

Barbara G Turgeon

List of Publications by Year in descending order

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90
papers

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citations

66343

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docs citations

94
times ranked

7410
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	The <i>Fusarium graminearum</i> Genome Reveals a Link Between Localized Polymorphism and Pathogen Specialization. <i>Science</i> , 2007, 317, 1400-1402.	12.6	837
3	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
4	Phylogenomic analysis of type I polyketide synthase genes in pathogenic and saprobic ascomycetes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15670-15675.	7.1	485
5	Effector diversification within compartments of the <i>Leptosphaeria maculans</i> genome affected by Repeat-Induced Point mutations. <i>Nature Communications</i> , 2011, 2, 202.	12.8	481
6	Early Events in the Infection of Soybean (<i>Glycine max</i> L. Merr) by <i>Rhizobium japonicum</i> . <i>Plant Physiology</i> , 1980, 66, 1027-1031.	4.8	368
7	Siderophores in Fungal Physiology and Virulence. <i>Annual Review of Phytopathology</i> , 2008, 46, 149-187.	7.8	365
8	NPS6, Encoding a Nonribosomal Peptide Synthetase Involved in Siderophore-Mediated Iron Metabolism, Is a Conserved Virulence Determinant of Plant Pathogenic Ascomycetes. <i>Plant Cell</i> , 2006, 18, 2836-2853.	6.6	311
9	Proposed Nomenclature for Mating Type Genes of Filamentous Ascomycetes. <i>Fungal Genetics and Biology</i> , 2000, 31, 1-5.	2.1	305
10	Split-Marker Recombination for Efficient Targeted Deletion of Fungal Genes. <i>Fungal Genetics Reports</i> , 2003, 50, 9-11.	0.6	287
11	Whole-Genome Analysis of Two-Component Signal Transduction Genes in Fungal Pathogens. <i>Eukaryotic Cell</i> , 2003, 2, 1151-1161.	3.4	267
12	Comparative Genome Structure, Secondary Metabolite, and Effector Coding Capacity across <i>Cochliobolus</i> Pathogens. <i>PLoS Genetics</i> , 2013, 9, e1003233.	3.5	232
13	APPLICATION OF MATING TYPE GENE TECHNOLOGY TO PROBLEMS IN FUNGAL BIOLOGY. <i>Annual Review of Phytopathology</i> , 1998, 36, 115-137.	7.8	225
14	Cloning and analysis of the mating type genes from <i>Cochliobolus heterostrophus</i> . <i>Molecular Genetics and Genomics</i> , 1993, 238-238, 270-284.	2.4	185
15	Phylogenomics reveals subfamilies of fungal nonribosomal peptide synthetases and their evolutionary relationships. <i>BMC Evolutionary Biology</i> , 2010, 10, 26.	3.2	184
16	Comparative Genomics of a Plant-Pathogenic Fungus, <i>Pyrenophora tritici-repentis</i> , Reveals Transduplication and the Impact of Repeat Elements on Pathogenicity and Population Divergence. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 41-63.	1.8	167
17	Shifting fungal reproductive mode by manipulation of mating type genes: obligatory heterothallism of <i>Gibberella zeae</i> . <i>Molecular Microbiology</i> , 2003, 50, 145-152.	2.5	159
18	ChLae1 and ChVel1 Regulate T-toxin Production, Virulence, Oxidative Stress Response, and Development of the Maize Pathogen <i>Cochliobolus heterostrophus</i> . <i>PLoS Pathogens</i> , 2012, 8, e1002542.	4.7	145

