

David S Holmes

List of Publications by Year in descending order

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papers

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66234

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docs citations

139
times ranked

4097
citing authors

#	ARTICLE	IF	CITATIONS
1	A Large-Scale Genome-Based Survey of Acidophilic Bacteria Suggests That Genome Streamlining Is an Adaptation for Life at Low pH. <i>Frontiers in Microbiology</i> , 2022, 13, 803241.	1.5	12
2	A Large-Scale Multiple Genome Comparison of Acidophilic Archaea (pH $\hat{\approx}$ 5.0) Extends Our Understanding of Oxidative Stress Responses in Polyextreme Environments. <i>Antioxidants</i> , 2022, 11, 59.	2.2	3
3	Draft Genome Sequence of the Novel, Moderately Thermophilic, Iron- and Sulfur-Oxidizing Firmicute Strain Y002, Isolated from an Extremely Acidic Geothermal Environment. <i>Microbiology Resource Announcements</i> , 2022, , e0014922.	0.3	1
4	Draft Genome Sequence of <i>Firmicutes</i> Strain S ⁰ AB, a Heterotrophic Iron/Sulfur-Oxidizing Extreme Acidophile. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.3	2
5	SinEx DB 2.0 update 2020: database for eukaryotic single-exon coding sequences. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	3
6	Integrative Genomics Sheds Light on Evolutionary Forces Shaping the Acidithiobacillia Class Acidophilic Lifestyle. <i>Frontiers in Microbiology</i> , 2021, 12, 822229.	1.5	10
7	Unlocking Survival Mechanisms for Metal and Oxidative Stress in the Extremely Acidophilic, Halotolerant Acidihalobacter Genus. <i>Genes</i> , 2020, 11, 1392.	1.0	8
8	AciDB 1.0: a database of acidophilic organisms, their genomic information and associated metadata. <i>Bioinformatics</i> , 2020, 36, 4970-4971.	1.8	9
9	Evolution of Predicted Acid Resistance Mechanisms in the Extremely Acidophilic <i>Leptospirillum</i> Genus. <i>Genes</i> , 2020, 11, 389.	1.0	23
10	Genome-based classification of <i>Acidihalobacter prosperus</i> F5 (=DSM 105917=JCM 32255) as <i>Acidihalobacter yilgarnensis</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 6226-6234.	0.8	13
11	Identification and Unusual Properties of the Master Regulator FNR in the Extreme Acidophile <i>Acidithiobacillus ferrooxidans</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1642.	1.5	19
12	Uncovering the Mechanisms of Halotolerance in the Extremely Acidophilic Members of the <i>Acidihalobacter</i> Genus Through Comparative Genome Analysis. <i>Frontiers in Microbiology</i> , 2019, 10, 155.	1.5	24
13	Effect of CO ₂ Concentration on Uptake and Assimilation of Inorganic Carbon in the Extreme Acidophile <i>Acidithiobacillus ferrooxidans</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 603.	1.5	22
14	Genome-based classification of two halotolerant extreme acidophiles, <i>Acidihalobacter prosperus</i> V6 (=DSM 14174 =JCM 32253) and ' <i>Acidihalobacter ferrooxidans</i> ' V8 (=DSM 14175 =JCM 32254) as two new species, <i>Acidihalobacter aeolianus</i> sp. nov. and <i>Acidihalobacter ferrooxydans</i> sp. nov., respectively. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1557-1565.	0.8	25
15	Improved ontology for eukaryotic single-exon coding sequences in biological databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, 1-6.	1.4	5
16	Mutantelec: An <i>In Silico</i> mutation simulation platform for comparative electrostatic potential profiling of proteins. <i>Journal of Computational Chemistry</i> , 2017, 38, 467-474.	1.5	6
17	16S rRNA and Multilocus Phylogenetic Analysis of the Iron Oxidizing Acidophiles of the <i>Acidiferrobacteraceae</i> Family. <i>Solid State Phenomena</i> , 2017, 262, 339-343.	0.3	1
18	Draft genome sequence of the type strain of the sulfur-oxidizing acidophile, <i>Acidithiobacillus albertensis</i> (DSM 14366). <i>Standards in Genomic Sciences</i> , 2017, 12, 77.	1.5	17

