

# Yvette M Piceno

## List of Publications by Year in descending order

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Version: 2024-02-01

58  
papers

10,471  
citations

87401

40  
h-index

162838

57  
g-index

61  
all docs

61  
docs citations

61  
times ranked

14566  
citing authors

#	ARTICLE	IF	CITATIONS
1	Fecal microbiota transplant for Crohn disease: A study evaluating safety, efficacy, and microbiome profile. <i>United European Gastroenterology Journal</i> , 2019, 7, 807-814.	1.6	51
2	Microbial Sulfate Reduction and Perchlorate Inhibition in a Novel Mesoscale Tank Experiment. <i>Energy &amp; Fuels</i> , 2018, 32, 12049-12065.	2.5	5
3	Metabolic and spatio-taxonomic response of uncultivated seafloor bacteria following the Deepwater Horizon oil spill. <i>ISME Journal</i> , 2017, 11, 2569-2583.	4.4	39
4	Bacterial community structure transformed after thermophilically composting human waste in Haiti. <i>PLoS ONE</i> , 2017, 12, e0177626.	1.1	37
5	Genome-Resolved Metagenomic Analysis Reveals Roles for Candidate Phyla and Other Microbial Community Members in Biogeochemical Transformations in Oil Reservoirs. <i>MBio</i> , 2016, 7, e01669-15.	1.8	151
6	Quo vadis? Microbial profiling revealed strong effects of cleanroom maintenance and routes of contamination in indoor environments. <i>Scientific Reports</i> , 2015, 5, 9156.	1.6	52
7	Comparing Bacterial Community Composition of Healthy and Dark Spot-Affected <i>Siderastrea siderea</i> in Florida and the Caribbean. <i>PLoS ONE</i> , 2014, 9, e108767.	1.1	30
8	Temperature and injection water source influence microbial community structure in four Alaskan North Slope hydrocarbon reservoirs. <i>Frontiers in Microbiology</i> , 2014, 5, 409.	1.5	37
9	Inhibition of microbial sulfate reduction in a flow-through column system by (per)chlorate treatment. <i>Frontiers in Microbiology</i> , 2014, 5, 315.	1.5	103
10	Effects of TiO <sub>2</sub> and Ag Nanoparticles on Polyhydroxybutyrate Biosynthesis By Activated Sludge Bacteria. <i>Environmental Science &amp; Technology</i> , 2014, 48, 14712-14720.	4.6	19
11	Expansion of Urease- and Uricase-Containing, Indole- and p-Cresol-Forming and Contraction of Short-Chain Fatty Acid-Producing Intestinal Microbiota in ESRD. <i>American Journal of Nephrology</i> , 2014, 39, 230-237.	1.4	478
12	Microbial biogeography across a full-scale wastewater treatment plant transect: evidence for immigration between coupled processes. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 4723-4736.	1.7	51
13	Coral transcriptome and bacterial community profiles reveal distinct Yellow Band Disease states in <i>Orbicella faveolata</i> . <i>ISME Journal</i> , 2014, 8, 2411-2422.	4.4	80
14	Bacterial communities in commercial aircraft high-efficiency particulate air (HEPA) filters assessed by PhyloChip analysis. <i>Indoor Air</i> , 2013, 23, 50-61.	2.0	43
15	Diversity of bacterioplankton in contrasting Tibetan lakes revealed by high-density microarray and clone library analysis. <i>FEMS Microbiology Ecology</i> , 2013, 86, 277-287.	1.3	41
16	Succession of Hydrocarbon-Degrading Bacteria in the Aftermath of the <i>Deepwater Horizon</i> Oil Spill in the Gulf of Mexico. <i>Environmental Science &amp; Technology</i> , 2013, 47, 10860-10867.	4.6	344
17	Tackling the minority: sulfate-reducing bacteria in an archaea-dominated subsurface biofilm. <i>ISME Journal</i> , 2013, 7, 635-651.	4.4	57
18	Biogeography of bacterioplankton in the tropical seawaters of Singapore. <i>FEMS Microbiology Ecology</i> , 2013, 84, 259-269.	1.3	19

