

Bernard Dumas

List of Publications by Year in descending order

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70
papers

4,808
citations

94433

37
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98798

67
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73
all docs

73
docs citations

73
times ranked

4558
citing authors

#	ARTICLE	IF	CITATIONS
1	A Comprehensive Assessment of the Secretome Responsible for Host Adaptation of the Legume Root Pathogen <i>Aphanomyces euteiches</i> . <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 88.	3.5	4
2	An oomycete effector targets a plant RNA helicase involved in root development and defense. <i>New Phytologist</i> , 2022, 233, 2232-2248.	7.3	12
3	Modification of Early Response of <i>Vitis vinifera</i> to Pathogens Relating to Esca Disease and Biocontrol Agent Vintec® Revealed By Untargeted Metabolomics on Woody Tissues. <i>Frontiers in Microbiology</i> , 2022, 13, 835463.	3.5	6
4	Phyllosphere Colonization by a Soil <i>Streptomyces</i> sp. Promotes Plant Defense Responses Against Fungal Infection. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 223-234.	2.6	29
5	MS-CleanR: A Feature-Filtering Workflow for Untargeted LC-MS Based Metabolomics. <i>Analytical Chemistry</i> , 2020, 92, 9971-9981.	6.5	55
6	Long-Read Genome Sequence of the Sugar Beet Rhizosphere Mycoparasite <i>Pythium oligandrum</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 431-436.	1.8	18
7	DNA-Damaging Effectors: New Players in the Effector Arena. <i>Trends in Plant Science</i> , 2019, 24, 1094-1101.	8.8	13
8	A local score approach improves GWAS resolution and detects minor QTL: application to <i>Medicago truncatula</i> quantitative disease resistance to multiple <i>Aphanomyces euteiches</i> isolates. <i>Heredity</i> , 2019, 123, 517-531.	2.6	36
9	Deciphering the phylogeny of violets based on multiplexed genetic and metabolomic approaches. <i>Phytochemistry</i> , 2019, 163, 99-110.	2.9	14
10	Lipo-chitooligosaccharide signalling blocks a rapid pathogen-induced ROS burst without impeding immunity. <i>New Phytologist</i> , 2019, 221, 743-749.	7.3	24
11	Genomics analysis of <i>Aphanomyces</i> spp. identifies a new class of oomycete effector associated with host adaptation. <i>BMC Biology</i> , 2018, 16, 43.	3.8	62
12	Plenty Is No Plague: <i>Streptomyces</i> Symbiosis with Crops. <i>Trends in Plant Science</i> , 2017, 22, 30-37.	8.8	98
13	Detection of nucleic acid-protein interactions in plant leaves using fluorescence lifetime imaging microscopy. <i>Nature Protocols</i> , 2017, 12, 1933-1950.	12.0	42
14	MtNF-YA1, A Central Transcriptional Regulator of Symbiotic Nodule Development, Is Also a Determinant of <i>Medicago truncatula</i> Susceptibility toward a Root Pathogen. <i>Frontiers in Plant Science</i> , 2016, 7, 1837.	3.6	25
15	High-throughput gene-expression quantification of grapevine defense responses in the field using microfluidic dynamic arrays. <i>BMC Genomics</i> , 2016, 17, 957.	2.8	37
16	CRN13 candidate effectors from plant and animal eukaryotic pathogens are DNA-binding proteins which trigger host DNA damage response. <i>New Phytologist</i> , 2016, 210, 602-617.	7.3	54
17	Transcriptome analysis highlights preformed defences and signalling pathways controlled by the quantitative trait locus (QTL), conferring partial resistance to <i>Aphanomyces euteiches</i> in <i>Medicago truncatula</i> . <i>Molecular Plant Pathology</i> , 2015, 16, 973-986.	4.2	18
18	Genomic Signature of Selective Sweeps Illuminates Adaptation of <i>Medicago truncatula</i> to Root-Associated Microorganisms. <i>Molecular Biology and Evolution</i> , 2015, 32, 2097-2110.	8.9	51