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19	Draft genome sequence of <i>Acidithiobacillus thiooxidans</i> CLST isolated from the acidic hypersaline Gorbea salt flat in northern Chile. <i>Standards in Genomic Sciences</i> , 2017, 12, 84.	1.5	20
20	Gene Loss and Horizontal Gene Transfer Contributed to the Genome Evolution of the Extreme Acidophile <i>Ferroplasma</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 797.	1.5	42
21	Aerobic Lineage of the Oxidative Stress Response Protein Rubrerythrin Emerged in an Ancient Microaerobic, (Hyper)Thermophilic Environment. <i>Frontiers in Microbiology</i> , 2016, 7, 1822.	1.5	38
22	Bioinformatic Analyses of Unique (Orphan) Core Genes of the Genus <i>Acidithiobacillus</i> : Functional Inferences and Use As Molecular Probes for Genomic and Metagenomic/Transcriptomic Interrogation. <i>Frontiers in Microbiology</i> , 2016, 7, 2035.	1.5	16
23	Genome Analysis of the Biotechnologically Relevant Acidophilic Iron Oxidising Strain JA12 Indicates Phylogenetic and Metabolic Diversity within the Novel Genus <i>Ferroplasma</i> . <i>PLoS ONE</i> , 2016, 11, e0146832.	1.1	48
24	Graphlet Based Metrics for the Comparison of Gene Regulatory Networks. <i>PLoS ONE</i> , 2016, 11, e0163497.	1.1	17
25	Genomic and metagenomic challenges and opportunities for bioleaching: a mini-review. <i>Research in Microbiology</i> , 2016, 167, 529-538.	1.0	61
26	SinEx DB: a database for single exon coding sequences in mammalian genomes. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw095.	1.4	16
27	Draft genome sequence of chloride-tolerant <i>Leptospirillum ferriphilum</i> Sp-Cl from industrial bioleaching operations in northern Chile. <i>Standards in Genomic Sciences</i> , 2016, 11, 19.	1.5	29
28	Multiple Osmotic Stress Responses in <i>Acidihalobacter prosperus</i> Result in Tolerance to Chloride Ions. <i>Frontiers in Microbiology</i> , 2016, 7, 2132.	1.5	48
29	Progress in Acidophile Genomics. , 2016, , 179-198.		11
30	Expression and activity of the Calvin-Benson-Bassham cycle transcriptional regulator CbbR from <i>Acidithiobacillus ferrooxidans</i> in <i>Ralstonia eutropha</i> . <i>FEMS Microbiology Letters</i> , 2015, 362, fmv108.	0.7	5
31	Metagenomic analysis reveals adaptations to a cold-adapted lifestyle in a low-temperature acid mine drainage stream. <i>FEMS Microbiology Ecology</i> , 2015, 91, .	1.3	75
32	Reclassification of <i>Thiobacillus prosperus</i> Huber and Stetter 1989 as <i>Acidihalobacter prosperus</i> gen. nov., sp. nov., a member of the family Ectothiorhodospiraceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 3641-3644.	0.8	32
33	Multi Locus Sequence Typing scheme for <i>Acidithiobacillus caldus</i> strain evaluation and differentiation. <i>Research in Microbiology</i> , 2014, 165, 735-742.	1.0	11
34	Draft Genome Sequence of the Iron-Oxidizing, Acidophilic, and Halotolerant <i>Thiobacillus prosperus</i> Type Strain DSM 5130. <i>Genome Announcements</i> , 2014, 2, .	0.8	15
35	Draft Genome Sequence of the Iron-Oxidizing Acidophile <i>Leptospirillum ferriphilum</i> Type Strain DSM 14647. <i>Genome Announcements</i> , 2014, 2, .	0.8	24
36	<i>fur</i> ⁻ , an antisense RNA gene to <i>fur</i> in the extreme acidophile <i>Acidithiobacillus ferrooxidans</i> . <i>Microbiology (United Kingdom)</i> , 2014, 160, 514-524.	0.7	3

