

Brett M Tyler

List of Publications by Year in descending order

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133
papers

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citations

31976
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142
all docs

142
docs citations

142
times ranked

7932
citing authors

#	ARTICLE	IF	CITATIONS
1	Phytophthora Genome Sequences Uncover Evolutionary Origins and Mechanisms of Pathogenesis. Science, 2006, 313, 1261-1266.	12.6	1,059
2	The Top 10 oomycete pathogens in molecular plant pathology. Molecular Plant Pathology, 2015, 16, 413-434.	4.2	695
3	Signatures of Adaptation to Obligate Biotrophy in the <i>Hyaloperonospora arabidopsidis</i> Genome. Science, 2010, 330, 1549-1551.	12.6	492
4	External Lipid PI3P Mediates Entry of Eukaryotic Pathogen Effectors into Plant and Animal Host Cells. Cell, 2010, 142, 284-295.	28.9	463
5	Transcriptional Programming and Functional Interactions within the <i>Phytophthora sojae</i> RXLR Effector Repertoire. Plant Cell, 2011, 23, 2064-2086.	6.6	455
6	A Secreted Effector Protein of <i>Laccaria bicolor</i> Is Required for Symbiosis Development. Current Biology, 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. Plant Cell, 2008, 20, 1930-1947.	6.6	440
8	<i>Phytophthora sojae</i> : root rot pathogen of soybean and model oomycete. Molecular Plant Pathology, 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. Plant Cell, 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. Proceedings of the National Academy of Sciences of the United States of America, 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. Genome Biology, 2010, 11, R73.	9.6	391
12	Protein secretion systems in bacterial-host associations, and their description in the Gene Ontology. BMC Microbiology, 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> . Molecular Plant-Microbe Interactions, 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. Plant Cell, 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> . Plant Cell, 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. Molecular Plant Pathology, 2016, 17, 127-139.	4.2	253
17	A paralogous decoy protects <i>Phytophthora sojae</i> apoplastic effector PsXEG1 from a host inhibitor. Science, 2017, 355, 710-714.	12.6	236
18	MOLECULAR BASIS OF RECOGNITION BETWEEN PHYTOPHTHORA PATHOGENS AND THEIR HOSTS. Annual Review of Phytopathology, 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>ScpA</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. BMC Microbiology, 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. PLoS Genetics, 2019, 15, e1008116.	3.5	38
75	Manipulating Endoplasmic Reticulum-Plasma Membrane Tethering in Plants Through Fluorescent Protein Complementation. Frontiers in Plant Science, 2019, 10, 635.	3.6	36
76	Assaying Effector Function in Planta Using Double-Barreled Particle Bombardment. Methods in Molecular Biology, 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. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	35
78	Structure of a <i>Neurospora</i> RNA polymerase I promoter defined by transcription in vitro with homologous extracts. Nucleic Acids Research, 1985, 13, 4311-4332.	14.5	33
79	Generation of long mRNA for membrane immunoglobulin β 2a chains by differential splicing. Nature, 1981, 293, 406-408.	27.8	30
80	Phylogenetic and transcriptional analysis of an expanded bZIP transcription factor family in <i>Phytophthora sojae</i> . BMC Genomics, 2013, 14, 839.	2.8	30
81	An Integrated BAC and Genome Sequence Physical Map of <i>Phytophthora sojae</i> . Molecular Plant-Microbe Interactions, 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. Journal of Experimental Botany, 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. PLoS Genetics, 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. Nucleic Acids Research, 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. Molecular Plant-Microbe Interactions, 2015, 28, 766-775.	2.6	28
86	Diverse Evolutionary Trajectories for Small RNA Biogenesis Genes in the Oomycete Genus <i>Phytophthora</i> . Frontiers in Plant Science, 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. Fungal Genetics and Biology, 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. Plant Direct, 2020, 4, e00252.	1.9	26
89	EumicrobeDBLite: a lightweight genomic resource and analytic platform for draft oomycete genomes. Molecular Plant Pathology, 2018, 19, 227-237.	4.2	24
90	Tethering of Multi-Vesicular Bodies and the Tonoplast to the Plasma Membrane in Plants. Frontiers in Plant Science, 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 of 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 novopanici</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

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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