Phytophthora Genome Sequences Uncover Evolutionar Pathogenesis

Science

313, 1261-6

DOI: 10.1126/science.1128796

Citation Report

#	Article	IF	Citations
1	An Integrated BAC and Genome Sequence Physical Map of Phytophthora sojae. Molecular Plant-Microbe Interactions, 2006, 19, 1302-10.	3.7	35
2	The Repertoire of Transfer RNA Genes Is Tuned to Codon Usage Bias in the Genomes of Phytophthora sojae and Phytophthora ramorum. Molecular Plant-Microbe Interactions, 2006, 19, 1322-8.	3.7	12
3	Phytophthora Genomics: The Plant Destroyers' Genome Decoded. Molecular Plant-Microbe Interactions, 2006, 19, 1295-301.	3.7	59
4	Comparative Analysis of Phytophthora Genes Encoding Secreted Proteins Reveals Conserved Synteny and Lineage-Specific Gene Duplications and Deletions. Molecular Plant-Microbe Interactions, 2006, 19, 1311-21.	3.7	46
5	Extensive Variation in Nuclear Mitochondrial DNA Content Between the Genomes of Phytophthora sojae and Phytophthora ramorum. Molecular Plant-Microbe Interactions, 2006, 19, 1329-36.	3.7	11
6	Genomewide Analysis of Phospholipid Signaling Genes in Phytophthora spp.: Novelties and a Missing Link. Molecular Plant-Microbe Interactions, 2006, 19, 1337-47.	3.7	42
7	Identification of Cell Wall-Associated Proteins From Phytophthora ramorum. Molecular Plant-Microbe Interactions, 2006, 19, 1348-58.	3.7	75
8	Targeted Gene Mutation in Phytophthora spp.. Molecular Plant-Microbe Interactions, 2006, 19, 1359-67.	3.7	29
9	Multiple, Non-Allelic, Intein-Coding Sequences in Eukaryotic RNA Polymerase Genes. BMC Biology, 2006, 4, 1-17.	5.2	18
10	Survey and Analysis of Microsatellites From Transcript Sequences in Phytophthora Species: Frequency, Distribution, and Potential as Markers for the Genus. BMC Genomics, 2006, 7, 1-11.	3.9	47
11	Plant Parasitic Oomycetes Such as Phytophthora Species Contain Genes Derived From Three Eukaryotic Lineages. Plant Signaling and Behavior, 2007, 2, 112-4.	4.7	16
12	CFGP: A Web-Based, Comparative Fungal Genomics Platform. Nucleic Acids Research, 2008, 36, D562-71.	19.7	73
13	Invasive Pathogens at Alpine Treeline: Consequences for Treeline Dynamics. Physical Geography, 2007, 28, 397-418.	1.8	69
14	Insights From Sequencing Fungal and Oomycete Genomes: What Can We Learn About Plant Disease and the Evolution of Pathogenicity?. Plant Cell, 2007, 19, 3318-26.	9.4	112
15	Adaptive Evolution Has Targeted the C-Terminal Domain of the RXLR Effectors of Plant Pathogenic Oomycetes. Plant Cell, 2007, 19, 2349-69.	9.4	307
16	Transport of Nuclear-Encoded Proteins Into Secondarily Evolved Plastids. Biological Chemistry, 2007, 388, 899-906.	2.3	41
17	Mycologia, Volume 117, Issue 5 (2025). Mycologia, 2007, 99, 868-76.	2.2	30
18	Expressed Sequence Tags From Phytophthora sojae Reveal Genes Specific to Development and Infection. Molecular Plant-Microbe Interactions, 2007, 20, 781-93.	3.7	59

#	Article	IF	Citations
19	Electrophoretic and Cytological Karyotyping of the Foliar Wheat Pathogen Mycosphaerella graminicola Reveals Many Chromosomes With a Large Size Range. Mycologia, 2007, 99, 868-876.	2.2	32
20	Photosynthetic Declines in Phytophthora ramorum-Infected Plants Develop Prior to Water Stress and in Response to Exogenous Application of Elicitins. Phytopathology, 2007, 97, 850-6.	3.7	25
21	Biochemical and Biological Functions of Class I Phosphatidylinositol Transfer Proteins. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2007, 1771, 677-691.	3.1	81
22	RXLR Effectors of Plant Pathogenic Oomycetes. Current Opinion in Microbiology, 2007, 10, 332-338.	8.6	160
23	Comparative Genomics of Protists: New Insights Into the Evolution of Eukaryotic Signal Transduction and Gene Regulation. Annual Review of Microbiology, 2007, 61, 453-475.	12.4	58
24	Flax Rust Resistance Gene Specificity Is Based on Direct Resistance-Avirulence Protein Interactions. Annual Review of Phytopathology, 2007, 45, 289-306.	13.2	204
25	Noel T. Keen—Pioneer Leader in Molecular Plant Pathology. Annual Review of Phytopathology, 2007, 45, 25-42.	13.2	3
26	Elicitors, Effectors, and R Genes: The New Paradigm and a Lifetime Supply of Questions. Annual Review of Phytopathology, 2007, 45, 399-436.	13.2	734
27	A Glimpse of Streptococcal Toxic Shock Syndrome From Comparative Genomics of S. Suis 2 Chinese Isolates. PLoS ONE, 2007, 2, e315.	3.2	246
28	Assessing the Monophyly of Chlorophyll-c Containing Plastids by Multi-Gene Phylogenies Under the Unlinked Model Conditions. Molecular Phylogenetics and Evolution, 2007, 45, 227-238.	4.0	23
29	Tandem Mass Spectrometry for the Detection of Plant Pathogenic Fungi and the Effects of Database Composition on Protein Inferences. Proteomics, 2007, 7, 3932-3942.	4.5	23
30	A Translocation Signal for Delivery of Oomycete Effector Proteins Into Host Plant Cells. Nature, 2007, 450, 115-118.	54.7	759
31	Phytophthora sojae: Root Rot Pathogen of Soybean and Model Oomycete. Molecular Plant Pathology, 2007, 8, 1-8.	5.2	455
32	Root Rot Disease of Legumes Caused by Aphanomyces Euteiches. Molecular Plant Pathology, 2007, 8, 539-548.	5.2	167
33	Secreted Proteins of Uromyces fabae: Similarities and Stage Specificity. Molecular Plant Pathology, 2008, 9, 59-66.	5.2	42
34	Identification and Comparative Genomic Analysis of Signaling and Regulatory Components in the Diatom Thalassiosira Pseudonana1. Journal of Phycology, 2007, 43, 585-604.	4.0	89
35	Fungal and Oomycete Genes Galore. New Phytologist, 2007, 174, 713-717.	8.9	7
36	Dyneins Across Eukaryotes: A Comparative Genomic Analysis. Traffic, 2007, 8, 1708-1721.	2.9	259

#	Article	IF	Citations
37	Identification of Phytophthora sojae Genes Upregulated During the Early Stage of Soybean Infection. FEMS Microbiology Letters, 2007, 269, 280-8.	2.1	36
38	Avirulence Proteins From Haustoria-Forming Pathogens. FEMS Microbiology Letters, 2007, 269, 181-8.	2.1	110
39	Oomycete Genomics: New Insights and Future Directions. FEMS Microbiology Letters, 2007, 274, 1-8.	2.1	80
40	Expressed Sequence Tags From the Oomycete Plasmopara halstedii, an Obligate Parasite of the Sunflower. BMC Microbiology, 2007, 7, 1-11.	5.5	9
41	Groovy Times: Filamentous Pathogen Effectors Revealed. Current Opinion in Plant Biology, 2007, 10, 358-365.	7.7	262
42	Characterization of Necrosis and Ethylene-Inducing Proteins (NEP) in the Basidiomycete Moniliophthora perniciosa, the Causal Agent of Witches' Broom in Theobroma cacao. Mycological Research, 2007, 111, 443-455.	3.0	79
43	Plastid Genome Sequence of the Cryptophyte Alga Rhodomonas salina CCMP1319: Lateral Transfer of Putative DNA Replication Machinery and a Test of Chromist Plastid Phylogeny. Molecular Biology and Evolution, 2007, 24, 1832-1842.	6.2	105
44	Tryptophan Biosynthesis in Stramenopiles: Eukaryotic Winners in the Diatom Complex Chloroplast. Journal of Molecular Evolution, 2007, 65, 496-511.	2.1	23
45	Mitochondrial Genome Sequences and Comparative Genomics of Phytophthora ramorum and P. Sojae. Current Genetics, 2007, 51, 285-296.	1.8	53
46	Alternate Intron Processing of Family 5 Endoglucanase Transcripts From the Genus Phytophthora. Current Genetics, 2007, 52, 115-123.	1.8	23
47	Correlation of Isozyme Profiles With Genomic Sequences of Phytophthora ramorum and Its P. Sojae Orthologues. Current Genetics, 2007, 52, 247-257.	1.8	5
48	Natural History of Arabidopsis thaliana and Oomycete Symbioses. European Journal of Plant Pathology, 2008, 122, 91-109.	2.5	50
49	Tapping Into Molecular Conversation Between Oomycete Plant Pathogens and Their Hosts. European Journal of Plant Pathology, 2008, 122, 57-69.	2.5	8
50	Comparative Epidemiology of Zoosporic Plant Pathogens. European Journal of Plant Pathology, 2008, 122, 111-126.	2.5	23
51	Classical and Molecular Genetics of Bremia lactucae, Cause of Lettuce Downy Mildew. European Journal of Plant Pathology, 2008, 122, 19-30.	2.5	54
52	Molecular Mechanisms of Plant and Microbe Coexistence. Soil Biology, 2008, .	0.0	49
53	Toward Improvements of Oomycete Transformation Protocols. Journal of Eukaryotic Microbiology, 2008, 55, 103-109.	2.8	69
54	The Phaeodactylum Genome Reveals the Evolutionary History of Diatom Genomes. Nature, 2008, 456, 239-244.	54.7	1,585

#	Article	IF	Citations
55	Genes in the Glass House. Nature, 2008, 456, 179-181.	54.7	3
56	Horizontal Gene Transfer in Eukaryotic Evolution. Nature Reviews Genetics, 2008, 9, 605-618.	59.2	1,217
57	Detecting Evolutionary Transfer of Genes Using PhIGs1. Journal of Phycology, 2008, 44, 19-22.	4.0	3
58	A Hypothesis for Plastid Evolution in CHROMALVEOLATES1. Journal of Phycology, 2008, 44, 1097-1107.	4.0	108
59	Exploration of the Late Stages of the Tomato–Phytophthora Parasitica Interactions Through Histological Analysis and Generation of Expressed Sequence Tags. New Phytologist, 2008, 177, 480-492.	8.9	50
60	Adaptive Eukaryote-to-Eukaryote Lateral Gene Transfer: Stress-Related Genes of Algal Origin in the Closest Unicellular Relatives of Animals. Journal of Evolutionary Biology, 2008, 21, 1852-1860.	2.3	42
61	The Evolution of Virulence and Pathogenicity in Plant Pathogen Populations. Molecular Plant Pathology, 2008, 9, 369-384.	5.2	241
62	Phytophthora infestans: The Plant (and R Gene) Destroyer. Molecular Plant Pathology, 2008, 9, 385-402.	5.2	712
63	Phytophthora ramorum: A Pathogen With a Remarkably Wide Host Range Causing Sudden Oak Death on Oaks and Ramorum Blight on Woody Ornamentals. Molecular Plant Pathology, 2008, 9, 729-740.	5.2	221
64	Reconstruction of the Sudden Oak Death Epidemic in California Through Microsatellite Analysis of the Pathogen Phytophthora ramorum. Molecular Ecology, 2008, 17, 2755-2768.	4.1	136
65	HECTAR: A Method to Predict Subcellular Targeting in Heterokonts. BMC Bioinformatics, 2008, 9, 1-13.	5.8	211
66	Origins of a Cyanobacterial 6-Phosphogluconate Dehydrogenase in Plastid-Lacking Eukaryotes. BMC Evolutionary Biology, 2008, 8, 1-10.	3.7	19
67	Chlamydial Genes Shed Light on the Evolution of Photoautotrophic Eukaryotes. BMC Evolutionary Biology, 2008, 8, 1-18.	3.7	99
68	cDNA-AFLP Analysis of Plant and Pathogen Genes Expressed in Grapevine Infected With Plasmopara viticola. BMC Genomics, 2008, 9, 1-14.	3.9	117
69	Altered Patterns of Gene Duplication and Differential Gene Gain and Loss in Fungal Pathogens. BMC Genomics, 2008, 9, 1-15.	3.9	54
70	Analysis of the Pythium ultimum Transcriptome Using Sanger and Pyrosequencing Approaches. BMC Genomics, 2008, 9, 1-10.	3.9	83
71	Use of Genome Sequence Data in the Design and Testing of SSR Markers for Phytophthora Species. BMC Genomics, 2008, 9, 1-23.	3.9	28
72	Cupin: A Candidate Molecular Structure for the Nep1-Like Protein Family. BMC Plant Biology, 2008, 8, 1-13.	5.6	11

#	Article	IF	Citations
73	Comparative Genomics of Transcription Factors and Chromatin Proteins in Parasitic Protists and Other Eukaryotes. International Journal for Parasitology, 2008, 38, 1-31.	3.3	256
74	Multiple Genes of Apparent Algal Origin Suggest Ciliates May Once Have Been Photosynthetic. Current Biology, 2008, 18, 956-962.	4.7	124
75	Sleep: Approaching the Fundamental Questions. Current Biology, 2008, 18, R665-R667.	4.7	2
76	Plastid Evolution: Remnant Algal Genes in Ciliates. Current Biology, 2008, 18, R663-R665.	4.7	20
77	Oomycete RXLR Effectors: Delivery, Functional Redundancy and Durable Disease Resistance. Current Opinion in Plant Biology, 2008, 11, 373-379.	7.7	169
78	Genome Biology Cracks Enigmas of Oomycete Plant Pathogens. , 2008, .		1
79	Fungal and Oomycete Biotrophy. , 2008, .		0
80	Molecular Biology of Plant Disease Development. , 2008, .		0
81	The Downy Mildews - Genetics, Molecular Biology and Control. , 2008, .		11
82	Cross-Kingdom Patterns of Alternative Splicing and Splice Recognition. Genome Biology, 2008, 9, 1-19.	9.8	131
83	Strategies of Attack and Defense in Plant–Oomycete Interactions, Accentuated for Phytophthora parasitica Dastur (Syn. P. Nicotianae Breda De Haan). Journal of Plant Physiology, 2008, 165, 83-94.	4.8	60
84	The Eukaryotic Tree of Life: Endosymbiosis Takes Its TOL. Trends in Ecology and Evolution, 2008, 23, 268-275.	9.7	240
85	Differences in the Induction of the Oxidative Burst in Compatible and Incompatible Interactions of Soybean and Phytophthora sojae. Physiological and Molecular Plant Pathology, 2008, 73, 16-24.	3.9	19
86	Moving Targets: Rapid Evolution of Oomycete Effectors. Trends in Microbiology, 2008, 16, 507-510.	15.1	16
87	A Multi-Locus Phylogeny for Phytophthora Utilizing Markers Derived From Complete Genome Sequences. Fungal Genetics and Biology, 2008, 45, 266-277.	2.9	463
88	Optimization of Transgene-Mediated Silencing in Phytophthora infestans and Its Association With Small-Interfering RNAs. Fungal Genetics and Biology, 2008, 45, 1197-1205.	2.9	78
89	Molecular Diversity at the Plant–Pathogen Interface. Developmental and Comparative Immunology, 2008, 32, 736-744.	2.5	67
90	Cell Wall Chitosaccharides Are Essential Components and Exposed Patterns of the Phytopathogenic Oomycete Aphanomyces Euteiches. Eukaryotic Cell, 2008, 7, 1980-93.	3.2	94

#	Article	IF	Citations
91	Plastid-Derived Genes in the Nonphotosynthetic Alveolate Oxyrrhis marina. Molecular Biology and Evolution, 2008, 25, 1297-306.	6.2	86
92	Natural History of Arabidopsis thaliana and Oomycete Symbioses. , 2008, .		4
93	RXLR-Mediated Entry of Phytophthora sojae Effector Avr1b Into Soybean Cells Does Not Require Pathogen-Encoded Machinery. Plant Cell, 2008, 20, 1930-1947.	9.4	422
94	Identification of Soluble Secreted Proteins From Appressoria of Colletotrichum higginsianum by Analysis of Expressed Sequence Tags. Microbiology (United Kingdom), 2008, 154, 1204-1217.	4.4	47
95	The Downy Mildew Effector Proteins ATR1 and ATR13 Promote Disease Susceptibility in Arabidopsis thaliana. Plant Cell, 2008, 19, 4077-4090.	9.4	240
96	RXLR Effector Reservoir in Two Phytophthora 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.	9.0	399
97	Whole-Genome Analysis Reveals Molecular Innovations and Evolutionary Transitions in Chromalveolate Species. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3427-3432.	9.0	55
98	A Phytophthora sojae G-Protein Alpha Subunit Is Involved in Chemotaxis to Soybean Isoflavones. Eukaryotic Cell, 2008, 7, 2133-40.	3.2	105
99	Cross-Species Global Proteomics Reveals Conserved and Unique Processes in Phytophthora sojae and Phytophthora ramorum. Molecular and Cellular Proteomics, 2008, 7, 1501-1516.	6.5	40
100	Conserved C-Terminal Motifs Required for Avirulence and Suppression of Cell Death by Phytophthora sojae Effector Avr1b. Plant Cell, 2008, 20, 1118-1133.	9.4	316
101	Phytophthora Database: A Forensic Database Supporting the Identification and Monitoring of Phytophthora. Plant Disease, 2008, 92, 966-972.	2.2	61
102	The Yeast Signal Sequence Trap Identifies Secreted Proteins of the Hemibiotrophic Corn Pathogen Colletotrichum graminicola. Molecular Plant-Microbe Interactions, 2008, 21, 1325-36.	3.7	44
103	Structure of the Glucanase Inhibitor Protein (GIP) Family From Phytophthora Species Suggests Coevolution With Plant Endo-β-1,3-Glucanases. Molecular Plant-Microbe Interactions, 2008, 21, 820-30.	3.7	76
104	Susceptibility in Viburnum to Phytophthora ramorum. Plant Disease, 2008, 92, 210-214.	2.2	18
105	Genetic Resistance to Peronospora tabacina in Nicotiana langsdorffii, a South American Wild Tobacco. Phytopathology, 2008, 98, 519-28.	3.7	7
106	The Phytophthora infestans Avirulence Gene Avr4 Encodes an RXLR-dEER Effector. Molecular Plant-Microbe Interactions, 2008, 21, 1460-70.	3.7	145
107	Gene Expression Profiling During Asexual Development of the Late Blight Pathogen Phytophthora infestans Reveals a Highly Dynamic Transcriptome. Molecular Plant-Microbe Interactions, 2008, 21, 433-47.	3.7	110
108	An Expanded Inventory of Conserved Meiotic Genes Provides Evidence for Sex in Trichomonas vaginalis. PLoS ONE, 2008, 3, e2879.	3.2	223

#	Article	IF	Citations
109	Recent Advances in Cotton Genomics. International Journal of Plant Genomics, 2008, 2008, 742304.	3.3	139
110	Genomes to Proteomes. , 2009, .		1
111	Automation in Proteomics and Genomics. , 2009, .		5
112	Oomycete Genetics and Genomics. , 2009, .		89
113	References. , 2009, .		0
114	Organization of Fungal, Oomycete and Lichen (1,3)-β-Glucans. , 2009, .		9
115	Copy Number Variation and Transcriptional Polymorphisms of Phytophthora sojae RXLR Effector Genes Avr1a and Avr3a. PLoS ONE, 2009, 4, e5066.	3.2	150
116	Relationship Between Phylogenetic Distribution and Genomic Features in Neurospora crassa. PLoS ONE, 2009, 4, e5286.	3.2	39
117	The Phytophthora sojae Avirulence Locus Avr3c Encodes a Multi-Copy RXLR Effector With Sequence Polymorphisms Among Pathogen Strains. PLoS ONE, 2009, 4, e5556.	3.2	102
118	Seeing Green and Red in Diatom Genomes. Science, 2009, 324, 1651-2.	43.1	27
119	Reverse Genetics for Functional Genomics of Phytopathogenic Fungi and Oomycetes. International Journal of Genomics, 2009, 2009, 380719.	1.8	32
120	Large-Scale Phylogenomic Analyses Reveal That Two Enigmatic Protist Lineages, Telonemia and Centroheliozoa, Are Related to Photosynthetic Chromalveolates. Genome Biology and Evolution, 2009, 1, 231-238.	3.2	146
121	In Planta Expression Screens of Phytophthora infestans RXLR Effectors Reveal Diverse Phenotypes, Including Activation of the Solanum bulbocastanum Disease Resistance Protein Rpi-blb2. Plant Cell, 2009, 21, 2928-2947.	9.4	368
122	Cell Wall Polysaccharide Synthases Are Located in Detergent-Resistant Membrane Microdomains in Oomycetes. Applied and Environmental Microbiology, 2009, 75, 1938-49.	4.2	21
123	Population Genetic Analysis Infers Migration Pathways of Phytophthora ramorum in US Nurseries. PLoS Pathogens, 2009, 5, e1000583.	5.0	138
124	Deletions in the Repertoire of Pseudomonas syringae pv. Tomato DC3000 Type III Secretion Effector Genes Reveal Functional Overlap Among Effectors. PLoS Pathogens, 2009, 5, e1000388.	5.0	260
125	Terrific Protein Traffic: The Mystery of Effector Protein Delivery by Filamentous Plant Pathogens. Science, 2009, 324, 748-50.	43.1	171
126	Computational Techniques for Elucidating Plant–Pathogen Interactions From Large-Scale Experiments on Fungi and Oomycetes. Briefings in Bioinformatics, 2009, 10, 654-663.	7.6	7

