

Ari Jumpponen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5635704/publications.pdf>

Version: 2024-02-01

96
papers

8,930
citations

47006

47
h-index

43889

91
g-index

98
all docs

98
docs citations

98
times ranked

9241
citing authors

#	ARTICLE	IF	CITATIONS
1	Improved software detection and extraction of ITS1 and <scp>ITS</scp>2 from ribosomal <scp>ITS</scp> sequences of fungi and other eukaryotes for analysis of environmental sequencing data. <i>Methods in Ecology and Evolution</i> , 2013, 4, 914-919.	5.2	868
2	Dark septate endophytes: a review of facultative biotrophic root-colonizing fungi. <i>New Phytologist</i> , 1998, 140, 295-310.	7.3	820
3	Dark septate endophytes - are they mycorrhizal?. <i>Mycorrhiza</i> , 2001, 11, 207-211.	2.8	534
4	Seeking the elusive function of the root-colonising dark septate endophytic fungi. <i>Studies in Mycology</i> , 2005, 53, 173-189.	7.2	529
5	Fire frequency drives decadal changes in soil carbon and nitrogen and ecosystem productivity. <i>Nature</i> , 2018, 553, 194-198.	27.8	325
6	DNA metabarcodingâ€™Need for robust experimental designs to draw sound ecological conclusions. <i>Molecular Ecology</i> , 2019, 28, 1857-1862.	3.9	300
7	Ecosystem properties and microbial community changes in primary succession on a glacier forefront. <i>Oecologia</i> , 1999, 119, 239-246.	2.0	235
8	Contrasting primary successional trajectories of fungi and bacteria in retreating glacier soils. <i>Molecular Ecology</i> , 2014, 23, 481-497.	3.9	208
9	Scraping the bottom of the barrel: are rare high throughput sequences artifacts?. <i>Fungal Ecology</i> , 2015, 13, 221-225.	1.6	196
10	The avian gut microbiota: community, physiology and function in wild birds. <i>Journal of Avian Biology</i> , 2018, 49, e01788.	1.2	194
11	Soil fungal community assembly in a primary successional glacier forefront ecosystem as inferred from rDNA sequence analyses. <i>New Phytologist</i> , 2003, 158, 569-578.	7.3	190
12	Characterization of â€™safe sitesâ€™™ for pioneers in primary succession on recently deglaciated terrain. <i>Journal of Ecology</i> , 1999, 87, 98-105.	4.0	167
13	Species abundance distributions and richness estimations in fungal metagenomics - lessons learned from community ecology. <i>Molecular Ecology</i> , 2011, 20, 275-285.	3.9	158
14	Massively parallel 454â€™sequencing of fungal communities in <i>Quercus</i> spp. ectomycorrhizas indicates seasonal dynamics in urban and rural sites. <i>Molecular Ecology</i> , 2010, 19, 41-53.	3.9	156
15	Diverse Helotiales associated with the roots of three species of Arctic Ericaceae provide no evidence for host specificity. <i>New Phytologist</i> , 2011, 191, 515-527.	7.3	150
16	Utilization of major detrital substrates by dark-septate, root endophytes. <i>Mycologia</i> , 2000, 92, 230-232.	1.9	133
17	Improving ITS sequence data for identification of plant pathogenic fungi. <i>Fungal Diversity</i> , 2014, 67, 11-19.	12.3	123
18	Foliar and fungal 15 N:14 N ratios reflect development of mycorrhizae and nitrogen supply during primary succession: testing analytical models. <i>Oecologia</i> , 2005, 146, 258-268.	2.0	122

