Jana M U'ren

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1248771/publications.pdf

Version: 2024-02-01

53 papers	3,435 citations	159585 30 h-index	175258 52 g-index
58 all docs	58 docs citations	58 times ranked	4282 citing authors

#	Article	IF	Citations
1	Ecological generalism drives hyperdiversity of secondary metabolite gene clusters in xylarialean endophytes. New Phytologist, 2022, 233, 1317-1330.	7.3	23
2	Methodological Approaches Frame Insights into Endophyte Richness and Community Composition. Microbial Ecology, 2021, 82, 21-34.	2.8	13
3	Climate and seasonality drive the richness and composition of tropical fungal endophytes at a landscape scale. Communications Biology, 2021, 4, 313.	4.4	45
4	Oaks provide new perspective on seed microbiome assembly. New Phytologist, 2021, 230, 1293-1295.	7.3	1
5	Two new endophytic species enrich the Coniochaeta endophytica / C. prunicola clade: Coniochaeta lutea sp. nov. and C. palaoa sp. nov.. Plant and Fungal Systematics, 2021, 66, 66-78.	0.5	3
6	Strobiloscyphones Aâ€“F, 6-Isopentylsphaeropsidones and Other Metabolites from Strobiloscypha sp. AZ0266, a Leaf-Associated Fungus of Douglas Fir. Journal of Natural Products, 2021, 84, 2575-2586.	3.0	2
7	Cyanolichen microbiome contains novel viruses that encode genes to promote microbial metabolism. ISME Communications, 2021, 1, .	4.2	3
8	Coniochaeta elegans sp. nov., Coniochaeta montana sp. nov. and Coniochaeta nivea sp. nov., three new species of endophytes with distinctive morphology and functional traits. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	1.7	3
9	Shed Light in the DaRk LineagES of the Fungal Tree of Lifeâ€”STRES. Life, 2020, 10, 362.	2.4	16
10	Teratopyrones Aâ€“C, Dimeric Naphtho-Î³-Pyrones and Other Metabolites from Teratosphaeria sp. AK1128, a Fungal Endophyte of Equisetum arvense. Molecules, 2020, 25, 5058.	3.8	1
11	Marine mammal skin microbiotas are influenced by host phylogeny. Royal Society Open Science, 2020, 7, 192046.	2.4	22
12	Coniochaeta endophytica sp. nov., a foliar endophyte associated with healthy photosynthetic tissue of Platycladus orientalis (Cupressaceae). Plant and Fungal Systematics, 2019, 64, 65-79.	0.5	17
13	T-BAS Version 2.1: Tree-Based Alignment Selector Toolkit for Evolutionary Placement of DNA Sequences and Viewing Alignments and Specimen Metadata on Curated and Custom Trees. Microbiology Resource Announcements, 2019, 8, .	0.6	35
14	Host availability drives distributions of fungal endophytes in the imperilled boreal realm. Nature Ecology and Evolution, 2019, 3, 1430-1437.	7.8	91
15	Age-related variation in the oral microbiome of urban Cooperâ€™s hawks (Accipiter cooperii). BMC Microbiology, 2019, 19, 47.	3.3	24
16	Cytotoxic and Noncytotoxic Metabolites from Teratosphaeria sp. FL2137, a Fungus Associated with Pinus clausa. Journal of Natural Products, 2018, 81, 616-624.	3.0	11
17	Phage hunters: Computational strategies for finding phages in large-scale â€˜omics datasets. Virus Research, 2018, 244, 110-115.	2.2	33
18	Using collections data to infer biogeographic, environmental, and host structure in communities of endophytic fungi. Mycologia, 2018, 110, 47-62.	1.9	19

