

Claude Murat

List of Publications by Year in descending order

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Version: 2024-02-01

78
papers

10,589
citations

101384

36
h-index

64668

79
g-index

82
all docs

82
docs citations

82
times ranked

9772
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.	6.0	1,424
2	454 Pyrosequencing analyses of forest soils reveal an unexpectedly high fungal diversity. <i>New Phytologist</i> , 2009, 184, 449-456.	3.5	908
3	Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 2015, 47, 410-415.	9.4	870
4	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.	3.3	717
5	Perigord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. <i>Nature</i> , 2010, 464, 1033-1038.	13.7	641
6	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
7	The Plant Cell Wall's Decomposing Machinery Underlies the Functional Diversity of Forest Fungi. <i>Science</i> , 2011, 333, 762-765.	6.0	512
8	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.	2.1	361
9	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.	3.3	359
10	Unearthing the roots of ectomycorrhizal symbioses. <i>Nature Reviews Microbiology</i> , 2016, 14, 760-773.	13.6	317
11	Pyrosequencing reveals a contrasted bacterial diversity between oak rhizosphere and surrounding soil. <i>Environmental Microbiology Reports</i> , 2010, 2, 281-288.	1.0	309
12	Large-scale genome sequencing of mycorrhizal fungi provides insights into the early evolution of symbiotic traits. <i>Nature Communications</i> , 2020, 11, 5125.	5.8	258
13	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
14	Comparative genomics and transcriptomics depict ericoid mycorrhizal fungi as versatile saprotrophs and plant mutualists. <i>New Phytologist</i> , 2018, 217, 1213-1229.	3.5	185
15	Truffles: much more than a prized and local fungal delicacy. <i>FEMS Microbiology Letters</i> , 2006, 260, 1-8.	0.7	177
16	Historical Biogeography and Diversification of Truffles in the Tuberales and Their Newly Identified Southern Hemisphere Sister Lineage. <i>PLoS ONE</i> , 2013, 8, e52765.	1.1	175
17	Ectomycorrhizal ecology is imprinted in the genome of the dominant symbiotic fungus <i>Cenococcum geophilum</i> . <i>Nature Communications</i> , 2016, 7, 12662.	5.8	156
18	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.	3.5	153

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19	ITS-1 versus ITS-2 pyrosequencing: a comparison of fungal populations in truffle grounds. <i>Mycologia</i> , 2011, 103, 1184-1193.	0.8	135
20	Molecular phylogeny and historical biogeography of the genus <i>Tuber</i> , the "true truffles". <i>Journal of Biogeography</i> , 2008, 35, 815-829.	1.4	117
21	Morphological and molecular typing of the below-ground fungal community in a natural <i>Tuber magnatum</i> truffle-ground. <i>FEMS Microbiology Letters</i> , 2005, 245, 307-313.	0.7	115
22	Pezizomycetes genomes reveal the molecular basis of ectomycorrhizal truffle lifestyle. <i>Nature Ecology and Evolution</i> , 2018, 2, 1956-1965.	3.4	95
23	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.	1.2	91
24	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.	3.5	83
25	454 Pyrosequencing Analysis of Fungal Assemblages from Geographically Distant, Disparate Soils Reveals Spatial Patterning and a Core Mycobiome. <i>Diversity</i> , 2013, 5, 73-98.	0.7	82
26	Gene expression in mycorrhizal orchid protocorms suggests a friendly plant-fungus relationship. <i>Planta</i> , 2014, 239, 1337-1349.	1.6	79
27	Forty years of inoculating seedlings with truffle fungi: past and future perspectives. <i>Mycorrhiza</i> , 2015, 25, 77-81.	1.3	71
28	Below-ground fine-scale distribution and soil versus fine root detection of fungal and soil oomycete communities in a French beech forest. <i>Fungal Ecology</i> , 2013, 6, 223-235.	0.7	69
29	Distribution and localization of microsatellites in the Perigord black truffle genome and identification of new molecular markers. <i>Fungal Genetics and Biology</i> , 2011, 48, 592-601.	0.9	67
30	<i>Tuber magnatum</i> Pico, a species of limited geographical distribution: its genetic diversity inside and outside a truffle ground. <i>Environmental Microbiology</i> , 2005, 7, 55-65.	1.8	63
31	Is the Perigord black truffle threatened by an invasive species? We dreaded it and it has happened!. <i>New Phytologist</i> , 2008, 178, 699-702.	3.5	63
32	Certainties and uncertainties about the life cycle of the Perigord black truffle (<i>Tuber melanosporum</i>) <i>Trends in Microbiology</i> , 2007, 15, 100-108.	0.8	61
33	Phylogenetic and populational study of the <i>Tuber indicum</i> complex. <i>Mycological Research</i> , 2006, 110, 1034-1045.	2.5	60
34	Soil analysis reveals the presence of an extended mycelial network in a <i>Tuber magnatum</i> truffle-ground. <i>FEMS Microbiology Ecology</i> , 2010, 71, 43-49.	1.3	52
35	Two ectomycorrhizal truffles, <i>Tuber melanosporum</i> and <i>T. aestivum</i> , endophytically colonise roots of non-ectomycorrhizal plants in natural environments. <i>New Phytologist</i> , 2020, 225, 2542-2556.	3.5	50
36	Climatic variations explain annual fluctuations in French Perigord black truffle wholesale markets but do not explain the decrease in black truffle production over the last 48 years. <i>Mycorrhiza</i> , 2014, 24, 115-125.	1.3	47