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37	AFAL: a web service for profiling amino acids surrounding ligands in proteins. <i>Journal of Computer-Aided Molecular Design</i> , 2014, 28, 1069-1076.	1.3	8
38	Metal resistance in acidophilic microorganisms and its significance for biotechnologies. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 8133-8144.	1.7	106
39	Genetic variability of psychrotolerant <i>Acidithiobacillus ferrivorans</i> revealed by (meta)genomic analysis. <i>Research in Microbiology</i> , 2014, 165, 726-734.	1.0	31
40	Metal resistance or tolerance? Acidophiles confront high metal loads via both abiotic and biotic mechanisms. <i>Frontiers in Microbiology</i> , 2014, 5, 157.	1.5	51
41	Draft Genome Sequence of the Nominated Type Strain of <i>Ferroplasma myxofaciens</i> , an Acidophilic, Iron-Oxidizing Betaproteobacterium. <i>Genome Announcements</i> , 2014, 2, .	0.8	24
42	Anaerobic Sulfur Metabolism Coupled to Dissimilatory Iron Reduction in the Extremophile <i>Acidithiobacillus ferrooxidans</i> . <i>Applied and Environmental Microbiology</i> , 2013, 79, 2172-2181.	1.4	135
43	Architecture and Gene Repertoire of the Flexible Genome of the Extreme Acidophile <i>Acidithiobacillus caldus</i> . <i>PLoS ONE</i> , 2013, 8, e78237.	1.1	68
44	TnpPred: A Web Service for the Robust Prediction of Prokaryotic Transposases. <i>Comparative and Functional Genomics</i> , 2012, 2012, 1-5.	2.0	46
45	Complete Genome Sequence of Temperate Bacteriophage <i>Aca</i> ML1 from the Extreme Acidophile <i>Acidithiobacillus caldus</i> ATCC 51756. <i>Journal of Virology</i> , 2012, 86, 12452-12453.	1.5	19
46	Comparative genomics of the oxidative stress response in bioleaching microorganisms. <i>Hydrometallurgy</i> , 2012, 127-128, 162-167.	1.8	57
47	ICE1, an Actively Excising Genetic Element from the Biomining Bacterium <i>Acidithiobacillus ferrooxidans</i> . <i>Journal of Molecular Microbiology and Biotechnology</i> , 2012, 22, 399-407.	1.0	36
48	An artifact in studies of gene regulation using β -galactosidase reporter gene assays. <i>Analytical Biochemistry</i> , 2012, 421, 333-335.	1.1	2
49	Genomic insights into microbial iron oxidation and iron uptake strategies in extremely acidic environments. <i>Environmental Microbiology</i> , 2012, 14, 1597-1611.	1.8	170
50	Draft Genome of the Psychrotolerant Acidophile <i>Acidithiobacillus ferrivorans</i> SS3. <i>Journal of Bacteriology</i> , 2011, 193, 4304-4305.	1.0	76
51	Draft Genome Sequence of the Extremely Acidophilic Biomining Bacterium <i>Acidithiobacillus thiooxidans</i> ATCC 19377 Provides Insights into the Evolution of the <i>Acidithiobacillus</i> Genus. <i>Journal of Bacteriology</i> , 2011, 193, 7003-7004.	1.0	75
52	Sulfur Metabolism in the Extreme Acidophile <i>Acidithiobacillus Caldus</i> . <i>Frontiers in Microbiology</i> , 2011, 2, 17.	1.5	145
53	Molecular dynamics study of the archaeal aquaporin AqpM. <i>BMC Genomics</i> , 2011, 12, S8.	1.2	16
54	Lessons from the genomes of extremely acidophilic bacteria and archaea with special emphasis on bioleaching microorganisms. <i>Applied Microbiology and Biotechnology</i> , 2010, 88, 605-620.	1.7	78

