

# 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	The Genome of Black Cottonwood, <i>Populus trichocarpa</i> (Torr. & Gray). <i>Science</i> , 2006, 313, 1596-1604.	6.0	3,945
2	The genome of <i>Laccaria bicolor</i> provides insights into mycorrhizal symbiosis. <i>Nature</i> , 2008, 452, 88-92.	13.7	1,003
3	P <sup>Å</sup> rigord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. <i>Nature</i> , 2010, 464, 1033-1038.	13.7	641
4	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
5	Oak genome reveals facets of long lifespan. <i>Nature Plants</i> , 2018, 4, 440-452.	4.7	303
6	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
7	Genome-wide identification of NBS resistance genes in <i>Populus trichocarpa</i> . <i>Plant Molecular Biology</i> , 2008, 66, 619-636.	2.0	247
8	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
9	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
10	Developmental cross talking in the ectomycorrhizal symbiosis: signals and communication genes. <i>New Phytologist</i> , 2001, 151, 145-154.	3.5	171
11	Transcript patterns associated with ectomycorrhiza development in <i>Eucalyptus globulus</i> and <i>Pisolithus microcarpus</i> . <i>New Phytologist</i> , 2005, 165, 599-611.	3.5	164
12	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
13	Transcript Profiling of Poplar Leaves upon Infection with Compatible and Incompatible Strains of the Foliar Rust <i>Melampsora larici-populina</i> . <i>Plant Physiology</i> , 2007, 144, 347-366.	2.3	156
14	Poplar Peroxiredoxin Q. A Thioredoxin-Linked Chloroplast Antioxidant Functional in Pathogen Defense. <i>Plant Physiology</i> , 2004, 134, 1027-1038.	2.3	155
15	Mining gene expression data with pattern structures in formal concept analysis. <i>Information Sciences</i> , 2011, 181, 1989-2001.	4.0	152
16	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
17	Gene expression patterns of trembling aspen trees following long-term exposure to interacting elevated CO <sub>2</sub> and tropospheric O <sub>3</sub> . <i>New Phytologist</i> , 2005, 167, 129-142.	3.5	112
18	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

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19	Effector proteins of rust fungi. <i>Frontiers in Plant Science</i> , 2014, 5, 416.	1.7	110
20	Advances in understanding obligate biotrophy in rust fungi. <i>New Phytologist</i> , 2019, 222, 1190-1206.	3.5	109
21	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
22	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
23	Poplar and Pathogen Interactions: Insights from <i>Populus</i> Genome-Wide Analyses of Resistance and Defense Gene Families and Gene Expression Profiling. <i>Critical Reviews in Plant Sciences</i> , 2009, 28, 309-334.	2.7	97
24	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
25	Living in harmony in the wood underground: ectomycorrhizal genomics. <i>Current Opinion in Plant Biology</i> , 2007, 10, 204-210.	3.5	90
26	Rust fungal effectors mimic host transit peptides to translocate into chloroplasts. <i>Cellular Microbiology</i> , 2016, 18, 453-465.	1.1	90
27	Infection assays in <i>Arabidopsis</i> reveal candidate effectors from the poplar rust fungus that promote susceptibility to bacteria and oomycete pathogens. <i>Molecular Plant Pathology</i> , 2018, 19, 191-200.	2.0	84
28	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
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. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 808-818.	1.4	80
30	RNA silencing in the model mycorrhizal fungus <i>Laccaria bicolor</i> : gene knockdown of nitrate reductase results in inhibition of symbiosis with <i>Populus</i> . <i>Environmental Microbiology</i> , 2009, 11, 1878-1896.	1.8	68
31	Phylogenetics and Phylogenomics of Rust Fungi. <i>Advances in Genetics</i> , 2017, 100, 267-307.	0.8	68
32	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
33	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
34	The Poplar-Poplar Rust Interaction: Insights from Genomics and Transcriptomics. <i>Journal of Pathogens</i> , 2011, 2011, 1-11.	0.9	66
35	Photosynthetic and respiratory changes in leaves of poplar elicited by rust infection. <i>Photosynthesis Research</i> , 2010, 104, 41-48.	1.6	59
36	Laser Capture Microdissection of Uredinia Formed by <i>Melampsora larici-populina</i> Revealed a Transcriptional Switch Between Biotrophy and Sporulation. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 1275-1286.	1.4	58

