Peter Baldrian

List of Publications by Year
in descending order

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229 papers	22,447 citations	8181 76 h-index	10158 140 g-index
244 all docs	244 docs citations	244 times ranked	20160 citing authors

#	Article	IF	Citations
1	Fungal laccases â€“ occurrence and properties. FEMS Microbiology Reviews, 2006, 30, 215-242.	8.6	1,751
2	The Variability of the 16S rRNA Gene in Bacterial Genomes and Its Consequences for Bacterial Community Analyses. PLoS ONE, 2013, 8, e57923.	2.5	957
3	Active and total microbial communities in forest soil are largely different and highly stratified during decomposition. ISME Journal, 2012, 6, 248-258.	9.8	725
4	Degradation of cellulose by basidiomycetous fungi. FEMS Microbiology Reviews, 2008, 32, 501-521.	8.6	671
5	Fungal community on decomposing leaf litter undergoes rapid successional changes. ISME Journal, 2013, 7, 477-486.	9.8	588
6	Mycobiome diversity: high-throughput sequencing and identification of fungi. Nature Reviews Microbiology, 2019, 17, 95-109.	28.6	580
7	Interactions of heavy metals with white-rot fungi. Enzyme and Microbial Technology, 2003, 32, 78-91.	3.2	539
8	Composition of fungal and bacterial communities in forest litter and soil is largely determined by dominant trees. Soil Biology and Biochemistry, 2015, 84, 53-64.	8.8	495
9	A genomic catalog of Earthâ€™s microbiomes. Nature Biotechnology, 2021, 39, 499-509.	17.5	457
10	Forest Soil Bacteria: Diversity, Involvement in Ecosystem Processes, and Response to Global Change. Microbiology and Molecular Biology Reviews, 2017, 81, .	6.6	456
11	FungalTraits: a user-friendly traits database of fungi and fungus-like stramenopiles. Fungal Diversity, 2020, 105, 1-16.	12.3	387
12	Cellulose utilization in forest litter and soil: identification of bacterial and fungal decomposers. FEMS Microbiology Ecology, 2012, 80, 735-746.	2.7	381
13	Forest microbiome: diversity, complexity and dynamics. FEMS Microbiology Reviews, 2017, 41, fuw040.	8.6	339
14	Cellulose and hemicellulose decomposition by forest soil bacteria proceeds by the action of structurally variable enzymatic systems. Scientific Reports, 2016, 6, 25279.	3.3	328
15	Microbial activity in forest soil reflects the changes in ecosystem properties between summer and winter. Environmental Microbiology, 2016, 18, 288-301.	3.8	321
16	Seasonal dynamics of fungal communities in a temperate oak forest soil. New Phytologist, 2014, 201, 269-278.	7.3	300
17	Climate fails to predict wood decomposition at regional scales. Nature Climate Change, 2014, 4, 625-630.	18.8	281
18	Spatial variability of enzyme activities and microbial biomass in the upper layers of Quercus petraea forest soil. Soil Biology and Biochemistry, 2008, 40, 2068-2075.	8.8	264

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19	Large-scale genome sequencing of mycorrhizal fungi provides insights into the early evolution of symbiotic traits. Nature Communications, 2020, 11, 5125.	12.8	258
20	A meta-analysis of global fungal distribution reveals climate-driven patterns. Nature Communications, 2019, 10, 5142.	12.8	232
21	Responses of the extracellular enzyme activities in hardwood forest to soil temperature and seasonality and the potential effects of climate change. Soil Biology and Biochemistry, 2013, 56, 60-68.	8.8	226
22	Copper and cadmium increase laccase activity inPleurotus ostreatus. FEMS Microbiology Letters, 2002, 206, 69-74.	1.8	222
23	SEED 2: a user-friendly platform for amplicon high-throughput sequencing data analyses. Bioinformatics, 2018, 34, 2292-2294.	4.1	202
