

Ricardo Cavicchioli

List of Publications by Year in descending order

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157
papers

12,462
citations

26630

56
h-index

28297

105
g-index

168
all docs

168
docs citations

168
times ranked

12423
citing authors

#	ARTICLE	IF	CITATIONS
1	Scientistsâ€™ warning to humanity: microorganisms and climate change. <i>Nature Reviews Microbiology</i> , 2019, 17, 569-586.	28.6	1,138
2	Cold-Adapted Enzymes. <i>Annual Review of Biochemistry</i> , 2006, 75, 403-433.	11.1	738
3	The genomic basis of trophic strategy in marine bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15527-15533.	7.1	685
4	Low-temperature extremophiles and their applications. <i>Current Opinion in Biotechnology</i> , 2002, 13, 253-261.	6.6	461
5	A genomic catalog of Earthâ€™s microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	17.5	457
6	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
7	Cold-adapted archaea. <i>Nature Reviews Microbiology</i> , 2006, 4, 331-343.	28.6	320
8	Biotechnological uses of enzymes from psychrophiles. <i>Microbial Biotechnology</i> , 2011, 4, 449-460.	4.2	283
9	The role of planktonic <i>Flavobacteria</i> in processing algal organic matter in coastal Antarctica revealed using metagenomics and metaproteomics. <i>Environmental Microbiology</i> , 2013, 15, 1302-1317.	3.8	277
10	Virophage control of antarctic algal hostâ€™ virus dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6163-6168.	7.1	252
11	Mechanisms of Thermal Adaptation Revealed From the Genomes of the Antarctic Archaea <i>Methanogenium frigidum</i> and <i>Methanococcoides burtonii</i> . <i>Genome Research</i> , 2003, 13, 1580-1588.	5.5	246
12	Global biogeography of SAR11 marine bacteria. <i>Molecular Systems Biology</i> , 2012, 8, 595.	7.2	215
13	An integrative study of a meromictic lake ecosystem in Antarctica. <i>ISME Journal</i> , 2011, 5, 879-895.	9.8	204
14	A metaproteomic assessment of winter and summer bacterioplankton from Antarctic Peninsula coastal surface waters. <i>ISME Journal</i> , 2012, 6, 1883-1900.	9.8	200
15	The genome sequence of the psychrophilic archaeon, <i>Methanococcoides burtonii</i> : the role of genome evolution in cold adaptation. <i>ISME Journal</i> , 2009, 3, 1012-1035.	9.8	178
16	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , 2016, 45, D457-D465.	14.5	177
17	Extremophiles and the Search for Extraterrestrial Life. <i>Astrobiology</i> , 2002, 2, 281-292.	3.0	172
18	Implications of rRNA Operon Copy Number and Ribosome Content in the Marine Oligotrophic Ultramicrobacterium <i>Sphingomonas</i> sp. Strain RB2256. <i>Applied and Environmental Microbiology</i> , 1998, 64, 4433-4438.	3.1	160

