

Peter Baldrian

List of Publications by Year in descending order

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Version: 2024-02-01

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	High-throughput sequencing view on the magnitude of global fungal diversity. <i>Fungal Diversity</i> , 2022, 114, 539-547.	12.3	94
2	Actinobacterial Strains as Genomic Candidates for Characterization of Genes Encoding Enzymes in Bioconversion of Lignocellulose. <i>Waste and Biomass Valorization</i> , 2022, 13, 1523-1534.	3.4	6
3	Functional soil mycobiome across ecosystems. <i>Journal of Proteomics</i> , 2022, 252, 104428.	2.4	15
4	Successional development of wood-inhabiting fungi associated with dominant tree species in a natural temperate floodplain forest. <i>Fungal Ecology</i> , 2022, 59, 101116.	1.6	8
5	Yeasts from temperate forests. <i>Yeast</i> , 2022, 39, 4-24.	1.7	18
6	Microbial phylogenetic relatedness links to distinct successional patterns of bacterial and fungal communities. <i>Environmental Microbiology</i> , 2022, 24, 3985-4000.	3.8	11
7	Composition and functioning of the soil microbiome in the highest altitudes of the Italian Alps and potential effects of climate change. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	2.7	7
8	Soil compartments (bulk soil, litter, root and rhizosphere) as main drivers of soil protistan communities distribution in forests with different nitrogen deposition. <i>Soil Biology and Biochemistry</i> , 2022, 168, 108628.	8.8	19
9	The invasive tree <i>Piper aduncum</i> alters soil microbiota and nutrient content in fallow land following small scale slash-and-burn farming in tropical lowland forest in Papua New Guinea. <i>Applied Soil Ecology</i> , 2022, 176, 104487.	4.3	0
10	Fungal Community Development in Decomposing Fine Deadwood Is Largely Affected by Microclimate. <i>Frontiers in Microbiology</i> , 2022, 13, 835274.	3.5	10
11	Specific utilization of biopolymers of plant and fungal origin reveals the existence of substrate-specific guilds for bacteria in temperate forest soils. <i>Soil Biology and Biochemistry</i> , 2022, 171, 108696.	8.8	7
12	Snags, logs, stumps, and microclimate as tools optimizing deadwood enrichment for forest biodiversity. <i>Biological Conservation</i> , 2022, 270, 109569.	4.1	11
13	Factors Controlling Dead Wood Decomposition in an Old-Growth Temperate Forest in Central Europe. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 673.	3.5	11
14	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	17.5	457
15	Composition of soil bacterial and fungal communities in relation to vegetation composition and soil characteristics along an altitudinal gradient. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	27
16	Termites Are Associated with External Species-Specific Bacterial Communities. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	10
17	Litter-inhabiting fungi show high level of specialization towards biopolymers composing plant and fungal biomass. <i>Biology and Fertility of Soils</i> , 2021, 57, 77-88.	4.3	30
18	Explorative Meta-Analysis of 417 Extant Archaeal Genomes to Predict Their Contribution to the Total Microbiome Functionality. <i>Microorganisms</i> , 2021, 9, 381.	3.6	2

