

Raquel Quatrini

List of Publications by Year in descending order

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73
papers

2,960
citations

218677

26
h-index

182427

51
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74
all docs

74
docs citations

74
times ranked

1939
citing authors

#	ARTICLE	IF	CITATIONS
1	Acidithiobacillus ferrooxidans metabolism: from genome sequence to industrial applications. BMC Genomics, 2008, 9, 597.	2.8	490
2	Extending the models for iron and sulfur oxidation in the extreme Acidophile Acidithiobacillus ferrooxidans. BMC Genomics, 2009, 10, 394.	2.8	309
3	Insights into the iron and sulfur energetic metabolism of Acidithiobacillus ferrooxidans by microarray transcriptome profiling. Hydrometallurgy, 2006, 83, 263-272.	4.3	112
4	Microbiomes in extremely acidic environments: functionalities and interactions that allow survival and growth of prokaryotes at low pH. Current Opinion in Microbiology, 2018, 43, 139-147.	5.1	106
5	Comparative genome analysis of Acidithiobacillus ferrooxidans, A. thiooxidans and A. caldus: Insights into their metabolism and ecophysiology. Hydrometallurgy, 2008, 94, 180-184.	4.3	102
6	Draft Genome Sequence of the Extremely Acidophilic Bacterium <i>Acidithiobacillus caldus</i> ATCC 51756 Reveals Metabolic Versatility in the Genus <i>Acidithiobacillus</i> . Journal of Bacteriology, 2009, 191, 5877-5878.	2.2	83
7	Bioinformatic prediction and experimental verification of Fur-regulated genes in the extreme acidophile Acidithiobacillus ferrooxidans. Nucleic Acids Research, 2007, 35, 2153-2166.	14.5	79
8	Lessons from the genomes of extremely acidophilic bacteria and archaea with special emphasis on bioleaching microorganisms. Applied Microbiology and Biotechnology, 2010, 88, 605-620.	3.6	78
9	Molecular Systematics of the Genus Acidithiobacillus: Insights into the Phylogenetic Structure and Diversification of the Taxon. Frontiers in Microbiology, 2017, 8, 30.	3.5	77
10	Draft Genome Sequence of the Extremely Acidophilic Biomining Bacterium Acidithiobacillus thiooxidans ATCC 19377 Provides Insights into the Evolution of the Acidithiobacillus Genus. Journal of Bacteriology, 2011, 193, 7003-7004.	2.2	75
11	Selection and evaluation of reference genes for improved interrogation of microbial transcriptomes: case study with the extremophile Acidithiobacillus ferrooxidans. BMC Molecular Biology, 2009, 10, 63.	3.0	74
12	Architecture and Gene Repertoire of the Flexible Genome of the Extreme Acidophile Acidithiobacillus caldus. PLoS ONE, 2013, 8, e78237.	2.5	68
13	Genomic and metagenomic challenges and opportunities for bioleaching: a mini-review. Research in Microbiology, 2016, 167, 529-538.	2.1	61
14	Comparative genomics of the oxidative stress response in bioleaching microorganisms. Hydrometallurgy, 2012, 127-128, 162-167.	4.3	57
15	Genomic insights into the iron uptake mechanisms of the biomining microorganism Acidithiobacillus ferrooxidans. Journal of Industrial Microbiology and Biotechnology, 2005, 32, 606-614.	3.0	56
16	Acidithiobacillus ferrooxidans. Trends in Microbiology, 2019, 27, 282-283.	7.7	56
17	Comparative Genomics Analysis of a New Exiguobacterium Strain from Salar de Huasco Reveals a Repertoire of Stress-Related Genes and Arsenic Resistance. Frontiers in Microbiology, 2017, 8, 456.	3.5	55
18	Microbial iron management mechanisms in extremely acidic environments: comparative genomics evidence for diversity and versatility. BMC Microbiology, 2008, 8, 203.	3.3	50

