

Sebastien Duplessis

List of Publications by Year in descending order

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84
papers

11,410
citations

81743

39
h-index

64668

79
g-index

103
all docs

103
docs citations

103
times ranked

11497
citing authors

#	ARTICLE	IF	CITATIONS
1	A point mutation and large deletion at the candidate avirulence locus <i>AvrMlp7</i> in the poplar rust fungus correlate with poplar RMLp7 resistance breakdown. <i>Molecular Ecology</i> , 2023, 32, 2472-2483.	2.0	10
2	Genomic Signatures of a Major Adaptive Event in the Pathogenic Fungus <i>Melampsora larici-populina</i> . <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	9
3	Annotation survey and life-cycle transcriptomics of transcription factors in rust fungi (Pucciniales) identify a possible role for cold shock proteins in dormancy exit. <i>Fungal Genetics and Biology</i> , 2022, , 103698.	0.9	0
4	Elevated Ozone Concentration and Nitrogen Addition Increase Poplar Rust Severity by Shifting the Phyllosphere Microbial Community. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 523.	1.5	8
5	Transposable Elements in Fungi: Coevolution With the Host Genome Shapes, Genome Architecture, Plasticity and Adaptation. , 2021, , 142-155.		5
6	Host Adaptation and Virulence in Heteroecious Rust Fungi. <i>Annual Review of Phytopathology</i> , 2021, 59, 403-422.	3.5	30
7	Two stripe rust effectors impair wheat resistance by suppressing import of host Fe-S protein into chloroplasts. <i>Plant Physiology</i> , 2021, 187, 2530-2543.	2.3	28
8	Transcriptome Analysis of Apple Leaves Infected by the Rust Fungus <i>Gymnosporangium yamadae</i> at Two Sporulation Stages. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 444-461.	1.4	17
9	Host-specialized transcriptome of plant-associated organisms. <i>Current Opinion in Plant Biology</i> , 2020, 56, 81-88.	3.5	26
10	Comparative transcriptomics of <i>Gymnosporangium</i> spp. teliospores reveals a conserved genetic program at this specific stage of the rust fungal life cycle. <i>BMC Genomics</i> , 2019, 20, 723.	1.2	6
11	Structural genomics applied to the rust fungus <i>Melampsora larici-populina</i> reveals two candidate effector proteins adopting cystine knot and NTF2-like protein folds. <i>Scientific Reports</i> , 2019, 9, 18084.	1.6	19
12	Advances in understanding obligate biotrophy in rust fungi. <i>New Phytologist</i> , 2019, 222, 1190-1206.	3.5	109
13	Show me the way: rust effector targets in heterologous plant systems. <i>Current Opinion in Microbiology</i> , 2018, 46, 19-25.	2.3	49
14	The Rust Fungus <i>Melampsora larici-populina</i> Expresses a Conserved Genetic Program and Distinct Sets of Secreted Protein Genes During Infection of Its Two Host Plants, Larch and Poplar. <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 695-706.	1.4	42
15	Intraspecific comparative genomics of isolates of the Norway spruce pathogen (Heterobasidion) Tj ETQq1 1 0.784314 rgBT /Qyerlock 10	1.2	37
16	Infection assays in <i>Arabidopsis</i> reveal candidate effectors from the poplar rust fungus that promote susceptibility to bacteria and oomycete pathogens. <i>Molecular Plant Pathology</i> , 2018, 19, 191-200.	2.0	84
17	A rust fungal effector binds plant DNA and modulates transcription. <i>Scientific Reports</i> , 2018, 8, 14718.	1.6	42
18	Oak genome reveals facets of long lifespan. <i>Nature Plants</i> , 2018, 4, 440-452.	4.7	303