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19	Complementary Roles of Wood-Inhabiting Fungi and Bacteria Facilitate Deadwood Decomposition. <i>MSystems</i> , 2021, 6, .	3.8	71
20	Fungal Communities Are Important Determinants of Bacterial Community Composition in Deadwood. <i>MSystems</i> , 2021, 6, .	3.8	28
21	Gene family expansions and transcriptome signatures uncover fungal adaptations to wood decay. <i>Environmental Microbiology</i> , 2021, 23, 5716-5732.	3.8	44
22	Niche differentiation of bacteria and fungi in carbon and nitrogen cycling of different habitats in a temperate coniferous forest: A metaproteomic approach. <i>Soil Biology and Biochemistry</i> , 2021, 155, 108170.	8.8	28
23	Genome-Resolved Metagenomics Is Essential for Unlocking the Microbial Black Box of the Soil. <i>Trends in Microbiology</i> , 2021, 29, 279-282.	7.7	11
24	Fungal diversity living in the root and sporophore of the endemic Korean fern <i>Mankyua chejuense</i> . <i>Fungal Ecology</i> , 2021, 50, 101038.	1.6	3
25	Successional Development of Fungal Communities Associated with Decomposing Deadwood in a Natural Mixed Temperate Forest. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 412.	3.5	14
26	Dynamics of Soil Bacterial and Fungal Communities During the Secondary Succession Following Swidden Agriculture IN Lowland Forests. <i>Frontiers in Microbiology</i> , 2021, 12, 676251.	3.5	6
27	Ecological Divergence Within the Enterobacterial Genus <i>Sodalis</i> : From Insect Symbionts to Inhabitants of Decomposing Deadwood. <i>Frontiers in Microbiology</i> , 2021, 12, 668644.	3.5	11
28	Deadwood-Inhabiting Bacteria Show Adaptations to Changing Carbon and Nitrogen Availability During Decomposition. <i>Frontiers in Microbiology</i> , 2021, 12, 685303.	3.5	21
29	Microbial activity in alpine soils under climate change. <i>Science of the Total Environment</i> , 2021, 783, 147012.	8.0	28
30	Metagenomes, metatranscriptomes and microbiomes of naturally decomposing deadwood. <i>Scientific Data</i> , 2021, 8, 198.	5.3	6
31	Distribution of Soil Extracellular Enzymatic, Microbial, and Biological Functions in the C and N-Cycle Pathways Along a Forest Altitudinal Gradient. <i>Frontiers in Microbiology</i> , 2021, 12, 660603.	3.5	15
32	The contribution of insects to global forest deadwood decomposition. <i>Nature</i> , 2021, 597, 77-81.	27.8	123
33	Predictors of soil fungal biomass and community composition in temperate mountainous forests in Central Europe. <i>Soil Biology and Biochemistry</i> , 2021, 161, 108366.	8.8	17
34	Forest Microhabitat Affects Succession of Fungal Communities on Decomposing Fine Tree Roots. <i>Frontiers in Microbiology</i> , 2021, 12, 541583.	3.5	12
35	Temporal turnover of the soil microbiome composition is guild-specific. <i>Ecology Letters</i> , 2021, 24, 2726-2738.	6.4	21
36	A Different Point of View of Plant-Bacterial Interactions: RNA-Seq Analysis of a PGP Bacterial Endophyte Colonizing Rapeseed Plants. <i>Biology and Life Sciences Forum</i> , 2021, 4, 90.	0.6	0

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37	In vitro elucidation of suppression effects of composts to soil-borne pathogen <i>Phytophthora nicotianae</i> on pepper plants using 16S amplicon sequencing and metaproteomics. <i>Renewable Agriculture and Food Systems</i> , 2020, 35, 206-214.	1.8	9
38	Evaluating the role of biotic and chemical components of plant-soil feedback of primary successional plants. <i>Biology and Fertility of Soils</i> , 2020, 56, 345-358.	4.3	11
39	Production of Fungal Mycelia in a Temperate Coniferous Forest Shows Distinct Seasonal Patterns. <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 190.	3.5	9
40	Stand age affects fungal community composition in a Central European temperate forest. <i>Fungal Ecology</i> , 2020, 48, 100985.	1.6	15
41	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
42	GlobalFungi, a global database of fungal occurrences from high-throughput-sequencing metabarcoding studies. <i>Scientific Data</i> , 2020, 7, 228.	5.3	92
43	Ligninolytic Enzyme Production and Decolorization Capacity of Synthetic Dyes by Saprotrophic White Rot, Brown Rot, and Litter Decomposing Basidiomycetes. <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 301.	3.5	33
44	Feeding on fungi: genomic and proteomic analysis of the enzymatic machinery of bacteria decomposing fungal biomass. <i>Environmental Microbiology</i> , 2020, 22, 4604-4619.	3.8	17
45	Metagenomics and stable isotope probing reveal the complementary contribution of fungal and bacterial communities in the recycling of dead biomass in forest soil. <i>Soil Biology and Biochemistry</i> , 2020, 148, 107875.	8.8	71
46	Alien ectomycorrhizal plants differ in their ability to interact with co-introduced and native ectomycorrhizal fungi in novel sites. <i>ISME Journal</i> , 2020, 14, 2336-2346.	9.8	19
47	Primary determinants of communities in deadwood vary among taxa but are regionally consistent. <i>Oikos</i> , 2020, 129, 1579-1588.	2.7	63
48	Explorative Meta-Analysis of 377 Extant Fungal Genomes Predicted a Total Mycobiome Functionality of 42.4 Million KEGG Functions. <i>Frontiers in Microbiology</i> , 2020, 11, 143.	3.5	8
49	Long-term decomposition of litter in the montane forest and the definition of fungal traits in the successional space. <i>Fungal Ecology</i> , 2020, 46, 100913.	1.6	22
50	Insights from enzymatic degradation of cellulose and hemicellulose to fermentable sugars – a review. <i>Biomass and Bioenergy</i> , 2020, 134, 105481.	5.7	172
51	Early successional ectomycorrhizal fungi are more likely to naturalize outside their native range than other ectomycorrhizal fungi. <i>New Phytologist</i> , 2020, 227, 1289-1293.	7.3	17
52	FungalTraits: a user-friendly traits database of fungi and fungus-like stramenopiles. <i>Fungal Diversity</i> , 2020, 105, 1-16.	12.3	387
53	Termites host specific fungal communities that differ from those in their ambient environments. <i>Fungal Ecology</i> , 2020, 48, 100991.	1.6	11
54	Seasonal influences on bacterial community dynamics in Mediterranean pyrophytic ecosystems. <i>Forest Ecology and Management</i> , 2020, 478, 118520.	3.2	3