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55	Genes and pathways for CO ₂ fixation in the obligate, chemolithoautotrophic acidophile, <i>Acidithiobacillus ferrooxidans</i> , Carbon fixation in <i>A. ferrooxidans</i> . <i>BMC Microbiology</i> , 2010, 10, 229.	1.3	65
56	Comparative genomics begins to unravel the ecophysiology of bioleaching. <i>Hydrometallurgy</i> , 2010, 104, 471-476.	1.8	43
57	Draft Genome Sequence of the Extremely Acidophilic Bacterium <i>Acidithiobacillus caldus</i> ATCC 51756 Reveals Metabolic Versatility in the Genus <i>Acidithiobacillus</i> . <i>Journal of Bacteriology</i> , 2009, 191, 5877-5878.	1.0	83
58	Genomic Lessons from Biomining Organisms: Case Study of the <i>Acidithiobacillus</i> Genus. <i>Advanced Materials Research</i> , 2009, 71-73, 215-218.	0.3	4
59	Extending the models for iron and sulfur oxidation in the extreme Acidophile <i>Acidithiobacillus ferrooxidans</i> . <i>BMC Genomics</i> , 2009, 10, 394.	1.2	309
60	Selection and evaluation of reference genes for improved interrogation of microbial transcriptomes: case study with the extremophile <i>Acidithiobacillus ferrooxidans</i> . <i>BMC Molecular Biology</i> , 2009, 10, 63.	3.0	74
61	Gene Organization and CO ₂ -Responsive Expression of Four <i>cbb</i> Operons in the Biomining Bacterium <i>Acidithiobacillus Ferrooxidans</i> . <i>Advanced Materials Research</i> , 2009, 71-73, 207-210.	0.3	12
62	Preparation and Analysis of an Expressed Sequence Tag Library from the Toxic Dinoflagellate <i>Alexandrium catenella</i> . <i>Marine Biotechnology</i> , 2008, 10, 692-700.	1.1	40
63	Review of International Biohydrometallurgy Symposium, Frankfurt, 2007. <i>Hydrometallurgy</i> , 2008, 92, 69-72.	1.8	13
64	Iron homeostasis strategies in acidophilic iron oxidizers: Studies in <i>Acidithiobacillus</i> and <i>Leptospirillum</i> . <i>Hydrometallurgy</i> , 2008, 94, 175-179.	1.8	13
65	Comparative genome analysis of <i>Acidithiobacillus ferrooxidans</i> , <i>A. thiooxidans</i> and <i>A. caldus</i> : Insights into their metabolism and ecophysiology. <i>Hydrometallurgy</i> , 2008, 94, 180-184.	1.8	102
66	<i>Acidithiobacillus ferrooxidans</i> metabolism: from genome sequence to industrial applications. <i>BMC Genomics</i> , 2008, 9, 597.	1.2	490
67	Microbial iron management mechanisms in extremely acidic environments: comparative genomics evidence for diversity and versatility. <i>BMC Microbiology</i> , 2008, 8, 203.	1.3	50
68	PRELIMINARY GENOMIC AND FUNCTIONAL ANALYSIS OF A CDNA LIBRARY FROM <i>BOTRYTIS CINEREA</i> . <i>Acta Horticulturae</i> , 2008, , 197-202.	0.1	0
69	AlterORF: a database of alternate open reading frames. <i>Nucleic Acids Research</i> , 2007, 36, D517-D518.	6.5	7
70	Discovery of Small Regulatory RNAs Extends Our Understanding of Gene Regulation in the <i>Acidithiobacillus</i> Genus. <i>Advanced Materials Research</i> , 2007, 20-21, 535-538.	0.3	2
71	Insights into the Metabolism and Ecophysiology of Three <i>Acidithiobacilli</i> by Comparative Genome Analysis. <i>Advanced Materials Research</i> , 2007, 20-21, 439-442.	0.3	7
72	Iron Homeostasis Strategies in Acidophilic Iron Oxidizers: Comparative Genomic Analyses. <i>Advanced Materials Research</i> , 2007, 20-21, 531-534.	0.3	1

