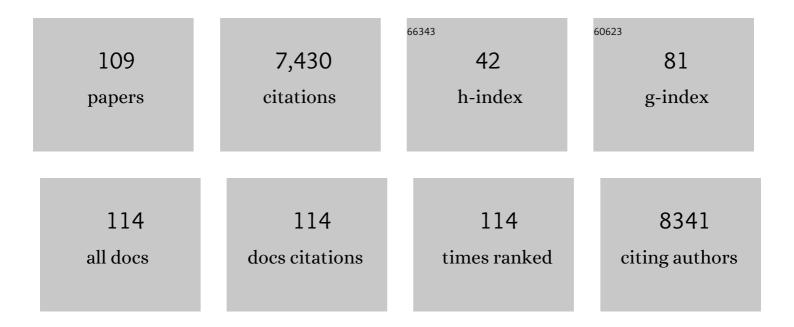
Céline Brochier-Armanet

List of Publications by Year in descending order

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| # | Article | IF | CITATIONS |
|----|---|--------------------------------|---------------|
| 1 | Mesophilic crenarchaeota: proposal for a third archaeal phylum, the Thaumarchaeota. Nature Reviews Microbiology, 2008, 6, 245-252. | 28.6 | 1,043 |
| 2 | Distinct gene set in two different lineages of ammonia-oxidizing archaea supports the phylum Thaumarchaeota. Trends in Microbiology, 2010, 18, 331-340. | 7.7 | 431 |
| 3 | <i>De novo</i> metagenomic assembly reveals abundant novel major lineage of Archaea in hypersaline microbial communities. ISME Journal, 2012, 6, 81-93. | 9.8 | 347 |
| 4 | The growing tree of Archaea: new perspectives on their diversity, evolution and ecology. ISME Journal, 2017, 11, 2407-2425. | 9.8 | 320 |
| 5 | A korarchaeal genome reveals insights into the evolution of the Archaea. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8102-8107. | 7.1 | 253 |
| 6 | The two-domain tree of life is linked to a new root for the Archaea. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6670-6675. | 7.1 | 234 |
| 7 | Giant viruses, giant chimeras: The multiple evolutionary histories of Mimivirus genes. BMC Evolutionary Biology, 2008, 8, 12. | 3.2 | 223 |
| 8 | The origin and evolution of Archaea: a state of the art. Philosophical Transactions of the Royal Society B: Biological Sciences, 2006, 361, 1007-1022. | 4.0 | 222 |
| 9 | Phylogeny and evolution of the Archaea: one hundred genomes later. Current Opinion in Microbiology, 2011, 14, 274-281. | 5.1 | 215 |
| 10 | Iron-Sulfur (Fe/S) Protein Biogenesis: Phylogenomic and Genetic Studies of A-Type Carriers. PLoS Genetics, 2009, 5, e1000497. | 3.5 | 166 |
| 11 | Genome sequence of the stramenopile Blastocystis, a human anaerobic parasite. Genome Biology, 2011, 12, R29. | 9.6 | 159 |
| 12 | The origin of eukaryotes and their relationship with the Archaea: are we at a phylogenomic impasse?. Nature Reviews Microbiology, 2010, 8, 743-752. | 28.6 | 140 |
| 13 | Structure, Function, and Evolution of the Thiomonas spp. Genome. PLoS Genetics, 2010, 6, e1000859. | 3.5 | 123 |
| 14 | Silencing of natural transformation by an RNA chaperone and a multitarget small RNA. Proceedings of the United States of America, 2016, 113, 8813-8818. | 7.1 | 104 |
| 15 | Phylogenetic and genetic variation among Fe(II)-oxidizing acidithiobacilli supports the view that these comprise multiple species with different ferrous iron oxidation pathways. Microbiology (United) Tj ETQq1 1 0.78 | 43 1.8 rgB T | ⊺/Quoarlock] |
| 16 | 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 |
| 17 | The Multiple Evolutionary Histories of Dioxygen Reductases: Implications for the Origin and Evolution of Aerobic Respiration. Molecular Biology and Evolution, 2009, 26, 285-297. | 8.9 | 93 |
| 18 | Anaerobic oxidation of long-chain <i>n</i> -alkanes by the hyperthermophilic sulfate-reducing archaeon, <i>Archaeoglobus fulgidus</i> . ISME Journal, 2014, 8, 2153-2166. | 9.8 | 88 |

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|----|--|------|-----------|
| 19 | Widespread distribution of archaeal reverse gyrase in thermophilic bacteria suggests a complex history of vertical inheritance and lateral gene transfers. Archaea, 2006, 2, 83-93. | 2.3 | 85 |
| 20 | On the last common ancestor and early evolution of eukaryotes: reconstructing the history of mitochondrial ribosomes. Research in Microbiology, 2011, 162, 53-70. | 2.1 | 85 |