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19	Microarray and bioinformatic analyses suggest models for carbon metabolism in the autotroph <i>Acidithiobacillus ferrooxidans</i> . <i>Hydrometallurgy</i> , 2006, 83, 273-280.	4.3	48
20	The ferric iron uptake regulator (Fur) from the extreme acidophile <i>Acidithiobacillus ferrooxidans</i> . <i>Microbiology (United Kingdom)</i> , 2005, 151, 2005-2015.	1.8	46
21	Comparative genomics begins to unravel the ecophysiology of bioleaching. <i>Hydrometallurgy</i> , 2010, 104, 471-476.	4.3	43
22	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.	3.5	38
23	ICE$\phi$$Afe$, an Actively Excising Genetic Element from the Biomining Bacterium $Acidithiobacillus ferrooxidans$. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2012, 22, 399-407.	1.0	36
24	<i>Acidithiobacillus ferrianus</i> sp. nov.: an ancestral extremely acidophilic and facultatively anaerobic chemolithoautotroph. <i>Extremophiles</i> , 2020, 24, 329-337.	2.3	35
25	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.	4.3	34
26	Genetic variability of psychrotolerant <i>Acidithiobacillus ferrivorans</i> revealed by (meta)genomic analysis. <i>Research in Microbiology</i> , 2014, 165, 726-734.	2.1	31
27	Genomic evolution of the class <i>Acidithiobacillia</i>: deep-branching Proteobacteria living in extreme acidic conditions. <i>ISME Journal</i> , 2021, 15, 3221-3238.	9.8	31
28	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
29	Insights into the biology of acidophilic members of the Acidiferrobacteraceae family derived from comparative genomic analyses. <i>Research in Microbiology</i> , 2018, 169, 608-617.	2.1	29
30	Thiol/Disulfide System Plays a Crucial Role in Redox Protection in the Acidophilic Iron-Oxidizing Bacterium <i>Leptospirillum ferriphilum</i> . <i>PLoS ONE</i> , 2012, 7, e44576.	2.5	27
31	Draft Genome Sequence of the Nominated Type Strain of $Ferroplasma myxofaciens$, an Acidophilic, Iron-Oxidizing Betaproteobacterium. <i>Genome Announcements</i> , 2014, 2, .	0.8	24
32	Detection, identification and typing of <i>Acidithiobacillus</i> species and strains: a review. <i>Research in Microbiology</i> , 2016, 167, 555-567.	2.1	24
33	A DNA segment encoding the anticodon stem/loop of tRNA determines the specific recombination of integrative-conjugative elements in <i>Acidithiobacillus</i> species. <i>RNA Biology</i> , 2018, 15, 492-499.	3.1	24
34	Acidophile Microbiology in Space and Time. <i>Current Issues in Molecular Biology</i> , 2020, 39, 63-76.	2.4	23
35	A 300 kpb Genome Segment, Including a Complete Set of tRNA Genes, is Dispensable for $Acidithiobacillus ferrooxidans$. <i>Advanced Materials Research</i> , 0, 71-73, 187-190.	0.3	21
36	Evolution of Type IV CRISPR-Cas Systems: Insights from CRISPR Loci in Integrative Conjugative Elements of <i>Acidithiobacillia</i>. <i>CRISPR Journal</i> , 2021, 4, 656-672.	2.9	21

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37	Acidithiobacillus sulfuriphilus sp. nov.: an extremely acidophilic sulfur-oxidizing chemolithotroph isolated from a neutral pH environment. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2907-2913.	1.7	21
38	Draft genome sequence of Acidithiobacillus thiooxidans CLST isolated from the acidic hypersaline Gorbea salt flat in northern Chile. Standards in Genomic Sciences, 2017, 12, 84.	1.5	20
39	Complete Genome Sequence of Temperate Bacteriophage <i>Aca</i> ML1 from the Extreme Acidophile Acidithiobacillus caldus ATCC 51756. Journal of Virology, 2012, 86, 12452-12453.	3.4	19
40	Nucleotide Second Messenger-Based Signaling in Extreme Acidophiles of the Acidithiobacillus Species Complex: Partition Between the Core and Variable Gene Complements. Frontiers in Microbiology, 2019, 10, 381.	3.5	19
41	The Flexible Genome of Acidophilic Prokaryotes. , 2016, , 199-220.		19
42	Occurrence, integrity and functionality of AcaML1-like viruses infecting extreme acidophiles of the Acidithiobacillus species complex. Research in Microbiology, 2018, 169, 628-637.	2.1	18
43	Acidiferrimicrobium australe gen. nov., sp. nov., an acidophilic and obligately heterotrophic, member of the Actinobacteria that catalyses dissimilatory oxido-reduction of iron isolated from metal-rich acidic water in Chile. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3348-3354.	1.7	18
44	Comparative Genomics Begins to Unravel the Ecophysiology of Bioleaching. Advanced Materials Research, 0, 71-73, 143-150.	0.3	17
45	Draft genome sequence of the type strain of the sulfur-oxidizing acidophile, Acidithiobacillus albertensis (DSM 14366). Standards in Genomic Sciences, 2017, 12, 77.	1.5	17
46	Variación morfológica y dieta en dos poblaciones de Liolaemus elongatus Koslowsky, 1896 (Iguania): Tj ETQq0 0 0 rgBT /Overlock 10	1.2	16
47	Temporal Dynamics of Genes Involved in Metabolic Pathways of C and N of <i>A. ferrophilum</i> and <i>A. ferrivorans</i> in the Industrial Bioleaching Process of Escondida Mine, Chile. Advanced Materials Research, 0, 825, 162-165.	0.3	15
48	Draft Genome Sequence of the Iron-Oxidizing, Acidophilic, and Halotolerant <i>Acidithiobacillus prosperus</i> Type Strain DSM 5130. Genome Announcements, 2014, 2, .	0.8	15
49	DNA, Cell Wall and General Oxidative Damage Underlie the Tellurite/Cefotaxime Synergistic Effect in Escherichia coli. PLoS ONE, 2013, 8, e79499.	2.5	15
50	Analysis of Gene Expression in Response to Copper Stress in <i>Acidithiobacillus ferrooxidans</i> Strain D2, Isolated from a Copper Bioleaching Operation. Advanced Materials Research, 0, 825, 157-161.	0.3	14
51	Iron homeostasis strategies in acidophilic iron oxidizers: Studies in Acidithiobacillus and Leptospirillum. Hydrometallurgy, 2008, 94, 175-179.	4.3	13
52	Endogenous and Foreign Nucleoid-Associated Proteins of Bacteria: Occurrence, Interactions and Effects on Mobile Genetic Elements and Host's Biology. Computational and Structural Biotechnology Journal, 2019, 17, 746-756.	4.1	13
53	Multi Locus Sequence Typing scheme for Acidithiobacillus caldus strain evaluation and differentiation. Research in Microbiology, 2014, 165, 735-742.	2.1	11
54	The Type IV Secretion System of ICEAfe1: Formation of a Conjugative Pilus in Acidithiobacillus ferrooxidans. Frontiers in Microbiology, 2019, 10, 30.	3.5	11