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37	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.	0.8	38
38	Characterization of Transposable Elements in the Ectomycorrhizal Fungus <i>Laccaria bicolor</i> . <i>PLoS ONE</i> , 2012, 7, e40197.	1.1	38
39	Genome-wide survey of repetitive DNA elements in the button mushroom <i>Agaricus bisporus</i> . <i>Fungal Genetics and Biology</i> , 2013, 55, 6-21.	0.9	37
40	Fine-scale spatial genetic structure analysis of the black truffle <i>Tuber aestivum</i> and its link to aroma variability. <i>Environmental Microbiology</i> , 2015, 17, 3039-3050.	1.8	36
41	Imaging mycorrhizal fungal transformants that express EGFP during ericoid endosymbiosis. <i>Current Genetics</i> , 2007, 52, 65-75.	0.8	35
42	Wild and cultivated mushrooms as a model of sustainable development. <i>Plant Biosystems</i> , 2013, 147, 226-236.	0.8	34
43	Five years investigation of female and male genotypes in Périgord black truffle (<i>Tuber</i> Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tj 5 Microbiology, 2017, 19, 2604-2615.	1.8	33
44	Phylogenetic relationships between <i>Tuber pseudoexcavatum</i> , a Chinese truffle, and other <i>Tuber</i> species based on parsimony and distance analysis of four different gene sequences. <i>FEMS Microbiology Letters</i> , 2006, 259, 269-281.	0.7	32
45	Cu,Zn superoxide dismutase and zinc stress in the metal-tolerant ericoid mycorrhizal fungus <i>Oidiodendron maius</i> Zn. <i>FEMS Microbiology Letters</i> , 2009, 293, 48-57.	0.7	31
46	Identification of Internal Transcribed Spacer Sequence Motifs in Truffles: a First Step toward Their DNA Bar Coding. <i>Applied and Environmental Microbiology</i> , 2007, 73, 5320-5330.	1.4	28
47	Fine-scale genetic structure of natural <i>Tuber aestivum</i> sites in southern Germany. <i>Mycorrhiza</i> , 2016, 26, 895-907.	1.3	27
48	Fungal Diversity Is Not Determined by Mineral and Chemical Differences in Serpentine Substrates. <i>PLoS ONE</i> , 2012, 7, e44233.	1.1	27
49	New Insights into the Complex Relationship between Weight and Maturity of Burgundy Truffles (<i>Tuber</i> Tj ETQq1 1,0,784314,rgBT / O Microbiology, 2017, 19, 2604-2615.	1.1	27
50	PCR primers specific for the genus <i>Tuber</i> reveal the presence of several truffle species in a truffle-ground. <i>FEMS Microbiology Letters</i> , 2009, 297, 67-72.	0.7	23
51	Phylogenetic affiliation of the desert truffles <i>Picoa juniperi</i> and <i>Picoa lefebvrei</i> . <i>Antonie Van Leeuwenhoek</i> , 2010, 98, 429-436.	0.7	20
52	Truffle Phylogenomics. <i>Advances in Botanical Research</i> , 2014, , 211-234.	0.5	20
53	Draft Genome Sequence of <i>Tuber borchii</i> Vittad., a Whitish Edible Truffle. <i>Genome Announcements</i> , 2018, 6, .	0.8	20
54	Influence of annual climatic variations, climate changes, and sociological factors on the production of the Périgord black truffle (<i>Tuber melanosporum</i> Vittad.) from 1903–1904 to 1988–1989 in the Vaucluse (France). <i>Mycorrhiza</i> , 2019, 29, 113-125.	1.3	20

