

Mika Tapio Tarkka

List of Publications by Year in descending order

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71
papers

5,146
citations

172457

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106344

65
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72
all docs

72
docs citations

72
times ranked

6286
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome sequencing analysis of maize roots reveals the effects of substrate and root hair formation in a spatial context. <i>Plant and Soil</i> , 2022, 478, 211-228.	3.7	9
2	Growth promotion and protection against root rot of sugar beet (<i>Beta vulgaris</i> L.) by two rock phosphate and potassium solubilizing <i>Streptomyces</i> spp. under greenhouse conditions. <i>Plant and Soil</i> , 2022, 472, 407-420.	3.7	7
3	Root hairs matter at field scale for maize shoot growth and nutrient uptake, but root trait plasticity is primarily triggered by texture and drought. <i>Plant and Soil</i> , 2022, 478, 119-141.	3.7	14
4	Designing Synergistic Biostimulants Formulation Containing Autochthonous Phosphate-Solubilizing Bacteria for Sustainable Wheat Production. <i>Frontiers in Microbiology</i> , 2022, 13, 889073.	3.5	8
5	Biofilm forming rhizobacteria affect the physiological and biochemical responses of wheat to drought. <i>AMB Express</i> , 2022, 12, .	3.0	6
6	Experimental platforms for the investigation of spatiotemporal patterns in the rhizosphere – Laboratory and field scale. <i>Journal of Plant Nutrition and Soil Science</i> , 2021, 184, 35-50.	1.9	49
7	Soil Texture, Sampling Depth and Root Hairs Shape the Structure of ACC Deaminase Bacterial Community Composition in Maize Rhizosphere. <i>Frontiers in Microbiology</i> , 2021, 12, 616828.	3.5	23
8	Spatiotemporal Dynamics of Maize (<i>Zea mays</i> L.) Root Growth and Its Potential Consequences for the Assembly of the Rhizosphere Microbiota. <i>Frontiers in Microbiology</i> , 2021, 12, 619499.	3.5	21
9	Interactions between soil properties, agricultural management and cultivar type drive structural and functional adaptations of the wheat rhizosphere microbiome to drought. <i>Environmental Microbiology</i> , 2021, 23, 5866-5882.	3.8	36
10	The wheat growth-promoting traits of <i>Ochrobactrum</i> and <i>Pantoea</i> species, responsible for solubilization of different P sources, are ensured by genes encoding enzymes of multiple P-releasing pathways. <i>Microbiological Research</i> , 2021, 246, 126703.	5.3	24
11	Multiple Potential Plant Growth Promotion Activities of Endemic <i>Streptomyces</i> spp. from Moroccan Sugar Beet Fields with Their Inhibitory Activities against <i>Fusarium</i> spp.. <i>Microorganisms</i> , 2021, 9, 1429.	3.6	21
12	Bridging Microbial Functional Traits With Localized Process Rates at Soil Interfaces. <i>Frontiers in Microbiology</i> , 2021, 12, 625697.	3.5	12
13	Ectomycorrhizal fungus supports endogenous rhythmic growth and corresponding resource allocation in oak during various below- and aboveground biotic interactions. <i>Scientific Reports</i> , 2021, 11, 23680.	3.3	5
14	Rhizosphere Spatiotemporal Organization – A Key to Rhizosphere Functions. <i>Frontiers in Agronomy</i> , 2020, 2, .	3.3	54
15	A multi-omics concentration-response framework uncovers novel understanding of triclosan effects in the chlorophyte <i>Scenedesmus vacuolatus</i> . <i>Journal of Hazardous Materials</i> , 2020, 397, 122727.	12.4	25
16	Compatibility of X-ray computed tomography with plant gene expression, rhizosphere bacterial communities and enzyme activities. <i>Journal of Experimental Botany</i> , 2020, 71, 5603-5614.	4.8	17
17	Oak displays common local but specific distant gene regulation responses to different mycorrhizal fungi. <i>BMC Genomics</i> , 2020, 21, 399.	2.8	14
18	Diversity and geographic distribution of soil streptomycetes with antagonistic potential against actinomycetoma-causing <i>Streptomyces sudanensis</i> in Sudan and South Sudan. <i>BMC Microbiology</i> , 2020, 20, 33.	3.3	11