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37	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
38	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
39	Show me the way: rust effector targets in heterologous plant systems. <i>Current Opinion in Microbiology</i> , 2018, 46, 19-25.	2.3	49
40	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
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. <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 695-706.	1.4	42
42	A rust fungal effector binds plant DNA and modulates transcription. <i>Scientific Reports</i> , 2018, 8, 14718.	1.6	42
43	Tâ€DNA insertion, plasmid rescue and integration analysis in the model mycorrhizal fungus <i>Laccaria bicolor</i> . <i>Microbial Biotechnology</i> , 2008, 1, 258-269.	2.0	38
44	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
45	Intraspecific comparative genomics of isolates of the Norway spruce pathogen (Heterobasidion) Tj ETQq1 1 0.784314 rgBT /Overlock	1.2	37
46	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
47	Advancing Knowledge on Biology of Rust Fungi Through Genomics. <i>Advances in Botanical Research</i> , 2014, , 173-209.	0.5	35
48	The poplar Phi class glutathione transferase: expression, activity and structure of GSTF1. <i>Frontiers in Plant Science</i> , 2014, 5, 712.	1.7	33
49	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
50	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
51	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
52	Host Adaptation and Virulence in Heteroecious Rust Fungi. <i>Annual Review of Phytopathology</i> , 2021, 59, 403-422.	3.5	30
53	Gene expression analysis of <i>Populus deltoides</i> roots subjected to copper stress. <i>Environmental and Experimental Botany</i> , 2009, 67, 335-344.	2.0	28
54	Two stripe rust effectors impair wheat resistance by suppressing import of host Fe protein into chloroplasts. <i>Plant Physiology</i> , 2021, 187, 2530-2543.	2.3	28

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55	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
56	Host-specialized transcriptome of plant-associated organisms. <i>Current Opinion in Plant Biology</i> , 2020, 56, 81-88.	3.5	26
57	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
58	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
59	Two FCA-Based Methods for Mining Gene Expression Data. <i>Lecture Notes in Computer Science</i> , 2009, , 251-266.	1.0	22
60	The application of genetic approaches for investigations of mycorrhizal symbioses. <i>Plant and Soil</i> , 2002, 244, 85-95.	1.8	21
61	On the current status of <i>Phakopsora pachyrhizi</i> genome sequencing. <i>Frontiers in Plant Science</i> , 2014, 5, 377.	1.7	21
62	Genomic Patterns of Positive Selection at the Origin of Rust Fungi. <i>PLoS ONE</i> , 2015, 10, e0143959.	1.1	20
63	Using Formal Concept Analysis for the Extraction of Groups of Co-expressed Genes. <i>Communications in Computer and Information Science</i> , 2008, , 439-449.	0.4	20
64	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
65	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
66	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
67	Computational Methods for Predicting Effectors in Rust Pathogens. <i>Methods in Molecular Biology</i> , 2017, 1659, 73-83.	0.4	19
68	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
69	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
70	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
71	More complexity in the mycorrhizal world. <i>New Phytologist</i> , 2006, 172, 600-604.	3.5	11
72	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

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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 RMIp7 resistance breakdown. <i>Molecular Ecology</i> , 2023, 32, 2472-2483.	2.0	10
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	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
76	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
77	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
78	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
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> . <i>Applied and Environmental Microbiology</i> , 2002, 68, 5788-5788.	1.4	4
81	12 Rust Fungi: Achievements and Future Challenges on Genomics and Host-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. <i>Frontiers in Agronomy</i> , 0, 4, .	1.5	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. <i>Fungal Genetics and Biology</i> , 2022, , 103698.	0.9	0