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19	Microbial ecology of Antarctic aquatic systems. <i>Nature Reviews Microbiology</i> , 2015, 13, 691-706.	28.6	150
20	Cold Adaptation in the Antarctic Archaeon <i>Methanococcoides burtonii</i> Involves Membrane Lipid Unsaturation. <i>Journal of Bacteriology</i> , 2004, 186, 8508-8515.	2.2	148
21	A proteomic determination of cold adaptation in the Antarctic archaeon, <i>Methanococcoides burtonii</i> . <i>Molecular Microbiology</i> , 2004, 53, 309-321.	2.5	146
22	Key microbial drivers in Antarctic aquatic environments. <i>FEMS Microbiology Reviews</i> , 2013, 37, 303-335.	8.6	144
23	Archaea – timeline of the third domain. <i>Nature Reviews Microbiology</i> , 2011, 9, 51-61.	28.6	142
24	Low temperature regulated DEAD-box RNA helicase from the antarctic archaeon, <i>Methanococcoides burtonii</i> . <i>Journal of Molecular Biology</i> , 2000, 297, 553-567.	4.2	139
25	A metagenomic assessment of winter and summer bacterioplankton from Antarctica Peninsula coastal surface waters. <i>ISME Journal</i> , 2012, 6, 1901-1915.	9.8	139
26	Unexpected host dependency of Antarctic Nanohaloarchaeota. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14661-14670.	7.1	134
27	Cold adaptation in the marine bacterium, <i>Sphingopyxis alaskensis</i> , assessed using quantitative proteomics. <i>Environmental Microbiology</i> , 2010, 12, 2658-2676.	3.8	130
28	Advection shapes Southern Ocean microbial assemblages independent of distance and environment effects. <i>Nature Communications</i> , 2013, 4, 2457.	12.8	123
29	Psychrophiles. <i>Annual Review of Earth and Planetary Sciences</i> , 2013, 41, 87-115.	11.0	121
30	Cold stress response in Archaea. <i>Extremophiles</i> , 2000, 4, 321-331.	2.3	115
31	Normalization and Statistical Analysis of Quantitative Proteomics Data Generated by Metabolic Labeling. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2227-2242.	3.8	111
32	A plasmid from an Antarctic haloarchaeon uses specialized membrane vesicles to disseminate and infect plasmid-free cells. <i>Nature Microbiology</i> , 2017, 2, 1446-1455.	13.3	108
33	Virus-mediated archaeal hecatomb in the deep seafloor. <i>Science Advances</i> , 2016, 2, e1600492.	10.3	107
34	High level of intergenera gene exchange shapes the evolution of haloarchaea in an isolated Antarctic lake. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16939-16944.	7.1	105
35	Influence of Temperature on tRNA Modification in Archaea: <i>Methanococcoides burtonii</i> (Optimum) Tj ETQq1 1 0.784314 rgBT /Overl <i>Bacteriology</i> , 2003, 185, 5483-5490.	2.2	99
36	The urgent need for microbiology literacy in society. <i>Environmental Microbiology</i> , 2019, 21, 1513-1528.	3.8	99

