

Mohammad Bahram

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6959774/publications.pdf>

Version: 2024-02-01

93
papers

15,657
citations

50276

46
h-index

45317

90
g-index

104
all docs

104
docs citations

104
times ranked

14187
citing authors

#	ARTICLE	IF	CITATIONS
1	Towards revealing the global diversity and community assembly of soil eukaryotes. <i>Ecology Letters</i> , 2022, 25, 65-76.	6.4	47
2	Designing PCR Primers for the Amplification-Refractory Mutation System. <i>Methods in Molecular Biology</i> , 2022, 2392, 93-99.	0.9	4
3	Global diversity and distribution of mushroom-inhabiting bacteria. <i>Environmental Microbiology Reports</i> , 2022, 14, 254-264.	2.4	13
4	Structure and function of the soil microbiome underlying N ₂ O emissions from global wetlands. <i>Nature Communications</i> , 2022, 13, 1430.	12.8	72
5	Global soil microbiomes: A new frontline of biome-ecology research. <i>Global Ecology and Biogeography</i> , 2022, 31, 1120-1132.	5.8	19
6	Fungi as mediators linking organisms and ecosystems. <i>FEMS Microbiology Reviews</i> , 2022, 46, .	8.6	47
7	Best practices in metabarcoding of fungi: From experimental design to results. <i>Molecular Ecology</i> , 2022, 31, 2769-2795.	3.9	87
8	Biotic interactions with mycorrhizal systems as extended nutrient acquisition strategies shaping forest soil communities and functions. <i>Basic and Applied Ecology</i> , 2021, 50, 25-42.	2.7	19
9	Metagenomic analysis reveals a dynamic microbiome with diversified adaptive functions to utilize high lignocellulosic forages in the cattle rumen. <i>ISME Journal</i> , 2021, 15, 1108-1120.	9.8	87
10	Metagenomic assessment of the global diversity and distribution of bacteria and fungi. <i>Environmental Microbiology</i> , 2021, 23, 316-326.	3.8	42
11	Temperature and pH define the realised niche space of arbuscular mycorrhizal fungi. <i>New Phytologist</i> , 2021, 231, 763-776.	7.3	126
12	Heavy metal pollution promotes antibiotic resistance potential in the aquatic environment. <i>Environmental Pollution</i> , 2021, 274, 116569.	7.5	91
13	Long- and short-read metabarcoding technologies reveal similar spatiotemporal structures in fungal communities. <i>Molecular Ecology Resources</i> , 2021, 21, 1833-1849.	4.8	16
14	Plant-microbe interactions in response to grassland herbivory and nitrogen eutrophication. <i>Soil Biology and Biochemistry</i> , 2021, 156, 108208.	8.8	9
15	A global overview of the trophic structure within microbiomes across ecosystems. <i>Environment International</i> , 2021, 151, 106438.	10.0	48
16	Seasonal dynamics of mycoplankton in the Yellow Sea reflect the combined effect of riverine inputs and hydrographic conditions. <i>Molecular Ecology</i> , 2021, 30, 3624-3637.	3.9	11
17	Dispersal strategies shape persistence and evolution of human gut bacteria. <i>Cell Host and Microbe</i> , 2021, 29, 1167-1176.e9.	11.0	66
18	Current Insight into Culture-Dependent and Culture-Independent Methods in Discovering Ascomycetous Taxa. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 703.	3.5	12