#	Article	IF	Citations
19	T-BAS: Tree-Based Alignment Selector toolkit for phylogenetic-based placement, alignment downloads and metadata visualization: an example with the Pezizomycotina tree of life. Bioinformatics, 2017, 33, 1160-1168.	4.1	55
20	Soilborne fungi have host affinity and host-specific effects on seed germination and survival in a lowland tropical forest. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 11458-11463.	7.1	97
21	An Endohyphal Bacterium (Chitinophaga, Bacteroidetes) Alters Carbon Source Use by Fusarium keratoplasticum (F. solani Species Complex, Nectriaceae). Frontiers in Microbiology, 2017, 8, 350.	3.5	69
22	Computational prospecting the great viral unknown. FEMS Microbiology Letters, 2016, 363, fnw077.	1.8	56
23	Viral metabolic reprogramming in marine ecosystems. Current Opinion in Microbiology, 2016, 31, 161-168.	5.1	192
24	Oxaspirol B with p97 Inhibitory Activity and Other Oxaspirols from Lecythophora sp. FL1375 and FL1031, Endolichenic Fungi Inhabiting Parmotrema tinctorum and Cladonia evansii. Journal of Natural Products, 2016, 79, 340-352.	3.0	29
25	Contributions of North American endophytes to the phylogeny, ecology, and taxonomy of Xylariaceae (Sordariomycetes, Ascomycota). Molecular Phylogenetics and Evolution, 2016, 98, 210-232.	2.7	110
26	Interaction type influences ecological network structure more than local abiotic conditions: evidence from endophytic and endolichenic fungi at a continental scale. Oecologia, 2016, 180, 181-191.	2.0	50
27	Pervasive Effects of Wildfire on Foliar Endophyte Communities in Montane Forest Trees. Microbial Ecology, 2016, 71, 452-468.	2.8	37
28	Diversity, taxonomic composition, and functional aspects of fungal communities in living, senesced, and fallen leaves at five sites across North America. PeerJ, 2016, 4, e2768.	2.0	48
29	Draft Genome Sequence of the Ale-Fermenting Saccharomyces cerevisiae Strain GSY2239. Genome Announcements, 2015, 3, .	0.8	5
30	Cytotoxic Cytochalasins and Other Metabolites from Xylariaceae sp. FL0390, a Fungal Endophyte of Spanish Moss. Natural Product Communications, 2015, 10, 1934578X1501001.	0.5	3
31	Fungal Endophytes in Aboveground Tissues of Desert Plants: Infrequent in Culture, but Highly Diverse and Distinctive Symbionts. Microbial Ecology, 2015, 70, 61-76.	2.8	84
32	Phylogenetic analyses of eurotiomycetous endophytes reveal their close affinities to Chaetothyriales, Eurotiales, and a new order â€“ Phaeomoniellales. Molecular Phylogenetics and Evolution, 2015, 85, 117-130.	2.7	66
33	Sesquiterpenes and other constituents of Xylaria sp. NC1214, a fungal endophyte of the moss Hypnum sp.. Phytochemistry, 2015, 118, 102-108.	2.9	41
34	Anteaglonialides Aâ€“F and Palmarumycins CE₁â€“CE₃ from Anteaglonium sp. FL0768, a Fungal Endophyte of the Spikemoss Selaginella arenicola. Journal of Natural Products, 2015, 78, 2738-2747.	3.0	22
35	Cytotoxic Cytochalasins and Other Metabolites from Xylariaceae sp. FL0390, a Fungal Endophyte of Spanish Moss. Natural Product Communications, 2015, 10, 1655-8.	0.5	4
36	Delitschiapyrone A, a Pyroneâ€“Naphthalenone Adduct Bearing a New Pentacyclic Ring System from the Leaf-Associated Fungus Delitschia sp. FL1581. Organic Letters, 2014, 16, 5944-5947.	4.6	27

#	Article	IF	Citations
37	Tissue storage and primer selection influence pyrosequencingâ€based inferences of diversity and community composition of endolichenic and endophytic fungi. Molecular Ecology Resources, 2014, 14, 1032-1048.	4.8	83
38	Genetic variation in horizontally transmitted fungal endophytes of pine needles reveals population structure in cryptic species. American Journal of Botany, 2014, 101, 1362-1374.	1.7	34
39	Host and geographic structure of endophytic and endolichenic fungi at a continental scale. American Journal of Botany, 2012, 99, 898-914.	1.7	304
40	Geopyxins Aâ€“E, ent-Kaurane Diterpenoids from Endolichenic Fungal Strains Geopyxis aff. majalis and Geopyxis sp. AZ0066: Structureâ€“Activity Relationships of Geopyxins and Their Analogues. Journal of Natural Products, 2012, 75, 361-369.	3.0	70
41	Smardaesidins Aâ€“G, Isopimarane and 20-nor-Isopimarane Diterpenoids from Smardaea sp., a Fungal Endophyte of the Moss Ceratodon purpureus. Journal of Natural Products, 2011, 74, 2052-2061.	3.0	63
42	Community Analysis Reveals Close Affinities Between Endophytic and Endolichenic Fungi in Mosses and Lichens. Microbial Ecology, 2010, 60, 340-353.	2.8	191
43	Diversity and evolutionary origins of fungi associated with seeds of a neotropical pioneer tree: a case study for analysing fungal environmental samples. Mycological Research, 2009, 113, 432-449.	2.5	131
44	Bacillus anthracis in China and its relationship to worldwide lineages. BMC Microbiology, 2009, 9, 71.	3.3	85
45	Is the hope for a cellulosic biofuel a lot of rot?. Environmental Microbiology, 2009, 11, 2475-2476.	3.8	0
46	Strain-Specific Single-Nucleotide Polymorphism Assays for the Bacillus anthracis Ames Strain. Journal of Clinical Microbiology, 2007, 45, 47-53.	3.9	126
47	Fine-Scale Genetic Diversity among Burkholderia pseudomallei Soil Isolates in Northeast Thailand. Applied and Environmental Microbiology, 2007, 73, 6678-6681.	3.1	24
48	Global Genetic Population Structure of Bacillus anthracis. PLoS ONE, 2007, 2, e461.	2.5	317
49	VNTR analysis of selected outbreaks of Burkholderia pseudomallei in Australia. Infection, Genetics and Evolution, 2007, 7, 416-423.	2.3	32
50	Tandem repeat regions within the Burkholderia pseudomallei genome and their application for high resolution genotyping. BMC Microbiology, 2007, 7, 23.	3.3	70
51	Use of a Real-Time PCR TaqMan Assay for Rapid Identification and Differentiation of Burkholderia pseudomallei and Burkholderia mallei. Journal of Clinical Microbiology, 2005, 43, 5771-5774.	3.9	50
52	Selection Versus Demography: A Multilocus Investigation of the Domestication Process in Maize. Molecular Biology and Evolution, 2004, 21, 1214-1225.	8.9	251
53	Phylogenetic discovery bias in Bacillus anthracis using single-nucleotide polymorphisms from whole-genome sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13536-13541.	7.1	243