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55	Identifying Active Members of Litter Fungal Communities by Precursor rRNA. , 2020, , 347-353.		0
56	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
57	Adaptive traits of bark and ambrosia beetle-associated fungi. Fungal Ecology, 2019, 41, 165-176.	1.6	21
58	A meta-analysis of global fungal distribution reveals climate-driven patterns. Nature Communications, 2019, 10, 5142.	12.8	232
59	Fungi associated with beetles dispersing from dead wood – Let's take the beetle bus!. Fungal Ecology, 2019, 39, 100-108.	1.6	41
60	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
61	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
62	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
63	Lignocellulolytic systems of soil bacteria: A vast and diverse toolbox for biotechnological conversion processes. Biotechnology Advances, 2019, 37, 107374.	11.7	71
64	Bacteria from the endosphere and rhizosphere of <i>Quercus</i> spp. use mainly cell wall-associated enzymes to decompose organic matter. PLoS ONE, 2019, 14, e0214422.	2.5	31
65	Editorial: special issue on the ecology of soil microorganisms. FEMS Microbiology Ecology, 2019, 95, .	2.7	1
66	Changes in Functional Response of Soil Microbial Community along Chronosequence of Spontaneous Succession on Post Mining Forest Sites Evaluated by Biolog and SIR Methods. Forests, 2019, 10, 1005.	2.1	5
67	Cellulase~Hemicellulase Activities and Bacterial Community Composition of Different Soils from Algerian Ecosystems. Microbial Ecology, 2019, 77, 713-725.	2.8	21
68	High-Throughput Sequencing Analysis of the Bacterial Community in Stone Fruit Phloem Tissues Infected by –Candidatus Phytoplasma prunorum–. Microbial Ecology, 2019, 77, 664-675.	2.8	4
69	Microbial communities in local and transplanted soils along a latitudinal gradient. Catena, 2019, 173, 456-464.	5.0	11
70	Mycobiome diversity: high-throughput sequencing and identification of fungi. Nature Reviews Microbiology, 2019, 17, 95-109.	28.6	580
71	The known and the unknown in soil microbial ecology. FEMS Microbiology Ecology, 2019, 95, .	2.7	64
72	The effect of traditional slash-and-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