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19	Glucose dehydrogenase gene containing phosphobacteria for biofortification of Phosphorus with growth promotion of rice. <i>Microbiological Research</i> , 2019, 223-225, 1-12.	5.3	59
20	Collembola interact with mycorrhizal fungi in modifying oak morphology, C and N incorporation and transcriptomics. <i>Royal Society Open Science</i> , 2019, 6, 181869.	2.4	15
21	Tree Response to Herbivory Is Affected by Endogenous Rhythmic Growth and Attenuated by Cotreatment With a Mycorrhizal Fungus. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 770-781.	2.6	5
22	DRomics: A Turnkey Tool to Support the Use of the Dose-Response Framework for Omics Data in Ecological Risk Assessment. <i>Environmental Science & Technology</i> , 2018, 52, 14461-14468.	10.0	37
23	Growing Research Networks on Mycorrhizae for Mutual Benefits. <i>Trends in Plant Science</i> , 2018, 23, 975-984.	8.8	51
24	Seeds with low phosphorus content: not so bad after all?. <i>Journal of Experimental Botany</i> , 2018, 69, 4993-4996.	4.8	7
25	Mycorrhizal microbiomes. <i>Mycorrhiza</i> , 2018, 28, 403-409.	2.8	22
26	Oak genome reveals facets of long lifespan. <i>Nature Plants</i> , 2018, 4, 440-452.	9.3	303
27	Transcriptome analysis in oak uncovers a strong impact of endogenous rhythmic growth on the interaction with plant-parasitic nematodes. <i>BMC Genomics</i> , 2016, 17, 627.	2.8	24
28	8 An Emerging Interdisciplinary Field: Fungal-Bacterial Interactions. , 2016, , 161-178.		4
29	Endogenous rhythmic growth, a trait suitable for the study of interplays between multitrophic interactions and tree development. <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2016, 19, 40-48.	2.7	20
30	Large scale transcriptome analysis reveals interplay between development of forest trees and a beneficial mycorrhiza helper bacterium. <i>BMC Genomics</i> , 2015, 16, 658.	2.8	28
31	Endogenous rhythmic growth in oak trees is regulated by internal clocks rather than resource availability. <i>Journal of Experimental Botany</i> , 2015, 66, 7113-7127.	4.8	27
32	Synergists and antagonists in the rhizosphere modulate microbial communities and growth of <i>Quercus robur</i> L.. <i>Soil Biology and Biochemistry</i> , 2015, 82, 65-73.	8.8	18
33	Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 2015, 47, 410-415.	21.4	870
34	The oak gene expression atlas: insights into Fagaceae genome evolution and the discovery of genes regulated during bud dormancy release. <i>BMC Genomics</i> , 2015, 16, 112.	2.8	49
35	Insights into organohalide respiration and the versatile catabolism of <i>Sulfurospirillum multivorans</i> gained from comparative genomics and physiological studies. <i>Environmental Microbiology</i> , 2014, 16, 3562-3580.	3.8	76
36	<i>Streptomyces</i> -Induced Resistance Against Oak Powdery Mildew Involves Host Plant Responses in Defense, Photosynthesis, and Secondary Metabolism Pathways. <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 891-900.	2.6	101

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37	Genome sequences of two dehalogenation specialists <i>Dehalococcoides mccartyi</i> strains BTF08 and DCMB5 enriched from the highly polluted Bitterfeld region. <i>FEMS Microbiology Letters</i> , 2013, 343, 101-104.	1.8	73
38	Detection and quantification of a mycorrhization helper bacterium and a mycorrhizal fungus in plant-soil microcosms at different levels of complexity. <i>BMC Microbiology</i> , 2013, 13, 205.	3.3	39
39	OakContig<sc>DF</sc>159.1, a reference library for studying differential gene expression in <i>Quercus robur</i> during controlled biotic interactions: use for quantitative transcriptomic profiling of oak roots in ectomycorrhizal symbiosis. <i>New Phytologist</i> , 2013, 199, 529-540.	7.3	97
40	Actinobacteria may influence white truffle (<i>Tuber magnatum</i> Pico) nutrition, ascocarp degradation and interactions with other soil fungi. <i>Fungal Ecology</i> , 2013, 6, 527-538.	1.6	27
41	Production of fungal and bacterial growth modulating secondary metabolites is widespread among mycorrhiza-associated streptomycetes. <i>BMC Microbiology</i> , 2012, 12, 164.	3.3	78
42	Protein-SIP enables time-resolved analysis of the carbon flux in a sulfate-reducing, benzene-degrading microbial consortium. <i>ISME Journal</i> , 2012, 6, 2291-2301.	9.8	109
43	Basidiomycetous Yeasts from Boletales Fruiting Bodies and Their Interactions with the Mycoparasite <i>Sepedonium chrysospermum</i> and the Host Fungus <i>Paxillus</i> . <i>Microbial Ecology</i> , 2012, 63, 295-303.	2.8	42
44	Bacterial-Fungal Interactions: Hyphens between Agricultural, Clinical, Environmental, and Food Microbiologists. <i>Microbiology and Molecular Biology Reviews</i> , 2011, 75, 583-609.	6.6	694
45	WS-5995 B, an antifungal agent inducing differential gene expression in the conifer pathogen <i>Heterobasidion annosum</i> but not in <i>Heterobasidion abietinum</i> . <i>Applied Microbiology and Biotechnology</i> , 2009, 85, 347-358.	3.6	6
46	Inter-kingdom encounters: recent advances in molecular bacterium-fungus interactions. <i>Current Genetics</i> , 2009, 55, 233-243.	1.7	95
47	Friends and foes: streptomycetes as modulators of plant disease and symbiosis. <i>Antonie Van Leeuwenhoek</i> , 2008, 94, 11-19.	1.7	154
48	Secondary Metabolites of Soil Streptomycetes in Biotic Interactions. <i>Soil Biology</i> , 2008, , 107-126.	0.8	28
49	Root inoculation with a forest soil streptomycete leads to locally and systemically increased resistance against phytopathogens in Norway spruce. <i>New Phytologist</i> , 2008, 177, 965-976.	7.3	103
50	Plant behavior upon contact with streptomycetes. <i>Plant Signaling and Behavior</i> , 2008, 3, 917-919.	2.4	31
51	Mycorrhiza Helper Bacteria. , 2008, , 113-132.		19
52	Plant Associated Soil Micro-organisms. <i>Soil Biology</i> , 2008, , 3-51.	0.8	14
53	Mycorrhizal Development and Cytoskeleton. , 2008, , 293-329.		0
54	Suppression of plant defence response by a mycorrhiza helper bacterium. <i>New Phytologist</i> , 2007, 174, 892-903.	7.3	77

