Gipsi Lima-Mendez

List of Publications by Year
in descending order

30 papers	9,638 citations	236925 25 h-index	434195 31 g-index
35 all docs	35 docs citations	35 times ranked	13789 citing authors

#	Article	IF	Citations
1	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. Communications Biology, 2021, 4, 604.	4.4	107
2	Disentangling environmental effects in microbial association networks. Microbiome, 2021, 9, 232.	11.1	21
3	Toxin-Antitoxin Gene Pairs Found in Tn *3* Family Transposons Appear To Be an Integral Part of the Transposition Module. MBio, 2020, 11, .	4.1	25
4	Community‐Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. Global Biogeochemical Cycles, 2019, 33, 391-419.	4.9	76
5	Population-level analysis of *Blastocystis* subtype prevalence and variation in the human gut microbiota. Gut, 2019, 68, 1180-1189.	12.1	149
6	A global ocean atlas of eukaryotic genes. Nature Communications, 2018, 9, 373.	12.8	297
7	Population-level analysis of gut microbiome variation. Science, 2016, 352, 560-564.	12.6	1,716
8	Species–function relationships shape ecological properties of the human gut microbiome. Nature Microbiology, 2016, 1, 16088.	13.3	279
9	Cyanobacterial symbionts diverged in the late Cretaceous towards lineage-specific nitrogen fixation factories in single-celled phytoplankton. Nature Communications, 2016, 7, 11071.	12.8	72
10	Cross-biome comparison of microbial association networks. Frontiers in Microbiology, 2015, 6, 1200.	3.5	154
11	Determinants of community structure in the global plankton interactome. Science, 2015, 348, 1262073.	12.6	842
12	Structure and function of the global ocean microbiome. Science, 2015, 348, 1261359.	12.6	2,137
13	Eukaryotic plankton diversity in the sunlit ocean. Science, 2015, 348, 1261605.	12.6	1,551
14	Metagenomic 16S rDNA Illumina tags are a powerful alternative to amplicon sequencing to explore diversity and structure of microbial communities. Environmental Microbiology, 2014, 16, 2659-2671.	3.8	291
15	Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. ISME Journal, 2013, 7, 1678-1695.	9.8	185
16	Towards a more accurate annotation of tyrosine-based site-specific recombinases in bacterial genomes. Mobile DNA, 2012, 3, 6.	3.6	32
17	Reticulate Classification of Mosaic Microbial Genomes Using NeAT Website. Methods in Molecular Biology, 2012, 804, 81-91.	0.9	7
18	A Holistic Approach to Marine Eco-Systems Biology. PLoS Biology, 2011, 9, e1001177.	5.6	353

#	Article	IF	Citations
19	A modular view of the bacteriophage genomic space: identification of host and lifestyle marker modules. Research in Microbiology, 2011, 162, 737-746.	2.1	60
20	Mainstreams of Horizontal Gene Exchange in Enterobacteria: Consideration of the Outbreak of Enterohemorrhagic E. coli O104:H4 in Germany in 2011. PLoS ONE, 2011, 6, e25702.	2.5	31
21	ACLAME: A CLAssification of Mobile genetic Elements, update 2010. Nucleic Acids Research, 2010, 38, D57-D61.	14.5	289
22	The powerful law of the power law and other myths in network biology. Molecular BioSystems, 2009, 5, 1482.	2.9	161
23	Comparative Analyses of Prophage-Like Elements Present in Bifidobacterial Genomes. Applied and Environmental Microbiology, 2009, 75, 6929-6936.	3.1	45
24	Network Analysis Tools: from biological networks to clusters and pathways. Nature Protocols, 2008, 3, 1616-1629.	12.0	101
25	NeAT: a toolbox for the analysis of biological networks, clusters, classes and pathways. Nucleic Acids Research, 2008, 36, W444-W451.	14.5	81
26	Prophinder: a computational tool for prophage prediction in prokaryotic genomes. Bioinformatics, 2008, 24, 863-865.	4.1	199
27	Reticulate Representation of Evolutionary and Functional Relationships between Phage Genomes. Molecular Biology and Evolution, 2008, 25, 762-777.	8.9	212
28	PhiGO, a phage ontology associated with the ACLAME database. Research in Microbiology, 2007, 158, 567-571.	2.1	16
29	Analysis of the phage sequence space: The benefit of structured information. Virology, 2007, 365, 241-249.	2.4	53
30	A first global analysis of plasmid encoded proteins in the ACLAME database. FEMS Microbiology Reviews, 2006, 30, 980-994.	8.6	48