

# Jose M Gonzalez

## List of Publications by Year in descending order

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Version: 2024-02-01

57  
papers

7,298  
citations

117453

34  
h-index

161609

54  
g-index

60  
all docs

60  
docs citations

60  
times ranked

7132  
citing authors

#	ARTICLE	IF	CITATIONS
1	Phylogenetically and functionally diverse microorganisms reside under the Ross Ice Shelf. <i>Nature Communications</i> , 2022, 13, 117.	5.8	17
2	Reduction of alternative electron acceptors drives biofilm formation in <i>Shewanella</i> algae. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 9.	2.9	15
3	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. <i>Communications Biology</i> , 2021, 4, 604.	2.0	107
4	Taxon-Specific Shifts in Bacterial and Archaeal Transcription of Dissolved Organic Matter Cycling Genes in a Stratified Fjord. <i>MSystems</i> , 2021, 6, e0057521.	1.7	1
5	Light supports cell integrity and growth rates of taxonomically diverse coastal photoheterotrophs. <i>Environmental Microbiology</i> , 2020, 22, 3823-3837.	1.8	6
6	Transcriptional Patterns of Biogeochemically Relevant Marker Genes by Temperate Marine Bacteria. <i>Frontiers in Microbiology</i> , 2020, 11, 465.	1.5	9
7	Evolutionary history of dimethylsulfoniopropionate (DMSP) demethylation enzyme DmdA in marine bacteria. <i>PeerJ</i> , 2020, 8, e9861.	0.9	4
8	Aerobic Hydrocarbon-Degrading Alphaproteobacteria: Rhodobacteraceae ( <i>Roseobacter</i> ). , 2019, , 1-13.		4
9	Repeated evolutionary transitions of flavobacteria from marine to non-marine habitats. <i>Environmental Microbiology</i> , 2019, 21, 648-666.	1.8	43
10	Functional annotation of orthologs in metagenomes: a case study of genes for the transformation of oceanic dimethylsulfoniopropionate. <i>ISME Journal</i> , 2019, 13, 1183-1197.	4.4	24
11	Aerobic Hydrocarbon-Degrading Alphaproteobacteria: Rhodobacteraceae ( <i>Roseobacter</i> ). , 2019, , 93-104.		7
12	Comparative proteomics reveals signature metabolisms of exponentially growing and stationary phase marine bacteria. <i>Environmental Microbiology</i> , 2017, 19, 2301-2319.	1.8	30
13	Diversity and Distribution of Freshwater Aerobic Anoxygenic Phototrophic Bacteria across a Wide Latitudinal Gradient. <i>Frontiers in Microbiology</i> , 2017, 8, 175.	1.5	44
14	Exploring Microdiversity in Novel <i>Kordia</i> sp. ( <i>Bacteroidetes</i> ) with Proteorhodopsin from the Tropical Indian Ocean via Single Amplified Genomes. <i>Frontiers in Microbiology</i> , 2017, 8, 1317.	1.5	7
15	Marine Bacterial and Archaeal Ion-Pumping Rhodopsins: Genetic Diversity, Physiology, and Ecology. <i>Microbiology and Molecular Biology Reviews</i> , 2016, 80, 929-954.	2.9	173
16	Response of marine bacterioplankton pH homeostasis gene expression to elevated CO <sub>2</sub> . <i>Nature Climate Change</i> , 2016, 6, 483-487.	8.1	68
17	Lipid remodelling is a widespread strategy in marine heterotrophic bacteria upon phosphorus deficiency. <i>ISME Journal</i> , 2016, 10, 968-978.	4.4	95
18	Proteorhodopsin light-enhanced growth linked to vitamin-B1 acquisition in marine Flavobacteria. <i>ISME Journal</i> , 2016, 10, 1102-1112.	4.4	58

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19	Marinomonas blandensis sp. nov., a novel marine gammaproteobacterium. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 5544-5549.	0.8	12
20	Transient Changes in Bacterioplankton Communities Induced by the Submarine Volcanic Eruption of El Hierro (Canary Islands). PLoS ONE, 2015, 10, e0118136.	1.1	22
21	Phosphate Limitation Induces Drastic Physiological Changes, Virulence-Related Gene Expression, and Secondary Metabolite Production in Pseudovibrio sp. Strain FO-BEG1. Applied and Environmental Microbiology, 2015, 81, 3518-3528.	1.4	49
22	Mannitolâ€¦phosphate dehydrogenases/phosphatases: a family of novel bifunctional enzymes for bacterial adaptation to osmotic stress. Environmental Microbiology, 2015, 17, 711-719.	1.8	21
23	Stimulation of growth by proteorhodopsin phototrophy involves regulation of central metabolic pathways in marine planktonic bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3650-8.	3.3	87
24	Dynamics of Metabolic Activities and Gene Expression in the Roseobacter Clade Bacterium Phaeobacter sp. Strain MED193 during Growth with Thiosulfate. Applied and Environmental Microbiology, 2014, 80, 6933-6942.	1.4	14
25	Master recyclers: features and functions of bacteria associated with phytoplankton blooms. Nature Reviews Microbiology, 2014, 12, 686-698.	13.6	947
26	Ecology of marine Bacteroidetes: a comparative genomics approach. ISME Journal, 2013, 7, 1026-1037.	4.4	614
27	Regulation of proteorhodopsin gene expression by nutrient limitation in the marine bacterium <i>Vibrio</i> sp. AND4. Environmental Microbiology, 2013, 15, 1400-1415.	1.8	39
28	Caffeate Respiration in the Acetogenic Bacterium Acetobacterium woodii: a Coenzyme A Loop Saves Energy for Caffeate Activation. Applied and Environmental Microbiology, 2013, 79, 1942-1947.	1.4	30
29	Assessing bacterial diversity in a seawaterâ€¦processing wastewater treatment plant by 454â€¦pyrosequencing of the 16S rRNA and <i>amoA</i> genes. Microbial Biotechnology, 2013, 6, 435-442.	2.0	30
30	Prevalent genome streamlining and latitudinal divergence of planktonic bacteria in the surface ocean. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11463-11468.	3.3	328
31	Genomics and Physiology of a Marine Flavobacterium Encoding a Proteorhodopsin and a Xanthorhodopsin-Like Protein. PLoS ONE, 2013, 8, e57487.	1.1	42
32	Comparative Genomic and Transcriptomic Analysis of Tandemly and Segmentally Duplicated Genes in Rice. PLoS ONE, 2013, 8, e63551.	1.1	36
33	Patterns and architecture of genomic islands in marine bacteria. BMC Genomics, 2012, 13, 347.	1.2	84
34	Bacterioplankton groups involved in the uptake of phosphate and dissolved organic phosphorus in a mesocosm experiment with Pâ€¦starved Mediterranean waters. Environmental Microbiology, 2012, 14, 2334-2347.	1.8	39
35	Biochemistry, evolution and physiological function of the Rnf complex, a novel ion-motive electron transport complex in prokaryotes. Cellular and Molecular Life Sciences, 2011, 68, 613-634.	2.4	352
36	Genomics of the Proteorhodopsin-Containing Marine Flavobacterium Dokdonia sp. Strain MED134. Applied and Environmental Microbiology, 2011, 77, 8676-8686.	1.4	56

