

Dave K Berger

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7484376/publications.pdf>

Version: 2024-02-01

94
papers

2,619
citations

159585

30
h-index

233421

45
g-index

96
all docs

96
docs citations

96
times ranked

2906
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>Calonectria</i> in the age of genes and genomes: Towards understanding an important but relatively unknown group of pathogens. <i>Molecular Plant Pathology</i> , 2022, 23, 1060-1072.	4.2	9
2	Pathogens of the Araucariaceae: How Much Do We Know?. <i>Current Forestry Reports</i> , 2022, 8, 124-147.	7.4	3
3	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.	2.2	107
4	Susceptibility of native New Zealand Myrtaceae to the South African strain of <i>Austropuccinia psidii</i> : A biosecurity threat. <i>Plant Pathology</i> , 2021, 70, 667-675.	2.4	6
5	Eucalyptus scab and shoot malformation: A new and serious foliar disease of <i>Eucalyptus</i> caused by <i>Elsinoe necatrix</i> sp. nov.. <i>Plant Pathology</i> , 2021, 70, 1230-1242.	2.4	11
6	Novel <i>Fusarium</i> mutualists of two <i>Euwallacea</i> species infesting <i>Acacia crassicarpa</i> in Indonesia. <i>Mycologia</i> , 2021, 113, 536-558.	1.9	9
7	Population genetic structure and migration patterns of the maize pathogenic fungus, <i>Cercospora zeina</i> in East and Southern Africa. <i>Fungal Genetics and Biology</i> , 2021, 149, 103527.	2.1	7
8	Global Genetic Diversity and Mating Type Distribution of <i>Calonectria pauciramosa</i> : An Important Wide-Host-Range Plant Pathogen. <i>Plant Disease</i> , 2021, 105, 1648-1656.	1.4	6
9	Population Diversity and Genetic Structure Reveal Patterns of Host Association and Anthropogenic Impact for the Globally Important Fungal Tree Pathogen <i>Ceratocystis manginecans</i> . <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 759.	3.5	4
10	Quantifying the Severity of Common Rust in Maize Using Mask R-CNN. <i>Lecture Notes in Computer Science</i> , 2021, , 202-213.	1.3	5
11	Phylogenomic incongruence in <i>Ceratocystis</i> : a clue to speciation?. <i>BMC Genomics</i> , 2020, 21, 362.	2.8	11
12	Time-Course RNAseq Reveals <i>Exserohilum turcicum</i> Effectors and Pathogenicity Determinants. <i>Frontiers in Microbiology</i> , 2020, 11, 360.	3.5	23
13	Genome comparisons suggest an association between <i>Ceratocystis</i> host adaptations and effector clusters in unique transposable element families. <i>Fungal Genetics and Biology</i> , 2020, 143, 103433.	2.1	9
14	Next generation sequencing reveals past and current widespread occurrence of maize yellow mosaic virus in South Africa. <i>European Journal of Plant Pathology</i> , 2020, 158, 237-249.	1.7	4
15	<i>Euwallacea perbrevis</i> (Coleoptera: Curculionidae: Scolytinae), a confirmed pest on <i>Acacia crassicarpa</i> in Riau, Indonesia, and a new fungal symbiont; <i>Fusarium rekanum</i> sp. nov.. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 803-823.	1.7	21
16	De novo Assembly of Transcriptomes From a B73 Maize Line Introgressed With a QTL for Resistance to Gray Leaf Spot Disease Reveals a Candidate Allele of a Lectin Receptor-Like Kinase. <i>Frontiers in Plant Science</i> , 2020, 11, 191.	3.6	9
17	Benefits of maize resistance breeding and chemical control against northern leaf blight in smallholder farms in South Africa. <i>South African Journal of Science</i> , 2020, 116, .	0.7	3
18	First report of maize yellow mosaic virus (MaYMV) on maize (<i>Zea mays</i>) in Tanzania. <i>Journal of Plant Pathology</i> , 2019, 101, 203-203.	1.2	13

