

Manuel Martinez-Garcia

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

3,736
citations

201385
27
h-index

143772
57
g-index

66
all docs

66
docs citations

66
times ranked

4622
citing authors

#	ARTICLE	IF	CITATIONS
1	Potential for Chemolithoautotrophy Among Ubiquitous Bacteria Lineages in the Dark Ocean. <i>Science</i> , 2011, 333, 1296-1300.	6.0	510
2	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	9.4	414
3	Prevalent genome streamlining and latitudinal divergence of planktonic bacteria in the surface ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11463-11468.	3.3	328
4	Capturing Single Cell Genomes of Active Polysaccharide Degraders: An Unexpected Contribution of Verrucomicrobia. <i>PLoS ONE</i> , 2012, 7, e35314.	1.1	236
5	High-throughput single-cell sequencing identifies photoheterotrophs and chemoautotrophs in freshwater bacterioplankton. <i>ISME Journal</i> , 2012, 6, 113-123.	4.4	168
6	Single-virus genomics reveals hidden cosmopolitan and abundant viruses. <i>Nature Communications</i> , 2017, 8, 15892.	5.8	165
7	Comparative single-cell genomics reveals potential ecological niches for the freshwater actinobacteria lineage. <i>ISME Journal</i> , 2014, 8, 2503-2516.	4.4	137
8	Unveiling <i>in situ</i> interactions between marine protists and bacteria through single cell sequencing. <i>ISME Journal</i> , 2012, 6, 703-707.	4.4	124
9	Genomic and Metabolic Diversity of Marine Group I Thaumarchaeota in the Mesopelagic of Two Subtropical Gyres. <i>PLoS ONE</i> , 2014, 9, e95380.	1.1	95
10	Metabolic potential of a single cell belonging to one of the most abundant lineages in freshwater bacterioplankton. <i>ISME Journal</i> , 2013, 7, 137-147.	4.4	94
11	Prokaryotic diversity in Tuz Lake, a hypersaline environment in Inland Turkey. <i>FEMS Microbiology Ecology</i> , 2008, 65, 474-483.	1.3	90
12	What's New Is Old: Resolving the Identity of <i>Leptothrix ochracea</i> Using Single Cell Genomics, Pyrosequencing and FISH. <i>PLoS ONE</i> , 2011, 6, e17769.	1.1	85
13	Productivity and salinity structuring of the microplankton revealed by comparative freshwater metagenomics. <i>Environmental Microbiology</i> , 2014, 16, 2682-2698.	1.8	80
14	Contrasting patterns of genome-level diversity across distinct co-occurring bacterial populations. <i>ISME Journal</i> , 2018, 12, 742-755.	4.4	76
15	Unveiling viral-host interactions within the "microbial dark matter". <i>Nature Communications</i> , 2014, 5, 4542.	5.8	69
16	Microbial community associated with the colonial ascidian <i>Cystodytes dellechiaiei</i> . <i>Environmental Microbiology</i> , 2007, 9, 521-534.	1.8	67
17	Tuning fresh: radiation through rewiring of central metabolism in streamlined bacteria. <i>ISME Journal</i> , 2016, 10, 1902-1914.	4.4	66
18	Ecogenomics of the SAR11 clade. <i>Environmental Microbiology</i> , 2020, 22, 1748-1763.	1.8	66

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19	Spatial and seasonal prokaryotic community dynamics in ponds of increasing salinity of Sfax solar saltern in Tunisia. <i>Antonie Van Leeuwenhoek</i> , 2012, 101, 845-857.	0.7	59
20	Distribution, abundance and diversity of the extremely halophilic bacterium <i>Salinibacter ruber</i> . <i>Saline Systems</i> , 2008, 4, 15.	2.0	54
21	From community approaches to single-cell genomics: the discovery of ubiquitous hyperhalophilic <i>Bacteroidetes</i> generalists. <i>ISME Journal</i> , 2015, 9, 16-31.	4.4	51
22	Caudovirales bacteriophages are associated with improved executive function and memory in flies, mice, and humans. <i>Cell Host and Microbe</i> , 2022, 30, 340-356.e8.	5.1	50
23	Ammonia-oxidizing <i>Crenarchaeota</i> and nitrification inside the tissue of a colonial ascidian. <i>Environmental Microbiology</i> , 2008, 10, 2991-3001.	1.8	48
24	Interactions between Closely Related Bacterial Strains Are Revealed by Deep Transcriptome Sequencing. <i>Applied and Environmental Microbiology</i> , 2015, 81, 8445-8456.	1.4	40
25	Structure and temporal dynamics of the bacterial communities associated to microhabitats of the coral <i>Scleractinia</i> <i>Oculina patagonica</i> . <i>Environmental Microbiology</i> , 2016, 18, 4564-4578.	1.8	37
26	Single-cell genomics uncover <i>Pelagibacter</i> as the putative host of the extremely abundant uncultured 37-F6 viral population in the ocean. <i>ISME Journal</i> , 2019, 13, 232-236.	4.4	36
27	Deciphering the Human Virome with Single-Virus Genomics and Metagenomics. <i>Viruses</i> , 2018, 10, 113.	1.5	31
28	Characterization of ecologically diverse viruses infecting co-occurring strains of cosmopolitan hyperhalophilic <i>Bacteroidetes</i> . <i>ISME Journal</i> , 2018, 12, 424-437.	4.4	29
29	Droplet Digital PCR for Estimating Absolute Abundances of Widespread <i>Pelagibacter</i> Viruses. <i>Frontiers in Microbiology</i> , 2019, 10, 1226.	1.5	29
30	Recovering microbial genomes from metagenomes in hypersaline environments: The Good, the Bad and the Ugly. <i>Systematic and Applied Microbiology</i> , 2019, 42, 30-40.	1.2	29
31	Cytotoxicity of the Ascidian <i>Cystodytes dellechiaiei</i> Against Tumor Cells and Study of the Involvement of Associated Microbiota in the Production of Cytotoxic Compounds. <i>Marine Drugs</i> , 2007, 5, 52-70.	2.2	26
32	Epibiosis of Oxygenic Phototrophs Containing Chlorophylls a, b, c, and d on the Colonial Ascidian <i>Cystodytes dellechiaiei</i> . <i>Microbial Ecology</i> , 2011, 61, 13-19.	1.4	23
33	Diversity of cultivable halophilic archaea and bacteria from superficial hypersaline sediments of Tunisian solar salterns. <i>Antonie Van Leeuwenhoek</i> , 2014, 106, 675-692.	0.7	23
34	<i>Vibrio</i> communities in scleractinian corals differ according to health status and geographic location in the Mediterranean Sea. <i>Systematic and Applied Microbiology</i> , 2018, 41, 131-138.	1.2	23
35	Insights into the antibiotic resistance dissemination in a wastewater effluent microbiome: bacteria, viruses and vesicles matter. <i>Environmental Microbiology</i> , 2019, 21, 4582-4596.	1.8	22
36	Prokaryotic and viral community structure in the singular chaotropic salt lake Salar de Uyuni. <i>Environmental Microbiology</i> , 2019, 21, 2029-2042.	1.8	22

