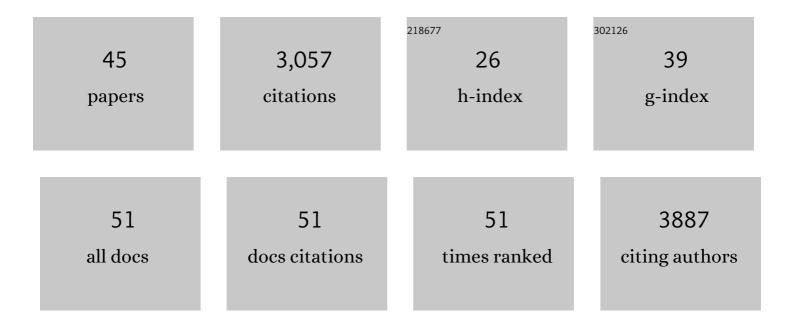
## Barbara J Macgregor

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Microbial Communities Under Distinct Thermal and Geochemical Regimes in Axial and Off-Axis Sediments of Guaymas Basin. Frontiers in Microbiology, 2021, 12, 633649.	3.5	28
2	Interactions between temperature and energy supply drive microbial communities in hydrothermal sediment. Communications Biology, 2021, 4, 1006.	4.4	10
3	Growth Patterns of Ciant Deep Sea Beggiatoaceae from a Guaymas Basin Vent Site. Springer Oceanography, 2020, , 173-181.	0.3	0
4	Identification, Expression and Activity of Candidate Nitrite Reductases From Orange Beggiatoaceae, Guaymas Basin. Frontiers in Microbiology, 2019, 10, 644.	3.5	15
5	Filamentous Giant Beggiatoaceae from the Guaymas Basin Are Capable of both Denitrification and Dissimilatory Nitrate Reduction to Ammonium. Applied and Environmental Microbiology, 2018, 84, .	3.1	30
6	10. Multiplication is vexation: a genomic perspective on cell division and DNA replication in the large sulfur bacteria. , 2017, , .		2
7	Microbial Communities in Methane- and Short Chain Alkane-Rich Hydrothermal Sediments of Guaymas Basin. Frontiers in Microbiology, 2016, 7, 17.	3.5	72
8	The Guaymas Basin Hiking Guide to Hydrothermal Mounds, Chimneys, and Microbial Mats: Complex Seafloor Expressions of Subsurface Hydrothermal Circulation. Frontiers in Microbiology, 2016, 7, 75.	3.5	82
9	Phylogeography, Salinity Adaptations and Metabolic Potential of the Candidate Division KB1 Bacteria Based on a Partial Single Cell Genome. Frontiers in Microbiology, 2016, 7, 1266.	3.5	32
10	Distinct Bacterial Communities in Surficial Seafloor Sediments Following the 2010 Deepwater Horizon Blowout. Frontiers in Microbiology, 2016, 7, 1384.	3.5	52
11	Visualizing Evolutionary Relationships of Multidomain Proteins: An Example from Receiver (REC) Domains of Sensor Histidine Kinases in the Candidatus Maribeggiatoa str. Orange Guaymas Draft Genome. Frontiers in Microbiology, 2016, 7, 1780.	3.5	2
12	Abundant Intergenic TAACTGA Direct Repeats and Putative Alternate RNA Polymerase β′ Subunits in Marine Beggiatoaceae Genomes: Possible Regulatory Roles and Origins. Frontiers in Microbiology, 2015, 6, 1397.	3.5	5
13	Clickâ€chemistry tagging of proteins in living cells: new possibilities for microbial (meta) proteomics. Environmental Microbiology, 2014, 16, 2353-2356.	3.8	0
14	Composition and enzymatic function of particle-associated and free-living bacteria: a coastal/offshore comparison. ISME Journal, 2014, 8, 2167-2179.	9.8	159
15	Sulfide oxidation, nitrate respiration, carbon acquisition, and electron transport pathways suggested by the draft genome of a single orange Guaymas Basin Beggiatoa (Cand. Maribeggiatoa) sp. filament. Marine Genomics, 2013, 11, 53-65.	1.1	32
16	Depth-Related Differences in Organic Substrate Utilization by Major Microbial Groups in Intertidal Marine Sediment. Applied and Environmental Microbiology, 2013, 79, 389-392.	3.1	24
17	Mobile Elements in a Single-Filament Orange Guaymas Basin Beggiatoa ("Candidatus Maribeggiatoaâ€ <del>)</del> sp. Draft Genome: Evidence for Genetic Exchange with Cyanobacteria. Applied and Environmental Microbiology, 2013, 79, 3974-3985.	3.1	33
18	Why Orange Guaymas Basin Beggiatoa spp. Are Orange: Single-Filament-Genome-Enabled Identification of an Abundant Octaheme Cytochrome with Hydroxylamine Oxidase, Hydrazine Oxidase, and Nitrite Reductase Activities. Applied and Environmental Microbiology, 2013, 79, 1183-1190.	3.1	36