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55	The Flexible Genome of Acidophilic Prokaryotes. <i>Current Issues in Molecular Biology</i> , 2021, 40, 231-266.	2.4	11
56	Acidophile Microbiology in Space and Time. , 2016, , 3-16.		11
57	Progress in Acidophile Genomics. , 2016, , 179-198.		11
58	Type IV Secretion Systems Diversity in the <i>Acidithiobacillus</i> Genus. <i>Solid State Phenomena</i> , 2017, 262, 429-433.	0.3	10
59	JMJD1B, a novel player in histone H3 and H4 processing to ensure genome stability. <i>Epigenetics and Chromatin</i> , 2020, 13, 6.	3.9	10
60	The Use Of Bioinformatics And Genome Biology To Advance Our Understanding Of Bioleaching Microorganisms. , 2007, , 221-239.		9
61	Respiratory Heme A-Containing Oxidases Originated in the Ancestors of Iron-Oxidizing Bacteria. <i>Frontiers in Microbiology</i> , 2021, 12, 664216.	3.5	9
62	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
63	AFAL: a web service for profiling amino acids surrounding ligands in proteins. <i>Journal of Computer-Aided Molecular Design</i> , 2014, 28, 1069-1076.	2.9	8
64	Insights into the Metabolism and Ecophysiology of Three Acidithiobacilli by Comparative Genome Analysis. <i>Advanced Materials Research</i> , 2007, 20-21, 439-442.	0.3	7
65	Domestication of Local Microbial Consortia for Efficient Recovery of Gold Through Top-Down Selection in Airlift Bioreactors. <i>Frontiers in Microbiology</i> , 2019, 10, 60.	3.5	7
66	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.	3.3	6
67	Predicted CO/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
68	Are there Viruses in Industrial Bioleaching Econiches?. <i>Solid State Phenomena</i> , 0, 262, 521-525.	0.3	2
69	Iron Homeostasis Strategies in Acidophilic Iron Oxidizers: Comparative Genomic Analyses. <i>Advanced Materials Research</i> , 2007, 20-21, 531-534.	0.3	1
70	Metagenome-Derived Draft Genome Sequence of <i>Acidithiobacillus ferroxidans</i> RV1 from an Abandoned Gold Tailing in Neuqu�n, Argentina. <i>Solid State Phenomena</i> , 0, 262, 439-442.	0.3	1
71	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
72	Insights into the Metabolism and Ecophysiology of Three Acidithiobacilli by Comparative Genome Analysis. <i>Advanced Materials Research</i> , 0, , 439-442.	0.3	1

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73	Genetic Basis of Metal Resistance in <i>Acidiphilium</i> sp. DSM 27270 (Yenapatur). Solid State Phenomena, 2017, 262, 358-363.	0.3	0