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19	Probing the Functions of Carbohydrate Binding Modules in the CBEL Protein from the Oomycete <i>Phytophthora parasitica</i> . <i>PLoS ONE</i> , 2015, 10, e0137481.	2.5	9
20	High-density genome-wide association mapping implicates an <i>F-box</i> encoding gene in <i>Medicago truncatula</i> resistance to <i>Aphanomyces euteiches</i> . <i>New Phytologist</i> , 2014, 201, 1328-1342.	7.3	86
21	Foliar treatments with <i>Gaultheria procumbens</i> essential oil induce defense responses and resistance against a fungal pathogen in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2014, 5, 477.	3.6	29
22	An experimental system to study responses of <i>Medicago truncatula</i> roots to chitin oligomers of high degree of polymerization and other microbial elicitors. <i>Plant Cell Reports</i> , 2013, 32, 489-502.	5.6	26
23	<i>NFP</i> , a <i>LysM</i> protein controlling <i>Nod</i> factor perception, also intervenes in <i>Medicago truncatula</i> resistance to pathogens. <i>New Phytologist</i> , 2013, 198, 875-886.	7.3	144
24	Distinctive Expansion of Potential Virulence Genes in the Genome of the Oomycete Fish Pathogen <i>Saprolegnia parasitica</i> . <i>PLoS Genetics</i> , 2013, 9, e1003272.	3.5	221
25	Pathogen-associated molecular pattern-triggered immunity and resistance to the root pathogen <i>Phytophthora parasitica</i> in <i>Arabidopsis</i> . <i>Journal of Experimental Botany</i> , 2013, 64, 3615-3625.	4.8	47
26	<i>Aphanomyces euteiches</i> Cell Wall Fractions Containing Novel Glucan-Chitosaccharides Induce Defense Genes and Nuclear Calcium Oscillations in the Plant Host <i>Medicago truncatula</i> . <i>PLoS ONE</i> , 2013, 8, e75039.	2.5	41
27	The unique architecture and function of cellulose-interacting proteins in oomycetes revealed by genomic and structural analyses. <i>BMC Genomics</i> , 2012, 13, 605.	2.8	40
28	Expression and purification of a biologically active <i>Phytophthora parasitica</i> cellulose binding elicitor lectin in <i>Pichia pastoris</i> . <i>Protein Expression and Purification</i> , 2011, 80, 217-223.	1.3	10
29	An <i>Ulva armoricana</i> extract protects plants against three powdery mildew pathogens. <i>European Journal of Plant Pathology</i> , 2011, 131, 393-401.	1.7	90
30	Hydrogen peroxide scavenging mechanisms are components of <i>Medicago truncatula</i> partial resistance to <i>Aphanomyces euteiches</i> . <i>European Journal of Plant Pathology</i> , 2011, 131, 559-571.	1.7	49
31	Host and Nonhost Resistance in <i>Medicago-Colletotrichum</i> Interactions. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 1107-1117.	2.6	15
32	Signatures of Adaptation to Obligate Biotrophy in the <i>Hyaloperonospora arabidopsidis</i> Genome. <i>Science</i> , 2010, 330, 1549-1551.	12.6	492
33	<i>Ste12</i> and <i>Ste12</i> -Like Proteins, Fungal Transcription Factors Regulating Development and Pathogenicity. <i>Eukaryotic Cell</i> , 2010, 9, 480-485.	3.4	131
34	Ulvan, a Sulfated Polysaccharide from Green Algae, Activates Plant Immunity through the Jasmonic Acid Signaling Pathway. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-11.	3.0	113
35	Sterol biosynthesis in oomycete pathogens. <i>Plant Signaling and Behavior</i> , 2010, 5, 258-260.	2.4	53
36	Genome sequence of the necrotrophic plant pathogen <i>Pythium ultimum</i> reveals original pathogenicity mechanisms and effector repertoire. <i>Genome Biology</i> , 2010, 11, R73.	9.6	391

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37	An <i>STE12</i> gene identified in the mycorrhizal fungus <i>Glomus intraradices</i> restores infectivity of a hemibiotrophic plant pathogen. <i>New Phytologist</i> , 2009, 181, 693-707.	7.3	23
38	Sterol metabolism in the oomycete <i>Aphanomyces euteiches</i> , a legume root pathogen. <i>New Phytologist</i> , 2009, 183, 291-300.	7.3	42
39	Partial Resistance of <i>Medicago truncatula</i> to <i>Aphanomyces euteiches</i> Is Associated with Protection of the Root Stele and Is Controlled by a Major QTL Rich in Proteasome-Related Genes. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 1043-1055.	2.6	82
40	Cellulose-binding domains: cellulose associated-defensive sensing partners?. <i>Trends in Plant Science</i> , 2008, 13, 160-164.	8.8	28
41	Cell Wall Chitosaccharides Are Essential Components and Exposed Patterns of the Phytopathogenic Oomycete <i>Aphanomyces euteiches</i> . <i>Eukaryotic Cell</i> , 2008, 7, 1980-1993.	3.4	77
42	Genetic Dissection of Resistance to Anthracnose and Powdery Mildew in <i>Medicago truncatula</i> . <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 61-69.	2.6	55
43	Transcriptome of <i>Aphanomyces euteiches</i> : New Oomycete Putative Pathogenicity Factors and Metabolic Pathways. <i>PLoS ONE</i> , 2008, 3, e1723.	2.5	109
44	Regulation and role of a STE12-like transcription factor from the plant pathogen <i>Colletotrichum lindemuthianum</i> . <i>Molecular Microbiology</i> , 2007, 64, 68-82.	2.5	47
45	Root rot disease of legumes caused by <i>Aphanomyces euteiches</i> . <i>Molecular Plant Pathology</i> , 2007, 8, 539-548.	4.2	140
46	AphanoDB: a genomic resource for <i>Aphanomyces</i> pathogens. <i>BMC Genomics</i> , 2007, 8, 471.	2.8	43
47	Transcriptomic approaches to unravel plant-pathogen interactions in legumes. <i>Euphytica</i> , 2006, 147, 25-36.	1.2	25
48	Cellulose Binding Domains of a <i>Phytophthora</i> Cell Wall Protein Are Novel Pathogen-Associated Molecular Patterns. <i>Plant Cell</i> , 2006, 18, 1766-1777.	6.6	149
49	Functional analysis of CLPT1, a Rab/GTPase required for protein secretion and pathogenesis in the plant fungal pathogen <i>Colletotrichum lindemuthianum</i> . <i>Journal of Cell Science</i> , 2005, 118, 323-329.	2.0	42
50	A Novel <i>Arabidopsis</i> - <i>Colletotrichum</i> Pathosystem for the Molecular Dissection of Plant-Fungal Interactions. <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 272-282.	2.6	214
51	Gene expression profiling and protection of <i>Medicago truncatula</i> against a fungal infection in response to an elicitor from green algae <i>Ulva</i> spp. <i>Plant, Cell and Environment</i> , 2004, 27, 917-928.	5.7	153
52	Production of a cell wall-associated endopolygalacturonase by <i>Colletotrichum lindemuthianum</i> and pectin degradation during bean infection. <i>Fungal Genetics and Biology</i> , 2004, 41, 140-147.	2.1	37
53	Cytological, Genetic, and Molecular Analysis to Characterize Compatible and Incompatible Interactions Between <i>Medicago truncatula</i> and <i>Colletotrichum trifolii</i> . <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 909-920.	2.6	74
54	Elicitor Activity of a Fungal Endopolygalacturonase in Tobacco Requires a Functional Catalytic Site and Cell Wall Localization. <i>Plant Physiology</i> , 2003, 131, 93-101.	4.8	48

