

Brett M Tyler

List of Publications by Year in descending order

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133
papers

13,566
citations

31974

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docs citations

142
times ranked

7932
citing authors

#	ARTICLE	IF	CITATIONS
1	Phytophthora Genome Sequences Uncover Evolutionary Origins and Mechanisms of Pathogenesis. <i>Science</i> , 2006, 313, 1261-1266.	12.6	1,059
2	The Top 10 oomycete pathogens in molecular plant pathology. <i>Molecular Plant Pathology</i> , 2015, 16, 413-434.	4.2	695
3	Signatures of Adaptation to Obligate Biotrophy in the <i>Hyaloperonospora arabidopsidis</i> Genome. <i>Science</i> , 2010, 330, 1549-1551.	12.6	492
4	External Lipid PI3P Mediates Entry of Eukaryotic Pathogen Effectors into Plant and Animal Host Cells. <i>Cell</i> , 2010, 142, 284-295.	28.9	463
5	Transcriptional Programming and Functional Interactions within the <i>Phytophthora sojae</i> RXLR Effector Repertoire. <i>Plant Cell</i> , 2011, 23, 2064-2086.	6.6	455
6	A Secreted Effector Protein of <i>Laccaria bicolor</i> Is Required for Symbiosis Development. <i>Current Biology</i> , 2011, 21, 1197-1203.	3.9	447
7	RXLR-Mediated Entry of <i>Phytophthora sojae</i> Effector <i>Avr1b</i> into Soybean Cells Does Not Require Pathogen-Encoded Machinery. <i>Plant Cell</i> , 2008, 20, 1930-1947.	6.6	440
8	<i>Phytophthora sojae</i> : root rot pathogen of soybean and model oomycete. <i>Molecular Plant Pathology</i> , 2007, 8, 1-8.	4.2	419
9	Differential Recognition of Highly Divergent Downy Mildew Avirulence Gene Alleles by RPP1 Resistance Genes from Two Arabidopsis Lines. <i>Plant Cell</i> , 2005, 17, 1839-1850.	6.6	416
10	RXLR effector reservoir in two <i>Phytophthora</i> species is dominated by a single rapidly evolving superfamily with more than 700 members. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 4874-4879.	7.1	409
11	Genome sequence of the necrotrophic plant pathogen <i>Pythium ultimum</i> reveals original pathogenicity mechanisms and effector repertoire. <i>Genome Biology</i> , 2010, 11, R73.	9.6	391
12	Protein secretion systems in bacterial-host associations, and their description in the Gene Ontology. <i>BMC Microbiology</i> , 2009, 9, S2.	3.3	346
13	The <i>Avr1b</i> Locus of <i>Phytophthora sojae</i> Encodes an Elicitor and a Regulator Required for Avirulence on Soybean Plants Carrying Resistance Gene <i>Rps1b</i> . <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 394-403.	2.6	343
14	A <i>Phytophthora sojae</i> Glycoside Hydrolase 12 Protein Is a Major Virulence Factor during Soybean Infection and Is Recognized as a PAMP. <i>Plant Cell</i> , 2015, 27, 2057-2072.	6.6	335
15	Conserved C-Terminal Motifs Required for Avirulence and Suppression of Cell Death by <i>Phytophthora sojae</i> effector <i>Avr1b</i> . <i>Plant Cell</i> , 2008, 20, 1118-1133.	6.6	323
16	Efficient disruption and replacement of an effector gene in the oomycete <i>Phytophthora sojae</i> using CRISPR-Cas9. <i>Molecular Plant Pathology</i> , 2016, 17, 127-139.	4.2	253
17	A paralogous decoy protects <i>Phytophthora sojae</i> apoplastic effector <i>PsXEG1</i> from a host inhibitor. <i>Science</i> , 2017, 355, 710-714.	12.6	236
18	MOLECULAR BASIS OF RECOGNITION BETWEEN PHYTOPHTHORA PATHOGENS AND THEIR HOSTS. <i>Annual Review of Phytopathology</i> , 2002, 40, 137-167.	7.8	224