24	Biotic interactions mediate soil microbial feedbacks to climate change. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7033-7038.	7.1	201
25	Influence of Cadmium and Mercury on Activities of Ligninolytic Enzymes and Degradation of Polycyclic Aromatic Hydrocarbons by Pleurotus ostreatus in Soil. Applied and Environmental Microbiology, 2000, 66, 2471-2478.	3.1	200
26	Transformation of Quercus petraea litter: successive changes in litter chemistry are reflected in differential enzyme activity and changes in the microbial community composition. FEMS Microbiology Ecology, 2011, 75, 291-303.	2.7	198
27	Laccaseâ€catalysed oxidations of naturally occurring phenols: from <i>in vivo</i> biosynthetic pathways to green synthetic applications. Microbial Biotechnology, 2012, 5, 318-332.	4.2	193
28	Dead fungal mycelium in forest soil represents a decomposition hotspot and a habitat for a specific microbial community. New Phytologist, 2016, 210, 1369-1381.	7.3	190
29	Increase of laccase activity during interspecific interactions of white-rot fungi. FEMS Microbiology Ecology, 2004, 50, 245-253.	2.7	182
30	Insights from enzymatic degradation of cellulose and hemicellulose to fermentable sugarsâ€“ a review. Biomass and Bioenergy, 2020, 134, 105481.	5.7	172
31	Analysis of soil fungal communities by amplicon pyrosequencing: current approaches to data analysis and the introduction of the pipeline SEED. Biology and Fertility of Soils, 2013, 49, 1027-1037.	4.3	168
32	Effects of soil properties and management on the activity of soil organic matter transforming enzymes and the quantification of soil-bound and free activity. Plant and Soil, 2011, 338, 99-110.	3.7	167
33	Is the effect of trees on soil properties mediated by soil fauna? A case study from post-mining sites. Forest Ecology and Management, 2013, 309, 87-95.	3.2	161
34	Production of extracellular enzymes and degradation of biopolymers by saprotrophic microfungi from the upper layers of forest soil. Plant and Soil, 2011, 338, 111-125.	3.7	158
35	Drivers of microbial community structure in forest soils. Applied Microbiology and Biotechnology, 2018, 102, 4331-4338.	3.6	157
36	Decolorization of synthetic dyes by hydrogen peroxide with heterogeneous catalysis by mixed iron oxides. Applied Catalysis B: Environmental, 2006, 66, 258-264.	20.2	156

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37	Production of lignocellulose-degrading enzymes and degradation of leaf litter by saprotrophic basidiomycetes isolated from a Quercus petraea forest. Soil Biology and Biochemistry, 2007, 39, 2651-2660.	8.8	155
38	Purification and characterization of laccase from the white-rot fungus Daedalea quercina and decolorization of synthetic dyes by the enzyme. Applied Microbiology and Biotechnology, 2004, 63, 560-563.	3.6	154
39	Potential of Cometabolic Transformation of Polysaccharides and Lignin in Lignocellulose by Soil Actinobacteria. PLoS ONE, 2014, 9, e89108.	2.5	152
40	The active microbial diversity drives ecosystem multifunctionality and is physiologically related to carbon availability in Mediterranean semiâ€arid soils. Molecular Ecology, 2016, 25, 4660-4673.	3.9	151
41	Differential sensitivity of total and active soil microbial communities to drought and forest management. Global Change Biology, 2017, 23, 4185-4203.	9.5	150
42	Wood-inhabiting ligninolytic basidiomycetes in soils: Ecology and constraints for applicability in bioremediation. Fungal Ecology, 2008, 1, 4-12.	1.6	146
43	Estimation of fungal biomass in forest litter and soil. Fungal Ecology, 2013, 6, 1-11.	1.6	142