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73	A conceptual framework for understanding the biogeochemistry of dry riverbeds through the lens of soil science. <i>Earth-Science Reviews</i> , 2019, 188, 441-453.	9.1	54
74	The concept of operational taxonomic units revisited: genomes of bacteria that are regarded as closely related are often highly dissimilar. <i>Folia Microbiologica</i> , 2019, 64, 19-23.	2.3	28
75	Decomposer food web in a deciduous forest shows high share of generalist microorganisms and importance of microbial biomass recycling. <i>ISME Journal</i> , 2018, 12, 1768-1778.	9.8	116
76	Inter-laboratory testing of the effect of DNA blocking reagent G2 on DNA extraction from low-biomass clay samples. <i>Scientific Reports</i> , 2018, 8, 5711.	3.3	9
77	SEED 2: a user-friendly platform for amplicon high-throughput sequencing data analyses. <i>Bioinformatics</i> , 2018, 34, 2292-2294.	4.1	202
78	Effects of oak, beech and spruce on the distribution and community structure of fungi in litter and soils across a temperate forest. <i>Soil Biology and Biochemistry</i> , 2018, 119, 162-173.	8.8	59
79	Independent effects of host and environment on the diversity of wood-inhabiting fungi. <i>Journal of Ecology</i> , 2018, 106, 1428-1442.	4.0	74
80	Nutrient content affects the turnover of fungal biomass in forest topsoil and the composition of associated microbial communities. <i>Soil Biology and Biochemistry</i> , 2018, 118, 187-198.	8.8	64
81	Clearcutting alters decomposition processes and initiates complex restructuring of fungal communities in soil and tree roots. <i>ISME Journal</i> , 2018, 12, 692-703.	9.8	100
82	Drivers of microbial community structure in forest soils. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 4331-4338.	3.6	157
83	Pezizomycetes genomes reveal the molecular basis of ectomycorrhizal truffle lifestyle. <i>Nature Ecology and Evolution</i> , 2018, 2, 1956-1965.	7.8	95
84	Specialisation events of fungal metacommunities exposed to a persistent organic pollutant are suggestive of augmented pathogenic potential. <i>Microbiome</i> , 2018, 6, 208.	11.1	16
85	A Short-Term Response of Soil Microbial Communities to Cadmium and Organic Substrate Amendment in Long-Term Contaminated Soil by Toxic Elements. <i>Frontiers in Microbiology</i> , 2018, 9, 2807.	3.5	13
86	Great differences in performance and outcome of high-throughput sequencing data analysis platforms for fungal metabarcoding. <i>MycKeys</i> , 2018, 39, 29-40.	1.9	52
87	Microbial expression profiles in the rhizosphere of two maize lines differing in N use efficiency. <i>Plant and Soil</i> , 2018, 433, 401-413.	3.7	39
88	Different twig litter (<i>Salix caprea</i>) diameter does affect microbial community activity and composition but not decay rate. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	11
89	Forest soil yeasts: Decomposition potential and the utilization of carbon sources. <i>Fungal Ecology</i> , 2018, 34, 10-19.	1.6	27
90	BTW – Bioinformatics Through Windows: an easy-to-install package to analyze marker gene data. <i>PeerJ</i> , 2018, 6, e5299.	2.0	13

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91	Forest microbiome: diversity, complexity and dynamics. FEMS Microbiology Reviews, 2017, 41, fuw040.	8.6	339
92	Efficient screening of potential cellulases and hemicellulases produced by <i>Bosea</i> sp. FBZP-16 using the combination of enzyme assays and genome analysis. World Journal of Microbiology and Biotechnology, 2017, 33, 29.	3.6	21
93	Statistical test for tolerability of effects of an antifungal biocontrol strain on fungal communities in three arable soils. Microbial Biotechnology, 2017, 10, 434-449.	4.2	13
94	Forest Soil Bacteria: Diversity, Involvement in Ecosystem Processes, and Response to Global Change. Microbiology and Molecular Biology Reviews, 2017, 81, .	6.6	456
95	Differential sensitivity of total and active soil microbial communities to drought and forest management. Global Change Biology, 2017, 23, 4185-4203.	9.5	150
96	Editorial: Special thematic issue on the ecology of soil microorganisms. FEMS Microbiology Ecology, 2017, 93, fiw237.	2.7	2
97	Development of microbial community during primary succession in areas degraded by mining activities. Land Degradation and Development, 2017, 28, 2574-2584.	3.9	89
98	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
99	Microbial activity and the dynamics of ecosystem processes in forest soils. Current Opinion in Microbiology, 2017, 37, 128-134.	5.1	92
100	Drivers of yeast community composition in the litter and soil of a temperate forest. FEMS Microbiology Ecology, 2017, 93, fiw223.	2.7	73
101	Spatial heterogeneity of cellulolytic activity and fungal communities within individual decomposing <i>Quercus petraea</i> leaves. Fungal Ecology, 2017, 27, 125-133.	1.6	6
102	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
103	Seasonal variation and distribution of total and active microbial community of β -glucosidase encoding genes in coniferous forest soil. Soil Biology and Biochemistry, 2017, 105, 71-80.	8.8	46
104	Bacteria associated with decomposing dead wood in a natural temperate forest. FEMS Microbiology Ecology, 2017, 93, .	2.7	67
105	Community-level physiological profiling analyses show potential to identify the copiotrophic bacteria present in soil environments. PLoS ONE, 2017, 12, e0171638.	2.5	66
106	Feed in summer, rest in winter: microbial carbon utilization in forest topsoil. Microbiome, 2017, 5, 122.	11.1	121
107	<i>Libkindia masarykiana</i> gen. et sp. nov., <i>Yurkovia mendeliana</i> gen. et sp. nov. and <i>Leucosporidium krtinense</i> f.a. sp. nov., isolated from temperate forest soils. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 902-908.	1.7	8
108	Back to the Future of Soil Metagenomics. Frontiers in Microbiology, 2016, 7, 73.	3.5	120

