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	Into the darkness: the ecologies of novel â€˜microbial dark matterâ€™ phyla in an Antarctic lake. Environmental Microbiology, 2022, 24, 2576-2603.	3.8	9
2	A genomic catalog of Earthâ€™s microbiomes. Nature Biotechnology, 2021, 39, 499-509.	17.5	457
3	Ecology and molecular targets of hypermutation in the global microbiome. Nature Communications, 2021, 12, 3076.	12.8	35
4	Linking genomic and physiological characteristics of psychrophilic Arthrobacter to metagenomic data to explain global environmental distribution. Microbiome, 2021, 9, 136.	11.1	9
5	Genome Analysis of a Verrucomicrobial Endosymbiont With a Tiny Genome Discovered in an Antarctic Lake. Frontiers in Microbiology, 2021, 12, 674758.	3.5	18
6	Shedding Light on Microbial â€œDark Matterâ€: Insights Into Novel Cloacimonadota and Omnitrophota From an Antarctic Lake. Frontiers in Microbiology, 2021, 12, 741077.	3.5	20
7	Remarkably coherent population structure for a dominant Antarctic Chlorobium species. Microbiome, 2021, 9, 231.	11.1	5
8	Influence of the polar light cycle on seasonal dynamics of an Antarctic lake microbial community. Microbiome, 2020, 8, 116.	11.1	32
9	Unexpected host dependency of Antarctic Nanohaloarchaeota. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14661-14670.	7.1	134
10	Sucrose Metabolism in Haloarchaea: Reassessment Using Genomics, Proteomics, and Metagenomics. Applied and Environmental Microbiology, 2019, 85, .	3.1	10
11	Scientistsâ€™ warning to humanity: microorganisms and climate change. Nature Reviews Microbiology, 2019, 17, 569-586.	28.6	1,138
12	The urgent need for microbiology literacy in society. Environmental Microbiology, 2019, 21, 1513-1528.	3.8	99
13	A vision for a â€˜microbcentricâ€™ future. Microbial Biotechnology, 2019, 12, 26-29.	4.2	6
14	Genomic variation and biogeography of Antarctic haloarchaea. Microbiome, 2018, 6, 113.	11.1	32
15	Cold adaptation of the Antarctic haloarchaea <i>Halohasta litchfieldiae</i> and <i>Halorubrum lacusprofundi</i>. Environmental Microbiology, 2017, 19, 2210-2227.	3.8	31
16	Enhancement of lipase stability and productivity through chemical modification and its application to latex-based polymer emulsions. Process Biochemistry, 2017, 57, 131-140.	3.7	18
17	Microbial communities of aquatic environments on Heard Island characterized by pyrotag sequencing and environmental data. Scientific Reports, 2017, 7, 44480.	3.3	12
18	A plasmid from an Antarctic haloarchaeon uses specialized membrane vesicles to disseminate and infect plasmid-free cells. Nature Microbiology, 2017, 2, 1446-1455.	13.3	108

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19	Glycerol metabolism of haloarchaea. Environmental Microbiology, 2017, 19, 864-877.	3.8	20
20	Single <scp>TRAM</scp> domain <scp>RNA</scp>â€binding proteins in <scp><i>A</i></scp><i>rchaea</i>: functional insight from <scp>C</scp>tr3 from the <scp>A</scp>ntarctic methanogen <scp><i>M</i></scp><i>ethanococcoides burtonii</i>. Environmental Microbiology, 2016, 18, 2810-2824.	3.8	21
21	Characterization of a temperature-responsive two component regulatory system from the Antarctic archaeon, Methanococcoides burtonii. Scientific Reports, 2016, 6, 24278.	3.3	17
22	Morphological and proteomic analysis of biofilms from the Antarctic archaeon, Halorubrum lacusprofundi. Scientific Reports, 2016, 6, 37454.	3.3	32
23	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. Nucleic Acids Research, 2016, 45, D457-D465.	14.5	177
24	Virus-mediated archaeal hecatomb in the deep seafloor. Science Advances, 2016, 2, e1600492.	10.3	107