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19	Distinctive Expansion of Potential Virulence Genes in the Genome of the Oomycete Fish Pathogen <i>Saprolegnia parasitica</i> . <i>PLoS Genetics</i> , 2013, 9, e1003272.	3.5	221
20	Mechanisms and Evolution of Virulence in Oomycetes. <i>Annual Review of Phytopathology</i> , 2012, 50, 295-318.	7.8	187
21	An expanded phylogeny for the genus <i>Phytophthora</i> . <i>IMA Fungus</i> , 2017, 8, 355-384.	3.8	170
22	<i>Phytophthora sojae</i> Avirulence Effector Avr3b is a Secreted NADH and ADP-ribose Pyrophosphorylase that Modulates Plant Immunity. <i>PLoS Pathogens</i> , 2011, 7, e1002353.	4.7	169
23	DNA sequence, organization and regulation of the qa gene cluster of <i>Neurospora crassa</i> . <i>Journal of Molecular Biology</i> , 1989, 207, 15-34.	4.2	163
24	MOLECULAR SIGNALS AND RECEPTORS: CONTROLLING RHIZOSPHERE INTERACTIONS BETWEEN PLANTS AND OTHER ORGANISMS. <i>Ecology</i> , 2003, 84, 858-868.	3.2	151
25	Copy Number Variation and Transcriptional Polymorphisms of <i>Phytophthora sojae</i> RXLR Effector Genes Avr1a and Avr3a. <i>PLoS ONE</i> , 2009, 4, e5066.	2.5	151
26	Leucine-rich repeat receptor-like gene screen reveals that <i>Nicotiana</i> RXEG1 regulates glycoside hydrolase 12 MAMP detection. <i>Nature Communications</i> , 2018, 9, 594.	12.8	142
27	Rust Secreted Protein Ps87 Is Conserved in Diverse Fungal Pathogens and Contains a RXLR-like Motif Sufficient for Translocation into Plant Cells. <i>PLoS ONE</i> , 2011, 6, e27217.	2.5	140
28	Chemotropic and Contact Responses of <i>Phytophthora sojae</i> Hyphae to Soybean Isoflavonoids and Artificial Substrates1. <i>Plant Physiology</i> , 1998, 117, 1171-1178.	4.8	135
29	Ancient Origin of Elicitin Gene Clusters in <i>Phytophthora</i> Genomes. <i>Molecular Biology and Evolution</i> , 2006, 23, 338-351.	8.9	127
30	Defense and Counterdefense During Plant-Pathogenic Oomycete Infection. <i>Annual Review of Microbiology</i> , 2019, 73, 667-696.	7.3	123
31	A <i>Phytophthora sojae</i> effector suppresses endoplasmic reticulum stress-mediated immunity by stabilizing plant Binding immunoglobulin Proteins. <i>Nature Communications</i> , 2016, 7, 11685.	12.8	119
32	The <i>Phytophthora sojae</i> Avirulence Locus Avr3c Encodes a Multi-Copy RXLR Effector with Sequence Polymorphisms among Pathogen Strains. <i>PLoS ONE</i> , 2009, 4, e5556.	2.5	116
33	Entry of oomycete and fungal effectors into plant and animal host cells. <i>Cellular Microbiology</i> , 2011, 13, 1839-1848.	2.1	115
34	Entering and breaking: virulence effector proteins of oomycete plant pathogens. <i>Cellular Microbiology</i> , 2009, 11, 13-20.	2.1	107
35	Ligand-induced monoubiquitination of BIK1 regulates plant immunity. <i>Nature</i> , 2020, 581, 199-203.	27.8	99
36	Stripe Rust Effector PstGSRE1 Disrupts Nuclear Localization of ROS-Promoting Transcription Factor TaLOL2 to Defeat ROS-Induced Defense in Wheat. <i>Molecular Plant</i> , 2019, 12, 1624-1638.	8.3	98

