

Francis Martin

List of Publications by Year in descending order

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109
papers

14,044
citations

34105

52
h-index

28297

105
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146
all docs

146
docs citations

146
times ranked

11432
citing authors

#	ARTICLE	IF	CITATIONS
1	The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 2012, 336, 1715-1719.	12.6	1,424
2	Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 2015, 47, 410-415.	21.4	870
3	Genome of an arbuscular mycorrhizal fungus provides insight into the oldest plant symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20117-20122.	7.1	717
4	PÃ©rigord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. <i>Nature</i> , 2010, 464, 1033-1038.	27.8	641
5	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.	7.1	640
6	Extensive sampling of basidiomycete genomes demonstrates inadequacy of the white-rot/brown-rot paradigm for wood decay fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9923-9928.	7.1	595
7	The Plant Cell Wallâ€Decomposing Machinery Underlies the Functional Diversity of Forest Fungi. <i>Science</i> , 2011, 333, 762-765.	12.6	512
8	A Secreted Effector Protein of <i>Laccaria bicolor</i> Is Required for Symbiosis Development. <i>Current Biology</i> , 2011, 21, 1197-1203.	3.9	447
9	Insights into evolution of multicellular fungi from the assembled chromosomes of the mushroom <i>Coprinopsis cinerea</i> (<i>Coprinus cinereus</i>). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 11889-11894.	7.1	389
10	Endophytic Life Strategies Decoded by Genome and Transcriptome Analyses of the Mutualistic Root Symbiont <i>Piriformospora indica</i> . <i>PLoS Pathogens</i> , 2011, 7, e1002290.	4.7	361
11	Genome sequence of the button mushroom <i>Agaricus bisporus</i> reveals mechanisms governing adaptation to a humic-rich ecological niche. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17501-17506.	7.1	359
12	Effector MiSSP7 of the mutualistic fungus <i>Laccaria bicolor</i> stabilizes the <i>Populus</i> JAZ6 protein and represses jasmonic acid (JA) responsive genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8299-8304.	7.1	329
13	Unearthing the roots of ectomycorrhizal symbioses. <i>Nature Reviews Microbiology</i> , 2016, 14, 760-773.	28.6	317
14	Pyrosequencing reveals a contrasted bacterial diversity between oak rhizosphere and surrounding soil. <i>Environmental Microbiology Reports</i> , 2010, 2, 281-288.	2.4	309
15	Ectomycorrhizal fungi decompose soil organic matter using oxidative mechanisms adapted from saprotrophic ancestors. <i>New Phytologist</i> , 2016, 209, 1705-1719.	7.3	264
16	Ectomycorrhizal <i>Cortinarius</i> species participate in enzymatic oxidation of humus in northern forest ecosystems. <i>New Phytologist</i> , 2014, 203, 245-256.	7.3	256
17	The Ectomycorrhizal Fungus <i>Laccaria bicolor</i> Stimulates Lateral Root Formation in Poplar and <i>Arabidopsis</i> through Auxin Transport and Signaling. <i>Plant Physiology</i> , 2009, 151, 1991-2005.	4.8	244
18	High intraspecific genome diversity in the model arbuscular mycorrhizal symbiont <i>Rhizophagus irregularis</i> . <i>New Phytologist</i> , 2018, 220, 1161-1171.	7.3	206