44	Ectomycorrhizal fungi and their enzymes in soils: is there enough evidence for their role as facultative soil saprotrophs?. Oecologia, 2009, 161, 657-660.	2.0	140
45	Purification of a new manganese peroxidase of the white-rot fungus Irpex lacteus, and degradation of polycyclic aromatic hydrocarbons by the enzyme. Research in Microbiology, 2006, 157, 248-253.	2.1	134
46	Enzyme activities and microbial biomass in topsoil layer during spontaneous succession in spoil heaps after brown coal mining. Soil Biology and Biochemistry, 2008, 40, 2107-2115.	8.8	126
47	When the forest dies: the response of forest soil fungi to a bark beetle-induced tree dieback. ISME Journal, 2014, 8, 1920-1931.	9.8	125
48	Degradation of cellulose and hemicelluloses by the brown rot fungus Piptoporus betulinus â€“ production of extracellular enzymes and characterization of the major cellulases. Microbiology (United Kingdom), 2006, 152, 3613-3622.	1.8	124
49	The contribution of insects to global forest deadwood decomposition. Nature, 2021, 597, 77-81.	27.8	123
50	Feed in summer, rest in winter: microbial carbon utilization in forest topsoil. Microbiome, 2017, 5, 122.	11.1	121
51	Back to the Future of Soil Metagenomics. Frontiers in Microbiology, 2016, 7, 73.	3.5	120
52	Distribution of microbial biomass and activity of extracellular enzymes in a hardwood forest soil reflect soil moisture content. Applied Soil Ecology, 2010, 46, 177-182.	4.3	119
53	Topâ€down control of soil fungal community composition by a globally distributed keystone consumer. Ecology, 2013, 94, 2518-2528.	3.2	119
54	Distribution of Extracellular Enzymes in Soils: Spatial Heterogeneity and Determining Factors at Various Scales. Soil Science Society of America Journal, 2014, 78, 11-18.	2.2	118

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55	Functional screening of abundant bacteria from acidic forest soil indicates the metabolic potential of Acidobacteria subdivision 1 for polysaccharide decomposition. Biology and Fertility of Soils, 2016, 52, 251-260.	4.3	116
56	Decomposer food web in a deciduous forest shows high share of generalist microorganisms and importance of microbial biomass recycling. ISME Journal, 2018, 12, 1768-1778.	9.8	116
57	The bacterial community inhabiting temperate deciduous forests is vertically stratified and undergoes seasonal dynamics. Soil Biology and Biochemistry, 2015, 87, 43-50.	8.8	112
58	Bacterial succession on decomposing leaf litter exhibits a specific occurrence pattern of cellulolytic taxa and potential decomposers of fungal mycelia. FEMS Microbiology Ecology, 2016, 92, fiw177.	2.7	110
59	Enzymatic systems involved in decomposition reflects the ecology and taxonomy of saprotrophic fungi. Fungal Ecology, 2015, 13, 10-22.	1.6	108
60	Phylogenetic composition and properties of bacteria coexisting with the fungus <i>Hypholoma fasciculare</i> in decaying wood. ISME Journal, 2009, 3, 1218-1221.	9.8	104
61	Degradation of lignocellulose by Pleurotus ostreatus in the presence of copper, manganese, lead and zinc. Research in Microbiology, 2005, 156, 670-676.	2.1	102
62	Dominant trees affect microbial community composition and activity in post-mining afforested soils. Soil Biology and Biochemistry, 2013, 56, 105-115.	8.8	101
63	Fungi associated with decomposing deadwood in a natural beech-dominated forest. Fungal Ecology, 2016, 23, 109-122.	1.6	100
64	Clearcutting alters decomposition processes and initiates complex restructuring of fungal communities in soil and tree roots. ISME Journal, 2018, 12, 692-703.	9.8	100
65	Changes in oxidative enzyme activity during interspecific mycelial interactions involving the white-rot fungus Trametes versicolor. Fungal Genetics and Biology, 2010, 47, 562-571.	2.1	98