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37	Different Domains of <i>Phytophthora sojae</i> Effector Avr4/6 Are Recognized by Soybean Resistance Genes <i>Rps4</i> and <i>Rps6</i> . <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 425-435.	2.6	97
38	Optimized vectors and selection for transformation of <i>Neurospora crassa</i> and <i>Aspergillus nidulans</i> to bleomycin and phleomycin resistance. <i>Gene</i> , 1990, 93, 157-162.	2.2	92
39	Homologous RXLR effectors from <i>Hyaloperonospora arabidopsidis</i> and <i>Phytophthora sojae</i> suppress immunity in distantly related plants. <i>Plant Journal</i> , 2012, 72, 882-893.	5.7	88
40	Inheritance of Avirulence Factors and Restriction Fragment Length Polymorphism Markers in Outcrosses of the Oomycete <i>Phytophthora sojae</i> . <i>Molecular Plant-Microbe Interactions</i> , 1995, 8, 515.	2.6	87
41	Structural Basis for Interactions of the <i>Phytophthora sojae</i> RXLR Effector Avh5 with Phosphatidylinositol 3-Phosphate and for Host Cell Entry. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 330-344.	2.6	81
42	Genetics and genomics of the oomycete "host interface. <i>Trends in Genetics</i> , 2001, 17, 611-614.	6.7	77
43	Sequence Variants of the <i>Phytophthora sojae</i> RXLR Effector Avr3a/5 Are Differentially Recognized by <i>Rps3a</i> and <i>Rps5</i> in Soybean. <i>PLoS ONE</i> , 2011, 6, e20172.	2.5	76
44	Efficient Genome Editing in the Oomycete <i>Phytophthora sojae</i> Using CRISPR/Cas9. <i>Current Protocols in Microbiology</i> , 2017, 44, 21A.1.1-21A.1.26.	6.5	74
45	Two RXLR Avirulence Genes in <i>Phytophthora sojae</i> Determine Soybean <i>Rps1k</i> -Mediated Disease Resistance. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 711-720.	2.6	73
46	Sequencing of the Litchi Downy Blight Pathogen Reveals It Is a <i>Phytophthora</i> Species With Downy Mildew-Like Characteristics. <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 573-583.	2.6	73
47	Transcription of <i>Neurospora crassa</i> 5 S rRNA genes requires a TATA box and three internal elements. <i>Journal of Molecular Biology</i> , 1987, 196, 801-811.	4.2	70
48	Transformation of the oomycete pathogen <i>Phytophthora megasperma</i> f. sp. <i>glycinea</i> occurs by DNA integration into single or multiple chromosomes. <i>Current Genetics</i> , 1993, 23, 211-218.	1.7	70
49	Potential Role of Elicitins in the Interaction between <i>Phytophthora</i> Species and Tobacco. <i>Applied and Environmental Microbiology</i> , 1994, 60, 1593-1598.	3.1	63
50	Regulatory sequences for expressing genes in oomycete fungi. <i>Molecular Genetics and Genomics</i> , 1992, 234, 138-146.	2.4	60
51	Conserved RXLR Effectors From Oomycetes <i>Hyaloperonospora arabidopsidis</i> and <i>Phytophthora sojae</i> Suppress PAMP- and Effector-Triggered Immunity in Diverse Plants. <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 374-385.	2.6	60
52	Mutations in ORP1 Conferring Oxathiapiprolin Resistance Confirmed by Genome Editing using CRISPR/Cas9 in <i>Phytophthora capsici</i> and <i>P. sojae</i> . <i>Phytopathology</i> , 2018, 108, 1412-1419.	2.2	60
53	A <i>Phytophthora</i> effector recruits a host cytoplasmic transacetylase into nuclear speckles to enhance plant susceptibility. <i>ELife</i> , 2018, 7, .	6.0	60
54	Expressed Sequence Tags from <i>Phytophthora sojae</i> Reveal Genes Specific to Development and Infection. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 781-793.	2.6	59

