

Annegret Kohler

List of Publications by Year in descending order

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91
papers

11,058
citations

61984

43
h-index

45317

90
g-index

100
all docs

100
docs citations

100
times ranked

9636
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolutionary innovations through gain and loss of genes in the ectomycorrhizal Boletales. <i>New Phytologist</i> , 2022, 233, 1383-1400.	7.3	19
2	Evolutionary transition to the ectomycorrhizal habit in the genomes of a hyperdiverse lineage of mushroom-forming fungi. <i>New Phytologist</i> , 2022, 233, 2294-2309.	7.3	21
3	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
4	Molecular basis of differential adventitious rooting competence in poplar genotypes. <i>Journal of Experimental Botany</i> , 2022, 73, 4046-4064.	4.8	14
5	Comparative Transcriptomics Analysis of the Symbiotic Germination of <i>D. officinale</i> (Orchidaceae) With Emphasis on Plant Cell Wall Modification and Cell Wall-Degrading Enzymes. <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	7
6	Ectomycorrhizal Symbiosis: From Genomics to Trans-Kingdom Molecular Communication and Signaling. <i>Rhizosphere Biology</i> , 2022, , 273-296.	0.6	2
7	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
8	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
9	Desert truffle genomes reveal their reproductive modes and new insights into plant-fungal interaction and ectomycorrhizal lifestyle. <i>New Phytologist</i> , 2021, 229, 2917-2932.	7.3	19
10	Evolution of the Mode of Nutrition in Symbiotic and Saprotrophic Fungi in Forest Ecosystems. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2021, 52, 385-404.	8.3	26
11	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
12	Genetic determinants of endophytism in the <i>Arabidopsis</i> root mycobiome. <i>Nature Communications</i> , 2021, 12, 7227.	12.8	58
13	A Transcriptomic Atlas of the Ectomycorrhizal Fungus <i>Laccaria bicolor</i> . <i>Microorganisms</i> , 2021, 9, 2612.	3.6	11
14	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
15	Large-scale genome sequencing of mycorrhizal fungi provides insights into the early evolution of symbiotic traits. <i>Nature Communications</i> , 2020, 11, 5125.	12.8	258
16	Alterations in the phenylpropanoid pathway affect poplar ability for ectomycorrhizal colonisation and susceptibility to root-knot nematodes. <i>Mycorrhiza</i> , 2020, 30, 555-566.	2.8	9
17	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
18	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

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19	The small secreted effector protein MiSSP7.6 of <i>Laccaria bicolor</i> is required for the establishment of ectomycorrhizal symbiosis. <i>Environmental Microbiology</i> , 2020, 22, 1435-1446.	3.8	37
20	Molecular Changes Concomitant with Vascular System Development in Mature Galls Induced by Root-Knot Nematodes in the Model Tree Host <i>Populus tremula</i> – <i>P. alba</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 406.	4.1	10
21	SLZRT2 Encodes a ZIP Family Zn Transporter With Dual Localization in the Ectomycorrhizal Fungus <i>Suillus luteus</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2251.	3.5	14
22	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
23	The ectomycorrhizal basidiomycete <i>Laccaria bicolor</i> releases a secreted β -1,4 endoglucanase that plays a key role in symbiosis development. <i>New Phytologist</i> , 2018, 220, 1309-1321.	7.3	49
24	Comparative genomics and transcriptomics depict ericoid mycorrhizal fungi as versatile saprotrophs and plant mutualists. <i>New Phytologist</i> , 2018, 217, 1213-1229.	7.3	185
25	Pezizomycetes genomes reveal the molecular basis of ectomycorrhizal truffle lifestyle. <i>Nature Ecology and Evolution</i> , 2018, 2, 1956-1965.	7.8	95
26	The Hydrophobin-Like OmSSP1 May Be an Effector in the Ericoid Mycorrhizal Symbiosis. <i>Frontiers in Plant Science</i> , 2018, 9, 546.	3.6	20
27	Secretome Analysis from the Ectomycorrhizal Ascomycete <i>Cenococcum geophilum</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 141.	3.5	24
28	<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
29	The SLZRT1 Gene Encodes a Plasma Membrane-Located ZIP (Zrt-, Irt-Like Protein) Transporter in the Ectomycorrhizal Fungus <i>Suillus luteus</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2320.	3.5	24
30	Ectomycorrhizal ecology is imprinted in the genome of the dominant symbiotic fungus <i>Cenococcum geophilum</i> . <i>Nature Communications</i> , 2016, 7, 12662.	12.8	156
31	Unearthing the roots of ectomycorrhizal symbioses. <i>Nature Reviews Microbiology</i> , 2016, 14, 760-773.	28.6	317
32	Comparative genomics, proteomics and transcriptomics give new insight into the exoproteome of the basidiomycete <i>Hebeloma cylindrosporum</i> and its involvement in ectomycorrhizal symbiosis. <i>New Phytologist</i> , 2015, 208, 1169-1187.	7.3	78
33	Diversity and evolution of ABC proteins in mycorrhiza-forming fungi. <i>BMC Evolutionary Biology</i> , 2015, 15, 249.	3.2	19
34	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
35	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
36	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