66	Small-scale spatial heterogeneity of ecosystem properties, microbial community composition and microbial activities in a temperate mountain forest soil. FEMS Microbiology Ecology, 2016, 92, fiw185.	2.7	95
67	Pezizomycetes genomes reveal the molecular basis of ectomycorrhizal truffle lifestyle. Nature Ecology and Evolution, 2018, 2, 1956-1965.	7.8	95
68	High-throughput sequencing view on the magnitude of global fungal diversity. Fungal Diversity, 2022, 114, 539-547.	12.3	94
69	Activity and spatial distribution of lignocellulose-degrading enzymes during forest soil colonization by saprotrophic basidiomycetes. Enzyme and Microbial Technology, 2008, 43, 186-192.	3.2	92
70	Microbial activity and the dynamics of ecosystem processes in forest soils. Current Opinion in Microbiology, 2017, 37, 128-134.	5.1	92
71	GlobalFungi, a global database of fungal occurrences from high-throughput-sequencing metabarcoding studies. Scientific Data, 2020, 7, 228.	5.3	92
72	Lignocellulose degradation byPleurotus ostreatusin the presence of cadmium. FEMS Microbiology Letters, 2003, 220, 235-240.	1.8	90

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73	Differential degradation of oak (Quercus petraea) leaf litter by litter-decomposing basidiomycetes. Research in Microbiology, 2007, 158, 447-455.	2.1	90
74	Development of microbial community during primary succession in areas degraded by mining activities. Land Degradation and Development, 2017, 28, 2574-2584.	3.9	89
75	Decolorization of dyes with copper(II)/organic acid/hydrogen peroxide systems. Applied Catalysis B: Environmental, 2003, 46, 287-292.	20.2	88
76	Laccase activity in soils: Considerations for the measurement of enzyme activity. Chemosphere, 2012, 88, 1154-1160.	8.2	81
77	Chapter 2 Enzymes of saprotrophic basidiomycetes. British Mycological Society Symposia Series, 2008, 28, 19-41.	0.5	79
78	Small-scale distribution of extracellular enzymes, fungal, and bacterial biomass in Quercus petraea forest topsoil. Biology and Fertility of Soils, 2010, 46, 717-726.	4.3	77
79	Production of ligninolytic enzymes by litter-decomposing fungi and their ability to decolorize synthetic dyes. Enzyme and Microbial Technology, 2006, 39, 1023-1029.	3.2	76
80	Ecological succession reveals potential signatures of marineâ€“terrestrial transition in salt marsh fungal communities. ISME Journal, 2016, 10, 1984-1997.	9.8	76
81	Polycyclic aromatic hydrocarbons degradation and microbial community shifts during co-composting of creosote-treated wood. Journal of Hazardous Materials, 2016, 301, 17-26.	12.4	76
82	Independent effects of host and environment on the diversity of woodâ€inhabiting fungi. Journal of Ecology, 2018, 106, 1428-1442.	4.0	74
83	Drivers of yeast community composition in the litter and soil of a temperate forest. FEMS Microbiology Ecology, 2017, 93, fiw223.	2.7	73
84	Influence of iron and copper nanoparticle powder on the production of lignocellulose degrading enzymes in the fungus Trametes versicolor. Journal of Hazardous Materials, 2010, 178, 1141-1145.	12.4	72
85	Lignocellulolytic systems of soil bacteria: A vast and diverse toolbox for biotechnological conversion processes. Biotechnology Advances, 2019, 37, 107374.	11.7	71
86	Metagenomics and stable isotope probing reveal the complementary contribution of fungal and bacterial communities in the recycling of dead biomass in forest soil. Soil Biology and Biochemistry, 2020, 148, 107875.	8.8	71
87	Complementary Roles of Wood-Inhabiting Fungi and Bacteria Facilitate Deadwood Decomposition. MSystems, 2021, 6, .	3.8	71