#	ARTICLE	IF	CITATIONS
19	Seasonal and temporal dynamics of arbuscular mycorrhizal and dark septate endophytic fungi in a tallgrass prairie ecosystem are minimally affected by nitrogen enrichment. <i>Mycorrhiza</i> , 2008, 18, 145-155.	2.8	119
20	Fungal Community Shifts in Structure and Function across a Boreal Forest Fire Chronosequence. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7869-7880.	3.1	119
21	Vertical distribution of fungal communities in tallgrass prairie soil. <i>Mycologia</i> , 2010, 102, 1027-1041.	1.9	118
22	Soil microbial communities are shaped by vegetation type and park age in cities under cold climate. <i>Environmental Microbiology</i> , 2017, 19, 1281-1295.	3.8	114
23	Isolation and morphological and metabolic characterization of common endophytes in annually burned tallgrass prairie. <i>Mycologia</i> , 2010, 102, 813-821.	1.9	110
24	Mycorrhiza-plant colonization patterns on a subalpine glacier forefront as a model system of primary succession. <i>Mycorrhiza</i> , 2005, 15, 405-416.	2.8	109
25	Mutualism–parasitism paradigm synthesized from results of root-endophyte models. <i>Frontiers in Microbiology</i> , 2014, 5, 776.	3.5	106
26	Occurrence of ectomycorrhizal fungi on the forefront of retreating Lyman Glacier (Washington, USA). <i>Journal of Biogeography</i> , 2010, 37, 104-114.	2.8	104
27	Urbanization Reduces Transfer of Diverse Environmental Microbiota Indoors. <i>Frontiers in Microbiology</i> , 2018, 9, 84.	3.5	95
28	Polymerase matters: non-proofreading enzymes inflate fungal community richness estimates by up to 15%. <i>Fungal Ecology</i> , 2015, 15, 86-89.	1.6	94
29	FOAM (Functional Ontology Assignments for Metagenomes): a Hidden Markov Model (HMM) database with environmental focus. <i>Nucleic Acids Research</i> , 2014, 42, e145-e145.	14.5	90
30	Deep Ion Torrent sequencing identifies soil fungal community shifts after frequent prescribed fires in a southeastern US forest ecosystem. <i>FEMS Microbiology Ecology</i> , 2013, 86, 557-566.	2.7	86
31	Soil fungal communities respond compositionally to recurring frequent prescribed burning in a managed southeastern US forest ecosystem. <i>Forest Ecology and Management</i> , 2015, 345, 1-9.	3.2	86
32	Vertical and seasonal dynamics of fungal communities in boreal Scots pine forest soil. <i>FEMS Microbiology Ecology</i> , 2016, 92, 170-179.	2.7	84
33	Nitrogen enrichment causes minimal changes in arbuscular mycorrhizal colonization but shifts community composition?evidence from rDNA data. <i>Biology and Fertility of Soils</i> , 2005, 41, 217-224.	4.3	82
34	Fungal colonization of shrub willow roots at the forefront of a receding glacier. <i>Mycorrhiza</i> , 2004, 14, 283-293.	2.8	77
35	Rootstocks Shape the Rhizobiome: Rhizosphere and Endosphere Bacterial Communities in the Grafted Tomato System. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	77
36	Septate endophyte colonization and host responses of grasses and forbs native to a tallgrass prairie. <i>Mycorrhiza</i> , 2012, 22, 109-119.	2.8	73

#	ARTICLE	IF	CITATIONS
37	Host Identity Impacts Rhizosphere Fungal Communities Associated with Three Alpine Plant Species. <i>Microbial Ecology</i> , 2012, 63, 682-693.	2.8	72
38	Vegetation Type and Age Drive Changes in Soil Properties, Nitrogen, and Carbon Sequestration in Urban Parks under Cold Climate. <i>Frontiers in Ecology and Evolution</i> , 2016, 4, .	2.2	72
39	Recruitment and establishment of the gut microbiome in arctic shorebirds. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	2.7	64
40	Spatial and successional dynamics of microbial biofilm communities in a grassland stream ecosystem. <i>Molecular Ecology</i> , 2016, 25, 4674-4688.	3.9	59
41	Effects of Established Willows on Primary Succession on Lyman Glacier Forefront, North Cascade Range, Washington, U.S.A.: Evidence for Simultaneous Canopy Inhibition and Soil Facilitation. <i>Arctic and Alpine Research</i> , 1998, 30, 31.	1.3	57
42	Soil Fungal Communities Underneath Willow Canopies on a Primary Successional Glacier Forefront: rDNA Sequence Results Can Be Affected by Primer Selection and Chimeric Data. <i>Microbial Ecology</i> , 2007, 53, 233-246.	2.8	57
43	Metaphenomic Responses of a Native Prairie Soil Microbiome to Moisture Perturbations. <i>MSystems</i> , 2019, 4, .	3.8	56
44	Habitat conditions and phenological tree traits overrule the influence of tree genotype in the needle mycobiome of <i>Picea glauca</i> system at an arctic treeline ecotone. <i>New Phytologist</i> , 2016, 211, 1221-1231.	7.3	55
45	Moth Outbreaks Alter Root-Associated Fungal Communities in Subarctic Mountain Birch Forests. <i>Microbial Ecology</i> , 2015, 69, 788-797.	2.8	54
46	The abundance of health-associated bacteria is altered in PAH polluted soils—Implications for health in urban areas?. <i>PLoS ONE</i> , 2017, 12, e0187852.	2.5	52
47	Half-lives of PAHs and temporal microbiota changes in commonly used urban landscaping materials. <i>PeerJ</i> , 2018, 6, e4508.	2.0	52
48	Fungal Communities and Functional Guilds Shift Along an Elevational Gradient in the Southern Appalachian Mountains. <i>Microbial Ecology</i> , 2018, 76, 156-168.	2.8	51
49	<i>Arabidopsis thaliana</i> model system reveals a continuum of responses to root endophyte colonization. <i>Fungal Biology</i> , 2013, 117, 250-260.	2.5	49
50	Phylogenetic diversity analyses reveal disparity between fungal and bacterial communities during microbial primary succession. <i>Soil Biology and Biochemistry</i> , 2015, 89, 52-60.	8.8	49
51	Composition and Drivers of Gut Microbial Communities in Arctic-Breeding Shorebirds. <i>Frontiers in Microbiology</i> , 2019, 10, 2258.	3.5	49
52	Repeated fire shifts carbon and nitrogen cycling by changing plant inputs and soil decomposition across ecosystems. <i>Ecological Monographs</i> , 2020, 90, e01409.	5.4	47
53	Can rDNA analyses of diverse fungal communities in soil and roots detect effects of environmental manipulations—a case study from tallgrass prairie. <i>Mycologia</i> , 2005, 97, 1177-1194.	1.9	46
54	Spatial distribution of discrete RAPD phenotypes of a root endophytic fungus, <i>Phialocephala fortinii</i> , at a primary successional site on a glacier forefront. <i>New Phytologist</i> , 1999, 141, 333-344.	7.3	44

