

Howard S Judelson

List of Publications by Year in descending order

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96
papers

7,034
citations

87888

38
h-index

62596

80
g-index

102
all docs

102
docs citations

102
times ranked

4465
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence and analysis of the Irish potato famine pathogen <i>Phytophthora infestans</i> . <i>Nature</i> , 2009, 461, 393-398.	27.8	1,405
2	The Top 10 oomycete pathogens in molecular plant pathology. <i>Molecular Plant Pathology</i> , 2015, 16, 413-434.	4.2	695
3	Signatures of Adaptation to Obligate Biotrophy in the <i>Hyaloperonospora arabidopsidis</i> Genome. <i>Science</i> , 2010, 330, 1549-1551.	12.6	492
4	The spores of <i>Phytophthora</i> : weapons of the plant destroyer. <i>Nature Reviews Microbiology</i> , 2005, 3, 47-58.	28.6	394
5	Oomycete pathogens encode RNA silencing suppressors. <i>Nature Genetics</i> , 2013, 45, 330-333.	21.4	238
6	Transformation of the Oomycete Pathogen, <i>Phytophthora infestans</i> . <i>Molecular Plant-Microbe Interactions</i> , 1991, 4, 602.	2.6	167
7	Large-Scale Gene Discovery in the Oomycete <i>Phytophthora infestans</i> Reveals Likely Components of Phytopathogenicity Shared with True Fungi. <i>Molecular Plant-Microbe Interactions</i> , 2005, 18, 229-243.	2.6	160
8	Genome analyses of the sunflower pathogen <i>Plasmopara halstedii</i> provide insights into effector evolution in downy mildews and <i>Phytophthora</i> . <i>BMC Genomics</i> , 2015, 16, 741.	2.8	135
9	Spray-induced gene silencing for disease control is dependent on the efficiency of pathogen RNA uptake. <i>Plant Biotechnology Journal</i> , 2021, 19, 1756-1768.	8.3	126
10	The <i>piO</i> Gene of <i>Phytophthora infestans</i> is Highly Expressed in Invading Hyphae during Infection. <i>Fungal Genetics and Biology</i> , 1998, 23, 126-138.	2.1	115
11	Gene Expression Profiling During Asexual Development of the Late Blight Pathogen <i>Phytophthora infestans</i> Reveals a Highly Dynamic Transcriptome. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 433-447.	2.6	105
12	Enhanced Polymerase Chain Reaction Methods for Detecting and Quantifying <i>Phytophthora infestans</i> in Plants. <i>Phytopathology</i> , 2000, 90, 1112-1119.	2.2	97
13	A bZIP transcription factor from <i>Phytophthora</i> interacts with a protein kinase and is required for zoospore motility and plant infection. <i>Molecular Microbiology</i> , 2005, 56, 638-648.	2.5	95
14	The Genetics and Biology of <i>Phytophthora infestans</i> : Modern Approaches to a Historical Challenge. <i>Fungal Genetics and Biology</i> , 1997, 22, 65-76.	2.1	94
15	Cell cycle regulator <i>Cdc14</i> is expressed during sporulation but not hyphal growth in the fungus-like oomycete <i>Phytophthora infestans</i> . <i>Molecular Microbiology</i> , 2003, 50, 487-494.	2.5	90
16	RNA-seq of life stages of the oomycete <i>Phytophthora infestans</i> reveals dynamic changes in metabolic, signal transduction, and pathogenesis genes and a major role for calcium signaling in development. <i>BMC Genomics</i> , 2017, 18, 198.	2.8	85
17	How Does <i>Phytophthora infestans</i> Evade Control Efforts? Modern Insight Into the Late Blight Disease. <i>Phytopathology</i> , 2018, 108, 916-924.	2.2	82
18	Dynamics and Innovations within Oomycete Genomes: Insights into Biology, Pathology, and Evolution. <i>Eukaryotic Cell</i> , 2012, 11, 1304-1312.	3.4	78