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55	Microbe-Independent Entry of Oomycete RxLR Effectors and Fungal RxLR-Like Effectors Into Plant and Animal Cells Is Specific and Reproducible. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 611-616.	2.6	57
56	A cosmopolitan fungal pathogen of dicots adopts an endophytic lifestyle on cereal crops and protects them from major fungal diseases. <i>ISME Journal</i> , 2020, 14, 3120-3135.	9.8	57
57	Crystal structure of the effector <i>AvrL4</i> of <i>Leptosphaeria maculans</i> reveals insights into its translocation into plant cells and recognition by resistance proteins. <i>Plant Journal</i> , 2015, 83, 610-624.	5.7	52
58	N-glycosylation shields <i>Phytophthora sojae</i> apoplastic effector PsXEG1 from a specific host aspartic protease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 27685-27693.	7.1	51
59	Mitotic Recombination and Rapid Genome Evolution in the Invasive Forest Pathogen <i>Phytophthora ramorum</i> . <i>MBio</i> , 2019, 10, .	4.1	50
60	Organization and Expression of Murine Immunoglobulin Genes. <i>Immunological Reviews</i> , 1981, 59, 5-32.	6.0	49
61	Mitochondrial genome sequences and comparative genomics of <i>Phytophthora ramorum</i> and <i>P. sojae</i> . <i>Current Genetics</i> , 2007, 51, 285-296.	1.7	48
62	Comparative Analysis of <i>Phytophthora</i> Genes Encoding Secreted Proteins Reveals Conserved Synteny and Lineage-Specific Gene Duplications and Deletions. <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 1311-1321.	2.6	47
63	Network-Based Prediction and Analysis of HIV Dependency Factors. <i>PLoS Computational Biology</i> , 2011, 7, e1002164.	3.2	47
64	Effector gene silencing mediated by histone methylation underpins host adaptation in an oomycete plant pathogen. <i>Nucleic Acids Research</i> , 2020, 48, 1790-1799.	14.5	47
65	Genetic and Physical Mapping of <i>Avr1a</i> in <i>Phytophthora sojae</i> . <i>Genetics</i> , 2002, 160, 949-959.	2.9	47
66	Unifying Themes in Microbial Associations with Animal and Plant Hosts Described Using the Gene Ontology. <i>Microbiology and Molecular Biology Reviews</i> , 2010, 74, 479-503.	6.6	46
67	Negative regulators of plant immunity derived from cinnamyl alcohol dehydrogenases are targeted by multiple <i>Phytophthora</i> <i>Avr3a</i> -like effectors. <i>New Phytologist</i> , 2019, .	7.3	46
68	Enhanced resistance in <i>Theobroma cacao</i> against oomycete and fungal pathogens by secretion of phosphatidylinositol 3-phosphate-binding proteins. <i>Plant Biotechnology Journal</i> , 2016, 14, 875-886.	8.3	45
69	Cis-acting and trans-acting regulatory mutations define two types of promoters controlled by the <i>qa-1F</i> gene of <i>Neurospora</i> . <i>Cell</i> , 1984, 36, 493-502.	28.9	42
70	Genome organization of <i>Phytophthora megasperma</i> f.sp.glycinea. <i>Experimental Mycology</i> , 1991, 15, 283-291.	1.6	39
71	Whole Genome Re-sequencing Reveals Natural Variation and Adaptive Evolution of <i>Phytophthora sojae</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2792.	3.5	39
72	Cosegregation of <i>Avr4</i> and <i>Avr6</i> in <i>Phytophthora sojae</i> . <i>Canadian Journal of Botany</i> , 1996, 74, 800-802.	1.1	38