#	ARTICLE	IF	CITATIONS
19	<i>Lecanosticta acicola</i> : A growing threat to expanding global pine forests and plantations. <i>Molecular Plant Pathology</i> , 2019, 20, 1327-1364.	4.2	28
20	QTL mapping of mycelial growth and aggressiveness to distinct hosts in <i>Ceratocystis</i> pathogens. <i>Fungal Genetics and Biology</i> , 2019, 131, 103242.	2.1	12
21	Influence of farming practices on the population genetics of the maize pathogen <i>Cercospora zeina</i> in South Africa. <i>Fungal Genetics and Biology</i> , 2019, 125, 36-44.	2.1	13
22	Biodiversity of <i>Lecanosticta</i> pine-needle blight pathogens suggests a Mesoamerican Centre of origin. <i>IMA Fungus</i> , 2019, 10, 2.	3.8	19
23	IMA Genome-F 11. <i>IMA Fungus</i> , 2019, 10, 13.	3.8	12
24	Ten new species of <i>Calonectria</i> from Indonesia and Vietnam. <i>Mycologia</i> , 2019, 111, 78-102.	1.9	38
25	Inheritance of phenotypic traits in the progeny of a <i>Ceratocystis</i> interspecific cross. <i>Fungal Biology</i> , 2018, 122, 717-729.	2.5	6
26	LOVe across kingdoms: Blue light perception vital for growth and development in plant-fungal interactions. <i>Fungal Biology Reviews</i> , 2018, 32, 86-103.	4.7	3
27	Application of Chloroplast Phylogenomics to Resolve Species Relationships Within the Plant Genus <i>Amaranthus</i> . <i>Journal of Molecular Evolution</i> , 2018, 86, 216-239.	1.8	25
28	New species of <i>Cylindrocladiella</i> from plantation soils in South-East Asia. <i>MycKeys</i> , 2018, 32, 1-24.	1.9	1
29	Nine novel species of <i>Huntia</i> from southern China with three distinct mating strategies and variable levels of pathogenicity. <i>Mycologia</i> , 2018, 110, 1145-1171.	1.9	7
30	The unified framework for biological invasions: a forest fungal pathogen perspective. <i>Biological Invasions</i> , 2017, 19, 3201-3214.	2.4	35
31	Evidence for salicylic acid signalling and histological changes in the defence response of <i>Eucalyptus grandis</i> to <i>Chrysosporium austroafricanum</i> . <i>Scientific Reports</i> , 2017, 7, 45402.	3.3	9
32	Complementation of <i>CTB7</i> in the Maize Pathogen <i>Cercospora zeina</i> Overcomes the Lack of In Vitro Cercosporin Production. <i>Molecular Plant-Microbe Interactions</i> , 2017, 30, 710-724.	2.6	25
33	Novel associations between ophiostomatoid fungi, insects and tree hosts: current status and future prospects. <i>Biological Invasions</i> , 2017, 19, 3215-3228.	2.4	49
34	A time series transcriptome analysis of cassava (<i>Manihot esculenta</i> Crantz) varieties challenged with Ugandan cassava brown streak virus. <i>Scientific Reports</i> , 2017, 7, 9747.	3.3	36
35	Systems genetics reveals a transcriptional network associated with susceptibility in the maize grey leaf spot pathosystem. <i>Plant Journal</i> , 2017, 89, 746-763.	5.7	49
36	Putative pathogenicity genes of <i>Phytophthora cinnamomi</i> identified via RNA-Seq analysis of pre-infection structures. <i>European Journal of Plant Pathology</i> , 2017, 147, 211-228.	1.7	18

