Sebastien Duplessis

List of Publications by Year
in descending order

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84 papers	11,410 citations	81900 39 h-index	64796 79 g-index
103 all docs	103 docs citations	103 times ranked	11497 citing authors

#	ARTICLE	IF	CITATIONS
1	The Genome of Black Cottonwood, <i>Populus trichocarpa</i> (Torr. & Gray). Science, 2006, 313, 1596-1604.	12.6	3,945
2	The genome of Laccaria bicolor provides insights into mycorrhizal symbiosis. Nature, 2008, 452, 88-92.	27.8	1,003
3	PÃ©rigord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. Nature, 2010, 464, 1033-1038.	27.8	641
4	Obligate biotrophy features unraveled by the genomic analysis of rust fungi. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9166-9171.	7.1	640
5	Oak genome reveals facets of long lifespan. Nature Plants, 2018, 4, 440-452.	9.3	303
6	Mitogen-Activated Protein Kinase Signaling in Plant-Interacting Fungi: Distinct Messages from Conserved Messengers. Plant Cell, 2012, 24, 1327-1351.	6.6	294
7	Genome-wide identification of NBS resistance genes in Populus trichocarpa. Plant Molecular Biology, 2008, 66, 619-636.	3.9	247
8	Insight into tradeâ€off between wood decay and parasitism from the genome of a fungal forest pathogen. New Phytologist, 2012, 194, 1001-1013.	7.3	210
9	Candidate Effector Proteins of the Rust Pathogen <i>Melampsora larici-populina</i> Target Diverse Plant Cell Compartments. Molecular Plant-Microbe Interactions, 2015, 28, 689-700.	2.6	172
10	Developmental cross talking in the ectomycorrhizal symbiosis: signals and communication genes. New Phytologist, 2001, 151, 145-154.	7.3	171
11	Transcript patterns associated with ectomycorrhiza development in Eucalyptus globulus and Pisolithus microcarpus. New Phytologist, 2005, 165, 599-611.	7.3	164
12	Identification of symbiosis-regulated genes in Eucalyptus globulus-Pisolithus tinctorius ectomycorrhiza by differential hybridization of arrayed cDNAs. Plant Journal, 2001, 25, 181-191.	5.7	158
13	Transcript Profiling of Poplar Leaves upon Infection with Compatible and Incompatible Strains of the Foliar Rust Melampsora larici-populina Â. Plant Physiology, 2007, 144, 347-366.	4.8	156
14	Poplar Peroxiredoxin Q. A Thioredoxin-Linked Chloroplast Antioxidant Functional in Pathogen Defense. Plant Physiology, 2004, 134, 1027-1038.	4.8	155
15	Mining gene expression data with pattern structures in formal concept analysis. Information Sciences, 2011, 181, 1989-2001.	6.9	152
16	A Comprehensive Analysis of Genes Encoding Small Secreted Proteins Identifies Candidate Effectors in <i>Melampsora larici-populina</i> (Poplar Leaf Rust). Molecular Plant-Microbe Interactions, 2012, 25, 279-293.	2.6	150
17	Gene expression patterns of trembling aspen trees following long-term exposure to interacting elevated CO2 and tropospheric O3. New Phytologist, 2005, 167, 129-142.	7.3	112
18	Genome-wide analysis of eukaryote thaumatin-like proteins (TLPs) with an emphasis on poplar. BMC Plant Biology, 2011, 11, 33.	3.6	111

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19	Effector proteins of rust fungi. Frontiers in Plant Science, 2014, 5, 416.	3.6	110
20	Advances in understanding obligate biotrophy in rust fungi. New Phytologist, 2019, 222, 1190-1206.	7.3	109
21	Decoding the oak genome: public release of sequence data, assembly, annotation and publication strategies. Molecular Ecology Resources, 2016, 16, 254-265.	4.8	108
22	Heterologous Expression Screens in Nicotiana benthamiana Identify a Candidate Effector of the Wheat Yellow Rust Pathogen that Associates with Processing Bodies. PLoS ONE, 2016, 11, e0149035.	2.5	99
23	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.	5.7	97
24	Forest tree genomics: 10 achievements from the past 10Âyears and future prospects. Annals of Forest Science, 2016, 73, 77-103.	2.0	91
25	Living in harmony in the wood underground: ectomycorrhizal genomics. Current Opinion in Plant Biology, 2007, 10, 204-210.	7.1	90
26	Rust fungal effectors mimic host transit peptides to translocate into chloroplasts. Cellular Microbiology, 2016, 18, 453-465.	2.1	90
27	Infection assays in <i>Arabidopsis</i> reveal candidate effectors from the poplar rust fungus that promote susceptibility to bacteria and oomycete pathogens. Molecular Plant Pathology, 2018, 19, 191-200.	4.2	84
28	454â€pyrosequencing of <i>Coffea arabica</i> leaves infected by the rust fungus <i>Hemileia vastatrix</i> reveals <i>in planta</i>â€expressed pathogenâ€secreted proteins and plant functions in a late compatible plantâ€"rust interaction. Molecular Plant Pathology, 2012, 13, 17-37.	4.2	81
29	<i>Melampsora larici-populina</i> Transcript Profiling During Germination and Timecourse Infection of Poplar Leaves Reveals Dynamic Expression Patterns Associated with Virulence and Biotrophy. Molecular Plant-Microbe Interactions, 2011, 24, 808-818.	2.6	80
30	RNA silencing in the model mycorrhizal fungus <i>Laccaria bicolor</i>: gene knockâ€down of nitrate reductase results in inhibition of symbiosis with <i>Populus</i>. Environmental Microbiology, 2009, 11, 1878-1896.	3.8	68
31	Phylogenetics and Phylogenomics of Rust Fungi. Advances in Genetics, 2017, 100, 267-307.	1.8	68
32	Analysis of expressed sequence tags from the ectomycorrhizal basidiomycetes Laccaria bicolor and Pisolithus microcarpus. New Phytologist, 2003, 159, 117-129.	7.3	67
33	Isolation and Characterization of Differentially Expressed Genes in the Mycelium and Fruit Body of <i>Tuber borchii</i>. Applied and Environmental Microbiology, 2002, 68, 4574-4582.	3.1	66
34	The Poplar-Poplar Rust Interaction: Insights from Genomics and Transcriptomics. Journal of Pathogens, 2011, 2011, 1-11.	1.4	66
35	Photosynthetic and respiratory changes in leaves of poplar elicited by rust infection. Photosynthesis Research, 2010, 104, 41-48.	2.9	59
36	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.	2.6	58