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37	T-RFPred: a nucleotide sequence size prediction tool for microbial community description based on terminal-restriction fragment length polymorphism chromatograms. <i>BMC Microbiology</i> , 2010, 10, 262.	1.3	8
38	Proteorhodopsin Phototrophy Promotes Survival of Marine Bacteria during Starvation. <i>PLoS Biology</i> , 2010, 8, e1000358.	2.6	206
39	<i>Bermanella marisrubri</i> gen. nov., sp. nov., a genome-sequenced gammaproteobacterium from the Red Sea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009, 59, 373-377.	0.8	24
40	High abundance of virulence gene homologues in marine bacteria. <i>Environmental Microbiology</i> , 2009, 11, 1348-1357.	1.8	98
41	Assembling the Marine Metagenome, One Cell at a Time. <i>PLoS ONE</i> , 2009, 4, e5299.	1.1	320
42	Genome analysis of the proteorhodopsin-containing marine bacterium <i>Polaribacter</i> sp. MED152 (Flavobacteria). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8724-8729.	3.3	231
43	<i>Reinekea blandensis</i> sp. nov., a marine, genome-sequenced gammaproteobacterium. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 2370-2375.	0.8	21
44	<i>Neptuniibacter caesariensis</i> gen. nov., sp. nov., a novel marine genome-sequenced gammaproteobacterium. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 1000-1006.	0.8	58
45	Light stimulates growth of proteorhodopsin-containing marine Flavobacteria. <i>Nature</i> , 2007, 445, 210-213.	13.7	349
46	Seasonality in bacterial diversity in north-west Mediterranean coastal waters: assessment through clone libraries, fingerprinting and FISH. <i>FEMS Microbiology Ecology</i> , 2007, 60, 98-112.	1.3	195
47	Phylogenetic identification and metabolism of marine dimethylsulfide-consuming bacteria. <i>Environmental Microbiology</i> , 2006, 8, 2189-2200.	1.8	73
48	Biochemical Characterization of VmL, a Seryl-tRNA Synthetase Encoded by the Valanimycin Biosynthetic Gene Cluster. <i>Journal of Biological Chemistry</i> , 2006, 281, 26785-26791.	1.6	51
49	Bacterial Taxa That Limit Sulfur Flux from the Ocean. <i>Science</i> , 2006, 314, 649-652.	6.0	296
50	Flow-Cytometric Cell Sorting and Subsequent Molecular Analyses for Culture-Independent Identification of Bacterioplankton Involved in Dimethylsulfoniopropionate Transformations. <i>Applied and Environmental Microbiology</i> , 2005, 71, 1405-1416.	1.4	33
51	<i>Saccharophagus degradans</i> gen. nov., sp. nov., a versatile marine degrader of complex polysaccharides. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2005, 55, 1545-1549.	0.8	133
52	Overview of the Marine Roseobacter Lineage. <i>Applied and Environmental Microbiology</i> , 2005, 71, 5665-5677.	1.4	753
53	Dimethylsulfoniopropionate Turnover Is Linked to the Composition and Dynamics of the Bacterioplankton Assemblage during a Microcosm Phytoplankton Bloom. <i>Applied and Environmental Microbiology</i> , 2005, 71, 7650-7660.	1.4	69
54	Use of Microautoradiography Combined with Fluorescence In Situ Hybridization To Determine Dimethylsulfoniopropionate Incorporation by Marine Bacterioplankton Taxa. <i>Applied and Environmental Microbiology</i> , 2004, 70, 4648-4657.	1.4	86

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55	Genome sequence of <i>Silicibacter pomeroyi</i> reveals adaptations to the marine environment. <i>Nature</i> , 2004, 432, 910-913.	13.7	415
56	Linking a Bacterial Taxon to Sulfur Cycling in the Sea: Studies of the Marine <i>Roseobacter</i> Group. <i>Geomicrobiology Journal</i> , 2003, 20, 375-388.	1.0	133
57	<i>Silicibacter pomeroyi</i> sp. nov. and <i>Roseovarius nubinhibens</i> sp. nov., dimethylsulfoniopropionate-demethylating bacteria from marine environments. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003, 53, 1261-1269.	0.8	231