#	ARTICLE	IF	CITATIONS
37	Ecology and population structure of a tree wound-infecting fungus in a native South African forest environment. <i>Fungal Biology</i> , 2017, 121, 69-81.	2.5	5
38	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.	3.8	37
39	RNA-Seq analysis of resistant and susceptible sub-tropical maize lines reveals a role for kauralexins in resistance to grey leaf spot disease, caused by <i>Cercospora zeina</i> . <i>BMC Plant Biology</i> , 2017, 17, 197.	3.6	43
40	<i>Calonectria</i> species isolated from Eucalyptus plantations and nurseries in South China. <i>IMA Fungus</i> , 2017, 8, 259-286.	3.8	37
41	Localization and Transcriptional Responses of <i>Chrysosporthe austroafricana</i> in <i>Eucalyptus grandis</i> Identify Putative Pathogenicity Factors. <i>Frontiers in Microbiology</i> , 2016, 7, 1953.	3.5	4
42	Dual RNA-Sequencing of <i>Eucalyptus nitens</i> during <i>Phytophthora cinnamomi</i> Challenge Reveals Pathogen and Host Factors Influencing Compatibility. <i>Frontiers in Plant Science</i> , 2016, 7, 191.	3.6	54
43	<i>Cercospora zeina</i> from Maize in South Africa Exhibits High Genetic Diversity and Lack of Regional Population Differentiation. <i>Phytopathology</i> , 2016, 106, 1194-1205.	2.2	11
44	Opportunities for unlocking the potential of genomics for African trees. <i>New Phytologist</i> , 2016, 210, 772-778.	7.3	11
45	Genetic Analyses Suggest Separate Introductions of the Pine Pathogen <i>Lecanosticta acicola</i> Into Europe. <i>Phytopathology</i> , 2016, 106, 1413-1425.	2.2	30
46	Functional characterization of a defense-related class-III chitinase promoter from <i>Lupinus albus</i> , active in legume and monocot tissues. <i>European Journal of Plant Pathology</i> , 2016, 146, 923-936.	1.7	0
47	The genetic landscape of <i>Ceratocystis albifundus</i> populations in South Africa reveals a recent fungal introduction event. <i>Fungal Biology</i> , 2016, 120, 690-700.	2.5	37
48	A possible centre of diversity in South East Asia for the tree pathogen, <i>Ceratocystis manginecans</i> . <i>Infection, Genetics and Evolution</i> , 2016, 41, 73-83.	2.3	25
49	Signals that stop the rot: Regulation of secondary metabolite defences in cereals. <i>Physiological and Molecular Plant Pathology</i> , 2016, 94, 156-166.	2.5	15
50	Draft genome sequences of <i>Ceratocystis eucalypticola</i> , <i>Chrysosporthe cubensis</i> , <i>C. deuterocubensis</i> , <i>Davidsoniella virescens</i> , <i>Fusarium temperatum</i> , <i>Graphilbum fragrans</i> , <i>Penicillium nordicum</i> , and <i>Thielaviopsis musarum</i> . <i>IMA Fungus</i> , 2015, 6, 493-506.	3.8	57
51	Molecular markers delimit cryptic species in <i>Ceratocystis sensu stricto</i> . <i>Mycological Progress</i> , 2015, 14, 1.	1.4	47
52	Genome-wide mapping of histone H3 lysine 4 trimethylation in <i>Eucalyptus grandis</i> developing xylem. <i>BMC Plant Biology</i> , 2015, 15, 117.	3.6	26
53	Investigating the molecular underpinnings underlying morphology and changes in carbon partitioning during tension wood formation in <i>Eucalyptus</i> . <i>New Phytologist</i> , 2015, 206, 1351-1363.	7.3	27
54	Population structure and diversity of an invasive pine needle pathogen reflects anthropogenic activity. <i>Ecology and Evolution</i> , 2014, 4, 3642-3661.	1.9	61

