Christina Dixelius

List of Publications by Year
in descending order

65 papers	2,982 citations	185998 28 h-index	174990 52 g-index
71 all docs	71 docs citations	71 times ranked	3617 citing authors

#	Article	IF	Citations
1	Phytophthora infestansâ€‰Ago1â€associated miRNA promotes potato late blight disease. New Phytologist, 2022, 233, 443-457.	3.5	14
2	Rhizoctonia solani Infection Assay of Young Sugar Beet and Arabidopsis plantlets. Bio-protocol, 2022, 12, e4300.	0.2	2
3	Major latex protein-like encoding genes contribute to Rhizoctonia solani defense responses in sugar beet. Molecular Genetics and Genomics, 2021, 296, 155-164.	1.0	20
4	Plant mitochondria and chloroplasts are targeted by the Rhizoctonia solani RsCRP1 effector. Biochemical and Biophysical Research Communications, 2021, 544, 86-90.	1.0	16
5	smartPARE: An R Package for Efficient Identification of True mRNA Cleavage Sites. International Journal of Molecular Sciences, 2021, 22, 4267.	1.8	5
6	Genome-wide identification of Argonautes in Solanaceae with emphasis on potato. Scientific Reports, 2020, 10, 20577.	1.6	10
7	The RsRlpA Effector Is a Protease Inhibitor Promoting Rhizoctonia solani Virulence through Suppression of the Hypersensitive Response. International Journal of Molecular Sciences, 2020, 21, 8070.	1.8	16
8	Dominance of Mating Type A1 and Indication of Epigenetic Effects During Early Stages of Mating in Phytophthora infestans. Frontiers in Microbiology, 2020, 11, 252.	1.5	9
9	The architecture of the Plasmodiophora brassicae nuclear and mitochondrial genomes. Scientific Reports, 2019, 9, 15753.	1.6	17
10	Induced Expression of Xerophyta viscosa XvSap1 Gene Enhances Drought Tolerance in Transgenic Sweet Potato. Frontiers in Plant Science, 2019, 10, 1119.	1.7	8
11	A LysM effector protein from the basidiomycete Rhizoctonia solani contributes to virulence through suppression of chitin-triggered immunity. Molecular Genetics and Genomics, 2019, 294, 1211-1218.	1.0	53
12	Xerophyta viscosa Aldose Reductase, XvAld1, Enhances Drought Tolerance in Transgenic Sweetpotato. Molecular Biotechnology, 2018, 60, 203-214.	1.3	16
13	The immunophilin repertoire of Plasmodiophora brassicae and functional analysis of PbCYP3 cyclophilin. Molecular Genetics and Genomics, 2018, 293, 381-390.	1.0	16
14	Analysis of the hybrid genomes of two field isolates of the soil-borne fungal species Verticillium longisporum. BMC Genomics, 2018, 19, 14.	1.2	23
15	Detection of Verticillium species in Swedish soils using real-time PCR. Archives of Microbiology, 2017, 199, 1383-1389.	1.0	20
16	Phytophthora infestans Argonaute 1 binds micro<scp>RNA</scp> and small <scp>RNA</scp>s from effector genes and transposable elements. New Phytologist, 2016, 211, 993-1007.	3.5	41
17	New kid on the block â€“ the clubroot pathogen genome moves the plasmodiophorids into the genomic era. European Journal of Plant Pathology, 2016, 145, 531-542.	0.8	30
18	Genome analysis of the sugar beet pathogen Rhizoctonia solani AG2-2IIIB revealed high numbers in secreted proteins and cell wall degrading enzymes. BMC Genomics, 2016, 17, 245.	1.2	69