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73	Bioinformatic prediction and experimental verification of Fur-regulated genes in the extreme acidophile <i>Acidithiobacillus ferrooxidans</i> . <i>Nucleic Acids Research</i> , 2007, 35, 2153-2166.	6.5	79
74	Second Acyl Homoserine Lactone Production System in the Extreme Acidophile <i>Acidithiobacillus ferrooxidans</i> . <i>Applied and Environmental Microbiology</i> , 2007, 73, 3225-3231.	1.4	78
75	Differential expression of two bc 1 complexes in the strict acidophilic chemolithoautotrophic bacterium <i>Acidithiobacillus ferrooxidans</i> suggests a model for their respective roles in iron or sulfur oxidation. <i>Microbiology (United Kingdom)</i> , 2007, 153, 102-110.	0.7	66
76	Genetic and Bioinformatic Insights into Iron and Sulfur Oxidation Mechanisms of Bioleaching Organisms. , 2007, , 281-307.		38
77	Regulation of a Novel <i>Acidithiobacillus caldus</i> Gene Cluster Involved in Metabolism of Reduced Inorganic Sulfur Compounds. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7367-7372.	1.4	57
78	The Use Of Bioinformatics And Genome Biology To Advance Our Understanding Of Bioleaching Microorganisms. , 2007, , 221-239.		9
79	Thermophiles like hot T. <i>Trends in Microbiology</i> , 2006, 14, 423-426.	3.5	17
80	Generation and analysis of expressed sequence tags from <i>Botrytis cinerea</i> . <i>Biological Research</i> , 2006, 39, 367-76.	1.5	14
81	Microarray and bioinformatic analyses suggest models for carbon metabolism in the autotroph <i>Acidithiobacillus ferrooxidans</i> . <i>Hydrometallurgy</i> , 2006, 83, 273-280.	1.8	48
82	Insights into the iron and sulfur energetic metabolism of <i>Acidithiobacillus ferrooxidans</i> by microarray transcriptome profiling. <i>Hydrometallurgy</i> , 2006, 83, 263-272.	1.8	112
83	Genomic insights into the iron uptake mechanisms of the biomining microorganism <i>Acidithiobacillus ferrooxidans</i> . <i>Journal of Industrial Microbiology and Biotechnology</i> , 2005, 32, 606-614.	1.4	56
84	A Lux-like Quorum Sensing System in the Extreme Acidophile <i>Acidithiobacillus ferrooxidans</i> . <i>Biological Research</i> , 2005, 38, 283-97.	1.5	62
85	Identification of a Gene Cluster for the Formation of Extracellular Polysaccharide Precursors in the Chemolithoautotroph <i>Acidithiobacillus ferrooxidans</i> . <i>Applied and Environmental Microbiology</i> , 2005, 71, 2902-2909.	1.4	109
86	The ferric iron uptake regulator (Fur) from the extreme acidophile <i>Acidithiobacillus ferrooxidans</i> . <i>Microbiology (United Kingdom)</i> , 2005, 151, 2005-2015.	0.7	46
87	Role of complementary proteins in autoimmunity: an old idea re-emerges with new twists. <i>Trends in Immunology</i> , 2005, 26, 367-372.	2.9	34
88	Large-Scale, Multi-Genome Analysis of Alternate Open Reading Frames in Bacteria and Archaea. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 91-105.	1.0	18
89	Aspects of the predicted physiology of <i>Acidithiobacillus ferrooxidans</i> deduced from an analysis of its partial genome sequence. <i>Hydrometallurgy</i> , 2003, 71, 97-105.	1.8	34
90	Characterization of the <i>petI</i> and <i>res</i> Operons of <i>Acidithiobacillus ferrooxidans</i> . <i>Journal of Bacteriology</i> , 2002, 184, 1498-1501.	1.0	45

