

Gipsi Lima-Mendez

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4937531/publications.pdf>

Version: 2024-02-01

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	Structure and function of the global ocean microbiome. <i>Science</i> , 2015, 348, 1261359.	12.6	2,137
2	Population-level analysis of gut microbiome variation. <i>Science</i> , 2016, 352, 560-564.	12.6	1,716
3	Eukaryotic plankton diversity in the sunlit ocean. <i>Science</i> , 2015, 348, 1261605.	12.6	1,551
4	Determinants of community structure in the global plankton interactome. <i>Science</i> , 2015, 348, 1262073.	12.6	842
5	A Holistic Approach to Marine Eco-Systems Biology. <i>PLoS Biology</i> , 2011, 9, e1001177.	5.6	353
6	A global ocean atlas of eukaryotic genes. <i>Nature Communications</i> , 2018, 9, 373.	12.8	297
7	Metagenomic <sc>16S rDNA I</sc>llumina tags are a powerful alternative to amplicon sequencing to explore diversity and structure of microbial communities. <i>Environmental Microbiology</i> , 2014, 16, 2659-2671.	3.8	291
8	ACLAME: A CLAssification of Mobile genetic Elements, update 2010. <i>Nucleic Acids Research</i> , 2010, 38, D57-D61.	14.5	289
9	Speciesâ€™function relationships shape ecological properties of the human gut microbiome. <i>Nature Microbiology</i> , 2016, 1, 16088.	13.3	279
10	Reticulate Representation of Evolutionary and Functional Relationships between Phage Genomes. <i>Molecular Biology and Evolution</i> , 2008, 25, 762-777.	8.9	212
11	Prophinder: a computational tool for prophage prediction in prokaryotic genomes. <i>Bioinformatics</i> , 2008, 24, 863-865.	4.1	199
12	Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. <i>ISME Journal</i> , 2013, 7, 1678-1695.	9.8	185
13	The powerful law of the power law and other myths in network biology. <i>Molecular BioSystems</i> , 2009, 5, 1482.	2.9	161
14	Cross-biome comparison of microbial association networks. <i>Frontiers in Microbiology</i> , 2015, 6, 1200.	3.5	154
15	Population-level analysis of <i>Blastocystis</i> subtype prevalence and variation in the human gut microbiota. <i>Gut</i> , 2019, 68, 1180-1189.	12.1	149
16	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. <i>Communications Biology</i> , 2021, 4, 604.	4.4	107
17	Network Analysis Tools: from biological networks to clusters and pathways. <i>Nature Protocols</i> , 2008, 3, 1616-1629.	12.0	101
18	NeAT: a toolbox for the analysis of biological networks, clusters, classes and pathways. <i>Nucleic Acids Research</i> , 2008, 36, W444-W451.	14.5	81

#	ARTICLE	IF	CITATIONS
19	Community-Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. <i>Global Biogeochemical Cycles</i> , 2019, 33, 391-419.	4.9	76
20	Cyanobacterial symbionts diverged in the late Cretaceous towards lineage-specific nitrogen fixation factories in single-celled phytoplankton. <i>Nature Communications</i> , 2016, 7, 11071.	12.8	72
21	A modular view of the bacteriophage genomic space: identification of host and lifestyle marker modules. <i>Research in Microbiology</i> , 2011, 162, 737-746.	2.1	60
22	Analysis of the phage sequence space: The benefit of structured information. <i>Virology</i> , 2007, 365, 241-249.	2.4	53
23	A first global analysis of plasmid encoded proteins in the ACLAME database. <i>FEMS Microbiology Reviews</i> , 2006, 30, 980-994.	8.6	48
24	Comparative Analyses of Prophage-Like Elements Present in Bifidobacterial Genomes. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6929-6936.	3.1	45
25	Towards a more accurate annotation of tyrosine-based site-specific recombinases in bacterial genomes. <i>Mobile DNA</i> , 2012, 3, 6.	3.6	32
26	Mainstreams of Horizontal Gene Exchange in Enterobacteria: Consideration of the Outbreak of Enterohemorrhagic <i>E. coli</i> O104:H4 in Germany in 2011. <i>PLoS ONE</i> , 2011, 6, e25702.	2.5	31
27	Toxin-Antitoxin Gene Pairs Found in Tn <i>3</i> Family Transposons Appear To Be an Integral Part of the Transposition Module. <i>MBio</i> , 2020, 11, .	4.1	25
28	Disentangling environmental effects in microbial association networks. <i>Microbiome</i> , 2021, 9, 232.	11.1	21
29	PhiGO, a phage ontology associated with the ACLAME database. <i>Research in Microbiology</i> , 2007, 158, 567-571.	2.1	16
30	Reticulate Classification of Mosaic Microbial Genomes Using NeAT Website. <i>Methods in Molecular Biology</i> , 2012, 804, 81-91.	0.9	7