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19	Involvement of auxin pathways in modulating root architecture during beneficial plant-microorganism interactions. <i>Plant, Cell and Environment</i> , 2013, 36, 909-919.	5.7	192
20	The Fungal Tree of Life: from Molecular Systematics to Genome-Scale Phylogenies. <i>Microbiology Spectrum</i> , 2017, 5, .	3.0	169
21	Blurred boundaries: lifestyle lessons from ectomycorrhizal fungal genomes. <i>Trends in Genetics</i> , 2011, 27, 14-22.	6.7	165
22	Genome-based estimates of fungal rDNA copy number variation across phylogenetic scales and ecological lifestyles. <i>Molecular Ecology</i> , 2019, 28, 721-730.	3.9	163
23	The importance of individuals: intraspecific diversity of mycorrhizal plants and fungi in ecosystems. <i>New Phytologist</i> , 2012, 194, 614-628.	7.3	157
24	Polymorphism at the ribosomal DNA ITS and its relation to postglacial recolonization routes of the Perigord truffle <i>Tuber melanosporum</i> . <i>New Phytologist</i> , 2004, 164, 401-411.	7.3	153
25	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.	2.6	150
26	Functional Assays and Metagenomic Analyses Reveals Differences between the Microbial Communities Inhabiting the Soil Horizons of a Norway Spruce Plantation. <i>PLoS ONE</i> , 2013, 8, e55929.	2.5	147
27	Fungal and plant gene expression in the <i>Tulasnella calospora</i> - <i>Serapias vomeracea</i> symbiosis provides clues about nitrogen pathways in orchid mycorrhizas. <i>New Phytologist</i> , 2017, 213, 365-379.	7.3	125
28	Functional guild classification predicts the enzymatic role of fungi in litter and soil biogeochemistry. <i>Soil Biology and Biochemistry</i> , 2015, 88, 441-456.	8.8	121
29	Isolation and characterization of <i>MAT</i> genes in the symbiotic ascomycete <i>Tuber melanosporum</i> . <i>New Phytologist</i> , 2011, 189, 710-722.	7.3	108
30	<i>Tuber melanosporum</i> : mating type distribution in a natural plantation and dynamics of strains of different mating types on the roots of nursery-inoculated host plants. <i>New Phytologist</i> , 2011, 189, 723-735.	7.3	104
31	The lichen symbiosis re-viewed through the genomes of <i>Cladonia grayi</i> and its algal partner <i>Asterochloris glomerata</i> . <i>BMC Genomics</i> , 2019, 20, 605.	2.8	98
32	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.	5.7	97
33	The <i>Laccaria</i> genome: a symbiont blueprint decoded. <i>New Phytologist</i> , 2008, 180, 296-310.	7.3	92
34	The genome of the white-rot fungus <i>Pycnoporus cinnabarinus</i> : a basidiomycete model with a versatile arsenal for lignocellulosic biomass breakdown. <i>BMC Genomics</i> , 2014, 15, 486.	2.8	91
35	Ethylene and jasmonic acid act as negative modulators during mutualistic symbiosis between <i>Laccaria bicolor</i> and <i>Populus</i> roots. <i>New Phytologist</i> , 2014, 202, 270-286.	7.3	87
36	Reconsidering mutualistic plant-fungal interactions through the lens of effector biology. <i>Current Opinion in Plant Biology</i> , 2015, 26, 45-50.	7.1	87

