

Francisco Rodriguez-Valera

List of Publications by Year in descending order

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220
papers

18,728
citations

11608

70
h-index

16127

124
g-index

241
all docs

241
docs citations

241
times ranked

15730
citing authors

#	ARTICLE	IF	CITATIONS
1	Unexpected diversity of small eukaryotes in deep-sea Antarctic plankton. <i>Nature</i> , 2001, 409, 603-607.	13.7	838
2	Explaining microbial population genomics through phage predation. <i>Nature Reviews Microbiology</i> , 2009, 7, 828-836.	13.6	596
3	Development of a Multilocus Sequence Typing Scheme for Characterization of Clinical Isolates of <i>Acinetobacter baumannii</i> . <i>Journal of Clinical Microbiology</i> , 2005, 43, 4382-4390.	1.8	595
4	Comparison of prokaryotic diversity at offshore oceanic locations reveals a different microbiota in the Mediterranean Sea. <i>FEMS Microbiology Ecology</i> , 2006, 56, 389-405.	1.3	580
5	Changes in archaeal, bacterial and eukaryal assemblages along a salinity gradient by comparison of genetic fingerprinting methods in a multipond solar saltern. <i>Environmental Microbiology</i> , 2002, 4, 338-348.	1.8	433
6	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	9.4	414
7	<i>Salinibacter ruber</i> gen. nov., sp. nov., a novel, extremely halophilic member of the Bacteria from saltern crystallizer ponds.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2002, 52, 485-491.	0.8	401
8	Viral and microbial community dynamics in four aquatic environments. <i>ISME Journal</i> , 2010, 4, 739-751.	4.4	387
9	The genome of <i>Salinibacter ruber</i> : Convergence and gene exchange among hyperhalophilic bacteria and archaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18147-18152.	3.3	299
10	Extremely Halophilic Bacteria in Crystallizer Ponds from Solar Salterns. <i>Applied and Environmental Microbiology</i> , 2000, 66, 3052-3057.	1.4	294
11	New Abundant Microbial Groups in Aquatic Hypersaline Environments. <i>Scientific Reports</i> , 2011, 1, 135.	1.6	288
12	Prokaryotic genetic diversity throughout the salinity gradient of a coastal solar saltern. <i>Environmental Microbiology</i> , 2002, 4, 349-360.	1.8	287
13	Long stretches of short tandem repeats are present in the largest replicons of the Archaea <i>Haloferax mediterranei</i> and <i>Haloferax volcanii</i> and could be involved in replicon partitioning. <i>Molecular Microbiology</i> , 1995, 17, 85-93.	1.2	266
14	Detection and identification of bacterial DNA in patients with cirrhosis and culture-negative, nonneutrocytic ascites. <i>Hepatology</i> , 2002, 36, 135-141.	3.6	264
15	Transcription at different salinities of <i>Haloferax mediterranei</i> sequences adjacent to partially modified PstI sites. <i>Molecular Microbiology</i> , 1993, 9, 613-621.	1.2	263
16	Expanding the Marine Virosphere Using Metagenomics. <i>PLoS Genetics</i> , 2013, 9, e1003987.	1.5	259
17	The genome of the square archaeon <i>Haloquadratum walsbyi</i> : life at the limits of water activity. <i>BMC Genomics</i> , 2006, 7, 169.	1.2	247
18	Characteristics of the heterotrophic bacterial populations in hypersaline environments of different salt concentrations. <i>Microbial Ecology</i> , 1981, 7, 235-243.	1.4	215

