

Takuro Nunoura

List of Publications by Year in descending order

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130
papers

9,094
citations

46984

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46771

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147
docs citations

147
times ranked

7729
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Asgard archaea illuminate the origin of eukaryotic cellular complexity. <i>Nature</i> , 2017, 541, 353-358. | 13.7 | 882 |
| 2 | Cell proliferation at 122Å°C and isotopically heavy CH ₄ production by a hyperthermophilic methanogen under high-pressure cultivation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 10949-10954. | 3.3 | 679 |
| 3 | Biogeographical distribution and diversity of microbes in methane hydrate-bearing deep marine sediments on the Pacific Ocean Margin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 2815-2820. | 3.3 | 644 |
| 4 | Insights into the evolution of Archaea and eukaryotic protein modifier systems revealed by the genome of a novel archaeal group. <i>Nucleic Acids Research</i> , 2011, 39, 3204-3223. | 6.5 | 303 |
| 5 | Hadal biosphere: Insight into the microbial ecosystem in the deepest ocean on Earth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1230-6. | 3.3 | 277 |
| 6 | Distribution, phylogenetic diversity and physiological characteristics of epsilon-Proteobacteria in a deep-sea hydrothermal field. <i>Environmental Microbiology</i> , 2005, 7, 1619-1632. | 1.8 | 247 |
| 7 | Major role of nitrite-oxidizing bacteria in dark ocean carbon fixation. <i>Science</i> , 2017, 358, 1046-1051. | 6.0 | 229 |
| 8 | Enzymatic and Genetic Characterization of Carbon and Energy Metabolisms by Deep-Sea Hydrothermal Chemolithoautotrophic Isolates of Epsilonproteobacteria. <i>Applied and Environmental Microbiology</i> , 2005, 71, 7310-7320. | 1.4 | 182 |
| 9 | Variability in microbial community and venting chemistry in a sediment-hosted backarc hydrothermal system: Impacts of subseafloor phase-separation. <i>FEMS Microbiology Ecology</i> , 2005, 54, 141-155. | 1.3 | 163 |
| 10 | A Deeply Branching Thermophilic Bacterium with an Ancient Acetyl-CoA Pathway Dominates a Subsurface Ecosystem. <i>PLoS ONE</i> , 2012, 7, e30559. | 1.1 | 161 |
| 11 | Microbial community in a sediment-hosted CO ₂ lake of the southern Okinawa Trough hydrothermal system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14164-14169. | 3.3 | 159 |
| 12 | A primordial and reversible TCA cycle in a facultatively chemolithoautotrophic thermophile. <i>Science</i> , 2018, 359, 559-563. | 6.0 | 155 |
| 13 | Isolation and phylogenetic diversity of members of previously uncultivated Å-Proteobacteria in deep-sea hydrothermal fields. <i>FEMS Microbiology Letters</i> , 2003, 218, 167-174. | 0.7 | 154 |
| 14 | Fungal diversity in deep-sea sediments â€“ the presence of novel fungal groups. <i>Fungal Ecology</i> , 2010, 3, 316-325. | 0.7 | 139 |
| 15 | Isolation and phylogenetic diversity of members of previously uncultivated Îµ-Proteobacteria in deep-sea hydrothermal fields. <i>FEMS Microbiology Letters</i> , 2003, 218, 167-174. | 0.7 | 135 |
| 16 | Characterization of C ₁ -Metabolizing Prokaryotic Communities in Methane Seep Habitats at the Kuroshima Knoll, Southern Ryukyu Arc, by Analyzing pmoA, mmoX, mxaF, mcrA, and 16S rRNA Genes. <i>Applied and Environmental Microbiology</i> , 2004, 70, 7445-7455. | 1.4 | 130 |
| 17 | Hydrothermal fluid geochemistry at the Iheya North field in the mid-Okinawa Trough: Implication for origin of methane in subseafloor fluid circulation systems. <i>Geochemical Journal</i> , 2011, 45, 109-124. | 0.5 | 122 |