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19	Optimization of transgene-mediated silencing in <i>Phytophthora infestans</i> and its association with small-interfering RNAs. <i>Fungal Genetics and Biology</i> , 2008, 45, 1197-1205.	2.1	73
20	Transformation of the oomycete pathogen <i>Phytophthora megasperma</i> f. sp. <i>glycinea</i> occurs by DNA integration into single or multiple chromosomes. <i>Current Genetics</i> , 1993, 23, 211-218.	1.7	70
21	Novel Protein Kinase Induced during Sporangial Cleavage in the Oomycete <i>Phytophthora infestans</i> . <i>Eukaryotic Cell</i> , 2002, 1, 687-695.	3.4	70
22	Transgene-Induced Silencing of the Zoosporogenesis-Specific NIFC Gene Cluster of <i>Phytophthora infestans</i> Involves Chromatin Alterations. <i>Eukaryotic Cell</i> , 2007, 6, 1200-1209.	3.4	70
23	Genetic Analysis of Metalaxyl Insensitivity Loci in <i>Phytophthora infestans</i> Using Linked DNA Markers. <i>Phytopathology</i> , 1997, 87, 1034-1040.	2.2	68
24	Regulatory sequences for expressing genes in oomycete fungi. <i>Molecular Genetics and Genomics</i> , 1992, 234, 138-146.	2.4	60
25	Multiple Loci Determining Insensitivity to Phenylamide Fungicides in <i>Phytophthora infestans</i> . <i>Phytopathology</i> , 1999, 89, 754-760.	2.2	60
26	Multiple Pathways Regulate the Induction of Genes During Zoosporogenesis in <i>Phytophthora infestans</i> . <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 330-337.	2.6	60
27	Lifestyle, gene gain and loss, and transcriptional remodeling cause divergence in the transcriptomes of <i>Phytophthora infestans</i> and <i>Pythium ultimum</i> during potato tuber colonization. <i>BMC Genomics</i> , 2017, 18, 764.	2.8	60
28	Expression and Inheritance of Sexual Preference and Selfing Potential in <i>Phytophthora infestans</i> . <i>Fungal Genetics and Biology</i> , 1997, 21, 188-197.	2.1	59
29	Expression and antisense inhibition of transgenes in <i>Phytophthora infestans</i> is modulated by choice of promoter and position effects. <i>Gene</i> , 1993, 133, 63-69.	2.2	58
30	Sporangium-Specific Gene Expression in the Oomycete Phytopathogen <i>Phytophthora infestans</i> . <i>Eukaryotic Cell</i> , 2003, 2, 1376-1385.	3.4	54
31	Genetic and Physical Variability at the Mating Type Locus of the Oomycete, <i>Phytophthora infestans</i> . <i>Genetics</i> , 1996, 144, 1005-1013.	2.9	53
32	Metalaxyl Resistance in <i>Phytophthora infestans</i> : Assessing Role of RPA190 Gene and Diversity Within Clonal Lineages. <i>Phytopathology</i> , 2015, 105, 1594-1600.	2.2	51
33	Stage-specific gene expression during sexual development in <i>Phytophthora infestans</i> . <i>Molecular Microbiology</i> , 2002, 45, 1057-1066.	2.5	49
34	Intermolecular ligation mediates efficient cotransformation in <i>Phytophthora infestans</i> . <i>Molecular Genetics and Genomics</i> , 1993, 239, 241-250.	2.4	47
35	Metabolic Diversity and Novelty in the Oomycetes. <i>Annual Review of Microbiology</i> , 2017, 71, 21-39.	7.3	47
36	Exchanges at the Plant-Oomycete Interface That Influence Disease. <i>Plant Physiology</i> , 2019, 179, 1198-1211.	4.8	46

