

Silvia G Acinas

List of Publications by Year in descending order

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Version: 2024-02-01

84
papers

15,959
citations

38660

50
h-index

54797

84
g-index

101
all docs

101
docs citations

101
times ranked

14496
citing authors

#	ARTICLE	IF	CITATIONS
1	A robust approach to estimate relative phytoplankton cell abundances from metagenomes. <i>Molecular Ecology Resources</i> , 2023, 23, 16-40.	2.2	29
2	Prevalence of Heterotrophic Methylmercury Detoxifying Bacteria across Oceanic Regions. <i>Environmental Science & Technology</i> , 2022, 56, 3452-3461.	4.6	9
3	Unifying the known and unknown microbial coding sequence space. <i>ELife</i> , 2022, 11, .	2.8	41
4	Cryptic and abundant marine viruses at the evolutionary origins of Earth's RNA virome. <i>Science</i> , 2022, 376, 156-162.	6.0	124
5	The Ocean Gene Atlas v2.0: online exploration of the biogeography and phylogeny of plankton genes. <i>Nucleic Acids Research</i> , 2022, 50, W516-W526.	6.5	26
6	Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. <i>Cell Genomics</i> , 2022, 2, 100123.	3.0	70
7	Biosynthetic potential of the global ocean microbiome. <i>Nature</i> , 2022, 607, 111-118.	13.7	128
8	Priorities for ocean microbiome research. <i>Nature Microbiology</i> , 2022, 7, 937-947.	5.9	27
9	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. <i>Communications Biology</i> , 2021, 4, 604.	2.0	107
10	Global distribution patterns of marine nitrogen-fixers by imaging and molecular methods. <i>Nature Communications</i> , 2021, 12, 4160.	5.8	58
11	mTAGs: taxonomic profiling using degenerate consensus reference sequences of ribosomal RNA genes. <i>Bioinformatics</i> , 2021, 38, 270-272.	1.8	5
12	Environmental vulnerability of the global ocean epipelagic plankton community interactome. <i>Science Advances</i> , 2021, 7, .	4.7	54
13	Macroscale patterns of oceanic zooplankton composition and size structure. <i>Scientific Reports</i> , 2021, 11, 15714.	1.6	24
14	Compendium of 530 metagenome-assembled bacterial and archaeal genomes from the polar Arctic Ocean. <i>Nature Microbiology</i> , 2021, 6, 1561-1574.	5.9	57
15	Diversity and distribution of marine heterotrophic bacteria from a large culture collection. <i>BMC Microbiology</i> , 2020, 20, 207.	1.3	27
16	Sequencing effort dictates gene discovery in marine microbial metagenomes. <i>Environmental Microbiology</i> , 2020, 22, 4589-4603.	1.8	13
17	Tara Oceans: towards global ocean ecosystems biology. <i>Nature Reviews Microbiology</i> , 2020, 18, 428-445.	13.6	227
18	A metagenomic assessment of microbial eukaryotic diversity in the global ocean. <i>Molecular Ecology Resources</i> , 2020, 20, 718-731.	2.2	70

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19	Disentangling the mechanisms shaping the surface ocean microbiota. <i>Microbiome</i> , 2020, 8, 55.	4.9	154
20	<i>Mesonia oceanica</i> sp. nov., isolated from oceans during the Tara oceans expedition, with a preference for mesopelagic waters. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4329-4338.	0.8	11
21	Important contribution of macroalgae to oceanic carbon sequestration. <i>Nature Geoscience</i> , 2019, 12, 748-754.	5.4	141
22	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019, 179, 1068-1083.e21.	13.5	268
23	Global Trends in Marine Plankton Diversity across Kingdoms of Life. <i>Cell</i> , 2019, 179, 1084-1097.e21.	13.5	271
24	Higher contribution of globally rare bacterial taxa reflects environmental transitions across the surface ocean. <i>Molecular Ecology</i> , 2019, 28, 1930-1945.	2.0	41
25	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019, 177, 1109-1123.e14.	13.5	541
26	Community-Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. <i>Global Biogeochemical Cycles</i> , 2019, 33, 391-419.	1.9	76
27	Delineation of ecologically distinct units of marine Bacteroidetes in the Northwestern Mediterranean Sea. <i>Molecular Ecology</i> , 2019, 28, 2846-2859.	2.0	31
28	Scaling of species distribution explains the vast potential marine prokaryote diversity. <i>Scientific Reports</i> , 2019, 9, 18710.	1.6	8
29	UCYN-3, a newly characterized open ocean sublineage of the symbiotic N ₂ -fixing cyanobacterium <i>Candidatus Atelocyanobacterium thalassa</i> . <i>Environmental Microbiology</i> , 2019, 21, 111-124.	1.8	31
30	Primer Design for an Accurate View of Picocyanobacterial Community Structure by Using High-Throughput Sequencing. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	9
31	Light color acclimation is a key process in the global ocean distribution of <i>Synechococcus cyanobacteria</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2010-E2019.	3.3	91
32	Large-scale ocean connectivity and planktonic body size. <i>Nature Communications</i> , 2018, 9, 142.	5.8	102
33	Single-virus genomics reveals hidden cosmopolitan and abundant viruses. <i>Nature Communications</i> , 2017, 8, 15892.	5.8	165
34	Phenotypic plasticity in freshwater picocyanobacteria. <i>Environmental Microbiology</i> , 2017, 19, 1120-1133.	1.8	31
35	A myovirus encoding both photosystem I and II proteins enhances cyclic electron flow in infected <i>Prochlorococcus</i> cells. <i>Nature Microbiology</i> , 2017, 2, 1350-1357.	5.9	74
36	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. <i>Scientific Data</i> , 2017, 4, 170093.	2.4	147