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19	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
20	Metagenomics of the Deep Mediterranean, a Warm Bathypelagic Habitat. <i>PLoS ONE</i> , 2007, 2, e914.	1.1	213
21	Variation of environmental features and microbial populations with salt concentrations in a multi-pond saltern. <i>Microbial Ecology</i> , 1985, 11, 107-115.	1.4	197
22	Transmission of Creutzfeldt-Jakob disease from man to the guinea pig. <i>Science</i> , 1975, 190, 571-572.	6.0	193
23	Comparative genomics of two ecotypes of the marine planktonic copiotroph <i>Alteromonas macleodii</i> suggests alternative lifestyles associated with different kinds of particulate organic matter. <i>ISME Journal</i> , 2008, 2, 1194-1212.	4.4	185
24	Metagenomics of the Water Column in the Pristine Upper Course of the Amazon River. <i>PLoS ONE</i> , 2011, 6, e23785.	1.1	183
25	Metagenomics uncovers a new group of low GC and ultra-small marine Actinobacteria. <i>Scientific Reports</i> , 2013, 3, 2471.	1.6	182
26	Effects of Culture Conditions on Poly(γ -Hydroxybutyric Acid) Production by <i>Haloferax mediterranei</i> . <i>Applied and Environmental Microbiology</i> , 1990, 56, 2517-2521.	1.4	181
27	Fluorescence in situ hybridization analysis of the prokaryotic community inhabiting crystallizer ponds. <i>Environmental Microbiology</i> , 1999, 1, 517-523.	1.8	177
28	Betaine is the main compatible solute of halophilic eubacteria. <i>Journal of Bacteriology</i> , 1984, 160, 478-479.	1.0	175
29	<i>Haloquadratum walsbyi</i> gen. nov., sp. nov., the square haloarchaeon of Walsby, isolated from saltern crystallizers in Australia and Spain. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 387-392.	0.8	173
30	Key roles for freshwater Actinobacteria revealed by deep metagenomic sequencing. <i>Molecular Ecology</i> , 2014, 23, 6073-6090.	2.0	170
31	The bacterial pan-genome: a new paradigm in microbiology. <i>International Microbiology</i> , 2010, 13, 45-57.	1.1	168
32	Single-virus genomics reveals hidden cosmopolitan and abundant viruses. <i>Nature Communications</i> , 2017, 8, 15892.	5.8	165
33	Accumulation of Poly (γ -Hydroxybutyrate) by Halobacteria. <i>Applied and Environmental Microbiology</i> , 1986, 51, 214-216.	1.4	162
34	Metagenomic Insights into the Uncultured Diversity and Physiology of Microbes in Four Hypersaline Soda Lake Brines. <i>Frontiers in Microbiology</i> , 2016, 7, 211.	1.5	161
35	Isolation and cultivation of Walsby's square archaeon. <i>Environmental Microbiology</i> , 2004, 6, 1287-1291.	1.8	150
36	Microdiversity of uncultured marine prokaryotes: the SAR11 cluster and the marine Archaea of Group I. <i>Molecular Ecology</i> , 2000, 9, 935-948.	2.0	139

