

Ioannis Stergiopoulos

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

4,711
citations

186265

28
h-index

197818

49
g-index

51
all docs

51
docs citations

51
times ranked

4703
citing authors

#	ARTICLE	IF	CITATIONS
1	Fungal Effector Proteins. Annual Review of Phytopathology, 2009, 47, 233-263.	7.8	801
2	Finished Genome of the Fungal Wheat Pathogen <i>Mycosphaerella graminicola</i> Reveals Dispersome Structure, Chromosome Plasticity, and Stealth Pathogenesis. PLoS Genetics, 2011, 7, e1002070.	3.5	532
3	Plant-Pathogen Effectors: Cellular Probes Interfering with Plant Defenses in Spatial and Temporal Manners. Annual Review of Phytopathology, 2016, 54, 419-441.	7.8	515
4	The novel <i>Cladosporium fulvum</i> lysin motif effector Ecp6 is a virulence factor with orthologues in other fungal species. Molecular Microbiology, 2008, 69, 119-136.	2.5	275
5	Fungal effector proteins: past, present and future. Molecular Plant Pathology, 2009, 10, 735-747.	4.2	264
6	The Genomes of the Fungal Plant Pathogens <i>Cladosporium fulvum</i> and <i>Dothistroma septosporum</i> Reveal Adaptation to Different Hosts and Lifestyles But Also Signatures of Common Ancestry. PLoS Genetics, 2012, 8, e1003088.	3.5	226
7	The Chitin-Binding <i>Cladosporium fulvum</i> Effector Protein Avr4 Is a Virulence Factor. Molecular Plant-Microbe Interactions, 2007, 20, 1092-1101.	2.6	223
8	Impact of fungal drug transporters on fungicide sensitivity, multidrug resistance and virulence. Pest Management Science, 2006, 62, 195-207.	3.4	171
9	Tomato Cf resistance proteins mediate recognition of cognate homologous effectors from fungi pathogenic on dicots and monocots. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7610-7615.	7.1	167
10	Phytotoxic secondary metabolites and peptides produced by plant pathogenic <i>Dothideomycete</i> fungi. FEMS Microbiology Reviews, 2013, 37, 67-93.	8.6	164
11	Horizontal gene and chromosome transfer in plant pathogenic fungi affecting host range. FEMS Microbiology Reviews, 2011, 35, 542-554.	8.6	143
12	Allelic Variation in the Effector Genes of the Tomato Pathogen <i>Cladosporium fulvum</i> Reveals Different Modes of Adaptive Evolution. Molecular Plant-Microbe Interactions, 2007, 20, 1271-1283.	2.6	123
13	In Silico Characterization and Molecular Evolutionary Analysis of a Novel Superfamily of Fungal Effector Proteins. Molecular Biology and Evolution, 2012, 29, 3371-3384.	8.9	90
14	Combating a Global Threat to a Clonal Crop: Banana Black Sigatoka Pathogen <i>Pseudocercospora fijiensis</i> (Synonym <i>Mycosphaerella fijiensis</i>) Genomes Reveal Clues for Disease Control. PLoS Genetics, 2016, 12, e1005876.	3.5	77
15	Title is missing!. European Journal of Plant Pathology, 2002, 108, 719-734.	1.7	76
16	ABC Transporters and Azole Susceptibility in Laboratory Strains of the Wheat Pathogen <i>Mycosphaerella graminicola</i> . Antimicrobial Agents and Chemotherapy, 2002, 46, 3900-3906.	3.2	72
17	The ABC Transporter MgAtr4 Is a Virulence Factor of <i>Mycosphaerella graminicola</i> that Affects Colonization of Substomatal Cavities in Wheat Leaves. Molecular Plant-Microbe Interactions, 2003, 16, 689-698.	2.6	72
18	Cryptic fungal infections: the hidden agenda of plant pathogens. Frontiers in Plant Science, 2014, 5, 506.	3.6	67

