

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
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241
all docs

241
docs citations

241
times ranked

15730
citing authors

#	ARTICLE	IF	CITATIONS
1	Long-Read Metagenomics Improves the Recovery of Viral Diversity from Complex Natural Marine Samples. <i>MSystems</i> , 2022, 7, .	1.7	11
2	±-cyanobacteria possessing form IA RuBisCO globally dominate aquatic habitats. <i>ISME Journal</i> , 2022, 16, 2421-2432.	4.4	14
3	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
4	RaFAH: Host prediction for viruses of Bacteria and Archaea based on protein content. <i>Patterns</i> , 2021, 2, 100274.	3.1	53
5	Enhanced Recovery of Microbial Genes and Genomes From a Marine Water Column Using Long-Read Metagenomics. <i>Frontiers in Microbiology</i> , 2021, 12, 708782.	1.5	17
6	Phylogenomics of SAR116 Clade Reveals Two Subclades with Different Evolutionary Trajectories and an Important Role in the Ocean Sulfur Cycle. <i>MSystems</i> , 2021, 6, e0094421.	1.7	12
7	Ecogenomics of the SAR11 clade. <i>Environmental Microbiology</i> , 2020, 22, 1748-1763.	1.8	66
8	Genomic Comparison and Spatial Distribution of Different <i>Synechococcus</i> Phylotypes in the Black Sea. <i>Frontiers in Microbiology</i> , 2020, 11, 1979.	1.5	13
9	Viral rhodopsins 1 are a unique family of light-gated cation channels. <i>Nature Communications</i> , 2020, 11, 5707.	5.8	33
10	Metagenome Mining Reveals Hidden Genomic Diversity of Pelagimyophages in Aquatic Environments. <i>MSystems</i> , 2020, 5, .	1.7	23
11	Microorganisms of Lake Baikal—the deepest and most ancient lake on Earth. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 6079-6090.	1.7	12
12	<i>Alteromonas</i> Myovirus V22 Represents a New Genus of Marine Bacteriophages Requiring a Tail Fiber Chaperone for Host Recognition. <i>MSystems</i> , 2020, 5, .	1.7	15
13	High-resolution structural insights into the heliorhodopsin family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 4131-4141.	3.3	58
14	Microbiome of the deep Lake Baikal, a unique oxic bathypelagic habitat. <i>Limnology and Oceanography</i> , 2020, 65, 1471-1488.	1.6	60
15	Uncovering a hidden diversity: optimized protocols for the extraction of dsDNA bacteriophages from soil. <i>Microbiome</i> , 2020, 8, 17.	4.9	52
16	The Evolutionary Success of the Marine Bacterium SAR11 Analyzed through a Metagenomic Perspective. <i>MSystems</i> , 2020, 5, .	1.7	22
17	Genomes of the <i>Candidatus</i> Actinomarinales-Order: Highly Streamlined Marine Epipelagic Actinobacteria. <i>MSystems</i> , 2020, 5, .	1.7	24
18	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

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19	Unique structure and function of viral rhodopsins. <i>Nature Communications</i> , 2019, 10, 4939.	5.8	59
20	Marine-freshwater prokaryotic transitions require extensive changes in the predicted proteome. <i>Microbiome</i> , 2019, 7, 117.	4.9	56
21	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
22	Genomic and metatranscriptomic analyses of carbon remineralization in an Antarctic polynya. <i>Microbiome</i> , 2019, 7, 29.	4.9	13
23	Numerous cultivated and uncultivated viruses encode ribosomal proteins. <i>Nature Communications</i> , 2019, 10, 752.	5.8	82
24	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
25	Trends of Microdiversity Reveal Depth-Dependent Evolutionary Strategies of Viruses in the Mediterranean. <i>MSystems</i> , 2019, 4, .	1.7	26
26	Prokaryotic Population Dynamics and Viral Predation in a Marine Succession Experiment Using Metagenomics. <i>Frontiers in Microbiology</i> , 2019, 10, 2926.	1.5	17
27	Single-cell genomics uncover Pelagibacter 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
28	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	9.4	414
29	Novel <i>Caudovirales</i> associated with Marine Group I Thaumarchaeota assembled from metagenomes. <i>Environmental Microbiology</i> , 2019, 21, 1980-1988.	1.8	33
30	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
31	Genomes of Novel Microbial Lineages Assembled from the Sub-Ice Waters of Lake Baikal. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	91
32	The enigmatic SAR202 cluster up close: shedding light on a globally distributed dark ocean lineage involved in sulfur cycling. <i>ISME Journal</i> , 2018, 12, 655-668.	4.4	101
33	Thousands of Novel Endolysins Discovered in Uncultured Phage Genomes. <i>Frontiers in Microbiology</i> , 2018, 9, 1033.	1.5	50
34	Fine metagenomic profile of the Mediterranean stratified and mixed water columns revealed by assembly and recruitment. <i>Microbiome</i> , 2018, 6, 128.	4.9	95
35	Ecological and genomic features of two widespread freshwater picocyanobacteria. <i>Environmental Microbiology</i> , 2018, 20, 3757-3771.	1.8	33
36	New insights into marine group III Euryarchaeota, from dark to light. <i>ISME Journal</i> , 2017, 11, 1102-1117.	4.4	72