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109	Cellulose and hemicellulose decomposition by forest soil bacteria proceeds by the action of structurally variable enzymatic systems. <i>Scientific Reports</i> , 2016, 6, 25279.	3.3	328
110	Dead-wood addition promotes non-saproxyllic epigeal arthropods but effects are mediated by canopy openness. <i>Biological Conservation</i> , 2016, 204, 181-188.	4.1	61
111	Microbial activity in forest soil reflects the changes in ecosystem properties between summer and winter. <i>Environmental Microbiology</i> , 2016, 18, 288-301.	3.8	321
112	Small-scale spatial heterogeneity of ecosystem properties, microbial community composition and microbial activities in a temperate mountain forest soil. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw185.	2.7	95
113	The active microbial diversity drives ecosystem multifunctionality and is physiologically related to carbon availability in Mediterranean semi-arid soils. <i>Molecular Ecology</i> , 2016, 25, 4660-4673.	3.9	151
114	Bacterial succession on decomposing leaf litter exhibits a specific occurrence pattern of cellulolytic taxa and potential decomposers of fungal mycelia. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw177.	2.7	110
115	Fungi associated with decomposing deadwood in a natural beech-dominated forest. <i>Fungal Ecology</i> , 2016, 23, 109-122.	1.6	100
116	Comparative assessment of fungal augmentation treatments of a fine-textured and historically oil-contaminated soil. <i>Science of the Total Environment</i> , 2016, 566-567, 250-259.	8.0	24
117	Decoding the complete arsenal for cellulose and hemicellulose deconstruction in the highly efficient cellulose decomposer <i>Paenibacillus</i> O199. <i>Biotechnology for Biofuels</i> , 2016, 9, 104.	6.2	56
118	Dead fungal mycelium in forest soil represents a decomposition hotspot and a habitat for a specific microbial community. <i>New Phytologist</i> , 2016, 210, 1369-1381.	7.3	190
119	The <i>rpb2</i> gene represents a viable alternative molecular marker for the analysis of environmental fungal communities. <i>Molecular Ecology Resources</i> , 2016, 16, 388-401.	4.8	66
120	Ecological succession reveals potential signatures of marine-terrestrial transition in salt marsh fungal communities. <i>ISME Journal</i> , 2016, 10, 1984-1997.	9.8	76
121	Effects of the soil microbial community on mobile proportions and speciation of mercury (Hg) in contaminated soil. <i>Journal of Environmental Science and Health - Part A Toxic/Hazardous Substances and Environmental Engineering</i> , 2016, 51, 364-370.	1.7	10
122	<i>Terracidiphilus gabretensis</i> gen. nov., sp. nov., an Abundant and Active Forest Soil Acidobacterium Important in Organic Matter Transformation. <i>Applied and Environmental Microbiology</i> , 2016, 82, 560-569.	3.1	67
123	Aerobic bacterial catabolism of persistent organic pollutants – potential impact of biotic and abiotic interaction. <i>Current Opinion in Biotechnology</i> , 2016, 38, 71-78.	6.6	30
124	Functional screening of abundant bacteria from acidic forest soil indicates the metabolic potential of Acidobacteria subdivision 1 for polysaccharide decomposition. <i>Biology and Fertility of Soils</i> , 2016, 52, 251-260.	4.3	116
125	<i>Silvibacterium bohemicum</i> gen. nov. sp. nov., an acidobacterium isolated from coniferous soil in the Bohemian Forest National Park. <i>Systematic and Applied Microbiology</i> , 2016, 39, 14-19.	2.8	31
126	Polycyclic aromatic hydrocarbons degradation and microbial community shifts during co-composting of creosote-treated wood. <i>Journal of Hazardous Materials</i> , 2016, 301, 17-26.	12.4	76

