

Silvia G Acinas

List of Publications by Year in descending order

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Version: 2024-02-01

85
papers

15,959
citations

38742

50
h-index

53230

85
g-index

101
all docs

101
docs citations

101
times ranked

14496
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	Eukaryotic plankton diversity in the sunlit ocean. <i>Science</i> , 2015, 348, 1261605.	12.6	1,551
3	Determinants of community structure in the global plankton interactome. <i>Science</i> , 2015, 348, 1262073.	12.6	842
4	Plankton networks driving carbon export in the oligotrophic ocean. <i>Nature</i> , 2016, 532, 465-470.	27.8	670
5	Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. <i>Nature</i> , 2016, 537, 689-693.	27.8	629
6	Patterns and ecological drivers of ocean viral communities. <i>Science</i> , 2015, 348, 1261498.	12.6	617
7	Ecology of marine Bacteroidetes: a comparative genomics approach. <i>ISME Journal</i> , 2013, 7, 1026-1037.	9.8	614
8	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019, 177, 1109-1123.e14.	28.9	541
9	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.	3.1	522
10	Divergence and Redundancy of 16S rRNA Sequences in Genomes with Multiple <i>rrn</i> Operons. <i>Journal of Bacteriology</i> , 2004, 186, 2629-2635.	2.2	520
11	Fine-scale phylogenetic architecture of a complex bacterial community. <i>Nature</i> , 2004, 430, 551-554.	27.8	475
12	A Holistic Approach to Marine Eco-Systems Biology. <i>PLoS Biology</i> , 2011, 9, e1001177.	5.6	353
13	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.	7.1	328
14	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.	3.1	319
15	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
16	Global Trends in Marine Plankton Diversity across Kingdoms of Life. <i>Cell</i> , 2019, 179, 1084-1097.e21.	28.9	271
17	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019, 179, 1068-1083.e21.	28.9	268
18	Tara Oceans: towards global ocean ecosystems biology. <i>Nature Reviews Microbiology</i> , 2020, 18, 428-445.	28.6	227

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19	Use of the 16Sâ€“23S ribosomal genes spacer region in studies of prokaryotic diversity. <i>Journal of Microbiological Methods</i> , 1999, 36, 55-64.	1.6	214
20	Global diversity and biogeography of deep-sea pelagic prokaryotes. <i>ISME Journal</i> , 2016, 10, 596-608.	9.8	191
21	Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. <i>ISME Journal</i> , 2013, 7, 1678-1695.	9.8	185
22	Large variability of bathypelagic microbial eukaryotic communities across the worldâ€™s oceans. <i>ISME Journal</i> , 2016, 10, 945-958.	9.8	171
23	Single-virus genomics reveals hidden cosmopolitan and abundant viruses. <i>Nature Communications</i> , 2017, 8, 15892.	12.8	165
24	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.	7.1	159
25	Environmental characteristics of Agulhas rings affect interocean plankton transport. <i>Science</i> , 2015, 348, 1261447.	12.6	158
26	Disentangling the mechanisms shaping the surface ocean microbiota. <i>Microbiome</i> , 2020, 8, 55.	11.1	154
27	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. <i>Scientific Data</i> , 2017, 4, 170093.	5.3	147
28	Important contribution of macroalgae to oceanic carbon sequestration. <i>Nature Geoscience</i> , 2019, 12, 748-754.	12.9	141
29	Biosynthetic potential of the global ocean microbiome. <i>Nature</i> , 2022, 607, 111-118.	27.8	128
30	Evaluation of 23S rRNA PCR Primers for Use in Phylogenetic Studies of Bacterial Diversity. <i>Applied and Environmental Microbiology</i> , 2006, 72, 2221-2225.	3.1	124
31	Cryptic and abundant marine viruses at the evolutionary origins of Earthâ€™s RNA virome. <i>Science</i> , 2022, 376, 156-162.	12.6	124
32	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.	2.7	123
33	Archaeal Biodiversity in Crystallizer Ponds from a Solar Saltern: Culture versus PCR. <i>Microbial Ecology</i> , 2001, 41, 12-19.	2.8	113
34	Particleâ€“association lifestyle is a phylogenetically conserved trait in bathypelagic prokaryotes. <i>Molecular Ecology</i> , 2015, 24, 5692-5706.	3.9	113
35	Evaluation of prokaryotic diversity by restrictase digestion of 16S rDNA directly amplified from hypersaline environments. <i>FEMS Microbiology Ecology</i> , 1995, 17, 247-255.	2.7	107
36	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. <i>Communications Biology</i> , 2021, 4, 604.	4.4	107