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37	Fast iodide-SAD phasing for high-throughput membrane protein structure determination. <i>Science Advances</i> , 2017, 3, e1602952.	4.7	38
38	Single-virus genomics reveals hidden cosmopolitan and abundant viruses. <i>Nature Communications</i> , 2017, 8, 15892.	5.8	165
39	Networking in microbes: conjugative elements and plasmids in the genus <i>Alteromonas</i> . <i>BMC Genomics</i> , 2017, 18, 36.	1.2	39
40	Inward H ⁺ pump xenorhodopsin: Mechanism and alternative optogenetic approach. <i>Science Advances</i> , 2017, 3, e1603187.	4.7	93
41	Metagenomic recovery of phage genomes of uncultured freshwater actinobacteria. <i>ISME Journal</i> , 2017, 11, 304-308.	4.4	52
42	Novel <i>Synechococcus</i> Genomes Reconstructed from Freshwater Reservoirs. <i>Frontiers in Microbiology</i> , 2017, 8, 1151.	1.5	69
43	Reconstruction of Diverse Verrucomicrobial Genomes from Metagenome Datasets of Freshwater Reservoirs. <i>Frontiers in Microbiology</i> , 2017, 8, 2131.	1.5	68
44	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
45	Transcriptome analysis of <i>Haloquadratum walsbyi</i> : vanity is but the surface. <i>BMC Genomics</i> , 2017, 18, 510.	1.2	10
46	Genome diversity of marine phages recovered from Mediterranean metagenomes: Size matters. <i>PLoS Genetics</i> , 2017, 13, e1007018.	1.5	82
47	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
48	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
49	The discovery of CRISPR in archaea and bacteria. <i>FEBS Journal</i> , 2016, 283, 3162-3169.	2.2	130
50	<i>Thalassospira australica</i> sp. nov. isolated from sea water. <i>Antonie Van Leeuwenhoek</i> , 2016, 109, 1091-1100.	0.7	10
51	Flexible genomic islands as drivers of genome evolution. <i>Current Opinion in Microbiology</i> , 2016, 31, 154-160.	2.3	81
52	Genomes of Abundant and Widespread Viruses from the Deep Ocean. <i>MBio</i> , 2016, 7, .	1.8	99
53	Marine Viruses. , 2016, , 155-183.		7
54	Pangenome Evolution in the Marine Bacterium <i>Alteromonas</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 1556-1570.	1.1	73