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37	The Evolutionary Success of the Marine Bacterium SAR11 Analyzed through a Metagenomic Perspective. MSystems, 2020, 5, .	1.7	22
38	Leuconostoc mesenteroides and Leuconostoc pseudomesenteroides bacteriophages: Genomics and cross-species host ranges. International Journal of Food Microbiology, 2017, 257, 128-137.	2.1	19
39	Single-virus genomics and beyond. Nature Reviews Microbiology, 2020, 18, 705-716.	13.6	18
40	Short-term high-fat feeding exacerbates degeneration in retinitis pigmentosa by promoting retinal oxidative stress and inflammation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	18
41	Geodermatophilus brasiliensis sp. nov., isolated from Brazilian soil. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 2841-2848.	0.8	16
42	Retinitis pigmentosa is associated with shifts in the gut microbiome. Scientific Reports, 2021, 11, 6692.	1.6	16
43	High-Throughput 16S rRNA Sequencing to Assess Potentially Active Bacteria and Foodborne Pathogens: A Case Example in Ready-to-Eat Food. Foods, 2019, 8, 480.	1.9	14
44	Diversity of <i>pufM</i> genes, involved in aerobic anoxygenic photosynthesis, in the bacterial communities associated with colonial ascidians. FEMS Microbiology Ecology, 2010, 71, 387-398.	1.3	13
45	Ecogenomics and Adaptation Strategies of Southern Ocean Viral Communities. MSystems, 2021, 6, e0039621.	1.7	11
46	Cationic Dendrimer G2-S16 Inhibits Herpes Simplex Type 2 Infection and Protects Mice Vaginal Microbiome. Pharmaceutics, 2020, 12, 515.	2.0	10
47	Prokaryotic and viral community of the sulfate-rich crust from Peñahueca ephemeral lake, an astrobiology analogue. Environmental Microbiology, 2019, 21, 3577-3600.	1.8	9
48	Diel cycling of the cosmopolitan abundant Pelagibacter virus 374F6: one of the most abundant viruses on earth. Environmental Microbiology Reports, 2020, 12, 214-219.	1.0	8
49	Unexpected myriad of co-occurring viral strains and species in one of the most abundant and microdiverse viruses on Earth. ISME Journal, 2022, 16, 1025-1035.	4.4	8
50	Benchmarking of single-virus genomics: a new tool for uncovering the virosphere. Environmental Microbiology, 2021, 23, 1584-1593.	1.8	7
51	Microarray tools to unveil viral-microbe interactions in nature. Frontiers in Ecology and Evolution, 2014, 2, .	1.1	6
52	Ancient saltern metagenomics: tracking changes in microbes and their viruses from the underground to the surface. Environmental Microbiology, 2021, 23, 3477-3498.	1.8	6
53	Cytotoxicity of the Ascidian Cystodytes dellechiaiei Against Tumor Cells and Study of the Involvement of Associated Microbiota in the Production of Cytotoxic Compounds. Marine Drugs, 2007, 5, 52-70.	2.2	6
54	A Resistome Roadmap: From the Human Body to Pristine Environments. Frontiers in Microbiology, 2022, 13, .	1.5	6

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55	Minimal-moderate variation of human oral virome and microbiome in IgA deficiency. Scientific Reports, 2021, 11, 14913.	1.6	5
56	Absolute quantification of infecting viral particles by chip-based digital polymerase chain reaction. Environmental Microbiology Reports, 2019, 11, 855-860.	1.0	4
57	Retinal-binding proteins mirror prokaryotic dynamics in multipond solar salterns. Environmental Microbiology, 2015, 17, 514-526.	1.8	3
58	Single-Virus Genomics: Studying Uncultured Viruses, One at a Time. , 2021, , 184-190.		3