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19	Functional Analysis of All Nonribosomal Peptide Synthetases in <i>Cochliobolus heterostrophus</i> Reveals a Factor, NPS6, Involved in Virulence and Resistance to Oxidative Stress. <i>Eukaryotic Cell</i> , 2005, 4, 545-555.	3.4	144
20	Two Polyketide Synthase-Encoding Genes Are Required for Biosynthesis of the Polyketide Virulence Factor, T-toxin, by <i>Cochliobolus heterostrophus</i> . <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 139-149.	2.6	135
21	Transformation of the fungal maize pathogen <i>Cochliobolus heterostrophus</i> using the <i>Aspergillus nidulans</i> amdS gene. <i>Molecular Genetics and Genomics</i> , 1985, 201, 450-453.	2.4	132
22	Lateral transfer of mating system in <i>Stemphylium</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 11390-11395.	7.1	110
23	Early events in the infection of soybean by <i>Rhizobium japonicum</i> . Time course and cytology of the initial infection process. <i>Canadian Journal of Botany</i> , 1982, 60, 152-161.	1.1	106
24	Sorbitol Modulates Resistance to <i>Alternaria alternata</i> by Regulating the Expression of an NLR Resistance Gene in Apple. <i>Plant Cell</i> , 2018, 30, 1562-1581.	6.6	97
25	Intracellular Siderophores Are Essential for Ascomycete Sexual Development in Heterothallic <i>Cochliobolus heterostrophus</i> and Homothallic <i>Gibberella zeae</i> . <i>Eukaryotic Cell</i> , 2007, 6, 1339-1353.	3.4	95
26	Organization of ribosomal RNA genes in the fungus <i>Cochliobolus heterostrophus</i> . <i>Current Genetics</i> , 1988, 14, 573-582.	1.7	93
27	Tracing the Origin of the Fungal $\hat{1}$ Domain Places Its Ancestor in the HMG-Box Superfamily: Implication for Fungal Mating-Type Evolution. <i>PLoS ONE</i> , 2010, 5, e15199.	2.5	93
28	Module evolution and substrate specificity of fungal nonribosomal peptide synthetases involved in siderophore biosynthesis. <i>BMC Evolutionary Biology</i> , 2008, 8, 328.	3.2	87
29	Root Border Cells and Their Role in Plant Defense. <i>Annual Review of Phytopathology</i> , 2016, 54, 143-161.	7.8	79
30	A Fungal Kinesin Required for Organelle Motility, Hyphal Growth, and Morphogenesis. <i>Molecular Biology of the Cell</i> , 1998, 9, 89-101.	2.1	76
31	A novel class of gene controlling virulence in plant pathogenic ascomycete fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5980-5985.	7.1	76
32	Hydrophobin genes of the entomopathogenic fungus, <i>Metarhizium brunneum</i> , are differentially expressed and corresponding mutants are decreased in virulence. <i>Current Genetics</i> , 2012, 58, 79-92.	1.7	70
33	Protoplast Transformation of Filamentous Fungi. <i>Methods in Molecular Biology</i> , 2010, 638, 3-19.	0.9	66
34	Six New Genes Required for Production of T-Toxin, a Polyketide Determinant of High Virulence of <i>Cochliobolus heterostrophus</i> to Maize. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 458-472.	2.6	64
35	Individual and combined roles of malonichrome, ferricrocin, and TAFC siderophores in <i>Fusarium graminearum</i> pathogenic and sexual development. <i>Frontiers in Microbiology</i> , 2014, 5, 759.	3.5	60
36	Genetic and Genomic Dissection of the <i>Cochliobolus heterostrophus</i> Tox1 Locus Controlling Biosynthesis of the Polyketide Virulence Factor T-toxin. <i>Advances in Genetics</i> , 2007, 57, 219-261.	1.8	56