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55	Genome Reconstruction from Metagenomic Data Sets Reveals Novel Microbes in the Brackish Waters of the Caspian Sea. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1599-1612.	1.4	59
56	Marine Group II Archaea, potentially important players in the global ocean carbon cycle. <i>Frontiers in Microbiology</i> , 2015, 6, 1108.	1.5	119
57	Replicating phages in the epidermal mucosa of the eel (<i>Anguilla anguilla</i>). <i>Frontiers in Microbiology</i> , 2015, 6, 3.	1.5	7
58	Genomes of Planktonic <i>Acidimicrobiales</i> : Widening Horizons for Marine <i>Actinobacteria</i> by Metagenomics. <i>MBio</i> , 2015, 6, .	1.8	88
59	<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
60	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
61	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
62	A new class of marine Euryarchaeota group II from the mediterranean deep chlorophyll maximum. <i>ISME Journal</i> , 2015, 9, 1619-1634.	4.4	95
63	<i>Spiribacter curvatus</i> sp. nov., a moderately halophilic bacterium isolated from a saltern. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 4638-4643.	0.8	18
64	Genomes of Two New Ammonia-Oxidizing Archaea Enriched from Deep Marine Sediments. <i>PLoS ONE</i> , 2014, 9, e96449.	1.1	32
65	Evidence for metaviromic islands in marine phages. <i>Frontiers in Microbiology</i> , 2014, 5, 27.	1.5	39
66	Genome Sequence of "Thalassospira australica" NP3b2T Isolated from St. Kilda Beach, Tasman Sea. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
67	Tales from a thousand and one phages. <i>Bacteriophage</i> , 2014, 4, e28265.	1.9	17
68	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
69	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
70	Comparison of prokaryotic community structure from Mediterranean and Atlantic saltern concentrator ponds by a metagenomic approach. <i>Frontiers in Microbiology</i> , 2014, 5, 196.	1.5	80
71	Pangenome Evidence for Extensive Interdomain Horizontal Transfer Affecting Lineage Core and Shell Genes in Uncultured Planktonic Thaumarchaeota and Euryarchaeota. <i>Genome Biology and Evolution</i> , 2014, 6, 1549-1563.	1.1	91
72	Metagenomics of the Mucosal Microbiota of European Eels. <i>Genome Announcements</i> , 2014, 2, .	0.8	15

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73	Metagenomics of Ancient Fermentation Pits Used for the Production of Chinese Strong-Aroma Liquor. <i>Genome Announcements</i> , 2014, 2, .	0.8	18
74	<i>Haloarcula marismortui</i> archaeellin genes as ecomparalogs. <i>Extremophiles</i> , 2014, 18, 341-349.	0.9	22
75	Prokaryotic taxonomic and metabolic diversity of an intermediate salinity hypersaline habitat assessed by metagenomics. <i>FEMS Microbiology Ecology</i> , 2014, 88, 623-635.	1.3	87
76	Key roles for freshwater <i>Actinobacteria</i> revealed by deep metagenomic sequencing. <i>Molecular Ecology</i> , 2014, 23, 6073-6090.	2.0	170
77	The Santa Pola saltern as a model for studying the microbiota of hypersaline environments. <i>Extremophiles</i> , 2014, 18, 811-824.	0.9	113
78	The Family Alteromonadaceae. , 2014, , 69-92.		15
79	Genomes of <i>Alteromonas australica</i> , a world apart. <i>BMC Genomics</i> , 2014, 15, 483.	1.2	45
80	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
81	Genomes of "Spiribacter", a streamlined, successful halophilic bacterium. <i>BMC Genomics</i> , 2013, 14, 787.	1.2	54
82	Intra- and Intergenomic Variation of Ribosomal RNA Operons in Concurrent <i>Alteromonas macleodii</i> Strains. <i>Microbial Ecology</i> , 2013, 65, 720-730.	1.4	5
83	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
84	Draft Genome of <i>Spiribacter salinus</i> M19-40, an Abundant Gammaproteobacterium in Aquatic Hypersaline Environments. <i>Genome Announcements</i> , 2013, 1, .	0.8	14
85	Reconstruction of Novel Cyanobacterial Siphovirus Genomes from Mediterranean Metagenomic Fosmids. <i>Applied and Environmental Microbiology</i> , 2013, 79, 688-695.	1.4	37
86	Expanding the Marine Virosphere Using Metagenomics. <i>PLoS Genetics</i> , 2013, 9, e1003987.	1.5	259
87	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
88	Fosmid System. , 2013, , 1-5.		0
89	Metagenomics uncovers a new group of low GC and ultra-small marine Actinobacteria. <i>Scientific Reports</i> , 2013, 3, 2471.	1.6	182
90	Novel group of podovirus infecting the marine bacterium <i>Alteromonas macleodii</i> . <i>Bacteriophage</i> , 2013, 3, e24766.	1.9	27