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37	The Neolithic revolution of bacterial genomes. Trends in Microbiology, 2006, 14, 200-206.	3.5	135
38	Environmental genomics, the big picture?. FEMS Microbiology Letters, 2004, 231, 153-158.	0.7	133
39	The discovery of <sc>CRISPR</sc> in archaea and bacteria. FEBS Journal, 2016, 283, 3162-3169.	2.2	130
40	Environmental genomics of "Haloquadratum walsbyi" in a saltern crystallizer indicates a large pool of accessory genes in an otherwise coherent species. BMC Genomics, 2006, 7, 171.	1.2	128
41	Diversity of free-living prokaryotes from a deep-sea site at the Antarctic Polar Front. , 2001, 36, 193-202.		124
42	Spatial and temporal variation in marine bacterioplankton diversity as shown by RFLP fingerprinting of PCR amplified 16S rDNA. FEMS Microbiology Ecology, 2006, 24, 27-40.	1.3	123
43	Marine Group II Archaea, potentially important players in the global ocean carbon cycle. Frontiers in Microbiology, 2015, 6, 1108.	1.5	119
44	ROBUST: The ROLE of BUFFERING capacities in STabilising coastal lagoon ecosystems. Continental Shelf Research, 2001, 21, 2021-2041.	0.9	118
45	Genomic plasticity in prokaryotes: the case of the square haloarchaeon. ISME Journal, 2007, 1, 235-245.	4.4	116
46	Archaeal Biodiversity in Crystallizer Ponds from a Solar Saltern: Culture versus PCR. Microbial Ecology, 2001, 41, 12-19.	1.4	113
47	Hindsight in the relative abundance, metabolic potential and genome dynamics of uncultivated marine archaea from comparative metagenomic analyses of bathypelagic plankton of different oceanic regions. ISME Journal, 2008, 2, 865-886.	4.4	113
48	The Santa Pola saltern as a model for studying the microbiota of hypersaline environments. Extremophiles, 2014, 18, 811-824.	0.9	113
49	Genomes of surface isolates of Alteromonas macleodii: the life of a widespread marine opportunistic copiotroph. Scientific Reports, 2012, 2, 696.	1.6	111
50	Prokaryotic Diversity in Zostera noltii -Colonized Marine Sediments. Applied and Environmental Microbiology, 2000, 66, 1715-1719.	1.4	110
51	Metagenome of the Mediterranean deep chlorophyll maximum studied by direct and fosmid library 454 pyrosequencing. ISME Journal, 2010, 4, 1154-1166.	4.4	109
52	Evaluation of prokaryotic diversity by restrictase digestion of 16S rDNA directly amplified from hypersaline environments. FEMS Microbiology Ecology, 1995, 17, 247-255.	1.3	107
53	Sequencing of Bacterial and Archaeal 16S rRNA Genes Directly Amplified from a Hypersaline Environment. Systematic and Applied Microbiology, 1995, 18, 574-581.	1.2	102
54	The enigmatic SAR202 cluster up close: shedding light on a globally distributed dark ocean lineage involved in sulfur cycling. ISME Journal, 2018, 12, 655-668.	4.4	101

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55	Genomes of Abundant and Widespread Viruses from the Deep Ocean. MBio, 2016, 7, .	1.8	99
56	A new class of marine Euryarchaeota group II from the mediterranean deep chlorophyll maximum. ISME Journal, 2015, 9, 1619-1634.	4.4	95
57	Fine metagenomic profile of the Mediterranean stratified and mixed water columns revealed by assembly and recruitment. Microbiome, 2018, 6, 128.	4.9	95
58	Inward H ⁺ pump xenorhodopsin: Mechanism and alternative optogenetic approach. Science Advances, 2017, 3, e1603187.	4.7	93
59	Pangenome Evidence for Extensive Interdomain Horizontal Transfer Affecting Lineage Core and Shell Genes in Uncultured Planktonic Thaumarchaeota and Euryarchaeota. Genome Biology and Evolution, 2014, 6, 1549-1563.	1.1	91
60	Genomes of Novel Microbial Lineages Assembled from the Sub-Ice Waters of Lake Baikal. Applied and Environmental Microbiology, 2018, 84, .	1.4	91
61	A novel haloarchaeal-related lineage is widely distributed in deep oceanic regions. Environmental Microbiology, 2001, 3, 72-78.	1.8	90
62	Halocins: salt-dependent bacteriocins produced by extremely halophilic rods. Canadian Journal of Microbiology, 1982, 28, 151-154.	0.8	88
63	Description of Alcanivorax venustensis sp. nov. and reclassification of Fundibacter jadensis DSM 12178T (Bruns and Berthe-Corti 1999) as Alcanivorax jadensis comb. nov., members of the emended genus Alcanivorax. International Journal of Systematic and Evolutionary Microbiology, 2003, 53, 331-338.	0.8	88
64	Genomes of Planktonic <i>Acidimicrobiales</i> : Widening Horizons for Marine <i>Actinobacteria</i> by Metagenomics. MBio, 2015, 6, .	1.8	88
65	Prokaryotic taxonomic and metabolic diversity of an intermediate salinity hypersaline habitat assessed by metagenomics. FEMS Microbiology Ecology, 2014, 88, 623-635.	1.3	87
66	Metagenomes of Mediterranean Coastal Lagoons. Scientific Reports, 2012, 2, 490.	1.6	85
67	Comparative analysis of a genome fragment of an uncultivated mesopelagic crenarchaeote reveals multiple horizontal gene transfers. Environmental Microbiology, 2004, 6, 19-34.	1.8	84
68	Numerous cultivated and uncultivated viruses encode ribosomal proteins. Nature Communications, 2019, 10, 752.	5.8	82
69	Genome diversity of marine phages recovered from Mediterranean metagenomes: Size matters. PLoS Genetics, 2017, 13, e1007018.	1.5	82
70	Flexible genomic islands as drivers of genome evolution. Current Opinion in Microbiology, 2016, 31, 154-160.	2.3	81
71	Comparison of prokaryotic community structure from Mediterranean and Atlantic saltern concentrator ponds by a metagenomic approach. Frontiers in Microbiology, 2014, 5, 196.	1.5	80
72	Prevalence and microdiversity of <i>Alteromonas macleodii</i> -like microorganisms in different oceanic regions. Environmental Microbiology, 2002, 4, 42-50.	1.8	79