#	ARTICLE	IF	CITATIONS
19	Revision of the genus <i>Restingomyces</i> , including two new species from Mexico. <i>Mycologia</i> , 2021, 113, 1-11.	1.9	1
20	Phylogenomics reveals the evolution of root nodulating alpha- and beta-Proteobacteria (rhizobia). <i>Microbiological Research</i> , 2021, 250, 126788.	5.3	18
21	Cropping systems with higher organic carbon promote soil microbial diversity. <i>Agriculture, Ecosystems and Environment</i> , 2021, 319, 107521.	5.3	33
22	The Global Soil Mycobiome consortium dataset for boosting fungal diversity research. <i>Fungal Diversity</i> , 2021, 111, 573-588.	12.3	42
23	Carbon content and pH as important drivers of fungal community structure in three Amazon forests. <i>Plant and Soil</i> , 2020, 450, 111-131.	3.7	23
24	Host tree organ is the primary driver of endophytic fungal community structure in a hemiboreal forest. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	19
25	Regional-Scale In-Depth Analysis of Soil Fungal Diversity Reveals Strong pH and Plant Species Effects in Northern Europe. <i>Frontiers in Microbiology</i> , 2020, 11, 1953.	3.5	126
26	Global patterns and determinants of bacterial communities associated with ectomycorrhizal root tips of <i>Alnus</i> species. <i>Soil Biology and Biochemistry</i> , 2020, 148, 107923.	8.8	5
27	Identifying the "unidentified" fungi: a global-scale long-read third-generation sequencing approach. <i>Fungal Diversity</i> , 2020, 103, 273-293.	12.3	48
28	Bacterial community dynamics across developmental stages of fungal fruiting bodies. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	17
29	Fruitbody chemistry underlies the structure of endofungal bacterial communities across fungal guilds and phylogenetic groups. <i>ISME Journal</i> , 2020, 14, 2131-2141.	9.8	20
30	How mycorrhizal associations drive plant population and community biology. <i>Science</i> , 2020, 367, .	12.6	453
31	Plant nutrient acquisition strategies drive topsoil microbiome structure and function. <i>New Phytologist</i> , 2020, 227, 1189-1199.	7.3	96
32	FungalTraits: a user-friendly traits database of fungi and fungus-like stramenopiles. <i>Fungal Diversity</i> , 2020, 105, 1-16.	12.3	387
33	A new <i>Stephanospora</i> (Agaricales, Basidiomycota) from the Yucatan peninsula, Mexico. <i>Phytotaxa</i> , 2020, 436, 63-71.	0.3	1
34	Newly designed 16S rRNA metabarcoding primers amplify diverse and novel archaeal taxa from the environment. <i>Environmental Microbiology Reports</i> , 2019, 11, 487-494.	2.4	91
35	Mycorrhizal types differ in ecophysiology and alter plant nutrition and soil processes. <i>Biological Reviews</i> , 2019, 94, 1857-1880.	10.4	178
36	Relative Performance of MinION (Oxford Nanopore Technologies) versus Sequel (Pacific Biosciences) Third-Generation Sequencing Instruments in Identification of Agricultural and Forest Fungal Pathogens. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	68

#	ARTICLE	IF	CITATIONS
37	Antibiotics-induced monodominance of a novel gut bacterial order. <i>Gut</i> , 2019, 68, 1781-1790.	12.1	73
38	The role of arbuscular mycorrhizal fungi in plant invasion trajectory. <i>Plant and Soil</i> , 2019, 441, 1-14.	3.7	30
39	Global mismatches in aboveground and belowground biodiversity. <i>Conservation Biology</i> , 2019, 33, 1187-1192.	4.7	103
40	Mycobiome diversity: high-throughput sequencing and identification of fungi. <i>Nature Reviews Microbiology</i> , 2019, 17, 95-109.	28.6	580
41	Host genetic variation strongly influences the microbiome structure and function in fungal fruiting bodies. <i>Environmental Microbiology</i> , 2018, 20, 1641-1650.	3.8	23
42	Complex effects of mammalian grazing on extramatrical mycelial biomass in the Scandes forest-tundra ecotone. <i>Ecology and Evolution</i> , 2018, 8, 1019-1030.	1.9	13
43	The genome and microbiome of a dikaryotic fungus (<i>Inocybe terrigena</i> , Inocybaceae) revealed by metagenomics. <i>Environmental Microbiology Reports</i> , 2018, 10, 155-166.	2.4	17
44	Seasonal and annual variation in fungal communities associated with epigeic springtails (Collembola) Tj ETQq0 0 0 ggBT /Overlock 10 Tf	8.8	47
45	Host preference and network properties in biotrophic plant-fungal associations. <i>New Phytologist</i> , 2018, 217, 1230-1239.	7.3	107
46	Tree species identity and diversity drive fungal richness and community composition along an elevational gradient in a Mediterranean ecosystem. <i>Mycorrhiza</i> , 2018, 28, 39-47.	2.8	48
47	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
48	High-level classification of the Fungi and a tool for evolutionary ecological analyses. <i>Fungal Diversity</i> , 2018, 90, 135-159.	12.3	450
49	Structure and function of the global topsoil microbiome. <i>Nature</i> , 2018, 560, 233-237.	27.8	1,370
50	Local-scale spatial structure and community composition of orchid mycorrhizal fungi in semi-natural grasslands. <i>Mycorrhiza</i> , 2017, 27, 355-367.	2.8	21
51	PipeCraft: Flexible open-source toolkit for bioinformatics analysis of custom high-throughput amplicon sequencing data. <i>Molecular Ecology Resources</i> , 2017, 17, e234-e240.	4.8	116
52	Physiological and molecular responses of resistant and susceptible wheat cultivars to <i>Fusarium graminearum</i> mycotoxin extract. <i>Canadian Journal of Plant Pathology</i> , 2017, 39, 444-453.	1.4	7
53	Plant species richness and productivity determine the diversity of soil fungal guilds in temperate coniferous forest and bog habitats. <i>Molecular Ecology</i> , 2017, 26, 4846-4858.	3.9	80
54	Elevation, space and host plant species structure Ericaceae root-associated fungal communities in Papua New Guinea. <i>Fungal Ecology</i> , 2017, 30, 112-121.	1.6	5

