

James K Hane

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6056966/publications.pdf>

Version: 2024-02-01

59
papers

5,617
citations

101496

36
h-index

128225

60
g-index

66
all docs

66
docs citations

66
times ranked

5425
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome Analysis of the Broad Host Range Necrotroph <i>Nalanthamala psidii</i> Highlights Genes Associated With Virulence. <i>Frontiers in Plant Science</i> , 2022, 13, 811152.	1.7	1
2	Chromosome-level genome assembly and manually-curated proteome of model necrotroph <i>Parastagonospora nodorum</i> Sn15 reveals a genome-wide trove of candidate effector homologs, and redundancy of virulence-related functions within an accessory chromosome. <i>BMC Genomics</i> , 2021, 22, 382.	1.2	12
3	Gene Validation and Remodelling Using Proteogenomics of <i>Phytophthora cinnamomi</i> , the Causal Agent of Dieback. <i>Frontiers in Microbiology</i> , 2021, 12, 665396.	1.5	3
4	Remote homology clustering identifies lowly conserved families of effector proteins in plant-pathogenic fungi. <i>Microbial Genomics</i> , 2021, 7, .	1.0	7
5	An automated and combinative method for the predictive ranking of candidate effector proteins of fungal plant pathogens. <i>Scientific Reports</i> , 2021, 11, 19731.	1.6	27
6	Crop-Zone Weed Mycobiomes of the South-Western Australian Grain Belt. <i>Frontiers in Microbiology</i> , 2020, 11, 581592.	1.5	4
7	Reference Genome Assembly for Australian <i>Ascochyta rabiei</i> Isolate ArME14. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2131-2140.	0.8	15
8	Prediction of pathogenicity genes involved in adaptation to a lupin host in the fungal pathogens <i>Botrytis cinerea</i> and <i>Sclerotinia sclerotiorum</i> via comparative genomics. <i>BMC Genomics</i> , 2019, 20, 385.	1.2	11
9	A whole genome scan of SNP data suggests a lack of abundant hard selective sweeps in the genome of the broad host range plant pathogenic fungus <i>Sclerotinia sclerotiorum</i> . <i>PLoS ONE</i> , 2019, 14, e0214201.	1.1	23
10	Adapting legume crops to climate change using genomic approaches. <i>Plant, Cell and Environment</i> , 2019, 42, 6-19.	2.8	74
11	“CATAstrophy,” a Genome-Informed Trophic Classification of Filamentous Plant Pathogens “How Many Different Types of Filamentous Plant Pathogens Are There?”. <i>Frontiers in Microbiology</i> , 2019, 10, 3088.	1.5	41
12	Bioinformatic prediction of plant “pathogenicity effector proteins of fungi. <i>Current Opinion in Microbiology</i> , 2018, 46, 43-49.	2.3	69
13	Accessories Make the Outfit: Accessory Chromosomes and Other Dispensable DNA Regions in Plant-Pathogenic Fungi. <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 779-788.	1.4	93
14	Comparative genomics of the wheat fungal pathogen <i>Pyrenophora tritici-repentis</i> reveals chromosomal variations and genome plasticity. <i>BMC Genomics</i> , 2018, 19, 279.	1.2	56
15	Genomic and Genetic Insights Into a Cosmopolitan Fungus, <i>Paecilomyces variotii</i> (Eurotiales). <i>Frontiers in Microbiology</i> , 2018, 9, 3058.	1.5	35
16	Pan- <i>Parastagonospora</i> Comparative Genome Analysis “Effector Prediction and Genome Evolution. <i>Genome Biology and Evolution</i> , 2018, 10, 2443-2457.	1.1	43
17	The western Mediterranean region provided the founder population of domesticated narrow-leafed lupin. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2543-2554.	1.8	28
18	Exploring the genetic and adaptive diversity of a pan-Mediterranean crop wild relative: narrow-leafed lupin. <i>Theoretical and Applied Genetics</i> , 2018, 131, 887-901.	1.8	50