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37	Phenotypic and genetic diversification of <i>Pseudanabaena</i> spp. (cyanobacteria). ISME Journal, 2009, 3, 31-46.	9.8	103
38	Large-scale ocean connectivity and planktonic body size. Nature Communications, 2018, 9, 142.	12.8	102
39	Spatial patterns of bacterial richness and evenness in the NW Mediterranean Sea explored by pyrosequencing of the 16S rRNA. Aquatic Microbial Ecology, 2010, 61, 221-233.	1.8	100
40	Light color acclimation is a key process in the global ocean distribution of <i>Synechococcus cyanobacteria</i> . Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E2010-E2019.	7.1	91
41	Patterns and architecture of genomic islands in marine bacteria. BMC Genomics, 2012, 13, 347.	2.8	84
42	Global genetic capacity for mixotrophy in marine picocyanobacteria. ISME Journal, 2016, 10, 2946-2957.	9.8	82
43	Prevalence and microdiversity of <i>Alteromonas macleodii</i> -like microorganisms in different oceanic regions. Environmental Microbiology, 2002, 4, 42-50.	3.8	79
44	Diversity and phylogeny of Baltic Sea picocyanobacteria inferred from their ITS and phycobiliprotein operons. Environmental Microbiology, 2008, 10, 174-188.	3.8	77
45	Global distribution and vertical patterns of a prymnesiophyte-cyanobacteria obligate symbiosis. ISME Journal, 2016, 10, 693-706.	9.8	76
46	Community-level Responses to Iron Availability in Open Ocean Plankton Ecosystems. Global Biogeochemical Cycles, 2019, 33, 391-419.	4.9	76
47	A myovirus encoding both photosystem I and II proteins enhances cyclic electron flow in infected <i>Prochlorococcus</i> cells. Nature Microbiology, 2017, 2, 1350-1357.	13.3	74
48	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
49	A metagenomic assessment of microbial eukaryotic diversity in the global ocean. Molecular Ecology Resources, 2020, 20, 718-731.	4.8	70
50	Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. Cell Genomics, 2022, 2, 100123.	6.5	70
51	Global distribution patterns of marine nitrogen-fixers by imaging and molecular methods. Nature Communications, 2021, 12, 4160.	12.8	58
52	Compendium of 530 metagenome-assembled bacterial and archaeal genomes from the polar Arctic Ocean. Nature Microbiology, 2021, 6, 1561-1574.	13.3	57
53	Description of prokaryotic biodiversity along the salinity gradient of a multipond solar saltern by direct PCR amplification of 16S rDNA. Hydrobiologia, 1996, 329, 19-31.	2.0	54
54	Environmental vulnerability of the global ocean epipelagic plankton community interactome. Science Advances, 2021, 7, .	10.3	54