#	Article	IF	Citations
127	Positive Selection in AvrP4 Avirulence Gene Homologues Across the Genus Melampsora. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 2913-22.	3.4	37
128	Phytophthora sojae: Diversity Among and Within Populations. , 2009, .		26
129	Influence of the Medium-Solidifying Agent, the Nutrient, and the Genotype on the Production of Gametangia by Phytophthora ramorum in Vitro. Mycological Research, 2009, 113, 110-116.	3.0	8
130	Cloning, Expression and Biochemical Characterization of Mitochondrial and Cytosolic Malate Dehydrogenase From Phytophthora infestans. Mycological Research, 2009, 113, 771-781.	3.0	21
131	Cyanobacterial Contribution to the Genomes of the Plastid-Lacking Protists. BMC Evolutionary Biology, 2009, 9, 1-15.	3.7	37
132	Are Algal Genes in Nonphotosynthetic Protists Evidence of Historical Plastid Endosymbioses?. BMC Genomics, 2009, 10, 1-16.	3.9	80
133	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, 1-8.	5.5	48
134	The Puzzle of Plastid Evolution. Current Biology, 2009, 19, R81-R88.	4.7	435
135	Phylogeny of the CDC25 Homology Domain Reveals Rapid Differentiation of Ras Pathways Between Early Animals and Fungi. Cellular Signalling, 2009, 21, 1579-1585.	4.8	22
136	Functional Analysis of Pcipg2 From the Straminopilous Plant Pathogen Phytophthora capsici. Genesis, 2009, 47, 535-544.	1.6	33
137	Intracellular Distribution of the Reductive and Oxidative Pentose Phosphate Pathways in Two Diatoms. Journal of Basic Microbiology, 2009, 49, 58-72.	3.7	43
138	Sizing Up the Genomic Footprint of Endosymbiosis. BioEssays, 2009, 31, 1273-1279.	3.2	48
139	Distribution and Phylogeny of the Blue Light Receptors Aureochromes in Eukaryotes. Planta, 2009, 230, 543-552.	4.7	76
140	Association of Blastocystis Subtype 3 and 1 With Patients From an Oregon Community Presenting With Chronic Gastrointestinal Illness. Parasitology Research, 2009, 104, 341-345.	2.0	97
141	Characterization of Cyclophilin-Encoding Genes in Phytophthora. Molecular Genetics and Genomics, 2009, 281, 565-578.	2.4	21
142	Identification of Phytophthora sojae Genes Involved in Asexual Sporogenesis. Journal of Genetics, 2009, 88, 141-148.	1.0	3
143	Green Fluorescent Protein (GFP) as a Vital Marker for Studying the Interaction of Phytophthora sojae and Soybean. Chinese Science Bulletin, 2009, 54, 2822-2829.	0.9	4
144	Progress in Mapping and Cloning Qualitative and Quantitative Resistance Against Phytophthora infestans in Potato and Its Wild Relatives. Potato Research, 2009, 52, 215-227.	3.9	63

#	Article	IF	Citations
145	Identification of Candidate Signaling Genes Including Regulators of Chromosome Condensation 1 Protein Family Differentially Expressed in the Soybean–Phytophthora Sojae Interaction. Theoretical and Applied Genetics, 2009, 118, 399-412.	4.3	16
146	Inventory and Comparative Evolution of the ABC Superfamily in the Genomes of Phytophthora ramorum and Phytophthora sojae. Journal of Molecular Evolution, 2009, 68, 563-575.	2.1	14
147	The Evolutionary History of Lysine Biosynthesis Pathways Within Eukaryotes. Journal of Molecular Evolution, 2009, 69, 240-248.	2.1	36
148	Solution Structure of the Phytotoxic Protein PcF: The First Characterized Member of the Phytophthora PcF Toxin Family. Protein Science, 2009, 18, 1786-1791.	6.0	31
149	Computational Models in Plant-Pathogen Interactions: The Case of Phytophthora infestans. Theoretical Biology and Medical Modelling, 2009, 6, 1-11.	1.7	15
150	Evidence for Inbreeding and Apomixis in Close Crosses of Phytophthora capsici. Plant Pathology, 2009, 58, 715-722.	2.9	21
151	The Zig-Zag-Zig in Oomycete–Plant Interactions. Molecular Plant Pathology, 2009, 10, 547-562.	5.2	146
152	Roadmap for Future Research on Plant Pathogen Effectors. Molecular Plant Pathology, 2009, 10, 805-813.	5.2	77
153	Ten Things to Know About Oomycete Effectors. Molecular Plant Pathology, 2009, 10, 795-803.	5.2	170
154	Ancient Isolation and Independent Evolution of the Three Clonal Lineages of the Exotic Sudden Oak Death Pathogen Phytophthora ramorum. Molecular Ecology, 2009, 18, 1161-1174.	4.1	129
155	Genome Sequence and Analysis of the Irish Potato Famine Pathogen Phytophthora infestans. Nature, 2009, 461, 393-398.	54.7	1,346
156	Protein Targeting Into Secondary Plastids1. Journal of Eukaryotic Microbiology, 2009, 56, 9-15.	2.8	90
157	Chromalveolates and the Evolution of Plastids by Secondary Endosymbiosis1. Journal of Eukaryotic Microbiology, 2009, 56, 1-8.	2.8	194
158	PCR-RFLP Markers Identify Three Lineages of the North American and European Populations of Phytophthora ramorum. Forest Pathology, 2009, 39, 266-278.	1.2	27
159	Entering and Breaking: Virulence Effector Proteins of Oomycete Plant Pathogens. Cellular Microbiology, 2009, 11, 13-20.	2.3	112
160	Sterol Metabolism in the Oomycete Aphanomyces Euteiches, a Legume Root Pathogen. New Phytologist, 2009, 183, 291-300.	8.9	52
161	Labyrinthulomycetes Phylogeny and Its Implications for the Evolutionary Loss of Chloroplasts and Gain of Ectoplasmic Gliding. Molecular Phylogenetics and Evolution, 2009, 50, 129-140.	4.0	113
162	Comparative Proteomic Studies of Root–Microbe Interactions. Journal of Proteomics, 2009, 72, 353-366.	3.1	86

#	Article	IF	Citations
163	Phosphite Induces Expression of a Putative Proteophosphoglycan Gene in Phytophthora cinnamomi. Australasian Plant Pathology, 2009, 38, 235-241.	1.3	10
164	Biosynthetic Enzymes for (1,3)-β-Glucans and (1,3;1,6)-β-Glucans in Protozoans and Chromistans: Biochemical Characterization and Molecular Biology. , 2009, .		2
165	Identification of the Cellulose Synthase Genes From the Oomycete Saprolegnia monoica and Effect of Cellulose Synthesis Inhibitors on Gene Expression and Enzyme Activity. Fungal Genetics and Biology, 2009, 46, 759-767.	2.9	33
166	Applying the Gene Ontology in Microbial Annotation. Trends in Microbiology, 2009, 17, 262-268.	15.1	15
167	Describing Commonalities in Microbial Effector Delivery Using the Gene Ontology. Trends in Microbiology, 2009, 17, 312-319.	15.1	8
168	Infection Strategies of Filamentous Microbes Described With the Gene Ontology. Trends in Microbiology, 2009, 17, 320-327.	15.1	9
169	The PsCZF1 Gene Encoding a C2H2 Zinc Finger Protein Is Required for Growth, Development and Pathogenesis in Phytophthora sojae. Microbial Pathogenesis, 2009, 47, 78-86.	4.2	52
170	Repeated Secondary Loss of Adaptin Complex Genes in the Apicomplexa. Parasitology International, 2009, 58, 86-94.	2.2	44
171	DNA Transfer From Organelles to the Nucleus: The Idiosyncratic Genetics of Endosymbiosis. Annual Review of Plant Biology, 2009, 60, 115-138.	27.3	349
172	Cellular and Molecular Biology of Phytophthora–Plant Interactions. , 2009, .		4
173	The Secretome of Plant-Associated Fungi and Oomycetes. , 2009, .		22
174	The Ectomycorrhizal Symbiosis: A Marriage of Convenience. , 2009, .		15
175	The Transferome of Metabolic Genes Explored: Analysis of the Horizontal Transfer of Enzyme Encoding Genes in Unicellular Eukaryotes. Genome Biology, 2009, 10, 1-13.	9.8	58
176	The HSP90-SGT1 Chaperone Complex for NLR Immune Sensors. Annual Review of Plant Biology, 2009, 60, 139-64.	27.3	359
177	Multiplex Real-Time Polymerase Chain Reaction (PCR) for Detection of Phytophthora ramorum, the Causal Agent of Sudden Oak Death. Canadian Journal of Plant Pathology, 2009, 31, 195-210.	1.8	29
178	Runaway Repeats Force Expansion of the Phytophthora infestans Genome. Genome Biology, 2009, 10, 1-4.	9.8	20
179	Ustilago maydis as a Pathogen. Annual Review of Phytopathology, 2009, 47, 423-445.	13.2	335
180	The Origin and Spread of Eukaryotic Photosynthesis: Evolving Views in Light of Genomics. Botanica Marina, 2009, 52, 95-103.	1.6	8

#	Article	IF	Citations
181	Evolution of Vacuolar Targeting in Algae. Botanica Marina, 2009, 52, 117-128.	1.6	6
182	Evolution and Genetics of the Invasive Sudden Oak Death Pathogen Phytophthora ramorum. , 2009, .		4
183	Migration Patterns of the Emerging Plant Pathogen Phytophthora ramorum on the West Coast of the United States of America. Phytopathology, 2009, 99, 739-49.	3.7	60
184	Pythium insidiosum and Mammalian Hosts. , 2009, .		9
185	The Role of Oomycete Effectors in Plant–Pathogen Interactions. Functional Plant Biology, 2010, 37, 919-925.	3.2	32
186	Plant Defense Responses to Pests and Pathogens. Acta Horticulturae, 2010, .	0.3	1
187	Different Domains of Phytophthora sojae Effector Avr4/6 Are Recognized by Soybean Resistance Genes Rps4 and Rps6. Molecular Plant-Microbe Interactions, 2010, 23, 425-35.	3.7	78
188	PsSAK1, A Stress-Activated MAP Kinase of Phytophthora sojae, Is Required for Zoospore Viability and Infection of Soybean. Molecular Plant-Microbe Interactions, 2010, 23, 1022-31.	3.7	48
189	Structural and Functional Profile of the Carbohydrate Esterase Gene Complement in Phytophthora infestans. Current Genetics, 2010, 56, 495-506.	1.8	21
190	Defining the Phosphite-Regulated Transcriptome of the Plant Pathogen Phytophthora cinnamomi. Molecular Genetics and Genomics, 2010, 284, 425-435.	2.4	62
191	Proteomic Studies of Phytopathogenic Fungi, Oomycetes and Their Interactions With Hosts. European Journal of Plant Pathology, 2010, 126, 81-95.	2.5	62
192	Genomics of Biotrophy in Fungi and Oomycetes — Emerging Patterns. Current Opinion in Plant Biology, 2010, 13, 409-414.	7.7	48
193	Oomycete–Plant Coevolution: Recent Advances and Future Prospects. Current Opinion in Plant Biology, 2010, 13, 427-433.	7.7	197
194	Armadillo-Repeat Protein Functions: Questions for Little Creatures. Trends in Cell Biology, 2010, 20, 470-481.	23.9	236
195	Taxonomic Distribution and Origins of the Extended LHC (Light-Harvesting Complex) Antenna Protein Superfamily. BMC Evolutionary Biology, 2010, 10, 1-15.	3.7	148
196	The Hidden Duplication Past of the Plant Pathogen Phytophthora and Its Consequences for Infection. BMC Genomics, 2010, 11, 1-16.	3.9	32
197	Comparative Analysis of Secreted Protein Evolution Using Expressed Sequence Tags From Four Poplar Leaf Rusts (Melampsora spp.). BMC Genomics, 2010, 11, 1-16.	3.9	70
198	A BAC/BIBAC-Based Physical Map of Chickpea, Cicer arietinum L. BMC Genomics, 2010, 11, 1-10.	3.9	31

#	Article	IF	Citations
199	The CAZyome of Phytophthora spp.: A Comprehensive Analysis of the Gene Complement Coding for Carbohydrate-Active Enzymes in Species of the Genus Phytophthora. BMC Genomics, 2010, 11, 1-16.	3.9	111
200	Analyses of Genome Architecture and Gene Expression Reveal Novel Candidate Virulence Factors in the Secretome of Phytophthora infestans. BMC Genomics, 2010, 11, 1-18.	3.9	182
201	The Kinome of Phytophthora infestans Reveals Oomycete-Specific Innovations and Links to Other Taxonomic Groups. BMC Genomics, 2010, 11, 1-20.	3.9	45
202	Proteomic Approaches to Study Plant–Pathogen Interactions. Phytochemistry, 2010, 71, 351-362.	3.7	95
203	Towards an Understanding on How RxLR-Effector Proteins Are Translocated From Oomycetes Into Host Cells. Fungal Biology Reviews, 2010, 24, 27-36.	5.4	9
204	Comparative Ecophysiology and Genomics of the Toxic Unicellular Alga Fibrocapsa Japonica. New Phytologist, 2010, 185, 446-458.	8.9	8
205	Calcium Channels in Photosynthetic Eukaryotes: Implications for Evolution of Calcium-Based Signalling. New Phytologist, 2010, 187, 23-43.	8.9	169
206	Central and Storage Carbon Metabolism of the Brown Alga Ectocarpus siliculosus: Insights Into the Origin and Evolution of Storage Carbohydrates in Eukaryotes. New Phytologist, 2010, 188, 67-81.	8.9	185
207	A Secreted Effector Protein (SNE1) From Phytophthora infestans Is a Broadly Acting Suppressor of Programmed Cell Death. Plant Journal, 2010, 62, 357-366.	6.5	114
208	Clonal Expansion of the Belgian Phytophthora ramorum Populations Based on New Microsatellite Markers. Molecular Ecology, 2010, 19, 92-107.	4.1	69
209	Plant Killers on the Spot. Nature Reviews Microbiology, 2010, 8, 615-615.	123.6	0
210	Recent Developments in Effector Biology of Filamentous Plant Pathogens. Cellular Microbiology, 2010, 12, 705-715.	2.3	111
211	Development of New Oomycete Taxon-Specific Mitochondrial Cytochrome b Region Primers for Use in Phylogenetic and Phylogeographic Studies. Journal of Phytopathology, 2010, 158, 321-327.	1.3	13
212	Comparative Genome Analysis Reveals an Absence of Leucine-Rich Repeat Pattern-Recognition Receptor Proteins in the Kingdom Fungi. PLoS ONE, 2010, 5, e12725.	3.2	35
213	Algal Genes in the Closest Relatives of Animals. Molecular Biology and Evolution, 2010, 27, 2879-89.	6.2	38
214	Rewiring and Regulation of Cross-Compartmentalized Metabolism in Protists. Philosophical Transactions of the Royal Society B: Biological Sciences, 2010, 365, 831-45.	5.2	50
215	GPR11, A Putative Seven-Transmembrane G Protein-Coupled Receptor, Controls Zoospore Development and Virulence of Phytophthora sojae. Eukaryotic Cell, 2010, 9, 242-50.	3.2	36
216	Signatures of Adaptation to Obligate Biotrophy in the Hyaloperonospora arabidopsidis Genome. Science, 2010, 330, 1549-1551.	43.1	437

#	Article	IF	Citations
217	Unifying Themes in Microbial Associations With Animal and Plant Hosts Described Using the Gene Ontology. Microbiology and Molecular Biology Reviews, 2010, 74, 479-503.	11.5	50
218	Mediation of the Transition From Biotrophy to Necrotrophy in Hemibiotrophic Plant Pathogens by Secreted Effector Proteins. Plant Signaling and Behavior, 2010, 5, 769-72.	4.7	92
219	Eukaryotic and Eubacterial Contributions to the Establishment of Plastid Proteome Estimated by Large-Scale Phylogenetic Analyses. Molecular Biology and Evolution, 2010, 27, 581-90.	6.2	55
220	Genomics of Fungal Disease Resistance in Tomato. Current Genomics, 2010, 11, 30-39.	4.2	88
221	Sterol Biosynthesis in Oomycete Pathogens. Plant Signaling and Behavior, 2010, 5, 258-60.	4.7	63
222	Evolutionary Biology - Concepts, Molecular and Morphological Evolution. , 2010, .		15
223	A Hierarchical Classification of Polysaccharide Lyases for Glycogenomics. Biochemical Journal, 2010, 432, 437-444.	4.0	358
224	Functional Analysis of Pcpme6 From Oomycete Plant Pathogen Phytophthora capsici. Microbial Pathogenesis, 2010, 49, 23-31.	4.2	29
225	External Lipid PI3P Mediates Entry of Eukaryotic Pathogen Effectors Into Plant and Animal Host Cells. Cell, 2010, 142, 284-295.	38.3	448
226	Virulence, Sporulation, and Elicitin Production in Three Clonal Lineages of Phytophthora ramorum. Physiological and Molecular Plant Pathology, 2010, 74, 317-322.	3.9	26
227	Development of a SNP Genetic Marker System Based on Variation in Microsatellite Flanking Regions of Phytophthora infestans. Canadian Journal of Plant Pathology, 2010, 32, 440-457.	1.8	16
228	The Endosymbiotic Origin, Diversification and Fate of Plastids. Philosophical Transactions of the Royal Society B: Biological Sciences, 2010, 365, 729-48.	5.2	652
229	Getting the Most From the Host: How Pathogens Force Plants to Cooperate in Disease. Molecular Plant-Microbe Interactions, 2010, 23, 1253-9.	3.7	50
230	Introduction to Marine Genomics. , 2010, .		8
231	Genome Sequence of the Necrotrophic Plant Pathogen Pythium ultimum Reveals Original Pathogenicity Mechanisms and Effector Repertoire. Genome Biology, 2010, 11, 1-22.	9.8	357
232	Genome-Wide Analysis of the Diatom Cell Cycle Unveils a Novel Type of Cyclins Involved in Environmental Signaling. Genome Biology, 2010, 11, 1-19.	9.8	106
233	A Common Red Algal Origin of the Apicomplexan, Dinoflagellate, and Heterokont Plastids. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10949-10954.	9.0	459
234	Characterization of Intronic Structures and Alternative Splicing in Phytophthora sojae by Comparative Analysis of Expressed Sequence Tags and Genomic Sequences. Canadian Journal of Microbiology, 2011, 57, 84-90.	2.5	18

#	Article	IF	Citations
235	Purification of Effector–Target Protein Complexes via Transient Expression in Nicotiana benthamiana. Methods in Molecular Biology, 2011, 712, 181-194.	1.2	68
236	Do Red and Green Make Brown?: Perspectives on Plastid Acquisitions Within Chromalveolates. Eukaryotic Cell, 2011, 10, 856-68.	3.2	137
237	Targeted Metabolic Reconstruction: A Novel Approach for the Characterization of Plant-Pathogen Interactions. Briefings in Bioinformatics, 2011, 12, 151-62.	7.6	17
238	Plant ABC Transporters. The Arabidopsis Book, 2011, 9, e0153.	0.0	509
239	Cross-Species Protein Sequence and Gene Structure Prediction With Fine-Tuned Webscipio 2.0 and Scipio. BMC Research Notes, 2011, 4, 1-20.	1.8	51
240	Phytophthora infestans Effector AVRblb2 Prevents Secretion of a Plant Immune Protease at the Haustorial Interface. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 20832-20837.	9.0	291
241	Plant Immunity. Methods in Molecular Biology, 2011, .	1.2	3
242	Expressed Sequence Tags Reveal Genetic Diversity and Putative Virulence Factors of the Pathogenic Oomycete Pythium insidiosum. Fungal Biology, 2011, 115, 683-696.	3.1	40
243	Genome-Wide Identification of Phytophthora sojae SNARE Genes and Functional Characterization of the Conserved SNARE PsYKT6. Fungal Genetics and Biology, 2011, 48, 241-251.	2.9	32
244	Aberrant Genome Size and Instability of Phytophthora ramorum Oospore Progenies. Fungal Genetics and Biology, 2011, 48, 537-543.	2.9	39
245	On the Last Common Ancestor and Early Evolution of Eukaryotes: Reconstructing the History of Mitochondrial Ribosomes. Research in Microbiology, 2011, 162, 53-70.	4.2	92
246	Dothideomycete Effectors Facilitating Biotrophic and Necrotrophic Lifestyles. , 2011, .		3
247	Entry of Oomycete and Fungal Effectors Into Host Cells. , 2011, .		30
248	The Second Phytophthora Mating Hormone Defines Interspecies Biosynthetic Crosstalk. Nature Chemical Biology, 2011, 7, 591-593.	16.4	48
249	Silencing of the PiAvr3a Effector-Encoding Gene From Phytophthora infestans by Transcriptional Fusion to a Short Interspersed Element. Fungal Biology, 2011, 115, 1225-1233.	3.1	20
250	Use of a 15N-Tracer Method as a Tool to Indicate the Assimilation of Elicitin-Sterol Complexes by Phytophthorasojae. International Journal of Biology, 2011, 3, p119.	0.3	1
251	Identification of 18 Genes Encoding Necrosis-Inducing Proteins From the Plant Pathogen Phytophthora capsici (Pythiaceae: Oomycetes). Genetics and Molecular Research, 2011, 10, 910-22.	0.4	16
252	Mining Effector Proteins in Phytopathogenic Fungi. , 2011, .		0

#	Article	IF	Citations
253	Identification of Hyaloperonospora arabidopsidis Transcript Sequences Expressed During Infection Reveals Isolate-Specific Effectors. PLoS ONE, 2011, 6, e19328.	3.2	54
254	The Plant Pathogen Phytophthora Andina Emerged via Hybridization of an Unknown Phytophthora Species and the Irish Potato Famine Pathogen, P. Infestans. PLoS ONE, 2011, 6, e24543.	3.2	90
255	Red and Problematic Green Phylogenetic Signals Among Thousands of Nuclear Genes From the Photosynthetic and Apicomplexa-Related Chromera velia. Genome Biology and Evolution, 2011, 3, 1220-30.	3.2	79
256	Entry of Oomycete and Fungal Effectors Into Plant and Animal Host Cells. Cellular Microbiology, 2011, 13, 1839-1848.	2.3	124
257	Phenotypic Differences Among Three Clonal Lineages of Phytophthora ramorum. Forest Pathology, 2011, 41, 7-14.	1.2	35
258	Infection of Arabidopsis thaliana by Phytophthora parasitica and Identification of Variation in Host Specificity. Molecular Plant Pathology, 2011, 12, 187-201.	5.2	82
259	How Do Oomycete Effectors Interfere With Plant Life?. Current Opinion in Plant Biology, 2011, 14, 407-414.	7.7	131
260	Comparison of Three Microsatellite Analysis Methods for Detecting Genetic Diversity in Phytophthora sojae (Stramenopila: Oomycete). Biotechnology Letters, 2011, 33, 2217-2223.	2.6	25
261	After the Primary Endosymbiosis: An Update on the Chromalveolate Hypothesis and the Origins of Algae With Chl c. Photosynthesis Research, 2011, 107, 103-115.	3.9	80
262	Identification and Analysis of Phytophthora cactorum Genes Up-Regulated During Cyst Germination and Strawberry Infection. Current Genetics, 2011, 57, 297-315.	1.8	16
263	Fifty Years of Oomycetes—From Consolidation to Evolutionary and Genomic Exploration. Fungal Diversity, 2011, 50, 35-46.	19.8	59
264	The Genetic Basis of Resistance to Downy Mildew in Cucumis spp.—Latest Developments and Prospects. Journal of Applied Genetics, 2011, 52, 249-255.	2.4	35
265	Resistance to Plasmopara Viticolain a Grapevine Segregating Population Is Associated With Stilbenoid Accumulation and With Specific Host Transcriptional Responses. BMC Plant Biology, 2011, 11, 1-13.	5.6	113
266	Observing Copepods Through a Genomic Lens. Frontiers in Zoology, 2011, 8, 1-15.	2.8	74
267	Experimental Design and Statistical Rigor in Phylogenomics of Horizontal and Endosymbiotic Gene Transfer. BMC Evolutionary Biology, 2011, 11, 1-8.	3.7	39
268	The Aspartic Proteinase Family of Three Phytophthora Species. BMC Genomics, 2011, 12, 1-15.	3.9	23
269	EST Mining Identifies Proteins Putatively Secreted by the Anthracnose Pathogen Colletotrichum truncatum. BMC Genomics, 2011, 12, 1-16.	3.9	43
270	De Novo Sequence Assembly of Albugo candida Reveals a Small Genome Relative to Other Biotrophic Oomycetes. BMC Genomics, 2011, 12, 1-12.	3.9	112

