

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
g-index

74
all docs

74
docs citations

74
times ranked

1939
citing authors

#	ARTICLE	IF	CITATIONS
1	The Flexible Genome of Acidophilic Prokaryotes. <i>Current Issues in Molecular Biology</i> , 2021, 40, 231-266.	2.4	11
2	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
3	Respiratory Heme A-Containing Oxidases Originated in the Ancestors of Iron-Oxidizing Bacteria. <i>Frontiers in Microbiology</i> , 2021, 12, 664216.	3.5	9
4	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
5	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
6	<i>Acidithiobacillus ferrianus</i> sp. nov.: an ancestral extremely acidophilic and facultatively anaerobic chemolithoautotroph. <i>Extremophiles</i> , 2020, 24, 329-337.	2.3	35
7	<i>Acidiferrimicrobium australe</i> 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. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3348-3354.	1.7	18
8	Acidophile Microbiology in Space and Time. <i>Current Issues in Molecular Biology</i> , 2020, 39, 63-76.	2.4	23
9	Endogenous and Foreign Nucleoid-Associated Proteins of Bacteria: Occurrence, Interactions and Effects on Mobile Genetic Elements and Host's Biology. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 746-756.	4.1	13
10	Nucleotide Second Messenger-Based Signaling in Extreme Acidophiles of the <i>Acidithiobacillus</i> Species Complex: Partition Between the Core and Variable Gene Complements. <i>Frontiers in Microbiology</i> , 2019, 10, 381.	3.5	19
11	The Type IV Secretion System of ICEAfe1: Formation of a Conjugative Pilus in <i>Acidithiobacillus ferrooxidans</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 30.	3.5	11
12	<i>Acidithiobacillus ferrooxidans</i> . <i>Trends in Microbiology</i> , 2019, 27, 282-283.	7.7	56
13	<i>Acidithiobacillus sulfuriphilus</i> sp. nov.: an extremely acidophilic sulfur-oxidizing chemolithotroph isolated from a neutral pH environment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2907-2913.	1.7	21
14	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
15	Microbiomes in extremely acidic environments: functionalities and interactions that allow survival and growth of prokaryotes at low pH. <i>Current Opinion in Microbiology</i> , 2018, 43, 139-147.	5.1	106
16	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
17	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
18	Occurrence, integrity and functionality of AcaML1-like viruses infecting extreme acidophiles of the <i>Acidithiobacillus</i> species complex. <i>Research in Microbiology</i> , 2018, 169, 628-637.	2.1	18

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19	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
20	Genetic Basis of Metal Resistance in <i>Acidiphilium</i> sp. DSM 27270 (Yenapatur). <i>Solid State Phenomena</i> , 2017, 262, 358-363.	0.3	0
21	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
22	Molecular Systematics of the Genus <i>Acidithiobacillus</i> : Insights into the Phylogenetic Structure and Diversification of the Taxon. <i>Frontiers in Microbiology</i> , 2017, 8, 30.	3.5	77
23	Comparative Genomics Analysis of a New <i>Exiguobacterium</i> Strain from Salar de Huasco Reveals a Repertoire of Stress-Related Genes and Arsenic Resistance. <i>Frontiers in Microbiology</i> , 2017, 8, 456.	3.5	55
24	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
25	Draft genome sequence of <i>Acidithiobacillus thiooxidans</i> CLST isolated from the acidic hypersaline Corbea salt flat in northern Chile. <i>Standards in Genomic Sciences</i> , 2017, 12, 84.	1.5	20
26	Type IV Secretion Systems Diversity in the <i>Acidithiobacillus</i> Genus. <i>Solid State Phenomena</i> , 2017, 262, 429-433.	0.3	10
27	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
28	Genomic and metagenomic challenges and opportunities for bioleaching: a mini-review. <i>Research in Microbiology</i> , 2016, 167, 529-538.	2.1	61
29	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
30	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
31	Acidophile Microbiology in Space and Time. , 2016, , 3-16.		11
32	Progress in Acidophile Genomics. , 2016, , 179-198.		11
33	The Flexible Genome of Acidophilic Prokaryotes. , 2016, , 199-220.		19
34	Multi Locus Sequence Typing scheme for <i>Acidithiobacillus caldus</i> strain evaluation and differentiation. <i>Research in Microbiology</i> , 2014, 165, 735-742.	2.1	11
35	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
36	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