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19	The Large Subunit rDNA Sequence of Plasmodiophora brassicae Does not Contain Intra-species Polymorphism. Protist, 2016, 167, 544-554.	0.6	30
20	Draft genome sequence of the sugar beet pathogen Rhizoctonia solani AG2-2IIIB strain BBA69670. Journal of Biotechnology, 2016, 222, 11-12.	1.9	20
21	Evolutionary Origins of Rhizarian Parasites. Molecular Biology and Evolution, 2016, 33, 980-983.	3.5	47
22	The Plasmodiophora brassicae genome reveals insights in its life cycle and ancestry of chitin synthases. Scientific Reports, 2015, 5, 11153.	1.6	202
23	Plant-mediated gene silencing restricts growth of the potato late blight pathogen Phytophthora infestans. Journal of Experimental Botany, 2015, 66, 2785-2794.	2.4	124
24	Genetic and morphological evidence for introgression between three species of willows. BMC Evolutionary Biology, 2015, 15, 193.	3.2	29
25	Susceptibility to Verticillium longisporum is linked to monoterpene production by <scp>TPS</scp>23/27 in Arabidopsis. Plant Journal, 2015, 81, 572-585.	2.8	19
26	Fragmentation of tRNA in Phytophthora infestans asexual life cycle stages and during host plant infection. BMC Microbiology, 2014, 14, 308.	1.3	24
27	Clubroot, a persistent threat to Swedish oilseed rape production. Canadian Journal of Plant Pathology, 2014, 36, 135-141.	0.8	21
28	RabGAP22 Is Required for Defense to the Vascular Pathogen Verticillium longisporum and Contributes to Stomata Immunity. PLoS ONE, 2014, 9, e88187.	1.1	28
29	A novel role of <scp>PR</scp>2 in abscisic acid (<scp>ABA</scp>) mediated, pathogenâ€induced callose deposition in Arabidopsis thaliana. New Phytologist, 2013, 200, 1187-1199.	3.5	129
30	Phenotypic diversification by gene silencing inPhytophthoraplant pathogens. Communicative and Integrative Biology, 2013, 6, e25890.	0.6	9
31	A Network of HMG-box Transcription Factors Regulates Sexual Cycle in the Fungus Podospora anserina. PLoS Genetics, 2013, 9, e1003642.	1.5	58
32	Can silencing of transposons contribute to variation in effector gene expression inPhytophthora infestans?. Mobile Genetic Elements, 2012, 2, 110-114.	1.8	43
33	Stop worrying; start growing. EMBO Reports, 2012, 13, 493-497.	2.0	15
34	European agricultural policy goes down the tubers. Nature Biotechnology, 2012, 30, 492-493.	9.4	10
35	Two loci in sorghum with NB-LRR encoding genes confer resistance to Colletotrichum sublineolum. Theoretical and Applied Genetics, 2012, 124, 1005-1015.	1.8	34
36	Evidence for Small RNAs Homologous to Effector-Encoding Genes and Transposable Elements in the Oomycete Phytophthora infestans. PLoS ONE, 2012, 7, e51399.	1.1	79