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55	An improved method compatible with metagenomic analyses to extract genomic DNA from soils in <i>Tuber melanosporum</i> orchards. <i>Journal of Applied Microbiology</i> , 2013, 115, 163-170.	1.4	19
56	First production of Italian white truffle (<i>Tuber magnatum</i> Pico) ascocarps in an orchard outside its natural range distribution in France. <i>Mycorrhiza</i> , 2021, 31, 383-388.	1.3	19
57	Sex and truffles: first evidence of Perigord black truffle outcrosses. <i>New Phytologist</i> , 2008, 180, 260-263.	3.5	18
58	Beech roots are simultaneously colonized by multiple genets of the ectomycorrhizal fungus <i>Laccaria amethystina</i> clustered in two genetic groups. <i>Molecular Ecology</i> , 2012, 21, 2116-2129.	2.0	18
59	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.	2.2	18
60	SSR-based identification of genetic groups within European populations of <i>Tuber aestivum</i> Vittad. <i>Mycorrhiza</i> , 2016, 26, 99-110.	1.3	17
61	Diversity and Structure of Fungal Communities in Neotropical Rainforest Soils: The Effect of Host Recurrence. <i>Microbial Ecology</i> , 2017, 73, 310-320.	1.4	17
62	Modulation of Plant and Fungal Gene Expression Upon Cd Exposure and Symbiosis in Ericoid Mycorrhizal <i>Vaccinium myrtillus</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 341.	1.5	17
63	<i>Trichocybe</i> , a new genus for <i>Clitocybe puberula</i> (Agaricomycetes, Agaricales). <i>Fungal Diversity</i> , 2010, 42, 97-105.	4.7	16
64	First Identification of Polymorphic Microsatellite Markers in the Burgundy Truffle, <i>Tuber aestivum</i> (Tuberaceae). <i>Applications in Plant Sciences</i> , 2013, 1, 1200220.	0.8	16
65	Ascoma genotyping and mating type analyses of mycorrhizas and soil mycelia of <i>Tuber borchii</i> in a truffle orchard established by mycelial inoculated plants. <i>Environmental Microbiology</i> , 2020, 22, 964-975.	1.8	16
66	Specific regions in the <i>Sod1</i> locus of the ericoid mycorrhizal fungus <i>Oidiodendron maius</i> from metal-enriched soils show a different sequence polymorphism. <i>FEMS Microbiology Ecology</i> , 2011, 75, 321-331.	1.3	15
67	The Black Truffles <i>Tuber melanosporum</i> and <i>Tuber indicum</i> . <i>Soil Biology</i> , 2016, , 19-32.	0.6	13
68	Soil temperature and hydric potential influences the monthly variations of soil <i>Tuber aestivum</i> DNA in a highly productive orchard. <i>Scientific Reports</i> , 2019, 9, 12964.	1.6	11
69	New insights into black truffle biology: discovery of the potential connecting structure between a <i>Tuber aestivum</i> ascocarp and its host root. <i>Mycorrhiza</i> , 2019, 29, 219-226.	1.3	9
70	Reconstructing the evolutionary history of gypsy retrotransposons in the Périgord black truffle (<i>Tuber melanosporum</i> Vittad.). <i>Mycorrhiza</i> , 2016, 26, 553-563.	1.3	7
71	Draft Genome Sequences of the Black Truffles <i>Tuber brumale</i> Vittad. and <i>Tuber indicum</i> Cook & Masee. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	7
72	Frequency of the two mating types in the soil under productive and non-productive trees in five French orchards of the Périgord black truffle (<i>Tuber melanosporum</i> Vittad.). <i>Mycorrhiza</i> , 2021, 31, 361-369.	1.3	7

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73	Genomic suppression subtractive hybridization as a tool to identify differences in mycorrhizal fungal genomes. <i>FEMS Microbiology Letters</i> , 2011, 318, 115-122.	0.7	6
74	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.	2.0	6
75	Correction for Morin et al., 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> , 2013, 110, 4146-4146.	3.3	4
76	Draft Genome Sequence of the Ectomycorrhizal Ascomycete <i>Sphaerospora brunnea</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
77	Truffle Genomics: Investigating an Early Diverging Lineage of Pezizomycotina. <i>Soil Biology</i> , 2016, , 137-149.	0.6	2
78	Identification and In Situ Distribution of a Fungal Gene Marker: The Mating Type Genes of the Black Truffle. <i>Methods in Molecular Biology</i> , 2016, 1399, 141-149.	0.4	1