| 18 | Genetic and functional properties of uncultivated thermophilic crenarchaeotes from a subsurface gold mine as revealed by analysis of genome fragments. <i>Environmental Microbiology</i> , 2005, 7, 1967-1984. | 1.8 | 119 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 19 | Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994. | 5.9 | 115 |
| 20 | Spatial Distribution of Marine Crenarchaeota Group I in the Vicinity of Deep-Sea Hydrothermal Systems. <i>Applied and Environmental Microbiology</i> , 2004, 70, 2404-2413. | 1.4 | 107 |
| 21 | Virus-mediated archaeal hecatomb in the deep seafloor. <i>Science Advances</i> , 2016, 2, e1600492. | 4.7 | 107 |
| 22 | Metagenomic Analysis of Viral Communities in (Hado)Pelagic Sediments. <i>PLoS ONE</i> , 2013, 8, e57271. | 1.1 | 105 |
| 23 | Culture-Dependent and -Independent Characterization of Microbial Communities Associated with a Shallow Submarine Hydrothermal System Occurring within a Coral Reef off Taketomi Island, Japan. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7642-7656. | 1.4 | 104 |
| 24 | Microbial Diversity in Deep-sea Methane Seep Sediments Presented by SSU rRNA Gene Tag Sequencing. <i>Microbes and Environments</i> , 2012, 27, 382-390. | 0.7 | 99 |
| 25 | Microbial community and geochemical analyses of trans-trench sediments for understanding the roles of hadal environments. <i>ISME Journal</i> , 2020, 14, 740-756. | 4.4 | 99 |
| 26 | Quantification of mcrA by fluorescent PCR in methanogenic and methanotrophic microbial communities. <i>FEMS Microbiology Ecology</i> , 2008, 64, 240-247. | 1.3 | 98 |
| 27 | Phylogenetic and enzymatic diversity of deep subseafloor aerobic microorganisms in organics- and methane-rich sediments off Shimokita Peninsula. <i>Extremophiles</i> , 2008, 12, 519-527. | 0.9 | 93 |
| 28 | Variability in the microbial communities and hydrothermal fluid chemistry at the newly discovered Mariner hydrothermal field, southern Lau Basin. <i>Journal of Geophysical Research</i> , 2008, 113, . | 3.3 | 91 |
| 29 | Liquid CO ₂ venting on the seafloor: Yonaguni Knoll IV hydrothermal system, Okinawa Trough. <i>Geophysical Research Letters</i> , 2006, 33, . | 1.5 | 89 |
| 30 | Isolation and Characterization of a Thermophilic, Obligately Anaerobic and Heterotrophic Marine <i>Chloroflexi</i> Bacterium from a <i>Chloroflexi</i>-dominated Microbial Community Associated with a Japanese Shallow Hydrothermal System, and Proposal for <i>Thermomarinilinea lacunofontalis</i> gen. nov., sp. nov.. <i>Microbes and Environments</i> , 2013, 28, 228-235. | 0.7 | 89 |
| 31 | FLDS: A Comprehensive dsRNA Sequencing Method for Intracellular RNA Virus Surveillance. <i>Microbes and Environments</i> , 2016, 31, 33-40. | 0.7 | 84 |
| 32 | Archaeal Diversity and Distribution along Thermal and Geochemical Gradients in Hydrothermal Sediments at the Yonaguni Knoll IV Hydrothermal Field in the Southern Okinawa Trough. <i>Applied and Environmental Microbiology</i> , 2010, 76, 1198-1211. | 1.4 | 83 |
| 33 | Host-Symbiont Relationships in Hydrothermal Vent Gastropods of the Genus <i>Alviniconcha</i> from the Southwest Pacific. <i>Applied and Environmental Microbiology</i> , 2006, 72, 1388-1393. | 1.4 | 81 |
| 34 | Microbial Diversity in Sediments from the Bottom of the Challenger Deep, the Mariana Trench. <i>Microbes and Environments</i> , 2018, 33, 186-194. | 0.7 | 75 |
| 35 | <i>Methylomarinovum caldicuralii</i> gen. nov., sp. nov., a moderately thermophilic methanotroph isolated from a shallow submarine hydrothermal system, and proposal of the family <i>Methylothermaceae</i> fam. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 989-999. | 0.8 | 73 |
| 36 | Geochemical origin of hydrothermal fluid methane in sediment-associated fields and its relevance to the geographical distribution of whole hydrothermal circulation. <i>Chemical Geology</i> , 2013, 339, 213-225. | 1.4 | 70 |

