

Teresita M Porter

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

3,052
citations

218381

26
h-index

276539

41
g-index

56
all docs

56
docs citations

56
times ranked

4422
citing authors

#	ARTICLE	IF	CITATIONS
1	Simultaneous assessment of the macrobiome and microbiome in a bulk sample of tropical arthropods through DNA metasytematics. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 8007-8012.	3.3	252
2	Scaling up: A guide to high-throughput genomic approaches for biodiversity analysis. Molecular Ecology, 2018, 27, 313-338.	2.0	248
3	A Comprehensive, Automatically Updated Fungal ITS Sequence Dataset for Reference-Based Chimera Control in Environmental Sequencing Efforts. Microbes and Environments, 2015, 30, 145-150.	0.7	231
4	Massively parallel multiplex DNA sequencing for specimen identification using an Illumina MiSeq platform. Scientific Reports, 2015, 5, 9687.	1.6	217
5	Five simple guidelines for establishing basic authenticity and reliability of newly generated fungal ITS sequences. MycoKeys, 0, 4, 37-63.	0.8	157
6	The cantharelloid clade: dealing with incongruent gene trees and phylogenetic reconstruction methods. Mycologia, 2006, 98, 937-948.	0.8	135
7	Over 2.5 million COI sequences in GenBank and growing. PLoS ONE, 2018, 13, e0200177.	1.1	125
8	Improving ITS sequence data for identification of plant pathogenic fungi. Fungal Diversity, 2014, 67, 11-19.	4.7	123
9	Automated high throughput animal CO1 metabarcoding classification. Scientific Reports, 2018, 8, 4226.	1.6	112
10	Rapid Degradation of <i>Deepwater Horizon</i> Spilled Oil by Indigenous Microbial Communities in Louisiana Saltmarsh Sediments. Environmental Science & Technology, 2013, 47, 13303-13312.	4.6	108
11	Widespread occurrence and phylogenetic placement of a soil clone group adds a prominent new branch to the fungal tree of life. Molecular Phylogenetics and Evolution, 2008, 46, 635-644.	1.2	95
12	The cantharelloid clade: dealing with incongruent gene trees and phylogenetic reconstruction methods. Mycologia, 2006, 98, 937-948.	0.8	89
13	COI metabarcoding primer choice affects richness and recovery of indicator taxa in freshwater systems. PLoS ONE, 2019, 14, e0220953.	1.1	86
14	Studying Ecosystems With DNA Metabarcoding: Lessons From Biomonitoring of Aquatic Macroinvertebrates. Frontiers in Ecology and Evolution, 2019, 7, .	1.1	85
15	DNA metabarcoding and morphological macroinvertebrate metrics reveal the same changes in boreal watersheds across an environmental gradient. Scientific Reports, 2017, 7, 12777.	1.6	80
16	Fruiting body and soil rDNA sampling detects complementary assemblage of Agaricomycotina (Basidiomycota, Fungi) in a hemlock-dominated forest plot in southern Ontario. Molecular Ecology, 2008, 17, 3037-3050.	2.0	78
17	Structure, Function, and Phylogeny of the Mating Locus in the Rhizopus oryzae Complex. PLoS ONE, 2010, 5, e15273.	1.1	72
18	Key Questions for Next-Generation Biomonitoring. Frontiers in Environmental Science, 2020, 7, .	1.5	68

