

Et Steenkamp

List of Publications by Year in descending order

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110
papers

5,059
citations

70961

41
h-index

106150

65
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119
all docs

119
docs citations

119
times ranked

4850
citing authors

#	ARTICLE	IF	CITATIONS
1	The Protistan Origins of Animals and Fungi. <i>Molecular Biology and Evolution</i> , 2006, 23, 93-106.	3.5	283
2	Whole Genome Analyses Suggests that <i>Burkholderia sensu lato</i> Contains Two Additional Novel Genera (<i>Mycetohabitans</i> gen. nov., and <i>Trinickia</i> gen. nov.): Implications for the Evolution of Diazotrophy and Nodulation in the <i>Burkholderiaceae</i> . <i>Genes</i> , 2018, 9, 389.	1.0	252
3	Pitch canker caused by <i>Fusarium circinatum</i> “ a growing threat to pine plantations and forests worldwide. <i>Australasian Plant Pathology</i> , 2008, 37, 319.	0.5	219
4	One Fungus, One Name: Defining the Genus <i>Fusarium</i> in a Scientifically Robust Way That Preserves Longstanding Use. <i>Phytopathology</i> , 2013, 103, 400-408.	1.1	219
5	Microsatellite discovery by deep sequencing of enriched genomic libraries. <i>BioTechniques</i> , 2009, 46, 217-223.	0.8	180
6	PCR-Based Identification of MAT-1 and MAT-2 in the <i>Gibberella fujikuroi</i> Species Complex. <i>Applied and Environmental Microbiology</i> , 2000, 66, 4378-4382.	1.4	149
7	Evolutionary Relationships among the <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> Vegetative Compatibility Groups. <i>Applied and Environmental Microbiology</i> , 2009, 75, 4770-4781.	1.4	130
8	Genome Data Provides High Support for Generic Boundaries in <i>Burkholderia sensu lato</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1154.	1.5	122
9	Phylogenomic analyses predict sistergroup relationship of nucleariids and Fungi and parphyly of zygomycetes with significant support. <i>BMC Evolutionary Biology</i> , 2009, 9, 272.	3.2	119
10	Cowpea and peanut in southern Africa are nodulated by diverse <i>Bradyrhizobium</i> strains harboring nodulation genes that belong to the large pantropical clade common in Africa. <i>Molecular Phylogenetics and Evolution</i> , 2008, 48, 1131-1144.	1.2	111
11	Current status of the taxonomic position of <i>Fusarium oxysporum</i> formae specialis <i>cubense</i> within the <i>Fusarium oxysporum</i> complex. <i>Infection, Genetics and Evolution</i> , 2011, 11, 533-542.	1.0	111
12	Phylogenomic Analysis of a 55.1-kb 19-Gene Dataset Resolves a Monophyletic <i>Fusarium</i> that Includes the <i>Fusarium solani</i> Species Complex. <i>Phytopathology</i> , 2021, 111, 1064-1079.	1.1	107
13	Mango Malformation Disease and the Associated <i>Fusarium</i> Species. <i>Phytopathology</i> , 2006, 96, 667-672.	1.1	79
14	Homothallism: an umbrella term for describing diverse sexual behaviours. <i>IMA Fungus</i> , 2015, 6, 207-214.	1.7	75
15	A plant pathology perspective of fungal genome sequencing. <i>IMA Fungus</i> , 2017, 8, 1-15.	1.7	75
16	Novel taxa in the <i>Fusarium fujikuroi</i> species complex from <i>Pinus</i> spp.. <i>Studies in Mycology</i> , 2015, 80, 131-150.	4.5	74
17	First outbreak of pitch canker in a South African pine plantation. <i>Australasian Plant Pathology</i> , 2007, 36, 256.	0.5	72
18	South African Papilionoid Legumes Are Nodulated by Diverse <i>Burkholderia</i> with Unique Nodulation and Nitrogen-Fixation Loci. <i>PLoS ONE</i> , 2013, 8, e68406.	1.1	70

