

Dave K Berger

List of Publications by Year in descending order

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94
papers

2,619
citations

159585

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233421

45
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96
all docs

96
docs citations

96
times ranked

2906
citing authors

#	ARTICLE	IF	CITATIONS
1	SND2, a NAC transcription factor gene, regulates genes involved in secondary cell wall development in Arabidopsis fibres and increases fibre cell area in Eucalyptus. BMC Plant Biology, 2011, 11, 173.	3.6	164
2	Role of integration host factor in stimulating transcription from the Īf54-dependent nifH promoter. Journal of Molecular Biology, 1992, 227, 602-620.	4.2	112
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. Phytopathology, 2021, 111, 1064-1079.	2.2	107
4	Tolerance in banana to Fusarium wilt is associated with early up-regulation of cell wall-strengthening genes in the roots. Molecular Plant Pathology, 2007, 8, 333-341.	4.2	99
5	The isolated catalytic domain of NIFA, a bacterial enhancer-binding protein, activates transcription in vitro: activation is inhibited by NIFL.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 103-107.	7.1	94
6	Activity of purified NIFA, a transcriptional activator of nitrogen fixation genes.. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 2266-2270.	7.1	92
7	Population structure and diversity of an invasive pine needle pathogen reflects anthropogenic activity. Ecology and Evolution, 2014, 4, 3642-3661.	1.9	61
8	Microsatellite markers reflect intra-specific relationships between isolates of the vascular wilt pathogen Ceratocystis fimbriata. Molecular Plant Pathology, 2001, 2, 319-325.	4.2	58
9	Draft genome sequences of Ceratocystis eucalypticola, Chrysosporthe cubensis, C. deuterocubensis, Davidsoniella virescens, Fusarium temperatum, Graphilbum fragrans, Penicillium nordicum, and Thielaviopsis musarum. IMA Fungus, 2015, 6, 493-506.	3.8	57
10	Characterization of Seiridium spp. Associated with Cypress Canker Based on ÅŸ-Tubulin and Histone Sequences. Plant Disease, 2001, 85, 317-321.	1.4	56
11	Dual RNA-Sequencing of Eucalyptus nitens during Phytophthora cinnamomi Challenge Reveals Pathogen and Host Factors Influencing Compatibility. Frontiers in Plant Science, 2016, 7, 191.	3.6	54
12	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. New Phytologist, 2008, 179, 722-737.	7.3	49
13	Novel associations between ophiostomatoid fungi, insects and tree hosts: current status“future prospects. Biological Invasions, 2017, 19, 3215-3228.	2.4	49
14	Systems genetics reveals a transcriptional network associated with susceptibility in the maize“grey leaf spot pathosystem. Plant Journal, 2017, 89, 746-763.	5.7	49
15	Molecular markers delimit cryptic species in Ceratocystis sensu stricto. Mycological Progress, 2015, 14, 1.	1.4	47
16	Development and assessment of microarray-based DNA fingerprinting in Eucalyptus grandis. Theoretical and Applied Genetics, 2004, 109, 1329-1336.	3.6	45
17	Quantitative phenotyping of grey leaf spot disease in maize using real-time PCR. European Journal of Plant Pathology, 2012, 133, 461-471.	1.7	44
18	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 Cercospora zeina. BMC Plant Biology, 2017, 17, 197.	3.6	43

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19	<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
20	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
21	Ten new species of <i>Calonectria</i> from Indonesia and Vietnam. <i>Mycologia</i> , 2019, 111, 78-102.	1.9	38
22	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
23	High-throughput screening of suppression subtractive hybridization cDNA libraries using DNA microarray analysis. <i>BioTechniques</i> , 2004, 37, 818-824.	1.8	37
24	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
25	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
26	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
27	<i>Calonectria</i> species isolated from Eucalyptus plantations and nurseries in South China. <i>IMA Fungus</i> , 2017, 8, 259-286.	3.8	37
28	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
29	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
30	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
31	The unified framework for biological invasions: a forest fungal pathogen perspective. <i>Biological Invasions</i> , 2017, 19, 3201-3214.	2.4	35
32	Diurnal and circadian patterns of gene expression in the developing xylem of Eucalyptus trees. <i>South African Journal of Botany</i> , 2010, 76, 425-439.	2.5	32
33	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
34	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
35	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
36	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

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37	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
38	<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
39	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
40	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
41	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
42	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
43	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
44	Time-Course RNAseq Reveals <i>Exserohilum turcicum</i> Effectors and Pathogenicity Determinants. <i>Frontiers in Microbiology</i> , 2020, 11, 360.	3.5	23
45	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
46	MADIBA: A web server toolkit for biological interpretation of Plasmodium and plant gene clusters. <i>BMC Genomics</i> , 2008, 9, 105.	2.8	21
47	Gene-for-Gene Tolerance to Bacterial Wilt in <i>Arabidopsis</i> . <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 398-406.	2.6	21
48	<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
49	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
50	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
51	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
52	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
53	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
54	Anthracoze of lupins in South Africa is caused by <i>Colletotrichum lupinivar.setosum</i> . <i>Australasian Plant Pathology</i> , 2005, 34, 385.	1.0	17

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55	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
56	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
57	Biolistic transformation of chinchinchee (<i>Ornithogalum</i>) and regeneration of transgenic plants. <i>Physiologia Plantarum</i> , 2000, 109, 450-455.	5.2	13
58	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
59	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
60	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
61	IMA Genome-F 11. <i>IMA Fungus</i> , 2019, 10, 13.	3.8	12
62	<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
63	Opportunities for unlocking the potential of genomics for African trees. <i>New Phytologist</i> , 2016, 210, 772-778.	7.3	11
64	Phylogenomic incongruence in <i>Ceratocystis</i> : a clue to speciation?. <i>BMC Genomics</i> , 2020, 21, 362.	2.8	11
65	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
66	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
67	Maize microarray annotation database. <i>Plant Methods</i> , 2011, 7, 31.	4.3	9
68	Evidence for salicylic acid signalling and histological changes in the defence response of <i>Eucalyptus grandis</i> to <i>Chrysosporthe austroafricana</i> . <i>Scientific Reports</i> , 2017, 7, 45402.	3.3	9
69	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
70	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
71	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
72	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

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73	<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
74	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
75	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
76	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
77	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
78	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
79	Exo-β-1,3-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
80	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
81	Screening of cDNA Libraries on Glass Slide Microarrays. <i>Methods in Molecular Biology</i> , 2007, 382, 177-203.	0.9	5
82	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
83	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
84	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
85	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
86	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
87	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
88	A <i>Eucalyptus</i> bacterial wilt isolate from South Africa is pathogenic on <i>Arabidopsis</i> and manipulates host defences. <i>Forest Pathology</i> , 2011, 41, 101-113.	1.1	3
89	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
90	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

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91	Pathogens of the Araucariaceae: How Much Do We Know?. <i>Current Forestry Reports</i> , 2022, 8, 124-147.	7.4	3
92	New species of <i>Cylindrocladiella</i> from plantation soils in South-East Asia. <i>MycKeys</i> , 2018, 32, 1-24.	1.9	1
93	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
94	Identification of genes expressed during the compatible interaction of grapevine with <i>Plasmopara viticola</i> through suppression subtractive hybridization (SSH). , 2010, , 149-169.		0