| 21 | The <i>Pseudomonas aeruginosa</i> patatinâ€like protein PlpD is the archetype of a novel Type V secretion system. Environmental Microbiology, 2010, 12, 1498-1512. | 3.8 | 84 |
| 22 | Unsuspected Diversity of Arsenite-Oxidizing Bacteria as Revealed by Widespread Distribution of the <i>aoxB</i> Gene in Prokaryotes. Applied and Environmental Microbiology, 2011, 77, 4685-4692. | 3.1 | 84 |
| 23 | Molecular organization, biochemical function, cellular role and evolution of NfuA, an atypical Feâ€S carrier. Molecular Microbiology, 2012, 86, 155-171. | 2.5 | 80 |
| 24 | Emergence and Modular Evolution of a Novel Motility Machinery in Bacteria. PLoS Genetics, 2011, 7, e1002268. | 3.5 | 77 |
| 25 | 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 |
| 26 | Comparative RNomics and Modomics in Mollicutes: Prediction of Gene Function and Evolutionary Implications. IUBMB Life, 2007, 59, 634-658. | 3.4 | 76 |
| 27 | Biosynthesis of Wyosine Derivatives in tRNA: An Ancient and Highly Diverse Pathway in Archaea. Molecular Biology and Evolution, 2010, 27, 2062-2077. | 8.9 | 71 |
| 28 | Phylogenomic Test of the Hypotheses for the Evolutionary Origin of Eukaryotes. Molecular Biology and Evolution, 2014, 31, 832-845. | 8.9 | 69 |
| 29 | Phylogenomic analysis supports the ancestral presence of LPS-outer membranes in the Firmicutes. ELife, 2016, 5, . | 6.0 | 69 |
| 30 | Global Phylogenomic Analysis Disentangles the Complex Evolutionary History of DNA Replication in Archaea. Genome Biology and Evolution, 2014, 6, 192-212. | 2.5 | 68 |
| 31 | PASTA repeats of the protein kinase StkP interconnect cell constriction and separation of Streptococcus pneumoniae. Nature Microbiology, 2018, 3, 197-209. | 13.3 | 63 |
| 32 | The Environmental Acinetobacter baumannii 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 |
| 33 | Life in an Arsenic-Containing Gold Mine: Genome and Physiology of the Autotrophic Arsenite-Oxidizing Bacterium Rhizobium sp. NT-26. Genome Biology and Evolution, 2013, 5, 934-953. | 2.5 | 60 |
| 34 | Extending the Conserved Phylogenetic Core of Archaea Disentangles the Evolution of the Third Domain of Life. Molecular Biology and Evolution, 2015, 32, 1242-1254. | 8.9 | 59 |
| 35 | A DNA topoisomerase IB in Thaumarchaeota testifies for the presence of this enzyme in the last common ancestor of Archaea and Eucarya. Biology Direct, 2008, 3, 54. | 4.6 | 55 |
| 36 | Qri7/OSGEPL, the mitochondrial version of the universal Kae1/YgjD protein, is essential for mitochondrial genome maintenance. Nucleic Acids Research, 2009, 37, 5343-5352. | 14.5 | 55 |

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| 37 | Complete-fosmid and fosmid-end sequences reveal frequent horizontal gene transfers in marine uncultured planktonic archaea. ISME Journal, 2011, 5, 1291-1302. | 9.8 | 55 |
| 38 | Mesotoga infera sp. nov., a mesophilic member of the order Thermotogales , isolated from an underground gas storage aquifer. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 3003-3008. | 1.7 | 52 |
| 39 | Extreme halophilic archaea derive from two distinct methanogen Class II lineages. Molecular Phylogenetics and Evolution, 2018, 127, 46-54. | 2.7 | 52 |
| 40 | Cultivation of the first mesophilic representative ("mesotogaâ€) within the order Thermotogales. Systematic and Applied Microbiology, 2011, 34, 581-585. | 2.8 | 51 |
| 41 | Plant, Animal, and Fungal Micronutrient Queuosine Is Salvaged by Members of the DUF2419 Protein Family. ACS Chemical Biology, 2014, 9, 1812-1825. | 3.4 | 48 |
| 42 | Phylogenomics of the archaeal flagellum: rare horizontal gene transfer in a unique motility structure. BMC Evolutionary Biology, 2007, 7, 106. | 3.2 | 47 |