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37	Exploring Microdiversity in Novel <i>Kordia</i> sp. (Bacteroidetes) with Proteorhodopsin from the Tropical Indian Ocean via Single Amplified Genomes. <i>Frontiers in Microbiology</i> , 2017, 8, 1317.	1.5	7
38	Global genetic capacity for mixotrophy in marine picocyanobacteria. <i>ISME Journal</i> , 2016, 10, 2946-2957.	4.4	82
39	Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. <i>Nature</i> , 2016, 537, 689-693.	13.7	629
40	Cyanobacterial symbionts diverged in the late Cretaceous towards lineage-specific nitrogen fixation factories in single-celled phytoplankton. <i>Nature Communications</i> , 2016, 7, 11071.	5.8	72
41	Delineating ecologically significant taxonomic units from global patterns of marine picocyanobacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3365-74.	3.3	159
42	Plankton networks driving carbon export in the oligotrophic ocean. <i>Nature</i> , 2016, 532, 465-470.	13.7	670
43	Global distribution and vertical patterns of a prymnesiophyte-cyanobacteria obligate symbiosis. <i>ISME Journal</i> , 2016, 10, 693-706.	4.4	76
44	Large variability of bathypelagic microbial eukaryotic communities across the world's oceans. <i>ISME Journal</i> , 2016, 10, 945-958.	4.4	171
45	Global diversity and biogeography of deep-sea pelagic prokaryotes. <i>ISME Journal</i> , 2016, 10, 596-608.	4.4	191
46	Closing the gaps on the viral photosystem I gene organization. <i>Environmental Microbiology</i> , 2015, 17, 5100-5108.	1.8	7
47	Deep sequencing of amplified <i>Pirasinovirus</i> and host green algal genes from an Indian Ocean transect reveals interacting trophic dependencies and new genotypes. <i>Environmental Microbiology Reports</i> , 2015, 7, 979-989.	1.0	8
48	Particle-association lifestyle is a phylogenetically conserved trait in bathypelagic prokaryotes. <i>Molecular Ecology</i> , 2015, 24, 5692-5706.	2.0	113
49	Life-Style and Genome Structure of Marine Pseudoalteromonas Siphovirus B8b Isolated from the Northwestern Mediterranean Sea. <i>PLoS ONE</i> , 2015, 10, e0114829.	1.1	13
50	Determinants of community structure in the global plankton interactome. <i>Science</i> , 2015, 348, 1262073.	6.0	842
51	Patterns and ecological drivers of ocean viral communities. <i>Science</i> , 2015, 348, 1261498.	6.0	617
52	Structure and function of the global ocean microbiome. <i>Science</i> , 2015, 348, 1261359.	6.0	2,137
53	Eukaryotic plankton diversity in the sunlit ocean. <i>Science</i> , 2015, 348, 1261605.	6.0	1,551
54	Environmental characteristics of Agulhas rings affect interocean plankton transport. <i>Science</i> , 2015, 348, 1261447.	6.0	158

