <i>Journal of Experimental Botany</i> , 2020, 71, 5323-5332.	4.8	21
59	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
60	Development of three fusarium 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
61	Heterologous expression of intact biosynthetic gene clusters in <i>Fusarium graminearum</i> . <i>Fungal Genetics and Biology</i> , 2019, 132, 103248.	2.1	15
62	Coverage and Consistency: Bioinformatics Aspects of the Analysis of Multirun iTRAQ Experiments with Wheat Leaves. <i>Journal of Proteome Research</i> , 2013, 12, 4870-4881.	3.7	14
63	Genome Sequences of <i>Pseudomonas</i> spp. Isolated from Cereal Crops. <i>Genome Announcements</i> , 2013, 1, .	0.8	12
64	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
65	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
66	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
67	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
68	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
69	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
70	11 Application of Genomics to the Study of Pathogenicity and Development in <i>Fusarium</i> . , 2014, , 267-300.		9
71	Regulation of a novel <i>Fusarium</i> cytokinin in <i>Fusarium pseudograminearum</i> . <i>Fungal Biology</i> , 2019, 123, 255-266.	2.5	9
72	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

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73	Gene technologies in weed management: a technical feasibility analysis. <i>Current Opinion in Insect Science</i> , 2020, 38, 6-14.	4.4	9
74	The Fdb3 transcription factor of the Fusarium 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
75	Fusarium Virulence Assay on Wheat and Barley Seedlings. <i>Bio-protocol</i> , 2013, 3, .	0.4	8
76	Genome Sequences of Three Isolates of <i>Fusarium verticillioides</i> . <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	7
77	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
78	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
79	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
80	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
81	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
82	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
83	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
84	A method for high-throughput image-based antifungal screening. <i>Journal of Microbiological Methods</i> , 2021, 190, 106342.	1.6	2
85	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
86	4 Fungal Toxins of Agricultural Importance. , 2013, , 75-113.		1