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73	From Metagenomics to Pure Culture: Isolation and Characterization of the Moderately Halophilic Bacterium <i>Spiribacter salinus</i> gen. nov., sp. nov. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3850-3857.	1.4	78
74	Reconstructing Viral Genomes from the Environment Using Fosmid Clones: The Case of Haloviruses. <i>PLoS ONE</i> , 2012, 7, e33802.	1.1	78
75	Survey of lipids of a new group of extremely halophilic bacteria from salt ponds in Spain. <i>Canadian Journal of Microbiology</i> , 1982, 28, 1365-1372.	0.8	76
76	Intragenomic 16S rDNA Divergence in <i>Haloarcula marismortui</i> Is an Adaptation to Different Temperatures. <i>Journal of Molecular Evolution</i> , 2007, 65, 687-696.	0.8	76
77	Adapting to environmental changes using specialized paralogs. <i>Trends in Genetics</i> , 2008, 24, 154-158.	2.9	76
78	Types and properties of some bacteria isolated from hypersaline soils. <i>Journal of Applied Bacteriology</i> , 1982, 53, 155-161.	1.1	74
79	Pangenome Evolution in the Marine Bacterium <i>Alteromonas</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 1556-1570.	1.1	73
80	Behaviour of mixed populations of halophilic bacteria in continuous cultures. <i>Canadian Journal of Microbiology</i> , 1980, 26, 1259-1263.	0.8	72
81	Characterization of Microbial Diversity in Hypersaline Environments by Melting Profiles and Reassociation Kinetics in Combination with Terminal Restriction Fragment Length Polymorphism (T-RFLP). <i>Microbial Ecology</i> , 2003, 46, 291-301.	1.4	72
82	New insights into marine group III Euryarchaeota, from dark to light. <i>ISME Journal</i> , 2017, 11, 1102-1117.	4.4	72
83	Genomic Diversity of Deep Ecotype <i>Alteromonas macleodii</i> Isolates: Evidence for Pan-Mediterranean Clonal Frames. <i>Genome Biology and Evolution</i> , 2013, 5, 1220-1232.	1.1	71
84	Genetic analysis of housekeeping genes reveals a deep-sea ecotype of <i>Alteromonas macleodii</i> in the Mediterranean Sea. <i>Environmental Microbiology</i> , 2005, 7, 649-659.	1.8	70
85	Novel <i>Synechococcus</i> Genomes Reconstructed from Freshwater Reservoirs. <i>Frontiers in Microbiology</i> , 2017, 8, 1151.	1.5	69
86	Reconstruction of Diverse Verrucomicrobial Genomes from Metagenome Datasets of Freshwater Reservoirs. <i>Frontiers in Microbiology</i> , 2017, 8, 2131.	1.5	68
87	Breaking a paradigm: cosmopolitan and abundant freshwater actinobacteria are low GC. <i>Environmental Microbiology Reports</i> , 2012, 4, 29-35.	1.0	66
88	Ecogenomics of the SAR11 clade. <i>Environmental Microbiology</i> , 2020, 22, 1748-1763.	1.8	66
89	Metagenomic islands of hyperhalophiles: the case of <i>Salinibacter ruber</i> . <i>BMC Genomics</i> , 2009, 10, 570.	1.2	64
90	Evolutionary relationships of <i>Fusobacterium nucleatum</i> based on phylogenetic analysis and comparative genomics. <i>BMC Evolutionary Biology</i> , 2004, 4, 50.	3.2	63