#	ARTICLE	IF	CITATIONS
19	Comparative secretome analysis of <i>Rhizoctonia solani</i> isolates with different host ranges reveals unique secretomes and cell death inducing effectors. <i>Scientific Reports</i> , 2017, 7, 10410.	1.6	62
20	A comprehensive draft genome sequence for lupin (<i>Lupinus angustifolius</i>), an emerging health food: insights into plant-microbe interactions and legume evolution. <i>Plant Biotechnology Journal</i> , 2017, 15, 318-330.	4.1	153
21	Comprehensive Annotation of the <i>Parastagonospora nodorum</i> Reference Genome Using Next-Generation Genomics, Transcriptomics and Proteogenomics. <i>PLoS ONE</i> , 2016, 11, e0147221.	1.1	47
22	OcculterCut: A Comprehensive Survey of AT-Rich Regions in Fungal Genomes. <i>Genome Biology and Evolution</i> , 2016, 8, 2044-2064.	1.1	123
23	Utilizing Gene Tree Variation to Identify Candidate Effector Genes in <i>Zymoseptoria tritici</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 779-791.	0.8	24
24	Mass-spectrometry data for <i>Rhizoctonia solani</i> proteins produced during infection of wheat and vegetative growth. <i>Data in Brief</i> , 2016, 8, 267-271.	0.5	5
25	Comparative genomics and prediction of conditionally dispensable sequences in legume-infecting <i>Fusarium oxysporum</i> formae speciales facilitates identification of candidate effectors. <i>BMC Genomics</i> , 2016, 17, 191.	1.2	109
26	Proteomic Analysis of <i>Rhizoctonia solani</i> Identifies Infection-specific, Redox Associated Proteins and Insight into Adaptation to Different Plant Hosts. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1188-1203.	2.5	37
27	Reactive Oxygen Species Play a Role in the Infection of the Necrotrophic Fungi, <i>Rhizoctonia solani</i> in Wheat. <i>PLoS ONE</i> , 2016, 11, e0152548.	1.1	77
28	Evaluation of Secretion Prediction Highlights Differing Approaches Needed for Oomycete and Fungal Effectors. <i>Frontiers in Plant Science</i> , 2015, 6, 1168.	1.7	85
29	Repeat-Induced Point Mutation: A Fungal-Specific, Endogenous Mutagenesis Process. <i>Fungal Biology</i> , 2015, , 55-68.	0.3	49
30	Analysis of conglutin seed storage proteins across lupin species using transcriptomic, protein and comparative genomic approaches. <i>BMC Plant Biology</i> , 2015, 15, 106.	1.6	49
31	Overview of genomic and bioinformatic resources for <i>Zymoseptoria tritici</i> . <i>Fungal Genetics and Biology</i> , 2015, 79, 13-16.	0.9	17
32	Next-generation re-sequencing as a tool for rapid bioinformatic screening of presence and absence of genes and accessory chromosomes across isolates of <i>Zymoseptoria tritici</i> . <i>Fungal Genetics and Biology</i> , 2015, 79, 71-75.	0.9	7
33	CodingQuarry: highly accurate hidden Markov model gene prediction in fungal genomes using RNA-seq transcripts. <i>BMC Genomics</i> , 2015, 16, 170.	1.2	158
34	Transcriptome sequencing of different narrow-leaved lupin tissue types provides a comprehensive uni-gene assembly and extensive gene-based molecular markers. <i>Plant Biotechnology Journal</i> , 2015, 13, 14-25.	4.1	70
35	The Arabidopsis KH-Domain RNA-Binding Protein ESR1 Functions in Components of Jasmonate Signalling, Unlinking Growth Restraint and Resistance to Stress. <i>PLoS ONE</i> , 2015, 10, e0126978.	1.1	45
36	Genome Sequencing and Comparative Genomics of the Broad Host-Range Pathogen <i>Rhizoctonia solani</i> AG8. <i>PLoS Genetics</i> , 2014, 10, e1004281.	1.5	145

