

Akifumi S Tanabe

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

3,262
citations

331259

21
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329751

37
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44
docs citations

44
times ranked

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citing authors

#	ARTICLE	IF	CITATIONS
1	Specialized mycorrhizal association between a partially mycoheterotrophic orchid <i>Oreorchis indica</i> and a <i>Tomentella</i> taxon. <i>Mycorrhiza</i> , 2021, 31, 243-250.	1.3	16
2	Mycorrhizal communities of two closely related species, <i>Pyrola subaphylla</i> and <i>P. japonica</i> , with contrasting degrees of mycoheterotrophy in a sympatric habitat. <i>Mycorrhiza</i> , 2021, 31, 219-229.	1.3	6
3	Aboveground herbivores drive stronger plant species-specific feedback than belowground fungi to regulate tree community assembly. <i>Oecologia</i> , 2021, 195, 773-784.	0.9	2
4	Rapid detection of macroalgal seed bank on cobbles: application of DNA metabarcoding using next-generation sequencing. <i>Journal of Applied Phycology</i> , 2019, 31, 2743-2753.	1.5	12
5	The fauna of freshwater calanoid copepods in Japan in the early decades of the 21 st Century: Implications for the assessment and conservation of biodiversity. <i>Limnology and Oceanography</i> , 2018, 63, 758-772.	1.6	10
6	Mycorrhizal fungi mediate the direction and strength of plant–soil feedbacks differently between arbuscular mycorrhizal and ectomycorrhizal communities. <i>Communications Biology</i> , 2018, 1, 196.	2.0	73
7	Structural diversity across arbuscular mycorrhizal, ectomycorrhizal, and endophytic plant–fungus networks. <i>BMC Plant Biology</i> , 2018, 18, 292.	1.6	9
8	Improving the standards for gut microbiome analysis of fecal samples: insights from the field biology of Japanese macaques on Yakushima Island. <i>Primates</i> , 2018, 59, 423-436.	0.7	18
9	Network hubs in root-associated fungal metacommunities. <i>Microbiome</i> , 2018, 6, 116.	4.9	112
10	Composition and Diversity of Soil Fungi in Dipterocarpaceae-Dominated Seasonal Tropical Forests in Thailand. <i>Microbes and Environments</i> , 2018, 33, 135-143.	0.7	4
11	Eukaryotic diversity in late Pleistocene marine sediments around a shallow methane hydrate deposit in the Japan Sea. <i>Geobiology</i> , 2017, 15, 715-727.	1.1	5
12	Host shifts enhance diversification of ectomycorrhizal fungi: diversification rate analysis of the ectomycorrhizal fungal genera <i>Strobilomyces</i> and <i>Afroboletus</i> with an 80% gene phylogeny. <i>New Phytologist</i> , 2017, 214, 443-454.	3.5	32
13	Phylogeny and biogeography of the genus <i>Stevia</i> (Asteraceae: Eupatorieae): an example of diversification in the Asteraceae in the new world. <i>Journal of Plant Research</i> , 2017, 130, 953-972.	1.2	12
14	Deep microbial life in high-quality granitic groundwater from geochemically and geographically distinct underground boreholes. <i>Environmental Microbiology Reports</i> , 2016, 8, 285-294.	1.0	35
15	Comparative study of the validity of three regions of the 18S rRNA gene for massively parallel sequencing-based monitoring of the planktonic eukaryote community. <i>Molecular Ecology Resources</i> , 2016, 16, 402-414.	2.2	80
16	A new resource of single nucleotide polymorphisms in the Japanese eel <i>Anguilla japonica</i> derived from restriction site-associated DNA. <i>Ichthyological Research</i> , 2016, 63, 496-504.	0.5	3
17	Structure of phyllosphere fungal communities in a tropical dipterocarp plantation: A massively parallel next-generation sequencing analysis. <i>Mycoscience</i> , 2016, 57, 171-180.	0.3	18
18	Network modules and hubs in plant-root fungal biomes. <i>Journal of the Royal Society Interface</i> , 2016, 13, 20151097.	1.5	100

