

Martin Hartmann

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

70
papers

21,323
citations

35
h-index

75
g-index

75
ext. papers

27,027
ext. citations

5.7
avg, IF

6.26
L-index

#	Paper	IF	Citations
70	Worldwide diversity of endophytic fungi and insects associated with dormant tree twigs.. <i>Scientific Data</i> , 2022 , 9, 62	8.2	2
69	Improving Soil Resource Uptake by Plants Through Capitalizing on Synergies Between Root Architecture and Anatomy and Root-Associated Microorganisms.. <i>Frontiers in Plant Science</i> , 2022 , 13, 827369	6.2	2
68	Microbial Community-Level Physiological Profiles and Genetic Prokaryotic Structure of Burned Soils Under Mediterranean Sclerophyll Forests in Central Chile.. <i>Frontiers in Microbiology</i> , 2022 , 13, 824813	5.7	1
67	Positive Effects of Crop Diversity on Productivity Driven by Changes in Soil Microbial Composition. <i>Frontiers in Microbiology</i> , 2021 , 12, 660749	5.7	13
66	Long-term stability of soil bacterial and fungal community structures revealed in their abundant and rare fractions. <i>Molecular Ecology</i> , 2021 , 30, 4305-4320	5.7	4
65	Limited resilience of the soil microbiome to mechanical compaction within four growing seasons of agricultural management. <i>ISME Communications</i> , 2021 , 1,		5
64	Mixed Effects of Soil Compaction on the Nitrogen Cycle Under Pea and Wheat.. <i>Frontiers in Microbiology</i> , 2021 , 12, 822487	5.7	0
63	Rhizosphere Soil Fungal Communities of Aluminum-Tolerant and -Sensitive Soybean Genotypes Respond Differently to Aluminum Stress in an Acid Soil. <i>Frontiers in Microbiology</i> , 2020 , 11, 1177	5.7	8
62	Thinning Partially Mitigates the Impact of Atlantic Forest Replacement by Pine Monocultures on the Soil Microbiome. <i>Frontiers in Microbiology</i> , 2020 , 11, 1491	5.7	5
61	Drivers of richness and community composition of fungal endophytes of tree seeds. <i>FEMS Microbiology Ecology</i> , 2020 , 96,	4.3	3
60	Microbial succession on decomposing root litter in a drought-prone Scots pine forest. <i>ISME Journal</i> , 2019 , 13, 2346-2362	11.9	43
59	The Pedological Context Modulates the Response of Soil Microbial Communities to Agroecological Management. <i>Frontiers in Ecology and Evolution</i> , 2019 , 7,	3.7	8
58	Taxon-specific fungal preference for distinct soil particle size fractions. <i>European Journal of Soil Biology</i> , 2019 , 94, 103103	2.9	14
57	Are traded forest tree seeds a potential source of nonnative pests?. <i>Ecological Applications</i> , 2019 , 29, e01971	4.9	18
56	The -Resistant Olive Cultivar "Leccino" Has Stable Endophytic Microbiota during the Olive Quick Decline Syndrome (OQDS). <i>Pathogens</i> , 2019 , 9,	4.5	23
55	Kinematics of perceived dyadic coordination in dance. <i>Scientific Reports</i> , 2019 , 9, 15594	4.9	3
54	Response of soil microbial communities to the application of a formulated <i>Metarhizium brunneum</i> biocontrol strain. <i>Biocontrol Science and Technology</i> , 2019 , 29, 547-564	1.7	7