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|----|---|-----|-----------|
| 37 | Molecular biological and isotopic biogeochemical prognoses of the nitrification-driven dynamic microbial nitrogen cycle in hadal pelagic sediments. <i>Environmental Microbiology</i> , 2013, 15, 3087-3107. | 1.8 | 68 |
| 38 | <i>Methylomarinum vadi</i> gen. nov., sp. nov., a methanotroph isolated from two distinct marine environments. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 1073-1082. | 0.8 | 65 |
| 39 | Distribution and Niche Separation of Planktonic Microbial Communities in the Water Columns from the Surface to the Hadal Waters of the Japan Trench under the Eutrophic Ocean. <i>Frontiers in Microbiology</i> , 2016, 7, 1261. | 1.5 | 62 |
| 40 | Comparison of microbial communities associated with phase-separation-induced hydrothermal fluids at the Yonaguni Knoll IV hydrothermal field, the Southern Okinawa Trough. <i>FEMS Microbiology Ecology</i> , 2009, 67, 351-370. | 1.3 | 61 |
| 41 | Quantification of <i>mcrA</i> by quantitative fluorescent PCR in sediments from methane seep of the Nankai Trough. <i>FEMS Microbiology Ecology</i> , 2006, 57, 149-157. | 1.3 | 60 |
| 42 | Unveiling the RNA virosphere associated with marine microorganisms. <i>Molecular Ecology Resources</i> , 2018, 18, 1444-1455. | 2.2 | 59 |
| 43 | Metagenomic insights into zooplankton-associated bacterial communities. <i>Environmental Microbiology</i> , 2018, 20, 492-505. | 1.8 | 57 |
| 44 | Subseafloor microbial communities associated with rapid turbidite deposition in the Gulf of Mexico continental slope (IODP Expedition 308). <i>FEMS Microbiology Ecology</i> , 2009, 69, 410-424. | 1.3 | 55 |
| 45 | Disturbance of deep-sea environments induced by the M9.0 Tohoku Earthquake. <i>Scientific Reports</i> , 2012, 2, 270. | 1.6 | 55 |
| 46 | A Long-Term Cultivation of an Anaerobic Methane-Oxidizing Microbial Community from Deep-Sea Methane-Seep Sediment Using a Continuous-Flow Bioreactor. <i>PLoS ONE</i> , 2014, 9, e105356. | 1.1 | 55 |
| 47 | Development of 16S rRNA gene-targeted primers for detection of archaeal anaerobic methanotrophs (ANMEs). <i>FEMS Microbiology Letters</i> , 2009, 297, 31-37. | 0.7 | 54 |
| 48 | Molecular Characterization of Potential Nitrogen Fixation by Anaerobic Methane-Oxidizing Archaea in the Methane Seep Sediments at the Number 8 Kumano Knoll in the Kumano Basin, Offshore of Japan. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7153-7162. | 1.4 | 50 |
| 49 | Variance and potential niche separation of microbial communities in subseafloor sediments off Shimokita Peninsula, Japan. <i>Environmental Microbiology</i> , 2016, 18, 1889-1906. | 1.8 | 48 |
| 50 | <i>Mariprofundus micogutta</i> sp. nov., a novel iron-oxidizing zetaproteobacterium isolated from a deep-sea hydrothermal field at the Bayonnaise knoll of the Izu-Ogasawara arc, and a description of <i>Mariprofundales</i> ord. nov. and <i>Zetaproteobacteria classis</i> nov.. <i>Archives of Microbiology</i> , 2017, 199, 335-346. | 1.0 | 48 |
| 51 | <i>Kosmotoga arenicorallina</i> sp. nov. a thermophilic and obligately anaerobic heterotroph isolated from a shallow hydrothermal system occurring within a coral reef, southern part of the Yaeyama Archipelago, Japan, reclassification of <i>Thermococcoides shengliensis</i> as <i>Kosmotoga shengliensis</i> comb. nov., and emended description of the genus <i>Kosmotoga</i> . <i>Archives of Microbiology</i> , 2010, 192, 811-819. | 1.0 | 47 |
| 52 | <i>Thermosulfidibacter takaii</i> gen. nov., sp. nov., a thermophilic, hydrogen-oxidizing, sulfur-reducing chemolithoautotroph isolated from a deep-sea hydrothermal field in the Southern Okinawa Trough. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 659-665. | 0.8 | 46 |
| 53 | Variability in Microbial Communities in Black Smoker Chimneys at the NW Caldera Vent Field, Brothers Volcano, Kermadec Arc. <i>Geomicrobiology Journal</i> , 2009, 26, 552-569. | 1.0 | 46 |
| 54 | Library Construction from Subnanogram DNA for Pelagic Sea Water and Deep-Sea Sediments. <i>Microbes and Environments</i> , 2017, 32, 336-343. | 0.7 | 46 |