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37	Fine-scale spatial genetic structure of the black truffle (<i>Tuber melanosporum</i>) investigated with neutral microsatellites and functional mating type genes. <i>New Phytologist</i> , 2013, 199, 176-187.	7.3	83
38	The Mutualist <i>Laccaria bicolor</i> Expresses a Core Gene Regulon During the Colonization of Diverse Host Plants and a Variable Regulon to Counteract Host-Specific Defenses. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 261-273.	2.6	82
39	Genomic and transcriptomic analysis of <i>Laccaria bicolor</i> CAZome reveals insights into polysaccharides remodelling during symbiosis establishment. <i>Fungal Genetics and Biology</i> , 2014, 72, 168-181.	2.1	81
40	<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.	2.6	80
41	Comparative genomics, proteomics and transcriptomics give new insight into the exoproteome of the basidiomycete <i>Hyaloscypha cylindrospora</i> and its involvement in ectomycorrhizal symbiosis. <i>New Phytologist</i> , 2015, 208, 1169-1187.	7.3	78
42	Genomic Analysis Enlightens Agaricales Lifestyle Evolution and Increasing Peroxidase Diversity. <i>Molecular Biology and Evolution</i> , 2021, 38, 1428-1446.	8.9	72
43	Development of the Poplar- <i>Laccaria bicolor</i> Ectomycorrhiza Modifies Root Auxin Metabolism, Signaling, and Response. <i>Plant Physiology</i> , 2015, 169, 890-902.	4.8	70
44	<i>Populus trichocarpa</i> and <i>Populus deltoides</i> Exhibit Different Metabolomic Responses to Colonization by the Symbiotic Fungus <i>Laccaria bicolor</i> . <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 546-556.	2.6	69
45	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.	3.8	68
46	Non-exhaustive DNA methylation-mediated transposon silencing in the black truffle genome, a complex fungal genome with massive repeat element content. <i>Genome Biology</i> , 2014, 15, 411.	8.8	67
47	A fungal family of lytic polysaccharide monoxygenase-like copper proteins. <i>Nature Chemical Biology</i> , 2020, 16, 345-350.	8.0	63
48	Laser microdissection and microarray analysis of <i>Tuber melanosporum</i> ectomycorrhizas reveal functional heterogeneity between mantle and Hartig net compartments. <i>Environmental Microbiology</i> , 2013, 15, 1853-1869.	3.8	62
49	Certainties and uncertainties about the life cycle of the Périgord black truffle (<i>Tuber melanosporum</i>) Tj ETQq1 1 0.784314 16 BT / Ove 2.0 69	2.0	69
50	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.	2.5	57
51	Microbe-Independent Entry of Oomycete RxLR Effectors and Fungal RxLR-Like Effectors Into Plant and Animal Cells Is Specific and Reproducible. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 611-616.	2.6	57
52	Genome-wide inventory of metal homeostasis-related gene products including a functional phytochelatin synthase in the hypogeous mycorrhizal fungus <i>Tuber melanosporum</i> . <i>Fungal Genetics and Biology</i> , 2011, 48, 573-584.	2.1	56
53	On the road to understanding truffles in the underground. <i>Fungal Genetics and Biology</i> , 2011, 48, 555-560.	2.1	54
54	Extreme diversification of the mating type <i>h</i> high-mobility group (<i>MATA</i> / <i>HMG</i>) gene family in a plant-associated arbuscular mycorrhizal fungus. <i>New Phytologist</i> , 2014, 201, 254-268.	7.3	53

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55	Fungal Endophytes of <i>Populus trichocarpa</i> Alter Host Phenotype, Gene Expression, and Rhizobiome Composition. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 853-864.	2.6	52
56	The ectomycorrhizal basidiomycete <i>Laccaria bicolor</i> releases a secreted Î²-1,4 endoglucanase that plays a key role in symbiosis development. <i>New Phytologist</i> , 2018, 220, 1309-1321.	7.3	49
57	Secretome of the Free-living Mycelium from the Ectomycorrhizal Basidiomycete <i>Laccaria bicolor</i> . <i>Journal of Proteome Research</i> , 2012, 11, 157-171.	3.7	47
58	Phylogenetic, genomic organization and expression analysis of hydrophobin genes in the ectomycorrhizal basidiomycete <i>Laccaria bicolor</i> . <i>Fungal Genetics and Biology</i> , 2012, 49, 199-209.	2.1	47
59	The Perigord black truffle responds to cold temperature with an extensive reprogramming of its transcriptional activity. <i>Fungal Genetics and Biology</i> , 2011, 48, 585-591.	2.1	45
60	Gene family expansions and transcriptome signatures uncover fungal adaptations to wood decay. <i>Environmental Microbiology</i> , 2021, 23, 5716-5732.	3.8	44
61	Poplar root exudates contain compounds that induce the expression of MiSSP7 in <i>Laccaria bicolor</i> . <i>Plant Signaling and Behavior</i> , 2012, 7, 12-15.	2.4	43
62	The effect of elevated carbon dioxide on the interaction between <i>Eucalyptus grandis</i> and diverse isolates of <i>Pisolithus</i> sp. is associated with a complex shift in the root transcriptome. <i>New Phytologist</i> , 2015, 206, 1423-1436.	7.3	43
63	Mutualistic interactions on a knife-edge between saprotrophy and pathogenesis. <i>Current Opinion in Plant Biology</i> , 2011, 14, 444-450.	7.1	42
64	The Identification of Phytohormone Receptor Homologs in Early Diverging Fungi Suggests a Role for Plant Sensing in Land Colonization by Fungi. <i>MBio</i> , 2017, 8, .	4.1	41
65	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.	4.2	38
66	Survey and analysis of simple sequence repeats in the <i>Laccaria bicolor</i> genome, with development of microsatellite markers. <i>Current Genetics</i> , 2011, 57, 75-88.	1.7	38
67	Characterization of Transposable Elements in the Ectomycorrhizal Fungus <i>Laccaria bicolor</i> . <i>PLoS ONE</i> , 2012, 7, e40197.	2.5	38
68	<i>Populus trichocarpa</i> encodes small, effector-like secreted proteins that are highly induced during mutualistic symbiosis. <i>Scientific Reports</i> , 2017, 7, 382.	3.3	36
69	Genome-wide search and functional identification of transcription factors in the mycorrhizal fungus <i>Tuber melanosporum</i> . <i>New Phytologist</i> , 2011, 189, 736-750.	7.3	35
70	Carbohydrate utilization and metabolism is highly differentiated in <i>Agaricus bisporus</i> . <i>BMC Genomics</i> , 2013, 14, 663.	2.8	35
71	Metagenome sequence of <i>Eucalyptus</i> from sporocarp tissue reveals Ascomycota ectomycorrhizal fingerprints of genome expansion and a Proteobacteria-rich microbiome. <i>Environmental Microbiology</i> , 2015, 17, 2952-2968.	3.8	34
72	Five years investigation of female and male genotypes in pÃ©rigord black truffle (<i>Tuber</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 67 Td <i>Microbiology</i> , 2017, 19, 2604-2615.	3.8	33