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37	Sex and parasites: genomic and transcriptomic analysis of Microbotryum lychnidis-dioicae, the biotrophic and plant-castrating anther smut fungus. BMC Genomics, 2015, 16, 461.	2.8	58
38	RNA-Seq of Early-Infected Poplar Leaves by the Rust Pathogen Melampsora larici-populina Uncovers PtSultr3;5, a Fungal-Induced Host Sulfate Transporter. PLoS ONE, 2012, 7, e44408.	2.5	57
39	Show me the way: rust effector targets in heterologous plant systems. Current Opinion in Microbiology, 2018, 46, 19-25.	5.1	49
40	Patterns of genomic variation in the poplar rust fungus Melampsora larici-populina identify pathogenesis-related factors. Frontiers in Plant Science, 2014, 5, 450.	3.6	48
41	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. Molecular Plant-Microbe Interactions, 2018, 31, 695-706.	2.6	42
42	A rust fungal effector binds plant DNA and modulates transcription. Scientific Reports, 2018, 8, 14718.	3.3	42
43	Tâ€ÐNA insertion, plasmid rescue and integration analysis in the model mycorrhizal fungus<i>Laccaria bicolor</i>. Microbial Biotechnology, 2008, 1, 258-269.	4.2	38
44	Validation of Melampsora larici-populina reference genes for in planta RT-quantitative PCR expression profiling during time-course infection of poplar leaves. Physiological and Molecular Plant Pathology, 2011, 75, 106-112.	2.5	38
45	Intraspecific comparative genomics of isolates of the Norway spruce pathogen (Heterobasidion) Tj ETQq1 1 0.784314 rgBT /Overlock	2.8	37
46	Validation of RT-qPCR reference genes for in planta expression studies in Hemileia vastatrix, the causal agent of coffee leaf rust. Fungal Biology, 2011, 115, 891-901.	2.5	36
47	Advancing Knowledge on Biology of Rust Fungi Through Genomics. Advances in Botanical Research, 2014, , 173-209.	1.1	35
48	The poplar Phi class glutathione transferase: expression, activity and structure of GSTF1. Frontiers in Plant Science, 2014, 5, 712.	3.6	33
49	Transcript Profiling Reveals Novel Marker Genes Involved in Fruiting Body Formation in Tuber borchii. Eukaryotic Cell, 2005, 4, 1599-1602.	3.4	30
50	Transcriptome analysis of poplar rust telia reveals overwintering adaptation and tightly coordinated karyogamy and meiosis processes. Frontiers in Plant Science, 2013, 4, 456.	3.6	30
51	Genome analysis of poplar LRR-RLP gene clusters reveals RISP, a defense-related gene coding a candidate endogenous peptide elicitor. Frontiers in Plant Science, 2014, 5, 111.	3.6	30
52	Host Adaptation and Virulence in Heteroecious Rust Fungi. Annual Review of Phytopathology, 2021, 59, 403-422.	7.8	30
53	Gene expression analysis of Populus deltoides roots subjected to copper stress. Environmental and Experimental Botany, 2009, 67, 335-344.	4.2	28
54	Two stripe rust effectors impair wheat resistance by suppressing import of host Feâ€“S protein into chloroplasts. Plant Physiology, 2021, 187, 2530-2543.	4.8	28

