

# Senthil K Murugapiran

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5723052/publications.pdf>

Version: 2024-02-01

25  
papers

1,084  
citations

586496

16  
h-index

685536

24  
g-index

27  
all docs

27  
docs citations

27  
times ranked

1767  
citing authors

#	ARTICLE	IF	CITATIONS
1	Temperature and Geographic Location Impact the Distribution and Diversity of Photoautotrophic Gene Variants in Alkaline Yellowstone Hot Springs. <i>Microbiology Spectrum</i> , 2022, 10, e0146521.	1.2	7
2	Recharge from glacial meltwater is critical for alpine springs and their microbiomes. <i>Environmental Research Letters</i> , 2021, 16, 064012.	2.2	8
3	Genomics, Exometabolomics, and Metabolic Probing Reveal Conserved Proteolytic Metabolism of <i>Thermoflexus hugenholtzii</i> and Three Candidate Species From China and Japan. <i>Frontiers in Microbiology</i> , 2021, 12, 632731.	1.5	8
4	Diverse respiratory capacity among <i>Thermus</i> strains from US Great Basin hot springs. <i>Extremophiles</i> , 2020, 24, 71-80.	0.9	13
5	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.	1.0	52
6	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.	1.5	12
7	Anoxygenic Phototrophs Span Geochemical Gradients and Diverse Morphologies in Terrestrial Geothermal Springs. <i>MSystems</i> , 2019, 4, .	1.7	24
8	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.	1.8	53
9	<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.	0.9	20
10	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, .	1.4	23
11	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.	1.5	19
12	High-Quality Draft Genomes from <i>Thermus caliditerrae</i> YIM 77777 and <i>T. Âtengchongensis</i> YIM 77401, Isolates from Tengchong, China. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
13	High-Quality Draft Genome Sequence of <i>Thermocrinis jamiesonii</i> GBS1 <sup>T</sup> Isolated from Great Boiling Spring, Nevada. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
14	High-quality draft genome sequence of the <i>Thermus amyloliquefaciens</i> type strain YIM 77409T with an incomplete denitrification pathway. <i>Standards in Genomic Sciences</i> , 2016, 11, 20.	1.5	7
15	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.	1.4	36
16	Phylogeny and physiology of candidate phylum <i>Âtribacteria</i> <sup>TM</sup> (OP9/JS1) inferred from cultivation-independent genomics. <i>ISME Journal</i> , 2016, 10, 273-286.	4.4	166
17	High-Quality Draft Genome Sequence of <i>Kallotenuis papyrolyticum</i> JKG1 T Reveals Broad Heterotrophic Capacity Focused on Carbohydrate and Amino Acid Metabolism. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
18	Uncultivated thermophiles: current status and spotlight on <i>Âigarchaeota</i> <sup>TM</sup> . <i>Current Opinion in Microbiology</i> , 2015, 25, 136-145.	2.3	70

#	ARTICLE	IF	CITATIONS
19	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
20	<i>Thermoflexus hugenholtzii</i> gen. nov., sp. nov., a thermophilic, microaerophilic, filamentous bacterium representing a novel class in the Chloroflexi, Thermoflexia classis nov., and description of Thermoflexaceae fam. nov. and Thermoflexales ord. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 2119-2127.	0.8	90
21	Impact of single-cell genomics and metagenomics on the emerging view of extremophile microbial dark matter. <i>Extremophiles</i> , 2014, 18, 865-875.	0.9	133
22	Single-cell and metagenomic analyses indicate a fermentative and saccharolytic lifestyle for members of the OP9 lineage. <i>Nature Communications</i> , 2013, 4, 1854.	5.8	199
23	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
24	<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
25	Pyrosequencing Reveals High-Temperature Cellulolytic Microbial Consortia in Great Boiling Spring after In Situ Lignocellulose Enrichment. <i>PLoS ONE</i> , 2013, 8, e59927.	1.1	42