#	ARTICLE	IF	CITATIONS
55	Novel soil-inhabiting clades fill gaps in the fungal tree of life. <i>Microbiome</i> , 2017, 5, 42.	11.1	152
56	Bacterial Communities in Boreal Forest Mushrooms Are Shaped Both by Soil Parameters and Host Identity. <i>Frontiers in Microbiology</i> , 2017, 8, 836.	3.5	62
57	Biogeography and Specificity of Ectomycorrhizal Fungi of <i>Coccoloba uvifera</i> . <i>Ecological Studies</i> , 2017, , 345-359.	1.2	11
58	Lack of association between <i>Fusarium graminearum</i> resistance in spike and crude extract tolerance in seedling of wheat. <i>European Journal of Plant Pathology</i> , 2016, 144, 525-538.	1.7	12
59	Ectomycorrhizal and saprotrophic fungi respond differently to long-term experimentally increased snow depth in the High Arctic. <i>MicrobiologyOpen</i> , 2016, 5, 856-869.	3.0	30
60	Alpine bistort (<i>Bistorta vivipara</i>) in edge habitat associates with fewer but distinct ectomycorrhizal fungal species: a comparative study of three contrasting soil environments in Svalbard. <i>Mycorrhiza</i> , 2016, 26, 809-818.	2.8	17
61	Millions of reads, thousands of taxa: microbial community structure and associations analyzed via marker genes. <i>FEMS Microbiology Reviews</i> , 2016, 40, 686-700.	8.6	159
62	Temporal changes in fungal communities associated with guts and appendages of <i>Collembola</i> as based on culturing and high-throughput sequencing. <i>Soil Biology and Biochemistry</i> , 2016, 96, 152-159.	8.8	42
63	Stochastic distribution of small soil eukaryotes resulting from high dispersal and drift in a local environment. <i>ISME Journal</i> , 2016, 10, 885-896.	9.8	256
64	Tree diversity and species identity effects on soil fungi, protists and animals are context dependent. <i>ISME Journal</i> , 2016, 10, 346-362.	9.8	307
65	Temporal variation of <i>Bistorta vivipara</i> -associated ectomycorrhizal fungal communities in the High Arctic. <i>Molecular Ecology</i> , 2015, 24, 6289-6302.	3.9	39
66	Ectomycorrhizal impacts on plant nitrogen nutrition: emerging isotopic patterns, latitudinal variation and hidden mechanisms. <i>Ecology Letters</i> , 2015, 18, 96-107.	6.4	48
67	Host diversity and trophic status as determinants of species richness and community composition of fungus gnats. <i>Basic and Applied Ecology</i> , 2015, 16, 46-53.	2.7	12
68	Niche partitioning in arbuscular mycorrhizal communities in temperate grasslands: a lesson from adjacent serpentine and nonserpentine habitats. <i>Molecular Ecology</i> , 2015, 24, 1831-1843.	3.9	31
69	Response to Comment on "Global diversity and geography of soil fungi". <i>Science</i> , 2015, 349, 936-936.	12.6	43
70	Local-scale biogeography and spatiotemporal variability in communities of mycorrhizal fungi. <i>New Phytologist</i> , 2015, 205, 1454-1463.	7.3	197
71	Global diversity and geography of soil fungi. <i>Science</i> , 2014, 346, 1256688.	12.6	2,513
72	Global biogeography of <i>Alnus</i> -associated <i>Frankia</i> actinobacteria. <i>New Phytologist</i> , 2014, 204, 979-988.	7.3	41