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19	Burkholderia kirstenboschensis sp. nov. nodulates papilionoid legumes indigenous to South Africa. Systematic and Applied Microbiology, 2015, 38, 545-554.	1.2	68
20	Intron Derived Size Polymorphism in the Mitochondrial Genomes of Closely Related Chrysoporthe Species. PLoS ONE, 2016, 11, e0156104.	1.1	68
21	Draft genome sequences of Diplodia sapinea, Ceratocystis manginecans, and Ceratocystis moniliformis. IMA Fungus, 2014, 5, 135-140.	1.7	64
22	Concerted Evolution in the Ribosomal RNA Cistron. PLoS ONE, 2013, 8, e59355.	1.1	61
23	The pitch canker fungus, <i>Fusarium circinatum</i> : implications for South African forestry. Southern Forests, 2011, 73, 1-13.	0.2	58
24	Structure and evolution of the Fusarium mating type locus: New insights from the Gibberella fujikuroi complex. Fungal Genetics and Biology, 2011, 48, 731-740.	0.9	58
25	Draft genome sequences of Ceratocystis eucalypticola, Chrysoporthe cubensis, C. deuterocubensis, Davidsoniella virescens, Fusarium temperatum, Graphilbum fragrans, Penicillium nordicum, and Thielaviopsis musarum. IMA Fungus, 2015, 6, 493-506.	1.7	57
26	Development of simple sequence repeat (SSR) markers in Eucalyptus from amplified inter-simple sequence repeats (ISSR). Plant Breeding, 2000, 119, 433-436.	1.0	56
27	Causes and Consequences of Variability in Peptide Mating Pheromones of Ascomycete Fungi. Molecular Biology and Evolution, 2011, 28, 1987-2003.	3.5	54
28	Mixta gen. nov., a new genus in the Erwiniaceae. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1396-1407.	0.8	53
29	Evidence for inter-specific recombination among the mitochondrial genomes of Fusarium species in the Gibberella fujikuroi complex. BMC Genomics, 2013, 14, 605.	1.2	52
30	Three novel lineages of <i>Candidatus Liberibacter africanus</i> ™ associated with native rutaceous hosts of Trioza erytreae in South Africa. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 723-731.	0.8	52
31	Cryptic Speciation in Fusarium subglutinans. Mycologia, 2002, 94, 1032.	0.8	51
32	Fungal species and their boundaries matter – Definitions, mechanisms and practical implications. Fungal Biology Reviews, 2018, 32, 104-116.	1.9	51
33	Distinct Bradyrhizbium communities nodulate legumes native to temperate and tropical monsoon Australia. Molecular Phylogenetics and Evolution, 2012, 63, 265-277.	1.2	49
34	DNA Loss at the Ceratocystis fimbriata Mating Locus Results in Self-Sterility. PLoS ONE, 2014, 9, e92180.	1.1	48
35	Phylogenomic resolution of the bacterial genus Pantoea and its relationship with Erwinia and Tatumella. Antonie Van Leeuwenhoek, 2017, 110, 1287-1309.	0.7	48
36	Species-specific primers for Fusarium redolens and a PCR-RFLP technique to distinguish among three clades of Fusarium oxysporum. FEMS Microbiology Letters, 2007, 271, 27-32.	0.7	47

