

# Simonetta Gribaldo

## List of Publications by Year in descending order

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Version: 2024-02-01

101  
papers

9,717  
citations

44069

48  
h-index

40979

93  
g-index

117  
all docs

117  
docs citations

117  
times ranked

10751  
citing authors

#	ARTICLE	IF	CITATIONS
1	BMGE (Block Mapping and Gathering with Entropy): a new software for selection of phylogenetic informative regions from multiple sequence alignments. <i>BMC Evolutionary Biology</i> , 2010, 10, 210.	3.2	1,153
2	Mesophilic crenarchaeota: proposal for a third archaeal phylum, the Thaumarchaeota. <i>Nature Reviews Microbiology</i> , 2008, 6, 245-252.	28.6	1,043
3	The growing tree of Archaea: new perspectives on their diversity, evolution and ecology. <i>ISME Journal</i> , 2017, 11, 2407-2425.	9.8	320
4	Origin and evolution of DNA topoisomerases. <i>Biochimie</i> , 2007, 89, 427-446.	2.6	298
5	Ancient Phylogenetic Relationships. <i>Theoretical Population Biology</i> , 2002, 61, 391-408.	1.1	276
6	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
7	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
8	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
9	Phylogenomics of Sterol Synthesis: Insights into the Origin, Evolution, and Diversity of a Key Eukaryotic Feature. <i>Genome Biology and Evolution</i> , 2009, 1, 364-381.	2.5	229
10	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
11	Phylogeny and evolution of the Archaea: one hundred genomes later. <i>Current Opinion in Microbiology</i> , 2011, 14, 274-281.	5.1	215
12	Highly plastic genome of <i>Microcystis aeruginosa</i> PCC 7806, a ubiquitous toxic freshwater cyanobacterium. <i>BMC Genomics</i> , 2008, 9, 274.	2.8	210
13	Wide diversity of methane and short-chain alkane metabolisms in uncultured archaea. <i>Nature Microbiology</i> , 2019, 4, 603-613.	13.3	187
14	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
15	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
16	Genome Sequence of <i>Candidatus Methanomethylophilus alvus</i> 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
17	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
18	A horizontal gene transfer at the origin of phenylpropanoid metabolism: a key adaptation of plants to land. <i>Biology Direct</i> , 2009, 4, 7.	4.6	138

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19	Nanoarchaea: representatives of a novel archaeal phylum or a fast-evolving euryarchaeal lineage related to Thermococcales?. <i>Genome Biology</i> , 2005, 6, R42.	9.6	136
20	The host-associated archaeome. <i>Nature Reviews Microbiology</i> , 2020, 18, 622-636.	28.6	122
21	Biology of a widespread uncultivated archaeon that contributes to carbon fixation in the subsurface. <i>Nature Communications</i> , 2014, 5, 5497.	12.8	119
22	A hidden reservoir of integrative elements is the major source of recently acquired foreign genes and ORFans in archaeal and bacterial genomes. <i>Genome Biology</i> , 2009, 10, R65.	9.6	118
23	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994.	13.3	115
24	Archaeal phylogeny based on proteins of the transcription and translation machineries: tackling the <i>Methanopyrus kandleri</i> paradox. <i>Genome Biology</i> , 2004, 5, R17.	9.6	104
25	Large-Scale Phylogenomic Analyses Indicate a Deep Origin of Primary Plastids within Cyanobacteria. <i>Molecular Biology and Evolution</i> , 2011, 28, 3019-3032.	8.9	97
26	Discontinuous Occurrence of the <i>hsp70</i> ( <i>dnaK</i> ) Gene among Archaea and Sequence Features of HSP70 Suggest a Novel Outlook on Phylogenies Inferred from This Protein. <i>Journal of Bacteriology</i> , 1999, 181, 434-443.	2.2	97
27	The Root of the Universal Tree of Life Inferred from Anciently Duplicated Genes Encoding Components of the Protein-Targeting Machinery. <i>Journal of Molecular Evolution</i> , 1998, 47, 508-516.	1.8	96
28	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
29	Deciphering the role of the chitin synthase families 1 and 2 in the <i>in vivo</i> and <i>in vitro</i> growth of <i>Aspergillus fumigatus</i> by multiple gene targeting deletion. <i>Cellular Microbiology</i> , 2014, 16, 1784-1805.	2.1	90
30	An emerging phylogenetic core of Archaea: phylogenies of transcription and translation machineries converge following addition of new genome sequences. <i>BMC Evolutionary Biology</i> , 2005, 5, 36.	3.2	85
31	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
32	Genome Sequence of <i>Candidatus</i> <i>Methanomassiliicoccus intestinalis</i> -Issoire-Mx1, a Third <i>Thermoplasmatales</i> -Related Methanogenic Archaeon from Human Feces. <i>Genome Announcements</i> , 2013, 1, .	0.8	85
33	Diversity of virus-host systems in hypersaline Lake Retba, Senegal. <i>Environmental Microbiology</i> , 2011, 13, 1956-1972.	3.8	82
34	Comparative analyses of <i>Legionella</i> species identifies genetic features of strains causing Legionnaires™ disease. <i>Genome Biology</i> , 2014, 15, 505.	8.8	82
35	Eukaryotic Origins: How and When Was the Mitochondrion Acquired?. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a015990-a015990.	5.5	80
36	The changing view of eukaryogenesis – fossils, cells, lineages and how they all come together. <i>Journal of Cell Science</i> , 2016, 129, 3695-3703.	2.0	77

