

# Jean François Brugère

## List of Publications by Year in descending order

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Version: 2024-02-01

39  
papers

2,540  
citations

304602

22  
h-index

330025

37  
g-index

50  
all docs

50  
docs citations

50  
times ranked

3168  
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.	5.9	72
2	The host-associated archaeome. <i>Nature Reviews Microbiology</i> , 2020, 18, 622-636.	13.6	122
3	Archaea, specific genetic traits, and development of improved bacterial live biotherapeutic products: another face of next-generation probiotics. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 4705-4716.	1.7	18
4	Pyrrolysine in archaea: a 22nd amino acid encoded through a genetic code expansion. <i>Emerging Topics in Life Sciences</i> , 2018, 2, 607-618.	1.1	22
5	The Evolution of Living Beings Started with Prokaryotes and in Interaction with Prokaryotes. , 2018, , 241-338.		2
6	ASaiM: a Galaxy-based framework to analyze microbiota data. <i>GigaScience</i> , 2018, 7, .	3.3	25
7	Fecal microbiota variation across the lifespan of the healthy laboratory rat. <i>Gut Microbes</i> , 2017, 8, 428-439.	4.3	93
8	Comparative genomics of microsporidian genomes reveals a minimal non-coding RNA set and new insights for transcription in minimal eukaryotic genomes. <i>DNA Research</i> , 2017, 24, 251-260.	1.5	8
9	Functional amplification and preservation of human gut microbiota. <i>Microbial Ecology in Health and Disease</i> , 2017, 28, 1308070.	3.8	10
10	Genomics and metagenomics of trimethylamine-utilizing Archaea in the human gut microbiome. <i>ISME Journal</i> , 2017, 11, 2059-2074.	4.4	112
11	Colonic Transit Time Is a Driven Force of the Gut Microbiota Composition and Metabolism: In Vitro Evidence. <i>Journal of Neurogastroenterology and Motility</i> , 2017, 23, 124-134.	0.8	89
12	Whole Rye Consumption Improves Blood and Liver n-3 Fatty Acid Profile and Gut Microbiota Composition in Rats. <i>PLoS ONE</i> , 2016, 11, e0148118.	1.1	21
13	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.	1.7	24
14	In-vitro model for studying methanogens in human gut microbiota. <i>Anaerobe</i> , 2015, 34, 50-52.	1.0	10
15	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
16	Archaea and the human gut: New beginning of an old story. <i>World Journal of Gastroenterology</i> , 2014, 20, 16062.	1.4	308
17	PhylOPDb: a 16S rRNA oligonucleotide probe database for prokaryotic identification. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau036-bau036.	1.4	18
18	Three-stage continuous culture system with a self-generated anaerobia to study the regionalized metabolism of the human gut microbiota. <i>Journal of Microbiological Methods</i> , 2014, 96, 111-118.	0.7	32

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19	Archaeobiotics. Gut Microbes, 2014, 5, 5-10.	4.3	201
20	Comparative genomics highlights the unique biology of Methanomassiliicoccales, a Thermoplasmatales-related seventh order of methanogenic archaea that encodes pyrrolysine. BMC Genomics, 2014, 15, 679.	1.2	246
21	Design and Validation of a Colorimetric Test for the Genetic Diagnosis of Hemochromatosis Using $\hat{\pm}$ -Phosphorothioate Nucleotides. Biochemical Genetics, 2013, 51, 635-643.	0.8	0
22	Genome Sequence of <i>Candidatus</i> Methanomassiliicoccus intestinalis <sup>Issoire-Mx1</sup> , a Third Thermoplasmatales-Related Methanogenic Archaeon from Human Feces. Genome Announcements, 2013, 1, .	0.8	85
23	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.	1.1	249
24	The Human Gut Chip <i>HuGChip</i> , an Explorative Phylogenetic Microarray for Determining Gut Microbiome Diversity at Family Level. PLoS ONE, 2013, 8, e62544.	1.1	46
25	Genome Sequence of <i>Candidatus</i> Methanomethylophilus alvus <sup>Mx1201</sup> , a Methanogenic Archaeon from the Human Gut Belonging to a Seventh Order of Methanogens. Journal of Bacteriology, 2012, 194, 6944-6945.	1.0	155
26	In vitro maintenance of a human proximal colon microbiota using the continuous fermentation system P-ECSIM. Applied Microbiology and Biotechnology, 2011, 91, 1425-1433.	1.7	31
27	Molecular evaluation of the human gut methanogenic archaeal microbiota reveals an age-associated increase of the diversity. Environmental Microbiology Reports, 2010, 2, 272-280.	1.0	121
28	Tools for stools: the challenge of assessing human intestinal microbiota using molecular diagnostics. Expert Review of Molecular Diagnostics, 2009, 9, 353-365.	1.5	27
29	Single-tube genotyping using a solid-phase method that combines $\hat{\pm}$ -phosphorothioate-mediated primer extension and ExoIII: Proof of concept with the F508del cystic fibrosis diagnosis. Molecular and Cellular Probes, 2008, 22, 320-323.	0.9	4
30	A putative new order of methanogenic Archaea inhabiting the human gut, as revealed by molecular analyses of the mcrA gene. Research in Microbiology, 2008, 159, 516-521.	1.0	94
31	Characterisation and expression of phospholipases B from the opportunistic fungus <i>Aspergillus fumigatus</i> . FEMS Microbiology Letters, 2004, 239, 87-93.	0.7	53
32	In vitro susceptibility of <i>Aspergillus</i> spp. clinical isolates to albendazole. Journal of Antimicrobial Chemotherapy, 2003, 51, 1419-1422.	1.3	5
33	Inter-Strain Variability of Insertion/Deletion Events in the <i>Encephalitozoon cuniculi</i> Genome: A Comparative KARD-PFGE Analysis. Journal of Eukaryotic Microbiology, 2001, 48, 50s-55s.	0.8	5
34	Occurrence of subtelomeric rearrangements in the genome of the microsporidian parasite <i>Encephalitozoon cuniculi</i> , as revealed by a new fingerprinting procedure based on two-dimensional pulsed field gel electrophoresis. Electrophoresis, 2000, 21, 2576-2581.	1.3	23
35	<i>Encephalitozoon cuniculi</i> (Microspora) genome: physical map and evidence for telomere-associated rDNA units on all chromosomes. Nucleic Acids Research, 2000, 28, 2026-2033.	6.5	56
36	In-gel DNA radiolabelling and two-dimensional pulsed field gel electrophoresis procedures suitable for fingerprinting and mapping small eukaryotic genomes. Nucleic Acids Research, 2000, 28, 48e-48.	6.5	42

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37	The ECSIM Concept (Environmental Control System for Intestinal Microbiota) and Its Derivative Versions to Help Better Understand Human Gut Biology. , 0, , .		4
38	Archaeobiotics: Archaea as Pharmabiotics for Treating Chronic Disease in Humans?. , 0, , .		5
39	A Comprehensive Analysis of the Global Human Gut Archaeome from a Thousand Genome Catalogue. SSRN Electronic Journal, 0, , .	0.4	0