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19	Contrasting Diversity and Host Association of Ectomycorrhizal Basidiomycetes versus Root-Associated Ascomycetes in a Dipterocarp Rainforest. <i>PLoS ONE</i> , 2015, 10, e0125550.	1.1	31
20	Diversity and Spatial Structure of Belowground Plantâ€Fungal Symbiosis in a Mixed Subtropical Forest of Ectomycorrhizal and Arbuscular Mycorrhizal Plants. <i>PLoS ONE</i> , 2014, 9, e86566.	1.1	81
21	Spatial Segregation and Aggregation of Ectomycorrhizal and Root-Endophytic Fungi in the Seedlings of Two <i>Quercus</i> Species. <i>PLoS ONE</i> , 2014, 9, e96363.	1.1	32
22	Diet disparity among sympatric herbivorous cichlids in the same ecomorphs in Lake Tanganyika: amplicon pyrosequences on algal farms and stomach contents. <i>BMC Biology</i> , 2014, 12, 90.	1.7	23
23	Detection of the horizontal spatial structure of soil fungal communities in a natural forest. <i>Population Ecology</i> , 2014, 56, 301-310.	0.7	29
24	<i>Palpitomonas bilix</i> represents a basal cryptist lineage: insight into the character evolution in Cryptista. <i>Scientific Reports</i> , 2014, 4, 4641.	1.6	80
25	Diversification of endosymbiosis: replacements, co-speciation and promiscuity of bacteriocyte symbionts in weevils. <i>ISME Journal</i> , 2013, 7, 1378-1390.	4.4	90
26	How are plant and fungal communities linked to each other in belowground ecosystems? A massively parallel pyrosequencing analysis of the association specificity of rootâ€associated fungi and their host plants. <i>Ecology and Evolution</i> , 2013, 3, 3112-3124.	0.8	71
27	Community composition of rootâ€associated fungi in a <i>Quercus</i> -dominated temperate forest: â€ocodominanceâ€of mycorrhizal and rootâ€endophytic fungi. <i>Ecology and Evolution</i> , 2013, 3, 1281-1293.	0.8	133
28	Two New Computational Methods for Universal DNA Barcoding: A Benchmark Using Barcode Sequences of Bacteria, Archaea, Animals, Fungi, and Land Plants. <i>PLoS ONE</i> , 2013, 8, e76910.	1.1	224
29	Sharing of Diverse Mycorrhizal and Root-Endophytic Fungi among Plant Species in an Oak-Dominated Coolâ€Temperate Forest. <i>PLoS ONE</i> , 2013, 8, e78248.	1.1	76
30	Entangling Ancient Allotetraploidization in Asian <i>Mitella</i> : An Integrated Approach for Multilocus Combinations. <i>Molecular Biology and Evolution</i> , 2012, 29, 429-439.	3.5	24
31	An asynchronous parallel genetic algorithm for the maximum likelihood phylogenetic tree search. , 2012, , .		0
32	High-Coverage ITS Primers for the DNA-Based Identification of Ascomycetes and Basidiomycetes in Environmental Samples. <i>PLoS ONE</i> , 2012, 7, e40863.	1.1	895
33	Kakusan4 and Aminosan: two programs for comparing nonpartitioned, proportional and separate models for combined molecular phylogenetic analyses of multilocus sequence data. <i>Molecular Ecology Resources</i> , 2011, 11, 914-921.	2.2	608
34	Extreme population genetic differentiation and secondary contact in the freshwater copepod <i>Acanthodiaptomus pacificus</i> in the Japanese Archipelago. <i>Molecular Ecology</i> , 2009, 18, 3699-3713.	2.0	34
35	New Records of Hairworms (Nematomorpha: Gordiida) from Japan. <i>Species Diversity</i> , 2009, 14, 131-135.	0.1	2
36	kakusan: a computer program to automate the selection of a nucleotide substitution model and the configuration of a mixed model on multilocus data. <i>Molecular Ecology Notes</i> , 2007, 7, 962-964.	1.7	263

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37	Sedimentary Facies and Depositional Rates of Submarine Cave Sediment in a Coral Reef of Okinawa. The Quaternary Research, 2003, 42, 99-104.	0.2	8