#	Article	IF	Citations
271	Comparative Structural and Functional Characterization of Putative Protein Effectors Belonging to the PcF Toxin Family From Phytophthora spp. Protein Science, 2011, 20, 2047-2059.	6.0	16
272	Isolation of Nine Phytophthora capsici Pectin Methylesterase Genes Which Are Differentially Expressed in Various Plant Species. Journal of Basic Microbiology, 2011, 51, 61-70.	3.7	20
273	A Domain-Centric Analysis of Oomycete Plant Pathogen Genomes Reveals Unique Protein Organization. Plant Physiology, 2011, 155, 628-644.	6.5	74
274	Horizontal Gene Transfer Facilitated the Evolution of Plant Parasitic Mechanisms in the Oomycetes. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 15258-15263.	9.0	239
275	Characterization of Single-Nucleotide-Polymorphism Markers for Plasmopara viticola, the Causal Agent of Grapevine Downy Mildew. Applied and Environmental Microbiology, 2011, 77, 7861-3.	4.2	13
276	The Comprehensive Phytopathogen Genomics Resource: A Web-Based Resource for Data-Mining Plant Pathogen Genomes. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar053.	2.7	26
277	Effector Diversification Within Compartments of the Leptosphaeria maculans Genome Affected by Repeat-Induced Point Mutations. Nature Communications, 2011, 2, 1-10.	18.1	464
278	Perturbation of Arabidopsis Amino Acid Metabolism Causes Incompatibility With the Adapted Biotrophic Pathogen Hyaloperonospora arabidopsidis. Plant Cell, 2011, 23, 2788-2803.	9.4	110
279	Transcriptional Programming and Functional Interactions Within the Phytophthora sojae RXLR Effector Repertoire. Plant Cell, 2011, 23, 2064-2086.	9.4	413
280	Two Host Cytoplasmic Effectors Are Required for Pathogenesis of Phytophthora sojae by Suppression of Host Defenses. Plant Physiology, 2011, 155, 490-501.	6.5	102
281	Structures of Phytophthora RXLR Effector Proteins: A Conserved but Adaptable Fold Underpins Functional Diversity. Journal of Biological Chemistry, 2011, 286, 35834-35842.	4.2	184
282	Digital Gene Expression Profiling of the Phytophthora sojae Transcriptome. Molecular Plant-Microbe Interactions, 2011, 24, 1530-9.	3.7	113
283	Unexpected Repertoire of Metazoan Transcription Factors in the Unicellular Holozoan Capsaspora Owczarzaki. Molecular Biology and Evolution, 2011, 28, 1241-1254.	6.2	186
284	The Inclusion of Downy Mildews in a Multi-Locus-Dataset and Its Reanalysis Reveals a High Degree of Paraphyly in Phytophthora. IMA Fungus, 2011, 2, 163-171.	3.8	49
285	Gene Gain and Loss During Evolution of Obligate Parasitism in the White Rust Pathogen of Arabidopsis thaliana. PLoS Biology, 2011, 9, e1001094.	5.9	241
286	Phytophthora sojae Avirulence Effector Avr3b Is a Secreted NADH and ADP-Ribose Pyrophosphorylase That Modulates Plant Immunity. PLoS Pathogens, 2011, 7, e1002353.	5.0	173
287	Multiple Candidate Effectors From the Oomycete Pathogen Hyaloperonospora arabidopsidis Suppress Host Plant Immunity. PLoS Pathogens, 2011, 7, e1002348.	5.0	195
288	Fungal and Oomycete Effectors – Strategies to Subdue a Host. Canadian Journal of Plant Pathology, 2011, 33, 425-446.	1.8	15

#	Article	IF	Citations
289	Genome, Functional Gene Annotation, and Nuclear Transformation of the Heterokont Oleaginous Alga Nannochloropsis oceanica CCMP1779. PLoS Genetics, 2012, 8, e1003064.	3.9	415
290	Comparative Analysis of the Genomes of Two Field Isolates of the Rice Blast Fungus Magnaporthe oryzae. PLoS Genetics, 2012, 8, e1002869.	3.9	168
291	Computational Prediction and Molecular Characterization of an Oomycete Effector and the Cognate Arabidopsis Resistance Gene. PLoS Genetics, 2012, 8, e1002502.	3.9	52
292	Sequence Divergent RXLR Effectors Share a Structural Fold Conserved Across Plant Pathogenic Oomycete Species. PLoS Pathogens, 2012, 8, e1002400.	5.0	148
293	Molecular Linkage Mapping and Marker-Trait Associations With NlRPT, a Downy Mildew Resistance Gene in Nicotiana langsdorffii. Frontiers in Plant Science, 2012, 3, 29035.	5.8	12
294	Conserved and Diversified Gene Families of Monovalent Cation/H+ Antiporters From Algae to Flowering Plants. Frontiers in Plant Science, 2012, 3, 17646.	5.8	216
295	Dynamics and Innovations Within Oomycete Genomes: Insights Into Biology, Pathology, and Evolution. Eukaryotic Cell, 2012, 11, 1304-12.	3.2	73
296	Can Silencing of Transposons Contribute to Variation in Effector Gene Expression in Phytophthora infestans?. Mobile Genetic Elements, 2012, 2, 110-114.	3.7	42
297	Algal Genes in Aplastidic Eukaryotes Are Not Necessarily Derived From Historical Plastids. Mobile Genetic Elements, 2012, 2, 193-196.	3.7	2
298	Re-Evaluating the Green Versus Red Signal in Eukaryotes With Secondary Plastid of Red Algal Origin. Genome Biology and Evolution, 2012, 4, 626-35.	3.2	71
299	Nontoxic Nep1-Like Proteins of the Downy Mildew Pathogen Hyaloperonospora arabidopsidis: Repression of Necrosis-Inducing Activity by a Surface-Exposed Region. Molecular Plant-Microbe Interactions, 2012, 25, 697-708.	3.7	68
300	Sudden Oak Death: Interactions of the Exotic Oomycete Phytophthora ramorum With Naïve North American Hosts. Eukaryotic Cell, 2012, 11, 1313-23.	3.2	46
301	Reconstruction of Oomycete Genome Evolution Identifies Differences in Evolutionary Trajectories Leading to Present-Day Large Gene Families. Genome Biology and Evolution, 2012, 4, 199-211.	3.2	46
302	Host-Targeting Protein 1 (SpHtp1) From the Oomycete Saprolegnia parasitica Translocates Specifically Into Fish Cells in a Tyrosine-O-Sulphate–Dependent Manner. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2096-2101.	9.0	85
303	The Genome Portal of the Department of Energy Joint Genome Institute. Nucleic Acids Research, 2012, 40, D26-32.	19.7	463
304	A Comprehensive Analysis of Genes Encoding Small Secreted Proteins Identifies Candidate Effectors in Melampsora larici-Populina (Poplar Leaf Rust). Molecular Plant-Microbe Interactions, 2012, 25, 279-93.	3.7	138
305	The NLP Toxin Family in Phytophthora sojae Includes Rapidly Evolving Groups That Lack Necrosis-Inducing Activity. Molecular Plant-Microbe Interactions, 2012, 25, 896-909.	3.7	97
306	Tomato Immune Receptor Ve1 Recognizes Effector of Multiple Fungal Pathogens Uncovered by Genome and RNA Sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5110-5115.	9.0	478

#	Article	IF	Citations
307	Genome Evolution in Filamentous Plant Pathogens: Why Bigger Can Be Better. Nature Reviews Microbiology, 2012, 10, 417-430.	123.6	639
308	Learning More About Why Effectors Promote Disease. Physiological and Molecular Plant Pathology, 2012, 77, ix.	3.9	0
309	Effects of Latrunculin B on the Actin Cytoskeleton and Hyphal Growth in Phytophthora infestans. Fungal Genetics and Biology, 2012, 49, 1014-1022.	2.9	35
310	Draft Genome Sequence and Genetic Transformation of the Oleaginous Alga Nannochloropsis gaditana. Nature Communications, 2012, 3, 1-11.	18.1	505
311	Borrelidin, a Potent Antifungal Agent: Insight Into the Antifungal Mechanism Against Phytophthora sojae. Journal of Agricultural and Food Chemistry, 2012, 60, 9874-81.	6.6	41
312	Genome Sequences of Phytophthora Enable Translational Plant Disease Management and Accelerate Research. Canadian Journal of Plant Pathology, 2012, 34, 13-19.	1.8	11
313	The Clavibacter michiganensis subsp. Michiganensis–Tomato Interactome Reveals the Perception of Pathogen by the Host and Suggests Mechanisms of Infection. Journal of Proteome Research, 2012, 11, 736-50.	4.0	61
314	Phytophthora sojae Effector Avh331 Suppresses the Plant Defence Response by Disturbing the MAPK Signalling Pathway. Physiological and Molecular Plant Pathology, 2012, 77, 1-9.	3.9	27
315	Plant Disease Resistance Genes: Current Status and Future Directions. Physiological and Molecular Plant Pathology, 2012, 78, 51-65.	3.9	383
316	Emergence of the Sudden Oak Death Pathogen Phytophthora ramorum. Trends in Microbiology, 2012, 20, 131-138.	15.1	277
317	The RxLR Effector Avh241 From Phytophthora sojae Requires Plasma Membrane Localization to Induce Plant Cell Death. New Phytologist, 2012, 196, 247-260.	8.9	139
318	Mechanisms and Evolution of Virulence in Oomycetes. Annual Review of Phytopathology, 2012, 50, 295-318.	13.2	201
319	The Oomycete Pythium oligandrum Expresses Putative Effectors During Mycoparasitism of Phytophthora infestans and Is Amenable to Transformation. Fungal Biology, 2012, 116, 24-41.	3.1	88
320	Differential Expression of the Putative Kex2 Processed and Secreted Aspartic Proteinase Gene Family of Cryphonectria parasitica. Fungal Biology, 2012, 116, 363-378.	3.1	2
321	Genome Sequencing and Mapping Reveal Loss of Heterozygosity as a Mechanism for Rapid Adaptation in the Vegetable Pathogen Phytophthora capsici. Molecular Plant-Microbe Interactions, 2012, 25, 1350-60.	3.7	248
322	Ancient Gene Transfer From Algae to Animals: Mechanisms and Evolutionary Significance. BMC Evolutionary Biology, 2012, 12, 1-10.	3.7	34
323	Systematic and Searchable Classification of Cytochrome P450 Proteins Encoded by Fungal and Oomycete Genomes. BMC Genomics, 2012, 13, 1-13.	3.9	152
324	Homologous RXLR Effectors From Hyaloperonospora arabidopsidis and Phytophthora sojae Suppress Immunity in Distantly Related Plants. Plant Journal, 2012, 72, 882-893.	6.5	89

#	Article	IF	Citations
325	Mitochondrial Origins. , 2012, .		1
326	Effectors of Fungi and Oomycetes: Their Virulence and Avirulence Functions and Translocation From Pathogen to Host Cells. , 2012, .		20
327	The Evolution of Algae by Secondary and Tertiary Endosymbiosis. Advances in Botanical Research, 2012, 64, 87-118.	4.0	50
328	Secondary and Tertiary Endosymbiosis and Kleptoplasty. Advances in Photosynthesis and Respiration, 2012, .	0.0	4
329	Discovery of a Fourth Evolutionary Lineage of Phytophthora ramorum: EU2. Fungal Biology, 2012, 116, 1178-1191.	3.1	89
330	Oomycetes, Effectors, and All That Jazz. Current Opinion in Plant Biology, 2012, 15, 483-492.	7.7	249
331	Roles and Delivery Mechanisms of Fungal Effectors During Infection Development: Common Threads and New Directions. Current Opinion in Microbiology, 2012, 15, 692-698.	8.6	21
332	Secretion, Delivery and Function of Oomycete Effector Proteins. Current Opinion in Microbiology, 2012, 15, 685-691.	8.6	95
333	Construction of BIBAC and BAC Libraries From a Variety of Organisms for Advanced Genomics Research. Nature Protocols, 2012, 7, 479-499.	19.2	24
334	Plastid Origins. , 2012, .		1
335	Signaling and Communication in Plant Symbiosis. Signaling and Communication in Plants, 2012, .	0.0	14
336	Phenotypic Diversification Is Associated With Host-Induced Transposon Derepression in the Sudden Oak Death Pathogen Phytophthora ramorum. PLoS ONE, 2012, 7, e34728.	3.2	57
337	mRNA-Seq Analysis of the Pseudoperonospora cubensis Transcriptome During Cucumber (Cucumis sativus L.) Infection. PLoS ONE, 2012, 7, e35796.	3.2	53
338	Moniliophthora perniciosa Necrosis- and Ethylene-Inducing Protein 2 (MpNep2) as a Metastable Dimer in Solution: Structural and Functional Implications. PLoS ONE, 2012, 7, e45620.	3.2	18
339	Evolution of Virulence in Eukaryotic Microbes. , 2012, .		1
340	Gene Differential Expression of Phytophthora sojae During Sporangium Formation Process. African Journal of Microbiology Research, 2012, 6, 6911-6917.	0.6	3
341	Insights Into the Molecular Mechanism of Tolerance to Carboxylic Acid Amide (CAA) Fungicides in Pythium aphanidermatum. Pest Management Science, 2012, 68, 1171-1183.	4.4	15
342	Preparation of Megabase-Sized DNA From a Variety of Organisms Using the Nuclei Method for Advanced Genomics Research. Nature Protocols, 2012, 7, 467-478.	19.2	111

#	Article	IF	Citations
343	Potato and Tomato Late Blight Caused by Phytophthora infestans: An Overview of Pathology and Resistance Breeding. Plant Disease, 2012, 96, 4-17.	2.2	327
344	Plastid Genomes of Parasitic Plants: A Trail of Reductions and Losses. , 2012, .		17
345	Identification and Detection of Phytophthora: Reviewing Our Progress, Identifying Our Needs. Plant Disease, 2012, 96, 1080-1103.	2.2	208
346	Phylogeny and Molecular Evolution of the Green Algae. Critical Reviews in Plant Sciences, 2012, 31, 1-46.	8.4	827
347	Impacts of Exotic Forest Pathogens on Mediterranean Ecosystems: Four Case Studies. European Journal of Plant Pathology, 2012, 133, 101-116.	2.5	56
348	Oomycete and Fungal Effector Entry, a Microbial Trojan Horse. New Phytologist, 2012, 193, 874-881.	8.9	36
349	Analysis of Polymorphism and Transcription of the Effector Gene Avr1b in Phytophthora sojae Isolates From China Virulent to Rps1b. Molecular Plant Pathology, 2012, 13, 114-122.	5.2	29
350	Subcellular Localization of the Hpa RxLR Effector Repertoire Identifies a Tonoplast-Associated Protein HaRxL17 That Confers Enhanced Plant Susceptibility. Plant Journal, 2012, 69, 252-265.	6.5	153
351	Analysis of Expressed Sequence Tags From the Marine Microalga Pseudochattonella Farcimen (Dictyochophyceae). Protist, 2012, 163, 143-161.	2.1	15
352	RNA-Seq Reveals Infection-Related Global Gene Changes in Phytophthora phaseoli, the Causal Agent of Lima Bean Downy Mildew. Molecular Plant Pathology, 2012, 13, 454-466.	5.2	40
353	Effector Identification in the Lettuce Downy Mildew Bremia lactucae by Massively Parallel Transcriptome Sequencing. Molecular Plant Pathology, 2012, 13, 719-731.	5.2	40
354	The Evolutionary Phylogeny of the Oomycete “Fungi”. Protoplasma, 2012, 249, 3-19.	3.3	314
355	Phytophthora capsici-Tomato Interaction Features Dramatic Shifts in Gene Expression Associated With a Hemi-Biotrophic Lifestyle. Genome Biology, 2013, 14, 1-18.	9.8	125
356	E-Probe Diagnostic Nucleic Acid Analysis (EDNA): A Theoretical Approach for Handling of Next Generation Sequencing Data for Diagnostics. Journal of Microbiological Methods, 2013, 94, 356-366.	2.5	65
357	Antimicrobial Defenses and Resistance in Forest Trees: Challenges and Perspectives in a Genomic Era. Annual Review of Phytopathology, 2013, 51, 221-244.	13.2	67
358	Lateral Gene Transfer in Evolution. , 2013, .		3
359	A Predicted Functional Gene Network for the Plant Pathogen Phytophthora Infestansas a Framework for Genomic Biology. BMC Genomics, 2013, 14, 1-16.	3.9	10
360	From Pathogen Genomes to Host Plant Processes: The Power of Plant Parasitic Oomycetes. Genome Biology, 2013, 14, 1-10.	9.8	58

#	Article	IF	Citations
361	Epigenetics and the Evolution of Virulence. Trends in Microbiology, 2013, 21, 575-582.	15.1	35
362	Host-Related Metabolic Cues Affect Colonization Strategies of a Root Endophyte. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 13965-13970.	9.0	166
363	Phylogenetic and Transcriptional Analysis of an Expanded bZIP Transcription Factor Family in Phytophthora sojae. BMC Genomics, 2013, 14, 1-13.	3.9	24
364	Recent Developments in Blastocystis Research. Advances in Parasitology, 2013, 82, 1-32.	5.0	264
365	Genome-Wide Sequencing of Phytophthora lateralis Reveals Genetic Variation Among Isolates From Lawson Cypress (Chamaecyparis lawsoniana) in Northern Ireland. FEMS Microbiology Letters, 2013, 344, 179-85.	2.1	35
366	Chemotaxis and Oospore Formation in Phytophthora sojae Are Controlled by G-Protein-Coupled Receptors With a Phosphatidylinositol Phosphate Kinase Domain. Molecular Microbiology, 2013, 88, 382-394.	3.2	45
367	Identification and Characterization of in Planta–Expressed Secreted Effector Proteins From Magnaporthe oryzae That Induce Cell Death in Rice. Molecular Plant-Microbe Interactions, 2013, 26, 191-202.	3.7	136
368	Microbial Cytochromes P450: Biodiversity and Biotechnology. Where Do Cytochromes P450 Come From, What Do They Do and What Can They Do for Us?. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120476.	5.2	206
369	Developing a Taxonomic Identification System of Phytophthora Species Based on Microsatellites. Revista Iberoamericana De Micologia, 2013, 30, 88-95.	1.3	7
370	Structural Basis for Interactions of the Phytophthora sojae RxLR Effector Avh5 With Phosphatidylinositol 3-Phosphate and for Host Cell Entry. Molecular Plant-Microbe Interactions, 2013, 26, 330-44.	3.7	78
371	Oomycete Pathogens Encode RNA Silencing Suppressors. Nature Genetics, 2013, 45, 330-333.	25.5	266
372	GK4, A G-Protein-Coupled Receptor With a Phosphatidylinositol Phosphate Kinase Domain in Phytophthora infestans, Is Involved in Sporangia Development and Virulence. Molecular Microbiology, 2013, 88, 352-370.	3.2	39
373	Horizontal Gene Transfer in the Evolution of Photosynthetic Eukaryotes. Journal of Systematics and Evolution, 2013, 51, 13-29.	3.4	26
374	The Number, Speed, and Impact of Plastid Endosymbioses in Eukaryotic Evolution. Annual Review of Plant Biology, 2013, 64, 583-607.	27.3	445
375	Two RxLR Avirulence Genes in Phytophthora sojae Determine Soybean Rps1k-Mediated Disease Resistance. Molecular Plant-Microbe Interactions, 2013, 26, 711-20.	3.7	58
376	Phytophthora Viruses. Advances in Virus Research, 2013, 86, 327-350.	5.7	34
377	The Phytophthora sojae Avr1d Gene Encodes an RxLR-dEER Effector With Presence and Absence Polymorphisms Among Pathogen Strains. Molecular Plant-Microbe Interactions, 2013, 26, 958-68.	3.7	45
378	Phenotypic Diversification by Gene Silencing in Phytophthora Plant Pathogens. Communicative and Integrative Biology, 2013, 6, e25890.	2.6	9