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55	Prokaryotic functional gene diversity in the sunlit ocean: Stumbling in the dark. <i>Current Opinion in Microbiology</i> , 2015, 25, 33-39.	2.3	24
56	Validation of a new catalysed reporter depositionâ€“fluorescence <i>in situ</i> hybridization probe for the accurate quantification of marine <i>Bacteroidetes</i> populations. <i>Environmental Microbiology</i> , 2015, 17, 3557-3569.	1.8	21
57	Metagenomic 16S rDNA Illumina tags are a powerful alternative to amplicon sequencing to explore diversity and structure of microbial communities. <i>Environmental Microbiology</i> , 2014, 16, 2659-2671.	1.8	291
58	The phylogenetic and ecological context of cultured and whole genome-sequenced planktonic bacteria from the coastal NW Mediterranean Sea. <i>Systematic and Applied Microbiology</i> , 2014, 37, 216-228.	1.2	22
59	Spatial and temporal variability among marine <i>Bacteroidetes</i> populations in the NW Mediterranean Sea. <i>Systematic and Applied Microbiology</i> , 2014, 37, 68-78.	1.2	33
60	Ecology of marine <i>Bacteroidetes</i> : a comparative genomics approach. <i>ISME Journal</i> , 2013, 7, 1026-1037.	4.4	614
61	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
62	Exploring nucleocytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. <i>ISME Journal</i> , 2013, 7, 1678-1695.	4.4	185
63	Patterns and architecture of genomic islands in marine bacteria. <i>BMC Genomics</i> , 2012, 13, 347.	1.2	84
64	Evaluation of Marine <i>Bacteroidetes</i> -Specific Primers for Microbial Diversity and Dynamics Studies. <i>Microbial Ecology</i> , 2012, 64, 1047-1055.	1.4	38
65	A Holistic Approach to Marine Eco-Systems Biology. <i>PLoS Biology</i> , 2011, 9, e1001177.	2.6	353
66	Transcriptome Fingerprinting Analysis: An Approach to Explore Gene Expression Patterns in Marine Microbial Communities. <i>PLoS ONE</i> , 2011, 6, e22950.	1.1	3
67	Diversity of nitrogen-fixing bacteria in cyanobacterial mats. <i>FEMS Microbiology Ecology</i> , 2010, 73, no-no.	1.3	43
68	Spatial patterns of bacterial richness and evenness in the NW Mediterranean Sea explored by pyrosequencing of the 16S rRNA. <i>Aquatic Microbial Ecology</i> , 2010, 61, 221-233.	0.9	100
69	Phenotypic and genetic diversification of <i>Pseudanabaena</i> spp. (cyanobacteria). <i>ISME Journal</i> , 2009, 3, 31-46.	4.4	103
70	Diversity and phylogeny of Baltic Sea picocyanobacteria inferred from their ITS and phycobiliprotein operons. <i>Environmental Microbiology</i> , 2008, 10, 174-188.	1.8	77
71	Evaluation of 23S rRNA PCR Primers for Use in Phylogenetic Studies of Bacterial Diversity. <i>Applied and Environmental Microbiology</i> , 2006, 72, 2221-2225.	1.4	124
72	Spatial and temporal variation in marine bacterioplankton diversity as shown by RFLP fingerprinting of PCR amplified 16S rDNA. <i>FEMS Microbiology Ecology</i> , 2006, 24, 27-40.	1.3	123

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73	PCR-Induced Sequence Artifacts and Bias: Insights from Comparison of Two 16S rRNA Clone Libraries Constructed from the Same Sample. <i>Applied and Environmental Microbiology</i> , 2005, 71, 8966-8969.	1.4	522
74	Divergence and Redundancy of 16S rRNA Sequences in Genomes with Multiple <i>rrn</i> Operons. <i>Journal of Bacteriology</i> , 2004, 186, 2629-2635.	1.0	520
75	Fine-scale phylogenetic architecture of a complex bacterial community. <i>Nature</i> , 2004, 430, 551-554.	13.7	475
76	A(r)Ray of Hope in Analysis of the Function and Diversity of Microbial Communities. <i>Biological Bulletin</i> , 2003, 204, 196-199.	0.7	18
77	Prevalence and microdiversity of <i>Alteromonas macleodii</i> -like microorganisms in different oceanic regions. <i>Environmental Microbiology</i> , 2002, 4, 42-50.	1.8	79
78	Archaeal Biodiversity in Crystallizer Ponds from a Solar Saltern: Culture versus PCR. <i>Microbial Ecology</i> , 2001, 41, 12-19.	1.4	113
79	Use of the 16S-23S ribosomal genes spacer region in studies of prokaryotic diversity. <i>Journal of Microbiological Methods</i> , 1999, 36, 55-64.	0.7	214
80	Diversity of Free-Living and Attached Bacteria in Offshore Western Mediterranean Waters as Depicted by Analysis of Genes Encoding 16S rRNA. <i>Applied and Environmental Microbiology</i> , 1999, 65, 514-522.	1.4	319
81	Heterotrophic bacteria, activity and bacterial diversity in two coastal lagoons as detected by culture and 16S rRNA genes PCR amplification and partial sequencing. <i>Hydrobiologia</i> , 1996, 329, 3-17.	1.0	3
82	Description of prokaryotic biodiversity along the salinity gradient of a multipond solar saltern by direct PCR amplification of 16S rDNA. <i>Hydrobiologia</i> , 1996, 329, 19-31.	1.0	54
83	Evaluation of prokaryotic diversity by restrictase digestion of 16S rDNA directly amplified from hypersaline environments. <i>FEMS Microbiology Ecology</i> , 1995, 17, 247-255.	1.3	47
84	Evaluation of prokaryotic diversity by restrictase digestion of 16S rDNA directly amplified from hypersaline environments. <i>FEMS Microbiology Ecology</i> , 1995, 17, 247-255.	1.3	107