

# 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

516710  
16  
h-index

610901  
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 “Atribacteria”™ (OP9/J1) 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 “microbial dark matter”. <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, 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. | 1.7  | 90        |
| 5  | Uncultivated thermophiles: current status and spotlight on “Aigarchaeota”™. <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        |

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|----|--|-----|-----------|
| 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 Kallotenue 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 <sup>T</sup> Isolated from Great Boiling Spring, Nevada. Genome Announcements, 2016, 4, .   | 0.8 | 0         |