#	ARTICLE	IF	CITATIONS
55	Analyses of ITS and LSU gene regions provide congruent results on fungal community responses. <i>Fungal Ecology</i> , 2014, 9, 65-68.	1.6	44
56	Twenty years of research on fungal-plant interactions on Lyman Glacier forefront – lessons learned and questions yet unanswered. <i>Fungal Ecology</i> , 2012, 5, 430-442.	1.6	41
57	Tallgrass prairie soil fungal communities are resilient to climate change. <i>Fungal Ecology</i> , 2014, 10, 44-57.	1.6	41
58	Fungi and Algae Co-Occur in Snow: An Issue of Shared Habitat or Algal Facilitation of Heterotrophs?. <i>Arctic, Antarctic, and Alpine Research</i> , 2015, 47, 729-749.	1.1	41
59	Long-term biodiversity intervention shapes health-associated commensal microbiota among urban day-care children. <i>Environment International</i> , 2021, 157, 106811.	10.0	36
60	Fire as a driver of fungal diversity – A synthesis of current knowledge. <i>Mycologia</i> , 2022, 114, 215-241.	1.9	36
61	EcM fungal community structure, but not diversity, altered in a Pb-contaminated shooting range in a boreal coniferous forest site in Southern Finland. <i>FEMS Microbiology Ecology</i> , 2011, 76, 121-132.	2.7	35
62	Context dependent fungal and bacterial soil community shifts in response to recent wildfires in the Southern Appalachian Mountains. <i>Forest Ecology and Management</i> , 2019, 451, 117520.	3.2	35
63	Woody plant encroachment, and its removal, impact bacterial and fungal communities across stream and terrestrial habitats in a tallgrass prairie ecosystem. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv109.	2.7	34
64	Ectomycorrhizal fungi in Lyman Lake Basin: a comparison between primary and secondary successional sites. <i>Mycologia</i> , 1999, 91, 575-582.	1.9	33
65	Ectomycorrhizal Fungi in Lyman Lake Basin: A Comparison between Primary and Secondary Successional Sites. <i>Mycologia</i> , 1999, 91, 575.	1.9	33
66	Biogeography of Root-Associated Fungal Endophytes. <i>Ecological Studies</i> , 2017, , 195-222.	1.2	30
67	Ectomycorrhizal Fungal Communities in Urban Parks Are Similar to Those in Natural Forests but Shaped by Vegetation and Park Age. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	29
68	Microbial Ecology of Snow Reveals Taxa-Specific Biogeographical Structure. <i>Microbial Ecology</i> , 2019, 77, 946-958.	2.8	28
69	Unraveling the Dark Septate Endophyte Functions: Insights from the Arabidopsis Model. , 2014, , 115-141.		27
70	Over twenty years farmland reforestation decreases fungal diversity of soils, but stimulates the return of ectomycorrhizal fungal communities. <i>Plant and Soil</i> , 2018, 427, 231-244.	3.7	26
71	Filamentous ascomycetes inhabiting the rhizoid environment of the liverwort <i>Cephaloziella varians</i> in Antarctica are assessed by direct PCR and cloning. <i>Mycologia</i> , 2003, 95, 457-466.	1.9	25
72	Soil fungal community changes in response to long-term fire cessation and N fertilization in tallgrass prairie. <i>Fungal Ecology</i> , 2019, 41, 45-55.	1.6	25

