

Anja Spang

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

7,067
citations

159525

30
h-index

206029

48
g-index

59
all docs

59
docs citations

59
times ranked

6700
citing authors

#	ARTICLE	IF	CITATIONS
1	Origin of eukaryotes: What can be learned from the first successfully isolated Asgard archaeon. Faculty Reviews, 2022, 11, 3.	1.7	2
2	Evolving Perspective on the Origin and Diversification of Cellular Life and the Virosphere. Genome Biology and Evolution, 2022, 14, .	1.1	13
3	An estimate of the deepest branches of the tree of life from ancient vertically evolving genes. ELife, 2022, 11, .	2.8	43
4	The importance of biofilm formation for cultivation of a Micrarchaeon and its interactions with its Thermoplasmatales host. Nature Communications, 2022, 13, 1735.	5.8	12
5	A rooted phylogeny resolves early bacterial evolution. Science, 2021, 372, .	6.0	128
6	Undinarchaeota illuminate DPANN phylogeny and the impact of gene transfer on archaeal evolution. Nature Communications, 2020, 11, 3939.	5.8	102
7	Chlamydial contribution to anaerobic metabolism during eukaryotic evolution. Science Advances, 2020, 6, eabb7258.	4.7	18
8	Hikarchaeia demonstrate an intermediate stage in the methanogen-to-halophile transition. Nature Communications, 2020, 11, 5490.	5.8	39
9	Roadmap for naming uncultivated Archaea and Bacteria. Nature Microbiology, 2020, 5, 987-994.	5.9	115
10	Marine Sediments Illuminate Chlamydiae Diversity and Evolution. Current Biology, 2020, 30, 1032-1048.e7.	1.8	52
11	Complex subsurface hydrothermal fluid mixing at a submarine arc volcano supports distinct and highly diverse microbial communities. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 32627-32638.	3.3	36
12	Archaea – An Introduction. , 2019, , .		0
13	Asgard archaea capable of anaerobic hydrocarbon cycling. Nature Communications, 2019, 10, 1822.	5.8	165
14	An archaeal symbiont-host association from the deep terrestrial subsurface. ISME Journal, 2019, 13, 2135-2139.	4.4	39
15	Virus Genomes from Deep Sea Sediments Expand the Ocean Megavirome and Support Independent Origins of Viral Gigantism. MBio, 2019, 10, .	1.8	85
16	Proposal of the reverse flow model for the origin of the eukaryotic cell based on comparative analyses of Asgard archaeal metabolism. Nature Microbiology, 2019, 4, 1138-1148.	5.9	143
17	The Emergence of Life. Space Science Reviews, 2019, 215, 1.	3.7	53
18	Towards a systematic understanding of differences between archaeal and bacterial diversity. Environmental Microbiology Reports, 2019, 11, 9-12.	1.0	3

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19	Genomic diversity, lifestyles and evolutionary origins of DPANN archaea. <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	167
20	Symbiosis in the microbial world: from ecology to genome evolution. <i>Biology Open</i> , 2018, 7, .	0.6	34
21	Genome size evolution in the Archaea. <i>Emerging Topics in Life Sciences</i> , 2018, 2, 595-605.	1.1	23
22	Complex Evolutionary History of Translation Elongation Factor 2 and Diphthamide Biosynthesis in Archaea and Parabasalids. <i>Genome Biology and Evolution</i> , 2018, 10, 2380-2393.	1.1	37
23	Genomes of two archaeal endosymbionts show convergent adaptations to an intracellular lifestyle. <i>ISME Journal</i> , 2018, 12, 2655-2667.	4.4	26
24	Asgard archaea are the closest prokaryotic relatives of eukaryotes. <i>PLoS Genetics</i> , 2018, 14, e1007080.	1.5	114
25	Asgard archaea illuminate the origin of eukaryotic cellular complexity. <i>Nature</i> , 2017, 541, 353-358.	13.7	882
26	Integrative modeling of gene and genome evolution roots the archaeal tree of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4602-E4611.	3.3	232
27	Archaeal evolution: The methanogenic roots of Archaea. <i>Nature Microbiology</i> , 2017, 2, 17109.	5.9	13
28	Genomic exploration of the diversity, ecology, and evolution of the archaeal domain of life. <i>Science</i> , 2017, 357, .	6.0	247
29	Archaea and the origin of eukaryotes. <i>Nature Reviews Microbiology</i> , 2017, 15, 711-723.	13.6	388
30	Microbial diversity: The tree of life comes of age. <i>Nature Microbiology</i> , 2016, 1, 16056.	5.9	14
31	Tracing the Archaeal Origins of Eukaryotic Membrane-Trafficking System Building Blocks. <i>Molecular Biology and Evolution</i> , 2016, 33, 1528-1541.	3.5	77
32	Complex archaea that bridge the gap between prokaryotes and eukaryotes. <i>Nature</i> , 2015, 521, 173-179.	13.7	995
33	Exploring microbial dark matter to resolve the deep archaeal ancestry of eukaryotes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140328.	1.8	40
34	â€˜Geoarchaeote NAG1â€™™ is a deeply rooting lineage of the archaeal order Thermoproteales rather than a new phylum. <i>ISME Journal</i> , 2014, 8, 1353-1357.	4.4	19
35	Variability of the transporter gene complement in ammonia-oxidizing archaea. <i>Trends in Microbiology</i> , 2014, 22, 665-675.	3.5	81
36	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.	1.0	46

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37	Archaea in Biogeochemical Cycles. Annual Review of Microbiology, 2013, 67, 437-457.	2.9	393
38	Methylotrophic methanogenic Thermoplasmata implicated in reduced methane emissions from bovine rumen. Nature Communications, 2013, 4, 1428.	5.8	328
39	Close Encounters of the Third Domain: The Emerging Genomic View of Archaeal Diversity and Evolution. Archaea, 2013, 2013, 1-12.	2.3	24
40	The genome of the ammonia-oxidizing <i>Candidatus Nitrososphaera gargensis</i> : insights into metabolic versatility and environmental adaptations. Environmental Microbiology, 2012, 14, 3122-3145.	1.8	332
41	Metagenomic Analysis of Ammonia-Oxidizing Archaea Affiliated with the Soil Group. Frontiers in Microbiology, 2012, 3, 208.	1.5	41
42	A thaumarchaeal provirus testifies for an ancient association of tailed viruses with archaea. Biochemical Society Transactions, 2011, 39, 82-88.	1.6	50
43	<i>Nitrososphaera viennensis</i> , an ammonia oxidizing archaeon from soil. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 8420-8425.	3.3	810
44	A bacterial genome in transition - an exceptional enrichment of IS elements but lack of evidence for recent transposition in the symbiont <i>Amoebophilus asiaticus</i> . BMC Evolutionary Biology, 2011, 11, 270.	3.2	22
45	Genome Sequence of the Arctic Methanotroph <i>Methylobacter tundripaludum</i> SV96. Journal of Bacteriology, 2011, 193, 6418-6419.	1.0	78
46	Distinct gene set in two different lineages of ammonia-oxidizing archaea supports the phylum Thaumarchaeota. Trends in Microbiology, 2010, 18, 331-340.	3.5	431