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37	Phylogenetic Depth of the Bacterial Genera Aquifex and Thermotoga Inferred from Analysis of Ribosomal Protein, Elongation Factor, and RNA Polymerase Subunit Sequences. <i>Journal of Molecular Evolution</i> , 2000, 50, 366-380.	1.8	75
38	A catalogue of 1,167 genomes from the human gut archaeome. <i>Nature Microbiology</i> , 2022, 7, 48-61.	13.3	72
39	One or two membranes? Diderm Firmicutes challenge the Gram <sup>+</sup> /Gram <sup>-</sup> divide. <i>Molecular Microbiology</i> , 2020, 113, 659-671.	2.5	71
40	Phylogenomic analysis supports the ancestral presence of LPS-outer membranes in the Firmicutes. <i>ELife</i> , 2016, 5, .	6.0	69
41	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
42	The Evolutionary History of Archaeal MCM Helicases: A Case Study of Vertical Evolution Combined with Hitchhiking of Mobile Genetic Elements. <i>Molecular Biology and Evolution</i> , 2010, 27, 2716-2732.	8.9	65
43	Comparative analyses of <i>Legionella</i> species identifies genetic features of strains causing Legionnaires' disease. <i>Genome Biology</i> , 2014, 15, 505.	9.6	62
44	Ribonucleotide reduction - horizontal transfer of a required function spans all three domains. <i>BMC Evolutionary Biology</i> , 2010, 10, 383.	3.2	61
45	Phylogeny of prokaryotes: does it exist and why should we care?. <i>Research in Microbiology</i> , 2009, 160, 513-521.	2.1	60
46	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
47	Crenarchaeal CdvA Forms Double-Helical Filaments Containing DNA and Interacts with ESCRT-III-Like CdvB. <i>PLoS ONE</i> , 2011, 6, e21921.	2.5	56
48	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
49	Outer Membrane Proteome of <i>Veillonella parvula</i> : A Diderm Firmicute of the Human Microbiome. <i>Frontiers in Microbiology</i> , 2017, 8, 1215.	3.5	55
50	The rise of diversity in metabolic platforms across the Candidate Phyla Radiation. <i>BMC Biology</i> , 2020, 18, 69.	3.8	54
51	Genome-wide analysis of the Firmicutes illuminates the diderm/monoderm transition. <i>Nature Ecology and Evolution</i> , 2020, 4, 1661-1672.	7.8	52
52	Taxonomic and functional prokaryote diversity in mildly arsenic-contaminated sediments. <i>Research in Microbiology</i> , 2011, 162, 877-887.	2.1	51
53	An archaeal origin of the Wood'land Ljungdahl H4MPT branch and the emergence of bacterial methylophily. <i>Nature Microbiology</i> , 2019, 4, 2155-2163.	13.3	51
54	Functional Divergence Prediction from Evolutionary Analysis: A Case Study of Vertebrate Hemoglobin. <i>Molecular Biology and Evolution</i> , 2003, 20, 1754-1759.	8.9	50

