

Guillaume Borrel

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

3,447
citations

257450

24
h-index

330143

37
g-index

39
all docs

39
docs citations

39
times ranked

4146
citing authors

#	ARTICLE	IF	CITATIONS
1	A catalogue of 1,167 genomes from the human gut archaeome. <i>Nature Microbiology</i> , 2022, 7, 48-61.	13.3	72
2	A microbe that uses crude oil to make methane. <i>Nature</i> , 2022, 601, 196-197.	27.8	1
3	Factors shaping the abundance and diversity of the gut archaeome across the animal kingdom. <i>Nature Communications</i> , 2022, 13, .	12.8	36
4	Diversity and Evolution of Methane-Related Pathways in Archaea. <i>Annual Review of Microbiology</i> , 2022, 76, 727-755.	7.3	37
5	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
6	New Insights into the Ecology and Physiology of Methanomassiliicoccales from Terrestrial and Aquatic Environments. <i>Microorganisms</i> , 2021, 9, 30.	3.6	23
7	Genome-wide analysis of the Firmicutes illuminates the diderm/monoderm transition. <i>Nature Ecology and Evolution</i> , 2020, 4, 1661-1672.	7.8	52
8	The host-associated archaeome. <i>Nature Reviews Microbiology</i> , 2020, 18, 622-636.	28.6	122
9	Resource availability drives bacterial succession during leaf-litter decomposition in a bromeliad ecosystem. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	9
10	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
11	Wide diversity of methane and short-chain alkane metabolisms in uncultured archaea. <i>Nature Microbiology</i> , 2019, 4, 603-613.	13.3	187
12	Evolutionary placement of Methanonatronarchaea. <i>Nature Microbiology</i> , 2019, 4, 558-559.	13.3	24
13	Evolutionary history of carbon monoxide dehydrogenase/acetyl-CoA synthase, one of the oldest enzymatic complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1166-E1173.	7.1	160
14	Simulated drought regimes reveal community resilience and hydrological thresholds for altered decomposition. <i>Oecologia</i> , 2018, 187, 267-279.	2.0	7
15	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
16	Fecal microbiota variation across the lifespan of the healthy laboratory rat. <i>Gut Microbes</i> , 2017, 8, 428-439.	9.8	93
17	The growing tree of Archaea: new perspectives on their diversity, evolution and ecology. <i>ISME Journal</i> , 2017, 11, 2407-2425.	9.8	320
18	Genomics and metagenomics of trimethylamine-utilizing Archaea in the human gut microbiome. <i>ISME Journal</i> , 2017, 11, 2059-2074.	9.8	112

#	ARTICLE	IF	CITATIONS
19	Methanogenesis and the Wood–Ljungdahl Pathway: An Ancient, Versatile, and Fragile Association. <i>Genome Biology and Evolution</i> , 2016, 8, 1706-1711.	2.5	167
20	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
21	In-vitro model for studying methanogens in human gut microbiota. <i>Anaerobe</i> , 2015, 34, 50-52.	2.1	10
22	Unique Characteristics of the Pyrrolysine System in the 7th Order of Methanogens: Implications for the Evolution of a Genetic Code Expansion Cassette. <i>Archaea</i> , 2014, 2014, 1-11.	2.3	58
23	Archaea and the human gut: New beginning of an old story. <i>World Journal of Gastroenterology</i> , 2014, 20, 16062.	3.3	308
24	Archaeobiotics. <i>Gut Microbes</i> , 2014, 5, 5-10.	9.8	201
25	Comparative genomics highlights the unique biology of Methanomassiliicoccales, a Thermoplasmatales-related seventh order of methanogenic archaea that encodes pyrrolysine. <i>BMC Genomics</i> , 2014, 15, 679.	2.8	246
26	Genome Sequence of <i>Candidatus</i> Methanomassiliicoccus intestinalis-Issoire-Mx1, a Third Thermoplasmatales-Related Methanogenic Archaeon from Human Feces. <i>Genome Announcements</i> , 2013, 1, .	0.8	85
27	Phylogenomic Data Support a Seventh Order of Methylophilic Methanogens and Provide Insights into the Evolution of Methanogenesis. <i>Genome Biology and Evolution</i> , 2013, 5, 1769-1780.	2.5	249
28	The Human Gut Chip –HuGChip–, an Explorative Phylogenetic Microarray for Determining Gut Microbiome Diversity at Family Level. <i>PLoS ONE</i> , 2013, 8, e62544.	2.5	46
29	Genome Sequence of <i>Candidatus</i> Methanomethylophilus alvus-Mx1201, a Methanogenic Archaeon from the Human Gut Belonging to a Seventh Order of Methanogens. <i>Journal of Bacteriology</i> , 2012, 194, 6944-6945.	2.2	155
30	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
31	Methanobacterium lacus 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
32	Production and consumption of methane in freshwater lake ecosystems. <i>Research in Microbiology</i> , 2011, 162, 832-847.	2.1	240
33	Identification of microbial communities involved in the methane cycle of a freshwater meromictic lake. <i>FEMS Microbiology Ecology</i> , 2011, 77, 533-545.	2.7	110
34	Identification of Sulfur-Cycle Prokaryotes in a Low-Sulfate Lake (Lake Pavin) Using aprA and 16S rRNA Gene Markers. <i>Microbial Ecology</i> , 2011, 61, 313-327.	2.8	47
35	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