

# CÃ©line Brochier-Armanet

## List of Publications by Year in descending order

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Version: 2024-02-01

109  
papers

7,430  
citations

66343

42  
h-index

60623

81  
g-index

114  
all docs

114  
docs citations

114  
times ranked

8341  
citing authors

#	ARTICLE	IF	CITATIONS
1	A divide-and-conquer phylogenomic approach based on character supermatrices resolves early steps in the evolution of the Archaea. <i>Bmc Ecology and Evolution</i> , 2022, 22, 1.	1.6	32
2	Structural and functional analysis of the <i>Francisella</i> lysine decarboxylase as a key actor in oxidative stress resistance. <i>Scientific Reports</i> , 2021, 11, 972.	3.3	9
3	A Comprehensive Evolutionary Scenario of Cell Division and Associated Processes in the Firmicutes. <i>Molecular Biology and Evolution</i> , 2021, 38, 2396-2412.	8.9	4
4	Plant genera <i>Cannabis</i> and <i>Humulus</i> share the same pair of well-differentiated sex chromosomes. <i>New Phytologist</i> , 2021, 231, 1599-1611.	7.3	17
5	Phylogenetics and biochemistry elucidate the evolutionary link between l-malate and l-lactate dehydrogenases and disclose an intermediate group of sequences with mix functional properties. <i>Biochimie</i> , 2021, 191, 140-153.	2.6	7
6	The Molecular Determinants of Thermoadaptation: <i>Methanococcales</i> as a Case Study. <i>Molecular Biology and Evolution</i> , 2021, 38, 1761-1776.	8.9	14
7	Evolutionary relationships between Archaea and eukaryotes. <i>Nature Ecology and Evolution</i> , 2020, 4, 20-21.	7.8	11
8	Hepatitis B virus preS2 <sup>1</sup> 38 <sup>â€</sup> 55 variants: A newly identified risk factor for hepatocellular carcinoma. <i>JHEP Reports</i> , 2020, 2, 100144.	4.9	21
9	The TERB1-TERB2-MAJIN complex of mouse meiotic telomeres dates back to the common ancestor of metazoans. <i>BMC Evolutionary Biology</i> , 2020, 20, 55.	3.2	16
10	<i>Dickeya poaceiphila</i> sp. nov., a plant-pathogenic bacterium isolated from sugar cane ( <i>Saccharum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.7	30
11	GeneSpy, a user-friendly and flexible genomic context visualizer. <i>Bioinformatics</i> , 2019, 35, 329-331.	4.1	33
12	Taxonomic assignment of uncultured prokaryotes with long range PCR targeting the spectinomycin operon. <i>Research in Microbiology</i> , 2019, 170, 280-287.	2.1	2
13	Structure, Function, and Evolution of the <i>Pseudomonas aeruginosa</i> Lysine Decarboxylase LdcA. <i>Structure</i> , 2019, 27, 1842-1854.e4.	3.3	9
14	The bacterial MrpORP is a novel Mrp/NBP35 protein involved in iron-sulfur biogenesis. <i>Scientific Reports</i> , 2019, 9, 712.	3.3	7
15	<i>Francisella tularensis</i> : FupA mutation contributes to fluoroquinolone resistance by increasing vesicle secretion and biofilm formation. <i>Emerging Microbes and Infections</i> , 2019, 8, 808-822.	6.5	38
16	Comparative genomics and proteogenomics highlight key molecular players involved in <i>Frankia</i> sporulation. <i>Research in Microbiology</i> , 2019, 170, 202-213.	2.1	5
17	The phytopathogenic nature of <i>Dickeya aquatica</i> 174/2 and the dynamic early evolution of <i>Dickeya</i> pathogenicity. <i>Environmental Microbiology</i> , 2019, 21, 2809-2835.	3.8	32
18	Evolutionary placement of Methanonatronarchaea. <i>Nature Microbiology</i> , 2019, 4, 558-559.	13.3	24