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|----|--|-----|-----------|
| 55 | Subseafloor Microbial Communities in Methane Hydrate-Bearing Sediment at Two Distinct Locations (ODP Leg204) in the Cascadia Margin. <i>Microbes and Environments</i> , 2008, 23, 317-325. | 0.7 | 44 |
| 56 | Spatial Distribution of Viruses Associated with Planktonic and Attached Microbial Communities in Hydrothermal Environments. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1311-1320. | 1.4 | 42 |
| 57 | Biogeography of <i>Persephonella</i> in deep-sea hydrothermal vents of the Western Pacific. <i>Frontiers in Microbiology</i> , 2013, 4, 107. | 1.5 | 41 |
| 58 | Genome-enabled metabolic reconstruction of dominant chemosynthetic colonizers in deep-sea massive sulfide deposits. <i>Environmental Microbiology</i> , 2018, 20, 862-877. | 1.8 | 41 |
| 59 | <i>Geofilum rubicundum</i> gen. nov., sp. nov., isolated from deep subseafloor sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012, 62, 1075-1080. | 0.8 | 40 |
| 60 | The first microbiological contamination assessment by deep-sea drilling and coring by the D/V Chikyu at the Iheya North hydrothermal field in the Mid-Okinawa Trough (IODP Expedition 331). <i>Frontiers in Microbiology</i> , 2013, 4, 327. | 1.5 | 40 |
| 61 | Enantioselective Utilization of D-Amino Acids by Deep-Sea Microorganisms. <i>Frontiers in Microbiology</i> , 2016, 7, 511. | 1.5 | 40 |
| 62 | Physiological and Genomic Features of a Novel Sulfur-Oxidizing Gammaproteobacterium Belonging to a Previously Uncultivated Symbiotic Lineage Isolated from a Hydrothermal Vent. <i>PLoS ONE</i> , 2014, 9, e104959. | 1.1 | 40 |
| 63 | <i>Thermotomaculum hydrothermale</i> gen. nov., sp. nov., a novel heterotrophic thermophile within the phylum Acidobacteria from a deep-sea hydrothermal vent chimney in the Southern Okinawa Trough. <i>Extremophiles</i> , 2012, 16, 245-253. | 0.9 | 39 |
| 64 | <i>Sunxiuqinia faeciviva</i> sp. nov., a facultatively anaerobic organoheterotroph of the Bacteroidetes isolated from deep subseafloor sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 1602-1609. | 0.8 | 39 |
| 65 | Genomics insights into ecotype formation of ammonia-oxidizing archaea in the deep ocean. <i>Environmental Microbiology</i> , 2019, 21, 716-729. | 1.8 | 39 |
| 66 | Pangenomics Analysis Reveals Diversification of Enzyme Families and Niche Specialization in Globally Abundant SAR202 Bacteria. <i>MBio</i> , 2020, 11, . | 1.8 | 39 |
| 67 | Single host and symbiont lineages of hydrothermal-vent gastropods <i>Ipremeria nautili</i> (Provannidae): biogeography and evolution. <i>Marine Ecology - Progress Series</i> , 2006, 315, 167-175. | 0.9 | 38 |
| 68 | <i>Exilispira thermophila</i> gen. nov., sp. nov., an anaerobic, thermophilic spirochaete isolated from a deep-sea hydrothermal vent chimney. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 2258-2265. | 0.8 | 33 |
| 69 | <i>Desulfothermus okinawensis</i> sp. nov., a thermophilic and heterotrophic sulfate-reducing bacterium isolated from a deep-sea hydrothermal field. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 2360-2364. | 0.8 | 30 |
| 70 | Endemicity of the cosmopolitan mesophilic chemolithoautotroph <i>Sulfurimonas</i> at deep-sea hydrothermal vents. <i>ISME Journal</i> , 2017, 11, 909-919. | 4.4 | 30 |
| 71 | <i>Marinitoga okinawensis</i> sp. nov., a novel thermophilic and anaerobic heterotroph isolated from a deep-sea hydrothermal field, Southern Okinawa Trough. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 467-471. | 0.8 | 29 |
| 72 | Microbial Community Stratification Controlled by the Subseafloor Fluid Flow and Geothermal Gradient at the Iheya North Hydrothermal Field in the Mid-Okinawa Trough (Integrated Ocean Drilling) <i>Tj ETQq0 0 Q. BT / Overd</i> | 1.4 | 28 |