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73	Common and contrasting themes in host cell-targeted effectors from bacterial, fungal, oomycete and nematode plant symbionts described using the Gene Ontology. <i>BMC Microbiology</i> , 2009, 9, S3.	3.3	38
74	Infection mechanisms and putative effector repertoire of the mosquito pathogenic oomycete <i>Pythium guiyangense</i> uncovered by genomic analysis. <i>PLoS Genetics</i> , 2019, 15, e1008116.	3.5	38
75	Manipulating Endoplasmic Reticulum-Plasma Membrane Tethering in Plants Through Fluorescent Protein Complementation. <i>Frontiers in Plant Science</i> , 2019, 10, 635.	3.6	36
76	Assaying Effector Function in Planta Using Double-Barreled Particle Bombardment. <i>Methods in Molecular Biology</i> , 2011, 712, 153-172.	0.9	35
77	<i>Phytophthora sojae</i> effector Avr1d functions as an E2 competitor and inhibits ubiquitination activity of GmPUB13 to facilitate infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	35
78	Structure of a <i>Neurospora</i> RNA polymerase I promoter defined by transcription in vitro with homologous extracts. <i>Nucleic Acids Research</i> , 1985, 13, 4311-4332.	14.5	33
79	Generation of long mRNA for membrane immunoglobulin β 2a chains by differential splicing. <i>Nature</i> , 1981, 293, 406-408.	27.8	30
80	Phylogenetic and transcriptional analysis of an expanded bZIP transcription factor family in <i>Phytophthora sojae</i> . <i>BMC Genomics</i> , 2013, 14, 839.	2.8	30
81	An Integrated BAC and Genome Sequence Physical Map of <i>Phytophthora sojae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 1302-1310.	2.6	29
82	Two <i>Theobroma cacao</i> genotypes with contrasting pathogen tolerance show aberrant transcriptional and ROS responses after salicylic acid treatment. <i>Journal of Experimental Botany</i> , 2015, 66, 6245-6258.	4.8	29
83	Long transposon-rich centromeres in an oomycete reveal divergence of centromere features in Stramenopila-Alveolata-Rhizaria lineages. <i>PLoS Genetics</i> , 2020, 16, e1008646.	3.5	29
84	A <i>Neurospora crassa</i> ribosomal protein gene, homologous to yeast CRY1, contains sequences potentially coordinating its transcription with rRNA genes. <i>Nucleic Acids Research</i> , 1990, 18, 5759-5765.	14.5	28
85	Characterization of Cell-Death-Inducing Members of the Pectate Lyase Gene Family in <i>Phytophthora capsici</i> and Their Contributions to Infection of Pepper. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 766-775.	2.6	28
86	Diverse Evolutionary Trajectories for Small RNA Biogenesis Genes in the Oomycete Genus <i>Phytophthora</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 284.	3.6	27
87	Carbon Regulation of Ribosomal Genes in <i>Neurospora crassa</i> Occurs by a Mechanism Which Does Not Require Cre-1, the Homologue of the <i>Aspergillus</i> Carbon Catabolite Repressor, CreA. <i>Fungal Genetics and Biology</i> , 1999, 26, 253-269.	2.1	26
88	Plant science decadal vision 2020–2030: Reimagining the potential of plants for a healthy and sustainable future. <i>Plant Direct</i> , 2020, 4, e00252.	1.9	26
89	EumicrobeDBLite: a lightweight genomic resource and analytic platform for draft oomycete genomes. <i>Molecular Plant Pathology</i> , 2018, 19, 227-237.	4.2	24
90	Tethering of Multi-Vesicular Bodies and the Tonoplast to the Plasma Membrane in Plants. <i>Frontiers in Plant Science</i> , 2019, 10, 636.	3.6	24

