

Jeffrey A Rollins

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7132137/publications.pdf>

Version: 2024-02-01

74
papers

5,328
citations

134610

34
h-index

100535

70
g-index

75
all docs

75
docs citations

75
times ranked

5298
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic Analysis of the Necrotrophic Fungal Pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . <i>PLoS Genetics</i> , 2011, 7, e1002230.	1.5	902
2	Lifestyle transitions in plant pathogenic <i>Colletotrichum</i> fungi deciphered by genome and transcriptome analyses. <i>Nature Genetics</i> , 2012, 44, 1060-1065.	9.4	840
3	Green Fluorescent Protein Is Lighting Up Fungal Biology. <i>Applied and Environmental Microbiology</i> , 2001, 67, 1987-1994.	1.4	286
4	The <i>Sclerotinia sclerotiorum</i> <i>pac1</i> Gene Is Required for Sclerotial Development and Virulence. <i>Molecular Plant-Microbe Interactions</i> , 2003, 16, 785-795.	1.4	272
5	pH Signaling in <i>Sclerotinia sclerotiorum</i> : Identification of a <i>pacC/RIM1</i> Homolog. <i>Applied and Environmental Microbiology</i> , 2001, 67, 75-81.	1.4	243
6	The Complete Genome Sequence of the Phytopathogenic Fungus <i>Sclerotinia sclerotiorum</i> Reveals Insights into the Genome Architecture of Broad Host Range Pathogens. <i>Genome Biology and Evolution</i> , 2017, 9, 593-618.	1.1	187
7	Silicon influences cytological and molecular events in compatible and incompatible rice- <i>Magnaporthe grisea</i> interactions. <i>Physiological and Molecular Plant Pathology</i> , 2005, 66, 144-159.	1.3	174
8	Mechanisms of Broad Host Range Necrotrophic Pathogenesis in <i>Sclerotinia sclerotiorum</i> . <i>Phytopathology</i> , 2018, 108, 1128-1140.	1.1	132
9	Ribosomal DNA systematics of <i>Ceratobasidium</i> and <i>Thanatephorus</i> with <i>Rhizoctonia</i> anamorphs. <i>Mycologia</i> , 2001, 93, 1138-1150.	0.8	126
10	Oxaloacetate acetylhydrolase gene mutants of <i>Sclerotinia sclerotiorum</i> do not accumulate oxalic acid, but do produce limited lesions on host plants. <i>Molecular Plant Pathology</i> , 2015, 16, 559-571.	2.0	110
11	Transcriptomic changes in the plant pathogenic fungus <i>Rhizoctonia solani</i> AG-3 in response to the antagonistic bacteria <i>Serratia proteamaculans</i> and <i>Serratia plymuthica</i> . <i>BMC Genomics</i> , 2015, 16, 630.	1.2	97
12	Deletion of the adenylate cyclase (<i>sac1</i>) gene affects multiple developmental pathways and pathogenicity in <i>Sclerotinia sclerotiorum</i> . <i>Fungal Genetics and Biology</i> , 2007, 44, 521-530.	0.9	94
13	Introduction of Large Sequence Inserts by CRISPR-Cas9 To Create Pathogenicity Mutants in the Multinucleate Filamentous Pathogen <i>Sclerotinia sclerotiorum</i> . <i>MBio</i> , 2018, 9, .	1.8	89
14	How many fungi make sclerotia?. <i>Fungal Ecology</i> , 2015, 13, 211-220.	0.7	81
15	Multi-factor regulation of pectate lyase secretion by <i>Colletotrichum gloeosporioides</i> pathogenic on avocado fruits. <i>Molecular Plant Pathology</i> , 2008, 9, 281-291.	2.0	79
16	The GATA-type IVb zinc-finger transcription factor <i>SsNsd1</i> regulates asexual sexual development and appressoria formation in <i>Sclerotinia sclerotiorum</i> . <i>Molecular Plant Pathology</i> , 2018, 19, 1679-1689.	2.0	75
17	Increase in Endogenous and Exogenous Cyclic AMP Levels Inhibits Sclerotial Development in <i>Sclerotinia sclerotiorum</i> . <i>Applied and Environmental Microbiology</i> , 1998, 64, 2539-2544.	1.4	71
18	<i>Sclerotinia sclerotiorum</i> β -Glutamyl Transpeptidase (<i>Ss-Ggt1</i>) Is Required for Regulating Glutathione Accumulation and Development of Sclerotia and Compound Appressoria. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 412-420.	1.4	66