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|----|---|-----|-----------|
| 73 | Fluid chemistry in the Solitaire and Dodo hydrothermal fields of the Central Indian Ridge. <i>Geofluids</i> , 2016, 16, 988-1005. | 0.3 | 29 |
| 74 | <i>Hydrogenivirga okinawensis</i> sp. nov., a thermophilic sulfur-oxidizing chemolithoautotroph isolated from a deep-sea hydrothermal field, Southern Okinawa Trough. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 676-681. | 0.8 | 28 |
| 75 | Sedimentary organic matter contents and porewater chemistry at upper bathyal depths influenced by the 2011 off the Pacific coast of Tohoku Earthquake and tsunami. <i>Journal of Oceanography</i> , 2016, 72, 99-111. | 0.7 | 28 |
| 76 | Hadal water biogeochemistry over the Izu Ogasawara Trench observed with a full-depth CTD-CMS. <i>Ocean Science</i> , 2018, 14, 575-588. | 1.3 | 28 |
| 77 | <i>Sulfurivirga caldicuralii</i> gen. nov., sp. nov., a novel microaerobic, thermophilic, thiosulfate-oxidizing chemolithoautotroph, isolated from a shallow marine hydrothermal system occurring in a coral reef, Japan. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 1921-1929. | 0.8 | 27 |
| 78 | Genomes of Thaumarchaeota from deep sea sediments reveal specific adaptations of three independently evolved lineages. <i>ISME Journal</i> , 2021, 15, 2792-2808. | 4.4 | 27 |
| 79 | Variability of seafloor viral abundance at the geographically and geologically distinct continental margins. <i>FEMS Microbiology Ecology</i> , 2014, 88, 60-68. | 1.3 | 26 |
| 80 | Comparative Analysis of Microbial Communities in Iron-Dominated Flocculent Mats in Deep-Sea Hydrothermal Environments. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5741-5755. | 1.4 | 26 |
| 81 | Deep-sea vent phage DNA polymerase specifically initiates DNA synthesis in the absence of primers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E2310-E2318. | 3.3 | 26 |
| 82 | <i>Thermaerobacter nagasakiensis</i> sp. nov., a novel aerobic and extremely thermophilic marine bacterium. <i>Archives of Microbiology</i> , 2002, 177, 339-344. | 1.0 | 25 |
| 83 | Nitrification-driven forms of nitrogen metabolism in microbial mat communities thriving along an ammonium-enriched subsurface geothermal stream. <i>Geochimica Et Cosmochimica Acta</i> , 2013, 113, 152-173. | 1.6 | 23 |
| 84 | Effects of mass sedimentation events after the 2011 off the Pacific coast of Tohoku Earthquake on benthic prokaryotes and meiofauna inhabiting the upper bathyal sediments. <i>Journal of Oceanography</i> , 2016, 72, 113-128. | 0.7 | 23 |
| 85 | Quantitative Viral Community DNA Analysis Reveals the Dominance of Single-Stranded DNA Viruses in Offshore Upper Bathyal Sediment from Tohoku, Japan. <i>Frontiers in Microbiology</i> , 2018, 9, 75. | 1.5 | 23 |
| 86 | Genome sequence of a novel deep-sea vent epsilonproteobacterial phage provides new insight into the co-evolution of Epsilonproteobacteria and their phages. <i>Extremophiles</i> , 2013, 17, 405-419. | 0.9 | 22 |
| 87 | Expedition reveals changes in Lau Basin Hydrothermal System. <i>Eos</i> , 2006, 87, 13. | 0.1 | 21 |
| 88 | Domain-level identification and quantification of relative prokaryotic cell abundance in microbial communities by MicroFTIR spectroscopy. <i>Environmental Microbiology Reports</i> , 2012, 4, 42-49. | 1.0 | 21 |
| 89 | <i>Lebetimonas natsushimae</i> sp. nov., a novel strictly anaerobic, moderately thermophilic chemoautotroph isolated from a deep-sea hydrothermal vent polychaete nest in the Mid-Okinawa Trough. <i>Systematic and Applied Microbiology</i> , 2017, 40, 352-356. | 1.2 | 21 |