| 43 | Evolution of the haem copper oxidases superfamily: a rooting tale. Trends in Biochemical Sciences, 2009, 34, 375-381. | 7.5 | 47 |
| 44 | Metagenomics of Kamchatkan hot spring filaments reveal two new major (hyper)thermophilic lineages related to Thaumarchaeota. Research in Microbiology, 2013, 164, 425-438. | 2.1 | 46 |
| 45 | Acquisition of a bacterial RumAâ€type tRNA(uracilâ€54, C5)â€methyltransferase by Archaea through an ancient horizontal gene transfer. Molecular Microbiology, 2008, 67, 323-335. | 2.5 | 45 |
| 46 | Characterization of heterotrophic prokaryote subgroups in the Sfax coastal solar salterns by combining flow cytometry cell sorting and phylogenetic analysis. Extremophiles, 2011, 15, 347-358. | 2.3 | 40 |
| 47 | 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 |
| 48 | Evolution of Helicobacter: Acquisition by Gastric Species of Two Histidine-Rich Proteins Essential for Colonization. PLoS Pathogens, 2015, 11, e1005312. | 4.7 | 40 |
| 49 | Characteristics of a phylogenetically ambiguous, arsenic-oxidizing Thiomonas sp., Thiomonas arsenitoxydans strain 3AsT sp. nov. Archives of Microbiology, 2011, 193, 439-449. | 2.2 | 38 |
| 50 | Promiscuous Nickel Import in Human Pathogens: Structure, Thermodynamics, and Evolution of Extracytoplasmic Nickel-Binding Proteins. Structure, 2014, 22, 1421-1432. | 3.3 | 38 |
| 51 | <i>Francisella tularensis</i> : FupA mutation contributes to fluoroquinolone resistance by increasing vesicle secretion and biofilm formation. Emerging Microbes and Infections, 2019, 8, 808-822. | 6.5 | 38 |
| 52 | 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 |
| 53 | Evolutionary history of the mammalian synaptonemal complex. Chromosoma, 2016, 125, 355-360. | 2.2 | 36 |
| 54 | Horizontal gene transfer of a chloroplast DnaJ-Fer protein to Thaumarchaeota and the evolutionary history of the DnaK chaperone system in Archaea. BMC Evolutionary Biology, 2012, 12, 226. | 3.2 | 34 |

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| 55 | 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. BMC Evolutionary Biology, 2011, 11, 265. | 3.2 | 33 |
| 56 | Evolution and Design Governing Signal Precision and Amplification in a Bacterial Chemosensory Pathway. PLoS Genetics, 2015, 11, e1005460. | 3.5 | 33 |
| 57 | GeneSpy, a user-friendly and flexible genomic context visualizer. Bioinformatics, 2019, 35, 329-331. | 4.1 | 33 |
| 58 | The phytopathogenic nature of <i>Dickeya aquatica</i> 174/2 and the dynamic early evolution of <i>Dickeya</i> pathogenicity. Environmental Microbiology, 2019, 21, 2809-2835. | 3.8 | 32 |
| 59 | A divide-and-conquer phylogenomic approach based on character supermatrices resolves early steps in the evolution of the Archaea. Bmc Ecology and Evolution, 2022, 22, 1. | 1.6 | 32 |
| 60 | Specificity shifts in the rRNA and tRNA nucleotide targets of archaeal and bacterial m ⁵ U methyltransferases. Rna, 2011, 17, 45-53. | 3.5 | 31 |
| 61 | Constitutive arsenite oxidase expression detected in arsenic-hypertolerant Pseudomonas xanthomarina S11. Research in Microbiology, 2015, 166, 205-214. | 2.1 | 31 |
| 62 | Ribosomal proteins: Toward a next generation standard for prokaryotic systematics?. Molecular Phylogenetics and Evolution, 2014, 75, 103-117. | 2.7 | 30 |
| 63 | Dickeya poaceiphila sp. nov., a plant-pathogenic bacterium isolated from sugar cane (Saccharum) Tj ETQq1 1 0.78 | 34314 rgB 1.7 | T /Overlock |
| 64 | A New Highly Conserved Antibiotic Sensing/Resistance Pathway in Firmicutes Involves an ABC Transporter Interplaying with a Signal Transduction System. PLoS ONE, 2011, 6, e15951. | 2.5 | 28 |