#	ARTICLE	IF	CITATIONS
19	The Arabidopsis Mediator Complex Subunit16 Is a Key Component of Basal Resistance against the Necrotrophic Fungal Pathogen <i>Sclerotinia sclerotiorum</i> . <i>Plant Physiology</i> , 2015, 169, 856-872.	2.3	64
20	Effect of Ammonia Production by <i>Colletotrichum gloeosporioides</i> on pelB Activation, Pectate Lyase Secretion, and Fruit Pathogenicity. <i>Applied and Environmental Microbiology</i> , 2006, 72, 1034-1039.	1.4	62
21	Phylogenetic relationships of <i>Rhizoctonia</i> fungi within the Cantharellales. <i>Fungal Biology</i> , 2016, 120, 603-619.	1.1	56
22	A CRY-DASH-type photolyase/cryptochrome from <i>Sclerotinia sclerotiorum</i> mediates minor UV-A-specific effects on development. <i>Fungal Genetics and Biology</i> , 2008, 45, 1265-1276.	0.9	55
23	Fungal oxalate decarboxylase activity contributes to <i>Sclerotinia sclerotiorum</i> early infection by affecting both compound appressoria development and function. <i>Molecular Plant Pathology</i> , 2015, 16, 825-836.	2.0	52
24	pH modulation differs during sunflower cotyledon colonization by the two closely related necrotrophic fungi <i>Botrytis cinerea</i> and <i>Sclerotinia sclerotiorum</i> . <i>Molecular Plant Pathology</i> , 2012, 13, 568-578.	2.0	51
25	Genetic diversity of <i>Rhizoctonia solani</i> AG-3 from potato and tobacco in North Carolina. <i>Mycologia</i> , 2002, 94, 437-449.	0.8	50
26	Laurel Wilt in Natural and Agricultural Ecosystems: Understanding the Drivers and Scales of Complex Pathosystems. <i>Forests</i> , 2017, 8, 48.	0.9	50
27	The development-specific protein (Ssp1) from <i>Sclerotinia sclerotiorum</i> is encoded by a novel gene expressed exclusively in sclerotium tissues. <i>Mycologia</i> , 2009, 101, 34-43.	0.8	49
28	Draft Genome Sequence of the Plant-Pathogenic Soil Fungus <i>Rhizoctonia solani</i> Anastomosis Group 3 Strain Rhs1AP. <i>Genome Announcements</i> , 2014, 2, .	0.8	49
29	The infection cushion of <i>Botrytis cinerea</i> : a fungal "weapon" of plant biomass destruction. <i>Environmental Microbiology</i> , 2021, 23, 2293-2314.	1.8	48
30	Mating Type and Simple Sequence Repeat Markers Indicate a Clonal Population of <i>Phyllosticta citricarpa</i> in Florida. <i>Phytopathology</i> , 2016, 106, 1300-1310.	1.1	46
31	Pathogenic adaptations of <i>Colletotrichum</i> fungi revealed by genome wide gene family evolutionary analyses. <i>PLoS ONE</i> , 2018, 13, e0196303.	1.1	46
32	Characterization and functional analysis of a cAMP-dependent protein kinase A catalytic subunit gene (<i>pka1</i>) in <i>Sclerotinia sclerotiorum</i> . <i>Physiological and Molecular Plant Pathology</i> , 2004, 64, 155-163.	1.3	44
33	An atypical forkhead-containing transcription factor <i>SsFKH1</i> is involved in sclerotial formation and is essential for pathogenicity in <i>Sclerotinia sclerotiorum</i> . <i>Molecular Plant Pathology</i> , 2017, 18, 963-975.	2.0	43
34	Chemotaxonomy of fungi in the <i>Rhizoctonia solani</i> species complex performing GC/MS metabolite profiling. <i>Metabolomics</i> , 2013, 9, 159-169.	1.4	34
35	Sexual Reproduction in the Citrus Black Spot Pathogen, <i>Phyllosticta citricarpa</i> . <i>Phytopathology</i> , 2017, 107, 732-739.	1.1	33
36	An In Planta Method for Assessing the Role of Basidiospores in <i>Rhizoctonia</i> Foliar Disease of Tomato. <i>Plant Disease</i> , 2010, 94, 515-520.	0.7	32