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37	Pathogenic archaea: do they exist?. <i>BioEssays</i> , 2003, 25, 1119-1128.	2.5	98
38	Metaproteogenomic analysis of a dominant green sulfur bacterium from Ace Lake, Antarctica. <i>ISME Journal</i> , 2010, 4, 1002-1019.	9.8	97
39	Integrating metagenomic and amplicon databases to resolve the phylogenetic and ecological diversity of the <i>Chlamydiae</i> . <i>ISME Journal</i> , 2014, 8, 115-125.	9.8	94
40	<i>Sphingomonas alaskensis</i> Strain AFO1, an Abundant Oligotrophic Ultramicrobacterium from the North Pacific. <i>Applied and Environmental Microbiology</i> , 2001, 67, 4945-4954.	3.1	82
41	Biogeographic partitioning of Southern Ocean microorganisms revealed by metagenomics. <i>Environmental Microbiology</i> , 2013, 15, 1318-1333.	3.8	82
42	Biology of the Cold Adapted Archaeon, <i>Methanococcoides burtonii</i> Determined by Proteomics Using Liquid Chromatography-Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2004, 3, 1164-1176.	3.7	77
43	Identification and characterization of narQ, a second nitrate sensor for nitrate-dependent gene regulation in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 1992, 6, 1913-1923.	2.5	75
44	Terrestrial models for extraterrestrial life: methanogens and halophiles at Martian temperatures. <i>International Journal of Astrobiology</i> , 2006, 5, 89-97.	1.6	75
45	Metagenomic insights into strategies of carbon conservation and unusual sulfur biogeochemistry in a hypersaline Antarctic lake. <i>ISME Journal</i> , 2013, 7, 1944-1961.	9.8	75
46	On the concept of a psychrophile. <i>ISME Journal</i> , 2016, 10, 793-795.	9.8	75
47	Cold Adaptation of the Antarctic Archaeon, <i>Methanococcoides burtonii</i> Assessed by Proteomics Using ICAT. <i>Journal of Proteome Research</i> , 2005, 4, 473-480.	3.7	73
48	Life under Nutrient Limitation in Oligotrophic Marine Environments: An Eco/Physiological Perspective of <i>Sphingopyxis alaskensis</i> (formerly <i>Sphingomonas alaskensis</i>). <i>Microbial Ecology</i> , 2003, 46, 249-256.	2.8	72
49	Structure and Function of Cold Shock Proteins in Archaea. <i>Journal of Bacteriology</i> , 2007, 189, 5738-5748.	2.2	70
50	Mitochondrial and cytoplasmic protein syntheses are not required for heat shock acquisition of ethanol and thermotolerance in yeast. <i>FEBS Letters</i> , 1984, 172, 299-302.	2.8	68
51	Improved thermal stability and activity in the cold-adapted lipase B from <i>Candida antarctica</i> following chemical modification with oxidized polysaccharides. <i>Extremophiles</i> , 2005, 9, 471-476.	2.3	65
52	Role of lysine versus arginine in enzyme cold-adaptation: Modifying lysine to homo-arginine stabilizes the cold-adapted α -amylase from <i>Pseudoalteromonas haloplanktis</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 486-501.	2.6	65
53	Defining the response of a microorganism to temperatures that span its complete growth temperature range ($\sim 2^{\circ}\text{C}$ to 28°C) using multiplex quantitative proteomics. <i>Environmental Microbiology</i> , 2011, 13, 2186-2203.	3.8	64
54	Role of the periplasmic domain of the <i>Escherichia coli</i> NarX sensor-transmitter protein in nitrate-dependent signal transduction and gene regulation. <i>Molecular Microbiology</i> , 1996, 21, 901-911.	2.5	62

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55	Temperature-dependent global gene expression in the Antarctic archaeon <i>Methanococcoides burtonii</i> . <i>Environmental Microbiology</i> , 2011, 13, 2018-2038.	3.8	62
56	Role of Disulfide Bridges in the Activity and Stability of a Cold-Active α -Amylase. <i>Journal of Bacteriology</i> , 2005, 187, 6206-6212.	2.2	61
57	Physiological Responses to Starvation in the Marine Oligotrophic Ultramicrobacterium <i>Sphingomonas</i> sp. Strain RB2256. <i>Applied and Environmental Microbiology</i> , 2000, 66, 2037-2044.	3.1	55
58	Microbial ecology of an Antarctic hypersaline lake: genomic assessment of ecophysiology among dominant haloarchaea. <i>ISME Journal</i> , 2014, 8, 1645-1658.	9.8	54
59	Marine metaproteomics: deciphering the microbial metabolic food web. <i>Trends in Microbiology</i> , 2014, 22, 248-260.	7.7	54
60	Sphingomonads from marine environments. <i>Journal of Industrial Microbiology and Biotechnology</i> , 1999, 23, 268-272.	3.0	53
61	Serpins in Unicellular Eukarya, Archaea, and Bacteria: Sequence Analysis and Evolution. <i>Journal of Molecular Evolution</i> , 2004, 59, 437-447.	1.8	53
62	Viruses of Haloarchaea. <i>Life</i> , 2014, 4, 681-715.	2.4	51
63	Effect of Temperature on Stability and Activity of Elongation Factor 2 Proteins from Antarctic and Thermophilic Methanogens. <i>Journal of Bacteriology</i> , 2000, 182, 1328-1332.	2.2	50
64	The NarX and NarQ sensor-transmitter proteins of <i>Escherichia coli</i> each require two conserved histidines for nitrate-dependent signal transduction to NarL. <i>Journal of Bacteriology</i> , 1995, 177, 2416-2424.	2.2	49
65	Life and applications of extremophiles. <i>Environmental Microbiology</i> , 2011, 13, 1903-1907.	3.8	49
66	Archaeal cold-adapted proteins: structural and evolutionary analysis of the elongation factor 2 proteins from psychrophilic, mesophilic and thermophilic methanogens 1. <i>FEBS Letters</i> , 1998, 439, 281-286.	2.8	48
67	"Locked-on" and "locked-off" signal transduction mutations in the periplasmic domain of the <i>Escherichia coli</i> NarQ and NarX sensors affect nitrate- and nitrite-dependent regulation by NarL and NarP. <i>Molecular Microbiology</i> , 1997, 24, 1049-1060.	2.5	47
68	Global Proteomic Analysis of the Insoluble, Soluble, and Supernatant Fractions of the Psychrophilic Archaeon <i>Methanococcoides burtonii</i> Part I: The Effect of Growth Temperature. <i>Journal of Proteome Research</i> , 2010, 9, 640-652.	3.7	47
69	Thermodynamic activation properties of elongation factor 2 (EF-2) proteins from psychrotolerant and thermophilic Archaea. <i>Extremophiles</i> , 2002, 6, 143-150.	2.3	46
70	The Active Site Is the Least Stable Structure in the Unfolding Pathway of a Multidomain Cold-Adapted α -Amylase. <i>Journal of Bacteriology</i> , 2005, 187, 6197-6205.	2.2	46
71	Carbon and nitrogen substrate utilization in the marine bacterium <i>Sphingopyxis alaskensis</i> strain RB2256. <i>ISME Journal</i> , 2009, 3, 1036-1052.	9.8	46
72	Antarctic archaea-virus interactions: metaproteome-led analysis of invasion, evasion and adaptation. <i>ISME Journal</i> , 2015, 9, 2094-2107.	9.8	44