| 65 | Obligate sugar oxidation in <i>Mesotoga</i> spp., phylum <i>Thermotogae</i> , in the presence of either elemental sulfur or hydrogenotrophic sulfateâ€reducers as electron acceptor. Environmental Microbiology, 2018, 20, 281-292. | 3.8 | 28 |
| 66 | Happy together: genomic insights into the unique Nanoarchaeum/Ignicoccus association. Journal of Biology, 2009, 8, 7. | 2.7 | 27 |
| 67 | Time for order in microbial systematics. Trends in Microbiology, 2012, 20, 209-210. | 7.7 | 27 |
| 68 | A eukaryoticâ€like sulfiredoxin involved in oxidative stress responses and in the reduction of the sulfinic form of 2â€Cys peroxiredoxin in the cyanobacterium <i>Anabaena</i> PCC 7120. New Phytologist, 2011, 191, 1108-1118. | 7.3 | 26 |
| 69 | An oxygen reduction chain in the hyperthermophilic anaerobe <i>Thermotoga maritima</i> highlights horizontal gene transfer between <i>Thermococcales</i> and <i>Thermotogales</i> . Environmental Microbiology, 2011, 13, 2132-2145. | 3.8 | 25 |
| 70 | In Vitro Detection of the Enzymatic Activity of Folateâ€Dependent tRNA (Uracilâ€54, 5)â€Methyltransferase: Evolutionary Implications. Methods in Enzymology, 2007, 425, 103-119. | 1.0 | 24 |
| 71 | Evolutionary placement of Methanonatronarchaeia. Nature Microbiology, 2019, 4, 558-559. | 13.3 | 24 |
| 72 | Adaptation in Toxic Environments: Arsenic Genomic Islands in the Bacterial Genus Thiomonas. PLoS ONE, 2015, 10, e0139011. | 2.5 | 24 |

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| 73 | RiboDB Database: A Comprehensive Resource for Prokaryotic Systematics. Molecular Biology and Evolution, 2016, 33, 2170-2172. | 8.9 | 23 |
| 74 | Cell division of Streptococcus pneumoniae: think positive!. Current Opinion in Microbiology, 2016, 34, 18-23. | 5.1 | 23 |
| 75 | Halomonas olivaria sp. nov., a moderately halophilic bacterium isolated from olive-processing effluents. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 46-54. | 1.7 | 22 |
| 76 | Hepatitis B virus preS2Δ38–55 variants: A newly identified risk factor for hepatocellular carcinoma. JHEP Reports, 2020, 2, 100144. | 4.9 | 21 |
| 77 | A Complex Cell Division Machinery Was Present in the Last Common Ancestor of Eukaryotes. PLoS ONE, 2009, 4, e5021. | 2.5 | 21 |
| 78 | Phylogenies of Central Element Proteins Reveal the Dynamic Evolutionary History of the Mammalian Synaptonemal Complex: Ancient and Recent Components. Genetics, 2013, 195, 781-793. | 2.9 | 20 |
| 79 | The Assembly Mode of the Pseudopilus. Journal of Biological Chemistry, 2011, 286, 24407-24416. | 3.4 | 19 |
| 80 | Comparative genomic analysis of the DUF71/COG2102 family predicts roles in diphthamide biosynthesis and B12 salvage. Biology Direct, 2012, 7, 32. | 4.6 | 19 |
| 81 | Comparison of alignment free string distances for complete genome phylogeny. Advances in Data Analysis and Classification, 2009, 3, 95-108. | 1.4 | 18 |
| 82 | Plant genera <i>Cannabis</i> and <i>Humulus</i> share the same pair of wellâ€differentiated sex chromosomes. New Phytologist, 2021, 231, 1599-1611. | 7.3 | 17 |
| 83 | Evolutionary history of phosphatidylinositol- 3-kinases: ancestral origin in eukaryotes and complex duplication patterns. BMC Evolutionary Biology, 2015, 15, 226. | 3.2 | 16 |
| 84 | An evolutionary link between capsular biogenesis and surface motility in bacteria. Nature Reviews Microbiology, 2015, 13, 318-326. | 28.6 | 16 |
| 85 | The TERB1-TERB2-MAJIN complex of mouse meiotic telomeres dates back to the common ancestor of metazoans. BMC Evolutionary Biology, 2020, 20, 55. | 3.2 | 16 |