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19	Draft genome sequences for three unisolated <i>Alnus</i> -infective <i>Frankia</i> Sp+ strains, AgTrS, AiOr and AvVan, the first sequenced <i>Frankia</i> strains able to sporulate <i>in-planta</i> . Journal of Genomics, 2019, 7, 50-55.	0.9	8
20	Extreme halophilic archaea derive from two distinct methanogen Class II lineages. Molecular Phylogenetics and Evolution, 2018, 127, 46-54.	2.7	52
21	Loss-of-Function Mutations in UNC45A Cause a Syndrome Associating Cholestasis, Diarrhea, Impaired Hearing, and Bone Fragility. American Journal of Human Genetics, 2018, 102, 364-374.	6.2	40
22	PASTA repeats of the protein kinase StkP interconnect cell constriction and separation of <i>Streptococcus pneumoniae</i> . Nature Microbiology, 2018, 3, 197-209.	13.3	63
23	Obligate sugar oxidation in <i>Mesotoga</i> spp., phylum <i>Thermotogae</i> , in the presence of either elemental sulfur or hydrogenotrophic sulfate reducers as electron acceptor. Environmental Microbiology, 2018, 20, 281-292.	3.8	28
24	A novel subfamily of bacterial AAT-fold basic amino acid decarboxylases and functional characterization of its first representative: <i>Pseudomonas aeruginosa</i> LdcA. Genome Biology and Evolution, 2018, 10, 3058-3075.	2.5	11
25	The Environmental <i>Acinetobacter baumannii</i> Isolate DSM30011 Reveals Clues into the Preantibiotic Era Genome Diversity, Virulence Potential, and Niche Range of a Predominant Nosocomial Pathogen. Genome Biology and Evolution, 2017, 9, 2292-2307.	2.5	61
26	The growing tree of Archaea: new perspectives on their diversity, evolution and ecology. ISME Journal, 2017, 11, 2407-2425.	9.8	320
27	IsoSel: Protein Isoform Selector for phylogenetic reconstructions. PLoS ONE, 2017, 12, e0174250.	2.5	7
28	RiboDB Database: A Comprehensive Resource for Prokaryotic Systematics. Molecular Biology and Evolution, 2016, 33, 2170-2172.	8.9	23
29	The changing view of eukaryogenesis – fossils, cells, lineages and how they all come together. Journal of Cell Science, 2016, 129, 3695-3703.	2.0	77
30	Cell division of <i>Streptococcus pneumoniae</i> : think positive!. Current Opinion in Microbiology, 2016, 34, 18-23.	5.1	23
31	Silencing of natural transformation by an RNA chaperone and a multitarget small RNA. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 8813-8818.	7.1	104
32	Transcriptional start site turnover in the evolution of bacterial paralogous genes – the <i>pelE</i> virulence genes in <i>Dickeya</i> . FEBS Journal, 2016, 283, 4192-4207.	4.7	15
33	Gene Acquisitions from Bacteria at the Origins of Major Archaeal Clades Are Vastly Overestimated. Molecular Biology and Evolution, 2016, 33, 305-310.	8.9	37
34	Novel genomic island modifies DNA with 7-deazaguanine derivatives. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1452-9.	7.1	99
35	Evolutionary history of the mammalian synaptonemal complex. Chromosoma, 2016, 125, 355-360.	2.2	36
36	Phylogenomic analysis supports the ancestral presence of LPS-outer membranes in the Firmicutes. ELife, 2016, 5, .	6.0	69