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55	A thaumarchaeal provirus testifies for an ancient association of tailed viruses with archaea. <i>Biochemical Society Transactions</i> , 2011, 39, 82-88.	3.4	50
56	The SUF system: an ABC ATPase-dependent protein complex with a role in Fe-S cluster biogenesis. <i>Research in Microbiology</i> , 2019, 170, 426-434.	2.1	49
57	Bacteria with a eukaryotic touch: A glimpse of ancient evolution?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 12739-12740.	7.1	48
58	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
59	Evolution of the haem copper oxidases superfamily: a rooting tale. <i>Trends in Biochemical Sciences</i> , 2009, 34, 375-381.	7.5	47
60	The origin of modern terrestrial life. <i>HFSP Journal</i> , 2007, 1, 156-168.	2.5	43
61	Evidence for a Xer/dif System for Chromosome Resolution in Archaea. <i>PLoS Genetics</i> , 2010, 6, e1001166.	3.5	43
62	Toward More Accurate Ancestral Protein Genotype-Phenotype Reconstructions with the Use of Species Tree-Aware Gene Trees. <i>Molecular Biology and Evolution</i> , 2015, 32, 13-22.	8.9	43
63	Genome-wide analyses of chitin synthases identify horizontal gene transfers towards bacteria and allow a robust and unifying classification into fungi. <i>BMC Evolutionary Biology</i> , 2016, 16, 252.	3.2	43
64	A third purine biosynthetic pathway encoded by aminoadenine-based viral DNA genomes. <i>Science</i> , 2021, 372, 516-520.	12.6	40
65	Heterotachy and Functional Shift in Protein Evolution. <i>IUBMB Life</i> , 2003, 55, 257-265.	3.4	38
66	Diversity and Evolution of Methane-Related Pathways in Archaea. <i>Annual Review of Microbiology</i> , 2022, 76, 727-755.	7.3	37
67	Factors shaping the abundance and diversity of the gut archaeome across the animal kingdom. <i>Nature Communications</i> , 2022, 13, .	12.8	36
68	Geographic Structuring of the Plasmodium falciparum Sarco(endo)plasmic Reticulum Ca <sup>2+</sup> ATPase (PF SERCA) Gene Diversity. <i>PLoS ONE</i> , 2010, 5, e9424.	2.5	35
69	SepF is the FtsZ anchor in archaea, with features of an ancestral cell division system. <i>Nature Communications</i> , 2021, 12, 3214.	12.8	35
70	Histone variants in archaea and the evolution of combinatorial chromatin complexity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 33384-33395.	7.1	34
71	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
72	S-layers at second glance? Altiarchaeal grappling hooks (hami) resemble archaeal S-layer proteins in structure and sequence. <i>Frontiers in Microbiology</i> , 2015, 6, 543.	3.5	31