#	ARTICLE	IF	CITATIONS
55	Mapping QTL conferring resistance in maize to gray leaf spot disease caused by <i>Cercospora zeina</i> . <i>BMC Genetics</i> , 2014, 15, 60.	2.7	41
56	Gene-for-Gene Tolerance to Bacterial Wilt in Arabidopsis. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 398-406.	2.6	21
57	The identification and differential expression of <i>Eucalyptus grandis</i> pathogenesis-related genes in response to salicylic acid and methyl jasmonate. <i>Frontiers in Plant Science</i> , 2013, 4, 43.	3.6	31
58	Quantitative phenotyping of grey leaf spot disease in maize using real-time PCR. <i>European Journal of Plant Pathology</i> , 2012, 133, 461-471.	1.7	44
59	Bin mapping of tomato diversity array (DArT) markers to genomic regions of <i>Solanum lycopersicum</i> – <i>Solanum pennellii</i> introgression lines. <i>Theoretical and Applied Genetics</i> , 2012, 124, 947-956.	3.6	18
60	A <i>Eucalyptus</i> bacterial wilt isolate from South Africa is pathogenic on Arabidopsis and manipulates host defences. <i>Forest Pathology</i> , 2011, 41, 101-113.	1.1	3
61	SND2, a NAC transcription factor gene, regulates genes involved in secondary cell wall development in Arabidopsis fibres and increases fibre cell area in <i>Eucalyptus</i> . <i>BMC Plant Biology</i> , 2011, 11, 173.	3.6	164
62	Identification of genes expressed during the compatible interaction of grapevine with <i>Plasmopara viticola</i> through suppression subtractive hybridization (SSH). <i>European Journal of Plant Pathology</i> , 2011, 129, 281-301.	1.7	28
63	High population diversity and increasing importance of the <i>Eucalyptus</i> stem canker pathogen, <i>Teratosphaeria zuluensis</i> , in South China. <i>Australasian Plant Pathology</i> , 2011, 40, 407-415.	1.0	22
64	Maize microarray annotation database. <i>Plant Methods</i> , 2011, 7, 31.	4.3	9
65	Diurnal and circadian patterns of gene expression in the developing xylem of <i>Eucalyptus</i> trees. <i>South African Journal of Botany</i> , 2010, 76, 425-439.	2.5	32
66	SSHscreen and SSHdb, generic software for microarray based gene discovery: application to the stress response in cowpea. <i>Plant Methods</i> , 2010, 6, 10.	4.3	15
67	Identification of genes expressed during the compatible interaction of grapevine with <i>Plasmopara viticola</i> through suppression subtractive hybridization (SSH). , 2010, , 149-169.		0
68	<i>Cercospora zeina</i> is the causal agent of grey leaf spot disease of maize in southern Africa. <i>European Journal of Plant Pathology</i> , 2009, 124, 577-583.	1.7	41
69	Salicylic acid confers resistance to a biotrophic rust pathogen, <i>Puccinia substriata</i> , in pearl millet (<i>Pennisetum glaucum</i>). <i>Molecular Plant Pathology</i> , 2009, 10, 291-304.	4.2	37
70	Exo-β-1,3-α-D-Glucanase from Yeast Inhibits <i>Colletotrichum lupini</i> and <i>Botrytis cinerea</i> Spore Germination. <i>Journal of Phytopathology</i> , 2009, 157, 1-6.	1.0	5
71	Comparative analysis of orthologous cellulose synthase promoters from <i>Arabidopsis</i> , <i>Populus</i> and <i>Eucalyptus</i> : evidence of conserved regulatory elements in angiosperms. <i>New Phytologist</i> , 2008, 179, 722-737.	7.3	49
72	MADIBA: A web server toolkit for biological interpretation of Plasmodium and plant gene clusters. <i>BMC Genomics</i> , 2008, 9, 105.	2.8	21