53	Improved recovery of ancient DNA from subfossil wood - application to the world's oldest Late Glacial pine forest. <i>New Phytologist</i> , 2018 , 217, 1737-1748	9.8	16
52	Biochar affects community composition of nitrous oxide reducers in a field experiment. <i>Soil Biology and Biochemistry</i> , 2018 , 119, 143-151	7.5	34
51	Positive diversity-functioning relationships in model communities of methanotrophic bacteria. <i>Ecology</i> , 2018 , 99, 714-723	4.6	18
50	Metaxa2 Database Builder: enabling taxonomic identification from metagenomic or metabarcoding data using any genetic marker. <i>Bioinformatics</i> , 2018 , 34, 4027-4033	7.2	26
49	Effects of titanium dioxide nanoparticles on soil microbial communities and wheat biomass. <i>Soil Biology and Biochemistry</i> , 2017 , 111, 85-93	7.5	47
48	Tolerance of the forest soil microbiome to increasing mercury concentrations. <i>Soil Biology and Biochemistry</i> , 2017 , 105, 162-176	7.5	63
47	A decade of irrigation transforms the soil microbiome of a semi-arid pine forest. <i>Molecular Ecology</i> , 2017 , 26, 1190-1206	5.7	82
46	A metagenomic survey of forest soil microbial communities more than a decade after timber harvesting. <i>Scientific Data</i> , 2017 , 4, 170092	8.2	9
45	Interaction features for prediction of perceptual segmentation: Effects of musicianship and experimental task. <i>Journal of New Music Research</i> , 2017 , 46, 156-174	1.1	6
44	Assessing effects of the entomopathogenic fungus <i>Metarhizium brunneum</i> on soil microbial communities in <i>Agriotes</i> spp. biological pest control. <i>FEMS Microbiology Ecology</i> , 2017 , 93,	4.3	18
43	Temporal Dynamics of Soil Microbial Communities below the Seedbed under Two Contrasting Tillage Regimes. <i>Frontiers in Microbiology</i> , 2017 , 8, 1127	5.7	72
42	Ecology of Alpine Macrofungi - Combining Historical with Recent Data. <i>Frontiers in Microbiology</i> , 2017 , 8, 2066	5.7	13
41	Assimilation of microbial and plant carbon by active prokaryotic and fungal populations in glacial forefields. <i>Soil Biology and Biochemistry</i> , 2016 , 98, 30-41	7.5	21
40	Potential sources of microbial colonizers in an initial soil ecosystem after retreat of an alpine glacier. <i>ISME Journal</i> , 2016 , 10, 1625-41	11.9	57
39	Microbial diversity in European alpine permafrost and active layers. <i>FEMS Microbiology Ecology</i> , 2016 , 92,	4.3	139
38	Networking in the Plant Microbiome. <i>PLoS Biology</i> , 2016 , 14, e1002378	9.7	204
37	Microbes as Engines of Ecosystem Function: When Does Community Structure Enhance Predictions of Ecosystem Processes?. <i>Frontiers in Microbiology</i> , 2016 , 7, 214	5.7	321
36	Stable isotope probing implicates a species of <i>Cortinarius</i> in carbon transfer through ectomycorrhizal fungal mycelial networks in Arctic tundra. <i>New Phytologist</i> , 2016 , 210, 383-90	9.8	25

35	A Comprehensive, Automatically Updated Fungal ITS Sequence Dataset for Reference-Based Chimera Control in Environmental Sequencing Efforts. <i>Microbes and Environments</i> , 2015 , 30, 145-50	2.6	144
34	METAXA2: improved identification and taxonomic classification of small and large subunit rRNA in metagenomic data. <i>Molecular Ecology Resources</i> , 2015 , 15, 1403-14	8.4	252
33	Distinct soil microbial diversity under long-term organic and conventional farming. <i>ISME Journal</i> , 2015 , 9, 1177-94	11.9	668
32	Vertical distribution of the soil microbiota along a successional gradient in a glacier forefield. <i>Molecular Ecology</i> , 2015 , 24, 1091-108	5.7	104
31	Improving ITS sequence data for identification of plant pathogenic fungi. <i>Fungal Diversity</i> , 2014 , 67, 11-19	7.6	101
30	Resistance and resilience of the forest soil microbiome to logging-associated compaction. <i>ISME Journal</i> , 2014 , 8, 226-44	11.9	194
29	Improved software detection and extraction of ITS1 and ITS2 from ribosomal ITS sequences of fungi and other eukaryotes for analysis of environmental sequencing data. <i>Methods in Ecology and Evolution</i> , 2013 , 4, n/a-n/a	7.7	312
28	Towards a unified paradigm for sequence-based identification of fungi. <i>Molecular Ecology</i> , 2013 , 22, 5271-7	11.7	2019
27	Isolation of a substantial proportion of forest soil bacterial communities detected via pyrotag sequencing. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 2096-8	4.8	29
26	Temporal stability of the mouse gut microbiota in relation to innate and adaptive immunity. <i>Environmental Microbiology Reports</i> , 2013 , 5, 200-10	3.7	63
25	Nutrient enrichment increased species richness of leaf litter fungal assemblages in a tropical forest. <i>Molecular Ecology</i> , 2013 , 22, 2827-38	5.7	44
24	Long-term warming alters the composition of Arctic soil microbial communities. <i>FEMS Microbiology Ecology</i> , 2012 , 82, 303-15	4.3	151
23	Megraft: a software package to graft ribosomal small subunit (16S/18S) fragments onto full-length sequences for accurate species richness and sequencing depth analysis in pyrosequencing-length metagenomes and similar environmental datasets. <i>Research in Microbiology</i> , 2012 , 163, 407-12	4	12
22	Neutrophil elastase alters the murine gut microbiota resulting in enhanced <i>Salmonella</i> colonization. <i>PLoS ONE</i> , 2012 , 7, e49646	3.7	46
21	Early life antibiotic-driven changes in microbiota enhance susceptibility to allergic asthma. <i>EMBO Reports</i> , 2012 , 13, 440-7	6.5	566
20	Significant and persistent impact of timber harvesting on soil microbial communities in Northern coniferous forests. <i>ISME Journal</i> , 2012 , 6, 2199-218	11.9	203
19	Five simple guidelines for establishing basic authenticity and reliability of newly generated fungal ITS sequences. <i>MycoKeys</i> , 2012 , 4, 37-63	2.4	126
18	Long-term experimental manipulation of climate alters the ectomycorrhizal community of <i>Betula nana</i> in Arctic tundra. <i>Global Change Biology</i> , 2011 , 17, 1625-1636	11.4	146