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73	A novel approach for enhancing the catalytic efficiency of a protease at low temperature: Reduction in substrate inhibition by chemical modification. <i>Biotechnology and Bioengineering</i> , 2009, 103, 676-686.	3.3	43
74	Kinetic and thermodynamic characterization of the functional properties of a hybrid versatile peroxidase using isothermal titration calorimetry: Insight into manganese peroxidase activation and lignin peroxidase inhibition. <i>Biochimie</i> , 2012, 94, 1221-1231.	2.6	43
75	Effects of Ribosomes and Intracellular Solutes on Activities and Stabilities of Elongation Factor 2 Proteins from Psychrotolerant and Thermophilic Methanogens. <i>Journal of Bacteriology</i> , 2001, 183, 1974-1982.	2.2	41
76	The response of the marine bacterium <i>Sphingopyxis alaskensis</i> to solar radiation assessed by quantitative proteomics. <i>Environmental Microbiology</i> , 2009, 11, 2660-2675.	3.8	41
77	Acquisition of ethanol tolerance in yeast cells by heat shock. <i>Biotechnology Letters</i> , 1983, 5, 683-688.	2.2	40
78	Methanogenesis. , 0, , 288-314.		39
79	Specific Growth Rate Plays a Critical Role in Hydrogen Peroxide Resistance of the Marine Oligotrophic Ultramicrobacterium <i>Sphingomonas alaskensis</i> Strain RB2256. <i>Applied and Environmental Microbiology</i> , 2001, 67, 1292-1299.	3.1	35
80	Ecology and molecular targets of hypermutation in the global microbiome. <i>Nature Communications</i> , 2021, 12, 3076.	12.8	35
81	Predicted Roles for Hypothetical Proteins in the Low-Temperature Expressed Proteome of the Antarctic Archaeon <i>Methanococcoides burtonii</i> . <i>Journal of Proteome Research</i> , 2005, 4, 464-472.	3.7	34
82	endAFS, a novel family E endoglucanase gene from <i>Fibrobacter succinogenes</i> AR1. <i>Journal of Bacteriology</i> , 1991, 173, 3265-3268.	2.2	33
83	Proteomic and Computational Analysis of Secreted Proteins with Type I Signal Peptides from the Antarctic Archaeon <i>Methanococcoides burtonii</i> . <i>Journal of Proteome Research</i> , 2006, 5, 2457-2464.	3.7	33
84	A chemically modified α -amylase with a molten-globule state has entropically driven enhanced thermal stability. <i>Protein Engineering, Design and Selection</i> , 2010, 23, 769-780.	2.1	33
85	Versatile peroxidase degradation of humic substances: Use of isothermal titration calorimetry to assess kinetics, and applications to industrial wastes. <i>Journal of Biotechnology</i> , 2014, 178, 1-11.	3.8	32
86	Morphological and proteomic analysis of biofilms from the Antarctic archaeon, <i>Halorubrum lacusprofundi</i> . <i>Scientific Reports</i> , 2016, 6, 37454.	3.3	32
87	Genomic variation and biogeography of Antarctic haloarchaea. <i>Microbiome</i> , 2018, 6, 113.	11.1	32
88	Influence of the polar light cycle on seasonal dynamics of an Antarctic lake microbial community. <i>Microbiome</i> , 2020, 8, 116.	11.1	32
89	Cold adaptation of the Antarctic haloarchaea <i>Halohasta litchfieldiae</i> and <i>Halorubrum lacusprofundi</i> . <i>Environmental Microbiology</i> , 2017, 19, 2210-2227.	3.8	31
90	Proteinaceous Surface Layers of Archaea: Ultrastructure and Biochemistry. , 0, , 315-340.		28