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37	A complete inventory of fungal kinesins in representative filamentous ascomycetes. <i>Fungal Genetics and Biology</i> , 2003, 39, 1-15.	2.1	54
38	Deletion of the <i>Cochliobolus heterostrophus</i> mating-type (MAT) locus promotes the function of MAT transgenes. <i>Current Genetics</i> , 1996, 29, 241-249.	1.7	52
39	Shared ITS DNA substitutions in isolates of opposite mating type reveal a recombining history for three presumed asexual species in the filamentous ascomycete genus <i>Alternaria</i> . <i>Mycological Research</i> , 2003, 107, 169-182.	2.5	51
40	Fungal Sex: The <i>Ascomycota</i> . <i>Microbiology Spectrum</i> , 2016, 4, .	3.0	50
41	Physical map of defective interfering particles of bacteriophage ϕ 1. <i>Journal of Molecular Biology</i> , 1977, 111, 395-414.	4.2	49
42	Single mating type-specific genes and their 3' UTRs control mating and fertility in <i>Cochliobolus heterostrophus</i> . <i>Molecular Genetics and Genomics</i> , 1998, 259, 272-281.	2.4	44
43	G-Protein β 2 Subunit of <i>Cochliobolus heterostrophus</i> Involved in Virulence, Asexual and Sexual Reproductive Ability, and Morphogenesis. <i>Eukaryotic Cell</i> , 2004, 3, 1653-1663.	3.4	44
44	Systematics and mating systems of two fungal pathogens of opium poppy: the heterothallic <i>Crivellia papaveracea</i> with a <i>Brachycladium penicillatum</i> asexual state and a homothallic species with a <i>Brachycladium papaveris</i> asexual state. <i>Canadian Journal of Botany</i> , 2006, 84, 1304-1326.	1.1	44
45	Histidine Kinase Two-Component Response Regulator Proteins Regulate Reproductive Development, Virulence, and Stress Responses of the Fungal Cereal Pathogens <i>Cochliobolus heterostrophus</i> and <i>Gibberella zeae</i> . <i>Eukaryotic Cell</i> , 2010, 9, 1867-1880.	3.4	44
46	A Polyketide Synthase Is Required for Fungal Virulence and Production of the Polyketide T-Toxin. <i>Plant Cell</i> , 1996, 8, 2139.	6.6	41
47	Victorin, the host-selective cyclic peptide toxin from the oat pathogen <i>Cochliobolus victoriae</i> , is ribosomally encoded. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 24243-24250.	7.1	41
48	Creating and screening <i>Cochliobolus heterostrophus</i> non-ribosomal peptide synthetase mutants. <i>Mycological Research</i> , 2008, 112, 200-206.	2.5	37
49	A mitochondrial plasmid from the plant pathogenic fungus <i>Cochliobolus heterostrophus</i> . <i>Molecular Genetics and Genomics</i> , 1984, 196, 301-310.	2.4	35
50	The two <i>Cochliobolus</i> mating type genes are conserved among species but one of them is missing in <i>C. victoriae</i> . <i>Mycological Research</i> , 1998, 102, 919-929.	2.5	35
51	A Decarboxylase Encoded at the <i>Cochliobolus heterostrophus</i> Translocation-Associated Tox1B Locus Is Required for Polyketide (T-toxin) Biosynthesis and High Virulence on T-cytoplasm Maize. <i>Molecular Plant-Microbe Interactions</i> , 2002, 15, 883-893.	2.6	34
52	Determinants of Virulence and In Vitro Development Colocalize on a Genetic Map of <i>Setosphaeria turcica</i> . <i>Phytopathology</i> , 2018, 108, 254-263.	2.2	34
53	Efficient Gene Knockout in the Maize Pathogen <i>Setosphaeria turcica</i> Using <i>Agrobacterium tumefaciens</i> -Mediated Transformation. <i>Phytopathology</i> , 2013, 103, 641-647.	2.2	33
54	Characterization and potential evolutionary impact of transposable elements in the genome of <i>Cochliobolus heterostrophus</i> . <i>BMC Genomics</i> , 2014, 15, 536.	2.8	32

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55	Molecular-genetic evaluation of fungal molecules for roles in pathogenesis to plants. <i>Journal of Genetics</i> , 1996, 75, 425-440.	0.7	30
56	A ToxA-like protein from <i>Cochliobolus heterostrophus</i> induces light-dependent leaf necrosis and acts as a virulence factor with host selectivity on maize. <i>Fungal Genetics and Biology</i> , 2015, 81, 12-24.	2.1	30
57	Structure and function of mating type genes in <i>Cochliobolus</i> spp. and asexual fungi. <i>Canadian Journal of Botany</i> , 1995, 73, 778-783.	1.1	28
58	Deletion of all <i>Cochliobolus heterostrophus</i> Monofunctional Catalase-Encoding Genes Reveals a Role for One in Sensitivity to Oxidative Stress but None with a Role in Virulence. <i>Molecular Plant-Microbe Interactions</i> , 2003, 16, 1013-1021.	2.6	28
59	Transcripts at the mating type locus of <i>Cochliobolus heterostrophus</i> . <i>Molecular Genetics and Genomics</i> , 1997, 256, 661-673.	2.4	27
60	Fungal genome sequencing and bioenergy. <i>Fungal Biology Reviews</i> , 2008, 22, 1-5.	4.7	27
61	Reductive Iron Assimilation and Intracellular Siderophores Assist Extracellular Siderophore-Driven Iron Homeostasis and Virulence. <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 793-808.	2.6	27
62	Comparative chemical screening and genetic analysis reveal tentoxin as a new virulence factor in <i>Cochliobolus miyabeanus</i> , the causal agent of brown spot disease on rice. <i>Molecular Plant Pathology</i> , 2016, 17, 805-817.	4.2	26
63	A DNase from a Fungal Phytopathogen Is a Virulence Factor Likely Deployed as Counter Defense against Host-Secreted Extracellular DNA. <i>MBio</i> , 2019, 10, .	4.1	25
64	<i>Cochliobolus heterostrophus</i> Llm1 – A Lae1-like methyltransferase regulates T-toxin production, virulence, and development. <i>Fungal Genetics and Biology</i> , 2013, 51, 21-33.	2.1	23
65	Iron, Oxidative Stress, and Virulence: Roles of Iron-Sensitive Transcription Factor Sre1 and the Redox Sensor ChAp1 in the Maize Pathogen <i>Cochliobolus heterostrophus</i> . <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 1473-1485.	2.6	21
66	Altering sexual reproductive mode by interspecific exchange of MAT loci. <i>Fungal Genetics and Biology</i> , 2011, 48, 714-724.	2.1	20
67	Natural roles of nonribosomal peptide metabolites in fungi. <i>Mycoscience</i> , 2020, 61, 101-110.	0.8	20
68	Nematode ascaroside enhances resistance in a broad spectrum of plant-pathogen systems. <i>Journal of Phytopathology</i> , 2019, 167, 265-272.	1.0	18
69	Evolution of Host Specific Virulence in <i>Cochliobolus heterostrophus</i> . , 2000, , 93-126.		16
70	Structure and function of the mating-type locus in the homothallic ascomycete, <i>Didymella zaeae-maydis</i> . <i>Journal of Microbiology</i> , 2013, 51, 814-820.	2.8	15
71	Septins are required for reproductive propagule development and virulence of the maize pathogen <i>Cochliobolus heterostrophus</i> . <i>Fungal Genetics and Biology</i> , 2020, 135, 103291.	2.1	14
72	Molecular Bases of Fungal Pathogenicity to Plants. , 1985, , 417-448.		13

