

# 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	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
2	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
3	Multi-marker DNA metabarcoding detects suites of environmental gradients from an urban harbour. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
4	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
5	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
6	eDNA and Bioassessment of Rivers. , 2021, , .		0
7	Key Questions for Next-Generation Biomonitoring. <i>Frontiers in Environmental Science</i> , 2020, 7, .	1.5	68
8	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
9	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
10	Drivers of tropical soil invertebrate community composition and richness across tropical secondary forests using DNA metasytematics. <i>Scientific Reports</i> , 2020, 10, 18429.	1.6	5
11	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
12	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
13	Freshwater diatom biomonitoring through benthic kick-net metabarcoding. <i>PLoS ONE</i> , 2020, 15, e0242143.	1.1	9
14	Studying Ecosystems With DNA Metabarcoding: Lessons From Biomonitoring of Aquatic Macroinvertebrates. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	85
15	COI metabarcoding primer choice affects richness and recovery of indicator taxa in freshwater systems. <i>PLoS ONE</i> , 2019, 14, e0220953.	1.1	86
16	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
17	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
18	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

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19	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
20	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
21	Scaling up: A guide to high-throughput genomic approaches for biodiversity analysis. <i>Molecular Ecology</i> , 2018, 27, 313-338.	2.0	248
22	Automated high throughput animal CO1 metabarcode classification. <i>Scientific Reports</i> , 2018, 8, 4226.	1.6	112
23	Over 2.5 million COI sequences in GenBank and growing. <i>PLoS ONE</i> , 2018, 13, e0200177.	1.1	125
24	DNA metabarcoding and morphological macroinvertebrate metrics reveal the same changes in boreal watersheds across an environmental gradient. <i>Scientific Reports</i> , 2017, 7, 12777.	1.6	80
25	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
26	A Comprehensive, Automatically Updated Fungal ITS Sequence Dataset for Reference-Based Chimera Control in Environmental Sequencing Efforts. <i>Microbes and Environments</i> , 2015, 30, 145-150.	0.7	231
27	Massively parallel multiplex DNA sequencing for specimen identification using an Illumina MiSeq platform. <i>Scientific Reports</i> , 2015, 5, 9687.	1.6	217
28	Rapid and accurate taxonomic classification of insect (class Insecta) cytochrome c oxidase subunit 1 (COI) using a 10 Tm primer. <i>PLoS ONE</i> , 2014, 9, e929-942.	2.2	50
29	Simultaneous assessment of the macrobiome and microbiome in a bulk sample of tropical arthropods through DNA metabarcoding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8007-8012.	3.3	252
30	Improving ITS sequence data for identification of plant pathogenic fungi. <i>Fungal Diversity</i> , 2014, 67, 11-19.	4.7	123
31	Ancient pathogen DNA in archaeological samples detected with a Microbial Detection Array. <i>Scientific Reports</i> , 2014, 4, 4245.	1.6	48
32	Rapid Degradation of Deepwater Horizon Spilled Oil by Indigenous Microbial Communities in Louisiana Saltmarsh Sediments. <i>Environmental Science &amp; Technology</i> , 2013, 47, 13303-13312.	4.6	108
33	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
34	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
35	Molecular phylogeny of the Blastocladiomycota (Fungi) based on nuclear ribosomal DNA. <i>Fungal Biology</i> , 2011, 115, 381-392.	1.1	45
36	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

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37	Structure, Function, and Phylogeny of the Mating Locus in the <i>Rhizopus oryzae</i> Complex. <i>PLoS ONE</i> , 2010, 5, e15273.	1.1	72
38	Widespread occurrence and phylogenetic placement of a soil clone group adds a prominent new branch to the fungal tree of life. <i>Molecular Phylogenetics and Evolution</i> , 2008, 46, 635-644.	1.2	95
39	Fruiting body and soil rDNA sampling detects complementary assemblage of Agaricomycotina (Basidiomycota, Fungi) in a hemlock-dominated forest plot in southern Ontario. <i>Molecular Ecology</i> , 2008, 17, 3037-3050.	2.0	78
40	The cantharelloid clade: dealing with incongruent gene trees and phylogenetic reconstruction methods. <i>Mycologia</i> , 2006, 98, 937-948.	0.8	89
41	The cantharelloid clade: dealing with incongruent gene trees and phylogenetic reconstruction methods. <i>Mycologia</i> , 2006, 98, 937-948.	0.8	135
42	Five simple guidelines for establishing basic authenticity and reliability of newly generated fungal ITS sequences. <i>MycKeys</i> , 0, 4, 37-63.	0.8	157