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91	General Characteristics and Important Model Organisms. , 0 , 14-92.		27
92	Shotgun Redox Proteomics: Identification and Quantitation of Carbonylated Proteins in the UVB-Resistant Marine Bacterium, Photobacterium angustum S14. PLoS ONE, 2013, 8, e68112.	2.5	27
93	Global Proteomic Analysis of the Insoluble, Soluble, and Supernatant Fractions of the Psychrophilic Archaeon <i>Methanococoides burtonii</i> Part II: The Effect of Different Methylated Growth Substrates. Journal of Proteome Research, 2010, 9, 653-663.	3.7	25
94	Ecophysiological Distinctions of Haloarchaea from a Hypersaline Antarctic Lake as Determined by Metaproteomics. Applied and Environmental Microbiology, 2016, 82, 3165-3173.	3.1	24
95	Cross-species identification of proteins from proteome profiles of the marine oligotrophic ultramicrobacterium, <i>Sphingopyxis alaskensis</i> . Proteomics, 2004, 4, 1779-1788.	2.2	23
96	Cold Adaptation of Archaeal Elongation Factor 2 (EF-2) Proteins. Current Protein and Peptide Science, 2002, 3, 223-230.	1.4	22
97	Proteomics of extremophiles. Environmental Microbiology, 2011, 13, 1934-1955.	3.8	21
98	Single TRAM domain RNA-binding proteins in Archaea: functional insight from Ctr3 from the Antarctic methanogen <i>Methanococoides burtonii</i> . Environmental Microbiology, 2016, 18, 2810-2824.	3.8	21
99	Complete genome sequence of the Antarctic Halorubrum lacusprofundi type strain ACAM 34. Standards in Genomic Sciences, 2016, 11, 70.	1.5	21
100	Central Metabolism. , 0 , 260-287.		21
101	Molecular cloning, expression, and characterization of endoglucanase genes from Fibrobacter succinogenes AR1. Applied and Environmental Microbiology, 1991, 57, 359-365.	3.1	21
102	Aptamer based peptide enrichment for quantitative analysis of gonadotropin-releasing hormone by LC-MS/MS. Talanta, 2016, 150, 671-680.	5.5	20
103	Glycerol metabolism of haloarchaea. Environmental Microbiology, 2017, 19, 864-877.	3.8	20
104	Shedding Light on Microbial "Dark Matter": Insights Into Novel Cloacimonadota and Omnitrophota From an Antarctic Lake. Frontiers in Microbiology, 2021, 12, 741077.	3.5	20
105	Characterization of the aegA locus of Escherichia coli: control of gene expression in response to anaerobiosis and nitrate. Journal of Bacteriology, 1996, 178, 6968-6974.	2.2	19
106	Remarkable resistance to UVB of the marine bacterium Photobacterium angustum explained by an unexpected role of photolyase. Photochemical and Photobiological Sciences, 2009, 8, 1313-1320.	2.9	19
107	A new broad specificity alkaline metalloprotease from a Pseudomonas sp. isolated from refrigerated milk: Role of calcium in improving enzyme productivity. Journal of Molecular Catalysis B: Enzymatic, 2015, 113, 1-8.	1.8	19
108	An assessment of protein profiles from the marine oligotrophic ultramicrobacterium, Sphingomonas sp. strain RB2256. Electrophoresis, 1999, 20, 2094-2098.	2.4	18