#	ARTICLE	IF	CITATIONS
73	Host-Environment Interplay Shapes Fungal Diversity in Mosquitoes. <i>MSphere</i> , 2021, 6, e0064621.	2.9	21
74	Analysis of ribosomal RNA indicates seasonal fungal community dynamics in <i>Andropogon gerardii</i> roots. <i>Mycorrhiza</i> , 2011, 21, 453-464.	2.8	19
75	Experimental drought re-ordered assemblages of root-associated fungi across North American grasslands. <i>Journal of Ecology</i> , 2021, 109, 776-792.	4.0	17
76	Biogeography of root-associated fungi in foundation grasses of North American plains. <i>Journal of Biogeography</i> , 2022, 49, 22-37.	3.0	17
77	Nitrogen enrichment suppresses other environmental drivers and homogenizes salt marsh leaf microbiome. <i>Ecology</i> , 2018, 99, 1411-1418.	3.2	13
78	Can rDNA analyses of diverse fungal communities in soil and roots detect effects of environmental manipulations—a case study from tallgrass prairie. <i>Mycologia</i> , 2005, 97, 1177-1194.	1.9	12
79	Chestnuts bred for blight resistance depart nursery with distinct fungal rhizobiomes. <i>Mycorrhiza</i> , 2019, 29, 313-324.	2.8	12
80	Urbanization minimizes the effects of plant traits on soil provisioned ecosystem services across climatic regions. <i>Global Change Biology</i> , 2021, 27, 4139-4153.	9.5	12
81	Fire, Hypogeous Fungi and Mycophagous Marsupials. <i>Mycological Research</i> , 2005, 109, 516-518.	2.5	8
82	Bacterial but Not Fungal Rhizosphere Community Composition Differ among Perennial Grass Ecotypes under Abiotic Environmental Stress. <i>Microbiology Spectrum</i> , 2022, 10, e0239121.	3.0	8
83	Draft Genome Sequence of <i>Fusarium</i> sp. Strain DS 682, a Novel Fungal Isolate from the Grass Rhizosphere. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	7
84	The rich and the sensitive: diverse fungal communities change functionally with the warming Arctic. <i>Molecular Ecology</i> , 2014, 23, 3127-3129.	3.9	6
85	Analyses of Sporocarps, Morphotyped Ectomycorrhizae, Environmental ITS and LSU Sequences Identify Common Genera that Occur at a Periglacial Site. <i>Journal of Fungi (Basel, Switzerland)</i> , 2015, 1, 76-93.	3.5	6
86	Mycorrhizal Fungi in Successional Environments. <i>Mycology</i> , 2005, , 139-168.	0.5	6
87	<i>Darksidea phi</i> , sp. nov., a dark septate root-associated fungus in foundation grasses in North American Great Plains. <i>Mycologia</i> , 2022, 114, 254-269.	1.9	6
88	Watershed and fire severity are stronger determinants of soil chemistry and microbiomes than within-watershed woody encroachment in a tallgrass prairie system. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	5
89	Multi-element fingerprinting and high throughput sequencing identify multiple elements that affect fungal communities in <i>Quercus macrocarpa</i> foliage. <i>Plant Signaling and Behavior</i> , 2010, 5, 1157-1161.	2.4	4
90	Terabase Metagenome Sequencing of Grassland Soil Microbiomes. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	4

#	ARTICLE	IF	CITATIONS
91	Filamentous ascomycetes inhabiting the rhizoid environment of the liverwort <i>Cephaloziella varians</i> in Antarctica are assessed by direct PCR and cloning. <i>Mycologia</i> , 2003, 95, 457-66.	1.9	4
92	Soil fungal communities are compositionally resistant to drought manipulations – Evidence from culture-dependent and culture-independent analyses. <i>Fungal Ecology</i> , 2021, 51, 101062.	1.6	3
93	Changes in Ectomycorrhizal Colonization and Root Peroxidase Activity in <i>Pinus sylvestris</i> Nursery Seedlings Planted in Forest Humus. <i>Scandinavian Journal of Forest Research</i> , 2004, 19, 400-408.	1.4	2
94	Analysis of Rhizosphere Fungal Communities Using rRNA and rDNA. <i>Soil Biology</i> , 2009, , 29-40.	0.8	1
95	Improving Instructional Fitness Requires Change. <i>BioScience</i> , 2020, 70, 1027-1035.	4.9	1
96	Precipitation, Not Land Use, Primarily Determines the Composition of Both Plant and Phyllosphere Fungal Communities. <i>Frontiers in Fungal Biology</i> , 0, 3, .	2.0	0