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73	Fungal ecological strategies reflected in gene transcription – a case study of two litter decomposers. <i>Environmental Microbiology</i> , 2020, 22, 1089-1103.	3.8	32
74	Genome-wide analysis of cell wall-related genes in <i>Tuber melanosporum</i> . <i>Current Genetics</i> , 2012, 58, 165-177.	1.7	30
75	An ectomycorrhizal fungus alters sensitivity to jasmonate, salicylate, gibberellin, and ethylene in host roots. <i>Plant, Cell and Environment</i> , 2020, 43, 1047-1068.	5.7	30
76	Fine-scale genetic structure of natural <i>Tuber aestivum</i> sites in southern Germany. <i>Mycorrhiza</i> , 2016, 26, 895-907.	2.8	27
77	Study of nitrogen and carbon transfer from soil organic matter to <i>Tuber melanosporum</i> mycorrhizas and ascocarps using ¹⁵ N and ¹³ C soil labelling and whole-genome oligoarrays. <i>Plant and Soil</i> , 2015, 395, 351-373.	3.7	26
78	Community genetics in the time of next-generation molecular technologies. <i>Molecular Ecology</i> , 2013, 22, 3198-3207.	3.9	25
79	The Fungal Tree of Life: From Molecular Systematics to Genome-Scale Phylogenies. , 2017, , 1-34.		25
80	Understanding plant cell-wall remodelling during the symbiotic interaction between <i>Tuber melanosporum</i> and <i>Corylus avellana</i> using a carbohydrate microarray. <i>Planta</i> , 2016, 244, 347-359.	3.2	24
81	Secretome Analysis from the Ectomycorrhizal Ascomycete <i>Cenococcum geophilum</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 141.	3.5	24
82	Multi-omic Analyses of Extensively Decayed <i>Pinus contorta</i> Reveal Expression of a Diverse Array of Lignocellulose-Degrading Enzymes. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	24
83	Mycorrhizal effector PaMiSSP10b alters polyamine biosynthesis in <i>Eucalyptus</i> root cells and promotes root colonization. <i>New Phytologist</i> , 2020, 228, 712-727.	7.3	24
84	The ectomycorrhizal basidiomycete <i>Hebeloma cylindrosporum</i> undergoes early waves of transcriptional reprogramming prior to symbiotic structures differentiation. <i>Environmental Microbiology</i> , 2017, 19, 1338-1354.	3.8	22
85	The mutualism effector MiSSP7 of <i>Laccaria bicolor</i> alters the interactions between the poplar JAZ6 protein and its associated proteins. <i>Scientific Reports</i> , 2020, 10, 20362.	3.3	21
86	C-STABILITY an innovative modeling framework to leverage the continuous representation of organic matter. <i>Nature Communications</i> , 2021, 12, 810.	12.8	21
87	Diversity and evolution of ABC proteins in mycorrhiza-forming fungi. <i>BMC Evolutionary Biology</i> , 2015, 15, 249.	3.2	19
88	A survey of genome-wide single nucleotide polymorphisms through genome resequencing in the Périgord black truffle (<i>Tuber melanosporum</i> Vittad.). <i>Molecular Ecology Resources</i> , 2015, 15, 1243-1255.	4.8	18
89	Broad-specificity GH131 β -glucanases are a hallmark of fungi and oomycetes that colonize plants. <i>Environmental Microbiology</i> , 2019, 21, 2724-2739.	3.8	18
90	Genome sequencing of <i>Rigidoporus microporus</i> provides insights on genes important for wood decay, latex tolerance and interspecific fungal interactions. <i>Scientific Reports</i> , 2020, 10, 5250.	3.3	16