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109	Developing a genetic manipulation system for the Antarctic archaeon, <i>Halorubrum lacusprofundi</i> : investigating acetamidase gene function. <i>Scientific Reports</i> , 2016, 6, 34639.	3.3	18
110	Enhancement of lipase stability and productivity through chemical modification and its application to latex-based polymer emulsions. <i>Process Biochemistry</i> , 2017, 57, 131-140.	3.7	18
111	Genome Analysis of a Verrucomicrobial Endosymbiont With a Tiny Genome Discovered in an Antarctic Lake. <i>Frontiers in Microbiology</i> , 2021, 12, 674758.	3.5	18
112	Characterization of a temperature-responsive two component regulatory system from the Antarctic archaeon, <i>Methanococoides burtonii</i> . <i>Scientific Reports</i> , 2016, 6, 24278.	3.3	17
113	Loss of heat-shock acquisition of thermotolerance in yeast is not correlated with loss of heat-shock proteins. <i>FEBS Letters</i> , 1986, 207, 149-152.	2.8	16
114	Metagenomic studies reveal the critical and wide-ranging ecological importance of uncultivated archaea: the role of ammonia oxidizers. <i>BioEssays</i> , 2007, 29, 11-14.	2.5	16
115	Integration of genomics and proteomics into marine microbial ecology. <i>Marine Ecology - Progress Series</i> , 2007, 332, 291-299.	1.9	15
116	Analyzing the Hydrophobic Proteome of the Antarctic Archaeon <i>Methanococoides burtonii</i> Using Differential Solubility Fractionation. <i>Journal of Proteome Research</i> , 2010, 9, 664-676.	3.7	14
117	Psychrophiles: Genetics, Genomics, Evolution. , 2011, , 865-890.		14
118	The discovery of Antarctic <i>scp</i> RNA viruses: a new game changer. <i>Molecular Ecology</i> , 2015, 24, 4809-4811.	3.9	14
119	Lost cold Antarctic deserts inferred from unusual sulfate formation and isotope signatures. <i>Nature Communications</i> , 2015, 6, 7579.	12.8	14
120	Pathogenic archaeobacteria: do they not exist because archaeobacteria use different vitamins?. <i>BioEssays</i> , 2004, 26, 592-593.	2.5	12
121	Microbial communities of aquatic environments on Heard Island characterized by pyrotag sequencing and environmental data. <i>Scientific Reports</i> , 2017, 7, 44480.	3.3	12
122	Structural analysis of the elongation factor G protein from the low-temperature-adapted bacterium <i>Arthrobacter globiformis</i> SI55. <i>Extremophiles</i> , 2000, 4, 123-130.	2.3	11
123	Influence of growth temperature and starvation state on survival and DNA damage induction in the marine bacterium <i>Sphingopyxis alaskensis</i> exposed to UV radiation. <i>Journal of Photochemistry and Photobiology B: Biology</i> , 2010, 100, 51-56.	3.8	10
124	Sucrose Metabolism in Haloarchaea: Reassessment Using Genomics, Proteomics, and Metagenomics. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	10
125	Flagellation and Chemotaxis. , 0, , 385-410.		10
126	Transcription: Mechanism and Regulation. , 0, , 139-157.		10