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19	Phylogenetics and Phylogenomics of Rust Fungi. <i>Advances in Genetics</i> , 2017, 100, 267-307.	0.8	68
20	Computational Methods for Predicting Effectors in Rust Pathogens. <i>Methods in Molecular Biology</i> , 2017, 1659, 73-83.	0.4	19
21	Heterologous Expression Screens in <i>Nicotiana benthamiana</i> Identify a Candidate Effector of the Wheat Yellow Rust Pathogen that Associates with Processing Bodies. <i>PLoS ONE</i> , 2016, 11, e0149035.	1.1	99
22	The Poplar Rust-Induced Secreted Protein (RISP) Inhibits the Growth of the Leaf Rust Pathogen <i>Melampsora larici-populina</i> and Triggers Cell Culture Alkalinisation. <i>Frontiers in Plant Science</i> , 2016, 7, 97.	1.7	11
23	Editorial: Genomics Research on Non-model Plant Pathogens: Delivering Novel Insights into Rust Fungus Biology. <i>Frontiers in Plant Science</i> , 2016, 7, 216.	1.7	7
24	Rust fungal effectors mimic host transit peptides to translocate into chloroplasts. <i>Cellular Microbiology</i> , 2016, 18, 453-465.	1.1	90
25	Forest tree genomics: 10 achievements from the past 10 years and future prospects. <i>Annals of Forest Science</i> , 2016, 73, 77-103.	0.8	91
26	Decoding the oak genome: public release of sequence data, assembly, annotation and publication strategies. <i>Molecular Ecology Resources</i> , 2016, 16, 254-265.	2.2	108
27	Genomic Patterns of Positive Selection at the Origin of Rust Fungi. <i>PLoS ONE</i> , 2015, 10, e0143959.	1.1	20
28	Effector-Mining in the Poplar Rust Fungus <i>Melampsora larici-populina</i> Secretome. <i>Frontiers in Plant Science</i> , 2015, 6, 1051.	1.7	26
29	Candidate Effector Proteins of the Rust Pathogen <i>Melampsora larici-populina</i> Target Diverse Plant Cell Compartments. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 689-700.	1.4	172
30	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus. <i>BMC Genomics</i> , 2015, 16, 461.	1.2	58
31	Effector proteins of rust fungi. <i>Frontiers in Plant Science</i> , 2014, 5, 416.	1.7	110
32	Overview of the functional virulent genome of the coffee leaf rust pathogen <i>Hemileia vastatrix</i> with an emphasis on early stages of infection. <i>Frontiers in Plant Science</i> , 2014, 5, 88.	1.7	25
33	Genome analysis of poplar LRR-RLP gene clusters reveals RISP, a defense-related gene coding a candidate endogenous peptide elicitor. <i>Frontiers in Plant Science</i> , 2014, 5, 111.	1.7	30
34	Genome-wide patterns of segregation and linkage disequilibrium: the construction of a linkage genetic map of the poplar rust fungus <i>Melampsora larici-populina</i> . <i>Frontiers in Plant Science</i> , 2014, 5, 454.	1.7	19
35	On the current status of <i>Phakopsora pachyrhizi</i> genome sequencing. <i>Frontiers in Plant Science</i> , 2014, 5, 377.	1.7	21
36	The poplar Phi class glutathione transferase: expression, activity and structure of GSTF1. <i>Frontiers in Plant Science</i> , 2014, 5, 712.	1.7	33