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55	Evaluation of prokaryotic diversity by restrictase digestion of 16S rDNA directly amplified from hypersaline environments. <i>FEMS Microbiology Ecology</i> , 1995, 17, 247-255.	2.7	47
56	Diversity of nitrogen-fixing bacteria in cyanobacterial mats. <i>FEMS Microbiology Ecology</i> , 2010, 73, no-no.	2.7	43
57	Higher contribution of globally rare bacterial taxa reflects environmental transitions across the surface ocean. <i>Molecular Ecology</i> , 2019, 28, 1930-1945.	3.9	41
58	Unifying the known and unknown microbial coding sequence space. <i>ELife</i> , 2022, 11, .	6.0	41
59	Evaluation of Marine Bacteroidetes-Specific Primers for Microbial Diversity and Dynamics Studies. <i>Microbial Ecology</i> , 2012, 64, 1047-1055.	2.8	38
60	Spatial and temporal variability among marine Bacteroidetes populations in the NW Mediterranean Sea. <i>Systematic and Applied Microbiology</i> , 2014, 37, 68-78.	2.8	33
61	Phenotypic plasticity in freshwater picocyanobacteria. <i>Environmental Microbiology</i> , 2017, 19, 1120-1133.	3.8	31
62	Delineation of ecologically distinct units of marine Bacteroidetes in the Northwestern Mediterranean Sea. <i>Molecular Ecology</i> , 2019, 28, 2846-2859.	3.9	31
63	UCYNâ€A3, a newly characterized open ocean sublineage of the symbiotic N₂-fixing cyanobacterium <i>Candidatus</i> <i>Atelocyanobacterium thalassa</i> . <i>Environmental Microbiology</i> , 2019, 21, 111-124.	3.8	31
64	A robust approach to estimate relative phytoplankton cell abundances from metagenomes. <i>Molecular Ecology Resources</i> , 2023, 23, 16-40.	4.8	29
65	Diversity and distribution of marine heterotrophic bacteria from a large culture collection. <i>BMC Microbiology</i> , 2020, 20, 207.	3.3	27
66	Priorities for ocean microbiome research. <i>Nature Microbiology</i> , 2022, 7, 937-947.	13.3	27
67	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.	14.5	26
68	Prokaryotic functional gene diversity in the sunlit ocean: Stumbling in the dark. <i>Current Opinion in Microbiology</i> , 2015, 25, 33-39.	5.1	24
69	Macroscale patterns of oceanic zooplankton composition and size structure. <i>Scientific Reports</i> , 2021, 11, 15714.	3.3	24
70	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.	2.8	22
71	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.	3.8	21
72	A(r)Ray of Hope in Analysis of the Function and Diversity of Microbial Communities. <i>Biological Bulletin</i> , 2003, 204, 196-199.	1.8	18

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73	Life-Style and Genome Structure of Marine Pseudoalteromonas Siphovirus B8b Isolated from the Northwestern Mediterranean Sea. PLoS ONE, 2015, 10, e0114829.	2.5	13
74	Sequencing effort dictates gene discovery in marine microbial metagenomes. Environmental Microbiology, 2020, 22, 4589-4603.	3.8	13
75	Mesonion oceanica sp. nov., isolated from oceans during the Tara oceans expedition, with a preference for mesopelagic waters. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4329-4338.	1.7	11
76	Primer Design for an Accurate View of Picocyanobacterial Community Structure by Using High-Throughput Sequencing. Applied and Environmental Microbiology, 2019, 85, .	3.1	9
77	Prevalence of Heterotrophic Methylmercury Detoxifying Bacteria across Oceanic Regions. Environmental Science & Technology, 2022, 56, 3452-3461.	10.0	9
78	Deep sequencing of amplified <i>Pcrasinovirus</i> and host green algal genes from an Indian Ocean transect reveals interacting trophic dependencies and new genotypes. Environmental Microbiology Reports, 2015, 7, 979-989.	2.4	8
79	Scaling of species distribution explains the vast potential marine prokaryote diversity. Scientific Reports, 2019, 9, 18710.	3.3	8
80	Closing the gaps on the viral photosystem <i>psaDCAB</i> gene organization. Environmental Microbiology, 2015, 17, 5100-5108.	3.8	7
81	Exploring Microdiversity in Novel <i>Kordia</i> sp. (Bacteroidetes) with Proteorhodopsin from the Tropical Indian Ocean via Single Amplified Genomes. Frontiers in Microbiology, 2017, 8, 1317.	3.5	7
82	Spatial and temporal variation in marine bacterioplankton diversity as shown by RFLP fingerprinting of PCR amplified 16S rDNA. FEMS Microbiology Ecology, 1997, 24, 27-40.	2.7	6
83	mTAGs: taxonomic profiling using degenerate consensus reference sequences of ribosomal RNA genes. Bioinformatics, 2021, 38, 270-272.	4.1	5
84	Heterotrophic bacteria, activity and bacterial diversity in two coastal lagoons as detected by culture and 16S rRNA genes PCR amplification and partial sequencing. Hydrobiologia, 1996, 329, 3-17.	2.0	3
85	Transcriptome Fingerprinting Analysis: An Approach to Explore Gene Expression Patterns in Marine Microbial Communities. PLoS ONE, 2011, 6, e22950.	2.5	3