| 86 | Transcriptional start site turnover in the evolution of bacterial paralogous genes – the <i>pelEâ€pelD</i> virulence genes in <i>Dickeya</i> . FEBS Journal, 2016, 283, 4192-4207. | 4.7 | 15 |
| 87 | The Molecular Determinants of Thermoadaptation: <i>Methanococcales</i> as a Case Study. Molecular Biology and Evolution, 2021, 38, 1761-1776. | 8.9 | 14 |
| 88 | Survival of extremely and moderately halophilic isolates of Tunisian solar salterns after UV-B or oxidative stress. Canadian Journal of Microbiology, 2011, 57, 923-933. | 1.7 | 13 |
| 89 | Characterization of <i>Halorubrum sfaxense</i> sp. nov., a New Halophilic Archaeon Isolated from the Solar Saltern of Sfax in Tunisia. International Journal of Microbiology, 2011, 2011, 1-8. | 2.3 | 13 |
| 90 | Genome-wide survey of two-component signal transduction systems in the plant growth-promoting bacterium Azospirillum. BMC Genomics, 2015, 16, 833. | 2.8 | 13 |

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| 91 | Protein SYCP2 Is an Ancient Component of the Metazoan Synaptonemal Complex. Cytogenetic and Genome Research, 2015, 144, 299-305. | 1.1 | 11 |
| 92 | A novel subfamily of bacterial AAT-fold basic amino acid decarboxylases and functional characterization of its first representative: Pseudomonas aeruginosa LdcA. Genome Biology and Evolution, 2018, 10, 3058-3075. | 2.5 | 11 |
| 93 | Evolutionary relationships between Archaea and eukaryotes. Nature Ecology and Evolution, 2020, 4, 20-21. | 7.8 | 11 |
| 94 | The GTPase Function of YvcJ and Its Subcellular Relocalization Are Dependent on Growth Conditions in Bacillus subtilis. Journal of Molecular Microbiology and Biotechnology, 2011, 20, 156-167. | 1.0 | 10 |
| 95 | Structure, Function, and Evolution of the Pseudomonas aeruginosa Lysine Decarboxylase LdcA. Structure, 2019, 27, 1842-1854.e4. | 3.3 | 9 |
| 96 | Structural and functional analysis of the Francisella lysine decarboxylase as a key actor in oxidative stress resistance. Scientific Reports, 2021, 11, 972. | 3.3 | 9 |
| 97 | Editorial: Archaea and the Tree of Life. Research in Microbiology, 2011, 162, 1-4. | 2.1 | 8 |
| 98 | Draft genome sequence of Mesotoga strain PhosAC3, a mesophilic member of the bacterial order Thermotogales, isolated from a digestor treating phosphogypsum in Tunisia. Standards in Genomic Sciences, 2015, 10, 12. | 1.5 | 8 |
| 99 | 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 |
| 100 | IsoSel: Protein Isoform Selector for phylogenetic reconstructions. PLoS ONE, 2017, 12, e0174250. | 2.5 | 7 |
| 101 | The bacterial MrpORP is a novel Mrp/NBP35 protein involved in iron-sulfur biogenesis. Scientific Reports, 2019, 9, 712. | 3.3 | 7 |
| 102 | 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. Biochimie, 2021, 191, 140-153. | 2.6 | 7 |
| 103 | Taxonomy and Phylogeny of Prokaryotes. , 2015, , 145-190. | | 6 |
| 104 | For Three Billion Years, Microorganisms Were the Only Inhabitants of the Earth. , 2015, , 75-106. | | 6 |
| 105 | Comparative genomics and proteogenomics highlight key molecular players involved in Frankia sporulation. Research in Microbiology, 2019, 170, 202-213. | 2.1 | 5 |
| 106 | A Comprehensive Evolutionary Scenario of Cell Division and Associated Processes in the Firmicutes. Molecular Biology and Evolution, 2021, 38, 2396-2412. | 8.9 | 4 |
| 107 | Natural History of the Archaeal Domain. , 0, , 17-28. | | 3 |
| 108 | Taxonomic assignment of uncultured prokaryotes with long range PCR targeting the spectinomycin operon. Research in Microbiology, 2019, 170, 280-287. | 2.1 | 2 |

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| 109 | Minimal cell: the biologist's point of view. , 2011, , 26-46. | | 0 |