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37	Evolutionary history of phosphatidylinositol- 3-kinases: ancestral origin in eukaryotes and complex duplication patterns. <i>BMC Evolutionary Biology</i> , 2015, 15, 226.	3.2	16
38	Genome-wide survey of two-component signal transduction systems in the plant growth-promoting bacterium <i>Azospirillum</i> . <i>BMC Genomics</i> , 2015, 16, 833.	2.8	13
39	Draft genome sequence of <i>Mesotoga</i> strain PhosAC3, a mesophilic member of the bacterial order Thermotogales, isolated from a digester treating phosphogypsum in Tunisia. <i>Standards in Genomic Sciences</i> , 2015, 10, 12.	1.5	8
40	Evolution and Design Governing Signal Precision and Amplification in a Bacterial Chemosensory Pathway. <i>PLoS Genetics</i> , 2015, 11, e1005460.	3.5	33
41	Extending the Conserved Phylogenetic Core of Archaea Disentangles the Evolution of the Third Domain of Life. <i>Molecular Biology and Evolution</i> , 2015, 32, 1242-1254.	8.9	59
42	Constitutive arsenite oxidase expression detected in arsenic-hypertolerant <i>Pseudomonas xanthomarina</i> S11. <i>Research in Microbiology</i> , 2015, 166, 205-214.	2.1	31
43	An evolutionary link between capsular biogenesis and surface motility in bacteria. <i>Nature Reviews Microbiology</i> , 2015, 13, 318-326.	28.6	16
44	The two-domain tree of life is linked to a new root for the Archaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6670-6675.	7.1	234
45	Taxonomy and Phylogeny of Prokaryotes. , 2015, , 145-190.		6
46	Protein SYCP2 Is an Ancient Component of the Metazoan Synaptonemal Complex. <i>Cytogenetic and Genome Research</i> , 2015, 144, 299-305.	1.1	11
47	For Three Billion Years, Microorganisms Were the Only Inhabitants of the Earth. , 2015, , 75-106.		6
48	Adaptation in Toxic Environments: Arsenic Genomic Islands in the Bacterial Genus <i>Thiomonas</i> . <i>PLoS ONE</i> , 2015, 10, e0139011.	2.5	24
49	Evolution of <i>Helicobacter</i> : Acquisition by Gastric Species of Two Histidine-Rich Proteins Essential for Colonization. <i>PLoS Pathogens</i> , 2015, 11, e1005312.	4.7	40
50	Global Phylogenomic Analysis Disentangles the Complex Evolutionary History of DNA Replication in Archaea. <i>Genome Biology and Evolution</i> , 2014, 6, 192-212.	2.5	68
51	Phylogenomic Test of the Hypotheses for the Evolutionary Origin of Eukaryotes. <i>Molecular Biology and Evolution</i> , 2014, 31, 832-845.	8.9	69
52	<i>Halomonas olivaria</i> sp. nov., a moderately halophilic bacterium isolated from olive-processing effluents. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 46-54.	1.7	22
53	Ribosomal proteins: Toward a next generation standard for prokaryotic systematics?. <i>Molecular Phylogenetics and Evolution</i> , 2014, 75, 103-117.	2.7	30
54	Plant, Animal, and Fungal Micronutrient Queuosine Is Salvaged by Members of the DUF2419 Protein Family. <i>ACS Chemical Biology</i> , 2014, 9, 1812-1825.	3.4	48

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55	Promiscuous Nickel Import in Human Pathogens: Structure, Thermodynamics, and Evolution of Extracytoplasmic Nickel-Binding Proteins. <i>Structure</i> , 2014, 22, 1421-1432.	3.3	38
56	Anaerobic oxidation of long-chain <i>n</i> -alkanes by the hyperthermophilic sulfate-reducing archaeon, <i>Archaeoglobus fulgidus</i> . <i>ISME Journal</i> , 2014, 8, 2153-2166.	9.8	88
57	Phylogenies of Central Element Proteins Reveal the Dynamic Evolutionary History of the Mammalian Synaptonemal Complex: Ancient and Recent Components. <i>Genetics</i> , 2013, 195, 781-793.	2.9	20
58	Metagenomics of Kamchatkan hot spring filaments reveal two new major (hyper)thermophilic lineages related to Thaumarchaeota. <i>Research in Microbiology</i> , 2013, 164, 425-438.	2.1	46
59	<i>Mesotoga infera</i> sp. nov., a mesophilic member of the order Thermotogales, isolated from an underground gas storage aquifer. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 3003-3008.	1.7	52
60	Life in an Arsenic-Containing Gold Mine: Genome and Physiology of the Autotrophic Arsenite-Oxidizing Bacterium <i>Rhizobium</i> sp. NT-26. <i>Genome Biology and Evolution</i> , 2013, 5, 934-953.	2.5	60
61	Molecular organization, biochemical function, cellular role and evolution of NfuA, an atypical Fe <sup>2+</sup> carrier. <i>Molecular Microbiology</i> , 2012, 86, 155-171.	2.5	80
62	Time for order in microbial systematics. <i>Trends in Microbiology</i> , 2012, 20, 209-210.	7.7	27
63	Comparative genomic analysis of the DUF71/COG2102 family predicts roles in diphthamide biosynthesis and B12 salvage. <i>Biology Direct</i> , 2012, 7, 32.	4.6	19
64	<i>De novo</i> metagenomic assembly reveals abundant novel major lineage of Archaea in hypersaline microbial communities. <i>ISME Journal</i> , 2012, 6, 81-93.	9.8	347
65	Horizontal gene transfer of a chloroplast DnaJ-Fer protein to Thaumarchaeota and the evolutionary history of the DnaK chaperone system in Archaea. <i>BMC Evolutionary Biology</i> , 2012, 12, 226.	3.2	34
66	Minimal cell: the biologist's point of view. , 2011, , 26-46.		0
67	Phylogenetic and genetic variation among Fe(II)-oxidizing acidithiobacilli supports the view that these comprise multiple species with different ferrous iron oxidation pathways. <i>Microbiology (United Kingdom)</i> 151:1414-1424. doi:10.1099/mic/0/000000.0	1.0	14
68	Emergence and Modular Evolution of a Novel Motility Machinery in Bacteria. <i>PLoS Genetics</i> , 2011, 7, e1002268.	3.5	77
69	Genome sequence of the stramenopile <i>Blastocystis</i> , a human anaerobic parasite. <i>Genome Biology</i> , 2011, 12, R29.	9.6	159
70	Phylogeny and evolution of the Archaea: one hundred genomes later. <i>Current Opinion in Microbiology</i> , 2011, 14, 274-281.	5.1	215
71	On the last common ancestor and early evolution of eukaryotes: reconstructing the history of mitochondrial ribosomes. <i>Research in Microbiology</i> , 2011, 162, 53-70.	2.1	85
72	Editorial: Archaea and the Tree of Life. <i>Research in Microbiology</i> , 2011, 162, 1-4.	2.1	8