#	Article	IF	Citations
379	Sequence Comparative Analysis Using Networks: Software for Evaluating De Novo Transcript Assembly From Next-Generation Sequencing. Molecular Biology and Evolution, 2013, 30, 1975-86.	6.2	12
380	The Repertoires of Ubiquitinating and Deubiquitinating Enzymes in Eukaryotic Genomes. Molecular Biology and Evolution, 2013, 30, 1172-87.	6.2	77
381	Distinctive Expansion of Potential Virulence Genes in the Genome of the Oomycete Fish Pathogen Saprolegnia parasitica. PLoS Genetics, 2013, 9, e1003272.	3.9	169
382	Hooked and Cooked: A Fish Killer Genome Exposed. PLoS Genetics, 2013, 9, e1003590.	3.9	14
383	An RxLR Effector From Phytophthora infestans Prevents Re-Localisation of Two Plant NAC Transcription Factors From the Endoplasmic Reticulum to the Nucleus. PLoS Pathogens, 2013, 9, e1003670.	5.0	247
384	Review of Soybean Resistance to Pathogens. Ratarstvo I Povrtarstvo, 2013, 50, 52-61.	0.5	16
385	Cloning, Expression, Purification and Initial Analysis of a Novel Pectate Lyase Pcpel1 From Phytophthora capsici. Journal of Phytopathology, 2013, 161, 230-238.	1.3	3
386	New Types of Metacaspases in Phytoplankton Reveal Diverse Origins of Cell Death Proteases. Cell Death and Disease, 2013, 4, e490-e490.	12.1	108
387	Horizontal Transfer and Evolution of Prokaryote Transposable Elements in Eukaryotes. Genome Biology and Evolution, 2013, 5, 822-32.	3.2	52
388	Analyses of Extracellular Carbohydrates in Oomycetes Unveil the Existence of Three Different Cell Wall Types. Eukaryotic Cell, 2013, 12, 194-203.	3.2	167
389	Deletion of the Phytophthora sojae Avirulence Gene Avr1d Causes Gain of Virulence on Rps1d. Molecular Plant-Microbe Interactions, 2013, 26, 969-76.	3.7	38
390	Evolution of Virulence in Oomycete Plant Pathogens. , 2012, .		0
391	Identification and Characterisation CRN Effectors in Phytophthora capsici Shows Modularity and Functional Diversity. PLoS ONE, 2013, 8, e59517.	3.2	144
392	Still Acting Green: Continued Expression of Photosynthetic Genes in the Heterotrophic Dinoflagellate Pfiesteria piscicida (Peridiniales, Alveolata). PLoS ONE, 2013, 8, e68232.	3.2	7
393	Carbohydrate-Active Enzymes in Pythium and Their Role in Plant Cell Wall and Storage Polysaccharide Degradation. PLoS ONE, 2013, 8, e72572.	3.2	100
394	RNA-Seq Reveals Infection-Related Gene Expression Changes in Phytophthora capsici. PLoS ONE, 2013, 8, e74588.	3.2	52
395	Comparative Genomics Reveals Insight Into Virulence Strategies of Plant Pathogenic Oomycetes. PLoS ONE, 2013, 8, e75072.	3.2	147
396	Phytophthora Have Distinct Endogenous Small RNA Populations That Include Short Interfering and microRNAs. PLoS ONE, 2013, 8, e77181.	3.2	64

#	Article	IF	Citations
397	Evolution of RXLR-Class Effectors in the Oomycete Plant Pathogen Phytophthora ramorum. PLoS ONE, 2013, 8, e79347.	3.2	30
398	Characterization of Cell Death Inducing Phytophthora capsici CRN Effectors Suggests Diverse Activities in the Host Nucleus. Frontiers in Plant Science, 2013, 4, 57589.	5.8	56
399	An Ephemeral Sexual Population of Phytophthora infestans in the Northeastern United States and Canada. PLoS ONE, 2014, 9, e116354.	3.2	38
400	Genome Re-Sequencing and Functional Analysis Places the Phytophthora sojae Avirulence Genes Avr1c and Avr1a in a Tandem Repeat at a Single Locus. PLoS ONE, 2014, 9, e89738.	3.2	29
401	Identification of Transcription Factor Genes and Their Correlation With the High Diversity of Stramenopiles. PLoS ONE, 2014, 9, e111841.	3.2	10
402	A Tale of Effectors; Their Secretory Mechanisms and Computational Discovery in Pathogenic, Non-Pathogenic and Commensal Microbes. Molecular Biology (Los Angeles, Calif), 2014, .	0.2	2
403	Small Homologous Blocks in Phytophthora Genomes Do Not Point to an Ancient Whole-Genome Duplication. Genome Biology and Evolution, 2014, 6, 1079-85.	3.2	8
404	Unconventionally Secreted Effectors of Two Filamentous Pathogens Target Plant Salicylate Biosynthesis. Nature Communications, 2014, 5, 1-10.	18.1	337
405	Functionally Redundant RXLR Effectors From Phytophthora infestans Act at Different Steps to Suppress Early flg22-Triggered Immunity. PLoS Pathogens, 2014, 10, e1004057.	5.0	131
406	Duplications and Losses in Gene Families of Rust Pathogens Highlight Putative Effectors. Frontiers in Plant Science, 2014, 5, 89536.	5.8	49
407	Epigenetic Control of Effectors in Plant Pathogens. Frontiers in Plant Science, 2014, 5, 117827.	5.8	46
408	Sex or No Sex: Evolutionary Adaptation Occurs Regardless. BioEssays, 2014, 36, 335-345.	3.2	111
409	Effectors as Tools in Disease Resistance Breeding Against Biotrophic, Hemibiotrophic, and Necrotrophic Plant Pathogens. Molecular Plant-Microbe Interactions, 2014, 27, 196-206.	3.7	348
410	A New Oil-Based Formulation of Trichoderma asperellum for the Biological Control of Cacao Black Pod Disease Caused by Phytophthora megakarya. Biological Control, 2014, 77, 15-22.	3.9	63
411	Sequence Diversity in the Large Subunit of RNA Polymerase I Contributes to Mefenoxam Insensitivity in Phytophthora infestans. Molecular Plant Pathology, 2014, 15, 664-676.	5.2	81
412	Profiling the Secretome and Extracellular Proteome of the Potato Late Blight Pathogen Phytophthora infestans. Molecular and Cellular Proteomics, 2014, 13, 2101-2113.	6.5	67
413	Transcriptomic Analysis of the Phytopathogenic Oomycete Phytophthora cactorum Provides Insights Into Infection-Related Effectors. BMC Genomics, 2014, 15, 1-24.	3.9	34
414	Transcriptome Analysis Reveals Pathogenicity and Evolutionary History of the Pathogenic Oomycete Pythium insidiosum. Fungal Biology, 2014, 118, 640-653.	3.1	27

#	Article	IF	Citations
415	Dual RNA-Seq of the Plant Pathogen Phytophthora ramorum and Its Tanoak Host. Tree Genetics and Genomes, 2014, 10, 489-502.	2.1	53
416	Strategies of Attack and Defence in Woody Plant–Phytophthora Interactions. Forest Pathology, 2014, 44, 169-190.	1.2	107
417	Drechslerella Stenobrocha Genome Illustrates the Mechanism of Constricting Rings and the Origin of Nematode Predation in Fungi. BMC Genomics, 2014, 15, 1-14.	3.9	78
418	Phylogeny and Evolution of Plant Pathogenic Oomycetes—A Global Overview. European Journal of Plant Pathology, 2014, 138, 431-447.	2.5	201
419	Molecular Response to the Pathogen Phytophthora sojae Among Ten Soybean Near Isogenic Lines Revealed by Comparative Transcriptomics. BMC Genomics, 2014, 15, 1-13.	3.9	67
420	Endosymbiotic Gene Transfer in Tertiary Plastid-Containing Dinoflagellates. Eukaryotic Cell, 2014, 13, 246-55.	3.2	59
421	Phytophthora parasitica: A Model Oomycete Plant Pathogen. Mycology, 2014, 5, 43-51.	6.7	98
422	Reprogramming of Plant Cells by Filamentous Plant-Colonizing Microbes. New Phytologist, 2014, 204, 803-814.	8.9	39
423	3 Systematics of the Straminipila: Labyrinthulomycota, Hyphochytriomycota, and Oomycota. , 2014, .		71
424	Phytophthora Suppressor of RNA Silencing 2 Is a Conserved RxLR Effector That Promotes Infection in Soybean and Arabidopsis thaliana. Molecular Plant-Microbe Interactions, 2014, 27, 1379-89.	3.7	88
425	Gene Transfers Shaped the Evolution of De Novo NAD+ Biosynthesis in Eukaryotes. Genome Biology and Evolution, 2014, 6, 2335-49.	3.2	20
426	Quantitative Label-Free Phosphoproteomics of Six Different Life Stages of the Late Blight Pathogen Phytophthora infestans Reveals Abundant Phosphorylation of Members of the CRN Effector Family. Journal of Proteome Research, 2014, 13, 1848-59.	4.0	24
427	Genomics of Plant-Associated Fungi and Oomycetes: Dicot Pathogens. , 2014, .		14
428	Clotrimazole as a Potent Agent for Treating the Oomycete Fish Pathogen Saprolegnia parasitica Through Inhibition of Sterol 14α-Demethylase (CYP51). Applied and Environmental Microbiology, 2014, 80, 6154-66.	4.2	51
429	Gene Expression Profiling of Candidate Virulence Factors in the Laminated Root Rot Pathogen Phellinus sulphurascens. BMC Genomics, 2014, 15, 1-17.	3.9	8
430	Plant ABC Transporters. Signaling and Communication in Plants, 2014, .	0.0	10
431	Carbohydrate-Related Enzymes of Important Phytophthora Plant Pathogens. Fungal Genetics and Biology, 2014, 72, 192-200.	2.9	47
432	A Multilocus Timescale for Oomycete Evolution Estimated Under Three Distinct Molecular Clock Models. BMC Evolutionary Biology, 2014, 14, 1-11.	3.7	67

#	Article	IF	Citations
433	Characterization of Necrosis-Inducing NLP Proteins in Phytophthora capsici. BMC Plant Biology, 2014, 14, 1-19.	5.6	64
434	Recognition of an Avr3a Homologue Plays a Major Role in Mediating Nonhost Resistance to Phytophthora capsici in Nicotiana Species. Molecular Plant-Microbe Interactions, 2014, 27, 770-80.	3.7	64
435	Molecular and Genetic Aspects of Controlling the Soilborne Necrotrophic Pathogens Rhizoctonia and Pythium. Plant Science, 2014, 228, 61-70.	4.9	77
436	Single Amino Acid Mutations in the Potato Immune Receptor R3a Expand Response to Phytophthora Effectors. Molecular Plant-Microbe Interactions, 2014, 27, 624-37.	3.7	128
437	Codon-Based Phylogenetics Introduces Novel Flagellar Gene Markers to Oomycete Systematics. Molecular Phylogenetics and Evolution, 2014, 79, 279-291.	4.0	11
438	Comparative Genomics of the Pine Pathogens and Beetle Symbionts in the Genus Grosmannia. Molecular Biology and Evolution, 2014, 31, 1454-74.	6.2	7
439	Agroinfiltration and PVX Agroinfection in Potato and Nicotiana benthamiana. Journal of Visualized Experiments, 2014, .	0.7	45
440	Recent Progress in RXLR Effector Research. Molecular Plant-Microbe Interactions, 2015, 28, 1063-72.	3.7	146
441	Characterization of Cell-Death-Inducing Members of the Pectate Lyase Gene Family in Phytophthora capsici and Their Contributions to Infection of Pepper. Molecular Plant-Microbe Interactions, 2015, 28, 766-75.	3.7	40
442	Polyphyly of Nuclear Lamin Genes Indicates an Early Eukaryotic Origin of the Metazoan-Type Intermediate Filament Proteins. Scientific Reports, 2015, 5, 1-10.	5.2	44
443	A Phytophthora sojae Cytoplasmic Effector Mediates Disease Resistance and Abiotic Stress Tolerance in Nicotiana benthamiana. Scientific Reports, 2015, 5, 1-15.	5.2	33
444	Genome Sequence and Architecture of the Tobacco Downy Mildew Pathogen Peronospora tabacina. Molecular Plant-Microbe Interactions, 2015, 28, 1198-215.	3.7	52
445	Current Possibilities and Prospects of Using Fungicides in Forestry. Forest Research Papers, 2015, 76, 191-206.	0.1	22
446	Draft Genome Sequences of Phytophthora Kernoviae and Phytophthora ramorum Lineage EU2 From Scotland. Genomics Data, 2015, 6, 193-194.	2.1	19
447	Genome Analyses of the Sunflower Pathogen Plasmopara halstedii Provide Insights Into Effector Evolution in Downy Mildews and Phytophthora. BMC Genomics, 2015, 16, 1-23.	3.9	100
448	Proteomic Profile of the Plant-Pathogenic Oomycete Phytophthora capsici in Response to the Fungicide Pyrimorph. Proteomics, 2015, 15, 2972-2982.	4.5	34
449	In Silico Analysis of Correlations Between Protein Disorder and Post-Translational Modifications in Algae. International Journal of Molecular Sciences, 2015, 16, 19812-19835.	5.9	21
450	Coordination of MicroRNAs, PhasiRNAs, and NB-LRR Genes in Response to a Plant Pathogen: Insights From Analyses of a Set of Soybean Rps Gene Near-Isogenic Lines. Plant Genome, 2015, 8, plantgenome2014.09.0044.	5.4	34

#	Article	IF	Citations
451	The Elicitin-Like Glycoprotein, ELI025, Is Secreted by the Pathogenic Oomycete Pythium insidiosum and Evades Host Antibody Responses. PLoS ONE, 2015, 10, e0118547.	3.2	23
452	A Virulence Essential CRN Effector of Phytophthora capsici Suppresses Host Defense and Induces Cell Death in Plant Nucleus. PLoS ONE, 2015, 10, e0127965.	3.2	45
453	Ancient Origin of the U2 Small Nuclear RNA Gene-Targeting Non-LTR Retrotransposons Utopia. PLoS ONE, 2015, 10, e0140084.	3.2	11
454	The Pectin Methylesterase Gene Complement of Phytophthora sojae: Structural and Functional Analyses, and the Evolutionary Relationships With Its Oomycete Homologs. PLoS ONE, 2015, 10, e0142096.	3.2	12
455	Fungal Biomolecules. , 2015, .		26
456	Oomycete Interactions With Plants: Infection Strategies and Resistance Principles. Microbiology and Molecular Biology Reviews, 2015, 79, 263-80.	11.5	189
457	Evidence for Homoploid Speciation in Phytophthora alni Supports Taxonomic Reclassification in This Species Complex. Fungal Genetics and Biology, 2015, 77, 12-21.	2.9	92
458	A Recent Expansion of the RXLR Effector Gene Avrblb2 Is Maintained in Global Populations of Phytophthora infestans Indicating Different Contributions to Virulence. Molecular Plant-Microbe Interactions, 2015, 28, 901-12.	3.7	34
459	Phytophthora sojae and Soybean Isoflavones, a Model to Study Zoospore Chemotaxis. Physiological and Molecular Plant Pathology, 2015, 92, 161-165.	3.9	20
460	Overexpression of a Phytophthora Cytoplasmic CRN Effector Confers Resistance to Disease, Salinity and Drought in Nicotiana benthamiana. Plant and Cell Physiology, 2015, 56, 2423-35.	4.3	22
461	A New Approach for Detecting Fungal and Oomycete Plant Pathogens in Next Generation Sequencing Metagenome Data Utilising Electronic Probes. International Journal of Data Mining and Bioinformatics, 2015, 12, 115-28.	0.5	30
462	The Two-Speed Genomes of Filamentous Pathogens: Waltz With Plants. Current Opinion in Genetics and Development, 2015, 35, 57-65.	4.4	451
463	Draft Genome Sequences of Seven Isolates of Phytophthora ramorum EU2 From Northern Ireland. Genomics Data, 2015, 6, 191-192.	2.1	4
464	Comparative Proteomic Analysis of Hyphae and Germinating Cysts of Phytophthora pisi and Phytophthora sojae. Journal of Proteomics, 2015, 117, 24-40.	3.1	15
465	Host–Microbe and Microbe–Microbe Interactions in the Evolution of Obligate Plant Parasitism. New Phytologist, 2015, 206, 1207-1228.	8.9	70
466	Acquired Resistance to Mefenoxam in Sensitive Isolates of Phytophthora infestans. Phytopathology, 2015, 105, 342-9.	3.7	63
467	Environmental Microbiology: Fundamentals and Applications. , 2015, .		253
468	Secreted Biomolecules in Fungal Plant Pathogenesis. , 2015, .		13

#	Article	IF	Citations
469	Evolution of Alternative Biosynthetic Pathways for Vitamin C Following Plastid Acquisition in Photosynthetic Eukaryotes. ELife, 2015, .	5.2	162
470	The Histone Acetyltransferase PsGcn5 Mediates Oxidative Stress Responses and Is Required for Full Virulence of Phytophthora sojae. Microbial Pathogenesis, 2015, 87, 51-58.	4.2	16
471	Diversity and Evolution of Cytochrome P450 Monooxygenases in Oomycetes. Scientific Reports, 2015, 5, 1-13.	5.2	36
472	Characterization of the Secretome of Plasmopara viticola by De Novo Transcriptome Analysis. Physiological and Molecular Plant Pathology, 2015, 91, 1-10.	3.9	46
473	A GRASP-Based Memetic Algorithm With Path Relinking for the Far From Most String Problem. Engineering Applications of Artificial Intelligence, 2015, 41, 183-194.	10.2	19
474	The Role of Horizontal Gene Transfer in the Evolution of the Oomycetes. PLoS Pathogens, 2015, 11, e1004805.	5.0	87
475	Experimental Approaches to Investigate Effector Translocation Into Host Cells in the Ustilago maydis/Maize Pathosystem. European Journal of Cell Biology, 2015, 94, 349-358.	4.4	19
476	The Evolution of Parasite Genomes and the Origins of Parasitism. Parasitology, 2015, 142, S1-S5.	2.3	47
477	Phylogenomic Analysis of Emiliania huxleyi Provides Evidence for Haptophyte–Stramenopile Association and a Chimeric Haptophyte Nuclear Genome. Marine Genomics, 2015, 21, 31-42.	1.4	8
478	Phytophthora Effector Targets a Novel Component of Small RNA Pathway in Plants to Promote Infection. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5850-5855.	9.0	193
479	Globalisation, the Founder Effect, Hybrid Phytophthora Species and Rapid Evolution: New Headaches for Biosecurity. Australasian Plant Pathology, 2015, 44, 255-262.	1.3	23
480	Insect Effectors and Gene-for-Gene Interactions With Host Plants. Current Opinion in Insect Science, 2015, 9, 56-61.	4.6	63
481	The Heat Shock Transcription Factor PsHSF1 of Phytophthora sojae Is Required for Oxidative Stress Tolerance and Detoxifying the Plant Oxidative Burst. Environmental Microbiology, 2015, 17, 1351-1364.	4.5	39
482	Genetic Analysis of Environmental Strains of the Plant Pathogen Phytophthora capsici Reveals Heterogeneous Repertoire of Effectors and Possible Effector Evolution via Genomic Island. FEMS Microbiology Letters, 2015, 362, fnv189.	2.1	6
483	Comparative Genomics Including the Early-Diverging Smut Fungus Ceraceosorus Bombacis Reveals Signatures of Parallel Evolution Within Plant and Animal Pathogens of Fungi and Oomycetes. Genome Biology and Evolution, 2015, 7, 2781-98.	3.2	16
484	The Sunflower Downy Mildew Pathogen Plasmopara halstedii. Molecular Plant Pathology, 2015, 16, 109-122.	5.2	94
485	Molecular Phylogenetic Study and Expression Analysis of ATP-Binding Cassette Transporter Gene Family in Oryza sativa in Response to Salt Stress. Computational Biology and Chemistry, 2015, 54, 18-32.	3.8	58
486	Rerouting of Plant Late Endocytic Trafficking Toward a Pathogen Interface. Traffic, 2015, 16, 204-226.	2.9	92

#	Article	IF	Citations
487	Achievements and Challenges in Legume Breeding for Pest and Disease Resistance. Critical Reviews in Plant Sciences, 2015, 34, 195-236.	8.4	214
488	What Lies Beneath: Belowground Defense Strategies in Plants. Trends in Plant Science, 2015, 20, 91-101.	15.2	214
489	The Top 10 Oomycete Pathogens in Molecular Plant Pathology. Molecular Plant Pathology, 2015, 16, 413-434.	5.2	886
490	Single Cell Genome Analysis of an Uncultured Heterotrophic Stramenopile. Scientific Reports, 2014, 4, 1-8.	5.2	49
491	Roles of Rack1 Proteins in Fungal Pathogenesis. BioMed Research International, 2016, 2016, 4130376.	3.8	9
492	Elucidating the Role of Effectors in Plant-Fungal Interactions: Progress and Challenges. Frontiers in Microbiology, 2016, 7, 188193.	5.6	221
493	Studying the Mechanism of Plasmopara viticola RxLR Effectors on Suppressing Plant Immunity. Frontiers in Microbiology, 2016, 7, 191946.	5.6	63
494	Comparative Genomic Analysis Among Four Representative Isolates of Phytophthora sojae Reveals Genes Under Evolutionary Selection. Frontiers in Microbiology, 2016, 7, 205982.	5.6	10
495	Thousand Cankers Disease Complex: A Forest Health Issue That Threatens Juglans Species Across the U.S.. Forests, 2016, 7, 260.	3.1	18
496	Establishment of a Simple and Efficient Agrobacterium-Mediated Transformation System for Phytophthora palmivora. BMC Microbiology, 2016, 16, 1-8.	5.5	24
497	Diverse Evolutionary Trajectories for Small RNA Biogenesis Genes in the Oomycete Genus Phytophthora. Frontiers in Plant Science, 2016, 7, 174824.	5.8	13
498	Uptake of the Fusarium Effector Avr2 by Tomato Is Not a Cell Autonomous Event. Frontiers in Plant Science, 2016, 7, 219769.	5.8	22
499	The tRNA-Derived Small RNAs Regulate Gene Expression Through Triggering Sequence-Specific Degradation of Target Transcripts in the Oomycete Pathogen Phytophthora sojae. Frontiers in Plant Science, 2016, 7, 220129.	5.8	42
500	Splice Sites Seldom Slide: Intron Evolution in Oomycetes. Genome Biology and Evolution, 2016, 8, 2340-50.	3.2	11
501	High-Density Mapping of Resistance QTL Toward Phytophthora sojae, Pythium Irregulare, and Fusarium graminearum in the Same Soybean Population. Crop Science, 2016, 56, 2476-2492.	2.7	49
502	RTP1 Encodes a Novel Endoplasmic Reticulum (ER)-Localized Protein in Arabidopsis and Negatively Regulates Resistance Against Biotrophic Pathogens. New Phytologist, 2016, 209, 1641-1654.	8.9	63
503	Comparative Analysis of Expressed CRN and RXLR Effectors From Two Plasmopara Species Causing Grapevine and Sunflower Downy Mildew. Plant Pathology, 2016, 65, 767-781.	2.9	46
504	Molecular Soybean-Pathogen Interactions. Annual Review of Phytopathology, 2016, 54, 443-68.	13.2	104