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19	Watered-down biodiversity? A comparison of metabarcoding results from DNA extracted from matched water and bulk tissue biomonitoring samples. <i>PLoS ONE</i> , 2019, 14, e0225409.	1.1	65
20	Are similarity- or phylogeny-based methods more appropriate for classifying internal transcribed spacer (ITS) metagenomic amplicons?. <i>New Phytologist</i> , 2011, 192, 775-782.	3.5	58
21	Factors That Affect Large Subunit Ribosomal DNA Amplicon Sequencing Studies of Fungal Communities: Classification Method, Primer Choice, and Error. <i>PLoS ONE</i> , 2012, 7, e35749.	1.1	52
22	Rapid and accurate taxonomic classification of insect (class Insecta) cytochrome c oxidase subunit 1 () Tj ETQq0 0 0 rgBT /Overlock 10 T 929-942.	2.2	50
23	DNA metabarcoding reveals metacommunity dynamics in a threatened boreal wetland wilderness. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 8539-8545.	3.3	50
24	Ancient pathogen DNA in archaeological samples detected with a Microbial Detection Array. <i>Scientific Reports</i> , 2014, 4, 4245.	1.6	48
25	Metabarcoding of storage ethanol vs. conventional morphometric identification in relation to the use of stream macroinvertebrates as ecological indicators in forest management. <i>Ecological Indicators</i> , 2019, 101, 173-184.	2.6	46
26	Molecular phylogeny of the Blastocladiomycota (Fungi) based on nuclear ribosomal DNA. <i>Fungal Biology</i> , 2011, 115, 381-392.	1.1	45
27	Putting COI Metabarcoding in Context: The Utility of Exact Sequence Variants (ESVs) in Biodiversity Analysis. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	37
28	Network-Based Biomonitoring: Exploring Freshwater Food Webs With Stable Isotope Analysis and DNA Metabarcoding. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	31
29	The Ecobiomics project: Advancing metagenomics assessment of soil health and freshwater quality in Canada. <i>Science of the Total Environment</i> , 2020, 710, 135906.	3.9	25
30	Variations in terrestrial arthropod DNA metabarcoding methods recovers robust beta diversity but variable richness and site indicators. <i>Scientific Reports</i> , 2019, 9, 18218.	1.6	23
31	Amplicon pyrosequencing late Pleistocene permafrost: the removal of putative contaminant sequences and small-scale reproducibility. <i>Molecular Ecology Resources</i> , 2013, 13, 798-810.	2.2	16
32	Soil microbiomes associated with two dominant Costa Rican tree species, and implications for remediation: A case study from a Costa Rican conservation area. <i>Applied Soil Ecology</i> , 2019, 137, 139-153.	2.1	16
33	Ribosomal DNA and Plastid Markers Used to Sample Fungal and Plant Communities from Wetland Soils Reveals Complementary Biotas. <i>PLoS ONE</i> , 2016, 11, e0142759.	1.1	16
34	Profile hidden Markov model sequence analysis can help remove putative pseudogenes from DNA barcoding and metabarcoding datasets. <i>BMC Bioinformatics</i> , 2021, 22, 256.	1.2	15
35	Propylene glycol-based antifreeze is an effective preservative for DNA metabarcoding of benthic arthropods. <i>Freshwater Science</i> , 2021, 40, 77-87.	0.9	14
36	Freshwater diatom biomonitoring through benthic kick-net metabarcoding. <i>PLoS ONE</i> , 2020, 15, e0242143.	1.1	9

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37	Forest soil biotic communities show few responses to wood ash applications at multiple sites across Canada. <i>Scientific Reports</i> , 2022, 12, 4171.	1.6	8
38	Drivers of tropical soil invertebrate community composition and richness across tropical secondary forests using DNA metabystematics. <i>Scientific Reports</i> , 2020, 10, 18429.	1.6	5
39	LANDMark: an ensemble approach to the supervised selection of biomarkers in high-throughput sequencing data. <i>BMC Bioinformatics</i> , 2022, 23, 110.	1.2	5
40	Multi-marker DNA metabarcoding detects suites of environmental gradients from an urban harbour. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
41	Differences in the soil microbiomes of <i>Pentaclethra macroloba</i> across tree size and in contrasting land use histories. <i>Plant and Soil</i> , 2020, 452, 329-345.	1.8	3
42	eDNA and Bioassessment of Rivers. , 2021, , .		0