# Yasukazu Nakamura, 中村保一

## List of Publications by Year
in descending order

| | | |
|---|---|---|
| 145 papers | 25,443 citations | 60 h-index (20817) |
| 141 g-index (9861) | | |

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|---|---|---|
| 152 all docs | 152 docs citations | 152 times ranked |
| 25636 citing authors | | |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 1 | Analysis of the genome sequence of the flowering plant Arabidopsis thaliana. Nature, 2000, 408, 796-815. | 27.8 | 8,336 |
| 2 | The tomato genome sequence provides insights into fleshy fruit evolution. Nature, 2012, 485, 635-641. | 27.8 | 2,860 |
| 3 | Plant recognition of symbiotic bacteria requires two LysM receptor-like kinases. Nature, 2003, 425, 585-592. | 27.8 | 1,092 |
| 4 | Insights into Land Plant Evolution Garnered from the Marchantia polymorpha Genome. Cell, 2017, 171, 287-304.e15. | 28.9 | 973 |
| 5 | DFAST: a flexible prokaryotic genome annotation pipeline for faster genome publication. Bioinformatics, 2018, 34, 1037-1039. | 4.1 | 775 |
| 6 | Complete Genomic Sequence of Nitrogen-fixing Symbiotic Bacterium Bradyrhizobium japonicum USDA110. DNA Research, 2002, 9, 189-197. | 3.4 | 768 |
| 7 | Genome Structure of the Legume, Lotus japonicus. DNA Research, 2008, 15, 227-239. | 3.4 | 691 |
| 8 | Gene organization deduced from the complete sequence of liverwort Marchantia polymorpha mitochondrial DNA. Journal of Molecular Biology, 1992, 223, 1-7. | 4.2 | 602 |
| 9 | Klebsormidium flaccidum genome reveals primary factors for plant terrestrial adaptation. Nature Communications, 2014, 5, 3978. | 12.8 | 532 |
| 10 | From The Cover: A nucleoporin is required for induction of Ca2+ spiking in legume nodule development and essential for rhizobial and fungal symbiosis. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 359-364. | 7.1 | 361 |
| 11 | The International Nucleotide Sequence Database Collaboration. Nucleic Acids Research, 2012, 40, D33-D37. | 14.5 | 327 |
| 12 | Complete Genome Structure of the Thermophilic Cyanobacterium Thermosynechococcus elongatus BP-1. DNA Research, 2002, 9, 123-130. | 3.4 | 312 |
| 13 | Complete Genome Structure of Gloeobacter violaceus PCC 7421, a Cyanobacterium that Lacks Thylakoids. DNA Research, 2003, 10, 137-145. | 3.4 | 269 |
| 14 | Complete Genomic Structure of the Bloom-forming Toxic Cyanobacterium Microcystis aeruginosa NIES-843. DNA Research, 2007, 14, 247-256. | 3.4 | 253 |
| 15 | The Sulfate Transporter SST1 Is Crucial for Symbiotic Nitrogen Fixation in Lotus japonicus Root Nodules. Plant Cell, 2005, 17, 1625-1636. | 6.6 | 227 |
| 16 | DFAST and DAGA: web-based integrated genome annotation tools and resources. Bioscience of Microbiota, Food and Health, 2016, 35, 173-184. | 1.8 | 194 |
| 17 | Sequence and analysis of chromosome 3 of the plant Arabidopsis thaliana. Nature, 2000, 408, 820-823. | 27.8 | 188 |
| 18 | Expression Profiling-Based Identification of CO2-Responsive Genes Regulated by CCM1 Controlling a Carbon-Concentrating Mechanism in Chlamydomonas reinhardtii. Plant Physiology, 2004, 135, 1595-1607. | 4.8 | 188 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 19 | Role of the Putative Membrane-Bound Endo-1,4-Î²-Glucanase KORRIGAN in Cell Elongation and Cellulose Synthesis in Arabidopsis thaliana. Plant and Cell Physiology, 2001, 42, 251-263. | 3.1 | 185 |
| 20 | A Cluster of Genes Encodes the Two Types of Chalcone Isomerase Involved in the Biosynthesis of General Flavonoids and Legume-Specific 5-Deoxy(iso)flavonoids in Lotus japonicus Â. Plant Physiology, 2003, 131, 941-951. | 4.8 | 181 |
| 21 | Sequence and analysis of chromosome 5 of the plant Arabidopsis thaliana. Nature, 2000, 408, 823-826. | 27.8 | 175 |