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73	Setosphaeria rostrata: Insights from the sequenced genome of Setosphaeria turcica. Fungal Genetics and Biology, 2013, 61, 158-163.	2.1	12
74	Standardization of Functional Reporter and Antibiotic Resistance Cassettes to Facilitate the Genetic Engineering of Filamentous Fungi. ACS Synthetic Biology, 2014, 3, 960-962.	3.8	12
75	Disruptions of the genes involved in lysine biosynthesis, iron acquisition, and secondary metabolisms affect virulence and fitness in Metarhizium robertsii. Fungal Genetics and Biology, 2017, 98, 23-34.	2.1	12
76	Sequencing of individual chromosomes of plant pathogenic Fusarium oxysporum. Fungal Genetics and Biology, 2017, 98, 46-51.	2.1	12
77	Clues to an Evolutionary Mystery: The Genes for T-Toxin, Enabler of the Devastating 1970 Southern Corn Leaf Blight Epidemic, Are Present in Ancestral Species, Suggesting an Ancient Origin. Molecular Plant-Microbe Interactions, 2018, 31, 1154-1165.	2.6	12
78	Self-fertility in Chromocrea spinulosa is a consequence of direct repeat-mediated loss of MAT1-2, subsequent imbalance of nuclei differing in mating type, and recognition between unlike nuclei in a common cytoplasm. PLoS Genetics, 2017, 13, e1006981.	3.5	11
79	Virulence, Host-Selective Toxin Production, and Development of Three <i>Cochliobolus</i> Phytopathogens Lacking the Sfp-Type 4-Phosphopantetheinyl Transferase Ppt1. Molecular Plant-Microbe Interactions, 2015, 28, 1130-1141.	2.6	9
80	Population Genetics of <i>Verticillium dahliae</i> in Iran Based on Microsatellite and Single Nucleotide Polymorphism Markers. Phytopathology, 2018, 108, 780-788.	2.2	9
81	A Genome Resource of <i>Setosphaeria turcica</i> , Causal Agent of Northern Leaf Blight of Maize. Phytopathology, 2020, 110, 2014-2016.	2.2	9
82	Vel2 and Vos1 hold essential roles in ascospore and asexual spore development of the heterothallic maize pathogen Cochliobolus heterostrophus. Fungal Genetics and Biology, 2014, 70, 113-124.	2.1	8
83	Secondary Metabolism. , 0, , 376-395.		7
84	Pondering Mating: Pneumocystis jirovecii, the Human Lung Pathogen, Selfs without Mating Type Switching, in Contrast to Its Close Relative Schizosaccharomyces pombe. MBio, 2015, 6, e00583-15.	4.1	6
85	Evolution of Pathogenic and Reproductive Strategies in Cochliobolus and Related Genera. Developments in Plant Pathology, 1998, , 153-163.	0.1	6
86	Cochliobolus and Podospora: Mechanisms of Sex Determination and the Evolution of Reproductive Lifestyle. , 0, , 91-121.		6
87	Fungal Sex: The <i>Ascomycota</i> . , 0, , 115-145.		4
88	Cochliobolus heterostrophus: A Dothideomycete Pathogen of Maize. Soil Biology, 2013, , 213-228.	0.8	3
89	Deletion of the Cochliobolus heterostrophus mating-type (MAT) locus promotes the function of MAT transgenes. Current Genetics, 1996, 29, 241-249.	1.7	1
90	Transformation of plant pathogenic fungi. , 1989, , 195-207.		0