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127	Fungal Communities in Soils: Soil Organic Matter Degradation. <i>Methods in Molecular Biology</i> , 2016, 1399, 89-100.	0.9	2
128	Biotic interactions mediate soil microbial feedbacks to climate change. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 7033-7038.	7.1	201
129	Composition of fungal and bacterial communities in forest litter and soil is largely determined by dominant trees. <i>Soil Biology and Biochemistry</i> , 2015, 84, 53-64.	8.8	495
130	An in-depth analysis of actinobacterial communities shows their high diversity in grassland soils along a gradient of mixed heavy metal contamination. <i>Biology and Fertility of Soils</i> , 2015, 51, 827-837.	4.3	32
131	Olive mill wastewater biodegradation potential of white-rot fungi – Mode of action of fungal culture extracts and effects of ligninolytic enzymes. <i>Bioresource Technology</i> , 2015, 189, 121-130.	9.6	51
132	The bacterial community inhabiting temperate deciduous forests is vertically stratified and undergoes seasonal dynamics. <i>Soil Biology and Biochemistry</i> , 2015, 87, 43-50.	8.8	112
133	Reply to Veresoglou: Overdependence on ‘‘significance’’-testing in biology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5114-E5114.	7.1	2
134	Fungal succession in the needle litter of a montane <i>Picea abies</i> forest investigated through strain isolation and molecular fingerprinting. <i>Fungal Ecology</i> , 2015, 13, 157-166.	1.6	22
135	Enzymatic systems involved in decomposition reflects the ecology and taxonomy of saprotrophic fungi. <i>Fungal Ecology</i> , 2015, 13, 10-22.	1.6	108
136	Potential of Cometabolic Transformation of Polysaccharides and Lignin in Lignocellulose by Soil Actinobacteria. <i>PLoS ONE</i> , 2014, 9, e89108.	2.5	152
137	Draft Genome Sequence of <i>Burkholderia sordidicola</i> S170, a Potential Plant Growth Promoter Isolated from Coniferous Forest Soil in the Czech Republic. <i>Genome Announcements</i> , 2014, 2, .	0.8	10
138	Climate fails to predict wood decomposition at regional scales. <i>Nature Climate Change</i> , 2014, 4, 625-630.	18.8	281
139	Seasonal dynamics of fungal communities in a temperate oak forest soil. <i>New Phytologist</i> , 2014, 201, 269-278.	7.3	300
140	Litter decomposition along a primary post-mining chronosequence. <i>Biology and Fertility of Soils</i> , 2014, 50, 827-837.	4.3	25
141	When the forest dies: the response of forest soil fungi to a bark beetle-induced tree dieback. <i>ISME Journal</i> , 2014, 8, 1920-1931.	9.8	125
142	Microbial genomics, transcriptomics and proteomics: new discoveries in decomposition research using complementary methods. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 1531-1537.	3.6	49
143	Distribution of Extracellular Enzymes in Soils: Spatial Heterogeneity and Determining Factors at Various Scales. <i>Soil Science Society of America Journal</i> , 2014, 78, 11-18.	2.2	118
144	Wood resource and not fungi attract early-successional saproxylic species of Heteroptera – an experimental approach. <i>Insect Conservation and Diversity</i> , 2014, 7, 533-542.	3.0	24

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145	Top-down control of soil fungal community composition by a globally distributed keystone consumer. <i>Ecology</i> , 2013, 94, 2518-2528.	3.2	119
146	Is the effect of trees on soil properties mediated by soil fauna? A case study from post-mining sites. <i>Forest Ecology and Management</i> , 2013, 309, 87-95.	3.2	161
147	Fungal community on decomposing leaf litter undergoes rapid successional changes. <i>ISME Journal</i> , 2013, 7, 477-486.	9.8	588
148	Extracellular Enzymes of the White-Rot Fungus <i>Fomes fomentarius</i> and Purification of 1,4-β-Glucosidase. <i>Applied Biochemistry and Biotechnology</i> , 2013, 169, 100-109.	2.9	23
149	Estimation of fungal biomass in forest litter and soil. <i>Fungal Ecology</i> , 2013, 6, 1-11.	1.6	142
150	Responses of the extracellular enzyme activities in hardwood forest to soil temperature and seasonality and the potential effects of climate change. <i>Soil Biology and Biochemistry</i> , 2013, 56, 60-68.	8.8	226
151	Analysis of soil fungal communities by amplicon pyrosequencing: current approaches to data analysis and the introduction of the pipeline SEED. <i>Biology and Fertility of Soils</i> , 2013, 49, 1027-1037.	4.3	168
152	Bacterial communities in tetrachloroethene-polluted groundwaters: A case study. <i>Science of the Total Environment</i> , 2013, 454-455, 517-527.	8.0	56
153	Dominant trees affect microbial community composition and activity in post-mining afforested soils. <i>Soil Biology and Biochemistry</i> , 2013, 56, 105-115.	8.8	101
154	The Variability of the 16S rRNA Gene in Bacterial Genomes and Its Consequences for Bacterial Community Analyses. <i>PLoS ONE</i> , 2013, 8, e57923.	2.5	957
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