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19	Multiple mechanisms account for variation in base-line sensitivity to azole fungicides in field isolates of <i>Mycosphaerella graminicola</i> . <i>Pest Management Science</i> , 2003, 59, 1333-1343.	3.4	63
20	ABC transporters of the wheat pathogen <i>Mycosphaerella graminicola</i> function as protectants against biotic and xenobiotic toxic compounds. <i>Molecular Genetics and Genomics</i> , 2003, 269, 499-507.	2.1	61
21	Comparative Genomics of the Sigatoka Disease Complex on Banana Suggests a Link between Parallel Evolutionary Changes in <i>Pseudocercospora fijiensis</i> and <i>Pseudocercospora eumusae</i> and Increased Virulence on the Banana Host. <i>PLoS Genetics</i> , 2016, 12, e1005904.	3.5	51
22	Mating-type genes and the genetic structure of a world-wide collection of the tomato pathogen <i>Cladosporium fulvum</i> . <i>Fungal Genetics and Biology</i> , 2007, 44, 415-429.	2.1	39
23	FPLC and liquid-chromatography mass spectrometry identify candidate necrosis-inducing proteins from culture filtrates of the fungal wheat pathogen <i>Zymoseptoria tritici</i> . <i>Fungal Genetics and Biology</i> , 2015, 79, 54-62.	2.1	38
24	Structural Analysis of an Avr4 Effector Ortholog Offers Insight into Chitin Binding and Recognition by the Cf-4 Receptor. <i>Plant Cell</i> , 2016, 28, 1945-1965.	6.6	37
25	Structure of the <i>Cladosporium fulvum</i> Avr4 effector in complex with (GlcNAc) ₆ reveals the ligand-binding mechanism and uncouples its intrinsic function from recognition by the Cf-4 resistance protein. <i>PLoS Pathogens</i> , 2018, 14, e1007263.	4.7	37
26	Positive selection and intragenic recombination contribute to high allelic diversity in effector genes of <i>Mycosphaerella fijiensis</i> , causal agent of the black leaf streak disease of banana. <i>Molecular Plant Pathology</i> , 2014, 15, 447-460.	4.2	36
27	Novel Mutations Detected in Avirulence Genes Overcoming Tomato Cf Resistance Genes in Isolates of a Japanese Population of <i>Cladosporium fulvum</i> . <i>PLoS ONE</i> , 2015, 10, e0123271.	2.5	34
28	Molecular cloning and characterisation of three new ATP-binding cassette transporter genes from the wheat pathogen <i>Mycosphaerella graminicola</i> . <i>Gene</i> , 2002, 289, 141-149.	2.2	31
29	A conserved proline residue in Dothideomycete Avr4 effector proteins is required to trigger a Cf-dependent hypersensitive response. <i>Molecular Plant Pathology</i> , 2016, 17, 84-95.	4.2	24
30	A new mechanism for reduced sensitivity to demethylation inhibitor fungicides in the fungal banana black Sigatoka pathogen <i>Pseudocercospora fijiensis</i> . <i>Molecular Plant Pathology</i> , 2018, 19, 1491-1503.	4.2	21
31	<i>Agrobacterium tumefaciens</i> -Mediated Transformation of <i>Pseudocercospora fijiensis</i> to Determine the Role of PfHog1 in Osmotic Stress Regulation and Virulence Modulation. <i>Frontiers in Microbiology</i> , 2017, 8, 830.	3.5	17
32	Allele-Specific Detection Methods for Qol Fungicide-Resistant <i>Erysiphe necator</i> in Vineyards. <i>Plant Disease</i> , 2021, 105, 175-182.	1.4	17
33	Gene for Gene Models and Beyond: the <i>Cladosporium fulvum</i> Tomato Pathosystem. , 2009, , 135-156.		15
34	Inter- and intra-domain horizontal gene transfer, gain-loss asymmetry and positive selection mark the evolutionary history of the CBM14 family. <i>FEBS Journal</i> , 2015, 282, 2014-2028.	4.7	13
35	Silencing of the Mitogen-Activated Protein Kinases (MAPK) Fus3 and Slk2 in <i>Pseudocercospora fijiensis</i> Reduces Growth and Virulence on Host Plants. <i>Frontiers in Plant Science</i> , 2018, 9, 291.	3.6	13
36	Cloning of the Cytochrome b Gene From the Tomato Powdery Mildew Fungus <i>Leveillula taurica</i> Reveals High Levels of Allelic Variation and Heteroplasmy for the G143A Mutation. <i>Frontiers in Microbiology</i> , 2019, 10, 663.	3.5	13

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37	Targeted Delivery of Gene Silencing in Fungi Using Genetically Engineered Bacteria. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 125.	3.5	11
38	Activity of Azole Fungicides and ABC Transporter Modulators on <i>Mycosphaerella graminicola</i> . <i>Journal of Phytopathology</i> , 2002, 150, 313-320.	1.0	10
39	A diverse member of the fungal Avr4 effector family interacts with de-esterified pectin in plant cell walls to disrupt their integrity. <i>Science Advances</i> , 2021, 7, .	10.3	10
40	A chromosome-scale genome assembly of the tomato pathogen <i>Cladosporium fulvum</i> reveals a compartmentalized genome architecture and the presence of a dispensable chromosome. <i>Microbial Genomics</i> , 2022, 8, .	2.0	10
41	Characterization of the mitochondrial genomes of three powdery mildew pathogens reveals remarkable variation in size and nucleotide composition. <i>Microbial Genomics</i> , 2021, 7, .	2.0	9
42	A world-wide analysis of reduced sensitivity to DMI fungicides in the banana pathogen <i>Pseudocercospora fijiensis</i> . <i>Pest Management Science</i> , 2021, 77, 3273-3288.	3.4	8
43	The mitochondrial genome of the grape powdery mildew pathogen <i>Erysiphe necator</i> is intron rich and exhibits a distinct gene organization. <i>Scientific Reports</i> , 2021, 11, 13924.	3.3	7
44	Interruption of <i>Aspergillus niger</i> spore germination by the bacterially produced secondary metabolite collimomycin. <i>Environmental Microbiology Reports</i> , 2020, 12, 306-313.	2.4	6
45	Evolutionary analysis of the global landscape of protein domain types and domain architectures associated with family 14 carbohydrate-binding modules. <i>FEBS Letters</i> , 2015, 589, 1813-1818.	2.8	5
46	First Report of Powdery Mildew Caused by <i>Oidium lycopersici</i> in Field-grown Tomatoes in California. <i>Plant Disease</i> , 2016, 100, 1497-1497.	1.4	5
47	Identification of Putative SDHI Target Site Mutations in the SDHB, SDHC, and SDHD Subunits of the Grape Powdery Mildew Pathogen <i>Erysiphe necator</i> . <i>Plant Disease</i> , 2022, 106, 2310-2320.	1.4	5
48	First Draft Genome Resource for the Tomato Black Leaf Mold Pathogen <i>Pseudocercospora fuligena</i> . <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1441-1445.	2.6	3
49	Repeated Exposure of <i>Aspergillus niger</i> Spores to the Antifungal Bacterium <i>Collimonas fungivorans</i> Ter331 Selects for Delayed Spore Germination. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0023321.	3.1	2
50	Front Cover Image, Volume 77, Issue 7. <i>Pest Management Science</i> , 2021, 77, i.	3.4	0