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73	Identification, Purification, and Characterization of an Eukaryotic-like Phosphopantetheine Adenylyltransferase (Coenzyme A Biosynthetic Pathway) in the Hyperthermophilic Archaeon <i>Pyrococcus abyssi</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 31078-31087.	3.4	27
74	Happy together: genomic insights into the unique Nanoarchaeum/Ignicoccus association. <i>Journal of Biology</i> , 2009, 8, 7.	2.7	27
75	Time for order in microbial systematics. <i>Trends in Microbiology</i> , 2012, 20, 209-210.	7.7	27
76	An ancient divide in outer membrane tethering systems in bacteria suggests a mechanism for the diderm-to-monoderm transition. <i>Nature Microbiology</i> , 2022, 7, 411-422.	13.3	26
77	<i>Paenibacillus faecis</i> sp. nov., isolated from human faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 4621-4626.	1.7	25
78	The Flagellar Arginine Kinase in <i>Trypanosoma brucei</i> Is Important for Infection in Tsetse Flies. <i>PLoS ONE</i> , 2015, 10, e0133676.	2.5	25
79	Evolutionary placement of Methanonatronarchaeia. <i>Nature Microbiology</i> , 2019, 4, 558-559.	13.3	24
80	Transcriptional Analysis and Subcellular Protein Localization Reveal Specific Features of the Essential WalkR System in <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , 2016, 11, e0151449.	2.5	23
81	Autotransporters Drive Biofilm Formation and Autoaggregation in the Diderm Firmicute <i>Veillonella parvula</i> . <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	22
82	Spotlight on FtsZ-based cell division in Archaea. <i>Trends in Microbiology</i> , 2022, 30, 665-678.	7.7	22
83	An <i>rpoB</i> signature sequence provides unique resolution for the molecular typing of cyanobacteria. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 170-183.	1.7	21
84	A Genomic Survey of Reb Homologs Suggests Widespread Occurrence of R-Bodies in Proteobacteria. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 505-516.	1.8	20
85	The Evolution of Histidine Biosynthesis in Archaea: Insights into the his Genes Structure and Organization in LUCA. <i>Journal of Molecular Evolution</i> , 2009, 69, 512-526.	1.8	19
86	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
87	The genome reduction hypothesis and the phylogeny of eukaryotes. <i>Trends in Genetics</i> , 2003, 19, 696-700.	6.7	14
88	Phylogenetic and Functional Analysis of <i>Aspergillus fumigatus</i> MGTC, a Fungal Protein Homologous to a Bacterial Virulence Factor. <i>Applied and Environmental Microbiology</i> , 2011, 77, 4700-4703.	3.1	11
89	Evolutionary relationships between Archaea and eukaryotes. <i>Nature Ecology and Evolution</i> , 2020, 4, 20-21.	7.8	11
90	Cellular assays identify barriers impeding iron-sulfur enzyme activity in a non-native prokaryotic host. <i>ELife</i> , 2022, 11, .	6.0	9

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91	Updating Carbamoylphosphate Synthase (CPS) Phylogenies: Occurrence and Phylogenetic Identity of Archaeal CPS Genes. <i>Journal of Molecular Evolution</i> , 2002, 55, 153-160.	1.8	8
92	Editorial: Archaea and the Tree of Life. <i>Research in Microbiology</i> , 2011, 162, 1-4.	2.1	8
93	The <i>TET2</i> and <i>TET3</i> aminopeptidases from <i>Pyrococcus horikoshii</i> form a hetero-subunit peptidosome with enhanced peptide destruction properties. <i>Molecular Microbiology</i> , 2014, 94, 803-814.	2.5	8
94	Single-Stranded DNA-Binding Proteins in the. <i>Methods in Molecular Biology</i> , 2021, 2281, 23-47.	0.9	6
95	A dynamic, ring-forming MucB / RseB-like protein influences spore shape in <i>Bacillus subtilis</i> . <i>PLoS Genetics</i> , 2020, 16, e1009246.	3.5	5
96	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
97	Natural History of the Archaeal Domain. , 0, , 17-28.		3
98	Localization and functional characterization of the alternative oxidase in <i>Naegleria</i> . <i>Journal of Eukaryotic Microbiology</i> , 2022, 69, e12908.	1.7	3
99	Special section on Molecular biology of Archaea. <i>Biochimie</i> , 2015, 118, 253.	2.6	1
100	Structure and Evolution of Genomes. , 0, , 411-433.		0
101	A Comprehensive Analysis of the Global Human Gut Archaeome from a Thousand Genome Catalogue. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0