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37	Saprophytic and pathogenic fungi in the Ceratocystidaceae differ in their ability to metabolize plant-derived sucrose. <i>BMC Evolutionary Biology</i> , 2015, 15, 273.	3.2	47
38	Draft genome sequences of <i>Chrysosporthe austroafricana</i> , <i>Diplodia scrobiculata</i> , <i>Fusarium nygamai</i> , <i>Leptographium lundbergii</i> , <i>Limonomyces culmigenus</i> , <i>Stagonosporopsis tanacetii</i> , and <i>Thielaviopsis punctulata</i> . <i>IMA Fungus</i> , 2015, 6, 233-248.	1.7	46
39	Which MAT gene? Pezizomycotina (Ascomycota) mating-type gene nomenclature reconsidered. <i>Fungal Biology Reviews</i> , 2017, 31, 199-211.	1.9	45
40	Combined de novo and genome guided assembly and annotation of the <i>Pinus patula</i> juvenile shoot transcriptome. <i>BMC Genomics</i> , 2015, 16, 1057.	1.2	44
41	Molecular characterization of <i>Fusarium subglutinans</i> associated with mango malformation. <i>Molecular Plant Pathology</i> , 2000, 1, 187-193.	2.0	43
42	Simple sequence repeat markers for species in the <i>Fusarium oxysporum</i> complex. <i>Molecular Ecology Notes</i> , 2005, 5, 622-624.	1.7	43
43	A genetically homogenous population of <i>Fusarium circinatum</i> causes pitch canker of <i>Pinus radiata</i> in the Basque Country, Spain. <i>Fungal Biology</i> , 2011, 115, 288-295.	1.1	43
44	Chitosan application improves resistance to <i>Fusarium circinatum</i> in <i>Pinus patula</i> . <i>South African Journal of Botany</i> , 2013, 85, 70-78.	1.2	42
45	Draft nuclear genome sequence for the plant pathogen, <i>Ceratocystis fimbriata</i> . <i>IMA Fungus</i> , 2013, 4, 357-358.	1.7	42
46	Multigene phylogenetic and population differentiation data confirm the existence of a cryptic species within <i>Chrysosporthe cubensis</i> . <i>Fungal Biology</i> , 2010, 114, 966-979.	1.1	40
47	Diversity and dynamics of bacterial populations during spontaneous sorghum fermentations used to produce ting, a South African food. <i>Systematic and Applied Microbiology</i> , 2011, 34, 227-234.	1.2	39
48	IMA Genome-F 6. <i>IMA Fungus</i> , 2016, 7, 217-227.	1.7	39
49	Nodules from Fynbos legume <i>Virgilia divaricata</i> have high functional plasticity under variable P supply levels. <i>Journal of Plant Physiology</i> , 2014, 171, 1732-1739.	1.6	37
50	Draft genome of <i>Cercospora zeina</i> , <i>Fusarium pininemorale</i> , <i>Hawksworthiomyces lignivorus</i> , <i>Huntia decipiens</i> and <i>Ophiostoma ips</i> . <i>IMA Fungus</i> , 2017, 8, 385-396.	1.7	37
51	Draft genome sequence of <i>Annulohyphoxylon stygium</i> , <i>Aspergillus mulundensis</i> , <i>Berkeleyomyces basicola</i> (syn. <i>Thielaviopsis basicola</i>), <i>Ceratocystis smalleyi</i> , two <i>Cercospora beticola</i> strains, <i>Coleophoma cylindrospora</i> , <i>Fusarium fracticaudum</i> , <i>Phialophora cf. hyalina</i> , and <i>Morchella septimelata</i> . <i>IMA Fungus</i> , 2018, 9, 199-223.	1.7	37
52	Fungal Genomics Challenges the Dogma of Name-Based Biosecurity. <i>PLoS Pathogens</i> , 2016, 12, e1005475.	2.1	36
53	<i>Fusarium mangiferae</i> associated with mango malformation in the Sultanate of Oman. <i>European Journal of Plant Pathology</i> , 2008, 121, 195-199.	0.8	33
54	<i>Fusarium circinatum</i> and pitch canker of <i>Pinus</i> in Colombia. <i>Australasian Plant Pathology</i> , 2012, 41, 483-491.	0.5	33

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55	Crotalariaeae and Genisteae of the South African Great Escarpment are nodulated by novel Bradyrhizobium species with unique and diverse symbiotic loci. <i>Molecular Phylogenetics and Evolution</i> , 2016, 100, 206-218.	1.2	33
56	Draft genome sequences for <i>Ceratocystis fagacearum</i> , <i>C. harringtonii</i> , <i>Grosmannia penicillata</i> , and <i>Huntia bhutanensis</i> . <i>IMA Fungus</i> , 2016, 7, 317-323.	1.7	31
57	Genetic linkage map for <i>Amylostereum areolatum</i> reveals an association between vegetative growth and sexual and self-recognition. <i>Fungal Genetics and Biology</i> , 2009, 46, 632-641.	0.9	30
58	Variable P supply affects N metabolism in a legume tree, <i>Virgilia divaricata</i> , from nutrient-poor Mediterranean-type ecosystems. <i>Functional Plant Biology</i> , 2016, 43, 287.	1.1	29
59	Draft genome sequences of <i>Pantoea agglomerans</i> and <i>Pantoea vagans</i> isolates associated with termites. <i>Standards in Genomic Sciences</i> , 2016, 11, 23.	1.5	29
60	Mitochondrial introgression and interspecies recombination in the <i>Fusarium fujikuroi</i> species complex. <i>IMA Fungus</i> , 2018, 9, 37-48.	1.7	28
61	<i>Gibberella fujikuroi</i> mating population E is associated with maize and teosinte. <i>Molecular Plant Pathology</i> , 2001, 2, 215-221.	2.0	27
62	Legume nodules from nutrient-poor soils exhibit high plasticity of cellular phosphorus recycling and conservation during variable phosphorus supply. <i>Journal of Plant Physiology</i> , 2016, 191, 73-81.	1.6	27
63	Both mating types in the heterothallic fungus <i>Ophiostoma quercus</i> contain MAT1-1 and MAT1-2 genes. <i>Fungal Biology</i> , 2012, 116, 427-437.	1.1	26
64	Mate-recognition and species boundaries in the ascomycetes. <i>Fungal Diversity</i> , 2013, 58, 1-12.	4.7	25
65	The tolerance of <i>Pinus patula</i> — <i>Pinus tecunumanii</i> , and other pine hybrids, to <i>Fusarium circinatum</i> in greenhouse trials. <i>New Forests</i> , 2013, 44, 443-456.	0.7	24
66	Association of the pitch canker pathogen <i>Fusarium circinatum</i> with grass hosts in commercial pine production areas of South Africa. <i>Southern Forests</i> , 2014, 76, 161-166.	0.2	24
67	<i>Paraburkholderia strydomiana</i> sp. nov. and <i>Paraburkholderia steynii</i> sp. nov.: rhizobial symbionts of the fynbos legume <i>Hypocalyptus sophoroides</i> . <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 1369-1385.	0.7	24
68	Future outlook for <i>Pinus patula</i> in South Africa in the presence of the pitch canker fungus (<i>Fusarium</i>) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	0.2	23
69	Selection of <i>Pinus</i> spp. in South Africa for tolerance to infection by the pitch canker fungus. <i>New Forests</i> , 2012, 43, 473-489.	0.7	23
70	Evidence for a new introduction of the pitch canker fungus <i>Fusarium circinatum</i> in South Africa. <i>Plant Pathology</i> , 2014, 63, 530-538.	1.2	23
71	Diverse <i>Fusarium solani</i> isolates colonise agricultural environments in Ethiopia. <i>European Journal of Plant Pathology</i> , 2009, 124, 369-378.	0.8	22
72	Identification of the gene for β -fructofuranosidase from <i>Ceratocystis moniliformis</i> CMW 10134 and characterization of the enzyme expressed in <i>Saccharomyces cerevisiae</i> . <i>BMC Biotechnology</i> , 2013, 13, 100.	1.7	22