25	Developing a genetic manipulation system for the Antarctic archaeon, Halorubrum lacusprofundi: investigating acetamidase gene function. Scientific Reports, 2016, 6, 34639.	3.3	18
26	Complete genome sequence of the Antarctic Halorubrum lacusprofundi type strain ACAM 34. Standards in Genomic Sciences, 2016, 11, 70.	1.5	21
27	Aptamer based peptide enrichment for quantitative analysis of gonadotropin-releasing hormone by LCâ€“MS/MS. Talanta, 2016, 150, 671-680.	5.5	20
28	Ecophysiological Distinctions of Haloarchaea from a Hypersaline Antarctic Lake as Determined by Metaproteomics. Applied and Environmental Microbiology, 2016, 82, 3165-3173.	3.1	24
29	On the concept of a psychrophile. ISME Journal, 2016, 10, 793-795.	9.8	75
30	The discovery of Antarctic <scp>RNA</scp> viruses: a new game changer. Molecular Ecology, 2015, 24, 4809-4811.	3.9	14
31	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
32	Antarctic archaeaâ€“virus interactions: metaproteome-led analysis of invasion, evasion and adaptation. ISME Journal, 2015, 9, 2094-2107.	9.8	44
33	Lost cold Antarctic deserts inferred from unusual sulfate formation and isotope signatures. Nature Communications, 2015, 6, 7579.	12.8	14
34	Microbial ecology of Antarctic aquatic systems. Nature Reviews Microbiology, 2015, 13, 691-706.	28.6	150
35	Integrating metagenomic and amplicon databases to resolve the phylogenetic and ecological diversity of the <i>Chlamydiae</i>. ISME Journal, 2014, 8, 115-125.	9.8	94
36	Viruses of Haloarchaea. Life, 2014, 4, 681-715.	2.4	51

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37	Microbial ecology of an Antarctic hypersaline lake: genomic assessment of ecophysiology among dominant haloarchaea. ISME Journal, 2014, 8, 1645-1658.	9.8	54
38	Versatile peroxidase degradation of humic substances: Use of isothermal titration calorimetry to assess kinetics, and applications to industrial wastes. Journal of Biotechnology, 2014, 178, 1-11.	3.8	32
39	Marine metaproteomics: deciphering the microbial metabolic food web. Trends in Microbiology, 2014, 22, 248-260.	7.7	54
40	Metagenomic insights into strategies of carbon conservation and unusual sulfur biogeochemistry in a hypersaline Antarctic lake. ISME Journal, 2013, 7, 1944-1961.	9.8	75
41	High level of intergenera gene exchange shapes the evolution of haloarchaea in an isolated Antarctic lake. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 16939-16944.	7.1	105
42	Advection shapes Southern Ocean microbial assemblages independent of distance and environment effects. Nature Communications, 2013, 4, 2457.	12.8	123
43	Key microbial drivers in Antarctic aquatic environments. FEMS Microbiology Reviews, 2013, 37, 303-335.	8.6	144
44	Psychrophiles. Annual Review of Earth and Planetary Sciences, 2013, 41, 87-115.	11.0	121
45	Biogeographic partitioning of <scp>S</scp>outhern <scp>O</scp>cean microorganisms revealed by metagenomics. Environmental Microbiology, 2013, 15, 1318-1333.	3.8	82
46	The role of planktonic <i><scp>F</scp>lavobacteria</i> in processing algal organic matter in coastal <scp>E</scp>ast <scp>A</scp>ntarctica revealed using metagenomics and metaproteomics. Environmental Microbiology, 2013, 15, 1302-1317.	3.8	277
47	Prevalent genome streamlining and latitudinal divergence of planktonic bacteria in the surface ocean. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11463-11468.	7.1	328
48	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
49	Global biogeography of SAR11 marine bacteria. Molecular Systems Biology, 2012, 8, 595.	7.2	215
50	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. Biochimie, 2012, 94, 1221-1231.	2.6	43
51	A metaproteomic assessment of winter and summer bacterioplankton from Antarctic Peninsula coastal surface waters. ISME Journal, 2012, 6, 1883-1900.	9.8	200