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55	Effector-Mining in the Poplar Rust Fungus Melampsora larici-populina Secretome. Frontiers in Plant Science, 2015, 6, 1051.	3.6	26
56	Host-specialized transcriptome of plant-associated organisms. Current Opinion in Plant Biology, 2020, 56, 81-88.	7.1	26
57	Identification of symbiosisâ€regulated genes in <i>Eucalyptus globulusâ€"Pisolithus tinctorius</i> ectomycorrhiza by differential hybridization of arrayed cDNAs. Plant Journal, 2001, 25, 181-191.	5.7	25
58	Overview of the functional virulent genome of the coffee leaf rust pathogen Hemileia vastatrix with an emphasis on early stages of infection. Frontiers in Plant Science, 2014, 5, 88.	3.6	25
59	Two FCA-Based Methods for Mining Gene Expression Data. Lecture Notes in Computer Science, 2009, , 251-266.	1.3	22
60	The application of genetic approaches for investigations of mycorrhizal symbioses. Plant and Soil, 2002, 244, 85-95.	3.7	21
61	On the current status of Phakopsora pachyrhizi genome sequencing. Frontiers in Plant Science, 2014, 5, 377.	3.6	21
62	Genomic Patterns of Positive Selection at the Origin of Rust Fungi. PLoS ONE, 2015, 10, e0143959.	2.5	20
63	Using Formal Concept Analysis for the Extraction of Groups of Co-expressed Genes. Communications in Computer and Information Science, 2008, , 439-449.	0.5	20
64	Cloning and expression analysis of a new hydrophobin cDNA from the ectomycorrhizal basidiomycete Pisolithus. Current Genetics, 2001, 39, 335-339.	1.7	19
65	Genome-wide patterns of segregation and linkage disequilibrium: the construction of a linkage genetic map of the poplar rust fungus Melampsora larici-populina. Frontiers in Plant Science, 2014, 5, 454.	3.6	19
66	Structural genomics applied to the rust fungus Melampsora larici-populina reveals two candidate effector proteins adopting cystine knot and NTF2-like protein folds. Scientific Reports, 2019, 9, 18084.	3.3	19
67	Computational Methods for Predicting Effectors in Rust Pathogens. Methods in Molecular Biology, 2017, 1659, 73-83.	0.9	19
68	Transcriptome Analysis of Apple Leaves Infected by the Rust Fungus<i>Gymnosporangium yamadae</i>at Two Sporulation Stages. Molecular Plant-Microbe Interactions, 2020, 33, 444-461.	2.6	17
69	Isolation of differentially expressed genes during interactions between tomato cells and a protective or a non-protective strain of Fusarium oxysporum. Physiological and Molecular Plant Pathology, 2011, 76, 9-19.	2.5	14
70	Expression profiling of genes involved in the biotrophic colonisation of Coffea arabica leaves by Hemileia vastatrix. European Journal of Plant Pathology, 2012, 133, 261-277.	1.7	14
71	More complexity in the mycorrhizal world. New Phytologist, 2006, 172, 600-604.	7.3	11
72	The Poplar Rust-Induced Secreted Protein (RISP) Inhibits the Growth of the Leaf Rust Pathogen Melampsora larici-populina and Triggers Cell Culture Alkalinisation. Frontiers in Plant Science, 2016, 7, 97.	3.6	11

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73	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. Molecular Ecology, 2023, 32, 2472-2483.	3.9	10
74	T-DNA transfer from Agrobacterium tumefaciens to the ectomycorrhizal fungus Pisolithus microcarpus. Revista Argentina De Microbiologia, 2005, 37, 69-72.	0.7	9
75	Genomic Signatures of a Major Adaptive Event in the Pathogenic Fungus <i>Melampsora larici-populina</i>. Genome Biology and Evolution, 2022, 14, .	2.5	9
76	Elevated Ozone Concentration and Nitrogen Addition Increase Poplar Rust Severity by Shifting the Phyllosphere Microbial Community. Journal of Fungi (Basel, Switzerland), 2022, 8, 523.	3.5	8
77	Editorial: Genomics Research on Non-model Plant Pathogens: Delivering Novel Insights into Rust Fungus Biology. Frontiers in Plant Science, 2016, 7, 216.	3.6	7
78	Comparative transcriptomics of Gymnosporangium spp. teliospores reveals a conserved genetic program at this specific stage of the rust fungal life cycle. BMC Genomics, 2019, 20, 723.	2.8	6
79	Transposable Elements in Fungi: Coevolution With the Host Genome Shapes, Genome Architecture, Plasticity and Adaptation. , 2021, , 142-155.		5
80	<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>. Applied and Environmental Microbiology, 2002, 68, 5788-5788.	3.1	4
81	12 Rust Fungi: Achievements and Future Challenges on Genomics and Hostâ€"Parasite Interactions. , 2013, , 315-341.		1
82	Poplar Proteomics. , 2011, , 128-165.		1
83	A Short Review of Anti-Rust Fungi Peptides: Diversity and Bioassays. Frontiers in Agronomy, 0, 4, .	3.3	1
84	Annotation survey and life-cycle transcriptomics of transcription factors in rust fungi (Pucciniales) identify a possible role for cold shock proteins in dormancy exit. Fungal Genetics and Biology, 2022, , 103698.	2.1	0