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91	Latin American Genome Initiative, the Creation of a Network and Web Based Resource to Aid and Nurture Genome Biology in Developing Countries. <i>Electronic Journal of Biotechnology</i> , 2002, 5, .	1.2	0
92	ISAFE1, an ISL3 Family Insertion Sequence from <i>Acidithiobacillus ferrooxidans</i> ATCC 19859. <i>Journal of Bacteriology</i> , 2001, 183, 4323-4329.	1.0	22
93	Functional analysis of gapped microbial genomes: Amino acid metabolism of <i>Thiobacillus ferrooxidans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 3509-3514.	3.3	62
94	An RT-PCR artifact in the characterization of bacterial operons. <i>Electronic Journal of Biotechnology</i> , 2000, 3, .	1.2	1
95	IST1 insertional inactivation of the <i>theresB</i> gene: implications for phenotypic switching in <i>Thiobacillus ferrooxidans</i> . <i>FEMS Microbiology Letters</i> , 1999, 175, 223-229.	0.7	26
96	Sequence and expression of the rusticyanin structural gene from <i>Thiobacillus ferrooxidans</i> ATCC33020 strain. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1998, 1443, 99-112.	2.4	38
97	Biorecovery of metals from mining wastes. , 1998, , 517-545.		2
98	Biological cyanide destruction mediated by microorganisms. <i>World Journal of Microbiology and Biotechnology</i> , 1995, 11, 257-265.	1.7	115
99	Development of biosensors for the detection of mercury and copper ions. <i>Environmental Geochemistry and Health</i> , 1994, 16-16, 229-233.	1.8	14
100	Transposition of IST2 in <i>Thiobacillus ferrooxidans</i> . <i>Molecular Microbiology</i> , 1994, 12, 165-170.	1.2	12
101	Construction and Evaluation of a Self-Luminescent Biosensor. <i>Annals of the New York Academy of Sciences</i> , 1991, 646, 53-60.	1.8	22
102	IST2: an insertion sequence from <i>Thiobacillus ferrooxidans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1988, 85, 7284-7287.	3.3	41
103	Biotechnology in the mining and metal processing industries: challenges and opportunities. <i>Mining, Metallurgy and Exploration</i> , 1988, 5, 49-56.	0.4	5
104	Phenotypic switching of <i>Thiobacillus ferrooxidans</i> . <i>Journal of Bacteriology</i> , 1988, 170, 3915-3923.	1.0	68
105	Two families of repeated DNA sequences in <i>Thiobacillus ferrooxidans</i> . <i>Journal of Bacteriology</i> , 1987, 169, 1861-1870.	1.0	67
106	Use of x-ray computed tomography to examine microbial desulfurization of lump coal. <i>Energy & Fuels</i> , 1987, 1, 76-79.	2.5	13
107	The use of genetic probes to detect microorganisms in biomining operations. <i>Journal of Industrial Microbiology</i> , 1986, 1, 129-135.	0.9	23
108	<i>Acidiphilium organovorum</i> sp. nov., an Acidophilic Heterotroph Isolated from a <i>Thiobacillus ferrooxidans</i> Culture. <i>International Journal of Systematic Bacteriology</i> , 1986, 36, 139-144.	2.8	66