52	A metagenomic assessment of winter and summer bacterioplankton from Antarctica Peninsula coastal surface waters. ISME Journal, 2012, 6, 1901-1915.	9.8	139
53	Psychrophiles: Genetics, Genomics, Evolution. , 2011, , 865-890.		14
54	Physiology of Marine Oligotrophic Ultramicrobacteria. , 2011, , 1179-1199.		6

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55	Temperatureâ€dependent global gene expression in the Antarctic archaeon <i>Methanococcoides burtonii</i>. Environmental Microbiology, 2011, 13, 2018-2038.	3.8	62
56	The RNA polymerase subunits E/F from the Antarctic archaeon <i>Methanococcoides burtonii</i> bind to specific species of mRNA. Environmental Microbiology, 2011, 13, 2039-2055.	3.8	4
57	Defining the response of a microorganism to temperatures that span its complete growth temperature range (âˆ’2Â°C to 28Â°C) using multiplex quantitative proteomics. Environmental Microbiology, 2011, 13, 2186-2203.	3.8	64
58	Chaperonins from an Antarctic archaeon are predominantly monomeric: crystal structure of an open state monomer. Environmental Microbiology, 2011, 13, 2232-2249.	3.8	9
59	Proteomics of extremophiles. Environmental Microbiology, 2011, 13, 1934-1955.	3.8	21
60	Life and applications of extremophiles. Environmental Microbiology, 2011, 13, 1903-1907.	3.8	49
61	Archaea â€” timeline of the third domain. Nature Reviews Microbiology, 2011, 9, 51-61.	28.6	142
62	An integrative study of a meromictic lake ecosystem in Antarctica. ISME Journal, 2011, 5, 879-895.	9.8	204
63	Biotechnological uses of enzymes from psychrophiles. Microbial Biotechnology, 2011, 4, 449-460.	4.2	283
64	Virophage control of antarctic algal hostâ€“virus dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6163-6168.	7.1	252
65	Simple high-throughput annotation pipeline (SHAP). Bioinformatics, 2011, 27, 2431-2432.	4.1	3
66	Microbial communities in Antarctic lakes: Entirely new perspectives from metagenomics and metaproteomics. Microbiology Australia, 2011, 32, 157.	0.4	3
67	Influence of growth temperature and starvation state on survival and DNA damage induction in the marine bacterium Sphingopyxis alaskensis exposed to UV radiation. Journal of Photochemistry and Photobiology B: Biology, 2010, 100, 51-56.	3.8	10
68	Metaproteogenomic analysis of a dominant green sulfur bacterium from Ace Lake, Antarctica. ISME Journal, 2010, 4, 1002-1019.	9.8	97
69	Cold adaptation in the marine bacterium, <i>Sphingopyxis alaskensis</i>, assessed using quantitative proteomics. Environmental Microbiology, 2010, 12, 2658-2676.	3.8	130
70	A chemically modified Î±-amylase with a molten-globule state has entropically driven enhanced thermal stabilityâ€. Protein Engineering, Design and Selection, 2010, 23, 769-780.	2.1	33
71	Global Proteomic Analysis of the Insoluble, Soluble, and Supernatant Fractions of the Psychrophilic Archaeon <i>Methanococcoides burtonii</i> Part II: The Effect of Different Methylated Growth Substrates. Journal of Proteome Research, 2010, 9, 653-663.	3.7	25
72	Analyzing the Hydrophobic Proteome of the Antarctic Archaeon <i>Methanococcoides burtonii</i> Using Differential Solubility Fractionation. Journal of Proteome Research, 2010, 9, 664-676.	3.7	14

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73	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. Journal of Proteome Research, 2010, 9, 640-652.	3.7	47
74	Normalization and Statistical Analysis of Quantitative Proteomics Data Generated by Metabolic Labeling. Molecular and Cellular Proteomics, 2009, 8, 2227-2242.	3.8	111
75	The genomic basis of trophic strategy in marine bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 15527-15533.	7.1	685