| 22 | CyanoBase, a www database containing the complete nucleotide sequence of the genome of Synechocystis sp. strain PCC6803. Nucleic Acids Research, 1998, 26, 63-67. | 14.5 | 174 |
| 23 | A Large-scale Proteinâ€"protein Interaction Analysis in Synechocystis sp. PCC6803. DNA Research, 2007, 14, 207-216. | 3.4 | 170 |
| 24 | Chromatin Organization in Early Land Plants Reveals an Ancestral Association between H3K27me3, Transposons, and Constitutive Heterochromatin. Current Biology, 2020, 30, 573-588.e7. | 3.9 | 160 |
| 25 | Complete Genomic Structure of the Cultivated Rice Endophyte Azospirillum sp. B510. DNA Research, 2010, 17, 37-50. | 3.4 | 148 |
| 26 | Comprehensive Structural Analysis of the Genome of Red Clover (Trifolium pratense L.). DNA Research, 2005, 12, 301-364. | 3.4 | 145 |
| 27 | Gain-of-Function Phenotypes of Chemically Synthetic CLAVATA3/ESR-Related (CLE) Peptides in Arabidopsis thaliana and Oryza sativa. Plant and Cell Physiology, 2007, 48, 1821-1825. | 3.1 | 142 |
| 28 | CyanoBase: the cyanobacteria genome database update 2010. Nucleic Acids Research, 2010, 38, D379-D381. | 14.5 | 142 |
| 29 | Characterization of the Soybean Genome Using EST-derived Microsatellite Markers. DNA Research, 2007, 14, 271-281. | 3.4 | 133 |
| 30 | Autocatalytic differentiation of epigenetic modifications within the Arabidopsis genome. EMBO Journal, 2010, 29, 3496-3506. | 7.8 | 127 |
| 31 | Genome-wide association study and genomic prediction in citrus: Potential of genomics-assisted breeding for fruit quality traits. Scientific Reports, 2017, 7, 4721. | 3.3 | 125 |
| 32 | Structural Analysis of Four Large Plasmids Harboring in a Unicellular Cyanobacterium, Synechocystis sp. PCC 6803. DNA Research, 2003, 10, 221-228. | 3.4 | 124 |
| 33 | Condon usage tabulated from the international DNA sequence databases. Nucleic Acids Research, 1996, 24, 214-215. | 14.5 | 114 |
| 34 | The International Nucleotide Sequence Database Collaboration. Nucleic Acids Research, 2013, 41, D21-D24. | 14.5 | 110 |
| 35 | Development of a Bacterial Cell Enrichment Method and its Application to the Community Analysis in Soybean Stems. Microbial Ecology, 2009, 58, 703-714. | 2.8 | 108 |
| 36 | Generation of Expressed Sequence Tags from Low-CO2 and High-CO2 Adapted Cells of Chlamydomonas reinhardtii. DNA Research, 2000, 7, 305-307. | 3.4 | 107 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 37 | Host plant genome overcomes the lack of a bacterial gene for symbiotic nitrogen fixation. Nature, 2009, 462, 514-517. | 27.8 | 103 |
| 38 | COMPARISON OF RNA EXPRESSION PROFILES BETWEEN THE TWO GENERATIONS OF <i>PORPHYRA YEZOENSIS</i> (RHODOPHYTA), BASED ON EXPRESSED SEQUENCE TAG FREQUENCY ANALYSIS. Journal of Phycology, 2003, 39, 923-930. | 2.3 | 99 |
| 39 | The Integral Membrane Protein SEN1 is Required for Symbiotic Nitrogen Fixation in Lotus japonicus Nodules. Plant and Cell Physiology, 2012, 53, 225-236. | 3.1 | 95 |
| 40 | CyanoBase:Âa large-scale update on its 20th anniversary. Nucleic Acids Research, 2017, 45, D551-D554. | 14.5 | 95 |
| 41 | An interspecific linkage map of SSR and intronic polymorphism markers in tomato. Theoretical and Applied Genetics, 2010, 121, 731-739. | 3.6 | 92 |
| 42 | The International Nucleotide Sequence Database Collaboration. Nucleic Acids Research, 2011, 39, D15-D18. | 14.5 | 92 |
| 43 | SNP Discovery and Linkage Map Construction in Cultivated Tomato. DNA Research, 2010, 17, 381-391. | 3.4 | 87 |
| 44 | DDBJ launches a new archive database with analytical tools for next-generation sequence data. Nucleic Acids Research, 2010, 38, D33-D38. | 14.5 | 86 |