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73	A New Highly Conserved Antibiotic Sensing/Resistance Pathway in Firmicutes Involves an ABC Transporter Interplaying with a Signal Transduction System. <i>PLoS ONE</i> , 2011, 6, e15951.	2.5	28
74	An oxygen reduction chain in the hyperthermophilic anaerobe <i>Thermotoga maritima</i> highlights horizontal gene transfer between <i>Thermococcales</i> and <i>Thermotogales</i> . <i>Environmental Microbiology</i> , 2011, 13, 2132-2145.	3.8	25
75	A eukaryotic-like sulfiredoxin involved in oxidative stress responses and in the reduction of the sulfenic form of 2-Cys peroxiredoxin in the cyanobacterium <i>Anabaena</i> PCC 7120. <i>New Phytologist</i> , 2011, 191, 1108-1118.	7.3	26
76	Complete-fosmid and fosmid-end sequences reveal frequent horizontal gene transfers in marine uncultured planktonic archaea. <i>ISME Journal</i> , 2011, 5, 1291-1302.	9.8	55
77	Cultivation of the first mesophilic representative ( <i>Thermotoga</i> ) within the order Thermotogales. <i>Systematic and Applied Microbiology</i> , 2011, 34, 581-585.	2.8	51
78	The phylogenomic analysis of the anaphase promoting complex and its targets points to complex and modern-like control of the cell cycle in the last common ancestor of eukaryotes. <i>BMC Evolutionary Biology</i> , 2011, 11, 265.	3.2	33
79	Survival of extremely and moderately halophilic isolates of Tunisian solar salterns after UV-B or oxidative stress. <i>Canadian Journal of Microbiology</i> , 2011, 57, 923-933.	1.7	13
80	Characterization of heterotrophic prokaryote subgroups in the Sfax coastal solar salterns by combining flow cytometry cell sorting and phylogenetic analysis. <i>Extremophiles</i> , 2011, 15, 347-358.	2.3	40
81	Characteristics of a phylogenetically ambiguous, arsenic-oxidizing <i>Thiomonas</i> sp., <i>Thiomonas arsenitoxydans</i> strain 3AsT sp. nov. <i>Archives of Microbiology</i> , 2011, 193, 439-449.	2.2	38
82	Specificity shifts in the rRNA and tRNA nucleotide targets of archaeal and bacterial m <sup>5</sup> U methyltransferases. <i>Rna</i> , 2011, 17, 45-53.	3.5	31
83	Characterization of <i>Halorubrum sfaxense</i> sp. nov., a New Halophilic Archaeon Isolated from the Solar Saltern of Sfax in Tunisia. <i>International Journal of Microbiology</i> , 2011, 2011, 1-8.	2.3	13
84	The GTPase Function of YvcJ and Its Subcellular Relocalization Are Dependent on Growth Conditions in <i>Bacillus subtilis</i> . <i>Journal of Molecular Microbiology and Biotechnology</i> , 2011, 20, 156-167.	1.0	10
85	Unsuspected Diversity of Arsenite-Oxidizing Bacteria as Revealed by Widespread Distribution of the <i>aoxB</i> Gene in Prokaryotes. <i>Applied and Environmental Microbiology</i> , 2011, 77, 4685-4692.	3.1	84
86	The Assembly Mode of the Pseudopilus. <i>Journal of Biological Chemistry</i> , 2011, 286, 24407-24416.	3.4	19
87	The origin of eukaryotes and their relationship with the Archaea: are we at a phylogenomic impasse?. <i>Nature Reviews Microbiology</i> , 2010, 8, 743-752.	28.6	140
88	The <i>Pseudomonas aeruginosa</i> patatin-like protein PlpD is the archetype of a novel Type V secretion system. <i>Environmental Microbiology</i> , 2010, 12, 1498-1512.	3.8	84
89	Biosynthesis of Wyosine Derivatives in tRNA: An Ancient and Highly Diverse Pathway in Archaea. <i>Molecular Biology and Evolution</i> , 2010, 27, 2062-2077.	8.9	71
90	Structure, Function, and Evolution of the <i>Thiomonas</i> spp. Genome. <i>PLoS Genetics</i> , 2010, 6, e1000859.	3.5	123

