

# Terence L Marsh

## List of Publications by Year in descending order

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54  
papers

3,627  
citations

201674

27  
h-index

161849

54  
g-index

55  
all docs

55  
docs citations

55  
times ranked

4917  
citing authors

#	ARTICLE	IF	CITATIONS
1	Changes in Lake Sturgeon Gut Microbiomes Relative to Founding Origin and in Response to Chemotherapeutant Treatments. <i>Microorganisms</i> , 2022, 10, 1005.	3.6	3
2	Effects of Water Filtration and Temperature on Microbial Colonization and Survival of Lake Sturgeon Eggs. <i>North American Journal of Aquaculture</i> , 2021, 83, 26-37.	1.4	5
3	Watershed-scale landuse is associated with temporal and spatial compositional variation in Lake Michigan tributary bacterial communities. <i>Journal of Great Lakes Research</i> , 2021, 47, 862-874.	1.9	2
4	Genome Annotation of Poly(lactic acid) Degrading <i>Pseudomonas aeruginosa</i> , <i>Sphingobacterium</i> sp. and <i>Geobacillus</i> sp.. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7385.	4.1	5
5	Shedding of the Salmonid Herpesvirus-3 by Infected Lake Trout ( <i>Salvelinus namaycush</i> ). <i>Viruses</i> , 2019, 11, 580.	3.3	2
6	Effect of dietary prebiotics and probiotics on snakehead ( <i>Channa striata</i> ) health: Haematology and disease resistance parameters against <i>Aeromonas hydrophila</i> . <i>Fish and Shellfish Immunology</i> , 2018, 75, 99-108.	3.6	54
7	Development of the Tonsil Microbiome in Pigs and Effects of Stress on the Microbiome. <i>Frontiers in Veterinary Science</i> , 2018, 5, 220.	2.2	13
8	Development of the tonsillar microbiome in pigs from newborn through weaning. <i>BMC Microbiology</i> , 2018, 18, 35.	3.3	25
9	Analysing the effect of dietary prebiotics and probiotics on gut bacterial richness and diversity of Asian snakehead fingerlings using T-RFLP method. <i>Aquaculture Research</i> , 2018, 49, 3350-3361.	1.8	10
10	Biodegradation of Poly(lactic acid) in Soil Microcosms at Ambient Temperature: Evaluation of Natural Attenuation, Bio-augmentation and Bio-stimulation. <i>Journal of Polymers and the Environment</i> , 2018, 26, 3848-3857.	5.0	65
11	Dietary prebiotics and probiotics influence growth performance, nutrient digestibility and the expression of immune regulatory genes in snakehead ( <i>Channa striata</i> ) fingerlings. <i>Aquaculture</i> , 2016, 460, 59-68.	3.5	81
12	Effects of Family, Feeding Frequency, and Alternate Food Type on Body Size and Survival of Hatchery-Produced and Wild-Caught Lake Sturgeon Larvae. <i>North American Journal of Aquaculture</i> , 2016, 78, 136-144.	1.4	19
13	Phylogenetic Analysis of Anaerobic Co-Digestion of Animal Manure and Corn Stover Reveals Linkages between Bacterial Communities and Digestion Performance. <i>Advances in Microbiology</i> , 2016, 06, 879-897.	0.6	8
14	Intestinal microbial communities associated with acute enteric infections and disease recovery. <i>Microbiome</i> , 2015, 3, 45.	11.1	151
15	Properties of Soil Pore Space Regulate Pathways of Plant Residue Decomposition and Community Structure of Associated Bacteria. <i>PLoS ONE</i> , 2015, 10, e0123999.	2.5	98
16	Analysis of bacterial communities associated with the benthic amphipod <i>Diporeia</i> in the Laurentian Great Lakes Basin. <i>Canadian Journal of Microbiology</i> , 2015, 61, 72-81.	1.7	10
17	Dynamic Succession of Groundwater Functional Microbial Communities in Response to Emulsified Vegetable Oil Amendment during Sustained <i>In Situ</i> U(VI) Reduction. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4164-4172.	3.1	24
18	Microbial communities biostimulated by ethanol during uranium (VI) bioremediation in contaminated sediment as shown by stable isotope probing. <i>Frontiers of Environmental Science and Engineering</i> , 2015, 9, 453-464.	6.0	22