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37	Study of nitrogen and carbon transfer from soil organic matter to Tuber melanosporum mycorrhizas and ascocarps using 15N and 13C soil labelling and whole-genome oligoarrays. <i>Plant and Soil</i> , 2015, 395, 351-373.	3.7	26
38	Pta<sc>RHE</sc>1, a <i>Populus tremula</i>—<i>Populus alba</i> <sc>RING</sc>â€H2 protein of the <sc>ATL</sc> family, has a regulatory role in secondary phloem fibre development. <i>Plant Journal</i> , 2015, 82, 978-990.	5.7	17
39	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
40	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
41	Expanding genomics of mycorrhizal symbiosis. <i>Frontiers in Microbiology</i> , 2014, 5, 582.	3.5	25
42	Exploring the Transcriptome of Mycorrhizal Interactions. <i>Advances in Botanical Research</i> , 2014, 70, 53-78.	1.1	8
43	Transcriptomic profiles of <sc><i>H</i></sc> <sc><i>eterobasidion annosum</i></sc> under abiotic stresses and during saprotrophic growth in bark, sapwood and heartwood. <i>Environmental Microbiology</i> , 2014, 16, 1654-1667.	3.8	19
44	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
45	Ethylene and jasmonic acid act as negative modulators during mutualistic symbiosis between <sc><i>L</i></sc><sc><i>accaria bicolor</i></sc> and <sc><i>P</i></sc><sc><i>opulus</i></sc> roots. <i>New Phytologist</i> , 2014, 202, 270-286.	7.3	87
46	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
47	Transcriptomic Responses of <i>Phanerochaete chrysosporium</i> to Oak Acetonic Extracts: Focus on a New Glutathione Transferase. <i>Applied and Environmental Microbiology</i> , 2014, 80, 6316-6327.	3.1	34
48	<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
49	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
50	Laser microdissection and microarray analysis of <sc><i>T</i></sc><sc><i>uber melanosporum</i></sc> ectomycorrhizas reveal functional heterogeneity between mantle and <sc><i>H</i></sc>artig net compartments. <i>Environmental Microbiology</i> , 2013, 15, 1853-1869.	3.8	62
51	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.	3.6	30
52	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
53	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
54	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

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55	Secretome of the Free-living Mycelium from the Ectomycorrhizal Basidiomycete <i>Laccaria bicolor</i> . Journal of Proteome Research, 2012, 11, 157-171.	3.7	47
56	Insight into trade-off between wood decay and parasitism from the genome of a fungal forest pathogen. New Phytologist, 2012, 194, 1001-1013.	7.3	210
57	Phylogenetic, genomic organization and expression analysis of hydrophobin genes in the ectomycorrhizal basidiomycete <i>Laccaria bicolor</i> . Fungal Genetics and Biology, 2012, 49, 199-209.	2.1	47
58	The <i>AINTEGUMENTA LIKE1</i> Homeotic Transcription Factor <i>PtAIL1</i> Controls the Formation of Adventitious Root Primordia in Poplar. Plant Physiology, 2012, 160, 1996-2006.	4.8	118
59	The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. Science, 2012, 336, 1715-1719.	12.6	1,424
60	Genome-wide analysis of cell wall-related genes in <i>Tuber melanosporum</i> . Current Genetics, 2012, 58, 165-177.	1.7	30
61	<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
62	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
63	The Périgord black truffle responds to cold temperature with an extensive reprogramming of its transcriptional activity. Fungal Genetics and Biology, 2011, 48, 585-591.	2.1	45
64	Genome-wide inventory of metal homeostasis-related gene products including a functional phytochelatin synthase in the hypogeous mycorrhizal fungus <i>Tuber melanosporum</i> . Fungal Genetics and Biology, 2011, 48, 573-584.	2.1	56
65	Hyphal and cytoskeleton polarization in <i>Tuber melanosporum</i> : A genomic and cellular analysis. Fungal Genetics and Biology, 2011, 48, 561-572.	2.1	16
66	Tapping Genomics to Unravel Ectomycorrhizal Symbiosis. Methods in Molecular Biology, 2011, 722, 249-281.	0.9	11
67	Genome-wide search and functional identification of transcription factors in the mycorrhizal fungus <i>Tuber melanosporum</i> . New Phytologist, 2011, 189, 736-750.	7.3	35
68	A Secreted Effector Protein of <i>Laccaria bicolor</i> Is Required for Symbiosis Development. Current Biology, 2011, 21, 1197-1203.	3.9	447
69	The Plant Cell Wall "Decomposing Machinery Underlies the Functional Diversity of Forest Fungi. Science, 2011, 333, 762-765.	12.6	512
70	Périgord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. Nature, 2010, 464, 1033-1038.	27.8	641
71	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
72	Defense and Nutrient Mutualisms in <i>Populus</i> . , 2010, , 247-277.		8