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37	Transient expression of genes in the oomycete <i>Phytophthora infestans</i> using <i>Bremia lactucae</i> regulatory sequences. <i>Current Genetics</i> , 1991, 19, 453-459.	1.7	45
38	Gene Expression and Silencing Studies in <i>Phytophthora infestans</i> Reveal Infection-Specific Nutrient Transporters and a Role for the Nitrate Reductase Pathway in Plant Pathogenesis. <i>PLoS Pathogens</i> , 2016, 12, e1006097.	4.7	43
39	Vectors for fluorescent protein tagging in <i>Phytophthora</i> : tools for functional genomics and cell biology. <i>Fungal Biology</i> , 2011, 115, 882-890.	2.5	42
40	Stable transformation of the oomycete, <i>Phytophthora infestans</i> , using microprojectile bombardment. <i>Current Genetics</i> , 2003, 42, 228-235.	1.7	40
41	Activation of Zoosporogenesis-Specific Genes in <i>Phytophthora infestans</i> Involves a 7-Nucleotide Promoter Motif and Cold-Induced Membrane Rigidity. <i>Eukaryotic Cell</i> , 2006, 5, 745-752.	3.4	40
42	Niche-specific metabolic adaptation in biotrophic and necrotrophic oomycetes is manifested in differential use of nutrients, variation in gene content, and enzyme evolution. <i>PLoS Pathogens</i> , 2019, 15, e1007729.	4.7	37
43	Inactivation of transgenes in <i>Phytophthora infestans</i> is not associated with their deletion, methylation, or mutation. <i>Current Genetics</i> , 1995, 28, 571-579.	1.7	36
44	A Gene Expressed during Sexual and Asexual Sporulation in <i>Phytophthora infestans</i> Is a Member of the Puf Family of Translational Regulators. <i>Eukaryotic Cell</i> , 2003, 2, 465-473.	3.4	36
45	The kinome of <i>Phytophthora infestans</i> reveals oomycete-specific innovations and links to other taxonomic groups. <i>BMC Genomics</i> , 2010, 11, 700.	2.8	36
46	bZIP Transcription Factors in the Oomycete <i>Phytophthora infestans</i> with Novel DNA-Binding Domains Are Involved in Defense against Oxidative Stress. <i>Eukaryotic Cell</i> , 2013, 12, 1403-1412.	3.4	36
47	Myb Transcription Factors and Light Regulate Sporulation in the Oomycete <i>Phytophthora infestans</i> . <i>PLoS ONE</i> , 2014, 9, e92086.	2.5	36
48	Sequence Variation and Genomic Amplification of a Family of Gypsy-like Elements in the Oomycete Genus <i>Phytophthora</i> . <i>Molecular Biology and Evolution</i> , 2002, 19, 1313-1322.	8.9	35
49	Construction of a Bacterial Artificial Chromosome Library of <i>Phytophthora infestans</i> and Transformation of Clones into <i>P. infestans</i> . <i>Fungal Genetics and Biology</i> , 1999, 28, 160-170.	2.1	34
50	Genome-wide Prediction and Functional Validation of Promoter Motifs Regulating Gene Expression in Spore and Infection Stages of <i>Phytophthora infestans</i> . <i>PLoS Pathogens</i> , 2013, 9, e1003182.	4.7	34
51	Families of repeated DNA in the oomycete <i>Phytophthora infestans</i> and their distribution within the genus. <i>Genome</i> , 1998, 41, 605-615.	2.0	33
52	Quantitation of <i>Phytophthora cinnamomi</i> in Avocado Roots Using a Species-Specific DNA Probe. <i>Phytopathology</i> , 1996, 86, 763.	2.2	32
53	A Mating-Induced Protein of <i>Phytophthora infestans</i> Is a Member of a Family of Elicitors with Divergent Structures and Stage-Specific Patterns of Expression. <i>Molecular Plant-Microbe Interactions</i> , 2003, 16, 926-935.	2.6	31
54	Novel core promoter elements in the oomycete pathogen <i>Phytophthora infestans</i> and their influence on expression detected by genome-wide analysis. <i>BMC Genomics</i> , 2013, 14, 106.	2.8	31