88	Decolorization of structurally different synthetic dyes using cobalt(II)/ascorbic acid/hydrogen peroxide system. Chemosphere, 2003, 50, 975-979.	8.2	70
89	Estimation of bound and free fractions of lignocellulose-degrading enzymes of wood-rotting fungi Pleurotus ostreatus, Trametes versicolor and Piptoporus betulinus. Research in Microbiology, 2006, 157, 119-124.	2.1	70
90	Invertebrate grazing determines enzyme production by basidiomycete fungi. Soil Biology and Biochemistry, 2011, 43, 2060-2068.	8.8	67

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91	Terracidiphilus gabretensis gen. nov., sp. nov., an Abundant and Active Forest Soil Acidobacterium Important in Organic Matter Transformation. Applied and Environmental Microbiology, 2016, 82, 560-569.	3.1	67
92	Bacteria associated with decomposing dead wood in a natural temperate forest. FEMS Microbiology Ecology, 2017, 93, .	2.7	67
93	Biodegradation and detoxification of olive mill wastewater by selected strains of the mushroom genera Ganoderma and Pleurotus. Chemosphere, 2012, 88, 620-626.	8.2	66
94	The <i>rpb2</i> gene represents a viable alternative molecular marker for the analysis of environmental fungal communities. Molecular Ecology Resources, 2016, 16, 388-401.	4.8	66
95	Community-level physiological profiling analyses show potential to identify the copiotrophic bacteria present in soil environments. PLoS ONE, 2017, 12, e0171638.	2.5	66
96	Nutrient content affects the turnover of fungal biomass in forest topsoil and the composition of associated microbial communities. Soil Biology and Biochemistry, 2018, 118, 187-198.	8.8	64
97	The known and the unknown in soil microbial ecology. FEMS Microbiology Ecology, 2019, 95, .	2.7	64
98	Decolorization of textile dyes by whole cultures of Ischnoderma resinosum and by purified laccase and Mn-peroxidase. Enzyme and Microbial Technology, 2007, 40, 1673-1677.	3.2	63
99	Primary determinants of communities in deadwood vary among taxa but are regionally consistent. Oikos, 2020, 129, 1579-1588.	2.7	63
100	Intraspecific variability in growth response to cadmium of the wood-rotting fungus<i>Piptoporus betulinus</i>. Mycologia, 2002, 94, 428-436.	1.9	62
101	Dead-wood addition promotes non-saproxylic epigeal arthropods but effects are mediated by canopy openness. Biological Conservation, 2016, 204, 181-188.	4.1	61
102	Fungal bioremediation of the creosote-contaminated soil: Influence of Pleurotus ostreatus and Irpex lacteus on polycyclic aromatic hydrocarbons removal and soil microbial community composition in the laboratory-scale study. Chemosphere, 2008, 73, 1518-1523.	8.2	59
103	Effects of oak, beech and spruce on the distribution and community structure of fungi in litter and soils across a temperate forest. Soil Biology and Biochemistry, 2018, 119, 162-173.	8.8	59
104	Saprotrophic basidiomycete mycelia and their interspecific interactions affect the spatial distribution of extracellular enzymes in soil. FEMS Microbiology Ecology, 2011, 78, 80-90.	2.7	58
105	Diversity of foliar endophytes in wind-fallen Picea abies trees. Fungal Diversity, 2012, 54, 69-77.	12.3	58
106	Temperature affects the production, activity and stability of ligninolytic enzymes inPleurotus ostreatus andTrametes versicolor. Folia Microbiologica, 2007, 52, 498-502.	2.3	57
107	Bacterial communities in tetrachloroethene-polluted groundwaters: A case study. Science of the Total Environment, 2013, 454-455, 517-527.	8.0	56
108	Decoding the complete arsenal for cellulose and hemicellulose deconstruction in the highly efficient cellulose decomposer Paenibacillus O199. Biotechnology for Biofuels, 2016, 9, 104.	6.2	56