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73	The Ectomycorrhizal Fungus <i>Laccaria bicolor</i> Stimulates Lateral Root Formation in Poplar and Arabidopsis through Auxin Transport and Signaling. <i>Plant Physiology</i> , 2009, 151, 1991-2005.	4.8	244
74	Development and validation of an oligonucleotide microarray to characterise ectomycorrhizal fungal communities. <i>BMC Microbiology</i> , 2009, 9, 241.	3.3	11
75	Gene expression analysis of <i>Populus deltoides</i> roots subjected to copper stress. <i>Environmental and Experimental Botany</i> , 2009, 67, 335-344.	4.2	28
76	Fatty acid metabolism in the ectomycorrhizal fungus <i>Laccaria bicolor</i> . <i>New Phytologist</i> , 2009, 182, 950-964.	7.3	30
77	Expansion of signal pathways in the ectomycorrhizal fungus <i>Laccaria bicolor</i> – evolution of nucleotide sequences and expression patterns in families of protein kinases and RAS small GTPases. <i>New Phytologist</i> , 2009, 183, 365-379.	7.3	19
78	Genome-wide identification of NBS resistance genes in <i>Populus trichocarpa</i> . <i>Plant Molecular Biology</i> , 2008, 66, 619-636.	3.9	247
79	Comparison of the thiol-dependent antioxidant systems in the ectomycorrhizal <i>Laccaria bicolor</i> and the saprotrophic <i>Phanerochaete chrysosporium</i> . <i>New Phytologist</i> , 2008, 180, 391-407.	7.3	27
80	Gene organization of the mating type regions in the ectomycorrhizal fungus <i>Laccaria bicolor</i> reveals distinct evolution between the two mating type loci. <i>New Phytologist</i> , 2008, 180, 329-342.	7.3	59
81	A gene repertoire for nitrogen transporters in <i>Laccaria bicolor</i> . <i>New Phytologist</i> , 2008, 180, 343-364.	7.3	73
82	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.	4.8	156
83	Living in harmony in the wood underground: ectomycorrhizal genomics. <i>Current Opinion in Plant Biology</i> , 2007, 10, 204-210.	7.1	90
84	Mapping the proteome of poplar and application to the discovery of drought-stress responsive proteins. <i>Proteomics</i> , 2006, 6, 6509-6527.	2.2	155
85	Identification of Genes Differentially Expressed in Extraradical Mycelium and Ectomycorrhizal Roots during <i>Paxillus involutus</i> - <i>Betula pendula</i> Ectomycorrhizal Symbiosis. <i>Applied and Environmental Microbiology</i> , 2005, 71, 382-391.	3.1	62
86	Cloning and expression of multiple metallothioneins from hybrid poplar. <i>New Phytologist</i> , 2004, 164, 83-93.	7.3	123
87	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.	7.3	67
88	The poplar root transcriptome: analysis of 7000 expressed sequence tags. <i>FEBS Letters</i> , 2003, 542, 37-41.	2.8	89
89	Poplar Metal Tolerance Protein 1 Confers Zinc Tolerance and Is an Oligomeric Vacuolar Zinc Transporter with an Essential Leucine Zipper Motif. <i>Plant Cell</i> , 2003, 15, 2911-2928.	6.6	170
90	Transfer of hydroxycinnamoyl residues to microsomal proteins from parsley. <i>Phytochemistry</i> , 1997, 44, 225-228.	2.9	12

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91	Biosynthesis of ferulic acid esters of plant cell wall polysaccharides in endomembranes from parsley cells. FEBS Letters, 1991, 290, 209-212.	2.8	41