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109	Cloning of a Thiobacillus ferrooxidans plasmid in Escherichia coli. Journal of Bacteriology, 1984, 157, 324-326.	1.0	28
110	Rapid purification of bacterial plasmids and coliphage M13 RF without CsCl centrifugation. Analytical Biochemistry, 1982, 127, 428-433.	1.1	9
111	A note on the use of CsCl centrifugation to purify bacterial plasmids prepared by the rapid boiling method. Analytical Biochemistry, 1982, 127, 434.	1.1	12
112	The use of agar for gel electrophoresis of DNA. Analytical Biochemistry, 1982, 119, 164-166.	1.1	1
113	Specific increase of perchloric acid extractable chromosomal proteins during mammalian erythropoiesis. Comparative Biochemistry and Physiology Part B: Comparative Biochemistry, 1981, 69, 303-306.	0.2	0
114	A rapid boiling method for the preparation of bacterial plasmids. Analytical Biochemistry, 1981, 114, 193-197.	1.1	3,577
115	Structure of the chromosomal material in inactive nuclei of chicken red blood cells. Chromosoma, 1980, 79, 159-167.	1.0	7
116	The mesokaryote Gyrodiniumcohnii lacks nucleosomes. Biochemical and Biophysical Research Communications, 1979, 88, 1329-1336.	1.0	51
117	Application of the avidin-biotin method of gene enrichment to the isolation of long double-stranded DNA containing specific gene sequences. Nucleic Acids Research, 1977, 4, 2961-2974.	6.5	18
118	Positions of sea urchin (Strongylocentrotus purpuratus) histone genes relative to restriction endonuclease sites on the chimeric plasmids pSp2 and pSp17. Biochemistry, 1977, 16, 1504-1512.	1.2	40
119	The relative positions of sea urchin histone genes on the chimeric plasmids pSp2 and pSp17 as studied by electron microscopy. Cell, 1976, 9, 163-169.	13.5	43
120	Sequence composition of rat ascites chromosomal ribonucleic acid. Biochemistry, 1974, 13, 849-855.	1.2	21
121	Sequence composition of rat nuclear deoxyribonucleic acid and high molecular weight nuclear ribonucleic acid. Biochemistry, 1974, 13, 841-848.	1.2	66
122	Interspersion of Repetitive and Single-Copy Sequences in Nuclear Ribonucleic Acid of High Molecular Weight. Proceedings of the National Academy of Sciences of the United States of America, 1974, 71, 1108-1112.	3.3	43
123	Functional Organization of the Mammalian Genome. Cold Spring Harbor Symposia on Quantitative Biology, 1974, 38, 303-310.	2.0	50
124	Preparation, molecular weight, base composition, and secondary structure of giant nuclear ribonucleic acid. Biochemistry, 1973, 12, 2330-2338.	1.2	406
125	Chromosomal RNA: Its Properties. Science, 1972, 177, 72-74.	6.0	72
126	C-di-GMP Pathway in Biomining Bacteria. Advanced Materials Research, 0, 71-73, 223-226.	0.3	14

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127	Comparative Genomics Begins to Unravel the Ecophysiology of Bioleaching. <i>Advanced Materials Research</i> , 0, 71-73, 143-150.	0.3	17
128	Predicting the Function of Hypothetical Genes in Genomes of Bioleaching Microorganisms. <i>Advanced Materials Research</i> , 0, 71-73, 203-206.	0.3	0
129	Predicted CO ₂ Fixation in <i>Ferroplasma</i> spp. via a Novel Chimaeric Pathway. <i>Advanced Materials Research</i> , 0, 71-73, 219-222.	0.3	2
130	Protein Function in Extremely Acidic Conditions: Molecular Simulations of a Predicted Aquaporin and a Potassium Channel in <i>Acidithiobacillus Ferrooxidans</i> . <i>Advanced Materials Research</i> , 0, 71-73, 211-214.	0.3	8
131	Prediction of FNR Regulated Genes and Metabolic Pathways Potentially Involved in Anaerobic Growth of <i>Acidithiobacillus Ferrooxidans</i> . <i>Advanced Materials Research</i> , 0, 71-73, 195-198.	0.3	9
132	Regulation of Expression of the <i>PetI</i> Operon Involved in Iron Oxidation in the Biomining Bacterium <i>Acidithiobacillus Ferrooxidans</i> . <i>Advanced Materials Research</i> , 0, 71-73, 199-202.	0.3	8
133	Small Regulatory RNAs in <i>Acidithiobacillus Ferrooxidans</i> : Case Studies of 6S RNA and <i>Frr</i> . <i>Advanced Materials Research</i> , 0, 71-73, 191-194.	0.3	4
134	A 300 kpb Genome Segment, Including a Complete Set of tRNA Genes, is Dispensable for <i>Acidithiobacillus Ferrooxidans</i> . <i>Advanced Materials Research</i> , 0, 71-73, 187-190.	0.3	21
135	Analysis of Gene Expression in Response to Copper Stress in <i>Acidithiobacillus ferrooxidans</i> Strain D2, Isolated from a Copper Bioleaching Operation. <i>Advanced Materials Research</i> , 0, 825, 157-161.	0.3	14
136	Temporal Dynamics of Genes Involved in Metabolic Pathways of C and N of <i>L. ferriphilum</i> , in the Industrial Bioleaching Process of Escondida Mine, Chile. <i>Advanced Materials Research</i> , 0, 825, 162-165.	0.3	15