| 45 | Codon usage tabulated from the international DNA sequence databases. Nucleic Acids Research, 1997, 25, 244-245. | 14.5 | 83 |
| 46 | Codon usage tabulated from the international DNA sequence databases; its status 1999. Nucleic Acids Research, 1999, 27, 292-292. | 14.5 | 81 |
| 47 | Generation of 7137 Non-redundant Expressed Sequence Tags from a Legume, Lotus japonicus. DNA Research, 2000, 7, 127-130. | 3.4 | 80 |
| 48 | Gene clusters for ribosomal proteins in the mitochondrial genome of a liverwort,Marchantia polymorpha. Nucleic Acids Research, 1992, 20, 3199-3205. | 14.5 | 79 |
| 49 | DNA Data Bank of Japan. Nucleic Acids Research, 2017, 45, D25-D31. | 14.5 | 78 |
| 50 | Complete Genomic Sequence of Nitrogen-fixing Symbiotic Bacterium Bradyrhizobium japonicum USDA110 (Supplement). DNA Research, 2002, 9, 225-256. | 3.4 | 76 |
| 51 | Complete Genome Sequence of &lt;i&gt;Bradyrhizobium&lt;/i&gt; sp. S23321: Insights into Symbiosis Evolution in Soil Oligotrophs. Microbes and Environments, 2012, 27, 306-315. | 1.6 | 76 |
| 52 | DNA data bank of Japan (DDBJ) progress report. Nucleic Acids Research, 2016, 44, D51-D57. | 14.5 | 76 |
| 53 | Hybrid Origins of Citrus Varieties Inferred from DNA Marker Analysis of Nuclear and Organelle Genomes. PLoS ONE, 2016, 11, e0166969. | 2.5 | 76 |
| 54 | Codon usage tabulated from the international DNA sequence databases. Nucleic Acids Research, 1998, 26, 334-334. | 14.5 | 74 |

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| 55 | A Large Scale Analysis of Protein-Protein Interactions in the Nitrogen-fixing Bacterium Mesorhizobium loti. DNA Research, 2008, 15, 13-23. | 3.4 | 73 |
| 56 | Genome-wide analysis of ATP-binding cassette (ABC) proteins in a model legume plant, Lotus japonicus: comparison with Arabidopsis ABC protein family. DNA Research, 2006, 13, 205-228. | 3.4 | 71 |
| 57 | Genome-Wide Analysis of Intraspecific DNA Polymorphism in 'Micro-Tom', a Model Cultivar of Tomato (Solanum lycopersicum). Plant and Cell Physiology, 2014, 55, 445-454. | 3.1 | 69 |
| 58 | DDBJ Read Annotation Pipeline: A Cloud Computing-Based Pipeline for High-Throughput Analysis of Next-Generation Sequencing Data. DNA Research, 2013, 20, 383-390. | 3.4 | 68 |
| 59 | Characteristics of the Lotus Japonicus Gene Repertoire Deduced from Large-Scale Expressed Sequence Tag (EST) Analysis. Plant Molecular Biology, 2004, 54, 405-414. | 3.9 | 63 |
| 60 | Structural Analysis of a Lotus japonicus Genome. IV. Sequence Features and Mapping of Seventy-three TAC Clones Which Cover the 7.5 Mb Regions of the Genome. DNA Research, 2003, 10, 115-122. | 3.4 | 62 |
| 61 | The Naming of Names: Guidelines for Gene Nomenclature in *Marchantia*. Plant and Cell Physiology, 2016, 57, 257-261. | 3.1 | 60 |
| 62 | The genomic standards consortium: bringing standards to life for microbial ecology. ISME Journal, 2011, 5, 1565-1567. | 9.8 | 59 |
| 63 | Comparison of the Transcript Profiles from the Root and the Nodulating Root of the Model Legume Lotus japonicus by Serial Analysis of Gene Expression. Molecular Plant-Microbe Interactions, 2005, 18, 487-498. | 2.6 | 57 |
| 64 | The DDBJ Japanese Genotype-phenotype Archive for genetic and phenotypic human data. Nucleic Acids Research, 2015, 43, D18-D22. | 14.5 | 57 |
| 65 | CyanoBase and RhizoBase: databases of manually curated annotations for cyanobacterial and rhizobial genomes. Nucleic Acids Research, 2014, 42, D666-D670. | 14.5 | 56 |
| 66 | Transfer RNA genes in the mitochondrial genome from a liverwort,Marchantia polymorpha: the absence of chloroplast-like tRNAs. Nucleic Acids Research, 1992, 20, 3773-3777. | 14.5 | 54 |
| 67 | Group I introns in the liverwort mitochondrial genome: the gene coding for subunit 1 of cytochrome oxidase shares five intron positions with its fungal counterparts. Nucleic Acids Research, 1993, 21, 1297-1305. | 14.5 | 53 |