| 90 | Viral Communities in the Global Deep Ocean Conveyor Belt Assessed by Targeted Viromics. <i>Frontiers in Microbiology</i> , 2019, 10, 1801. | 1.5 | 21 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 91 | dsRNA-seq Reveals Novel RNA Virus and Virus-Like Putative Complete Genome Sequences from <i>Hymeniacidon</i> sp.; Sponge. <i>Microbes and Environments</i> , 2020, 35, n/a. | 0.7 | 21 |
| 92 | Three families of Asgard archaeal viruses identified in metagenome-assembled genomes. <i>Nature Microbiology</i> , 2022, 7, 962-973. | 5.9 | 21 |
| 93 | A New Fractionation and Recovery Method of Viral Genomes Based on Nucleic Acid Composition and Structure Using Tandem Column Chromatography. <i>Microbes and Environments</i> , 2015, 30, 199-203. | 0.7 | 18 |
| 94 | Defining boundaries for the distribution of microbial communities beneath the sediment-buried, hydrothermally active seafloor. <i>ISME Journal</i> , 2017, 11, 529-542. | 4.4 | 18 |
| 95 | Viral Infections Boost Prokaryotic Biomass Production and Organic C Cycling in Hadal Trench Sediments. <i>Frontiers in Microbiology</i> , 2019, 10, 1952. | 1.5 | 18 |
| 96 | Regulation of the aerobic respiratory chain in the facultatively aerobic and hyperthermophilic archaeon <i>Pyrobaculum oguniense</i> . <i>Microbiology (United Kingdom)</i> , 2003, 149, 673-688. | 0.7 | 17 |
| 97 | Viral RNA Genomes Identified from Marine Macroalgae and a Diatom. <i>Microbes and Environments</i> , 2020, 35, n/a. | 0.7 | 17 |
| 98 | RNA Viral Metagenome Analysis of Subnanogram dsRNA Using Fragmented and Primer Ligated dsRNA Sequencing (FLDS). <i>Microbes and Environments</i> , 2021, 36, n/a. | 0.7 | 17 |
| 99 | Nitrate Isotope Distribution in the Subarctic and Subtropical North Pacific. <i>Geochemistry, Geophysics, Geosystems</i> , 2018, 19, 2212-2224. | 1.0 | 16 |
| 100 | Genomic characterization of a temperate phage of the psychrotolerant deep-sea bacterium <i>Aurantimonas</i> sp.. <i>Extremophiles</i> , 2015, 19, 49-58. | 0.9 | 15 |
| 101 | d-Lactate electrochemical biosensor prepared by immobilization of thermostable dye-linked d-lactate dehydrogenase from <i>Candidatus Caldiarchaeum subterraneum</i> . <i>Journal of Bioscience and Bioengineering</i> , 2018, 126, 425-430. | 1.1 | 15 |
| 102 | Drivers of Bacterial α - and β -Diversity Patterns and Functioning in Subsurface Hadal Sediments. <i>Frontiers in Microbiology</i> , 2019, 10, 2609. | 1.5 | 14 |
| 103 | A new member of the family Totiviridae associated with arboreal ants (<i>Camponotus nipponicus</i>). <i>Archives of Virology</i> , 2016, 161, 2043-2045. | 0.9 | 13 |
| 104 | Biochemical and genetic characterization of β -1,3 glucanase from a deep subseafloor <i>Laceyella putida</i> . <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 203-214. | 1.7 | 13 |
| 105 | Bottleneck Size-Dependent Changes in the Genetic Diversity and Specific Growth Rate of a Rotavirus A Strain. <i>Journal of Virology</i> , 2020, 94, . | 1.5 | 13 |
| 106 | Identification and genomic analysis of temperate <i>Pseudomonas</i> bacteriophage PstS-1 from the Japan trench at a depth of 7000m. <i>Research in Microbiology</i> , 2015, 166, 668-676. | 1.0 | 12 |
| 107 | Distribution of eukaryotic serine racemases in the bacterial domain and characterization of a representative protein in <i>Roseobacter litoralis</i> Och 149. <i>Microbiology (United Kingdom)</i> , 2016, 162, 53-61. | 0.7 | 11 |
| 108 | Acquired Thermotolerance and Temperature-Induced Protein Accumulation in the Extremely Thermophilic Bacterium <i>Rhodothermus obamensis</i> . <i>Journal of Bacteriology</i> , 1998, 180, 2770-2774. | 1.0 | 11 |

