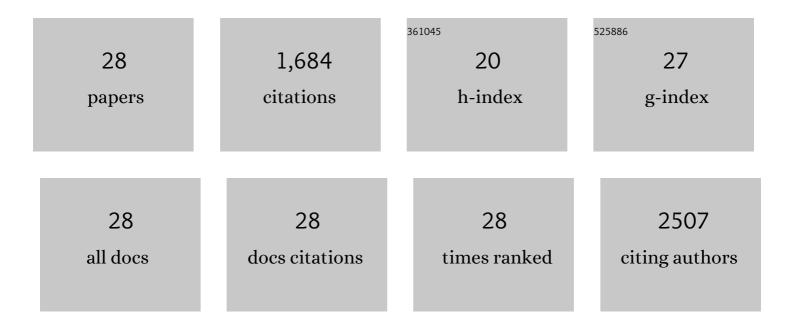
Itziar Lekunberri

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1661608/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Metagenomic exploration reveals a marked change in the river resistome and mobilome after treated wastewater discharges. Environmental Pollution, 2018, 234, 538-542.	3.7	44
2	Occurrence et devenir des polluants émergents (antibiotiques) dans un aquifère alluvial et leur influence sur les bactéries multi-résistantes (Bas-FluviÃ, Catalogne). Houille Blanche, 2018, 104, 47-52.	0.3	0
3	Contribution of bacteriophage and plasmid DNA to the mobilization of antibiotic resistance genes in a river receiving treated wastewater discharges. Science of the Total Environment, 2017, 601-602, 206-209.	3.9	97
4	Detection and quantification of the plasmid-mediated mcr-1 gene conferring colistin resistance in wastewater. International Journal of Antimicrobial Agents, 2017, 50, 734-736.	1.1	32
5	Exploring the contribution of bacteriophages to antibiotic resistance. Environmental Pollution, 2017, 220, 981-984.	3.7	107
6	Prokaryotic Responses to Ammonium and Organic Carbon Reveal Alternative CO2 Fixation Pathways and Importance of Alkaline Phosphatase in the Mesopelagic North Atlantic. Frontiers in Microbiology, 2016, 7, 1670.	1.5	47
7	Largeâ€scale distribution of microbial and viral populations in the <scp>S</scp> outh <scp>A</scp> tlantic <scp>O</scp> cean. Environmental Microbiology Reports, 2016, 8, 305-315.	1.0	38
8	Abundance of antibiotic resistance genes in five municipal wastewater treatment plants in the Monastir Governorate, Tunisia. Environmental Pollution, 2016, 219, 353-358.	3.7	107
9	Marinomonas blandensis sp. nov., a novel marine gammaproteobacterium. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 5544-5549.	0.8	12
10	The phylogenetic and ecological context of cultured and whole genome-sequenced planktonic bacteria from the coastal NW Mediterranean Sea. Systematic and Applied Microbiology, 2014, 37, 216-228.	1.2	22
11	Linkage between copepods and bacteria in the North Atlantic Ocean. Aquatic Microbial Ecology, 2014, 72, 215-225.	0.9	41
12	Culturing Bias in Marine Heterotrophic Flagellates Analyzed Through Seawater Enrichment Incubations. Microbial Ecology, 2013, 66, 489-499.	1.4	26
13	Spatial patterns of bacterial and archaeal communities along the Romanche Fracture Zone (tropical) Tj ETQq1 1	0.784314 1.3	rgBT /Over
14	Relationship between induced phytoplankton blooms and the structure and dynamics of the free-living heterotrophic bacterial community. Marine Ecology - Progress Series, 2012, 448, 23-37.	0.9	13
15	Mesoscale eddies: hotspots of prokaryotic activity and differential community structure in the ocean. ISME Journal, 2010, 4, 975-988.	4.4	86
16	Changes in bacterial activity and community composition caused by exposure to a simulated oil spill in microcosm and mesocosm experiments. Aquatic Microbial Ecology, 2010, 59, 169-183.	0.9	21
17	Particulate and dissolved primary production by contrasting phytoplankton assemblages during mesocosm experiments in the Ria de Vigo (NW Spain). Journal of Plankton Research, 2010, 32, 1231-1240.	0.8	18
18	Effects of a dust deposition event on coastal marine microbial abundance and activity, bacterial community structure and ecosystem function, Journal of Plankton Research, 2010, 32, 381-396	0.8	87

Itziar Lekunberri

#	Article	IF	CITATIONS
19	Bermanella marisrubri gen. nov., sp. nov., a genome-sequenced gammaproteobacterium from the Red Sea. International Journal of Systematic and Evolutionary Microbiology, 2009, 59, 373-377.	0.8	24
20	Bacterioplankton composition of the coastal upwelling system of â€~RÃa de Vigo', NW Spain. FEMS Microbiology Ecology, 2009, 70, 493-505.	1.3	46
21	Factors Controlling the Year-Round Variability in Carbon Flux Through Bacteria in a Coastal Marine System. Ecosystems, 2008, 11, 397-409.	1.6	121
22	Linkages between bacterioplankton community composition, heterotrophic carbon cycling and environmental conditions in a highly dynamic coastal ecosystem. Environmental Microbiology, 2008, 10, 906-917.	1.8	72
23	Genome analysis of the proteorhodopsin-containing marine bacterium <i>Polaribacter</i> sp. MED152 (Flavobacteria). Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8724-8729.	3.3	231
24	Reinekea blandensis sp. nov., a marine, genome-sequenced gammaproteobacterium. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 2370-2375.	0.8	21
25	Neptuniibacter caesariensis gen. nov., sp. nov., a novel marine genome-sequenced gammaproteobacterium. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 1000-1006.	0.8	58
26	Dynamics of the hydrocarbon-degrading Cycloclasticus bacteria during mesocosm-simulated oil spills. Environmental Microbiology, 2007, 9, 2551-2562.	1.8	91
27	Leeuwenhoekiella blandensis sp. nov., a genome-sequenced marine member of the family Flavobacteriaceae. International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 1489-1493.	0.8	57
28	Trace metal concentration, antioxidant enzyme activities and susceptibility to oxidative stress in the tricoptera larvae Hydropsyche exocellata from the Llobregat river basin (NE Spain). Aquatic Toxicology, 2005, 74, 3-19.	1.9	149