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55	Aromatic weapons: truffles attack plants by the production of volatiles. <i>New Phytologist</i> , 2007, 175, 381-383.	7.3	35
56	The mycorrhiza helper bacteria revisited. <i>New Phytologist</i> , 2007, 176, 22-36.	7.3	778
57	Interaction with mycorrhiza helper bacterium <i>Streptomyces</i> sp. Ach 505 modifies organisation of actin cytoskeleton in the ectomycorrhizal fungus <i>Amanita muscaria</i> (fly agaric). <i>Current Genetics</i> , 2007, 52, 77-85.	1.7	40
58	The β -tubulin gene AmTuba1: a marker for rapid mycelial growth in the ectomycorrhizal basidiomycete <i>Amanita muscaria</i> . <i>Current Genetics</i> , 2006, 49, 294-301.	1.7	16
59	Auxofuran, a Novel Metabolite That Stimulates the Growth of Fly Agaric, Is Produced by the Mycorrhiza Helper Bacterium <i>Streptomyces</i> Strain Ach 505. <i>Applied and Environmental Microbiology</i> , 2006, 72, 3550-3557.	3.1	153
60	Mycorrhiza helper bacterium <i>Streptomyces</i> Ach 505 induces differential gene expression in the ectomycorrhizal fungus <i>Amanita muscaria</i> . <i>New Phytologist</i> , 2005, 168, 205-216.	7.3	157
61	Two phylogenetically highly distinct β -tubulin genes of the basidiomycete <i>Suillus bovinus</i> . <i>Current Genetics</i> , 2005, 47, 253-263.	1.7	10
62	Physiology of Ectomycorrhiza (ECM). , 2005, , 247-276.		6
63	Heat shock protein synthesis is induced by diethyl phthalate but not by di(2-ethylhexyl) phthalate in radish (<i>Raphanus sativus</i>). <i>Journal of Plant Physiology</i> , 2003, 160, 1001-1010.	3.5	20
64	Einfluss von Bodenbakterien auf Transkriptom und Proteom des Mykorrhizapilzes <i>Amanita muscaria</i> . , 2003, , 68-74.		0
65	Characterization of Small GTPases Cdc42 and Rac and the Relationship Between Cdc42 and Actin Cytoskeleton in Vegetative and Ectomycorrhizal Hyphae of <i>Suillus bovinus</i> . <i>Molecular Plant-Microbe Interactions</i> , 2001, 14, 135-144.	2.6	41
66	Scots pine expresses short-root-specific peroxidases during development. <i>FEBS Journal</i> , 2001, 268, 86-93.	0.2	28
67	Molecular characterization of actin genes from homobasidiomycetes: two different actin genes from <i>Schizophyllum commune</i> and <i>Suillus bovinus</i> . <i>Gene</i> , 2000, 251, 27-35.	2.2	37
68	Developmentally regulated proteins during differentiation of root system and ectomycorrhiza in Scots pine (<i>Pinus sylvestris</i>) with <i>Suillus bovinus</i> . <i>Physiologia Plantarum</i> , 1998, 104, 449-455.	5.2	18
69	Tubulin and actin protein patterns in Scots pine (<i>Pinus sylvestris</i>) roots and developing ectomycorrhiza with <i>Suillus bovinus</i> . <i>Physiologia Plantarum</i> , 1996, 96, 186-192.	5.2	35
70	Tubulin and actin protein patterns in Scots pine (<i>Pinus sylvestris</i>) roots and developing ectomycorrhiza with <i>Suillus bovinus</i> . <i>Physiologia Plantarum</i> , 1996, 96, 186-192.	5.2	8
71	Water Deficit History Selects Plant Beneficial Soil Bacteria Differently Under Conventional and Organic Farming. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	6