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91	Haplotype-Phased Genome Assembly of Virulent <i>Phytophthora ramorum</i> Isolate ND886 Facilitated by Long-Read Sequencing Reveals Effector Polymorphisms and Copy Number Variation. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 1047-1060.	2.6	24
92	C239S Mutation in the β -Tubulin of <i>Phytophthora sojae</i> Confers Resistance to Zoxamide. <i>Frontiers in Microbiology</i> , 2016, 7, 762.	3.5	23
93	Whole Genome Sequences of the Raspberry and Strawberry Pathogens <i>Phytophthora rubi</i> and <i>P. fragariae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2017, 30, 767-769.	2.6	23
94	The fog of war: How network buffering protects plants' defense secrets from pathogens. <i>PLoS Genetics</i> , 2017, 13, e1006713.	3.5	22
95	Coordinated expression of ribosomal protein genes in <i>Neurospora Crassa</i> and identification of conserved upstream sequences. <i>Nucleic Acids Research</i> , 1991, 19, 6511-6517.	14.5	21
96	Distinctive Nuclear Localization Signals in the Oomycete <i>Phytophthora sojae</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 10.	3.5	21
97	PcMuORP1, an Oxathiapiprolin-Resistance Gene, Functions as a Novel Selection Marker for <i>Phytophthora</i> Transformation and CRISPR/Cas9 Mediated Genome Editing. <i>Frontiers in Microbiology</i> , 2019, 10, 2402.	3.5	21
98	Targeting of anti-microbial proteins to the hyphal surface amplifies protection of crop plants against <i>Phytophthora</i> pathogens. <i>Molecular Plant</i> , 2021, 14, 1391-1403.	8.3	21
99	Comparative Genomic Analysis among Four Representative Isolates of <i>Phytophthora sojae</i> Reveals Genes under Evolutionary Selection. <i>Frontiers in Microbiology</i> , 2016, 7, 1547.	3.5	20
100	The <i>Phytophthora sojae</i> Genome Sequence: Foundation for a Revolution. , 2014, , 133-157.		20
101	Cloning and Sequence Analysis of Elicitor Genes of <i>Phytophthora sojae</i> . <i>Fungal Genetics and Biology</i> , 1996, 20, 169-172.	2.1	18
102	Genetic resources for advanced biofuel production described with the Gene Ontology. <i>Frontiers in Microbiology</i> , 2014, 5, 528.	3.5	18
103	Biogenesis and Biological Functions of Extracellular Vesicles in Cellular and Organismal Communication With Microbes. <i>Frontiers in Microbiology</i> , 2022, 13, 817844.	3.5	18
104	The <i>Phytophthora sojae</i> Genome Contains Tandem Repeat Sequences Which Vary from Strain to Strain. <i>Fungal Genetics and Biology</i> , 1996, 20, 43-51.	2.1	16
105	Genetic resources for methane production from biomass described with the Gene Ontology. <i>Frontiers in Microbiology</i> , 2014, 5, 634.	3.5	16
106	Accurate transcription of homologous 5S rRNA and tRNA genes and splicing of tRNA in vitro by soluble extracts of <i>Neurospora</i> . <i>Nucleic Acids Research</i> , 1984, 12, 5737-5755.	14.5	15
107	Oxysterol-binding protein-related protein 2 is not essential for <i>Phytophthora sojae</i> based on CRISPR/Cas9 deletions. <i>Environmental Microbiology Reports</i> , 2018, 10, 293-298.	2.4	14
108	Expansion and Divergence of Argonaute Genes in the Oomycete Genus <i>Phytophthora</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2841.	3.5	14