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55	A cis-Acting Sequence Homologous to the Yeast Filamentation and Invasion Response Element Regulates Expression of a Pectinase Gene from the Bean Pathogen <i>Colletotrichum lindemuthianum</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 29125-29131.	3.4	21
56	Molecular characterization of CLPT1 , a SEC4 -like Rab/GTPase of the phytopathogenic fungus <i>Colletotrichum lindemuthianum</i> which is regulated by the carbon source. <i>Gene</i> , 2001, 272, 219-225.	2.2	21
57	Specific and constitutive expression of oxalate oxidase during the ageing of leaf sheaths of ryegrass stubble. <i>Plant, Cell and Environment</i> , 2001, 24, 1033-1043.	5.7	35
58	Cell wall degrading enzymes, inhibitory proteins, and oligosaccharides participate in the molecular dialogue between plants and pathogens. <i>Plant Physiology and Biochemistry</i> , 2000, 38, 157-163.	5.8	133
59	Use of Green Fluorescent Protein To Detect Expression of an Endopolygalacturonase Gene of <i>Colletotrichum lindemuthianum</i> during Bean Infection. <i>Applied and Environmental Microbiology</i> , 1999, 65, 1769-1771.	3.1	67
60	Endopolygalacturonase Genes from <i>Colletotrichum lindemuthianum</i> : Cloning of CLPG2 and Comparison of Its Expression to That of CLPG1 During Saprophytic and Parasitic Growth of the Fungus. <i>Molecular Plant-Microbe Interactions</i> , 1997, 10, 769-775.	2.6	64
61	Isolation and sequence analysis of Clpgl, a gene coding for an endopolygalacturonase of the phytopathogenic fungus <i>Colletotrichum lindemuthianum</i> . <i>Gene</i> , 1996, 170, 125-129.	2.2	42
62	Molecular characterization and expression of <i>Colletotrichum lindemuthianum</i> genes encoding endopolygalacturonase. <i>Progress in Biotechnology</i> , 1996, 14, 369-376.	0.2	0
63	Three Glycosylated Polypeptides Secreted by Several Embryogenic Cell Cultures of Pine Show Highly Specific Serological Affinity to Antibodies Directed against the Wheat Germin Apoprotein Monomer. <i>Plant Physiology</i> , 1995, 108, 141-148.	4.8	88
64	Tissue-Specific Expression of Germin-Like Oxalate Oxidase during Development and Fungal Infection of Barley Seedlings. <i>Plant Physiology</i> , 1995, 107, 1091-1096.	4.8	167
65	One-step purification and characterization of a lignin-specific O-methyltransferase from poplar. <i>Gene</i> , 1993, 133, 213-217.	2.2	21
66	Nucleotide Sequence of a Complementary DNA Encoding O-Methyltransferase from Poplar. <i>Plant Physiology</i> , 1992, 98, 796-797.	4.8	57
67	Regulation of Enzymes Involved in Lignin Biosynthesis: Induction of O-Methyltransferase mRNAs During the Hypersensitive Reaction of Tobacco to Tobacco Mosaic Virus. <i>Molecular Plant-Microbe Interactions</i> , 1992, 5, 294.	2.6	73
68	Plant Genes Involved in Resistance to Viruses. , 1991, , 153-166.		1
69	Purification of tobacco O-methyltransferases by affinity chromatography and estimation of the rate of synthesis of the enzymes during hypersensitive reaction to virus infection. <i>Planta</i> , 1988, 176, 36-41.	3.2	21
70	<i>Aphanomyces euteiches</i> and Legumes. , 0, , 345-360.		0