#	Article	IF	Citations
505	SCR96, A Small Cysteine-Rich Secretory Protein of Phytophthora cactorum, Can Trigger Cell Death in the Solanaceae and Is Important for Pathogenicity and Oxidative Stress Tolerance. Molecular Plant Pathology, 2016, 17, 577-587.	5.2	47
506	The Syntaxin Protein (MoSyn8) Mediates Intracellular Trafficking to Regulate Conidiogenesis and Pathogenicity of Rice Blast Fungus. New Phytologist, 2016, 209, 1655-1667.	8.9	95
507	Sequencing of the Litchi Downy Blight Pathogen Reveals It Is a Phytophthora Species With Downy Mildew-Like Characteristics. Molecular Plant-Microbe Interactions, 2016, 29, 573-83.	3.7	57
508	A Phytophthora sojae Effector Suppresses Endoplasmic Reticulum Stress-Mediated Immunity by Stabilizing Plant Binding Immunoglobulin Proteins. Nature Communications, 2016, 7, 1-17.	18.1	137
509	Emerging Oomycete Threats to Plants and Animals. Philosophical Transactions of the Royal Society B: Biological Sciences, 2016, 371, 20150459.	5.2	152
510	Insights Into the Adaptive Response of the Plant-Pathogenic Oomycete Phytophthora capsici to the Fungicide Flumorph. Scientific Reports, 2016, 6, 1-9.	5.2	12
511	New Kid on the Block – The Clubroot Pathogen Genome Moves the Plasmodiophorids Into the Genomic Era. European Journal of Plant Pathology, 2016, 145, 531-542.	2.5	29
512	Filamentous Pathogen Effectors Interfering With Small RNA Silencing in Plant Hosts. Current Opinion in Microbiology, 2016, 32, 1-6.	8.6	36
513	Genomes and Virulence Difference Between Two Physiological Races of Phytophthora nicotianae. GigaScience, 2016, 5, 3.	5.6	44
514	Genome Sequences of Six Phytophthora Species Threatening Forest Ecosystems. Genomics Data, 2016, 10, 85-88.	2.1	33
515	The Age of Effectors: Genome-Based Discovery and Applications. Phytopathology, 2016, 106, 1206-1212.	3.7	38
516	Population Structure Among and Within Iowa, Missouri, Ohio, and South Dakota Populations of Phytophthora sojae. Plant Disease, 2016, 100, 367-379.	2.2	34
517	Comparison of Five Detection and Quantification Methods for Phytophthora ramorum in Stream and Irrigation Water. Plant Disease, 2016, 100, 1202-1211.	2.2	23
518	Resurgence of Less-Studied Smut Fungi as Models of Phytopathogenesis in the Omics Age. Phytopathology, 2016, 106, 1244-1254.	3.7	13
519	Diversity, Evolution and Expression Profiles of Histone Acetyltransferases and Deacetylases in Oomycetes. BMC Genomics, 2016, 17, 1-14.	3.9	11
520	Engineering Barriers to Infection by Undermining Pathogen Effector Function or by Gaining Effector Recognition. , 2016, .		4
521	Systematic Search for Evidence of Interdomain Horizontal Gene Transfer From Prokaryotes to Oomycete Lineages. MSphere, 2016, .	4.1	21
522	Host-Induced Aneuploidy and Phenotypic Diversification in the Sudden Oak Death Pathogen Phytophthora ramorum. BMC Genomics, 2016, 17, 1-17.	3.9	61

#	Article	IF	Citations
523	Plant-Pathogen Effectors: Cellular Probes Interfering With Plant Defenses in Spatial and Temporal Manners. Annual Review of Phytopathology, 2016, 54, 419-41.	13.2	602
524	Population Genomics of Fungal and Oomycete Pathogens. Annual Review of Phytopathology, 2016, 54, 323-346.	13.2	88
525	CRN13 Candidate Effectors From Plant and Animal Eukaryotic Pathogens Are DNA-Binding Proteins Which Trigger Host DNA Damage Response. New Phytologist, 2016, 210, 602-617.	8.9	56
526	10 Pheromone Action in the Fungal Groups Chytridiomycetes and Zygomycetes and in the Oophytes. The mycota, 2016, .	0.0	5
527	Blue-Light-Regulated Transcription Factor, Aureochrome, in Photosynthetic Stramenopiles. Journal of Plant Research, 2016, 129, 189-197.	2.3	38
528	Novel Insights on ENTH Domain-Containing Proteins in Apicomplexan Parasites. Parasitology Research, 2016, 115, 2191-2202.	2.0	7
529	Omics-Driven Approaches in Plant–Microbe Interaction. , 2016, .		7
530	Mind the Gap; Seven Reasons to Close Fragmented Genome Assemblies. Fungal Genetics and Biology, 2016, 90, 24-30.	2.9	98
531	Efficient Disruption and Replacement of an Effector Gene in the Oomycete Phytophthora sojae Using CRISPR/Cas9. Molecular Plant Pathology, 2016, 17, 127-139.	5.2	298
532	Quantitative Proteomics Links Metabolic Pathways to Specific Developmental Stages of the Plant-Pathogenic Oomycete Phytophthora capsici. Molecular Plant Pathology, 2017, 18, 378-390.	5.2	17
533	PAMPs, PRRs, Effectors and R-Genes Associated With Citrus-Pathogen Interactions. Annals of Botany, 2017, 119, 749-774.	3.8	63
534	An LRR Receptor Kinase Regulates Growth, Development and Pathogenesis in Phytophthora capsici. Microbiological Research, 2017, 198, 8-15.	9.9	14
535	A Paralogous Decoy Protects Phytophthora sojae Apoplastic Effector PsXEG1 From a Host Inhibitor. Science, 2017, 355, 710-714.	43.1	241
536	Genetic Analysis of Phytophthora sojae Populations in Fujian, China. Plant Pathology, 2017, 66, 1182-1190.	2.9	14
537	Evolution of the Sterol Biosynthetic Pathway of Pythium insidiosum and Related Oomycetes Contributes to Antifungal Drug Resistance. Antimicrobial Agents and Chemotherapy, 2017, .	4.2	61
538	Adaptation of the Pathogen, Pseudomonas syringae, During Experimental Evolution on a Native vs. Alternative Host Plant. Molecular Ecology, 2017, 26, 1790-1801.	4.1	21
539	Harnessing Effector-Triggered Immunity for Durable Disease Resistance. Phytopathology, 2017, 107, 912-919.	3.7	35
540	Breeding for Grapevine Downy Mildew Resistance: A Review of “Omics” Approaches. Euphytica, 2017, 213, 1-21.	1.8	87

#	Article	IF	Citations
541	Genome Sequence of Plasmopara viticola and Insight Into the Pathogenic Mechanism. Scientific Reports, 2017, 7, 1-12.	5.2	85
542	Metabolic Diversity and Novelties in the Oomycetes. Annual Review of Microbiology, 2017, 71, 21-39.	12.4	58
543	Biological Invasions and Its Management in China. , 2017, .		20
544	Cloning and Functional Analysis of Succinate Dehydrogenase Gene PsSDHA in Phytophthora sojae. Microbial Pathogenesis, 2017, 108, 40-48.	4.2	9
545	Taking the Stage: Effectors in the Spotlight. Current Opinion in Plant Biology, 2017, 38, 25-33.	7.7	59
546	Microevolutionary Analyses of Pythium insidiosum Isolates of Brazil and Thailand Based on Exo-1,3-β-Glucanase Gene. Infection, Genetics and Evolution, 2017, 48, 58-63.	2.9	20
547	Endosymbiosis: The Feeling Is Not Mutual. Journal of Theoretical Biology, 2017, 434, 75-79.	1.9	96
548	Network and Role Analysis of Autophagy in Phytophthora sojae. Scientific Reports, 2017, 7, 1-12.	5.2	28
549	Phylogenomic Analysis Supports Multiple Instances of Polyphyly in the Oomycete Peronosporalean Lineage. Molecular Phylogenetics and Evolution, 2017, 114, 199-211.	4.0	18
550	Draft Genome of the Oomycete Pathogen Phytophthora cactorum Strain LV007 Isolated From European Beech (Fagus sylvatica). Genomics Data, 2017, 12, 155-156.	2.1	18
551	Phylogenomic Reconstruction of the Oomycete Phylogeny Derived From 37 Genomes. MSphere, 2017, .	4.1	95
552	Genome Sequences of 12 Isolates of the EU1 Lineage of Phytophthora ramorum, a Fungus-Like Pathogen That Causes Extensive Damage and Mortality to a Wide Range of Trees and Other Plants. Genomics Data, 2017, 12, 17-21.	2.1	11
553	Structural Characterization of a Putative Chitin Synthase Gene in Phytophthora spp. and Analysis of Its Transcriptional Activity During Pathogenesis on Potato and Soybean Plants. Current Genetics, 2017, 63, 909-921.	1.8	17
554	Effectors of Filamentous Plant Pathogens: Commonalities Amid Diversity. Microbiology and Molecular Biology Reviews, 2017, .	11.5	179
555	A Puccinia striiformis f. sp. Tritici Secreted Protein Activates Plant Immunity at the Cell Surface. Scientific Reports, 2017, 7, 1-10.	5.2	39
556	Hyphochytriomycota and Oomycota. , 2017, .		53
557	Intrinsic Disorder Is a Common Structural Characteristic of RxLR Effectors in Oomycete Pathogens. Fungal Biology, 2017, 121, 911-919.	3.1	18
558	Reductive Evolution of Apicomplexan Parasites From Phototrophic Ancestors. , 2017, .		4

#	Article	IF	Citations
559	Are Thraustochytrids Algae?. Fungal Biology, 2017, 121, 835-840.	3.1	108
560	Genomic, Network, and Phylogenetic Analysis of the Oomycete Effector Arsenal. MSphere, 2017, .	4.1	91
561	Genomic Data Quality Impacts Automated Detection of Lateral Gene Transfer in Fungi. G3: Genes, Genomes, Genetics, 2017, 7, 1301-1314.	2.6	24
562	Accessing the Genomic Information of Unculturable Oceanic Picoeukaryotes by Combining Multiple Single Cells. Scientific Reports, 2017, 7, 1-12.	5.2	55
563	Whole Genome Sequences of the Raspberry and Strawberry Pathogens Phytophthora Rubi and P. Fragariae. Molecular Plant-Microbe Interactions, 2017, 30, 767-769.	3.7	14
564	A Candidate RxLR Effector From Plasmopara viticola Can Elicit Immune Responses in Nicotiana benthamiana. BMC Plant Biology, 2017, 17, 1-14.	5.6	49
565	Putative Pathogenicity Genes of Phytophthora cinnamomi Identified via RNA-Seq Analysis of Pre-Infection Structures. European Journal of Plant Pathology, 2017, 147, 211-228.	2.5	18
566	Signatures of Selection and Host-Adapted Gene Expression of the Phytophthora infestans RNA Silencing Suppressor PSR2. Molecular Plant Pathology, 2017, 18, 110-124.	5.2	27
567	Differential Expression of Genes During the Interaction Between Colletotrichum lindemuthianum and Phaseolus vulgaris. European Journal of Plant Pathology, 2017, 147, 653-670.	2.5	9
568	Phytophthora megakarya and P. Palmivora, Closely Related Causal Agents of Cacao Black Pod Rot, Underwent Increases in Genome Sizes and Gene Numbers by Different Mechanisms. Genome Biology and Evolution, 2017, 9, 536-557.	3.2	69
569	Downy Mildew Disease of Crucifers: Biology, Ecology and Disease Management. , 2017, .		40
570	Phylogenetic Diversity of NTT Nucleotide Transport Proteins in Free-Living and Parasitic Bacteria and Eukaryotes. Genome Biology and Evolution, 2017, 9, 480-487.	3.2	40
571	Using Population and Comparative Genomics to Understand the Genetic Basis of Effector-Driven Fungal Pathogen Evolution. Frontiers in Plant Science, 2017, 8, 231749.	5.8	115
572	Genome-Wide Association Studies in Plant Pathosystems: Toward an Ecological Genomics Approach. Frontiers in Plant Science, 2017, 8, 262323.	5.8	145
573	Re-Analyses of “Algal” Genes Suggest a Complex Evolutionary History of Oomycetes. Frontiers in Plant Science, 2017, 8, 282883.	5.8	11
574	Rapid Turnover of Effectors in Grass Powdery Mildew (Blumeria graminis). BMC Evolutionary Biology, 2017, 17, 1-14.	3.7	50
575	β-Glucans, Production and Properties in Microalgae With Emphasis on Nannochloropsis Genus (Ochrophyta, Eustigmatales). Revista De Biologia Marina Y Oceanografia, 2019, 52, 33-49.	0.6	8
576	An Expanded Phylogeny for the Genus Phytophthora. IMA Fungus, 2017, 8, 355-384.	3.8	197

#	Article	IF	Citations
577	Alga-PrAS (Algal Protein Annotation Suite): A Database of Comprehensive Annotation in Algal Proteomes. Plant and Cell Physiology, 2017, 58, e6.	4.3	14
578	Distinct Trophic Specializations Affect How Phytophthora ramorum and Clade 6 Phytophthora spp. Colonize and Persist on Umbellularia californica Leaves in Streams. Phytopathology, 2018, 108, 858-869.	3.7	21
579	Phytophthora sojae Effectors Orchestrate Warfare With Host Immunity. Current Opinion in Microbiology, 2018, 46, 7-13.	8.6	56
580	A Conserved RxLR Effector Interacts With Host RABA-Type GTPases to Inhibit Vesicle-Mediated Secretion of Antimicrobial Proteins. Plant Journal, 2018, 95, 187-203.	6.5	56
581	The Ancient Link Between G-Protein-Coupled Receptors and C-Terminal Phospholipid Kinase Domains. MBio, 2018, .	5.5	23
582	The Succinate Dehydrogenase PsSDHB Is Involved in Hyphal Morphology, Chemical Stress Response and Pathogenicity of Phytophthora sojae. Physiological and Molecular Plant Pathology, 2018, 102, 8-16.	3.9	6
583	Transcription Profiling and Identification of Infection-Related Genes in Phytophthora cactorum. Molecular Genetics and Genomics, 2018, 293, 541-555.	2.4	27
584	Microbiome and Ecotypic Adaption of Holcus lanatus (L.) to Extremes of Its Soil pH Range, Investigated Through Transcriptome Sequencing. Microbiome, 2018, 6, 1-26.	14.8	29
585	The G-Protein γ Subunit of Phytophthora infestans Is Involved in Sporangial Development. Fungal Genetics and Biology, 2018, 116, 73-82.	2.9	12
586	The Phytophthora cactorum Genome Provides Insights Into the Adaptation to Host Defense Compounds and Fungicides. Scientific Reports, 2018, 8, 1-11.	5.2	50
587	Comparative Genomic Analysis of the 'Pseudofungus' Hyphochytrium Catenoides. Open Biology, 2018, 8, 170184.	3.3	34
588	Probing the Phylogenomics and Putative Pathogenicity Genes of Pythium insidiosum by Oomycete Genome Analyses. Scientific Reports, 2018, 8, 1-14.	5.2	41
589	Identification and Functional Analysis of the NLP-Encoding Genes From the Phytopathogenic Oomycete Phytophthora capsici. Molecular Genetics and Genomics, 2018, 293, 931-943.	2.4	29
590	EumicrobeDBLite: A Lightweight Genomic Resource and Analytic Platform for Draft Oomycete Genomes. Molecular Plant Pathology, 2018, 19, 227-237.	5.2	16
591	Phytophthora cinnamomi. Molecular Plant Pathology, 2018, 19, 260-285.	5.2	258
592	Did Some Red Alga-Derived Plastids Evolve via Kleptoplastidy? A Hypothesis. Biological Reviews, 2018, 93, 201-222.	12.7	44
593	ApoplastP: Prediction of Effectors and Plant Proteins in the Apoplast Using Machine Learning. New Phytologist, 2018, 217, 1764-1778.	8.9	161
594	Conserved RxLR Effectors From Oomycetes Hyaloperonospora arabidopsidis and Phytophthora sojae Suppress PAMP- and Effector-Triggered Immunity in Diverse Plants. Molecular Plant-Microbe Interactions, 2018, 31, 374-385.	3.7	51

#	Article	IF	Citations
595	Rediscovery and Analysis of Phytophthora Carbohydrate Esterase (CE) Genes Revealing Their Evolutionary Diversity. Journal of Integrative Agriculture, 2018, 17, 878-891.	4.8	1
596	Comparative Genomics of Downy Mildews Reveals Potential Adaptations to Biotrophy. BMC Genomics, 2018, 19, 1-23.	3.9	46
597	Expansion and Divergence of Argonaute Genes in the Oomycete Genus Phytophthora. Frontiers in Microbiology, 2018, 9, 418738.	5.6	7
598	The MADS-Box Transcription Factor PsMAD1 Is Involved in Zoosporogenesis and Pathogenesis of Phytophthora sojae. Frontiers in Microbiology, 2018, 9, 408252.	5.6	31
599	Bioinformatic Characterisation of the Effector Repertoire of the Strawberry Pathogen Phytophthora cactorum. PLoS ONE, 2018, 13, e0202305.	3.2	40
600	Phytophthora Methylomes Are Modulated by 6mA Methyltransferases and Associated With Adaptive Genome Regions. Genome Biology, 2018, 19, 1-16.	9.8	53
601	Characterization of Phenotypic Variation and Genome Aberrations Observed Among Phytophthora ramorum Isolates From Diverse Hosts. BMC Genomics, 2018, 19, 1-19.	3.9	22
602	Detection of Endogenous Phosphatidylinositol 4,5–Bisphosphate in Phytophthora cinnamomi. Lipids, 2018, 53, 835-839.	1.6	1
603	Application of Alignment-Free Bioinformatics Methods to Identify an Oomycete Protein With Structural and Functional Similarity to the Bacterial AvrE Effector Protein. PLoS ONE, 2018, 13, e0195559.	3.2	16
604	From Short Reads to Chromosome-Scale Genome Assemblies. Methods in Molecular Biology, 2018, 1848, 151-197.	1.2	7
605	Phytophthora infestans RXLR Effector SFI5 Requires Association With Calmodulin for PTI/MTI Suppressing Activity. New Phytologist, 2018, 219, 1433-1446.	8.9	39
606	Draft Genome Sequence for the Tree Pathogen Phytophthora plurivora. Genome Biology and Evolution, 2018, 10, 2432-2442.	3.2	24
607	Mitochondrial Glycolysis in a Major Lineage of Eukaryotes. Genome Biology and Evolution, 2018, 10, 2310-2325.	3.2	60
608	Stable Predictive Markers for Phytophthora sojae Avirulence Genes That Impair Infection of Soybean Uncovered by Whole Genome Sequencing of 31 Isolates. BMC Biology, 2018, 16, 1-16.	5.2	39
609	In Planta Functional Analysis and Subcellular Localization of the Oomycete Pathogen Plasmopara viticola Candidate RXLR Effector Repertoire. Frontiers in Plant Science, 2018, 9, 313581.	5.8	69
610	Abscisic Acid as a Dominant Signal in Tomato During Salt Stress Predisposition to Phytophthora Root and Crown Rot. Frontiers in Plant Science, 2018, 9, 363448.	5.8	26
611	Chimeric Structure of Plant Malic Enzyme Family: Different Evolutionary Scenarios for NAD- and NADP-Dependent Isoforms. Frontiers in Plant Science, 2018, 9, 340878.	5.8	17
612	Genome-Wide Identification of Long Non-Coding RNAs Suggests a Potential Association With Effector Gene Transcription in Phytophthora sojae. Molecular Plant Pathology, 2018, 19, 2177-2186.	5.2	32

#	Article	IF	Citations
613	Mining of Potential Drug Targets Through the Identification of Essential and Analogous Enzymes in the Genomes of Pathogens of Glycine max, Zea mays and Solanum lycopersicum. PLoS ONE, 2018, 13, e0197511.	3.2	4
614	Quantitative Proteomic Analysis of Four Developmental Stages of Saprolegnia parasitica. Frontiers in Microbiology, 2018, 8, 308790.	5.6	25
615	Aquatic Pseudomonads Inhibit Oomycete Plant Pathogens of Glycine max. Frontiers in Microbiology, 2018, 9, 337060.	5.6	28
616	A Possible Trifunctional β-Carotene Synthase Gene Identified in the Draft Genome of Aurantiochytrium sp. Strain KH105. Genes, 2018, 9, 200.	3.4	43
617	Transgenic Research on Tomato: Problems, Strategies, and Achievements. , 2018, .		2
618	A Phytophthora capsici RXLR Effector Targets and Inhibits a Plant PPIase to Suppress Endoplasmic Reticulum-Mediated Immunity. Molecular Plant, 2018, 11, 1067-1083.	27.3	116
619	Genomics Analysis of Aphanomyces spp. Identifies a New Class of Oomycete Effector Associated With Host Adaptation. BMC Biology, 2018, 16, 1-21.	5.2	48
620	Analysis of Microsatellites From Transcriptome Sequences of Phytophthora capsici and Applications for Population Studies. Scientific Reports, 2018, 8, 1-12.	5.2	29
621	The Gene Expression Analysis of Arabidopsis thaliana ABC Transporters by Real-Time PCR for Screening Monolignol-Transporter Candidates. Journal of Wood Science, 2018, 64, 477-484.	2.5	21
622	Chitin Synthase Is Involved in Vegetative Growth, Asexual Reproduction and Pathogenesis of Phytophthora capsici and Phytophthora sojae. Environmental Microbiology, 2019, 21, 4537-4547.	4.5	49
623	Updated Assembly of Phytophthora ramorum pr102 Isolate Incorporating Long Reads From PacBio Sequencing. Molecular Plant-Microbe Interactions, 2019, 32, 1472-1474.	3.7	16
624	Activity and Phylogenetics of the Broadly Occurring Family of Microbial Nep1-Like Proteins. Annual Review of Phytopathology, 2019, 57, 367-386.	13.2	88
625	Microbial Invasions in Terrestrial Ecosystems. Nature Reviews Microbiology, 2019, 17, 621-631.	123.6	117
626	The Nuclear-Localized RxLR Effector PvAvh74 From Plasmopara viticola Induces Cell Death and Immunity Responses in Nicotiana benthamiana. Frontiers in Microbiology, 2019, 10, 463779.	5.6	30
627	Effectors of Phytophthora Pathogens Are Powerful Weapons for Manipulating Host Immunity. Planta, 2019, 250, 413-425.	4.7	60
628	Oomycete Gene Table: An Online Database for Comparative Genomic Analyses of the Oomycete Microorganisms. Database: the Journal of Biological Databases and Curation, 2019, .	2.7	12
629	Diversity and Evolution of Chitin Synthases in Oomycetes (Straminipila: Oomycota). Molecular Phylogenetics and Evolution, 2019, 139, 106558.	4.0	24
630	Plasmopara viticola Effector PvRXLR159 Suppresses Immune Responses in Nicotiana benthamiana. Plant Signaling and Behavior, 2019, 14, 1682220.	4.7	21