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91	Halobacteria as producers of polyhydroxyalkanoates. FEMS Microbiology Letters, 1992, 103, 181-186.	0.7	62
92	Comparative genomics of gene-family size in closely related bacteria. Genome Biology, 2004, 5, R27.	13.9	62
93	Biogeography of the ubiquitous marine bacterium <i>Alteromonas macleodii</i> determined by multilocus sequence analysis. Molecular Ecology, 2008, 17, 4092-4106.	2.0	62
94	Isopranylglycerol diethers in non-alkaline evaporitic environments. Geochimica Et Cosmochimica Acta, 1993, 57, 4479-4489.	1.6	60
95	Microbiome of the deep Lake Baikal, a unique oxic bathypelagic habitat. Limnology and Oceanography, 2020, 65, 1471-1488.	1.6	60
96	Genome Reconstruction from Metagenomic Data Sets Reveals Novel Microbes in the Brackish Waters of the Caspian Sea. Applied and Environmental Microbiology, 2016, 82, 1599-1612.	1.4	59
97	Unique structure and function of viral rhodopsins. Nature Communications, 2019, 10, 4939.	5.8	59
98	Sequence Diversity in the 16S-23S Intergenic Spacer Region (ISR) of the rRNA Operons in Representatives of the Escherichia coli ECOR Collection. Journal of Molecular Evolution, 1998, 47, 62-72.	0.8	58
99	High-resolution structural insights into the heliorhodopsin family. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 4131-4141.	3.3	58
100	Polyclonality of Concurrent Natural Populations of <i>Alteromonas macleodii</i> . Genome Biology and Evolution, 2012, 4, 1360-1374.	1.1	57
101	Comparison of the small 16S to 23S intergenic spacer region (ISR) of the rRNA operons of some Escherichia coli strains of the ECOR collection and E. coli K-12. Journal of Bacteriology, 1996, 178, 6374-6377.	1.0	56
102	Marine-freshwater prokaryotic transitions require extensive changes in the predicted proteome. Microbiome, 2019, 7, 117.	4.9	56
103	Complete-fosmid and fosmid-end sequences reveal frequent horizontal gene transfers in marine uncultured planktonic archaea. ISME Journal, 2011, 5, 1291-1302.	4.4	55
104	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.	1.0	54
105	Evolution of rhodopsin ion pumps in haloarchaea. BMC Evolutionary Biology, 2007, 7, 79.	3.2	54
106	Genomes of <i>Spiribacter</i> , a streamlined, successful halophilic bacterium. BMC Genomics, 2013, 14, 787.	1.2	54
107	RaFAH: Host prediction for viruses of Bacteria and Archaea based on protein content. Patterns, 2021, 2, 100274.	3.1	53
108	Thalassospira lucentensis gen. nov., sp. nov., a new marine member of the alpha-Proteobacteria. International Journal of Systematic and Evolutionary Microbiology, 2002, 52, 1277-1283.	0.8	53