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37	Patterns of genomic variation in the poplar rust fungus <i>Melampsora larici-populina</i> identify pathogenesis-related factors. <i>Frontiers in Plant Science</i> , 2014, 5, 450.	1.7	48
38	Advancing Knowledge on Biology of Rust Fungi Through Genomics. <i>Advances in Botanical Research</i> , 2014, , 173-209.	0.5	35
39	12 Rust Fungi: Achievements and Future Challenges on Genomics and Host-Parasite Interactions. , 2013, , 315-341.		1
40	Transcriptome analysis of poplar rust telia reveals overwintering adaptation and tightly coordinated karyogamy and meiosis processes. <i>Frontiers in Plant Science</i> , 2013, 4, 456.	1.7	30
41	RNA-Seq of Early-Infected Poplar Leaves by the Rust Pathogen <i>Melampsora larici-populina</i> Uncovers PtSultr3;5, a Fungal-Induced Host Sulfate Transporter. <i>PLoS ONE</i> , 2012, 7, e44408.	1.1	57
42	A Comprehensive Analysis of Genes Encoding Small Secreted Proteins Identifies Candidate Effectors in <i>Melampsora larici-populina</i> (Poplar Leaf Rust). <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 279-293.	1.4	150
43	Mitogen-Activated Protein Kinase Signaling in Plant-Interacting Fungi: Distinct Messages from Conserved Messengers. <i>Plant Cell</i> , 2012, 24, 1327-1351.	3.1	294
44	Insight into trade-off between wood decay and parasitism from the genome of a fungal forest pathogen. <i>New Phytologist</i> , 2012, 194, 1001-1013.	3.5	210
45	Expression profiling of genes involved in the biotrophic colonisation of <i>Coffea arabica</i> leaves by <i>Hemileia vastatrix</i> . <i>European Journal of Plant Pathology</i> , 2012, 133, 261-277.	0.8	14
46	454-pyrosequencing of <i>Coffea arabica</i> leaves infected by the rust fungus <i>Hemileia vastatrix</i> reveals in planta-expressed pathogen-secreted proteins and plant functions in a late compatible plant-rust interaction. <i>Molecular Plant Pathology</i> , 2012, 13, 17-37.	2.0	81
47	<i>Melampsora larici-populina</i> Transcript Profiling During Germination and Timecourse Infection of Poplar Leaves Reveals Dynamic Expression Patterns Associated with Virulence and Biotrophy. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 808-818.	1.4	80
48	Obligate biotrophy features unraveled by the genomic analysis of rust fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9166-9171.	3.3	640
49	Validation of RT-qPCR reference genes for in planta expression studies in <i>Hemileia vastatrix</i> , the causal agent of coffee leaf rust. <i>Fungal Biology</i> , 2011, 115, 891-901.	1.1	36
50	Validation of <i>Melampsora larici-populina</i> reference genes for in planta RT-quantitative PCR expression profiling during time-course infection of poplar leaves. <i>Physiological and Molecular Plant Pathology</i> , 2011, 75, 106-112.	1.3	38
51	Isolation of differentially expressed genes during interactions between tomato cells and a protective or a non-protective strain of <i>Fusarium oxysporum</i> . <i>Physiological and Molecular Plant Pathology</i> , 2011, 76, 9-19.	1.3	14
52	Genome-wide analysis of eukaryote thaumatin-like proteins (TLPs) with an emphasis on poplar. <i>BMC Plant Biology</i> , 2011, 11, 33.	1.6	111
53	Mining gene expression data with pattern structures in formal concept analysis. <i>Information Sciences</i> , 2011, 181, 1989-2001.	4.0	152
54	The Poplar-Poplar Rust Interaction: Insights from Genomics and Transcriptomics. <i>Journal of Pathogens</i> , 2011, 2011, 1-11.	0.9	66

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55	Poplar Proteomics. , 2011, , 128-165.		1
56	Photosynthetic and respiratory changes in leaves of poplar elicited by rust infection. Photosynthesis Research, 2010, 104, 41-48.	1.6	59
57	PÃ©rigord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. Nature, 2010, 464, 1033-1038.	13.7	641
58	Laser Capture Microdissection of Uredinia Formed by <i>Melampsora larici-populina</i> Revealed a Transcriptional Switch Between Biotrophy and Sporulation. Molecular Plant-Microbe Interactions, 2010, 23, 1275-1286.	1.4	58
59	Gene expression analysis of <i>Populus deltoides</i> roots subjected to copper stress. Environmental and Experimental Botany, 2009, 67, 335-344.	2.0	28
60	RNA silencing in the model mycorrhizal fungus <i>Laccaria bicolor</i> : gene knock-down of nitrate reductase results in inhibition of symbiosis with <i>Populus</i> . Environmental Microbiology, 2009, 11, 1878-1896.	1.8	68
61	Poplar and Pathogen Interactions: Insights from <i>Populus</i> Genome-Wide Analyses of Resistance and Defense Gene Families and Gene Expression Profiling. Critical Reviews in Plant Sciences, 2009, 28, 309-334.	2.7	97
62	Two FCA-Based Methods for Mining Gene Expression Data. Lecture Notes in Computer Science, 2009, , 251-266.	1.0	22
63	Genome-wide identification of NBS resistance genes in <i>Populus trichocarpa</i> . Plant Molecular Biology, 2008, 66, 619-636.	2.0	247
64	The genome of <i>Laccaria bicolor</i> provides insights into mycorrhizal symbiosis. Nature, 2008, 452, 88-92.	13.7	1,003
65	Tâ€œDNA insertion, plasmid rescue and integration analysis in the model mycorrhizal fungus <i>Laccaria bicolor</i> . Microbial Biotechnology, 2008, 1, 258-269.	2.0	38
66	Using Formal Concept Analysis for the Extraction of Groups of Co-expressed Genes. Communications in Computer and Information Science, 2008, , 439-449.	0.4	20
67	Transcript Profiling of Poplar Leaves upon Infection with Compatible and Incompatible Strains of the Foliar Rust <i>Melampsora larici-populina</i> . Plant Physiology, 2007, 144, 347-366.	2.3	156
68	Living in harmony in the wood underground: ectomycorrhizal genomics. Current Opinion in Plant Biology, 2007, 10, 204-210.	3.5	90
69	More complexity in the mycorrhizal world. New Phytologist, 2006, 172, 600-604.	3.5	11
70	The Genome of Black Cottonwood, <i>Populus trichocarpa</i> (Torr. & Gray). Science, 2006, 313, 1596-1604.	6.0	3,945
71	Transcript patterns associated with ectomycorrhiza development in <i>Eucalyptus globulus</i> and <i>Pisolithus microcarpus</i> . New Phytologist, 2005, 165, 599-611.	3.5	164
72	Gene expression patterns of trembling aspen trees following long-term exposure to interacting elevated CO2 and tropospheric O3. New Phytologist, 2005, 167, 129-142.	3.5	112