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|-----|---|-----|-----------|
| 109 | An archaeal homing endonuclease I-Pogl cleaves at the insertion site of the neighboring intron, which has no nested open reading frame. <i>FEBS Letters</i> , 2003, 544, 165-170. | 1.3 | 10 |
| 110 | Abyssal fauna, benthic microbes, and organic matter quality across a range of trophic conditions in the western Pacific ocean. <i>Progress in Oceanography</i> , 2021, 195, 102591. | 1.5 | 10 |
| 111 | <i>Halopiger thermotolerans</i> sp. nov., a thermo-tolerant haloarchaeon isolated from commercial salt. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 4975-4980. | 0.8 | 10 |
| 112 | Culture-dependent and independent analyses of subsurface microbial communities in oil-bearing strata of the Sagara oil reservoir. <i>Island Arc</i> , 2006, 15, 328-337. | 0.5 | 9 |
| 113 | Complete Genome Sequence of a Novel RNA Virus Identified from a Deep-Sea Animal, &Osedax japonicus. <i>Microbes and Environments</i> , 2018, 33, 446-449. | 0.7 | 9 |
| 114 | A new polycipivirus identified in <i>Colobopsis shohki</i> . <i>Archives of Virology</i> , 2020, 165, 761-763. | 0.9 | 9 |
| 115 | Diverged and Active Partitiviruses in Lichen. <i>Frontiers in Microbiology</i> , 2020, 11, 561344. | 1.5 | 9 |
| 116 | Genomic Heterogeneity in a Natural Archaeal Population Suggests a Model of tRNA Gene Disruption. <i>PLoS ONE</i> , 2012, 7, e32504. | 1.1 | 9 |
| 117 | Diverse DNA modification in marine prokaryotic and viral communities. <i>Nucleic Acids Research</i> , 2022, 50, 1531-1550. | 6.5 | 9 |
| 118 | In situ experimental evidences for responses of abyssal benthic biota to shifts in phytodetritus compositions linked to global climate change. <i>Global Change Biology</i> , 2021, 27, 6139-6155. | 4.2 | 7 |
| 119 | Comparative Investigation of Microbial Communities Associated with Hydrothermal Activities in the Okinawa Trough. , 2015, , 421-435. | | 7 |
| 120 | Insights into the Methanogenic Population and Potential in Subsurface Marine Sediments Based on Coenzyme F430 as a Function-Specific Biomarker. <i>Jacs Au</i> , 2021, 1, 1743-1751. | 3.6 | 6 |
| 121 | Metagenomic Analysis of Five Phylogenetically Distant Anammox Bacterial Enrichment Cultures. <i>Microbes and Environments</i> , 2022, 37, n/a. | 0.7 | 6 |
| 122 | Hiding in Plain Sight: The Globally Distributed Bacterial Candidate Phylum PAUC34f. <i>Frontiers in Microbiology</i> , 2020, 11, 376. | 1.5 | 5 |
| 123 | Hydrogen and carbon isotope fractionation factors of aerobic methane oxidation in deep-sea water. <i>Biogeosciences</i> , 2021, 18, 5351-5362. | 1.3 | 5 |
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