

Guillaume Borrel

List of Publications by Year in descending order

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35
papers

3,447
citations

257450

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330143

37
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39
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39
docs citations

39
times ranked

4146
citing authors

#	ARTICLE	IF	CITATIONS
1	The growing tree of Archaea: new perspectives on their diversity, evolution and ecology. ISME Journal, 2017, 11, 2407-2425.	9.8	320
2	Archaea and the human gut: New beginning of an old story. World Journal of Gastroenterology, 2014, 20, 16062.	3.3	308
3	Phylogenomic Data Support a Seventh Order of Methylophilic Methanogens and Provide Insights into the Evolution of Methanogenesis. Genome Biology and Evolution, 2013, 5, 1769-1780.	2.5	249
4	Comparative genomics highlights the unique biology of Methanomassiliicoccales, a Thermoplasmatales-related seventh order of methanogenic archaea that encodes pyrrolysine. BMC Genomics, 2014, 15, 679.	2.8	246
5	Production and consumption of methane in freshwater lake ecosystems. Research in Microbiology, 2011, 162, 832-847.	2.1	240
6	Archaeobiotics. Gut Microbes, 2014, 5, 5-10.	9.8	201
7	Wide diversity of methane and short-chain alkane metabolisms in uncultured archaea. Nature Microbiology, 2019, 4, 603-613.	13.3	187
8	Methanogenesis and the Wood-Wjungdahl Pathway: An Ancient, Versatile, and Fragile Association. Genome Biology and Evolution, 2016, 8, 1706-1711.	2.5	167
9	Evolutionary history of carbon monoxide dehydrogenase/acetyl-CoA synthase, one of the oldest enzymatic complexes. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E1166-E1173.	7.1	160
10	Genome Sequence of <i>Candidatus Methanomethylophilus alvus</i> Mx1201, a Methanogenic Archaeon from the Human Gut Belonging to a Seventh Order of Methanogens. Journal of Bacteriology, 2012, 194, 6944-6945.	2.2	155
11	The host-associated archaeome. Nature Reviews Microbiology, 2020, 18, 622-636.	28.6	122
12	Genomics and metagenomics of trimethylamine-utilizing Archaea in the human gut microbiome. ISME Journal, 2017, 11, 2059-2074.	9.8	112
13	Identification of microbial communities involved in the methane cycle of a freshwater meromictic lake. FEMS Microbiology Ecology, 2011, 77, 533-545.	2.7	110
14	Fecal microbiota variation across the lifespan of the healthy laboratory rat. Gut Microbes, 2017, 8, 428-439.	9.8	93
15	Genome Sequence of <i>Candidatus Methanomassiliicoccus intestinalis</i> Issoire-Mx1, a Third Thermoplasmatales-Related Methanogenic Archaeon from Human Feces. Genome Announcements, 2013, 1, .	0.8	85
16	A catalogue of 1,167 genomes from the human gut archaeome. Nature Microbiology, 2022, 7, 48-61.	13.3	72
17	Unique Characteristics of the Pyrrolysine System in the 7th Order of Methanogens: Implications for the Evolution of a Genetic Code Expansion Cassette. Archaea, 2014, 2014, 1-11.	2.3	58
18	Genome-wide analysis of the Firmicutes illuminates the diderm/monoderm transition. Nature Ecology and Evolution, 2020, 4, 1661-1672.	7.8	52

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19	An archaeal origin of the Woodâ€“Ljungdahl H4MPT branch and the emergence of bacterial methylophony. <i>Nature Microbiology</i> , 2019, 4, 2155-2163.	13.3	51
20	Unexpected and novel putative viruses in the sediments of a deep-dark permanently anoxic freshwater habitat. <i>ISME Journal</i> , 2012, 6, 2119-2127.	9.8	48
21	Identification of Sulfur-Cycle Prokaryotes in a Low-Sulfate Lake (Lake Pavin) Using <i>aprA</i> and 16S rRNA Gene Markers. <i>Microbial Ecology</i> , 2011, 61, 313-327.	2.8	47
22	The Human Gut Chip â€œHuGChipâ€œ, an Explorative Phylogenetic Microarray for Determining Gut Microbiome Diversity at Family Level. <i>PLoS ONE</i> , 2013, 8, e62544.	2.5	46
23	<i>Methanobacterium lacus</i> sp. nov., isolated from the profundal sediment of a freshwater meromictic lake. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012, 62, 1625-1629.	1.7	45
24	Diversity and Evolution of Methane-Related Pathways in Archaea. <i>Annual Review of Microbiology</i> , 2022, 76, 727-755.	7.3	37
25	Factors shaping the abundance and diversity of the gut archaeome across the animal kingdom. <i>Nature Communications</i> , 2022, 13, .	12.8	36
26	Members of candidate divisions OP11, OD1 and SR1 are widespread along the water column of the meromictic Lake Pavin (France). <i>Archives of Microbiology</i> , 2010, 192, 559-567.	2.2	27
27	Molecular methods for studying methanogens of the human gastrointestinal tract: current status and future directions. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 5801-5815.	3.6	24
28	Evolutionary placement of Methanonatronarchaeia. <i>Nature Microbiology</i> , 2019, 4, 558-559.	13.3	24
29	New Insights into the Ecology and Physiology of Methanomassiliicoccales from Terrestrial and Aquatic Environments. <i>Microorganisms</i> , 2021, 9, 30.	3.6	23
30	Pyrrolysine in archaea: a 22nd amino acid encoded through a genetic code expansion. <i>Emerging Topics in Life Sciences</i> , 2018, 2, 607-618.	2.6	22
31	Comparative genomic analysis of <i>Methanimicrococcus blatticola</i> provides insights into host adaptation in archaea and the evolution of methanogenesis. <i>ISME Communications</i> , 2021, 1, .	4.2	17
32	In-vitro model for studying methanogens in human gut microbiota. <i>Anaerobe</i> , 2015, 34, 50-52.	2.1	10
33	Resource availability drives bacterial succession during leaf-litter decomposition in a bromeliad ecosystem. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	9
34	Simulated drought regimes reveal community resilience and hydrological thresholds for altered decomposition. <i>Oecologia</i> , 2018, 187, 267-279.	2.0	7
35	A microbe that uses crude oil to make methane. <i>Nature</i> , 2022, 601, 196-197.	27.8	1