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91	The ectomycorrhizal basidiomycete <i>Laccaria bicolor</i> releases a GH28 polygalacturonase that plays a key role in symbiosis establishment. <i>New Phytologist</i> , 2022, 233, 2534-2547.	7.3	16
92	Intra-species genetic variability drives carbon metabolism and symbiotic host interactions in the ectomycorrhizal fungus <i>Pisolithus microcarpus</i> . <i>Environmental Microbiology</i> , 2021, 23, 2004-2020.	3.8	14
93	Genomics of Arbuscular Mycorrhizal Fungi. <i>Advances in Botanical Research</i> , 2014, 70, 259-290.	1.1	13
94	Unearthing the truffle genome. <i>New Phytologist</i> , 2011, 189, 645-646.	7.3	12
95	The <i>Wolfiporia cocos</i> Genome and Transcriptome Shed Light on the Formation of Its Edible and Medicinal Sclerotium. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 455-467.	6.9	11
96	A Transcriptomic Atlas of the Ectomycorrhizal Fungus <i>Laccaria bicolor</i> . <i>Microorganisms</i> , 2021, 9, 2612.	3.6	11
97	A Viable New Strategy for the Discovery of Peptide Proteolytic Cleavage Products in Plant-Microbe Interactions. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1177-1188.	2.6	8
98	Reconstructing the evolutionary history of gypsy retrotransposons in the Périgord black truffle (<i>Tuber melanosporum</i> Vittad.). <i>Mycorrhiza</i> , 2016, 26, 553-563.	2.8	7
99	Contrasting demographic histories revealed in two invasive populations of the dry rot fungus <i>Serpula lacrymans</i> . <i>Molecular Ecology</i> , 2021, 30, 2772-2789.	3.9	6
100	Cryptic genetic structure and copy number variation in the ubiquitous forest symbiotic fungus <i>Cenococcum geophilum</i> . <i>Environmental Microbiology</i> , 2021, 23, 6536-6556.	3.8	5
101	Communication Between Plant, Ectomycorrhizal Fungi and Helper Bacteria. , 2012, , 229-247.		4
102	The transcriptional landscape of basidiosporogenesis in mature <i>Pisolithus microcarpus</i> basidiocarp. <i>BMC Genomics</i> , 2017, 18, 157.	2.8	3
103	Molecular Signalling During the Ectomycorrhizal Symbiosis. , 2019, , 95-109.		3
104	Draft Genome Sequence of the Ectomycorrhizal Ascomycete <i>Sphaerospora brunnea</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	3
105	Heterospecific Neighbor Plants Impact Root Microbiome Diversity and Molecular Function of Root Fungi. <i>Frontiers in Microbiology</i> , 2021, 12, 680267.	3.5	3
106	Truffle Genomics: Investigating an Early Diverging Lineage of Pezizomycotina. <i>Soil Biology</i> , 2016, , 137-149.	0.8	2
107	Mycorrhiza-induced mycocypins of <i>Laccaria bicolor</i> are potent protease inhibitors with nematotoxic and collembola antifeedant activity. <i>Environmental Microbiology</i> , 2022, 24, 4607-4622.	3.8	2
108	10 New Insights into Ectomycorrhizal Symbiosis Evolution and Function. , 2013, , 273-293.		1

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109	Genomics and Spectroscopy Provide Novel Insights into the Mechanisms of Litter Decomposition and Nitrogen Assimilation by Ectomycorrhizal Fungi. <i>Soil Biology</i> , 2013, , 191-211.	0.8	0