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109	A conceptual framework for understanding the biogeochemistry of dry riverbeds through the lens of soil science. Earth-Science Reviews, 2019, 188, 441-453.	9.1	54
110	Great differences in performance and outcome of high-throughput sequencing data analysis platforms for fungal metabarcoding. MycoKeys, 2018, 39, 29-40.	1.9	52
111	Fungal polysaccharide monooxygenases: new players in the decomposition of cellulose. Fungal Ecology, 2012, 5, 481-489.	1.6	51
112	Olive mill wastewater biodegradation potential of white-rot fungi â€“ Mode of action of fungal culture extracts and effects of ligninolytic enzymes. Bioresource Technology, 2015, 189, 121-130.	9.6	51
113	Development of bacterial community during spontaneous succession on spoil heaps after brown coal mining. FEMS Microbiology Ecology, 2011, 78, 59-69.	2.7	49
114	Microbial genomics, transcriptomics and proteomics: new discoveries in decomposition research using complementary methods. Applied Microbiology and Biotechnology, 2014, 98, 1531-1537.	3.6	49
115	Enzyme activities of fungi associated with Picea abies needles. Fungal Ecology, 2011, 4, 427-436.	1.6	46
116	Soil Food Web Changes during Spontaneous Succession at Post Mining Sites: A Possible Ecosystem Engineering Effect on Food Web Organization?. PLoS ONE, 2013, 8, e79694.	2.5	46
117	Seasonal variation and distribution of total and active microbial community of Î²-glucosidase encoding genes in coniferous forest soil. Soil Biology and Biochemistry, 2017, 105, 71-80.	8.8	46
118	Decolorization of synthetic dyes using a copper complex with glucaric acid. Chemosphere, 2004, 54, 291-295.	8.2	44
119	Gene family expansions and transcriptome signatures uncover fungal adaptations to wood decay. Environmental Microbiology, 2021, 23, 5716-5732.	3.8	44
120	Transformation of 14C-labelled lignin and humic substances in forest soil by the saprobic basidiomycetes Gymnopus erythropus and Hypholoma fasciculare. Soil Biology and Biochemistry, 2010, 42, 1541-1548.	8.8	43
121	Fungi associated with beetles dispersing from dead wood â€“ Let's take the beetle bus!. Fungal Ecology, 2019, 39, 100-108.	1.6	41
122	Ecology of coarse wood decomposition by the saprotrophic fungus Fomes fomentarius. Biodegradation, 2011, 22, 709-718.	3.0	40
123	Microbial expression profiles in the rhizosphere of two maize lines differing in N use efficiency. Plant and Soil, 2018, 433, 401-413.	3.7	39
124	Screening of Pleurotus ostreatus isolates for their ligninolytic properties during cultivation on natural substrates. Biodegradation, 2000, 11, 279-287.	3.0	37
125	ICP-MS determination of heavy metals in submerged cultures of wood-rotting fungi. Talanta, 2004, 62, 483-487.	5.5	37
126	Tracking of the activity of individual bacteria in temperate forest soils shows guild-specific responses to seasonality. Soil Biology and Biochemistry, 2019, 135, 275-282.	8.8	36

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127	Biosorption of cadmium to mycelial pellets of wood-rotting fungi. Biotechnology Letters, 1996, 10, 345.	0.5	34
128	Chemical composition of litter affects the growth and enzyme production by the saprotrophic basidiomycete Hypholoma fasciculare. Fungal Ecology, 2011, 4, 417-426.	1.6	34
129	Intraspecific Variability in Growth Response to Cadmium of the Wood-Rotting Fungus Piptoporus betulinus. Mycologia, 2002, 94, 428.	1.9	33
130	Ligninolytic Enzyme Production and Decolorization Capacity of Synthetic Dyes by Saprotrophic White Rot, Brown Rot, and Litter Decomposing Basidiomycetes. Journal of Fungi (Basel, Switzerland), 2020, 6, 301.	3.5	33