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19	Intra-aggregate Pore Structure Influences Phylogenetic Composition of Bacterial Community in Macroaggregates. <i>Soil Science Society of America Journal</i> , 2014, 78, 1924-1939.	2.2	69
20	Analysis of Microbial Communities with Denaturing Gradient Gel Electrophoresis and Terminal Restriction Fragment Length Polymorphism. , 2014, , 909-923.		3
21	Molecular characterization of bacterial communities associated with sediments in the Laurentian Great Lakes. <i>Journal of Great Lakes Research</i> , 2014, 40, 640-645.	1.9	14
22	Microbial Community Assembly and Succession on Lake Sturgeon Egg Surfaces as a Function of Simulated Spawning Stream Flow Rate. <i>Microbial Ecology</i> , 2013, 66, 500-511.	2.8	29
23	Defining the "core microbiome" of the microbial communities in the tonsils of healthy pigs. <i>BMC Microbiology</i> , 2012, 12, 20.	3.3	74
24	Genome sequence of <i>Desulfitobacterium hafniense</i> DCB-2, a Gram-positive anaerobe capable of dehalogenation and metal reduction. <i>BMC Microbiology</i> , 2012, 12, 21.	3.3	84
25	Heterogeneity of bacterial communities within the zebra mussel ( <i>Dreissena polymorpha</i> ) in the Laurentian Great Lakes Basin. <i>Journal of Great Lakes Research</i> , 2011, 37, 318-324.	1.9	23
26	Microbial communities in the tonsils of healthy pigs. <i>Veterinary Microbiology</i> , 2011, 147, 346-357.	1.9	63
27	Use of primer selection and restriction enzymes to assess bacterial community diversity in an agricultural soil used for potato production via terminal restriction fragment length polymorphism. <i>Applied Microbiology and Biotechnology</i> , 2011, 91, 1193-1202.	3.6	16
28	Dynamics of Microbial Community Composition and Function during In Situ Bioremediation of a Uranium-Contaminated Aquifer. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5063-5063.	3.1	4
29	Dynamics of Microbial Community Composition and Function during In Situ Bioremediation of a Uranium-Contaminated Aquifer. <i>Applied and Environmental Microbiology</i> , 2011, 77, 3860-3869.	3.1	51
30	Fecal bacterial diversity of human-habituated wild chimpanzees ( <i>Pan troglodytes</i> ). <i>Primate</i> 10 Tf 50 307 Td (sch) <i>Primate</i> , 2010, 72, 566-574.	1.7	24
31	Responses of microbial community functional structures to pilot-scale uranium in situ bioremediation. <i>ISME Journal</i> , 2010, 4, 1060-1070.	9.8	98
32	Significant Association between Sulfate-Reducing Bacteria and Uranium-Reducing Microbial Communities as Revealed by a Combined Massively Parallel Sequencing-Indicator Species Approach. <i>Applied and Environmental Microbiology</i> , 2010, 76, 6778-6786.	3.1	102
33	Biosequestration via cooperative binding of copper by <i>Ralstonia pickettii</i> . <i>Environmental Technology (United Kingdom)</i> , 2010, 31, 1045-1060.	2.2	27
34	Bacterial Assemblages Associated with Zebra Mussel ( <i>Dreissena polymorpha</i> ) Populations in the Laurentian Great Lakes Basin (USA). <i>Journal of Shellfish Research</i> , 2010, 29, 985-987.	0.9	7
35	Uranium Transformations in Static Microcosms. <i>Environmental Science &amp; Technology</i> , 2010, 44, 236-242.	10.0	44
36	Bacterial and Archaeal Phylogenetic Diversity of a Cold Sulfur-Rich Spring on the Shoreline of Lake Erie, Michigan. <i>Applied and Environmental Microbiology</i> , 2009, 75, 5025-5036.	3.1	28

