

Senthil K Murugapiran

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

1,084
citations

516681

16
h-index

610883

24
g-index

27
all docs

27
docs citations

27
times ranked

1542
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-cell and metagenomic analyses indicate a fermentative and saccharolytic lifestyle for members of the OP9 lineage. <i>Nature Communications</i> , 2013, 4, 1854.	12.8	199
2	Phylogeny and physiology of candidate phylum <i>~Atribacteria</i> TM (OP9/JJ1) inferred from cultivation-independent genomics. <i>ISME Journal</i> , 2016, 10, 273-286.	9.8	166
3	Impact of single-cell genomics and metagenomics on the emerging view of extremophile <i>~microbial dark matter</i> . <i>Extremophiles</i> , 2014, 18, 865-875.	2.3	133
4	<i>Thermoflexus hugenholtzii</i> gen. nov., sp. nov., a thermophilic, microaerophilic, filamentous bacterium representing a novel class in the Chloroflexi, <i>Thermoflexia</i> classis nov., and description of <i>Thermoflexaceae</i> fam. nov. and <i>Thermoflexales</i> ord. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 2119-2127.	1.7	90
5	Uncultivated thermophiles: current status and spotlight on <i>~Aigarchaeota</i> TM . <i>Current Opinion in Microbiology</i> , 2015, 25, 136-145.	5.1	70
6	Localized high abundance of Marine Group II archaea in the subtropical Pearl River Estuary: implications for their niche adaptation. <i>Environmental Microbiology</i> , 2018, 20, 734-754.	3.8	53
7	Temperature impacts community structure and function of phototrophic Chloroflexi and Cyanobacteria in two alkaline hot springs in Yellowstone National Park. <i>Environmental Microbiology Reports</i> , 2020, 12, 503-513.	2.4	52
8	Pyrosequencing Reveals High-Temperature Cellulolytic Microbial Consortia in Great Boiling Spring after In Situ Lignocellulose Enrichment. <i>PLoS ONE</i> , 2013, 8, e59927.	2.5	42
9	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
10	Single-Cell-Genomics-Facilitated Read Binning of Candidate Phylum EM19 Genomes from Geothermal Spring Metagenomes. <i>Applied and Environmental Microbiology</i> , 2016, 82, 992-1003.	3.1	36
11	<i>Thermus oshimai</i> JL-2 and <i>T. thermophilus</i> JL-18 genome analysis illuminates pathways for carbon, nitrogen, and sulfur cycling. <i>Standards in Genomic Sciences</i> , 2013, 7, 449-468.	1.5	31
12	Anoxygenic Phototrophs Span Geochemical Gradients and Diverse Morphologies in Terrestrial Geothermal Springs. <i>MSystems</i> , 2019, 4, .	3.8	24
13	Effect of the Synthetic Bile Salt Analog CamSA on the Hamster Model of <i>Clostridium difficile</i> Infection. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	23
14	<i>Thermus sediminis</i> sp. nov., a thiosulfate-oxidizing and arsenate-reducing organism isolated from Little Hot Creek in the Long Valley Caldera, California. <i>Extremophiles</i> , 2018, 22, 983-991.	2.3	20
15	Whole Genome Sequencing of <i>Thermus oshimai</i> JL-2 and <i>Thermus thermophilus</i> JL-18, Incomplete Denitrifiers from the United States Great Basin. <i>Genome Announcements</i> , 2013, 1, .	0.8	19
16	Genomic Comparison of Two Family-Level Groups of the Uncultivated NAG1 Archaeal Lineage from Chemically and Geographically Disparate Hot Springs. <i>Frontiers in Microbiology</i> , 2017, 8, 2082.	3.5	19
17	Diverse respiratory capacity among <i>Thermus</i> strains from US Great Basin hot springs. <i>Extremophiles</i> , 2020, 24, 71-80.	2.3	13
18	Position-Specific Metabolic Probing and Metagenomics of Microbial Communities Reveal Conserved Central Carbon Metabolic Network Activities at High Temperatures. <i>Frontiers in Microbiology</i> , 2019, 10, 1427.	3.5	12

#	ARTICLE	IF	CITATIONS
19	Recharge from glacial meltwater is critical for alpine springs and their microbiomes. Environmental Research Letters, 2021, 16, 064012.	5.2	8
20	Genomics, Exometabolomics, and Metabolic Probing Reveal Conserved Proteolytic Metabolism of Thermoflexus hugenholtzii and Three Candidate Species From China and Japan. Frontiers in Microbiology, 2021, 12, 632731.	3.5	8
21	High-quality draft genome sequence of the Thermus amyloliquefaciens type strain YIM 77409T with an incomplete denitrification pathway. Standards in Genomic Sciences, 2016, 11, 20.	1.5	7
22	Temperature and Geographic Location Impact the Distribution and Diversity of Photoautotrophic Gene Variants in Alkaline Yellowstone Hot Springs. Microbiology Spectrum, 2022, 10, e0146521.	3.0	7
23	High-Quality Draft Genomes from <i>Thermus caliditerrae</i> YIM 77777 and <i>T.Âtengchongensis</i> YIM 77401, Isolates from Tengchong, China. Genome Announcements, 2016, 4, .	0.8	5
24	High-Quality Draft Genome Sequence of Kallotenua papyrolyticum JKG1 T Reveals Broad Heterotrophic Capacity Focused on Carbohydrate and Amino Acid Metabolism. Genome Announcements, 2015, 3, .	0.8	4
25	High-Quality Draft Genome Sequence of Thermocrinis jamiesonii GBS1 ^T Isolated from Great Boiling Spring, Nevada. Genome Announcements, 2016, 4, .	0.8	0