

Antonio Fernandez-Guerra

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6548912/publications.pdf>

Version: 2024-02-01

30
papers

3,704
citations

331670

21
h-index

454955

30
g-index

37
all docs

37
docs citations

37
times ranked

5367
citing authors

#	ARTICLE	IF	CITATIONS
1	Unifying the known and unknown microbial coding sequence space. <i>ELife</i> , 2022, 11, .	6.0	41
2	Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. <i>Cell Genomics</i> , 2022, 2, 100123.	6.5	70
3	Community-led, integrated, reproducible multi-omics with anvio™. <i>Nature Microbiology</i> , 2021, 6, 3-6.	13.3	370
4	Community-curated and standardised metadata of published ancient metagenomic samples with AncientMetagenomeDir. <i>Scientific Data</i> , 2021, 8, 31.	5.3	23
5	Late Quaternary dynamics of Arctic biota from ancient environmental genomics. <i>Nature</i> , 2021, 600, 86-92.	27.8	81
6	Secondary metabolite biosynthetic diversity in Arctic Ocean metagenomes. <i>Microbial Genomics</i> , 2021, 7, .	2.0	4
7	A computational framework to explore large-scale biosynthetic diversity. <i>Nature Chemical Biology</i> , 2020, 16, 60-68.	8.0	569
8	Linking Spatial and Temporal Dynamic of Bacterioplankton Communities With Ecological Strategies Across a Coastal Frontal Area. <i>Frontiers in Marine Science</i> , 2020, 7, .	2.5	7
9	Verrucomicrobia use hundreds of enzymes to digest the algal polysaccharide fucoidan. <i>Nature Microbiology</i> , 2020, 5, 1026-1039.	13.3	182
10	Meta-SourceTracker: application of Bayesian source tracking to shotgun metagenomics. <i>PeerJ</i> , 2020, 8, e8783.	2.0	43
11	Fast and accurate average genome size and 16S rRNA gene average copy number computation in metagenomic data. <i>BMC Bioinformatics</i> , 2019, 20, 453.	2.6	15
12	Decoding the ocean's microbiological secrets for marine enzyme biodiscovery. <i>FEMS Microbiology Letters</i> , 2019, 366, .	1.8	26
13	Recurrent patterns of microdiversity in a temperate coastal marine environment. <i>ISME Journal</i> , 2018, 12, 237-252.	9.8	135
14	Organic matter processing by microbial communities throughout the Atlantic water column as revealed by metaproteomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E400-E408.	7.1	146
15	Determinants and Prediction of Esterase Substrate Promiscuity Patterns. <i>ACS Chemical Biology</i> , 2018, 13, 225-234.	3.4	106
16	Molecular recognition of the beta-glucans laminarin and pustulan by a SusD-like glycan-binding protein of a marine <i>Bacteroidetes</i> . <i>FEBS Journal</i> , 2018, 285, 4465-4481.	4.7	13
17	Geographic distribution at subspecies resolution level: closely related <i>Rhodopirellula</i> species in European coastal sediments. <i>ISME Journal</i> , 2017, 11, 478-489.	9.8	11
18	Comparative Genomic Analysis Reveals a Diverse Repertoire of Genes Involved in Prokaryote-Eukaryote Interactions within the <i>Pseudovibrio</i> Genus. <i>Frontiers in Microbiology</i> , 2016, 7, 387.	3.5	36

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19	MyOSD 2014: Evaluating Oceanographic Measurements Contributed by Citizen Scientists in Support of Ocean Sampling Day. <i>Journal of Microbiology and Biology Education</i> , 2016, 17, 163-171.	1.0	6
20	The ocean sampling day consortium. <i>GigaScience</i> , 2015, 4, 27.	6.4	185
21	Pheromone Evolution, Reproductive Genes, and Comparative Transcriptomics in Mediterranean Earthworms (Annelida, Oligochaeta, Hormogastridae). <i>Molecular Biology and Evolution</i> , 2013, 30, 1614-1629.	8.9	24
22	Patterns and architecture of genomic islands in marine bacteria. <i>BMC Genomics</i> , 2012, 13, 347.	2.8	84
23	Exploration of community traits as ecological markers in microbial metagenomes. <i>Molecular Ecology</i> , 2012, 21, 1909-1917.	3.9	84
24	A close relationship between primary nucleotides sequence structure and the composition of functional genes in the genome of prokaryotes. <i>Molecular Phylogenetics and Evolution</i> , 2011, 61, 650-658.	2.7	22
25	Phylogenetic ecology of widespread uncultured clades of the Kingdom Euryarchaeota. <i>Molecular Ecology</i> , 2011, 20, 1988-1996.	3.9	36
26	Genomics of the Proteorhodopsin-Containing Marine Flavobacterium <i>Dokdonia</i> sp. Strain MED134. <i>Applied and Environmental Microbiology</i> , 2011, 77, 8676-8686.	3.1	56
27	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.	3.3	8
28	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.	7.1	231
29	The Genome of the Sea Urchin <i>Strongylocentrotus purpuratus</i> . <i>Science</i> , 2006, 314, 941-952.	12.6	1,018
30	The genomic repertoire for cell cycle control and DNA metabolism in <i>S. purpuratus</i> . <i>Developmental Biology</i> , 2006, 300, 238-251.	2.0	48