76	A novel approach for enhancing the catalytic efficiency of a protease at low temperature: Reduction in substrate inhibition by chemical modification. Biotechnology and Bioengineering, 2009, 103, 676-686.	3.3	43
77	The genome sequence of the psychrophilic archaeon, <i>Methanococcoides burtonii</i>: the role of genome evolution in cold adaptation. ISME Journal, 2009, 3, 1012-1035.	9.8	178
78	Carbon and nitrogen substrate utilization in the marine bacterium <i>Sphingopyxis alaskensis</i> strain RB2256. ISME Journal, 2009, 3, 1036-1052.	9.8	46
79	The response of the marine bacterium <i>Sphingopyxis alaskensis</i> to solar radiation assessed by quantitative proteomics. Environmental Microbiology, 2009, 11, 2660-2675.	3.8	41
80	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
81	Structure and Function of Cold Shock Proteins in Archaea. Journal of Bacteriology, 2007, 189, 5738-5748.	2.2	70
82	Metagenomic studies reveal the critical and wide-ranging ecological importance of uncultivated archaea: the role of ammonia oxidizers. BioEssays, 2007, 29, 11-14.	2.5	16
83	Integration of genomics and proteomics into marine microbial ecology. Marine Ecology - Progress Series, 2007, 332, 291-299.	1.9	15
84	Proteomic and Computational Analysis of Secreted Proteins with Type I Signal Peptides from the Antarctic ArchaeonMethanococcoidesburtonii. Journal of Proteome Research, 2006, 5, 2457-2464.	3.7	33
85	Cold-Adapted Enzymes. Annual Review of Biochemistry, 2006, 75, 403-433.	11.1	738
86	17 Proteins from Psychrophiles. Methods in Microbiology, 2006, 35, 395-436.	0.8	9
87	Role of lysine versus arginine in enzyme cold-adaptation: Modifying lysine to homo-arginine stabilizes the cold-adapted Î±-amylase from Pseudoalteramonas haloplanktis. Proteins: Structure, Function and Bioinformatics, 2006, 64, 486-501.	2.6	65
88	Cold-adapted archaea. Nature Reviews Microbiology, 2006, 4, 331-343.	28.6	320
89	Terrestrial models for extraterrestrial life: methanogens and halophiles at Martian temperatures. International Journal of Astrobiology, 2006, 5, 89-97.	1.6	75
90	Cold-Adapted Enzymes. , 2006, , 615-638.		4

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91	Improved thermal stability and activity in the cold-adapted lipase B from Candida antarctica following chemical modification with oxidized polysaccharides. Extremophiles, 2005, 9, 471-476.	2.3	65
92	Proteomics of Archaea. Methods of Biochemical Analysis, 2005, 49, 57-72.	0.2	2
93	Role of Disulfide Bridges in the Activity and Stability of a Cold-Active Î±-Amylase. Journal of Bacteriology, 2005, 187, 6206-6212.	2.2	61
94	The Active Site Is the Least Stable Structure in the Unfolding Pathway of a Multidomain Cold-Adapted Î±-Amylase. Journal of Bacteriology, 2005, 187, 6197-6205.	2.2	46
95	Predicted Roles for Hypothetical Proteins in the Low-Temperature Expressed Proteome of the Antarctic ArchaeonMethanococcoidesburtonii. Journal of Proteome Research, 2005, 4, 464-472.	3.7	34
96	Cold Adaptation of the Antarctic Archaeon,Methanococcoides burtoniiAssessed by Proteomics Using ICAT. Journal of Proteome Research, 2005, 4, 473-480.	3.7	73
97	An online database for the detection of novel archaeal sequences in human ESTs. Bioinformatics, 2004, 20, 2361-2362.	4.1	1
98	A proteomic determination of cold adaptation in the Antarctic archaeon, Methanococcoides burtonii. Molecular Microbiology, 2004, 53, 309-321.	2.5	146
99	Serpins in Unicellular Eukarya, Archaea, and Bacteria: Sequence Analysis and Evolution. Journal of Molecular Evolution, 2004, 59, 437-447.	1.8	53
100	Crossâ€species identification of proteins from proteome profiles of the marine oligotrophic ultramicrobacterium, <i>Sphingopyxis alaskensis</i>. Proteomics, 2004, 4, 1779-1788.	2.2	23