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19	Spatial heterogeneity and underlying geochemistry of phylogenetically diverse orange and white Beggiatoa mats in Guaymas Basin hydrothermal sediments. Deep-Sea Research Part I: Oceanographic Research Papers, 2012, 67, 21-31.	1.4	73
20	Integrating microbial ecology into ecosystem models: challenges and priorities. Biogeochemistry, 2012, 109, 7-18.	3.5	206
21	Quantitative PCR methods for RNA and DNA in marine sediments: maximizing yield while overcoming inhibition. FEMS Microbiology Ecology, 2010, 72, 143-151.	2.7	62
22	Linking Microbial Community Function to Phylogeny of Sulfate-Reducing <i>Deltaproteobacteria</i> in Marine Sediments by Combining Stable Isotope Probing with Magnetic-Bead Capture Hybridization of 16S rRNA. Applied and Environmental Microbiology, 2009, 75, 4927-4935.	3.1	52
23	Improved 16S rRNA-targeted probe set for analysis of sulfate-reducing bacteria by fluorescence in situ hybridization. Journal of Microbiological Methods, 2007, 69, 523-528.	1.6	98
24	Diversity, relative abundance and metabolic potential of bacterial endosymbionts in three Bathymodiolus mussel species from cold seeps in the Gulf of Mexico. Environmental Microbiology, 2007, 9, 1423-1438.	3.8	133
25	Single-stranded conformational polymorphism for separation of mixed rRNAS (rRNA-SSCP), a new method for profiling microbial communities. Systematic and Applied Microbiology, 2006, 29, 661-670.	2.8	15
26	Comparison of rRNA and Polar-Lipid-Derived Fatty Acid Biomarkers for Assessment of 13 C-Substrate Incorporation by Microorganisms in Marine Sediments. Applied and Environmental Microbiology, 2006, 72, 5246-5253.	3.1	31
27	An improved fluorescence in situ hybridization protocol for the identification of bacteria and archaea in marine sediments. FEMS Microbiology Ecology, 2004, 50, 203-213.	2.7	165
28	Related assemblages of sulphate-reducing bacteria associated with ultradeep gold mines of South Africa and deep basalt aquifers of Washington State. Environmental Microbiology, 2003, 5, 267-277.	3.8	96
29	Evidence for a Dynamic Cycle between Mn and Co in the Water Column of a Stratified Lake. Environmental Science & Technology, 2002, 36, 468-476.	10.0	44
30	Isolation of small-subunit rRNA for stable isotopic characterization. Environmental Microbiology, 2002, 4, 451-464.	3.8	54
31	Phylum Bll. Thermotogae phy. nov , 2001, , 369-387.		34
32	Distribution and abundance of Gram-positive bacteria in the environment: development of a group-specific probe. Journal of Microbiological Methods, 2001, 44, 193-203.	1.6	13
33	Evidence for tight coupling between active bacteria and particulate organic carbon during seasonal stratification of Lake Michigan. Limnology and Oceanography, 2001, 46, 1202-1208.	3.1	10
34	Microbiological, molecular biological and stable isotopic evidence for nitrogen fixation in the open waters of Lake Michigan. Environmental Microbiology, 2001, 3, 205-219.	3.8	42
35	Seasonal and Spatial Variability in Lake Michigan Sediment Small-Subunit rRNA Concentrations. Applied and Environmental Microbiology, 2001, 67, 3908-3922.	3.1	35
36	Shewanella pealeana sp. nov., a member of the microbial community associated with the accessory nidamental gland of the squid Loligo pealei. International Journal of Systematic and Evolutionary Microbiology, 1999, 49, 1341-1351.	1.7	67

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37	Molecular approaches to the study of aquatic microbial communities. Current Opinion in Biotechnology, 1999, 10, 220-224.	6.6	16
38	Sulphate reduction and vertical distribution of sulphate-reducing bacteria quantified by rRNA slot-blot hybridization in a coastal marine sediment. Environmental Microbiology, 1999, 1, 65-74.	3.8	163
39	Polyphasic taxonomy of the genus Shewanella and description of Shewanella oneidensis sp. nov International Journal of Systematic and Evolutionary Microbiology, 1999, 49, 705-724.	1.7	574
40	Population Structure and Phylogenetic Characterization of Marine Benthic Archaea in Deep-Sea Sediments. Applied and Environmental Microbiology, 1999, 65, 4375-4384.	3.1	399
41	Transcription of the Rhodobacter sphaeroides cycA P1 Promoter by Alternate RNA Polymerase Holoenzymes. Journal of Bacteriology, 1998, 180, 1-9.	2.2	19
42	Genetic and physical mapping of the Rhodobacter sphaeroides photosynthetic gene cluster from R-prime pWS2. Plasmid, 1991, 25, 163-176.	1.4	11
43	Evidence for two promoters for the cytochrome c2 gene (cycA) of Rhodobacter sphaeroides. Journal of Bacteriology, 1991, 173, 3949-3957.	2.2	26
44	Soluble Cytochrome Synthesis in Rhodobacter Sphaeroides. , 1990, , 95-104.		2
45	Oxalobacter Allison, Dawson, Mayberry and Foss 1985b, 375VP (Effective publication: Allison, Dawson,) Tj ETQq1	. 1 0.7843	14 rgBT /Ove