#	ARTICLE	IF	CITATIONS
37	The development-specific <i>ssp1</i> and <i>ssp2</i> genes of <i>Sclerotinia sclerotiorum</i> encode lectins with distinct yet compensatory regulation. <i>Fungal Genetics and Biology</i> , 2010, 47, 531-538.	0.9	32
38	Genetic analysis of cross fertility between two self-sterile strains of <i>Glomerella graminicola</i> . <i>Mycologia</i> , 2000, 92, 430-435.	0.8	31
39	Genetic structure of populations of <i>Rhizoctonia solani</i> AG-3 on potato in eastern North Carolina. <i>Mycologia</i> , 2002, 94, 450-460.	0.8	31
40	An activating mutation of the <i>Sclerotinia sclerotiorum</i> <i>pac1</i> gene increases oxalic acid production at low pH but decreases virulence. <i>Molecular Plant Pathology</i> , 2007, 8, 611-622.	2.0	30
41	Genetic Analysis of Cross Fertility between Two Self-Sterile Strains of <i>Glomerella graminicola</i> . <i>Mycologia</i> , 2000, 92, 430.	0.8	29
42	A Global Perspective on the Population Structure and Reproductive System of <i>Phyllosticta citricarpa</i> . <i>Phytopathology</i> , 2017, 107, 758-768.	1.1	28
43	Fine-Scale Genetic Structure and Reproductive Biology of the Blueberry Pathogen <i>Monilinia vaccinii-corymbosi</i> . <i>Phytopathology</i> , 2017, 107, 231-239.	1.1	28
44	Characterization of MAT gene functions in the life cycle of <i>Sclerotinia sclerotiorum</i> reveals a lineage-specific MAT gene functioning in apothecium morphogenesis. <i>Fungal Biology</i> , 2016, 120, 1105-1117.	1.1	25
45	Peroxisomal Carnitine Acetyl Transferase Influences Host Colonization Capacity in <i>Sclerotinia sclerotiorum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 768-780.	1.4	22
46	Evidence for Morphological, Vegetative, Genetic, and Mating-Type Diversity in <i>Sclerotinia homoeocarpa</i> . <i>Phytopathology</i> , 2012, 102, 506-518.	1.1	21
47	Comparing Avocado, Swamp Bay, and Camphortree as Hosts of <i>Raffaelea lauricola</i> Using a Green Fluorescent Protein (GFP)-Labeled Strain of the Pathogen. <i>Phytopathology</i> , 2017, 107, 70-74.	1.1	20
48	Tomato spotted wilt virus on potato in eastern North Carolina. <i>American Journal of Potato Research</i> , 2005, 82, 255-261.	0.5	18
49	Thermal sensitivity of <i>Calonectria henricotiae</i> and <i>Calonectria pseudonaviculata</i> conidia and microsclerotia. <i>Mycologia</i> , 2018, 110, 546-558.	0.8	17
50	A gene with domains related to transcription regulation is required for pathogenicity in <i>Colletotrichum acutatum</i> causing Key lime anthracnose. <i>Molecular Plant Pathology</i> , 2005, 6, 513-525.	2.0	16
51	The Formaldehyde Dehydrogenase <i>SsFdh1</i> Is Regulated by and Functionally Cooperates with the GATA Transcription Factor <i>SsNsd1</i> in <i>Sclerotinia sclerotiorum</i> . <i>MSystems</i> , 2019, 4, .	1.7	16
52	Population Genomics Trace Clonal Diversification and Intercontinental Migration of an Emerging Fungal Pathogen of Boxwood. <i>Phytopathology</i> , 2021, 111, 184-193.	1.1	16
53	Molecular Dissection of Perithecial Mating Line Development in <i>Colletotrichum fructicola</i> , a Species with a Nontypical Mating System Featuring Plus-to-Minus Switch and Plus-Minus-Mediated Sexual Enhancement. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0047421.	1.4	13
54	Highly Contiguous Genome Resource of <i>Colletotrichum fructicola</i> Generated Using Long-Read Sequencing. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 790-793.	1.4	12