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109	RISSC: a novel database for ribosomal 16S-23S RNA genes spacer regions. <i>Nucleic Acids Research</i> , 2001, 29, 178-180.	6.5	52
110	Draft Genome Sequence of an Ammonia-Oxidizing Archaeon, <i>Candidatus Nitrosopumilus sediminis</i> AR2, from Svalbard in the Arctic Circle. <i>Journal of Bacteriology</i> , 2012, 194, 6948-6949.	1.0	52
111	Metagenomic recovery of phage genomes of uncultured freshwater actinobacteria. <i>ISME Journal</i> , 2017, 11, 304-308.	4.4	52
112	Wild eel microbiome reveals that skin mucus of fish could be a natural niche for aquatic mucosal pathogen evolution. <i>Microbiome</i> , 2017, 5, 162.	4.9	52
113	Uncovering a hidden diversity: optimized protocols for the extraction of dsDNA bacteriophages from soil. <i>Microbiome</i> , 2020, 8, 17.	4.9	52
114	Analysis of a genome fragment of a deep-sea uncultivated Group II euryarchaeote containing 16S rDNA, a spectinomycin-like operon and several energy metabolism genes. <i>Environmental Microbiology</i> , 2004, 6, 959-969.	1.8	51
115	Thousands of Novel Endolysins Discovered in Uncultured Phage Genomes. <i>Frontiers in Microbiology</i> , 2018, 9, 1033.	1.5	50
116	Spindle-shaped viruses infect marine ammonia-oxidizing thaumarchaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15645-15650.	3.3	49
117	Comparative analysis of genome fragments of <i>Acidobacteria</i> from deep Mediterranean plankton. <i>Environmental Microbiology</i> , 2008, 10, 2704-2717.	1.8	48
118	CRISPR analysis suggests that small circular single-stranded DNA smacoviruses infect Archaea instead of humans. <i>Nature Communications</i> , 2019, 10, 294.	5.8	46
119	<i>Halococcus saccharolyticus</i> sp. nov., a New Species of Extremely Halophilic Non-alkaliphilic Cocci. <i>Systematic and Applied Microbiology</i> , 1989, 12, 167-171.	1.2	45
120	Genomes of <i>Alteromonas australica</i> , a world apart. <i>BMC Genomics</i> , 2014, 15, 483.	1.2	45
121	Ecophysiological diversity of a novel member of the genus <i>Alteromonas</i> , and description of <i>Alteromonas mediterranea</i> sp. nov.. <i>Antonie Van Leeuwenhoek</i> , 2015, 107, 119-132.	0.7	44
122	Toward the Monophyly of Haeckel's Radiolaria: 18S rRNA Environmental Data Support the Sisterhood of Polycystinea and Acantharea. <i>Molecular Biology and Evolution</i> , 2002, 19, 118-121.	3.5	43
123	The structure of the exocellular polysaccharide produced by the Archaeon <i>Haloferax gibbonsii</i> (ATCC Tj ETQq1 1 0.784314 rgBT /Ove	1.1	42
124	Approaches to prokaryotic biodiversity: a population genetics perspective. <i>Environmental Microbiology</i> , 2002, 4, 628-633.	1.8	42
125	Evolutionary Model of Cluster Divergence of the Emergent Marine Pathogen <i>Vibrio vulnificus</i> : From Genotype to Ecotype. <i>MBio</i> , 2019, 10, .	1.8	41
126	Osmotically induced response in representatives of halophilic prokaryotes: the bacterium <i>Halomonas elongata</i> and the archaeon <i>Haloferax volcanii</i> . <i>Journal of Bacteriology</i> , 1997, 179, 5471-5481.	1.0	39