#	Article	IF	Citations
631	PcMuORP1, An Oxathiapiprolin-Resistance Gene, Functions as a Novel Selection Marker for Phytophthora Transformation and CRISPR/Cas9 Mediated Genome Editing. Frontiers in Microbiology, 2019, 10, 485903.	5.6	42
632	Candidate Effectors From Uromyces appendiculatus, the Causal Agent of Rust on Common Bean, Can Be Discriminated Based on Suppression of Immune Responses. Frontiers in Plant Science, 2019, 10, 474937.	5.8	21
633	Potato Germplasm Enhancement Enters the Genomics Era. Agronomy, 2019, 9, 575.	4.4	46
634	miR-129-5p Regulates the Immunomodulatory Functions of Adipose-Derived Stem Cells via Targeting Stat1 Signaling. Stem Cells International, 2019, 2019, 2631024.	4.1	7
635	Draft Assembly of Phytophthora capsici From Long-Read Sequencing Uncovers Complexity. Molecular Plant-Microbe Interactions, 2019, 32, 1559-1563.	3.7	33
636	Increased Expression of Phytophthora sojae Genes Encoding Membrane-Degrading Enzymes Appears to Suggest an Early Onset of Necrotrophy During Glycine max Infection. Fungal Genetics and Biology, 2019, 133, 103268.	2.9	7
637	Comprehensive, Classical and Molecular Characterization Methods of Saprolegnia (Oomycota; Stramnipila), an Important Fungal Pathogen of Fish. Fungal Biology Reviews, 2019, 33, 166-179.	5.4	21
638	Genomic Signatures of Heterokaryosis in the Oomycete Pathogen Bremia lactucae. Nature Communications, 2019, 10, 1-13.	18.1	59
639	Defense and Counterdefense During Plant-Pathogenic Oomycete Infection. Annual Review of Microbiology, 2019, 73, 667-696.	12.4	171
640	Ecology and Evolution of the Sudden Oak Death Pathogen Phytophthora ramorum. Annual Review of Phytopathology, 2019, 57, 301-321.	13.2	84
641	Small RNAs Generated by Bidirectional Transcription Mediate Silencing of RXLR Effector Genes in the Oomycete Phytophthora sojae. Phytopathology Research, 2019, 1, 1-11.	4.4	11
642	Comparative Genomics Approach to Build a Genome-Wide Database of High-Quality, Informative Microsatellite Markers: Application on Phytophthora sojae, a Soybean Pathogen. Scientific Reports, 2019, 9, 1-6.	5.2	6
643	Comparative Expression Analysis of Phytophthora sojae Polysaccharide Lyase Family 3 (Pectate Lyase) Genes During Infection of the Soybean Glycine max. Phytopathology Research, 2019, 1, 1-15.	4.4	4
644	Alternative Molecular-Based Diagnostic Methods of Plant Pathogenic Fungi Affecting Berry Crops—A Review. Molecules, 2019, 24, 1200.	5.4	19
645	Mitotic Recombination and Rapid Genome Evolution in the Invasive Forest Pathogen Phytophthora ramorum. MBio, 2019, .	5.5	69
646	The Emergence of the Multi-Species NIP1 Effector in Rhynchosporium Was Accompanied by High Rates of Gene Duplications and Losses. Environmental Microbiology, 2019, 21, 2677-2695.	4.5	25
647	Oomycete-Root Interactions. Rhizosphere Biology, 2019, .	0.0	10
648	A Phytophthora capsici Effector Targets ACD11 Binding Partners That Regulate ROS-Mediated Defense Response in Arabidopsis. Molecular Plant, 2019, 12, 565-581.	27.3	125

#	Article	IF	Citations
649	Phytophthora sojae Effector PsAvh240 Inhibits Host Aspartic Protease Secretion to Promote Infection. Molecular Plant, 2019, 12, 552-564.	27.3	66
650	A High-Quality Grapevine Downy Mildew Genome Assembly Reveals Rapidly Evolving and Lineage-Specific Putative Host Adaptation Genes. Genome Biology and Evolution, 2019, 11, 954-969.	3.2	67
651	A Genome-Wide Analysis of Coatomer Protein (COP) Subunits of Apicomplexan Parasites and Their Evolutionary Relationships. BMC Genomics, 2019, 20, 1-13.	3.9	6
652	A Single Loss of Photosynthesis in the Diatom Order Bacillariales (Bacillariophyta). American Journal of Botany, 2019, 106, 560-572.	2.7	15
653	The WY Domain in the Phytophthora Effector PSR1 Is Required for Infection and RNA Silencing Suppression Activity. New Phytologist, 2019, 223, 839-852.	8.9	45
654	effectR: An Expandable R Package to Predict Candidate RxLR and CRN Effectors in Oomycetes Using Motif Searches. Molecular Plant-Microbe Interactions, 2019, 32, 1067-1076.	3.7	41
655	Haplotype-Phased Genome Assembly of Virulent Phytophthora ramorum Isolate ND886 Facilitated by Long-Read Sequencing Reveals Effector Polymorphisms and Copy Number Variation. Molecular Plant-Microbe Interactions, 2019, 32, 1047-1060.	3.7	20
656	Molecular Characterization of Phytophthora palmivora Responsible for Bud Rot Disease of Oil Palm in Colombia. World Journal of Microbiology and Biotechnology, 2019, 35, 1-23.	5.0	15
657	A Phytophthora capsici Virulence Effector Associates With NPR1 and Suppresses Plant Immune Responses. Phytopathology Research, 2019, 1, 1-11.	4.4	50
658	A Sulfur-Containing Volatile Emitted by Potato-Associated Bacteria Confers Protection Against Late Blight Through Direct Anti-Oomycete Activity. Scientific Reports, 2019, 9, 1-15.	5.2	33
659	Whole Genome Re-Sequencing Reveals Natural Variation and Adaptive Evolution of Phytophthora sojae. Frontiers in Microbiology, 2019, 10, 496139.	5.6	47
660	Network Analysis Exposes Core Functions in Major Lifestyles of Fungal and Oomycete Plant Pathogens. BMC Genomics, 2019, 20, 1-15.	3.9	30
661	PpCRN7 And PpCRN20 of Phythophthora parasitica Regulate Plant Cell Death Leading to Enhancement of Host Susceptibility. BMC Plant Biology, 2019, 19, 1-17.	5.6	16
662	Comparative Analysis of Oomycete Genome Evolution Using the Oomycete Gene Order Browser (OGOB). Genome Biology and Evolution, 2019, 11, 189-206.	3.2	21
663	The Phytophthora sojae RXLR Effector Avh238 Destabilizes Soybean Type2 GmACSs to Suppress Ethylene Biosynthesis and Promote Infection. New Phytologist, 2019, 222, 425-437.	8.9	83
664	Arms Race: Diverse Effector Proteins With Conserved Motifs. Plant Signaling and Behavior, 2019, 14, 1557008.	4.7	67
665	Pectin Acetylesterase PAE5 Is Associated With the Virulence of Plant Pathogenic Oomycete Peronophythora litchii. Physiological and Molecular Plant Pathology, 2019, 106, 16-22.	3.9	50
666	An RXLR Effector Secreted by Phytophthora parasitica Is a Virulence Factor and Triggers Cell Death in Various Plants. Molecular Plant Pathology, 2019, 20, 356-371.	5.2	56

#	Article	IF	Citations
667	Phytophthora Urerae sp. nov., a New Clade 1c Relative of the Irish Famine Pathogen Phytophthora infestans From South America. Plant Pathology, 2019, 68, 557-565.	2.9	3
668	Pathogen Enrichment Sequencing (PenSeq) Enables Population Genomic Studies in Oomycetes. New Phytologist, 2019, 221, 1634-1648.	8.9	47
669	From Genomes to Forest Management – Tackling Invasive Phytophthora Species in the Era of Genomics. Canadian Journal of Plant Pathology, 2020, 42, 1-29.	1.8	21
670	Genomic Biosurveillance of Forest Invasive Alien Enemies: A Story Written in Code. Evolutionary Applications, 2020, 13, 95-115.	3.3	83
671	Dynamic Extreme Aneuploidy (DEA) in the Vegetable Pathogen Phytophthora capsici and the Potential for Rapid Asexual Evolution. PLoS ONE, 2020, 15, e0227250.	3.2	17
672	The Glycoside Hydrolase 18 Family Chitinases Are Associated With Development and Virulence in the Mosquito Pathogen Pythium Guiyangense. Fungal Genetics and Biology, 2020, 135, 103290.	2.9	17
673	Effector Gene Silencing Mediated by Histone Methylation Underpins Host Adaptation in an Oomycete Plant Pathogen. Nucleic Acids Research, 2020, 48, 1790-1799.	19.7	78
674	N-Glycosylation Shields Phytophthora sojae Apoplastic Effector PsXEG1 From a Specific Host Aspartic Protease. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 27685-27693.	9.0	93
675	Comparative Analyses of Saprotrophy in Salisapilia Sapeloensis and Diverse Plant Pathogenic Oomycetes Reveal Lifestyle-Specific Gene Expression. FEMS Microbiology Ecology, 2020, .	4.1	11
676	A Global Survey of Carbohydrate Esterase Families 1 and 10 in Oomycetes. Frontiers in Genetics, 2020, 11, 546276.	3.2	18
677	The Effector Repertoire of the Hop Downy Mildew Pathogen Pseudoperonospora humuli. Frontiers in Genetics, 2020, 11, 538988.	3.2	13
678	Genome-Wide Microsatellites and Species Specific Markers in Genus Phytophthora Revealed Through Whole Genome Analysis. 3 Biotech, 2020, 10, 1-8.	3.5	10
679	Horizontal Gene Transfer and Tandem Duplication Shape the Unique CAZyme Complement of the Mycoparasitic Oomycetes Pythium oligandrum and Pythium periplocum. Frontiers in Microbiology, 2020, 11, 581698.	5.6	22
680	Prediction and Characterization of RXLR Effectors in Pythium Species. Molecular Plant-Microbe Interactions, 2020, 33, 1046-1058.	3.7	41
681	The Genome of Peronospora belbahrii Reveals High Heterozygosity, a Low Number of Canonical Effectors, and TC-Rich Promoters. Molecular Plant-Microbe Interactions, 2020, 33, 742-753.	3.7	22
682	Genome Reconstruction of the Non-Culturable Spinach Downy Mildew Peronospora effusa by Metagenome Filtering. PLoS ONE, 2020, 15, e0225808.	3.2	22
683	Comparative Genomic and Proteomic Analyses of Three Widespread Phytophthora Species: Phytophthora chlamydospora, Phytophthora gonapodyides and Phytophthora pseudosyringae. Microorganisms, 2020, 8, 653.	5.1	46
684	Identification and Expression Analysis of Pathogenicity-Related Genes in Tilletia indica Inciting Karnal Bunt of Wheat. Australasian Plant Pathology, 2020, 49, 393-402.	1.3	21

#	Article	IF	Citations
685	Comparative Transcriptome Analysis Revealed Genes Regulated by Histone Acetylation and Genes Related to Sex Hormone Biosynthesis in Phytophthora infestans. Frontiers in Genetics, 2020, 11, 537969.	3.2	5
686	Characterization of Two Satellite DNA Families in the Genome of the Oomycete Plant Pathogen Phytophthora parasitica. Frontiers in Genetics, 2020, 11, 539016.	3.2	7
687	Organize, Don't Agonize: Strategic Success of Phytophthora Species. Microorganisms, 2020, 8, 917.	5.1	47
688	Long Transposon-Rich Centromeres in an Oomycete Reveal Divergence of Centromere Features in Stramenopila-Alveolata-Rhizaria Lineages. PLoS Genetics, 2020, 16, e1008646.	3.9	30
689	Screening of Lupine Germplasm for Resistance Against Phytophthora sojae. Botany, 2020, 98, 261-272.	1.5	2
690	Sensitivity of Different Developmental Stages and Resistance Risk Assessment of Phytophthora capsici to Fluopicolide in China. Frontiers in Microbiology, 2020, 11, 515749.	5.6	31
691	Pathotype and SSR Variation in Phytophthora sojae From the Argentinean Pampas. Journal of Phytopathology, 2020, 168, 228-243.	1.3	9
692	Divergent Evolution of PcF/SCR74 Effectors in Oomycetes Is Associated With Distinct Recognition Patterns in Solanaceous Plants. MBio, 2020, .	5.5	18
693	A Conserved Glycoside Hydrolase Family 7 Cellobiohydrolase PsGH7a of Phytophthora sojae Is Required for Full Virulence on Soybean. Frontiers in Microbiology, 2020, 11, 538365.	5.6	28
694	Molecular Assays to Detect the Presence and Viability of Phytophthora ramorum and Grosmannia clavigera. PLoS ONE, 2020, 15, e0221742.	3.2	14
695	Phytophthora capsici PcFtsZ2 Is Required for Asexual Development and Plant Infection (Retracted). Molecular Plant-Microbe Interactions, 2020, 33, 727-741.	3.7	3
696	G Protein α Subunit Suppresses Sporangium Formation Through a Serine/Threonine Protein Kinase in Phytophthora sojae. PLoS Pathogens, 2020, 16, e1008138.	5.0	20
697	A Phytophthora capsici Effector Suppresses Plant Immunity via Interaction With EDS1. Molecular Plant Pathology, 2020, 21, 502-511.	5.2	60
698	An RXLR Effector PlAvh142 From Peronophythora litchii Triggers Plant Cell Death and Contributes to Virulence. Molecular Plant Pathology, 2020, 21, 415-428.	5.2	55
699	Genomic Investigation of the Strawberry Pathogen Phytophthora fragariae Indicates Pathogenicity Is Associated With Transcriptional Variation in Three Key Races. Frontiers in Microbiology, 2020, 11, 516181.	5.6	17
700	Pan-Omics Focused to Crick's Central Dogma. , 2020, .		4
701	Insight Into Function and Subcellular Localization of Plasmopara viticola Putative RxLR Effectors. Frontiers in Microbiology, 2020, 11, 517018.	5.6	28
702	Pan-Genomics of Plant Pathogens and Its Applications. , 2020, .		6

#	Article	IF	Citations
703	Genetics of Pathogen–Host Interaction by the Example of Potato Late Blight Disease. Russian Journal of Genetics, 2020, 56, 261-268.	0.5	3
704	The ABC Transporter G Subfamily in Arabidopsis thaliana. Journal of Experimental Botany, 2021, 72, 92-106.	6.3	89
705	Pathogenicity and Infectivity of Phytophthora ramorum Vary Depending on Host Species, Infected Plant Part, Inoculum Potential, Pathogen Genotype, and Temperature. Plant Pathology, 2021, 70, 287-304.	2.9	22
706	A Conserved Oomycete CRN Effector Targets Tomato TCP14-2 to Enhance Virulence. Molecular Plant-Microbe Interactions, 2021, 34, 309-318.	3.7	31
707	The Expression of Pathogenicity-Related Genes in Phytophthora palmivora Causing Black Pod Rot Disease on Cacao (Theobroma cacao L.) in Indonesia. Journal of Plant Interactions, 2021, 16, 284-295.	3.6	1
708	Functional and Structural Analysis of a Novel Acyltransferase From Pathogenic Phytophthora melonis. ACS Omega, 2021, 6, 1797-1808.	5.2	11
709	PsGRGH, a TOS1 Family-Like Gene, Is Involved in the Vegetative Growth, Environmental Stress Response, and Pathogenicity of Phytophthora sojae. European Journal of Plant Pathology, 2021, 160, 67-79.	2.5	2
710	Comparative Analysis of Phytophthora Genomes Reveals Oomycete Pathogenesis in Crops. Heliyon, 2021, 7, e06317.	4.8	9
711	Mixed-Mating Model of Reproduction Revealed in European Phytophthora cactorum by ddRADseq and Effector Gene Sequence Data. Microorganisms, 2021, 9, 345.	5.1	7
712	Transcriptional Variability Associated With CRISPR-Mediated Gene Replacements at the Phytophthora sojae Avr1b-1 Locus. Frontiers in Microbiology, 2021, 12, 645331.	5.6	18
713	A Phytophthora sojae CRN Effector Mediates Phosphorylation and Degradation of Plant Aquaporin Proteins to Suppress Host Immune Signaling. PLoS Pathogens, 2021, 17, e1009388.	5.0	74
714	Innate Resistance and Phosphite Treatment Affect Both the Pathogen's and Host's Transcriptomes in the Tanoak-Phytophthora Ramorum Pathosystem. Journal of Fungi (Basel, Switzerland), 2021, 7, 198.	4.4	20
715	The Mitogen-Activated Protein Kinase PlMAPK2 Is Involved in Zoosporogenesis and Pathogenicity of Peronophythoralitchii. International Journal of Molecular Sciences, 2021, 22, 3524.	5.9	13
716	Characterization of CRN-Like Genes From Plasmopara viticola: Searching for the Most Virulent Ones. Frontiers in Microbiology, 2021, 12, 632047.	5.6	16
717	Genome of the Destructive Oomycete Phytophthora cinnamomi Provides Insights Into Its Pathogenicity and Adaptive Potential. BMC Genomics, 2021, 22, 1-15.	3.9	52
718	A Plasmopara viticola RXLR Effector Targets a Chloroplast Protein PsbP to Inhibit ROS Production in Grapevine. Plant Journal, 2021, 106, 1557-1570.	6.5	72
719	Genome Sequence Data of Three Formae Speciales of Phytophthora vignae Causing Phytophthora Stem Rot on Different Vigna Species. Plant Disease, 2021, 105, 3732-3735.	2.2	3
720	Effector Avr4 in Phytophthora infestans Escapes Host Immunity Mainly Through Early Termination. Frontiers in Microbiology, 2021, 12, 646062.	5.6	10

#	Article	IF	Citations
721	The bZIP Transcription Factor GmbZIP15 Facilitates Resistance Against Sclerotinia sclerotiorum and Phytophthora sojae Infection in Soybean. IScience, 2021, 24, 102642.	4.5	38
722	Predicting Lifestyle From Positive Selection Data and Genome Properties in Oomycetes. Pathogens, 2021, 10, 807.	4.1	13
723	Expression of Several Phytophthora cinnamomi Putative RxLRs Provides Evidence for Virulence Roles in Avocado. PLoS ONE, 2021, 16, e0254645.	3.2	9
724	PsGRASP, a Golgi Reassembly Stacking Protein in Phytophthora sojae, Is Required for Mycelial Growth, Stress Responses, and Plant Infection. Frontiers in Microbiology, 2021, 12, 702632.	5.6	9
725	Gene Validation and Remodelling Using Proteogenomics of Phytophthora cinnamomi, the Causal Agent of Dieback. Frontiers in Microbiology, 2021, 12, 665396.	5.6	4
726	Pathotype Complexity and Genetic Characterization of Phytophthora sojae Populations in Illinois, Indiana, Kentucky, and Ohio. Phytopathology, 2022, 112, 663-681.	3.7	23
727	A Phytophthora capsici RXLR Effector Targets and Inhibits the Central Immune Kinases to Suppress Plant Immunity. New Phytologist, 2021, 232, 264-278.	8.9	54
728	Phytophthora sojae Leucine-Rich Repeat Receptor-Like Kinases: Diverse and Essential Roles in Development and Pathogenicity. IScience, 2021, 24, 102725.	4.5	30
729	Targeting of Anti-Microbial Proteins to the Hyphal Surface Amplifies Protection of Crop Plants Against Phytophthora Pathogens. Molecular Plant, 2021, 14, 1391-1403.	27.3	35
730	Phytophthora Diseases Prevalence, Its Effects and Controls in Ghana. , 2021, .		3
731	Unexpected Organellar Locations of ESCRT Machinery in Giardia intestinalis and Complex Evolutionary Dynamics Spanning the Transition to Parasitism in the Lineage Fornicata. BMC Biology, 2021, 19, 1-23.	5.2	13
732	Genome Analysis of Phytophthora nicotianae JM01 Provides Insights Into Its Pathogenicity Mechanisms. Plants, 2021, 10, 1620.	5.0	7
733	Comparative Genomic Analysis Reveals Genetic Variation and Adaptive Evolution in the Pathogenicity-Related Genes of Phytophthora capsici. Frontiers in Microbiology, 2021, 12, 694136.	5.6	17
734	The Plant-Beneficial Rhizobacterium Bacillus velezensis FZB42 Controls the Soybean Pathogen Phytophthora sojae Due to Bacilysin Production. Applied and Environmental Microbiology, 2021, 87, e0160121.	4.2	104
735	4-Ethylphenol, a Volatile Organic Compound Produced by Disease-Resistant Soybean, Is a Potential Botanical Agrochemical Against Oomycetes. Frontiers in Plant Science, 2021, 12, 717258.	5.8	15
736	Comparative Analysis of Draft Genome Assemblies Developed From Whole Genome Sequences of Two Hyaloperonospora brassicae Isolate Samples Differing in Field Virulence on Brassica napus. Biotechnology Reports (Amsterdam, Netherlands), 2021, 31, e00653.	7.3	4
737	A Small Cysteine-Rich Phytotoxic Protein of Phytophthora capsici Functions as Both Plant Defense Elicitor and Virulence Factor. Molecular Plant-Microbe Interactions, 2021, 34, 891-903.	3.7	24
738	Encyclopedia of Life Sciences. , 2001, .		13,476

#	Article	IF	Citations
739	Aquaculture Genome Technologies. , 2007, .		127
740	Phytophthora sojae and Soybean. , 2009, .		16
741	Effectors. , 2009, .		14
742	In Planta Expression Systems. , 2009, .		9
743	Mechanisms and Application of Gene Silencing in Oomycetes. , 2009, .		4
744	Annual Plant Reviews Online. , 2018, .		3,098
745	Effectors in Plant–Microbe Interactions. , 2011, .		35
746	Evolutionary and Functional Dynamics of Oomycete Effector Genes. , 2011, .		5
747	Genomics of Fungal- and Oomycete-Soybean Interactions. , 2008, .		7
748	Structure and Function of RXLR Effectors of Plant Pathogenic Oomycetes. , 2008, .		1
749	Imaging Fluorescently Tagged Phytophthora Effector Proteins Inside Infected Plant Tissue. Methods in Molecular Biology, 2011, 712, 195-209.	1.2	8
750	Defence, Symbiosis and ABCG Transporters. Signaling and Communication in Plants, 2014, .	0.0	11
751	Hyphochytriomycota and Oomycota. , 2016, .		15
752	Plant Infection by Biotrophic Fungal and Oomycete Pathogens. Signaling and Communication in Plants, 2012, .	0.0	7
753	The Phytophthora sojae Genome Sequence: Foundation for a Revolution. , 2014, .		21
754	Phytophthora ramorum. , 2014, .		4
755	Phytophthora infestans. , 2014, .		7
756	Genomics of Marine Algae. , 2010, .		2