131	An in-depth analysis of actinobacterial communities shows their high diversity in grassland soils along a gradient of mixed heavy metal contamination. Biology and Fertility of Soils, 2015, 51, 827-837.	4.3	32
132	Silvibacterium bohemicum gen. nov. sp. nov., an acidobacterium isolated from coniferous soil in the Bohemian Forest National Park. Systematic and Applied Microbiology, 2016, 39, 14-19.	2.8	31
133	Bacteria from the endosphere and rhizosphere of Quercus spp. use mainly cell wall-associated enzymes to decompose organic matter. PLoS ONE, 2019, 14, e0214422.	2.5	31
134	Aerobic bacterial catabolism of persistent organic pollutants â€" potential impact of biotic and abiotic interaction. Current Opinion in Biotechnology, 2016, 38, 71-78.	6.6	30
135	Distinct environmental variables drive the community composition of mycorrhizal and saprotrophic fungi at the alpine treeline ecotone. Fungal Ecology, 2017, 27, 116-124.	1.6	30
136	Litter-inhabiting fungi show high level of specialization towards biopolymers composing plant and fungal biomass. Biology and Fertility of Soils, 2021, 57, 77-88.	4.3	30
137	The effect of traditional slashâ€andâ€burn agriculture on soil organic matter, nutrient content, and microbiota in tropical ecosystems of Papua New Guinea. Land Degradation and Development, 2019, 30, 166-177.	3.9	29
138	Copperâ€“ligand complex for the decolorization of synthetic dyes. Chemosphere, 2004, 57, 1207-1211.	8.2	28
139	Fungal Communities Are Important Determinants of Bacterial Community Composition in Deadwood. MSystems, 2021, 6, .	3.8	28
140	Niche differentiation of bacteria and fungi in carbon and nitrogen cycling of different habitats in a temperate coniferous forest: A metaproteomic approach. Soil Biology and Biochemistry, 2021, 155, 108170.	8.8	28
141	Microbial activity in alpine soils under climate change. Science of the Total Environment, 2021, 783, 147012.	8.0	28
142	The concept of operational taxonomic units revisited: genomes of bacteria that are regarded as closely related are often highly dissimilar. Folia Microbiologica, 2019, 64, 19-23.	2.3	28
143	Scaling Down the Analysis of Environmental Processes: Monitoring Enzyme Activity in Natural Substrates on a Millimeter Resolution Scale. Applied and Environmental Microbiology, 2012, 78, 3473-3475.	3.1	27
144	Forest soil yeasts: Decomposition potential and the utilization of carbon sources. Fungal Ecology, 2018, 34, 10-19.	1.6	27

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145	Composition of soil bacterial and fungal communities in relation to vegetation composition and soil characteristics along an altitudinal gradient. FEMS Microbiology Ecology, 2021, 97, .	2.7	27
146	Litter decomposition along a primary post-mining chronosequence. Biology and Fertility of Soils, 2014, 50, 827-837.	4.3	25
147	Wood resource and not fungi attract earlyâ€successional saproxylic species of <i>Heteroptera â€“</i> an experimental approach. Insect Conservation and Diversity, 2014, 7, 533-542.	3.0	24
148	Comparative assessment of fungal augmentation treatments of a fine-textured and historically oil-contaminated soil. Science of the Total Environment, 2016, 566-567, 250-259.	8.0	24
149	Diversity of fungi and bacteria in species-rich grasslands increases with plant diversity in shoots but not in roots and soil. FEMS Microbiology Ecology, 2019, 95, .	2.7	24
150	Tree species identity alters decomposition of understory litter and associated microbial communities: a case study. Biology and Fertility of Soils, 2019, 55, 525-538.	4.3	24