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73	Genome-Wide Macrosynteny among <i>Fusarium</i> Species in the <i>Gibberella fujikuroi</i> Complex Revealed by Amplified Fragment Length Polymorphisms. <i>PLoS ONE</i> , 2014, 9, e114682.	1.1	22
74	Host switching between native and non-native trees in a population of the canker pathogen <i>Chrysosporthe cubensis</i> from Colombia. <i>Plant Pathology</i> , 2013, 62, 642-648.	1.2	19
75	Diversity and evolution of polyketide biosynthesis gene clusters in the Ceratocystidaceae. <i>Fungal Biology</i> , 2018, 122, 856-866.	1.1	19
76	Panmixia defines the genetic diversity of a unique arthropod-dispersed fungus specific to <i>Protea</i> flowers. <i>Ecology and Evolution</i> , 2014, 4, 3444-3455.	0.8	17
77	Long-distance dispersal and recolonization of a fire-destroyed niche by a mite-associated fungus. <i>Fungal Biology</i> , 2015, 119, 245-256.	1.1	17
78	<i>Agrobacterium</i> -mediated transformation of <i>Ceratocystis albifundus</i> . <i>Microbiological Research</i> , 2019, 226, 55-64.	2.5	17
79	Characterization of <i>Fusarium graminearum</i> from <i>Acacia</i> and <i>Eucalyptus</i> Using β -Tubulin and Histone Gene Sequences. <i>Mycologia</i> , 2001, 93, 704.	0.8	15
80	Unexpected placement of the MAT1-1-2 gene in the MAT1-2 idiomorph of <i>Thielaviopsis</i> . <i>Fungal Genetics and Biology</i> , 2018, 113, 32-41.	0.9	15
81	Distribution and Evolution of Nonribosomal Peptide Synthetase Gene Clusters in the Ceratocystidaceae. <i>Genes</i> , 2019, 10, 328.	1.0	15
82	Plant-associated fungal biofilms—knowns and unknowns. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	15
83	Genetic basis for high population diversity in <i>Protea</i> -associated <i>Knoxdaviesia</i> . <i>Fungal Genetics and Biology</i> , 2016, 96, 47-57.	0.9	14
84	Genome-Based Selection and Characterization of <i>Fusarium circinatum</i> -Specific Sequences. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 631-639.	0.8	14
85	Nursery-linked plantation outbreaks and evidence for multiple introductions of the pitch canker pathogen <i>Fusarium circinatum</i> into South Africa. <i>Plant Pathology</i> , 2016, 65, 357-368.	1.2	14
86	Multiple independent origins for a subtelomeric locus associated with growth rate in <i>Fusarium circinatum</i> . <i>IMA Fungus</i> , 2018, 9, 27-36.	1.7	14
87	Genome-Based Characterization of Biological Processes That Differentiate Closely Related Bacteria. <i>Frontiers in Microbiology</i> , 2018, 9, 113.	1.5	14
88	Development of polymorphic microsatellite markers for the genetic characterisation of <i>Knoxdaviesia proteae</i> (Ascomycota: Microascales) using ISSR-PCR and pyrosequencing. <i>Mycological Progress</i> , 2014, 13, 439-444.	0.5	13
89	Culture-independent detection and quantification of <i>Fusarium circinatum</i> in a pine-producing seedling nursery. <i>Southern Forests</i> , 2014, 76, 137-143.	0.2	13
90	Practically delineating bacterial species with genealogical concordance. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 1311-1325.	0.7	12