17	V-REVCOMP: automated high-throughput detection of reverse complementary 16S rRNA gene sequences in large environmental and taxonomic datasets. <i>FEMS Microbiology Letters</i> , 2011 , 319, 140-5	2.9	10
16	A note on the incidence of reverse complementary fungal ITS sequences in the public sequence databases and a software tool for their detection and reorientation. <i>Mycoscience</i> , 2011 , 52, 278-282	1.2	7
15	Metaxa: a software tool for automated detection and discrimination among ribosomal small subunit (12S/16S/18S) sequences of archaea, bacteria, eukaryotes, mitochondria, and chloroplasts in metagenomes and environmental sequencing datasets. <i>Antonie Van Leeuwenhoek</i> , 2011 , 100, 471-5	2.1	61
14	Fungal community structure in soils of conventional and organic farming systems. <i>Fungal Ecology</i> , 2010 , 3, 215-224	4.1	21
13	An open source software package for automated extraction of ITS1 and ITS2 from fungal ITS sequences for use in high-throughput community assays and molecular ecology. <i>Fungal Ecology</i> , 2010 , 3, 284-287	4.1	170
12	V-Xtractor: an open-source, high-throughput software tool to identify and extract hypervariable regions of small subunit (16S/18S) ribosomal RNA gene sequences. <i>Journal of Microbiological Methods</i> , 2010 , 83, 250-3	2.8	93
11	Bacterial, archaeal and eukaryal community structures throughout soil horizons of harvested and naturally disturbed forest stands. <i>Environmental Microbiology</i> , 2009 , 11, 3045-62	5.2	143
10	Introducing mothur: open-source, platform-independent, community-supported software for describing and comparing microbial communities. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 7537-41	4.8	13777
9	Reliability for detecting composition and changes of microbial communities by T-RFLP genetic profiling. <i>FEMS Microbiology Ecology</i> , 2008 , 63, 249-60	4.3	66
8	Residual polymerase activity-induced bias in terminal restriction fragment length polymorphism analysis. <i>Environmental Microbiology</i> , 2007 , 9, 555-9	5.2	20
7	Community structure analyses are more sensitive to differences in soil bacterial communities than anonymous diversity indices. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 7804-12	4.8	137
6	Community structures and substrate utilization of bacteria in soils from organic and conventional farming systems of the DOK long-term field experiment. <i>Applied Soil Ecology</i> , 2006 , 33, 294-307	5	89
5	A novel strategy to extract specific phylogenetic sequence information from community T-RFLP. <i>Journal of Microbiological Methods</i> , 2006 , 66, 512-20	2.8	35
4	Ranking the magnitude of crop and farming system effects on soil microbial biomass and genetic structure of bacterial communities. <i>FEMS Microbiology Ecology</i> , 2006 , 57, 378-88	4.3	66
3	Bacterial community structure and activity in different Cd-treated forest soils. <i>FEMS Microbiology Ecology</i> , 2006 , 58, 278-92	4.3	26
2	Semi-automated genetic analyses of soil microbial communities: comparison of T-RFLP and RISA based on descriptive and discriminative statistical approaches. <i>Journal of Microbiological Methods</i> , 2005 , 61, 349-60	2.8	92
1	Musical interaction in music therapy for depression treatment. <i>Psychology of Music</i> , 030573562210843	1.2	