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19	Chronic kidney disease alters intestinal microbial flora. <i>Kidney International</i> , 2013, 83, 308-315.	2.6	828
20	Truffle BrÃs Have an Impact on the Diversity of Soil Bacterial Communities. <i>PLoS ONE</i> , 2013, 8, e61945.	1.1	55
21	Changes of Soil Bacterial Diversity as a Consequence of Agricultural Land Use in a Semi-Arid Ecosystem. <i>PLoS ONE</i> , 2013, 8, e59497.	1.1	95
22	Comparing Bacterial Community Composition between Healthy and White Plague-Like Disease States in <i>Orbicella annularis</i> Using PhyloChip, G3 Microarrays. <i>PLoS ONE</i> , 2013, 8, e79801.	1.1	32
23	Microbial Community Analysis of a Coastal Salt Marsh Affected by the Deepwater Horizon Oil Spill. <i>PLoS ONE</i> , 2012, 7, e41305.	1.1	146
24	Influence of geogenic factors on microbial communities in metallogenic Australian soils. <i>ISME Journal</i> , 2012, 6, 2107-2118.	4.4	79
25	PhyloChip, microarray comparison of sampling methods used for coral microbial ecology. <i>Journal of Microbiological Methods</i> , 2012, 88, 103-109.	0.7	19
26	Changes in the microbial community structure of bacteria, archaea and fungi in response to elevated CO <sub>2</sub> and warming in an Australian native grassland soil. <i>Environmental Microbiology</i> , 2012, 14, 3081-3096.	1.8	134
27	Comparison of the Fecal Microbiota in Feral and Domestic Goats. <i>Genes</i> , 2012, 3, 1-18.	1.0	19
28	The phylogenetic composition and structure of soil microbial communities shifts in response to elevated carbon dioxide. <i>ISME Journal</i> , 2012, 6, 259-272.	4.4	110
29	Bacterial Diversity in the Cecum of the World's Largest Living Rodent ( <i>Hydrochoerus hydrochaeris</i> ). <i>Microbial Ecology</i> , 2012, 63, 719-725.	1.4	16
30	Bacterial communities associated with a mineral weathering profile at a sulphidic mine tailings dump in arid Western Australia. <i>FEMS Microbiology Ecology</i> , 2012, 79, 298-311.	1.3	69
31	High-density PhyloChip profiling of stimulated aquifer microbial communities reveals a complex response to acetate amendment. <i>FEMS Microbiology Ecology</i> , 2012, 81, 188-204.	1.3	43
32	Comparison of Innovative Molecular Approaches and Standard Spore Assays for Assessment of Surface Cleanliness. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5438-5444.	1.4	27
33	Changes in Fecal Microbiota of Gulf War Veterans With Irritable Bowel Syndrome. <i>Gastroenterology</i> , 2011, 140, S-532.	0.6	0
34	Deciphering the Rhizosphere Microbiome for Disease-Suppressive Bacteria. <i>Science</i> , 2011, 332, 1097-1100.	6.0	2,135
35	PhyloChip hybridization uncovered an enormous bacterial diversity in the rhizosphere of different potato cultivars: many common and few cultivar-dependent taxa. <i>FEMS Microbiology Ecology</i> , 2011, 75, 497-506.	1.3	198
36	Bacterial Diversity of Terrestrial Crystalline Volcanic Rocks, Iceland. <i>Microbial Ecology</i> , 2011, 62, 69-79.	1.4	51

