

Anja Spang

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

7,067
citations

159585

30
h-index

206112

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.	3.9	2
2	Evolving Perspective on the Origin and Diversification of Cellular Life and the Virosphere. Genome Biology and Evolution, 2022, 14, .	2.5	13
3	An estimate of the deepest branches of the tree of life from ancient vertically evolving genes. ELife, 2022, 11, .	6.0	43
4	The importance of biofilm formation for cultivation of a Micrarchaeon and its interactions with its Thermoplasmatales host. Nature Communications, 2022, 13, 1735.	12.8	12
5	A rooted phylogeny resolves early bacterial evolution. Science, 2021, 372, .	12.6	128
6	Undinarchaeota illuminate DPANN phylogeny and the impact of gene transfer on archaeal evolution. Nature Communications, 2020, 11, 3939.	12.8	102
7	Chlamydial contribution to anaerobic metabolism during eukaryotic evolution. Science Advances, 2020, 6, eabb7258.	10.3	18
8	Hikarchaeia demonstrate an intermediate stage in the methanogen-to-halophile transition. Nature Communications, 2020, 11, 5490.	12.8	39
9	Roadmap for naming uncultivated Archaea and Bacteria. Nature Microbiology, 2020, 5, 987-994.	13.3	115
10	Marine Sediments Illuminate Chlamydiae Diversity and Evolution. Current Biology, 2020, 30, 1032-1048.e7.	3.9	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.	7.1	36
12	Archaea – An Introduction. , 2019, , .		0
13	Asgard archaea capable of anaerobic hydrocarbon cycling. Nature Communications, 2019, 10, 1822.	12.8	165
14	An archaeal symbiont-host association from the deep terrestrial subsurface. ISME Journal, 2019, 13, 2135-2139.	9.8	39
15	Virus Genomes from Deep Sea Sediments Expand the Ocean Megavirome and Support Independent Origins of Viral Gigantism. MBio, 2019, 10, .	4.1	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.	13.3	143
17	The Emergence of Life. Space Science Reviews, 2019, 215, 1.	8.1	53
18	Towards a systematic understanding of differences between archaeal and bacterial diversity. Environmental Microbiology Reports, 2019, 11, 9-12.	2.4	3

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19	Genomic diversity, lifestyles and evolutionary origins of DPANN archaea. <i>FEMS Microbiology Letters</i> , 2019, 366, .	1.8	167
20	Symbiosis in the microbial world: from ecology to genome evolution. <i>Biology Open</i> , 2018, 7, .	1.2	34
21	Genome size evolution in the Archaea. <i>Emerging Topics in Life Sciences</i> , 2018, 2, 595-605.	2.6	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.	2.5	37
23	Genomes of two archaeal endosymbionts show convergent adaptations to an intracellular lifestyle. <i>ISME Journal</i> , 2018, 12, 2655-2667.	9.8	26
24	Asgard archaea are the closest prokaryotic relatives of eukaryotes. <i>PLoS Genetics</i> , 2018, 14, e1007080.	3.5	114
25	Asgard archaea illuminate the origin of eukaryotic cellular complexity. <i>Nature</i> , 2017, 541, 353-358.	27.8	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.	7.1	232
27	Archaeal evolution: The methanogenic roots of Archaea. <i>Nature Microbiology</i> , 2017, 2, 17109.	13.3	13
28	Genomic exploration of the diversity, ecology, and evolution of the archaeal domain of life. <i>Science</i> , 2017, 357, .	12.6	247
29	Archaea and the origin of eukaryotes. <i>Nature Reviews Microbiology</i> , 2017, 15, 711-723.	28.6	388
30	Microbial diversity: The tree of life comes of age. <i>Nature Microbiology</i> , 2016, 1, 16056.	13.3	14
31	Tracing the Archaeal Origins of Eukaryotic Membrane-Trafficking System Building Blocks. <i>Molecular Biology and Evolution</i> , 2016, 33, 1528-1541.	8.9	77
32	Complex archaea that bridge the gap between prokaryotes and eukaryotes. <i>Nature</i> , 2015, 521, 173-179.	27.8	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.	4.0	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.	9.8	19
35	Variability of the transporter gene complement in ammonia-oxidizing archaea. <i>Trends in Microbiology</i> , 2014, 22, 665-675.	7.7	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.	2.1	46

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37	Archaea in Biogeochemical Cycles. Annual Review of Microbiology, 2013, 67, 437-457.	7.3	393
38	Methylotrophic methanogenic Thermoplasmata implicated in reduced methane emissions from bovine rumen. Nature Communications, 2013, 4, 1428.	12.8	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</i> Nitrososphaera gargensis: insights into metabolic versatility and environmental adaptations. Environmental Microbiology, 2012, 14, 3122-3145.	3.8	332
41	Metagenomic Analysis of Ammonia-Oxidizing Archaea Affiliated with the Soil Group. Frontiers in Microbiology, 2012, 3, 208.	3.5	41
42	A thaumarchaeal provirus testifies for an ancient association of tailed viruses with archaea. Biochemical Society Transactions, 2011, 39, 82-88.	3.4	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.	7.1	810
44	A bacterial genome in transition - an exceptional enrichment of IS elements but lack of evidence for recent transposition in the symbiont Amoebophilus asiaticus. BMC Evolutionary Biology, 2011, 11, 270.	3.2	22
45	Genome Sequence of the Arctic Methanotroph Methylobacter tundripaludum SV96. Journal of Bacteriology, 2011, 193, 6418-6419.	2.2	78
46	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