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55	Gene expression during oosporeogenesis in heterothallic and homothallic <i>Phytophthora</i> . <i>Fungal Genetics and Biology</i> , 2007, 44, 726-739.	2.1	30
56	Metabolic adaptation of <i>Phytophthora infestans</i> during growth on leaves, tubers and artificial media. <i>Molecular Plant Pathology</i> , 2009, 10, 843-855.	4.2	29
57	Myb transcription factors in the oomycete <i>Phytophthora</i> with novel diversified DNA-binding domains and developmental stage-specific expression. <i>Gene</i> , 2010, 453, 1-8.	2.2	29
58	Investigating the role of ABC transporters in multifungicide insensitivity in <i>Phytophthora infestans</i> . <i>Molecular Plant Pathology</i> , 2006, 7, 17-29.	4.2	28
59	Genetic Variation within Clonal Lineages of <i>Phytophthora infestans</i> Revealed through Genotyping-By-Sequencing, and Implications for Late Blight Epidemiology. <i>PLoS ONE</i> , 2016, 11, e0165690.	2.5	26
60	Chromosomal heteromorphism and an apparent translocation detected using a BAC contig spanning the mating type locus of <i>Phytophthora infestans</i> . <i>Fungal Genetics and Biology</i> , 2003, 38, 75-84.	2.1	25
61	Decay of Genes Encoding the Oomycete Flagellar Proteome in the Downy Mildew <i>Hyaloperonospora arabidopsidis</i> . <i>PLoS ONE</i> , 2012, 7, e47624.	2.5	24
62	Genome-Wide Increased Copy Number is Associated with Emergence of Dominant Clones of the Irish Potato Famine Pathogen <i>Phytophthora infestans</i> . <i>MBio</i> , 2020, 11, .	4.1	24
63	Rethinking the evolution of eukaryotic metabolism: novel cellular partitioning of enzymes in stramenopiles links serine biosynthesis to glycolysis in mitochondria. <i>BMC Evolutionary Biology</i> , 2017, 17, 241.	3.2	23
64	Metabolic Model of the <i>Phytophthora infestans</i> -Tomato Interaction Reveals Metabolic Switches during Host Colonization. <i>MBio</i> , 2019, 10, .	4.1	23
65	A Cas12a-based gene editing system for <i>Phytophthora infestans</i> reveals monoallelic expression of an elicitor. <i>Molecular Plant Pathology</i> , 2021, 22, 737-752.	4.2	22
66	Sexual Reproduction in Plant Pathogenic Oomycetes: Biology and Impact on Disease. , 0, , 445-458.		21
67	New Role for Cdc14 Phosphatase: Localization to Basal Bodies in the Oomycete <i>Phytophthora</i> and Its Evolutionary Coinheritance with Eukaryotic Flagella. <i>PLoS ONE</i> , 2011, 6, e16725.	2.5	21
68	Recombination pathways in <i>Phytophthora infestans</i> : polyploidy resulting from aberrant sexual development and zoospore-mediated heterokaryosis. <i>Mycological Research</i> , 1998, 102, 1245-1253.	2.5	20
69	A motif within a complex promoter from the oomycete <i>Phytophthora infestans</i> determines transcription during an intermediate stage of sporulation. <i>Fungal Genetics and Biology</i> , 2009, 46, 400-409.	2.1	20
70	Concerted evolution of a tandemly arrayed family of mating-specific genes in <i>Phytophthora</i> analyzed through inter- and intraspecific comparisons. <i>Molecular Genetics and Genomics</i> , 2006, 275, 169-184.	2.1	18
71	Architecture of the Sporulation-Specific <i>Cdc14</i> Promoter from the Oomycete <i>Phytophthora infestans</i> . <i>Eukaryotic Cell</i> , 2007, 6, 2222-2230.	3.4	18
72	Gene expression changes during asexual sporulation by the late blight agent <i>Phytophthora infestans</i> occur in discrete temporal stages. <i>Molecular Genetics and Genomics</i> , 2009, 281, 193-206.	2.1	18