#	ARTICLE	IF	CITATIONS
37	The genome sequence of the biocontrol fungus <i>Metarhizium anisopliae</i> and comparative genomics of <i>Metarhizium</i> species. <i>BMC Genomics</i> , 2014, 15, 660.	1.2	59
38	Draft genome sequence of chickpea (<i>Cicer arietinum</i>) provides a resource for trait improvement. <i>Nature Biotechnology</i> , 2013, 31, 240-246.	9.4	1,049
39	Comparative Genomics of a Plant-Pathogenic Fungus, <i>Pyrenophora tritici-repentis</i> , Reveals Transduplication and the Impact of Repeat Elements on Pathogenicity and Population Divergence. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 41-63.	0.8	167
40	Resequencing and Comparative Genomics of <i>Stagonospora nodorum</i> : Sectional Gene Absence and Effector Discovery. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 959-969.	0.8	66
41	Draft Genome Sequence of <i>Bacillus thuringiensis</i> Strain DAR 81934, Which Exhibits Molluscicidal Activity. <i>Genome Announcements</i> , 2013, 1, e0017512.	0.8	12
42	A comparative hidden Markov model analysis pipeline identifies proteins characteristic of cereal-infecting fungi. <i>BMC Genomics</i> , 2013, 14, 807.	1.2	26
43	Transcriptome analysis of <i>Stagonospora nodorum</i> : gene models, effectors, metabolism and pantothenate dispensability. <i>Molecular Plant Pathology</i> , 2012, 13, 531-545.	2.0	40
44	9 Genomic and Comparative Analysis of the Class Dothideomycetes. , 2011, , 205-229.		5
45	A novel mode of chromosomal evolution peculiar to filamentous Ascomycete fungi. <i>Genome Biology</i> , 2011, 12, R45.	13.9	126
46	Development of genomic resources for the narrow-leaved lupin (<i>Lupinus angustifolius</i>): construction of a bacterial artificial chromosome (BAC) library and BAC-end sequencing. <i>BMC Genomics</i> , 2011, 12, 521.	1.2	53
47	Effector diversification within compartments of the <i>Leptosphaeria maculans</i> genome affected by Repeat-Induced Point mutations. <i>Nature Communications</i> , 2011, 2, 202.	5.8	481
48	Finished Genome of the Fungal Wheat Pathogen <i>Mycosphaerella graminicola</i> Reveals Dispensome Structure, Chromosome Plasticity, and Stealth Pathogenesis. <i>PLoS Genetics</i> , 2011, 7, e1002070.	1.5	532
49	In silico reversal of repeat-induced point mutation (RIP) identifies the origins of repeat families and uncovers obscured duplicated genes. <i>BMC Genomics</i> , 2010, 11, 655.	1.2	41
50	Evolution of Linked Avirulence Effectors in <i>Leptosphaeria maculans</i> Is Affected by Genomic Environment and Exposure to Resistance Genes in Host Plants. <i>PLoS Pathogens</i> , 2010, 6, e1001180.	2.1	158
51	Ubiquity of ToxA and absence of ToxB in Australian populations of <i>Pyrenophora tritici-repentis</i> . <i>Australasian Plant Pathology</i> , 2010, 39, 63.	0.5	59
52	A first genome assembly of the barley fungal pathogen <i>Pyrenophora teres</i> f. <i>teres</i> . <i>Genome Biology</i> , 2010, 11, R109.	3.8	90
53	Deep proteogenomics; high throughput gene validation by multidimensional liquid chromatography and mass spectrometry of proteins from the fungal wheat pathogen <i>Stagonospora nodorum</i> . <i>BMC Bioinformatics</i> , 2009, 10, 301.	1.2	33
54	RIPCAL: a tool for alignment-based analysis of repeat-induced point mutations in fungal genomic sequences. <i>BMC Bioinformatics</i> , 2008, 9, 478.	1.2	151

#	ARTICLE	IF	CITATIONS
55	Construction of a comparative genetic map in faba bean (<i>Vicia faba</i> L.); conservation of genome structure with <i>Lens culinaris</i> . <i>BMC Genomics</i> , 2008, 9, 380.	1.2	103
56	A quantitative PCR approach to determine gene copy number. <i>Fungal Genetics Reports</i> , 2008, 55, 5-8.	0.6	53
57	Dothideomyceteâ€“Plant Interactions Illuminated by Genome Sequencing and EST Analysis of the Wheat Pathogen <i>Stagonospora nodorum</i> . <i>Plant Cell</i> , 2007, 19, 3347-3368.	3.1	235
58	Extensive macrosynteny between <i>Medicago truncatula</i> and <i>Lens culinaris</i> ssp. <i>culinaris</i> . <i>Theoretical and Applied Genetics</i> , 2007, 114, 549-558.	1.8	97
59	The first gene-based map of <i>Lupinus angustifolius</i> L.-location of domestication genes and conserved synteny with <i>Medicago truncatula</i> . <i>Theoretical and Applied Genetics</i> , 2006, 113, 225-238.	1.8	116