#	Article	IF	Citations
757	Phytophthora sojae. , 2017, .		7
758	Identification of Genes That Mediate Protection Against Soybean Pathogens. , 2012, .		2
759	Recent Advances in Oomycete Genomics. Advances in Genetics, 2020, 105, 175-228.	3.0	69
760	Determination of Virulence Contribution From Phytophthora infestans Effector IPI-O4 in a Resistant Potato Host Containing the RB Gene. Physiological and Molecular Plant Pathology, 2017, 100, 30-34.	3.9	9
761	Phytophthora parasitica Effector PpRxLR2 Suppresses Nicotiana benthamiana Immunity. Molecular Plant-Microbe Interactions, 2018, 31, 481-493.	3.7	25
762	Effectors as Tools in Disease Resistance Breeding Against Biotrophic, Hemibiotrophic, and Necrotrophic Plant Pathogens. Molecular Plant-Microbe Interactions, 2014, .	3.7	1
763	Effectors as Tools in Disease Resistance Breeding Against Biotrophic, Hemibiotrophic, and Necrotrophic Plant Pathogens. Molecular Plant-Microbe Interactions, 2015, 2015, 17-27.	3.7	5
764	Effectors as Tools in Disease Resistance Breeding Against Biotrophic, Hemibiotrophic, and Necrotrophic Plant Pathogens. Molecular Plant-Microbe Interactions, 2015, 2015, 40-50.	3.7	3
765	Draft Genomes of Two Australian Strains of the Plant Pathogen, Phytophthora cinnamomi. F1000Research, 2017, 6, 1972.	1.1	14
766	Transcriptome of Aphanomyces Euteiches: New Oomycete Putative Pathogenicity Factors and Metabolic Pathways. PLoS ONE, 2008, 3, e1723.	3.2	112
767	Comparative Genome Analysis of Filamentous Fungi Reveals Gene Family Expansions Associated With Fungal Pathogenesis. PLoS ONE, 2008, 3, e2300.	3.2	166
768	A Hypothesis for the Evolution of Nuclear-Encoded, Plastid-Targeted Glyceraldehyde-3-Phosphate Dehydrogenase Genes in “Chromalveolate” Members. PLoS ONE, 2009, 4, e4737.	3.2	28
769	Multiple Horizontal Gene Transfer Events and Domain Fusions Have Created Novel Regulatory and Metabolic Networks in the Oomycete Genome. PLoS ONE, 2009, 4, e6133.	3.2	35
770	Competition Between Phytophthora infestans Effectors Leads to Increased Aggressiveness on Plants Containing Broad-Spectrum Late Blight Resistance. PLoS ONE, 2010, 5, e10536.	3.2	55
771	Sequence Variants of the Phytophthora sojae RXLR Effector Avr3a/5 Are Differentially Recognized by Rps3a and Rps5 in Soybean. PLoS ONE, 2011, 6, e20172.	3.2	64
772	Novel Cellulose-Binding-Domain Protein in Phytophthora Is Cell Wall Localized. PLoS ONE, 2011, 6, e23555.	3.2	12
773	A Molecular Insight Into Algal-Oomycete Warfare: cDNA Analysis of Ectocarpus siliculosus Infected With the Basal Oomycete Eurychasma Dicksonii. PLoS ONE, 2011, 6, e24500.	3.2	38
774	Alternative Splicing of a Multi-Drug Transporter From Pseudoperonospora cubensis Generates an RXLR Effector Protein That Elicits a Rapid Cell Death. PLoS ONE, 2012, 7, e34701.	3.2	41

#	Article	IF	Citations
775	Bioinformatic Inference of Specific and General Transcription Factor Binding Sites in the Plant Pathogen Phytophthora infestans. PLoS ONE, 2012, 7, e51295.	3.2	17
776	Characterization of Pythium Transcriptome and Gene Expression Analysis at Different Stages of Fermentation. PLoS ONE, 2013, 8, e65552.	3.2	6
777	Gene Duplication and Fragment Recombination Drive Functional Diversification of a Superfamily of Cytoplasmic Effectors in Phytophthora sojae. PLoS ONE, 2013, 8, e70036.	3.2	48
778	The Genome Sequence of the Fungal Pathogen Fusarium virguliforme That Causes Sudden Death Syndrome in Soybean. PLoS ONE, 2014, 9, e81832.	3.2	49
779	Phytophthora sojae Effector PsCRN70 Suppresses Plant Defenses in Nicotiana benthamiana. PLoS ONE, 2014, 9, e98114.	3.2	56
780	Functional Analysis of Hyaloperonospora arabidopsidis RXLR Effectors. PLoS ONE, 2014, 9, e110624.	3.2	15
781	Strain Specific Factors Control Effector Gene Silencing in Phytophthora sojae. PLoS ONE, 2016, 11, e0150530.	3.2	19
782	Comparative Analysis of Sterol Acquisition in the Oomycetes Saprolegnia parasitica and Phytophthora infestans. PLoS ONE, 2017, 12, e0170873.	3.2	28
783	A Novel, Multiplexed, Probe-Based Quantitative PCR Assay for the Soybean Root- and Stem-Rot Pathogen, Phytophthora sojae, Utilizes Its Transposable Element. PLoS ONE, 2017, 12, e0176567.	3.2	12
784	Transcriptome Analysis of Phytophthora litchii Reveals Pathogenicity Arsenals and Confirms Taxonomic Status. PLoS ONE, 2017, 12, e0178245.	3.2	19
785	Multispecies Reconstructions Uncover Widespread Conservation, and Lineage-Specific Elaborations in Eukaryotic mRNA Metabolism. PLoS ONE, 2018, 13, e0192633.	3.2	19
786	Effector Prediction and Characterization in the Oomycete Pathogen Bremia lactucae Reveal Host-Recognized WY Domain Proteins That Lack the Canonical RXLR Motif. PLoS Pathogens, 2020, 16, e1009012.	5.0	47
787	Scientific Opinion on the Pest Risk Analysis onPhytophthora Ramorumprepared by the FP6 Project RAPRA. EFSA Journal, 2011, 9, 2186.	8.9	12
788	A Plethora of Virulence Strategies Hidden Behind Nuclear Targeting of Microbial Effectors. Frontiers in Plant Science, 2011, 2, 17689.	5.8	40
789	Algal Endosymbionts as Vectors of Horizontal Gene Transfer in Photosynthetic Eukaryotes. Frontiers in Plant Science, 2013, 4, 61722.	5.8	105
790	Ancient Origin of Chaperonin Gene Paralogs Involved in Ciliopathies. Journal of Phylogenetics & Evolutionary Biology, 2013, .	0.5	8
791	The Gene Repertoire of Pythium porphyrae (Oomycota) Suggests an Adapted Plant Pathogen Tackling Red Algae. Algae, 2020, 35, 133-144.	3.0	11
792	Interaction Between Phytophthora nicotianae and Candidatus Liberibacter asiaticus Damage to Citrus Fibrous Roots. Journal of Citrus Pathology, 2017, .	0.6	6

#	Article	IF	Citations
793	Oomycetes RXLR Effectors Function as Both Activator and Suppressor of Plant Immunity. Plant Pathology Journal, 2010, 26, 209-215.	2.9	12
794	Evidence for Suppression of Immunity as a Driver for Genomic Introgressions and Host Range Expansion in Races of Albugo candida, a Generalist Parasite. ELife, 2015, .	5.2	77
795	A Phytophthora Effector Recruits a Host Cytoplasmic Transacetylase Into Nuclear Speckles to Enhance Plant Susceptibility. ELife, 2018, .	5.2	81
796	Insights From the Proteome Profile of Phytophthora capsici in Response to the Novel Fungicide SYP-14288. PeerJ, 2019, 7, e7626.	2.9	15
797	Uncovering the Role of Metabolism in Oomycete–Host Interactions Using Genome-Scale Metabolic Models. Frontiers in Microbiology, 2021, 12, 748178.	5.6	6
798	Activity of the Novel Fungicide SYP-34773 Against Plant Pathogens and Its Mode of Action on Phytophthora infestans. Journal of Agricultural and Food Chemistry, 2021, 69, 11794-11803.	6.6	21
799	A Patched-Like Protein PsPTL Is Not Essential for the Growth and Response to Various Stresses in Phytophthora sojae. Frontiers in Microbiology, 2021, 12, 673784.	5.6	12
800	Specific Interaction of an RNA-Binding Protein With the 3'-UTR of Its Target mRNA Is Critical to Oomycete Sexual Reproduction. PLoS Pathogens, 2021, 17, e1010001.	5.0	21
801	Molecular Strategies for Identifying Determinants of Oomycete Pathogenicity. Soil Biology, 2008, .	0.0	1
802	Encyclopedia of Microbiology. , 2009, .		2,434
803	Unraveling the Senses of Phytophthora; Leads to Novel Control Strategies?. Acta Horticulturae, 2009, .	0.3	1
804	RNase P From Organelles. , 2010, .		1
805	Transferomics: Seeing the Evolutionary Forest Using Phylogenetic Trees. , 2010, .		0
806	Plants and Oomycetes, an Intimate Relationship: Co-Evolutionary Principles and Impact on Agricultural Practice. CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources, 2010, .	1.7	2
807	The Millardetian Conjunction in the Modern World. , 2011, .		2
808	A Re-Visit to the Evolution and Ecophysiology of the Labyrinthulomycetes. , 2012, .		1
809	Gene Transfer and the Chimeric Nature of Eukaryotic Genomes. , 2013, .		0
810	Genome Portal, Joint Genome Institute. , 2013, .		0

#	Article	IF	Citations
811	Hyaloperonospora arabidopsidis: A Model Pathogen of Arabidopsis. , 2014, .		10
812	Illuminating the Phytophthora capsici Genome. , 2014, .		0
813	Effectors as Tools in Disease Resistance Breeding Against Biotrophic, Hemibiotrophic, and Necrotrophic Plant Pathogens. Molecular Plant-Microbe Interactions, 2014, .	3.7	0
814	Validation and Expression Analysis of Predicted miRNAs in Phytophthora infestans and Phytophthora sojae. Journal of the Pennsylvania Academy of Science, 2018, 92, 53-67.	0.0	0
815	Role of Oomycete Elicitors in Plant Defense Signaling. , 2019, .		1
816	Pudrición de raíces y tallo de la soya por Phytophthora sojae Kaufm. & Gerd. en la altillanura plana del departamento del Meta. Summa Phytopathologica, 2020, 46, 113-120.	0.2	1
817	Forensics at the Port: Can Diagnostic Testing Benefit Trade?. Sustainability, 2021, 13, 106.	5.0	5
818	Functional Genomics and Bioinformatics of the Phytophthora sojae Soybean Interaction. , 2008, .		5
819	Classical and Molecular Genetics of Bremia lactucae, Cause of Lettuce Downy Mildew. , 2008, .		1
820	Tapping Into Molecular Conversation Between Oomycete Plant Pathogens and Their Hosts. , 2008, .		1
821	Comparative Epidemiology of Zoosporic Plant Pathogens. , 2008, .		0
822	An Atypical Phytophthora sojae RxLR Effector Manipulates Host Vesicle Trafficking to Promote Infection. PLoS Pathogens, 2021, 17, e1010104.	5.0	22
823	Molecular Mechanism of Crucifer's Host-Resistance. , 2021, .		14
824	Evaluation of the Anti-Oomycete Bioactivity of Rhizosphere Soil-Borne Isolates and the Biocontrol of Soybean Root Rot Caused by Phytophthora sojae. Biological Control, 2022, 166, 104818.	3.9	24
825	A Comprehensive Assessment of the Secretome Responsible for Host Adaptation of the Legume Root Pathogen Aphanomyces Euteiches. Journal of Fungi (Basel, Switzerland), 2022, 8, 88.	4.4	13
826	Combinatorial Synthesis of Sulfonate Derivatives of α/β-Naphthol as Anti- Oomycete Agents. Combinatorial Chemistry and High Throughput Screening, 2022, 25, 2026-2032.	1.9	10
827	ATAC-Seq Reveals the Landscape of Open Chromatin and Cis-Regulatory Elements in the Phytophthora sojae Genome. Molecular Plant-Microbe Interactions, 2022, 35, 301-310.	3.7	15
828	Pathogenicity Factors of Phytophthora melonis Revealed by Comparative Proteomics. Journal of Plant Interactions, 2022, 17, 183-197.	3.6	1

#	Article	IF	Citations
829	RXLR Effector Gene Avr3a From Phytophthora sojae Is Recognized by Rps8 in Soybean. Molecular Plant Pathology, 2022, 23, 693-706.	5.2	16
830	RNAi-Based Gene Silencing of RXLR Effectors Protects Plants Against the Oomycete Pathogen Phytophthora capsici. Molecular Plant-Microbe Interactions, 2022, 35, 440-449.	3.7	35
831	Ancestral Chromosomes for Family Peronosporaceae Inferred From a Telomere-to-Telomere Genome Assembly of Peronospora effusa. Molecular Plant-Microbe Interactions, 2022, 35, 450-463.	3.7	29
832	A Prophage-Encoded Nonclassical Secretory Protein of “Candidatus Liberibacter asiaticus” Induces a Strong Immune Response in Nicotiana benthamiana and Citrus. Molecular Plant Pathology, 2022, 23, 1022-1034.	5.2	34
833	Comparative Genome Analysis Across 128 Phytophthora Isolates Reveal Species-Specific Microsatellite Distribution and Localized Evolution of Compartmentalized Genomes. Frontiers in Microbiology, 2022, 13, 806398.	5.6	19
834	High-Quality, Phased Genomes of Phytophthora ramorum Clonal Lineages NA1 and EU1. Molecular Plant-Microbe Interactions, 2022, 35, 360-363.	3.7	12
835	An Enigmatic Stramenopile Sheds Light on Early Evolution in Ochrophyta Plastid Organellogenesis. Molecular Biology and Evolution, 2022, .	6.2	23
836	Monophyly of Diverse Bigyromonadea and Their Impact on Phylogenomic Relationships Within Stramenopiles. Molecular Phylogenetics and Evolution, 2022, 171, 107468.	4.0	18
837	Functional Analysis of a Phytophthora Host-Translocated Effector Using the Yeast Model System. PeerJ, 2021, 9, e12576.	2.9	0
838	The Mevalonate Pathway Is Important for Growth, Spore Production, and the Virulence of Phytophthora sojae. Frontiers in Microbiology, 2021, 12, 772994.	5.6	44
839	Short Linear Motifs (SLiMs) in "Core" RxLR Effectors of Phytophthora parasitica var. Nicotianae: A Case of PpRxLR1 Effector. Microbiology Spectrum, 2022, 10, e0177421.	4.2	7
840	The Evolutionary History of Meiotic Genes: Early Origins by Duplication and Subsequent Losses. , 2011, .		0
841	Systematics and Molecular Pathogenesis of Oomycetes With Emphasis on Flagellar Genes. , 2013, .		0
842	Eukaryotic Genomes: From Parasites to Primates. , 2009, .		0
843	Aphanomyces Euteiches and Legumes. , 2009, .		2
844	Global Proteomics and Phytophthora. , 2009, .		0
845	Strategy and Tactics for Genome Sequencing. , 2009, .		0
846	Genotypic and Phenotypic Structure of the Population of Phytophthora infestans in Egypt Revealed the Presence of European Genotypes. Journal of Fungi (Basel, Switzerland), 2022, 8, 468.	4.4	11

#	Article	IF	Citations
847	Two Typical Acyl-CoA-Binding Proteins (ACBPs) Are Required for the Asexual Development and Virulence of Phytophthora sojae. Fungal Genetics and Biology, 2022, 161, 103695.	2.9	5
848	Functional Analysis of the C-5 Sterol Desaturase PcErg3 in the Sterol Auxotrophic Oomycete Pathogen Phytophthora capsici. Frontiers in Microbiology, 2022, 13, 811132.	5.6	6
849	The Identification and Characterization of Endopolygalacturonases in a South African Isolate of Phytophthora cinnamomi. Microorganisms, 2022, 10, 1061.	5.1	2
850	Unraveling Plant Cell Death During Phytophthora Infection. Microorganisms, 2022, 10, 1139.	5.1	25
851	The Minichromosome Maintenance Complex Component 2 (MjMCM2) of Meloidogyne javanica Is a Potential Effector Regulating the Cell Cycle in Nematode-Induced Galls. Scientific Reports, 2022, 12, 1-15.	5.2	5
852	An Oomycete-Specific Leucine-Rich Repeat-Containing Protein Is Involved in Zoospore Flagellum Development in Phytophthora sojae. Phytopathology, 2022, 112, 2351-2359.	3.7	6
853	A Bursaphelenchus xylophilus Effector, BxSCD3, Suppresses Plant Defense and Contributes to Virulence. International Journal of Molecular Sciences, 2022, 23, 6417.	5.9	11
854	Transgenic Soybeans Expressing Phosphatidylinositol-3-Phosphate-Binding Proteins Show Enhanced Resistance Against the Oomycete Pathogen Phytophthora sojae. Frontiers in Microbiology, 2022, 13, 923281.	5.6	6
855	Differing Responses to Phytophthora cinnamomi Infection in Susceptible and Partially Resistant Persea americana (Mill.) Rootstocks: A Case for the Role of Receptor-Like Kinases and Apoplastic Proteases. Frontiers in Plant Science, 2022, 13, 928176.	5.8	12
856	The Contribution of DNA Repair Pathways to Genome Editing and Evolution in Filamentous Pathogens. FEMS Microbiology Reviews, 2022, .	17.0	45
857	Genome Analysis and CAZy Repertoire of a Novel Fungus Aspergillus sydowii C6d With Lignocellulolytic Ability Isolated From Camel Rumen. Electronic Journal of Biotechnology, 2022, 59, 36-45.	3.3	9
858	Current Status and Future Perspectives of Genomics Research in the Rust Fungi. International Journal of Molecular Sciences, 2022, 23, 9629.	5.9	17
859	An RxLR Effector From Plasmopara viticola Suppresses Plant Immunity in Grapevine by Targeting and Stabilizing VpBPA1. Plant Journal, 2022, 112, 104-114.	6.5	33
860	How Do Emerging Long-Read Sequencing Technologies Function in Transforming the Plant Pathology Research Landscape?. Plant Molecular Biology, 2022, 110, 469-484.	3.6	23
861	Transcriptome Reveals BCAAs Biosynthesis Pathway Is Influenced by Lovastatin and Can Act as a Potential Control Target in Phytophthora sojae. Journal of Applied Microbiology, 2022, 133, 3585-3595.	3.0	4
862	Signal and Regulatory Mechanisms Involved in Spore Development of Phytophthora and Peronophythora. Frontiers in Microbiology, 2022, 13, 984672.	5.6	25
863	Identification of a C2H2 Transcription Factor (PsCZF3) Associated With RxLR Effectors and Carbohydrate-Active Enzymes in Phytophthora sojae Based on WGCNA. Journal of Fungi (Basel, Switzerland), 2022, 8, 998.	4.4	4
864	Whole-Genome Sequence Resource of Phytophthora pini, the Causal Pathogen of Foliage Blight and Shoot Dieback of Rhododendron pulchrum. Molecular Plant-Microbe Interactions, 2022, 35, 944-948.	3.7	4

#	Article	IF	Citations
865	Bioinformatics Tools and Genomic Resources Available in Understanding the Structure and Function of Gossypium. , 2022, .		0
866	Ferroptosis Induced by the Biocontrol Agent Pythium oligandrum Enhances Soybean Resistance to Phytophthora sojae. Environmental Microbiology, 2022, 24, 6267-6278.	4.5	13
867	The Molecular Dialog Between Oomycete Effectors and Their Plant and Animal Hosts. Fungal Biology Reviews, 2023, 43, 100289.	5.4	24
868	Comparative Genomic Analysis of 31 Phytophthora Genomes Reveals Genome Plasticity and Horizontal Gene Transfer. Molecular Plant-Microbe Interactions, 2023, 36, 26-46.	3.7	35
869	Myo-D-Inositol Trisphosphate Signalling in Oomycetes. Microorganisms, 2022, 10, 2157.	5.1	5
870	Chromosome-Level Assembly of the Phytophthora Agathidicida Genome Reveals Adaptation in Effector Gene Families. Frontiers in Microbiology, 2022, 13, 1038444.	5.6	19
871	The Pythium periplocum Elicitin PpEli2 Confers Broad-Spectrum Disease Resistance by Triggering a Novel Receptor-Dependent Immune Pathway in Plants. Horticulture Research, 2023, 10, uhac255.	8.8	8
872	Progress and Challenges in Elucidating the Functional Role of Effectors in the Soybean-Phytophthora Sojae Interaction. Journal of Fungi (Basel, Switzerland), 2023, 9, 12.	4.4	5
873	Influence of Affinity Tags and Tobacco PR1a Signal Peptide on Detection, Purification and Bioactivity Analyses of the Small Oomycete Apoplastic Effectors. Biotechnology Letters, 2023, 45, 115-124.	2.6	3
874	The Phytophthora capsici RxLR Effector CRISIS2 Triggers Cell Death via Suppressing Plasma Membrane H+-ATPase in the Host Plant. Journal of Experimental Botany, 2023, 74, 1675-1689.	6.3	14
875	Two-Speed Genome Evolution Drives Pathogenicity in Fungal Pathogens of Animals. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, e2212633120.	9.0	41
876	Sterol-Sensing Domain (SSD)-Containing Proteins in Sterol Auxotrophic Phytophthora capsici Mediate Sterol Signaling and Play a Role in Asexual Reproduction and Pathogenicity. Microbiology Spectrum, 2023, 11, e0379722.	4.2	9
877	Molecular Mechanisms of Phytophthora sojae Avirulence Effectors Escaping Host Recognition. Frontiers in Microbiology, 2023, 13, 1111774.	5.6	11
878	SODplex, a Series of Hierarchical Multiplexed Real-Time PCR Assays for the Detection and Lineage Identification of Phytophthora ramorum, the Causal Agent of Sudden Oak Death and Sudden Larch Death. PhytoFrontiers, 2023, 3, 173-185.	1.3	4
879	A Tell Tail Sign: A Conserved C-Terminal Tail-Anchor Domain Targets a Subset of Pathogen Effectors to the Plant Endoplasmic Reticulum. Journal of Experimental Botany, 2023, 74, 3188-3202.	6.3	23
880	Synthesis, Anti-Oomycete Activity of 1-Sulfonyloxy/Acyloxysesamol Derivatives. Journal of Molecular Structure, 2023, 1283, 135260.	5.2	17
881	A Method for Quantifying Phytophthora Oospore Viability Using Fluorescent Dyes and Automated Image Analysis. PhytoFrontiers, 2023, 3, 497-505.	1.3	1
882	Virus-Induced Silencing of a Sequence Coding for Loricrin-Like Protein in Phytophthora infestans Upon Infection of a Recombinant Vector Based on Tobacco Mosaic Virus. Horticulturae, 2023, 9, 360.	3.6	2