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37	Rearrangement of bacterial community structure during peat diagenesis. <i>Soil Biology and Biochemistry</i> , 2009, 41, 135-143.	8.8	6
38	Changes in land use alter the structure of bacterial communities in Western Amazon soils. <i>ISME Journal</i> , 2009, 3, 1004-1011.	9.8	342
39	GeoChip-based analysis of functional microbial communities during the reoxidation of a bioreduced uranium-contaminated aquifer. <i>Environmental Microbiology</i> , 2009, 11, 2611-2626.	3.8	95
40	Predominance of <i>Tetragenococcus halophilus</i> as the cause of sugar thick juice degradation. <i>Food Microbiology</i> , 2008, 25, 413-421.	4.2	19
41	Speciation of Uranium in Sediments before and after In situ Biostimulation. <i>Environmental Science &amp; Technology</i> , 2008, 42, 1558-1564.	10.0	107
42	Microbial Communities in Contaminated Sediments, Associated with Bioremediation of Uranium to Submicromolar Levels. <i>Applied and Environmental Microbiology</i> , 2008, 74, 3718-3729.	3.1	154
43	Genetic and physiological diversity of <i>Tetragenococcus halophilus</i> strains isolated from sugar- and salt-rich environments. <i>Microbiology (United Kingdom)</i> , 2008, 154, 2600-2610.	1.8	39
44	Heterogeneous response to biostimulation for U(VI) reduction in replicated sediment microcosms. <i>Biodegradation</i> , 2006, 17, 303-316.	3.0	55
45	Colonization of the Cecal Mucosa by <i>Helicobacter hepaticus</i> Impacts the Diversity of the Indigenous Microbiota. <i>Infection and Immunity</i> , 2005, 73, 6952-6961.	2.2	72
46	Culture-independent Microbial Community Analysis with Terminal Restriction Fragment Length Polymorphism. <i>Methods in Enzymology</i> , 2005, 397, 308-329.	1.0	60
47	Characterization of the predominant anaerobic bacterium recovered from digital dermatitis lesions in three Michigan dairy cows. <i>Anaerobe</i> , 2003, 9, 151-155.	2.1	18
48	Effects of copper amendment on the bacterial community in agricultural soil analyzed by the T-RFLP technique. <i>FEMS Microbiology Ecology</i> , 2003, 46, 53-62.	2.7	72
49	Natural Biological Attenuation of Phenoxy Herbicides in Groundwater: Dow AgroSciences Paritutu Site, New Zealand. <i>Bioremediation Journal</i> , 2001, 5, 79-92.	2.0	11
50	Application of Denaturing Gradient Gel Electrophoresis (DGGE) To Study the Diversity of Marine Picoeukaryotic Assemblages and Comparison of DGGE with Other Molecular Techniques. <i>Applied and Environmental Microbiology</i> , 2001, 67, 2942-2951.	3.1	473
51	Terminal Restriction Fragment Length Polymorphism Analysis Program, a Web-Based Research Tool for Microbial Community Analysis. <i>Applied and Environmental Microbiology</i> , 2000, 66, 3616-3620.	3.1	272
52	Terminal restriction fragment length polymorphism (T-RFLP): An emerging method for characterizing diversity among homologous populations of amplification products. <i>Current Opinion in Microbiology</i> , 1999, 2, 323-327.	5.1	369
53	Beginning a molecular analysis of the eukaryal community in activated sludge. <i>Water Science and Technology</i> , 1998, 37, 455-460.	2.5	38
54	Parallel and Divergent Genotypic Evolution in Experimental Populations of <i>Ralstonia</i> sp. <i>Journal of Bacteriology</i> , 1998, 180, 4325-4331.	2.2	51