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73	Genomics of the Plant Pathogenic Oomycete <i>Phytophthora</i> : Insights into Biology and Evolution. <i>Advances in Genetics</i> , 2007, 57, 97-141.	1.8	17
74	A MADS-box transcription factor regulates a central step in sporulation of the oomycete <i>Phytophthora infestans</i> . <i>Molecular Microbiology</i> , 2018, 110, 562-575.	2.5	17
75	Novo&Stitch: accurate reconciliation of genome assemblies via optical maps. <i>Bioinformatics</i> , 2018, 34, i43-i51.	4.1	16
76	A cluster of NIF transcriptional regulators with divergent patterns of spore-specific expression in. <i>Fungal Genetics and Biology</i> , 2005, 42, 42-50.	2.1	15
77	Transcriptomic and proteomic analysis reveals wall-associated and glucan-degrading proteins with potential roles in <i>Phytophthora infestans</i> sexual spore development. <i>PLoS ONE</i> , 2018, 13, e0198186.	2.5	15
78	The Genome of <i>Peronospora belbahrii</i> Reveals High Heterozygosity, a Low Number of Canonical Effectors, and TC-Rich Promoters. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 742-753.	2.6	15
79	Investigating the role of ABC transporters in multifungicide insensitivity in <i>Phytophthora infestans</i> . <i>Molecular Plant Pathology</i> , 2006, 7, 17-29.	4.2	12
80	<i>Phytophthora infestans</i> Dihydroorotate Dehydrogenase Is a Potential Target for Chemical Control – A Comparison With the Enzyme From <i>Solanum tuberosum</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1479.	3.5	12
81	An RNA symbiont enhances heat tolerance and secondary homothallism in the oomycete <i>Phytophthora infestans</i> . <i>Microbiology (United Kingdom)</i> , 2010, 156, 2026-2034.	1.8	8
82	Performance of a tetracycline-responsive transactivator system for regulating transgenes in the oomycete <i>Phytophthora infestans</i> . <i>Current Genetics</i> , 2007, 51, 297-307.	1.7	7
83	Development of a bipartite ecdysone-responsive gene switch for the oomycete <i>Phytophthora infestans</i> and its use to manipulate transcription during axenic culture and plant infection. <i>Molecular Plant Pathology</i> , 2015, 16, 83-91.	4.2	6
84	Phosphagen kinase function in flagellated spores of the oomycete <i>Phytophthora infestans</i> integrates transcriptional regulation, metabolic dynamics and protein retargeting. <i>Molecular Microbiology</i> , 2018, 110, 296-308.	2.5	6
85	Invertases in <i>Phytophthora infestans</i> Localize to Haustoria and Are Programmed for Infection-Specific Expression. <i>MBio</i> , 2020, 11, .	4.1	6
86	Families of repeated DNA in the oomycete <i>Phytophthora infestans</i> and their distribution within the genus. <i>Genome</i> , 1998, 41, 605-615.	2.0	6
87	Chemical genetic approach using $\hat{2}$ -rubromycin reveals that a RIO kinase-like protein is involved in morphological development in <i>Phytophthora infestans</i> . <i>Scientific Reports</i> , 2020, 10, 22326.	3.3	6
88	Comparisons of Ribosomal Protein Gene Promoters Indicate Superiority of Heterologous Regulatory Sequences for Expressing Transgenes in <i>Phytophthora infestans</i> . <i>PLoS ONE</i> , 2015, 10, e0145612.	2.5	5
89	SNP-Based Differentiation of <i>Phytophthora infestans</i> Clonal Lineages Using Locked Nucleic Acid Probes and High-Resolution Melt Analysis. <i>Plant Disease</i> , 2016, 100, 1297-1306.	1.4	5
90	Defining Transgene Insertion Sites and Off-Target Effects of Homology-Based Gene Silencing Informs the Application of Functional Genomics Tools in <i>Phytophthora infestans</i> . <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 915-927.	2.6	5

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91	Illuminating Phytophthora Biology with Fluorescent Protein Tags. <i>Methods in Molecular Biology</i> , 2018, 1848, 119-129.	0.9	4
92	<i>Phytophthora infestans</i> Sporangia Produced in Artificial Media and Plant Lesions Have Subtly Divergent Transcription Profiles but Equivalent Infection Potential and Aggressiveness. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 1077-1087.	2.6	4
93	High-Quality Reference Genome Sequence for the Oomycete Vegetable Pathogen <i>Phytophthora capsici</i> Strain LT1534. <i>Microbiology Resource Announcements</i> , 2021, 10, e0029521.	0.6	4
94	Molecular Strategies for Identifying Determinants of Oomycete Pathogenicity. <i>Soil Biology</i> , 2008, , 383-410.	0.8	1
95	Nutritional factors modulating plant and fruit susceptibility to pathogens: BARD workshop, Haifa, Israel, February 25-26, 2018. <i>Phytoparasitica</i> , 2020, 48, 317-333.	1.2	0
96	Genomics of Oomycetes. , 2004, , 1-4.		0