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73	Transcript Profiling Reveals Novel Marker Genes Involved in Fruiting Body Formation in <i>Tuber borchii</i> . <i>Eukaryotic Cell</i> , 2005, 4, 1599-1602.	3.4	30
74	T-DNA transfer from <i>Agrobacterium tumefaciens</i> to the ectomycorrhizal fungus <i>Pisolithus microcarpus</i> . <i>Revista Argentina De Microbiologia</i> , 2005, 37, 69-72.	0.4	9
75	Poplar Peroxiredoxin Q. A Thioredoxin-Linked Chloroplast Antioxidant Functional in Pathogen Defense. <i>Plant Physiology</i> , 2004, 134, 1027-1038.	2.3	155
76	Analysis of expressed sequence tags from the ectomycorrhizal basidiomycetes <i>Laccaria bicolor</i> and <i>Pisolithus microcarpus</i> . <i>New Phytologist</i> , 2003, 159, 117-129.	3.5	67
77	<i>Albidovulum inexpectatum</i> gen. nov., sp. nov., a Nonphotosynthetic and Slightly Thermophilic Bacterium from a Marine Hot Spring That Is Very Closely Related to Members of the Photosynthetic Genus <i>Rhodovulum</i> . <i>Applied and Environmental Microbiology</i> , 2002, 68, 5788-5788.	1.4	4
78	Isolation and Characterization of Differentially Expressed Genes in the Mycelium and Fruit Body of <i>Tuber borchii</i> . <i>Applied and Environmental Microbiology</i> , 2002, 68, 4574-4582.	1.4	66
79	The application of genetic approaches for investigations of mycorrhizal symbioses. <i>Plant and Soil</i> , 2002, 244, 85-95.	1.8	21
80	Cloning and expression analysis of a new hydrophobin cDNA from the ectomycorrhizal basidiomycete <i>Pisolithus</i> . <i>Current Genetics</i> , 2001, 39, 335-339.	0.8	19
81	Developmental cross talking in the ectomycorrhizal symbiosis: signals and communication genes. <i>New Phytologist</i> , 2001, 151, 145-154.	3.5	171
82	Identification of symbiosis-regulated genes in <i>Eucalyptus globulus</i> - <i>Pisolithus tinctorius</i> ectomycorrhiza by differential hybridization of arrayed cDNAs. <i>Plant Journal</i> , 2001, 25, 181-191.	2.8	25
83	Identification of symbiosis-regulated genes in <i>Eucalyptus globulus</i> - <i>Pisolithus tinctorius</i> ectomycorrhiza by differential hybridization of arrayed cDNAs. <i>Plant Journal</i> , 2001, 25, 181-191.	2.8	158
84	A Short Review of Anti-Rust Fungi Peptides: Diversity and Bioassays. <i>Frontiers in Agronomy</i> , 0, 4, .	1.5	1