#	Article	IF	Citations
883	Genome Resource Announcement for Two Isolates of Phytophthora sansomeana With Varying Levels of Pathogenicity on Soybean. PhytoFrontiers, 2023, 3, 738-743.	1.3	3
884	Phase-Specific Transcriptional Patterns of the Oomycete Pathogen Phytophthora sojae Unravel Genes Essential for Asexual Development and Pathogenic Processes. PLoS Pathogens, 2023, 19, e1011256.	5.0	16
885	Phytophthora sojae Effector PsAvh113 Associates With the Soybean Transcription Factor GmDPB to Inhibit Catalase-Mediated Immunity. Plant Biotechnology Journal, 2023, 21, 1393-1407.	10.4	25
886	Genome-Wide Characterization of Effector Protein-Encoding Genes in Sclerospora graminicola and Its Validation in Response to Pearl Millet Downy Mildew Disease Stress. Journal of Fungi (Basel, Switzerland), 2023, 9, 431.	4.4	5
887	The Devastating Oomycete Phytopathogen Phytophthora cactorum: Insights Into Its Biology and Molecular Features. Molecular Plant Pathology, 2023, 24, 1017-1032.	5.2	30
888	First Detection of Potato Spindle Tuber Viroid in Natural Isolates of Potato Blight Agent Phytophthora infestans. Doklady Biological Sciences, 2023, 508, 55-62.	0.5	2
889	Genomics of Crucifer's Host- Pathosystem. , 2023, .		11
890	Rapid New Diagnostic LAMP (Loop-Mediated Isothermal Amplification) Assays to Distinguish Among the Four Lineages of Phytophthora ramorum. Plant Disease, 2023, 107, 3553-3559.	2.2	6
891	Genome-Enabled Insights Into Downy Mildew Biology and Evolution. Annual Review of Phytopathology, 2023, 61, 165-183.	13.2	7
892	Genome Resources and Whole Genome Resequencing of Phytophthora Rubi Isolates From Red Raspberry. Frontiers in Plant Science, 2023, 14, 1161864.	5.8	3
893	Phytophthora sojae Boosts Host Trehalose Accumulation to Acquire Carbon and Initiate Infection. Nature Microbiology, 2023, 8, 1561-1573.	18.2	43
894	A Novel FYVE Domain-Containing Protein Kinase, PsZFPK1, Plays a Critical Role in Vegetative Growth, Sporangium Formation, Oospore Production, and Virulence in Phytophthora sojae. Journal of Fungi (Basel, Switzerland), 2023, 9, 709.	4.4	2
895	Utilizing a New Target Gene, Ppinihp1, Identified From Genome Sequences to Detect Phytophthora pini. Crop Protection, 2023, 172, 106327.	3.3	3
896	An Overview of Phytophthora Species on Woody Plants in Sweden and Other Nordic Countries. Microorganisms, 2023, 11, 1309.	5.1	10
897	Genome Analysis of Phytophthora cactorum Strains Associated With Crown- and Leather-Rot in Strawberry. Frontiers in Microbiology, 2023, 14, 1214924.	5.6	7
898	Genome Analysis of Parmales, the Sister Group of Diatoms, Reveals the Evolutionary Specialization of Diatoms From Phago-Mixotrophs to Photoautotrophs. Communications Biology, 2023, 6, 1-14.	5.9	14
899	A Review of Biocontrol Agents in Controlling Late Blight of Potatoes and Tomatoes Caused by Phytophthora infestans and the Underlying Mechanisms. Pest Management Science, 2023, 79, 4715-4725.	4.4	27
900	Comparing the Inhibitory Effects of CuO-rGO, CuO NPs, and CuCl2 on the Oomycete Phytophthora sojae: Insights From Phenotypic and Transcriptomic Analyses. Environmental Science: Nano, 2023, 10, 2299-2311.	6.0	10

#	Article	IF	Citations
901	Gene Editing With an Oxathiapiprolin Resistance Selection Marker Reveals That PuLLP, a Loricrin-Like Protein, Is Required for Oospore Development in Pythium ultimum. Phytopathology Research, 2023, 5, 1-11.	4.4	4
902	Subcellular Proteomics for Determining Iron-Limited Remodeling of Plastids in the Model Diatom Thalassiosira pseudonana (Bacillariophyta). Journal of Phycology, 2023, 59, 1085-1099.	4.0	1
903	A Phytophthora Receptor-Like Kinase Regulates Oospore Development and Can Activate Pattern-Triggered Plant Immunity. Nature Communications, 2023, 14, 1-15.	18.1	24
904	Research Advances of Phytopathogen Effectors. Chinese Science Bulletin, 2023, 68, 4895-4917.	0.9	2
905	Stripe Rust Effector Pst21674 Compromises Wheat Resistance by Targeting Transcription Factor TaASR3. Plant Physiology, 2023, 193, 2806-2824.	6.5	29
906	Novel Function of the PsDMAP1 Protein in Regulating the Growth and Pathogenicity of Phytophthora sojae. International Journal of Biological Macromolecules, 2023, 253, 127198.	8.4	4
907	Advances in Understanding Grapevine Downy Mildew: From Pathogen Infection to Disease Management. Molecular Plant Pathology, 2024, 25, e13401.	5.2	30
908	The Oomycete-Specific BAG Subfamily Maintains Protein Homeostasis and Promotes Pathogenicity in an Atypical HSP70-Independent Manner. Cell Reports, 2023, 42, 113391.	7.7	7
909	Protein Kinase A Regulatory Subunit Is Required for Normal Growth, Zoosporogenesis, and Pathogenicity in Phytophthora sojae. Research in Microbiology, 2024, 175, 104152.	4.2	4
910	Specific Detection of Phytophthora parasitica by Recombinase Polymerase Amplification Assays Based on a Unique Multicopy Genomic Sequence. Plant Disease, 2024, 108, 987-995.	2.2	7
911	A Major Facilitator Superfamily Transporter PlMFS1 Contributes to Growth, Oosporogenesis, and Pathogenesis of Peronophythora litchii. Horticultural Plant Journal, 2025, 11, 189-198.	6.4	7
912	PcLRR-RK3, an LRR Receptor Kinase Is Required for Growth and In-Planta Infection Processes in Phytophthora capsici. Mycology, 2024, 15, 471-484.	6.7	3
913	PsAF5 Functions as an Essential Adapter for PsPHB2-Mediated Mitophagy Under ROS Stress in Phytophthora sojae. Nature Communications, 2024, 15, 1-15.	18.1	20
914	Integrative Transcriptome Analysis of mRNA and miRNA in Pepper's Response to Phytophthora capsici Infection. Biology, 2024, 13, 186.	4.6	5
915	Plant Genes Related to Phytophthora Pathogens Resistance. Phytopathology Research, 2024, 6, 1-11.	4.4	17
916	Design, Synthesis and Anti-Oomycete Activity of 2-Acyloxyhinokitiol Derivatives. Natural Product Research, 2025, 39, 4040-4049.	1.9	3
917	toGC: A Pipeline to Correct Gene Model for Functional Excavation of Dark GPCRs in Phytophthora sojae1. Journal of Integrative Agriculture, 2026, 25, 150-156.	4.8	0
918	Phytophthora sojae Effector PsAvh113 Targets Transcription Factors in Nicotiana benthamiana. Journal of Fungi (Basel, Switzerland), 2024, 10, 318.	4.4	1

#	Article	IF	Citations
919	A Novel Method for Extraction of High Purity and High Production Phytophthora sojae Oospores. Plant Methods, 2024, 20, 1-11.	5.8	2
920	CaWRKY01-10 And CaWRKY08-4 Confer Pepper's Resistance to Phytophthora capsici Infection by Directly Activating a Cluster of Defense-Related Genes. Journal of Agricultural and Food Chemistry, 2024, 72, 11682-11693.	6.6	22
921	PcAvh87, A Virulence Essential RxLR Effector of Phytophthora cinnamomi Suppresses Host Defense and Induces Cell Death in Plant Nucleus. Microbiological Research, 2024, 286, 127789.	9.9	5
922	Design, Synthesis, and Anti-Oomycete Activity of 3-Acyloxymaltol/Ethyl Maltol Derivatives. Journal of Asian Natural Products Research, 2024, 26, 1166-1174.	1.4	1
923	Complete Telomere-to-Telomere Genomes Uncover Virulence Evolution Conferred by Chromosome Fusion in Oomycete Plant Pathogens. Nature Communications, 2024, 15, 1-13.	18.1	18
924	The Extent, Role, and Timing of Endosymbiotic Gene Transfer in Plastids. , 2024, .		1
925	Integrated Overview of Stramenopile Ecology, Taxonomy, and Heterotrophic Origin. ISME Journal, 2024, .	10.0	27
926	A Conserved Oomycete Effector RxLR23 Triggers Plant Defense Responses by Targeting ERD15La to Release NbNAC68. Nature Communications, 2024, 15, 1-23.	18.1	11
927	AlphaFold-Guided Redesign of a Plant Pectin Methylesterase Inhibitor for Broad-Spectrum Disease Resistance. Molecular Plant, 2024, 17, 1344-1368.	27.3	69
928	Functional Genomics Identifies a Small Secreted Protein That Plays a Role During the Biotrophic to Necrotrophic Shift in the Root Rot Pathogen Phytophthora medicaginis. Frontiers in Plant Science, 2024, 15, 1439020.	5.8	0
929	Effector-Mediated Suppression of Programmed Cell Death by Phytophthora palmivora in Oil Palm. Journal of Fungi (Basel, Switzerland), 2024, 10, 750.	4.4	1
930	Two NPC1 Homologous Proteins Are Involved in Asexual Reproduction, Pathogenicity, and Lipid Trafficking in Phytophthora sojae. International Journal of Biological Macromolecules, 2025, 286, 138430.	8.4	0
931	CRISPR/Cas9-Mediated Gene-Knockout and in Situ Complementation System for Phytophthora sojae. Methods in Molecular Biology, 2025, 2892, 69-82.	1.2	2
932	Annotation of RxLR Effectors in Oomycete Genomes. Methods in Molecular Biology, 2025, 2892, 151-168.	1.2	0
933	PsDMAP1/PsTIP60-Regulated H4K16ac Is Required for ROS-Dependent Virulence Adaptation of Phytophthora sojae on Host Plants. Proceedings of the National Academy of Sciences of the United States of America, 2025, 122, e2413127122.	9.0	8
934	Blocking the Isoflavone Chemoreceptor in Phytophthora sojae to Prevent Disease. Science Advances, 2025, 11, eadt0925.	13.6	23
935	Technical Advances Drive the Molecular Understanding of Effectors From Wheat and Barley Powdery Mildew Fungi. Molecular Plant-Microbe Interactions, 2025, 38, 213-225.	3.7	9
936	Intraspecific Variation and Recent Loss of Ancient, Conserved Effector Genes in the Sudden Oak Death Pathogen Phytophthora ramorum. Molecular Plant-Microbe Interactions, 2025, 38, 440-453.	3.7	2

#	Article	IF	Citations
937	Sustainable Plant-Based Control Strategies for Late Blight Disease of Potato. CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources, 2025, .	1.7	5
938	Atypical RXLR Effectors Are Involved in Phytophthora cactorum Pathogenesis. ABIOTECH, 2025, 6, 50-62.	6.9	1
939	Upgrading of the Genetic Engineering Toolkit Accelerated the Discovery Process of the Virulence Effect of PsGH7d on Phytophthora sojae Invasion. Physiologia Plantarum, 2025, 177, e70083.	4.1	2
940	Pathogenomics Insights Into Phytophthora capsici and Phytophthora tropicalis -Sibling Species Causing Black Pepper Foot Rot: Genomic Architecture, Metabolic Pathways, and Effector Diversity. Gene, 2025, 947, 149328.	2.9	1
941	The Oligosaccharyltransferase Subunit PsSTT3A Regulates N-Glycosylation and Is Critical for Development and Virulence of Phytophthora sojae. Science China Life Sciences, 2025, 68, 1384-1399.	8.2	2
942	Enzymatic Oxidation of Galacturonides From Pectin Breakdown Contributes to Stealth Infection by Oomycota Phytopathogens. Nature Communications, 2025, 16, 3467.	18.1	20
943	A Core Plasmopara viticola Effector Attenuates the DNA-Binding Activity of bZIP Transcription Factor to Compromise Plant Immunity. Plant Journal, 2025, 122, e70143.	6.5	2
944	Pathogenomics for Tropical Tree Improvement and Conservation. , 2025, .		0
945	Plasmopara viticola Effector PvRXLR10 Targets a Host Phospholipase VvipPLA-IIδ2 to Suppress Plant Immunity in Grapevine. Molecular Plant Pathology, 2025, 26, e70095.	5.2	2
946	Comparative Genome Analysis of Phytophthora melonis MCC 9865 WB Isolated From Eastern India With Other Isolates Reveal Host Mediated Adaptation. Nucleus (India), 2026, 69, 1-15.	2.2	0
947	A Conserved Phytophthora Apoplastic Trypsin-Like Serine Protease Targets the Receptor-Like Kinase BAK1 to Dampen Plant Immunity. Nature Plants, 2025, 11, 1401-1415.	14.3	17
948	Genome Assembly, Polishing, and Analysis of the Chytrid Batrachochytrium salamandrivorans. Methods in Molecular Biology, 2025, 2955, 153-189.	1.2	0
949	Phytophthora Avr3a-Like Effectors Target and Inhibit Cinnamyl Alcohol Dehydrogenase CAD5 to Suppress Plant Immunity. Molecular Plant Pathology, 2025, 26, e70139.	5.2	3
950	The Anti-Oomycete Activity and Potential Mechanisms of Pamidronate Against Development and Pathogenicity in Phytophthora sojae. Physiological and Molecular Plant Pathology, 2026, 141, 102986.	3.9	0
951	Structural Insights Into WY Domain-SLiM Containing Conserved RxLR Effectors: A Case Study of Five Important Phytophthora Species. Molecular Plant-Microbe Interactions, 2026, 39, 14-30.	3.7	5
952	Oomycete Plant Pathogens: Biology, Pathogenesis and Emerging Control Strategies. Nature Reviews Microbiology, 2026, 24, 1-18.	123.6	15
953	Phytophthora: Timeline of Taxonomy and Identification From Plant Pathology's Origin to Molecular Technologies. Plant Disease, 2026, 110, 1038-1053.	2.2	2
954	Metagenomics of the MAST-3 Stramenopile, Incisomonas, and Its Associated Microbiome Reveals Unexpected Metabolic Attributes and Extensive Nutrient Dependencies: This Article Is Part of the Microbial Genomics of Eukaryotes Collection. Microbial Genomics, 2025, 11, 001510.	4.0	1

#	Article	IF	Citations
955	Genome-Wide Identification and Functional Characterization of RxLR Effectors in Phytophthora cinnamomi Infecting Carya cathayensis Sarg. Virulence, 2025, 16, 2590256.	6.6	2
956	Control Efficiency and Potential Mechanisms of 2,3-Butanedione Against Potato Leak Caused by Pythium ultimum. Postharvest Biology and Technology, 2026, 234, 114111.	7.6	1
957	Phytophthora Effector Exploits WY Module Truncation to Manipulate Nt-Acetylation–Mediated AtMBP-1 Turnover and Suppress Plant Immunity. Science Advances, 2025, 11, eady1482.	13.6	3
958	The Autophagy-Related Protein PlAtg26b Regulates Vegetative Growth, Reproductive Processes, Autophagy, and Pathogenicity in Peronophythora litchii. Virulence, 2026, 17, 2606498.	6.6	0
959	Evolutionary Relationships and a T-BAS Interactive Phylogeny of Emerging Lineages of the Plant Pathogen Phytophthora ramorum. Phytopathology, 2026, 116, 1119-1129.	3.7	1
960	Effector Gene Silencing Coordinated by Histone Methylation and Small RNAs Enhances Host Adaptation in a Plant Pathogen. Nucleic Acids Research, 2026, .	19.7	5
961	Phytophthora capsici Carries and Differentially Expresses Genes for the RNA Interference Pathway. PLoS ONE, 2026, 21, e0333769.	3.2	1
962	Characterization of the Effector Candidate Repertoire in the Arbuscular Mycorrhizal Fungus Rhizophagus irregularis. Journal of Fungi (Basel, Switzerland), 2026, 12, 122.	4.4	2
963	Building a Microecological Barrier: How Resistant Soybean Cultivars Integrate Metabolite Secretion and Microbial Consortia to Combat Root Rot. Plant, Cell and Environment, 2026, 49, 2225-2241.	7.8	0
964	New Draft Genomes Assemblies of Blastocystis Isolates From Subtypes 1 and 8 Confirm Conserved Synteny, Transposable Element Diversity, and Provide Insights Into Pathogenic Potential. Protist, 2026, 181, 126157.	2.1	0
965	Structuration et exploration d'informations génomiques et fonctionnelles des enzymes actives sur les glucides. , 0, .		0
966	Ecologie et évolution de l'interaction Plasmopara viticola / Vitis spp. et évaluation des risques de contournement de la résistance de la vigne au mildiou. , 0, .		0
967	Contribution à l'étude des déterminants génétiques impliqués dans le processus infectieux de Melampsora larici-populina, l'agent de la rouille foliaire du peuplier. , 0, .		0
968	Génomique et post-génomique du parasite intestinal Blastocystis sp. sous-type 7. Evaluation de son pouvoir pathogène. , 0, .		0
969	Contribution à l'analyse post-génomique de l'interaction entre le peuplier et Melampsora larici-populina, le champignon biotrophe responsable de la maladie de la rouille foliaire. , 0, .		0
970	Étude des conditions de l'émergence du phytophthora alni sur l'aulne glutineux. , 0, .		0
971	Génomique comparative et évolutive au sein du complexe d'espèces Leptosphaeria maculans-Leptosphaeria biglobosa. , 2013, .		0
972	Analyse fonctionnelle d'effecteurs fongiques impliqués dans le développement de la symbiose ectomycorhizienne Laccaria bicolor-Populus trichocarpa. , 0, .		0

#	Article	IF	Citations
973	Variation phénotypique de la résistance quantitative à Phytophthora capsici dans la diversité naturelle du piment, et diversité moléculaire et profil d'évolution du QTL majeur Pc5.1. , 0, .		0
974	Le contournement de résistance par Melampsora Larici-populina l'agent de la rouille du peuplier : impact démographique et déterminisme génétique. , 0, .		0
975	Identification et caractérisation de facteurs hôtes impliqués dans la résistance au Pepino Mosaic Virus chez la tomate. , 0, .		0
976	Origins and Early Evolution of Photosynthetic Eukaryotes. , 0, .		0
977	Etude des facteurs de transcription impliqués dans l'accumulation lipidique en condition de stress azoté chez la microalgue haptophyte Isochrysis affinis galbana. , 0, .		0
978	Étude des effecteurs de type RXLR de Plasmopara viticola pour la recherche de résistances durables au mildiou de la vigne. , 0, .		0
979	The Phytophthora parasitica Effector Avh195 : An Antagonist of Host Autophagy and Promoter of the Infection Cycle. , 2018, .		0
980	Interactions entre résistance induite chez Solanum tuberosum et traits d'histoire de vie et effecteurs de Phytophthora infestans. , 0, .		0
981	Origine et modes de dispersion des épidémies dues à Phytophthora megakarya dans les systèmes de cacaoculture innovants au Cameroun. , 0, .		0
982	Étude d'effecteurs de l'oomycète pathogène Phytophthora capsici exprimés au cours de l'interaction avec le piment et la tomate. , 0, .		0
983	Functional Characterization of Different Candidate Effectors From the Root Rot Oomycete Aphanomyces Euteiches. , 2020, .		0
984	Analyses évolutive et moléculaire des déterminants génétiques impliqués dans l'interaction entre l'agent de la rouille du peuplier et son hôte. , 0, .		0
985	Multiomics Identification of Effectors Candidates From Oomycete Root Plant Pathogen Aphanomyces Euteiches. , 2022, .		0
986	The Evolution of Red Algal Organellar Genomes and the Origin of Red Complex Plastids. , 2022, .		0
987	Integrative Proteomic and Biophysical Approaches to Elucidate Phytophthora Zoospore Sensing and Motility During Early Plant Interactions. , 2024, .		0
988	The Oligosaccharyltransferase Catalytic Subunit PsSTT3B Is Required for Asexual Development and Pathogenicity in Phytophthora sojae. Journal of Fungi (Basel, Switzerland), 2026, 12, 274.	4.4	1
989	Pheromone Action in Chytrids and Zygomycetes, and in Oophytes. The mycota, 2026, .	0.0	0
990	Phytophthora Targets Plant Extracellular Vesicles to Promote Infection. Nature Microbiology, 2026, 11, 1256-1270.	18.2	4

#	Article	IF	Citations
991	The 50 Most Researched Fungal and Oomycete Plant Pathogens. Fungal Diversity, 2026, .	19.8	6
992	Deciphering the Soybean Root Rot Pathogen Phytophthora sojae: Signaling Pathways, Transcriptional Regulation, and Effector Biology. New Plant Protection, 2026, 3, e70042.	1.5	0
993	Shining Light on Late Blight. Annual Review of Phytopathology, 2026, 64, 1-24.	13.2	2
994	Parasitisterols A–C, 24,25-Dihydroxycholestane-Type Triterpenoids, From Oomycete Fish Pathogen Saprolegnia parasitica. ACS Omega, 2026, 11, 27257-27265.	5.2	0
995	Next-Generation Sequencing for Plant Genomics. Interdisciplinary biotechnological advances, 2026, .	0.0	0
996	Dual Transcriptomic Analysis of Isolates of Phytophthora sansomeana With Varying Levels of Aggressiveness Compared to P. Sojae During a Time Course Infection Assay of Soybean. Phytopathology, 2026, .	3.7	0
997	Genome Re-Sequencing and Functional Analysis Reveal an α-1,3-Glucosyltransferase Conferring Metalaxyl Resistance in Phytophthora sojae. Journal of Fungi (Basel, Switzerland), 2026, 12, 479.	4.4	0
998	Eukaryotic Metagenome-Assembled Genomes Recovered From Deep Metagenomic Sequencing of the Seagrass, Zostera marina, Include a Novel Chytrid in the Order Lobulomycetales. Microbial Genomics, 2026, .	4.0	0
999	RXLR Effectors of Phytophthora infestans: Delivery, Host Targets and Immune Suppression. Molecular Biology Reports, 2026, 53, 1776.	3.6	0