#	ARTICLE	IF	CITATIONS
73	Tolerance in banana to <i>Fusarium</i> wilt is associated with early up-regulation of cell wall-strengthening genes in the roots. <i>Molecular Plant Pathology</i> , 2007, 8, 333-341.	4.2	99
74	Microarray analysis of the <i>Arabidopsis thaliana</i> cir1 (constitutively induced resistance 1) mutant reveals candidate defence response genes against <i>Pseudomonas syringae</i> pv tomato DC3000. <i>South African Journal of Botany</i> , 2007, 73, 412-421.	2.5	4
75	Screening of cDNA Libraries on Glass Slide Microarrays. <i>Methods in Molecular Biology</i> , 2007, 382, 177-203.	0.9	5
76	Apple polygalacturonase inhibiting protein1 expressed in transgenic tobacco inhibits polygalacturonases from fungal pathogens of apple and the anthracnose pathogen of lupins. <i>Phytochemistry</i> , 2006, 67, 255-263.	2.9	31
77	Molecular identification of some African strains of <i>Ralstonia solanacearum</i> from eucalypt and potato. <i>Journal of General Plant Pathology</i> , 2006, 72, 369-373.	1.0	10
78	Anthracnose of lupins in South Africa is caused by <i>Colletotrichum lupinivar.setosum</i> . <i>Australasian Plant Pathology</i> , 2005, 34, 385.	1.0	17
79	High-throughput screening of suppression subtractive hybridization cDNA libraries using DNA microarray analysis. <i>BioTechniques</i> , 2004, 37, 818-824.	1.8	37
80	Development and assessment of microarray-based DNA fingerprinting in <i>Eucalyptus grandis</i> . <i>Theoretical and Applied Genetics</i> , 2004, 109, 1329-1336.	3.6	45
81	High-level expression of apple PGIP1 is not sufficient to protect transgenic potato against <i>Verticillium dahliae</i> . <i>Physiological and Molecular Plant Pathology</i> , 2004, 65, 145-155.	2.5	20
82	Gene-mining the <i>Arabidopsis thaliana</i> genome: applications for biotechnology in Africa. <i>South African Journal of Botany</i> , 2004, 70, 173-180.	2.5	4
83	Characterization of <i>Seiridium</i> spp. Associated with Cypress Canker Based on α -Tubulin and Histone Sequences. <i>Plant Disease</i> , 2001, 85, 317-321.	1.4	56
84	Transformation of elite white maize using the particle inflow gun and detailed analysis of a low-copy integration event. <i>Plant Cell Reports</i> , 2001, 20, 721-730.	5.6	37
85	Microsatellite markers reflect intra-specific relationships between isolates of the vascular wilt pathogen <i>Ceratocystis fimbriata</i> . <i>Molecular Plant Pathology</i> , 2001, 2, 319-325.	4.2	58
86	Detection of <i>Xylophilus ampelinus</i> in grapevine cuttings using a nested polymerase chain reaction. <i>Plant Pathology</i> , 2001, 50, 515-526.	2.4	20
87	Biolistic transformation of chinchinchee (<i>Ornithogalum</i>) and regeneration of transgenic plants. <i>Physiologia Plantarum</i> , 2000, 109, 450-455.	5.2	13
88	Bean polygalacturonase inhibitor protein-1 (PGIP-1) inhibits polygalacturonases from <i>Stenocarpella maydis</i> . <i>Physiological and Molecular Plant Pathology</i> , 2000, 57, 5-14.	2.5	36
89	In vitro studies of the domains of the nitrogen fixation regulatory protein NIFA. <i>Journal of Bacteriology</i> , 1995, 177, 191-199.	2.2	35
90	The isolated catalytic domain of NIFA, a bacterial enhancer-binding protein, activates transcription in vitro: activation is inhibited by NIFL.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 103-107.	7.1	94

#	ARTICLE	IF	CITATIONS
91	Isolation of the <i>Thiobacillus ferrooxidans</i> ntrBC genes using a <i>T. ferrooxidans</i> nifH-lacZ fusion. <i>Microbiology (United Kingdom)</i> , 1994, 140, 2543-2553.	1.8	9
92	Activity of purified NIFA, a transcriptional activator of nitrogen fixation genes.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993, 90, 2266-2270.	7.1	92
93	Role of integration host factor in stimulating transcription from the σ^{54} -dependent nifH promoter. <i>Journal of Molecular Biology</i> , 1992, 227, 602-620.	4.2	112
94	Complementation of <i>Escherichia coli</i> sigma 54 (NtrA)-dependent formate hydrogenlyase activity by a cloned <i>Thiobacillus ferrooxidans</i> ntrA gene. <i>Journal of Bacteriology</i> , 1990, 172, 4399-4406.	2.2	28