#	ARTICLE	IF	CITATIONS
55	Transcriptional profile of oil palm pathogen, <i>Ganoderma boninense</i> , reveals activation of lignin degradation machinery and possible evasion of host immune response. <i>BMC Genomics</i> , 2021, 22, 326.	1.2	12
56	Competing sexual-aseexual generic names in Agaricomycotina (Basidiomycota) with recommendations for use. <i>IMA Fungus</i> , 2021, 12, 22.	1.7	11
57	Population Structure of the Blueberry Pathogen <i>Monilinia vaccinii-corymbosi</i> in the United States. <i>Phytopathology</i> , 2015, 105, 533-541.	1.1	10
58	One Clonal Lineage of <i>Calonectria pseudonaviculata</i> Is Primarily Responsible for the Boxwood Blight Epidemic in the United States. <i>Phytopathology</i> , 2020, 110, 1845-1853.	1.1	10
59	Development of an <i>Agrobacterium tumefaciens</i> -mediated gene disruption method for <i>Sclerotinia sclerotiorum</i> . <i>Canadian Journal of Plant Pathology</i> , 2007, 29, 394-400.	0.8	9
60	Seasonal Prevalence of Species of Binucleate Rhizoctonia Fungi in Growing Medium, Leaf Litter, and Stems of Container-Grown Azalea. <i>Plant Disease</i> , 2011, 95, 705-711.	0.7	9
61	<i>Coccinectria pachysandricola</i> , Causal Agent of a New Foliar Blight Disease of <i>Sarcococca hookeriana</i> . <i>Plant Disease</i> , 2019, 103, 1337-1346.	0.7	8
62	The cAMP-dependent protein kinase A pathway perturbs autophagy and plays important roles in development and virulence of <i>Sclerotinia sclerotiorum</i> . <i>Fungal Biology</i> , 2021, 126, 20-34.	1.1	8
63	Transmission of the M2 double-stranded RNA in <i>Rhizoctonia solani</i> anastomosis group 3 (AG-3). <i>Mycologia</i> , 2007, 99, 859-867.	0.8	7
64	Revisiting Graduate Student Training to Address Agricultural and Environmental Societal Challenges. <i>Agricultural and Environmental Letters</i> , 2017, 2, 170019.	0.8	7
65	Identification and characterization of <i>Septoria steviae</i> as the causal agent of <i>Septoria</i> leaf spot disease of <i>stevia</i> in North Carolina. <i>Mycologia</i> , 2019, 111, 456-465.	0.8	7
66	Efficient genome editing using endogenous U6 snRNA promoter-driven CRISPR/Cas9 sgRNA in <i>Sclerotinia sclerotiorum</i> . <i>Fungal Genetics and Biology</i> , 2021, 154, 103598.	0.9	7
67	Influence of soil calcium, potassium, and pH on development of leaf tipburn of cabbage in eastern North Carolina. <i>Communications in Soil Science and Plant Analysis</i> , 2000, 31, 259-275.	0.6	6
68	Genomic and transcriptomic insights into <i>Raffaelea lauricola</i> pathogenesis. <i>BMC Genomics</i> , 2020, 21, 570.	1.2	6
69	Genome sequence of <i>Monilinia vaccinii-corymbosi</i> sheds light on mummy berry disease infection of blueberry and mating type. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	4
70	Characterization and Aggressiveness of Take-All Root Rot Pathogens Isolated from Symptomatic Bermudagrass Putting Greens. <i>Phytopathology</i> , 2022, 112, 811-819.	1.1	4
71	Polyphasic identification and MAT1-2 isolates of <i>Phyllosticta citricarpa</i> in Cuba. <i>European Journal of Plant Pathology</i> , 2022, 162, 995-1003.	0.8	4
72	“Jumping Jack” Genomic Microsatellites Underscore the Distinctiveness of Closely Related <i>Pseudoperonospora cubensis</i> and <i>Pseudoperonospora humuli</i> and Provide New Insights Into Their Evolutionary Past. <i>Frontiers in Microbiology</i> , 2021, 12, 686759.	1.5	3

#	ARTICLE	IF	CITATIONS
73	The C2H2 Transcription Factor SsZFH1 Regulates the Size, Number, and Development of Apothecia in <i>Sclerotinia sclerotiorum</i> . <i>Phytopathology</i> , 2022, 112, 1476-1485.	1.1	2
74	Genomics of <i>Sclerotinia sclerotiorum</i> . , 2014, , 1-17.		1