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37	Silencing of the PiAvr3a effector-encoding gene from Phytophthora infestans by transcriptional fusion to a short interspersed element. Fungal Biology, 2011, 115, 1225-1233.	1.1	18
38	Evidence for involvement of Dicerâ€like, Argonaute and histone deacetylase proteins in gene silencing in Phytophthora infestans. Molecular Plant Pathology, 2011, 12, 772-785.	2.0	64
39	A highly conserved NB-LRR encoding gene cluster effective against Setosphaeria turcica in sorghum. BMC Plant Biology, 2011, 11, 151.	1.6	35
40	Phytophthora infestans effector AVR3a is essential for virulence and manipulates plant immunity by stabilizing host E3 ligase CMPG1. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9909-9914.	3.3	412
41	Tracing the Origin of the Fungal Î±1 Domain Places Its Ancestor in the HMG-Box Superfamily: Implication for Fungal Mating-Type Evolution. PLoS ONE, 2010, 5, e15199.	1.1	93
42	Studies on the mechanism of resistance to Bipolaris sorokiniana in the barley lesion mimic mutant bst1. Molecular Plant Pathology, 2009, 10, 587-598.	2.0	31
43	Layers of defense responses toLeptosphaeria maculansbelow theRLM1â€•and camalexinâ€dependent resistances. New Phytologist, 2009, 182, 470-482.	3.5	20
44	Genetic variability and genomic divergence of Elymus repens and related species. Plant Systematics and Evolution, 2008, 271, 143-156.	0.3	12
45	RLM3, a TIR domain encoding gene involved in broadâ€•range immunity of Arabidopsis to necrotrophic fungal pathogens. Plant Journal, 2008, 55, 188-200.	2.8	88
46	RLM3, a potential adaptor between specific TIR-NB-LRR receptors and DZC proteins. Communicative and Integrative Biology, 2008, 1, 59-61.	0.6	16
47	Tracing the ancient origins of plant innate immunity. Trends in Plant Science, 2007, 12, 334-342.	4.3	34
48	ABA Is Required for Leptosphaeria maculans Resistance via ABI1- and ABI4-Dependent Signaling. Molecular Plant-Microbe Interactions, 2007, 20, 335-345.	1.4	90
49	Early Responses in the Arabidopsis-Verticillium longisporum Pathosystem Are Dependent on NDR1, JA- and ET-Associated Signals via Cytosolic NPR1 and RFO1. Molecular Plant-Microbe Interactions, 2006, 19, 958-969.	1.4	130
50	Development of a rapid and simpleAgrobacterium tumefaciens-mediated transformation system for the fungal pathogenHeterobasidion annosum. FEMS Microbiology Letters, 2006, 255, 82-88.	0.7	15
51	Plant Host Range of Verticillium longisporum and Microsclerotia Density in Swedish Soils. European Journal of Plant Pathology, 2006, 114, 139-149.	0.8	40
52	Interactive Effects of Host, Pathogen and Mineral Nutrition on Grey Leaf Spot Epidemics in Uganda. European Journal of Plant Pathology, 2004, 110, 119-128.	0.8	13
53	Taxonomic characterization and plant colonizing abilities of some bacteria related to Bacillus amyloliquefaciens and Bacillus subtilis. FEMS Microbiology Ecology, 2004, 48, 249-259.	1.3	126
54	Phylogenetic analysis of Verticillium species based on nuclear and mitochondrial sequences. Archives of Microbiology, 2004, 181, 435-442.	1.0	43

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55	Characterisation of anArabidopsis-Leptosphaeria maculanspathosystem: resistance partially requires camalexin biosynthesis and is independent of salicylic acid, ethylene and jasmonic acid signalling. Plant Journal, 2004, 37, 9-20.	2.8	100
56	Estimation of Genetic Variation Among Verticillium Isolates using AFLP Analysis. European Journal of Plant Pathology, 2003, 109, 361-371.	0.8	38
57	Overexpression of a Brassica nigra cDNA Gives Enhanced Resistance to Leptosphaeria maculans in B. napus. Molecular Plant-Microbe Interactions, 2003, 16, 477-484.	1.4	20
58	Identification of the causal agent of Verticillium wilt of winter oilseed rape in Sweden, V. longisporum. Mycological Research, 2002, 106, 570-578.	2.5	58
59	The myrosinase-glucosinolate system in the interaction between Leptosphaeria maculans and Brassica napus. Molecular Plant Pathology, 2001, 2, 281-286.	2.0	15
60	B-genome derived resistance to Leptosphaeria maculans in near isogenic Brassica napus lines is independent of glucosinolate profile. Physiologia Plantarum, 2000, 110, 461-468.	2.6	12
61	Title is missing!. Euphytica, 2000, 115, 181-190.	0.6	4
62	UV dose-dependent DNA elimination in asymmetric somatic hybrids between Brassica napus and Arabidopsis thaliana. Plant Science, 1998, 131, 65-76.	1.7	74
63	Brassica napus (+) B. tournefortii, a somatic hybrid containing traits of agronomic importance for rapeseed breeding. Plant Science, 1995, 109, 75-86.	1.7	46
64	Presence of the pathogenesis-related proteins 2, Q and S in stressed Brassica napus and B. nigra plantlets. Physiological and Molecular Plant Pathology, 1994, 44, 1-8.	1.3	15
65	Transformation of Brassica napus by using the aadA gene as selectable marker and inheritance studies of the marker genes. Physiologia Plantarum, 1994, 92, 37-46.	2.6	9