151	Degradation of BTEX and PAHs by Co(II) and Cu(II)-based radical-generating systems. Applied Catalysis B: Environmental, 2004, 51, 159-164.	20.2	23
152	Extracellular Enzymes of the White-Rot Fungus Fomes fomentarius and Purification of 1,4-Î²-Glucosidase. Applied Biochemistry and Biotechnology, 2013, 169, 100-109.	2.9	23
153	Effect of forest fire prevention treatments on bacterial communities associated with productive <i>Boletus edulis</i> sites. Microbial Biotechnology, 2019, 12, 1188-1198.	4.2	23
154	Fungal succession in the needle litter of a montane Picea abies forest investigated through strain isolation and molecular fingerprinting. Fungal Ecology, 2015, 13, 157-166.	1.6	22
155	Long-term decomposition of litter in the montane forest and the definition of fungal traits in the successional space. Fungal Ecology, 2020, 46, 100913.	1.6	22
156	Efficient screening of potential cellulases and hemicellulases produced by Bosea sp. FBZP-16 using the combination of enzyme assays and genome analysis. World Journal of Microbiology and Biotechnology, 2017, 33, 29.	3.6	21
157	Interactions of saprotrophic fungi with tree roots: can we observe the emergence of novel ectomycorrhizal fungi?. New Phytologist, 2017, 215, 511-513.	7.3	21
158	Adaptive traits of bark and ambrosia beetle-associated fungi. Fungal Ecology, 2019, 41, 165-176.	1.6	21
159	Cellulaseâˆ’Hemicellulase Activities and Bacterial Community Composition of Different Soils from Algerian Ecosystems. Microbial Ecology, 2019, 77, 713-725.	2.8	21
160	Deadwood-Inhabiting Bacteria Show Adaptations to Changing Carbon and Nitrogen Availability During Decomposition. Frontiers in Microbiology, 2021, 12, 685303.	3.5	21
161	Temporal turnover of the soil microbiome composition is guildâ€specific. Ecology Letters, 2021, 24, 2726-2738.	6.4	21
162	Degradation of polycyclic aromatic hydrocarbons by hydrogen peroxide catalyzed by heterogeneous polymeric metal chelates. Applied Catalysis B: Environmental, 2005, 59, 267-274.	20.2	19

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163	Production of lignocellulose-degrading enzymes and changes in soil bacterial communities during the growth ofPleurotus ostreatus in soil with different carbon content. Folia Microbiologica, 2006, 51, 579-590.	2.3	19
164	Effect of long-term preservation of basidiomycetes on perlite in liquid nitrogen on their growth, morphological, enzymatic and genetic characteristics. Fungal Biology, 2010, 114, 929-935.	2.5	19
165	Effect of Heavy Metals on Saprotrophic Soil Fungi. Soil Biology, 2010, , 263-279.	0.8	19
166	Alien ectomycorrhizal plants differ in their ability to interact with co-introduced and native ectomycorrhizal fungi in novel sites. ISME Journal, 2020, 14, 2336-2346.	9.8	19
167	Soil compartments (bulk soil, litter, root and rhizosphere) as main drivers of soil protistan communities distribution in forests with different nitrogen deposition. Soil Biology and Biochemistry, 2022, 168, 108628.	8.8	19
168	Yeasts from temperate forests. Yeast, 2022, 39, 4-24.	1.7	18
169	Feeding on fungi: genomic and proteomic analysis of the enzymatic machinery of bacteria decomposing fungal biomass. Environmental Microbiology, 2020, 22, 4604-4619.	3.8	17
170	Early successional ectomycorrhizal fungi are more likely to naturalize outside their native range than other ectomycorrhizal fungi. New Phytologist, 2020, 227, 1289-1293.	7.3	17
171	Predictors of soil fungal biomass and community composition in temperate mountainous forests in Central Europe. Soil Biology and Biochemistry, 2021, 161, 108366.	8.8	17
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