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37	Bacterial Diversity of Weathered Terrestrial Icelandic Volcanic Glasses. <i>Microbial Ecology</i> , 2010, 60, 740-752.	1.4	66
38	Microbial secondary succession in a chronosequence of chalk grasslands. <i>ISME Journal</i> , 2010, 4, 711-715.	4.4	73
39	Bacterial community structure corresponds to performance during cathodic nitrate reduction. <i>ISME Journal</i> , 2010, 4, 1443-1455.	4.4	137
40	Bacterial Community Structure in Geographically Distributed Biological Wastewater Treatment Reactors. <i>Environmental Science &amp; Technology</i> , 2010, 44, 7391-7396.	4.6	180
41	Deep-Sea Oil Plume Enriches Indigenous Oil-Degrading Bacteria. <i>Science</i> , 2010, 330, 204-208.	6.0	1,109
42	Comprehensive Census of Bacteria in Clean Rooms by Using DNA Microarray and Cloning Methods. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6559-6567.	1.4	80
43	Environmental microarray analyses of Antarctic soil microbial communities. <i>ISME Journal</i> , 2009, 3, 340-351.	4.4	156
44	Bacterial diversity and White Plague Disease-associated community changes in the Caribbean coral <i>Montastraea faveolata</i> . <i>ISME Journal</i> , 2009, 3, 512-521.	4.4	364
45	Prokaryotic community profiles at different operational stages of a Greek solar saltern. <i>Research in Microbiology</i> , 2008, 159, 609-627.	1.0	52
46	Urban aerosols harbor diverse and dynamic bacterial populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 299-304.	3.3	593
47	High-Density Universal 16S rRNA Microarray Analysis Reveals Broader Diversity than Typical Clone Library When Sampling the Environment. <i>Microbial Ecology</i> , 2007, 53, 371-383.	1.4	416
48	NAST: a multiple sequence alignment server for comparative analysis of 16S rRNA genes. <i>Nucleic Acids Research</i> , 2006, 34, W394-W399.	6.5	918
49	Flash detection/identification of pathogens, bacterial spores and bioterrorism agent biomarkers from clinical and environmental matrices. <i>Journal of Microbiological Methods</i> , 2002, 48, 139-147.	0.7	28
50	Stability of a rhizosphere microbial community exposed to natural and manipulated environmental variability. <i>FEMS Microbiology Ecology</i> , 2001, 38, 69-76.	1.3	30
51	Stability in Natural Bacterial Communities: II. Plant Resource Allocation Effects on Rhizosphere Diazotroph Assemblage Composition. <i>Microbial Ecology</i> , 2000, 39, 41-48.	1.4	46
52	Stability in Natural Bacterial Communities: I. Nutrient Addition Effects on Rhizosphere Diazotroph Assemblage Composition. <i>Microbial Ecology</i> , 2000, 39, 32-40.	1.4	106
53	Molecular Analysis of Diazotroph Diversity in the Rhizosphere of the Smooth Cordgrass, <i>Spartina alterniflora</i> . <i>Applied and Environmental Microbiology</i> , 2000, 66, 3814-3822.	1.4	139
54	Spatial and Temporal Assessment of Diazotroph Assemblage Composition in Vegetated Salt Marsh Sediments Using Denaturing Gradient Gel Electrophoresis Analysis. <i>Microbial Ecology</i> , 1999, 38, 157-167.	1.4	80

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55	Physiological Diversity of the Rhizosphere Diazotroph Assemblages of Selected Salt Marsh Grasses. <i>Applied and Environmental Microbiology</i> , 1998, 64, 4276-4282.	1.4	76
56	SHORT-TERM CHANGES IN THE VERTICAL DISTRIBUTION OF BENTHIC MICROALGAL BIOMASS IN INTERTIDAL MUDDY SEDIMENTS. <i>Diatom Research</i> , 1994, 9, 143-153.	0.5	60
57	Purification of DNA from estuarine sediments. <i>Journal of Microbiological Methods</i> , 1994, 20, 161-174.	0.7	41
58	Bacterial numbers and activity, microalgal biomass and productivity, and meiofaunal distribution in sediments naturally contaminated with biogenic bromophenols. <i>Marine Ecology - Progress Series</i> , 1992, 90, 61-71.	0.9	27