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91	A Hybrid NRPS-PKS Gene Cluster Related to the Bleomycin Family of Antitumor Antibiotics in <i>Alteromonas macleodii</i> Strains. PLoS ONE, 2013, 8, e76021.	1.1	34
92	Draft Genome Sequence of an Ammonia-Oxidizing Archaeon, <i>Candidatus Nitrosopumilus sediminis</i> AR2, from Svalbard in the Arctic Circle. Journal of Bacteriology, 2012, 194, 6948-6949.	1.0	52
93	Complete Genome Sequence of the Copiotrophic Marine Bacterium <i>Alteromonas macleodii</i> Strain ATCC 27126. Journal of Bacteriology, 2012, 194, 6998-6998.	1.0	16
94	Draft Genome Sequence of the Sulfur-Oxidizing Bacterium <i>Candidatus Sulfurovum sediminum</i> AR, Which Belongs to the Epsilonproteobacteria. Journal of Bacteriology, 2012, 194, 4128-4129.	1.0	29
95	Polyclonality of Concurrent Natural Populations of <i>Alteromonas macleodii</i> . Genome Biology and Evolution, 2012, 4, 1360-1374.	1.1	57
96	Genomes of surface isolates of <i>Alteromonas macleodii</i> : the life of a widespread marine opportunistic copiotroph. Scientific Reports, 2012, 2, 696.	1.6	111
97	Metagenomes of Mediterranean Coastal Lagoons. Scientific Reports, 2012, 2, 490.	1.6	85
98	Breaking a paradigm: cosmopolitan and abundant freshwater actinobacteria are low GC. Environmental Microbiology Reports, 2012, 4, 29-35.	1.0	66
99	Is the pan-genome also a pan-selectome?. F1000Research, 2012, 1, 16.	0.8	33
100	Reconstructing Viral Genomes from the Environment Using Fosmid Clones: The Case of Haloviruses. PLoS ONE, 2012, 7, e33802.	1.1	78
101	New Abundant Microbial Groups in Aquatic Hypersaline Environments. Scientific Reports, 2011, 1, 135.	1.6	288
102	Metagenomics of the Water Column in the Pristine Upper Course of the Amazon River. PLoS ONE, 2011, 6, e23785.	1.1	183
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	Viral and microbial community dynamics in four aquatic environments. ISME Journal, 2010, 4, 739-751.	4.4	387
105	Metagenome of the Mediterranean deep chlorophyll maximum studied by direct and fosmid library 454 pyrosequencing. ISME Journal, 2010, 4, 1154-1166.	4.4	109
106	The bacterial pan-genome: a new paradigm in microbiology. International Microbiology, 2010, 13, 45-57.	1.1	168
107	CO Dehydrogenase Genes Found in Metagenomic Fosmid Clones from the Deep Mediterranean Sea. Applied and Environmental Microbiology, 2009, 75, 7436-7444.	1.4	35
108	Metagenomic islands of hyperhalophiles: the case of <i>Salinibacter ruber</i> . BMC Genomics, 2009, 10, 570.	1.2	64