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127	Evidence for metaviromic islands in marine phages. <i>Frontiers in Microbiology</i> , 2014, 5, 27.	1.5	39
128	Networking in microbes: conjugative elements and plasmids in the genus <i>Alteromonas</i> . <i>BMC Genomics</i> , 2017, 18, 36.	1.2	39
129	Fast iodide-SAD phasing for high-throughput membrane protein structure determination. <i>Science Advances</i> , 2017, 3, e1602952.	4.7	38
130	The ecology and taxonomy of aerobic chemoorganotrophic halophilic eubacteria. <i>FEMS Microbiology Letters</i> , 1986, 39, 17-22.	0.7	37
131	Reconstruction of Novel Cyanobacterial Siphovirus Genomes from Mediterranean Metagenomic Fosmids. <i>Applied and Environmental Microbiology</i> , 2013, 79, 688-695.	1.4	37
132	<i>Pseudorhizobium pelagicum</i> gen. nov., sp. nov. isolated from a pelagic Mediterranean zone. <i>Systematic and Applied Microbiology</i> , 2015, 38, 293-299.	1.2	37
133	Not All Particles Are Equal: The Selective Enrichment of Particle-Associated Bacteria from the Mediterranean Sea. <i>Frontiers in Microbiology</i> , 2016, 7, 996.	1.5	36
134	Single-cell genomics uncover <i>Pelagibacter</i> as the putative host of the extremely abundant uncultured 37-F6 viral population in the ocean. <i>ISME Journal</i> , 2019, 13, 232-236.	4.4	36
135	CO Dehydrogenase Genes Found in Metagenomic Fosmid Clones from the Deep Mediterranean Sea. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7436-7444.	1.4	35
136	Metagenome Sequencing of Prokaryotic Microbiota from Two Hypersaline Ponds of a Marine Saltern in Santa Pola, Spain. <i>Genome Announcements</i> , 2013, 1, .	0.8	35
137	Homologous recombination is involved in the diversity of replacement flexible genomic islands in aquatic prokaryotes. <i>Frontiers in Genetics</i> , 2014, 5, 147.	1.1	35
138	The microbiome of the Black Sea water column analyzed by shotgun and genome centric metagenomics. <i>Environmental Microbiomes</i> , 2021, 16, 5.	2.2	35
139	A Hybrid NRPS-PKS Gene Cluster Related to the Bleomycin Family of Antitumor Antibiotics in <i>Alteromonas macleodii</i> Strains. <i>PLoS ONE</i> , 2013, 8, e76021.	1.1	34
140	Ecological and genomic features of two widespread freshwater picocyanobacteria. <i>Environmental Microbiology</i> , 2018, 20, 3757-3771.	1.8	33
141	Novel <i>Caudovirales</i> associated with Marine Group I Thaumarchaeota assembled from metagenomes. <i>Environmental Microbiology</i> , 2019, 21, 1980-1988.	1.8	33
142	Viral rhodopsins 1 are a unique family of light-gated cation channels. <i>Nature Communications</i> , 2020, 11, 5707.	5.8	33
143	The structure of the exopolysaccharide produced by the halophilic Archaeon <i>Haloferax mediterranei</i> strain R4 (ATCC 33500). <i>Carbohydrate Research</i> , 1996, 295, 147-156.	1.1	33
144	Is the pan-genome also a pan-selectome?. <i>F1000Research</i> , 2012, 1, 16.	0.8	33

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145	Metagenomic analysis of mesopelagic Antarctic plankton reveals a novel deltaproteobacterial group. <i>Microbiology</i> (United Kingdom), 2006, 152, 505-517.	0.7	32
146	Genomes of Two New Ammonia-Oxidizing Archaea Enriched from Deep Marine Sediments. <i>PLoS ONE</i> , 2014, 9, e96449.	1.1	32
147	Benefit from decline: the primary transcriptome of <i>Alteromonas macleodii</i> str. Te101 during <i>Trichodesmium</i> demise. <i>ISME Journal</i> , 2018, 12, 981-996.	4.4	30
148	Effects of salt and temperature on plasmid topology in the halophilic archaeon <i>Haloferax volcanii</i> . <i>Journal of Bacteriology</i> , 1994, 176, 4966-4973.	1.0	29
149	Diversity of bacteriorhodopsins in different hypersaline waters from a single Spanish saltern. <i>Environmental Microbiology</i> , 2003, 5, 1039-1045.	1.8	29
150	Draft Genome Sequence of the Sulfur-Oxidizing Bacterium <i>Candidatus Sulfurovum sediminum</i> AR, Which Belongs to the Epsilonproteobacteria. <i>Journal of Bacteriology</i> , 2012, 194, 4128-4129.	1.0	29
151	RNA sequencing provides evidence for functional variability between naturally co-existing <i>Alteromonas macleodii</i> lineages. <i>BMC Genomics</i> , 2014, 15, 938.	1.2	29
152	Differentially transcribed regions of <i>Haloferax volcanii</i> genome depending on the medium salinity. <i>Journal of Bacteriology</i> , 1996, 178, 309-313.	1.0	27
153	Novel group of podovirus infecting the marine bacterium <i>Alteromonas macleodii</i> . <i>Bacteriophage</i> , 2013, 3, e24766.	1.9	27
154	Diversity of the cell-wall associated genomic island of the archaeon <i>Haloquadratum walsbyi</i> . <i>BMC Genomics</i> , 2015, 16, 603.	1.2	26
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