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109	Genomic Investigation of the Strawberry Pathogen <i>Phytophthora fragariae</i> Indicates Pathogenicity Is Associated With Transcriptional Variation in Three Key Races. <i>Frontiers in Microbiology</i> , 2020, 11, 490.	3.5	14
110	Sequence verification of synthetic DNA by assembly of sequencing reads. <i>Nucleic Acids Research</i> , 2013, 41, e25-e25.	14.5	13
111	A leucine tRNA gene adjacent to the <i>QAgene du</i> of <i>Neurospora crassa</i> . <i>Nucleic Acids Research</i> , 1984, 12, 5757-5765.	14.5	12
112	Strategies for high-efficiency cotransformation of <i>Neurospora crassa</i> . <i>Experimental Mycology</i> , 1990, 14, 9-17.	1.6	12
113	Two complex regions, including a TATA sequence, are required for transcription by RNA polymerase I in <i>Neurospora crassa</i> . <i>Nucleic Acids Research</i> , 1990, 18, 1805-1811.	14.5	11
114	<i>Phytophthora capsici</i> homologue of the cell cycle regulator <i>SDA1</i> is required for sporangial morphology, mycelial growth and plant infection. <i>Molecular Plant Pathology</i> , 2016, 17, 369-387.	4.2	11
115	The Repertoire of Transfer RNA Genes Is Tuned to Codon Usage Bias in the Genomes of <i>Phytophthora sojae</i> and <i>Phytophthora ramorum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 1322-1328.	2.6	10
116	Extensive Variation in Nuclear Mitochondrial DNA Content Between the Genomes of <i>Phytophthora sojae</i> and <i>Phytophthora ramorum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 1329-1336.	2.6	10
117	Interaction of <i>Phytophthora sojae</i> Effector Avr1b With E3 Ubiquitin Ligase GmPUB1 Is Required for Recognition by Soybeans Carrying <i>Phytophthora</i> Resistance Rps1-b and Rps1-k Genes. <i>Frontiers in Plant Science</i> , 2021, 12, 725571.	3.6	10
118	Pyrrolidine, a non-controlled substance, can replace piperidine for the chemical sequencing of DNA. <i>Nucleic Acids Research</i> , 1989, 17, 3317-3317.	14.5	9
119	Protocol of <i>Phytophthora capsici</i> Transformation Using the CRISPR-Cas9 System. <i>Methods in Molecular Biology</i> , 2018, 1848, 265-274.	0.9	9
120	Organization of the sequences flanking immunoglobulin heavy chain genes and their role in class switching. <i>Nucleic Acids Research</i> , 1980, 8, 5579-5598.	14.5	8
121	Viewing the microbial world through the lens of the Gene Ontology. <i>Trends in Microbiology</i> , 2009, 17, 259-261.	7.7	8
122	Stepwise accumulation of mutations in Cesa3 in <i>Phytophthora sojae</i> results in increasing resistance to CAA fungicides. <i>Evolutionary Applications</i> , 2021, 14, 996-1008.	3.1	8
123	Transcriptional Variability Associated With CRISPR-Mediated Gene Replacements at the <i>Phytophthora sojae</i> Avr1b-1 Locus. <i>Frontiers in Microbiology</i> , 2021, 12, 645331.	3.5	7
124	Identification and characterization of simple sequence repeats (SSRs) for population studies of <i>Puccinia novopanic</i> . <i>Journal of Microbiological Methods</i> , 2017, 139, 113-122.	1.6	6
125	Spatial and temporal expression patterns of Avr1b-1 and defense-related genes in soybean plants upon infection with <i>Phytophthora sojae</i> . <i>FEMS Microbiology Letters</i> , 2006, 265, 60-68.	1.8	5
126	An Improved Transformation System for <i>Phytophthora cinnamomi</i> Using Green Fluorescent Protein. <i>Frontiers in Microbiology</i> , 2021, 12, 682754.	3.5	5

#	ARTICLE	IF	CITATIONS
127	To kill or not to kill: the genetic relationship between a parasite and an endophyte. Trends in Microbiology, 1993, 1, 252-254.	7.7	4
128	Nuclear localization of a putative <i>Phytophthora sojae</i> bZIP1 transcription factor is mediated by multiple targeting motifs. Molecular Microbiology, 2017, 104, 621-635.	2.5	3
129	Enrichment of specific genes from genomic DNA or from clone library DNA, using R-looping. Gene, 1980, 10, 147-155.	2.2	2
130	Using Interpolation to Estimate System Uncertainty in Gene Expression Experiments. PLoS ONE, 2011, 6, e22071.	2.5	2
131	Transgenic Soybeans Expressing Phosphatidylinositol-3-Phosphate-Binding Proteins Show Enhanced Resistance Against the Oomycete Pathogen <i>Phytophthora sojae</i> . Frontiers in Microbiology, 0, 13, .	3.5	2
132	Two typical acyl-CoA-binding proteins (ACBPs) are required for the asexual development and virulence of <i>Phytophthora sojae</i> . Fungal Genetics and Biology, 2022, 161, 103695.	2.1	1
133	Microbe-Independent Entry of Oomycete RxLR Effectors and Fungal RxLR-Like Effectors Into Plant and Animal Cells Is Specific and Reproducible. Molecular Plant-Microbe Interactions, 2015, 2015, 51-56.	2.6	0