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91	Does P deficiency affect nodule bacterial composition and N source utilization in a legume from nutrient-poor Mediterranean-type ecosystems?. <i>Soil Biology and Biochemistry</i> , 2017, 104, 164-174.	4.2	12
92	Deciphering the effect of FUB1 disruption on fusaric acid production and pathogenicity in <i>Fusarium circinatum</i> . <i>Fungal Biology</i> , 2021, 125, 1036-1047.	1.1	11
93	Unidirectional mating-type switching confers self-fertility to <i>Thielaviopsis cerberus</i> , the only homothallic species in the genus. <i>Fungal Biology</i> , 2021, 125, 427-434.	1.1	11
94	<i>Knoxdaviesia proteae</i> is not the only <i>Knoxdaviesia</i> -symbiont of <i>Protea repens</i> . <i>IMA Fungus</i> , 2015, 6, 471-476.	1.7	10
95	Ras2 is important for growth and pathogenicity in <i>Fusarium circinatum</i> . <i>Fungal Genetics and Biology</i> , 2021, 150, 103541.	0.9	9
96	Culture-independent assessment of the diazotrophic <i>Bradyrhizobium</i> communities in the Pampa and Atlantic Forest Biomes localities in southern Brazil. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126228.	1.2	9
97	Tolerance of <i>Pinus patula</i> full-sib families to <i>Fusarium circinatum</i> in a greenhouse study. <i>Southern Forests</i> , 2012, 74, 247-252.	0.2	8
98	Re-use of seedling containers and <i>Fusarium circinatum</i> association with asymptomatic <i>Pinus patula</i> planting stock. <i>Southern Forests</i> , 2014, 76, 177-187.	0.2	8
99	Architecture and Distribution of Introns in Core Genes of Four <i>Fusarium</i> Species. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3809-3820.	0.8	7
100	Contrasting carbon metabolism in saprotrophic and pathogenic microascalean fungi from <i>Protea</i> trees. <i>Fungal Ecology</i> , 2017, 30, 88-100.	0.7	7
101	Gene expression associated with vegetative incompatibility in <i>Amylostereum areolatum</i> . <i>Fungal Genetics and Biology</i> , 2011, 48, 1034-1043.	0.9	6
102	Global forest research, science education and community service positively impacted by a unique Centre of Excellence in Tree Health Biotechnology. <i>Southern Forests</i> , 2013, 75, 71-80.	0.2	6
103	Comparison of the tolerance of <i>Pinus patula</i> seedlings and established trees to infection by <i>Fusarium circinatum</i> . <i>Southern Forests</i> , 2014, 76, 151-159.	0.2	6
104	Genome sequences of <i>Knoxdaviesia capensis</i> and <i>K. proteae</i> (Fungi: Ascomycota) from <i>Protea</i> trees in South Africa. <i>Standards in Genomic Sciences</i> , 2016, 11, 22.	1.5	6
105	Unique clones of the pitch canker fungus, <i>Fusarium circinatum</i> , associated with a new disease outbreak in South Africa. <i>European Journal of Plant Pathology</i> , 2017, 148, 97-107.	0.8	5
106	Extracellular Vesicles in Teasing Apart Complex Plant-Microbiota Links: Implications for Microbiome-Based Biotechnology. <i>MSystems</i> , 2021, 6, e0073421.	1.7	5
107	Grasses as a refuge for <i>Fusarium circinatum</i> L. – evidence from South Africa. <i>Southern Forests</i> , 2020, 82, 253-262.	0.2	4
108	Fungal genomes enhance our understanding of the pathogens affecting trees cultivated in Southern Hemisphere plantations. <i>Southern Forests</i> , 2020, 82, 215-232.	0.2	3

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109	Mutualism and asexual reproduction influence recognition genes in a fungal symbiont. <i>Fungal Biology</i> , 2013, 117, 439-450.	1.1	2
110	Diversity of <i>Fusarium</i> species associated with healthy and malformed <i>Syzygium cordatum</i> inflorescences in South Africa. <i>European Journal of Plant Pathology</i> , 2022, 162, 907.	0.8	1