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37	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
38	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
39	Architecture and Gene Repertoire of the Flexible Genome of the Extreme Acidophile <i>Acidithiobacillus caldus</i> . <i>PLoS ONE</i> , 2013, 8, e78237.	2.5	68
40	DNA, Cell Wall and General Oxidative Damage Underlie the Tellurite/Cefotaxime Synergistic Effect in <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2013, 8, e79499.	2.5	15
41	Complete Genome Sequence of Temperate Bacteriophage <i>ML1</i> from the Extreme Acidophile <i>Acidithiobacillus caldus</i> ATCC 51756. <i>Journal of Virology</i> , 2012, 86, 12452-12453.	3.4	19
42	Comparative genomics of the oxidative stress response in bioleaching microorganisms. <i>Hydrometallurgy</i> , 2012, 127-128, 162-167.	4.3	57
43	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
44	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
45	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.	2.2	75
46	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.	3.6	78
47	Comparative genomics begins to unravel the ecophysiology of bioleaching. <i>Hydrometallurgy</i> , 2010, 104, 471-476.	4.3	43
48	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.	2.2	83
49	Extending the models for iron and sulfur oxidation in the extreme Acidophile <i>Acidithiobacillus ferrooxidans</i> . <i>BMC Genomics</i> , 2009, 10, 394.	2.8	309
50	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
51	Iron homeostasis strategies in acidophilic iron oxidizers: Studies in <i>Acidithiobacillus</i> and <i>Leptospirillum</i> . <i>Hydrometallurgy</i> , 2008, 94, 175-179.	4.3	13
52	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.	4.3	102
53	<i>Acidithiobacillus ferrooxidans</i> metabolism: from genome sequence to industrial applications. <i>BMC Genomics</i> , 2008, 9, 597.	2.8	490
54	Microbial iron management mechanisms in extremely acidic environments: comparative genomics evidence for diversity and versatility. <i>BMC Microbiology</i> , 2008, 8, 203.	3.3	50

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55	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
56	Iron Homeostasis Strategies in Acidophilic Iron Oxidizers: Comparative Genomic Analyses. <i>Advanced Materials Research</i> , 2007, 20-21, 531-534.	0.3	1
57	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.	14.5	79
58	The Use Of Bioinformatics And Genome Biology To Advance Our Understanding Of Bioleaching Microorganisms. , 2007, , 221-239.		9
59	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
60	Insights into the iron and sulfur energetic metabolism of <i>Acidithiobacillus ferrooxidans</i> by microarray transcriptome profiling. <i>Hydrometallurgy</i> , 2006, 83, 263-272.	4.3	112
61	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.	3.0	56
62	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
63	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
64	Variación morfológica y dieta en dos poblaciones de <i>Liolaemus elongatus</i> Koslowsky, 1896 (Iguania): Tj ETQq0 0 0 rgBT /Overlock 10	1.2	16
65	Comparative Genomics Begins to Unravel the Ecophysiology of Bioleaching. <i>Advanced Materials Research</i> , 0, 71-73, 143-150.	0.3	17
66	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
67	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
68	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
69	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
70	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
71	Metagenome-Derived Draft Genome Sequence of <i>Acidithiobacillus ferrooxidans</i> RV1 from an Abandoned Gold Tailing in Neuquén, Argentina. <i>Solid State Phenomena</i> , 0, 262, 439-442.	0.3	1
72	Are there Viruses in Industrial Bioleaching Economies?. <i>Solid State Phenomena</i> , 0, 262, 521-525.	0.3	2

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73	Insights into the Metabolism and Ecophysiology of Three Acidithiobacilli by Comparative Genome Analysis. <i>Advanced Materials Research</i> , 0, , 439-442.	0.3	1