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127	17 Proteins from Psychrophiles. <i>Methods in Microbiology</i> , 2006, 35, 395-436.	0.8	9
128	Chaperonins from an Antarctic archaeon are predominantly monomeric: crystal structure of an open state monomer. <i>Environmental Microbiology</i> , 2011, 13, 2232-2249.	3.8	9
129	Linking genomic and physiological characteristics of psychrophilic <i>Arthrobacter</i> to metagenomic data to explain global environmental distribution. <i>Microbiome</i> , 2021, 9, 136.	11.1	9
130	Into the darkness: the ecologies of novel "microbial dark matter" phyla in an Antarctic lake. <i>Environmental Microbiology</i> , 2022, 24, 2576-2603.	3.8	9
131	Lipids: Biosynthesis, Function, and Evolution. , 0, , 341-353.		7
132	The involvement of transcriptional read-through from internal promoters in the expression of a novel endoglucanase gene <i>SendA</i> , from <i>Fibrobacter succinogenes</i> AR1. <i>Nucleic Acids Research</i> , 1991, 19, 1661-1669.	14.5	6
133	Physiology of Marine Oligotrophic Ultramicrobacteria. , 2011, , 1179-1199.		6
134	A vision for a "microcentric" future. <i>Microbial Biotechnology</i> , 2019, 12, 26-29.	4.2	6
135	Solute Transport. , 0, , 354-368.		6
136	Response to William Martin's letter. <i>BioEssays</i> , 2004, 26, 593-593.	2.5	5
137	Remarkably coherent population structure for a dominant Antarctic <i>Chlorobium</i> species. <i>Microbiome</i> , 2021, 9, 231.	11.1	5
138	The RNA polymerase subunits E/F from the Antarctic archaeon <i>Methanococcoides burtonii</i> bind to specific species of mRNA. <i>Environmental Microbiology</i> , 2011, 13, 2039-2055.	3.8	4
139	Cold-Adapted Enzymes. , 2006, , 615-638.		4
140	DNA-Binding Proteins and Chromatin. , 0, , 110-119.		4
141	Simple high-throughput annotation pipeline (SHAP). <i>Bioinformatics</i> , 2011, 27, 2431-2432.	4.1	3
142	Microbial communities in Antarctic lakes: Entirely new perspectives from metagenomics and metaproteomics. <i>Microbiology Australia</i> , 2011, 32, 157.	0.4	3
143	The Archaea: an Invitation to Evolution. , 0, , 1-13.		3
144	Protein Translocation into and across Archaeal Cytoplasmic Membranes. , 0, , 369-384.		3

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145	DNA Replication and Cell Cycle. , 0, , 93-109.		3
146	RNA Processing. , 0, , 158-174.		3
147	Proteomics of Archaea. Methods of Biochemical Analysis, 2005, 49, 57-72.	0.2	2
148	Archaeosome Vaccines. , 0, , 496-510.		2
149	Physical map location of the narQ gene of Escherichia coli.. Journal of Bacteriology, 1992, 174, 7882.	2.2	2
150	An online database for the detection of novel archaeal sequences in human ESTs. Bioinformatics, 2004, 20, 2361-2362.	4.1	1
151	Functional Genomics. , 0, , 434-462.		1
152	Molecular Genetics of Archaea. , 0, , 463-477.		1
153	Mechanisms of Genome Stability and Evolution^{â€}. , 0, , 120-138.		1
154	Features of Aminoacyl-tRNA Synthesis Unique to Archaea. , 0, , 198-208.		1
155	Protein-Folding Systems. , 0, , 209-223.		0
156	Structure and Evolution of Genomes. , 0, , 411-433.		0
157	Sensing, Signal Transduction, and Posttranslational Modification. , 0, , 224-259.		0