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91	Distinct gene set in two different lineages of ammonia-oxidizing archaea supports the phylum Thaumarchaeota. <i>Trends in Microbiology</i> , 2010, 18, 331-340.	7.7	431
92	Qri7/OSGEPL, the mitochondrial version of the universal Kae1/YgjD protein, is essential for mitochondrial genome maintenance. <i>Nucleic Acids Research</i> , 2009, 37, 5343-5352.	14.5	55
93	Evolution of the haem copper oxidases superfamily: a rooting tale. <i>Trends in Biochemical Sciences</i> , 2009, 34, 375-381.	7.5	47
94	Comparison of alignment free string distances for complete genome phylogeny. <i>Advances in Data Analysis and Classification</i> , 2009, 3, 95-108.	1.4	18
95	Happy together: genomic insights into the unique Nanoarchaeum/Ignicoccus association. <i>Journal of Biology</i> , 2009, 8, 7.	2.7	27
96	Iron-Sulfur (Fe/S) Protein Biogenesis: Phylogenomic and Genetic Studies of A-Type Carriers. <i>PLoS Genetics</i> , 2009, 5, e1000497.	3.5	166
97	The Multiple Evolutionary Histories of Dioxygen Reductases: Implications for the Origin and Evolution of Aerobic Respiration. <i>Molecular Biology and Evolution</i> , 2009, 26, 285-297.	8.9	93
98	A Complex Cell Division Machinery Was Present in the Last Common Ancestor of Eukaryotes. <i>PLoS ONE</i> , 2009, 4, e5021.	2.5	21
99	Acquisition of a bacterial RumA-type tRNA(uracil <sup>54</sup> , C5)-methyltransferase by Archaea through an ancient horizontal gene transfer. <i>Molecular Microbiology</i> , 2008, 67, 323-335.	2.5	45
100	Mesophilic crenarchaeota: proposal for a third archaeal phylum, the Thaumarchaeota. <i>Nature Reviews Microbiology</i> , 2008, 6, 245-252.	28.6	1,043
101	Giant viruses, giant chimeras: The multiple evolutionary histories of Mimivirus genes. <i>BMC Evolutionary Biology</i> , 2008, 8, 12.	3.2	223
102	A DNA topoisomerase IB in Thaumarchaeota testifies for the presence of this enzyme in the last common ancestor of Archaea and Eucarya. <i>Biology Direct</i> , 2008, 3, 54.	4.6	55
103	A korarchaeal genome reveals insights into the evolution of the Archaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8102-8107.	7.1	253
104	In Vitro Detection of the Enzymatic Activity of Folate-Dependent tRNA (Uracil <sup>54</sup> , C5)-Methyltransferase: Evolutionary Implications. <i>Methods in Enzymology</i> , 2007, 425, 103-119.	1.0	24
105	Phylogenomics of the archaeal flagellum: rare horizontal gene transfer in a unique motility structure. <i>BMC Evolutionary Biology</i> , 2007, 7, 106.	3.2	47
106	Comparative RNomics and Modomics in Mollicutes: Prediction of Gene Function and Evolutionary Implications. <i>IUBMB Life</i> , 2007, 59, 634-658.	3.4	76
107	Widespread distribution of archaeal reverse gyrase in thermophilic bacteria suggests a complex history of vertical inheritance and lateral gene transfers. <i>Archaea</i> , 2006, 2, 83-93.	2.3	85
108	The origin and evolution of Archaea: a state of the art. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 1007-1022.	4.0	222

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109	Natural History of the Archaeal Domain. , 0, , 17-28.		3