101	Response to William Martin's letter. BioEssays, 2004, 26, 593-593.	2.5	5
102	Pathogenic archaebacteria: do they not exist because archaebacteria use different vitamins?. BioEssays, 2004, 26, 592-593.	2.5	12
103	Cold Adaptation in the Antarctic Archaeon Methanococcoides burtonii Involves Membrane Lipid Unsaturation. Journal of Bacteriology, 2004, 186, 8508-8515.	2.2	148
104	Biology of the Cold Adapted Archaeon, <i>Methanococcoides </i><i>b</i><i>urtonii</i> Determined by Proteomics Using Liquid Chromatography-Tandem Mass Spectrometry. Journal of Proteome Research, 2004, 3, 1164-1176.	3.7	77
105	Life under Nutrient Limitation in Oligotrophic Marine Environments: An Eco/Physiological Perspective of Sphingopyxis alaskensis (formerly Sphingomonas alaskensis). Microbial Ecology, 2003, 46, 249-256.	2.8	72
106	Pathogenic archaea: do they exist?. BioEssays, 2003, 25, 1119-1128.	2.5	98
107	Influence of Temperature on tRNA Modification in Archaea: Methanococcoides burtonii (Optimum) Tj ETQq1 1 0.784314 rgBT /Overlock Bacteriology, 2003, 185, 5483-5490.	2.2	99
108	Mechanisms of Thermal Adaptation Revealed From the Genomes of the Antarctic Archaea Methanogenium frigidum and Methanococcoides burtonii. Genome Research, 2003, 13, 1580-1588.	5.5	246

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109	Cold Adaptation of Archaeal Elongation Factor 2 (EF-2) Proteins. Current Protein and Peptide Science, 2002, 3, 223-230.	1.4	22
110	Extremophiles and the Search for Extraterrestrial Life. Astrobiology, 2002, 2, 281-292.	3.0	172
111	Thermodynamic activation properties of elongation factor 2 (EF-2) proteins from psychrotolerant and thermophilic Archaea. Extremophiles, 2002, 6, 143-150.	2.3	46
112	Low-temperature extremophiles and their applications. Current Opinion in Biotechnology, 2002, 13, 253-261.	6.6	461
113	Sphingomonas alaskensis Strain AFO1, an Abundant Oligotrophic Ultramicrobacterium from the North Pacific. Applied and Environmental Microbiology, 2001, 67, 4945-4954.	3.1	82
114	Specific Growth Rate Plays a Critical Role in Hydrogen Peroxide Resistance of the Marine Oligotrophic Ultramicrobacterium Sphingomonas alaskensis Strain RB2256. Applied and Environmental Microbiology, 2001, 67, 1292-1299.	3.1	35
115	Effects of Ribosomes and Intracellular Solutes on Activities and Stabilities of Elongation Factor 2 Proteins from Psychrotolerant and Thermophilic Methanogens. Journal of Bacteriology, 2001, 183, 1974-1982.	2.2	41
116	Structural analysis of the elongation factor G protein from the low-temperature-adapted bacterium Arthrobacter globiformis SI55. Extremophiles, 2000, 4, 123-130.	2.3	11
117	Cold stress response in Archaea. Extremophiles, 2000, 4, 321-331.	2.3	115
118	Physiological Responses to Starvation in the Marine Oligotrophic Ultramicrobacterium Sphingomonas sp. Strain RB2256. Applied and Environmental Microbiology, 2000, 66, 2037-2044.	3.1	55
119	Effect of Temperature on Stability and Activity of Elongation Factor 2 Proteins from Antarctic and Thermophilic Methanogens. Journal of Bacteriology, 2000, 182, 1328-1332.	2.2	50
120	Low temperature regulated DEAD-box RNA helicase from the antarctic archaeon, Methanococcoides burtonii. Journal of Molecular Biology, 2000, 297, 553-567.	4.2	139
121	Sphingomonads from marine environments. Journal of Industrial Microbiology and Biotechnology, 1999, 23, 268-272.	3.0	53
122	An assessment of protein profiles from the marine oligotrophic ultramicrobacterium,Sphingomonas sp. strain RB2256. Electrophoresis, 1999, 20, 2094-2098.	2.4	18
123	Archaeal cold-adapted proteins: structural and evolutionary analysis of the elongation factor 2 proteins from psychrophilic, mesophilic and thermophilic methanogens 1. FEBS Letters, 1998, 439, 281-286.	2.8	48