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109	Explaining microbial population genomics through phage predation. <i>Nature Reviews Microbiology</i> , 2009, 7, 828-836.	13.6	596
110	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. <i>ISME Journal</i> , 2008, 2, 865-886.	4.4	113
111	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
112	Comparative analysis of genome fragments of <i>Acidobacteria</i> from deep Mediterranean plankton. <i>Environmental Microbiology</i> , 2008, 10, 2704-2717.	1.8	48
113	Biogeography of the ubiquitous marine bacterium <i>Alteromonas macleodii</i> determined by multilocus sequence analysis. <i>Molecular Ecology</i> , 2008, 17, 4092-4106.	2.0	62
114	Adapting to environmental changes using specialized paralogs. <i>Trends in Genetics</i> , 2008, 24, 154-158.	2.9	76
115	<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
116	Genomic plasticity in prokaryotes: the case of the square haloarchaeon. <i>ISME Journal</i> , 2007, 1, 235-245.	4.4	116
117	Evolution of rhodopsin ion pumps in haloarchaea. <i>BMC Evolutionary Biology</i> , 2007, 7, 79.	3.2	54
118	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
119	Metagenomics of the Deep Mediterranean, a Warm Bathypelagic Habitat. <i>PLoS ONE</i> , 2007, 2, e914.	1.1	213
120	Metagenomic analysis of mesopelagic Antarctic plankton reveals a novel deltaproteobacterial group. <i>Microbiology (United Kingdom)</i> , 2006, 152, 505-517.	0.7	32
121	The Neolithic revolution of bacterial genomes. <i>Trends in Microbiology</i> , 2006, 14, 200-206.	3.5	135
122	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
123	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
124	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
125	Environmental genomics of " <i>Haloquadratum walsbyi</i> " in a saltern crystallizer indicates a large pool of accessory genes in an otherwise coherent species. <i>BMC Genomics</i> , 2006, 7, 171.	1.2	128
126	IWoCS: analyzing ribosomal intergenic transcribed spacers configuration and taxonomic relationships. <i>Bioinformatics</i> , 2006, 22, 527-531.	1.8	13

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127	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
128	Micro-Mar: a database for dynamic representation of marine microbial biodiversity. <i>BMC Bioinformatics</i> , 2005, 6, 222.	1.2	10
129	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
130	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
131	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
132	Isolation and cultivation of Walsby's square archaeon. <i>Environmental Microbiology</i> , 2004, 6, 1287-1291.	1.8	150
133	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
134	Environmental genomics, the big picture?. <i>FEMS Microbiology Letters</i> , 2004, 231, 153-158.	0.7	133
135	Comparative analysis of a genome fragment of an uncultivated mesopelagic crenarchaeote reveals multiple horizontal gene transfers. <i>Environmental Microbiology</i> , 2004, 6, 19-34.	1.8	84
136	Comparative genomics of gene-family size in closely related bacteria. <i>Genome Biology</i> , 2004, 5, R27.	13.9	62
137	Red, Extremely Halophilic, but not Archaeal: The Physiology and Ecology of <i>Salinibacter ruber</i> , a Bacterium Isolated from Saltern Crystallizer Ponds. , 2004, , 63-76.		23
138	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
139	Diversity of bacteriorhodopsins in different hypersaline waters from a single Spanish saltern. <i>Environmental Microbiology</i> , 2003, 5, 1039-1045.	1.8	29
140	Diversity of Bacteria and Archaea in sulphate-reducing enrichment cultures inoculated from serial dilution of <i>Zostera noltii</i> rhizosphere samples. <i>Environmental Microbiology</i> , 2003, 5, 754-764.	1.8	20
141	Description of <i>Alcanivorax venustensis</i> sp. nov. and reclassification of <i>Fundibacter jadensis</i> DSM 12178T (Bruns and Berthe-Corti 1999) as <i>Alcanivorax jadensis</i> comb. nov., members of the emended genus <i>Alcanivorax</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003, 53, 331-338.	0.8	88
142	Amplified-Fragment Length Polymorphism as a Complement to IS 6110 -Based Restriction Fragment Length Polymorphism Analysis for Molecular Typing of <i>Mycobacterium tuberculosis</i> . <i>Journal of Clinical Microbiology</i> , 2003, 41, 4820-4822.	1.8	8
143	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
144	<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

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145	Molecular characterization of a Spanish isolate of <i>Mycobacterium malmoeense</i> . <i>Research in Microbiology</i> , 2002, 153, 33-36.	1.0	1
146	Sequence Diversity of the Internal Transcribed Spacer (ITS) Region of the rRNA Operons Among Different Serogroups of <i>Legionella pneumophila</i> Isolates. <i>Systematic and Applied Microbiology</i> , 2002, 25, 212-219.	1.2	5
147	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
148	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
149	Prokaryotic genetic diversity throughout the salinity gradient of a coastal solar saltern. <i>Environmental Microbiology</i> , 2002, 4, 349-360.	1.8	287
150	Approaches to prokaryotic biodiversity: a population genetics perspective. <i>Environmental Microbiology</i> , 2002, 4, 628-633.	1.8	42
151	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
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