#	ARTICLE	IF	CITATIONS
73	Network perspectives of ectomycorrhizal associations. <i>Fungal Ecology</i> , 2014, 7, 70-77.	1.6	77
74	Improving ITS sequence data for identification of plant pathogenic fungi. <i>Fungal Diversity</i> , 2014, 67, 11-19.	12.3	123
75	Global biogeography of the ectomycorrhizal /sebacina lineage (<sc>F</sc>ungi,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 667 2014, 23, 4168-4183.	3.9	58
76	Does host plant richness explain diversity of ectomycorrhizal fungi? Re-evaluation of Gao et al. (2013) data sets reveals sampling effects. <i>Molecular Ecology</i> , 2014, 23, 992-995.	3.9	42
77	Towards a unified paradigm for sequence-based identification of fungi. <i>Molecular Ecology</i> , 2013, 22, 5271-5277.	3.9	2,997
78	The distance decay of similarity in communities of ectomycorrhizal fungi in different ecosystems and scales. <i>Journal of Ecology</i> , 2013, 101, 1335-1344.	4.0	124
79	Ectomycorrhizal fungi of exotic pine plantations in relation to native host trees in Iran: evidence of host range expansion by local symbionts to distantly related host taxa. <i>Mycorrhiza</i> , 2013, 23, 11-19.	2.8	63
80	Biogeography of ectomycorrhizal fungi associated with alders (<i><sc>A</sc>lnus</i> spp.) in relation to biotic and abiotic variables at the global scale. <i>New Phytologist</i> , 2013, 198, 1239-1249.	7.3	191
81	Evolution of nutritional modes of Ceratobasidiaceae (Cantharellales, Basidiomycota) as revealed from publicly available ITS sequences. <i>Fungal Ecology</i> , 2013, 6, 256-268.	1.6	81
82	Phylogenetic relationships among host plants explain differences in fungal species richness and community composition in ectomycorrhizal symbiosis. <i>New Phytologist</i> , 2013, 199, 822-831.	7.3	151
83	Enzymatic activities and stable isotope patterns of ectomycorrhizal fungi in relation to phylogeny and exploration types in an afro-tropical rain forest. <i>New Phytologist</i> , 2012, 195, 832-843.	7.3	119
84	Regional and local patterns of ectomycorrhizal fungal diversity and community structure along an altitudinal gradient in the Hyrcanian forests of northern Iran. <i>New Phytologist</i> , 2012, 193, 465-473.	7.3	256
85	Towards global patterns in the diversity and community structure of ectomycorrhizal fungi. <i>Molecular Ecology</i> , 2012, 21, 4160-4170.	3.9	365
86	Fine root foraging strategies in <sc>N</sc>orway spruce forests across a <sc>E</sc>uropean climate gradient. <i>Global Change Biology</i> , 2011, 17, 3620-3632.	9.5	161
87	Spatial structure and the effects of host and soil environments on communities of ectomycorrhizal fungi in wooded savannas and rain forests of Continental Africa and Madagascar. <i>Molecular Ecology</i> , 2011, 20, 3071-3080.	3.9	108
88	A single European aspen (<i>Populus tremula</i>) tree individual may potentially harbour dozens of <i>Cenococcum geophilum</i> ITS genotypes and hundreds of species of ectomycorrhizal fungi. <i>FEMS Microbiology Ecology</i> , 2011, 75, 313-320.	2.7	115
89	Ericaceous dwarf shrubs affect ectomycorrhizal fungal community of the invasive <i>Pinus strobus</i> and native <i>Pinus sylvestris</i> in a pot experiment. <i>Mycorrhiza</i> , 2011, 21, 403-412.	2.8	78
90	454 Pyrosequencing and Sanger sequencing of tropical mycorrhizal fungi provide similar results but reveal substantial methodological biases. <i>New Phytologist</i> , 2010, 188, 291-301.	7.3	484

#	ARTICLE	IF	CITATIONS
91	Shotgun metagenomes and multiple primer pair-barcode combinations of amplicons reveal biases in metabarcoding analyses of fungi. MycoKeys, 0, 10, 1-43.	1.9	409
92	Top 50 most wanted fungi. MycoKeys, 0, 12, 29-40.	1.9	72
93	Vertical stratification of microbial communities in woody plants. Phytobiomes Journal, 0, , .	2.7	6