124	Implications of rRNA Operon Copy Number and Ribosome Content in the Marine Oligotrophic Ultramicrobacterium <i>Sphingomonas</i> sp. Strain RB2256. Applied and Environmental Microbiology, 1998, 64, 4433-4438.	3.1	160
125	â€˜Lockedâ€•onâ€™ and â€˜lockedâ€•offâ€™ signal transduction mutations in the periplasmic domain of the Escherichia coli NarQ and NarX sensors affect nitrateâ€•and nitriteâ€•dependent regulation by NarL and NarP. Molecular Microbiology, 1997, 24, 1049-1060.	2.5	47
126	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

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127	Role of the periplasmic domain of the Escherichia coli NarX sensorâ€transmitter protein in nitrateâ€dependent signal transduction and gene regulation. Molecular Microbiology, 1996, 21, 901-911.	2.5	62
128	The NarX and NarQ sensor-transmitter proteins of Escherichia coli each require two conserved histidines for nitrate-dependent signal transduction to NarL. Journal of Bacteriology, 1995, 177, 2416-2424.	2.2	49
129	Identification and characterization of narQ, a second nitrate sensor for nitrate-dependent gene regulation in Escherichia coli. Molecular Microbiology, 1992, 6, 1913-1923.	2.5	75
130	Physical map location of the narQ gene of Escherichia coli.. Journal of Bacteriology, 1992, 174, 7882.	2.2	2
131	endAFS, a novel family E endoglucanase gene from Fibrobacter succinogenes AR1. Journal of Bacteriology, 1991, 173, 3265-3268.	2.2	33
132	The involvement of transcriptional read-through from internal promoters in the expression of a novel endoglucanase geneFSendA, fromFibrobacter succinogenesAR1. Nucleic Acids Research, 1991, 19, 1661-1669.	14.5	6
133	Molecular cloning, expression, and characterization of endoglucanase genes from Fibrobacter succinogenes AR1. Applied and Environmental Microbiology, 1991, 57, 359-365.	3.1	21
134	Loss of heat-shock acquisition of thermotolerance in yeast is not correlated with loss of heat-shock proteins. FEBS Letters, 1986, 207, 149-152.	2.8	16
135	Mitochondrial and cytoplasmic protein syntheses are not required for heat shock acquisition of ethanol and thermotolerance in yeast. FEBS Letters, 1984, 172, 299-302.	2.8	68
136	Acquisition of ethanol tolerance in yeast cells by heat shock. Biotechnology Letters, 1983, 5, 683-688.	2.2	40
137	The Archaea: an Invitation to Evolutionâ€. , 0, , 1-13.		3
138	Central Metabolism. , 0, , 260-287.		21
139	Methanogenesis. , 0, , 288-314.		39
140	Proteinaceous Surface Layers of<i>Archaea</i>: Ultrastructure and Biochemistry. , 0, , 315-340.		28
141	Lipids: Biosynthesis, Function, and Evolution. , 0, , 341-353.		7
142	Solute Transport. , 0, , 354-368.		6
143	Protein Translocation into and across Archaeal Cytoplasmic Membranes. , 0, , 369-384.		3
144	Flagellation and Chemotaxis. , 0, , 385-410.		10

#	Article	IF	Citations
145	General Characteristics and Important Model Organisms. , 0, , 14-92.		27
146	Functional Genomics. , 0, , 434-462.		1
147	Molecular Genetics of Archaea. , 0, , 463-477.		1
148	Archaeosome Vaccines. , 0, , 496-510.		2
149	DNA Replication and Cell Cycle. , 0, , 93-109.		3
150	DNA-Binding Proteins and Chromatin. , 0, , 110-119.		4
151	Mechanisms of Genome Stability and Evolution^{â€}. , 0, , 120-138.		1
152	Transcription: Mechanism and Regulation. , 0, , 139-157.		10
153	RNA Processing. , 0, , 158-174.		3
154	Protein-Folding Systems. , 0, , 209-223.		0
155	Structure and Evolution of Genomes. , 0, , 411-433.		0
156	Features of Aminoacyl-tRNA Synthesis Unique to Archaea. , 0, , 198-208.		1
157	Sensing, Signal Transduction, and Posttranslational Modification. , 0, , 224-259.		0