| 68 | Genome Sequencing and Genome Resources in Model Legumes. Plant Physiology, 2007, 144, 588-593. | 4.8 | 53 |
| 69 | DNA Data Bank of Japan: 30th anniversary. Nucleic Acids Research, 2018, 46, D30-D35. | 14.5 | 51 |
| 70 | Structural Analysis of a Lotus japonicus Genome. II. Sequence Features and Mapping of Sixty-five TAC Clones Which Cover the 6.5-Mb Regions of the Genome. DNA Research, 2002, 9, 63-70. | 3.4 | 50 |
| 71 | Draft Sequencing of the Heterozygous Diploid Genome of Satsuma (Citrus unshiu Marc.) Using a Hybrid Assembly Approach. Frontiers in Genetics, 2017, 8, 180. | 2.3 | 49 |
| 72 | Structural Analysis of a Lotus japonicus Genome. V. Sequence Features and Mapping of Sixty-four TAC Clones Which Cover the 6.4 Mb Regions of the Genome. DNA Research, 2003, 10, 277-285. | 3.4 | 46 |

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| 73 | Complete genome sequence and analysis of Lactobacillus hokkaidonensis LOOC260T, a psychrotrophic lactic acid bacterium isolated from silage. BMC Genomics, 2015, 16, 240. | 2.8 | 44 |
| 74 | The DNA Data Bank of Japan launches a new resource, the DDBJ Omics Archive of functional genomics experiments. Nucleic Acids Research, 2012, 40, D38-D42. | 14.5 | 43 |
| 75 | Lactobacillus paragasseri sp. nov., a sister taxon of Lactobacillus gasseri, based on whole-genome sequence analyses. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3512-3517. | 1.7 | 43 |
| 76 | Complete Genome Structure of Gloeobacter violaceus PCC 7421, a Cyanobacterium that Lacks Thylakoids (Supplement). DNA Research, 2003, 10, 181-201. | 3.4 | 42 |
| 77 | DDBJ progress report. Nucleic Acids Research, 2011, 39, D22-D27. | 14.5 | 42 |
| 78 | Genome-wide Analyses of the Structural Gene Families Involved in the Legume-specific 5-Deoxyisoflavonoid Biosynthesis of Lotus japonicus. DNA Research, 2007, 14, 25-36. | 3.4 | 41 |
| 79 | Construction of Signature-tagged Mutant Library in Mesorhizobium loti as a Powerful Tool for Functional Genomics. DNA Research, 2008, 15, 297-308. | 3.4 | 41 |
| 80 | Large-scale genome analysis of bovine commensal *Escherichia coli* reveals that bovine-adapted *E. coli* lineages are serving as evolutionary sources of the emergence of human intestinal pathogenic strains. Genome Research, 2019, 29, 1495-1505. | 5.5 | 39 |
| 81 | Plant Genome DataBase Japan (PGDBj): A Portal Website for the Integration of Plant Genome-Related Databases. Plant and Cell Physiology, 2014, 55, e8-e8. | 3.1 | 38 |
| 82 | Toward richer metadata for microbial sequences: replacing strain-level NCBI taxonomy taxids with BioProject, BioSample and Assembly records. Standards in Genomic Sciences, 2014, 9, 1275-1277. | 1.5 | 38 |
| 83 | DDBJ new system and service refactoring. Nucleic Acids Research, 2012, 41, D25-D29. | 14.5 | 37 |
| 84 | DDBJ progress report: a new submission system for leading to a correct annotation. Nucleic Acids Research, 2014, 42, D44-D49. | 14.5 | 36 |
| 85 | Identification of the sex-determining factor in the liverwort Marchantia polymorpha reveals unique evolution of sex chromosomes in a haploid system. Current Biology, 2021, 31, 5522-5532.e7. | 3.9 | 36 |
| 86 | OryzaGenome: Genome Diversity Database of Wild *Oryza* Species. Plant and Cell Physiology, 2016, 57, e1-e1. | 3.1 | 34 |
| 87 | Survey of the genetic information carried in the genome of Eucalyptus camaldulensis. Plant Biotechnology, 2011, 28, 471-480. | 1.0 | 33 |
| 88 | Activation tagging approach in a model legume, Lotus japonicus. Journal of Plant Research, 2005, 118, 391-399. | 2.4 | 32 |
| 89 | Potential of Oryza officinalis to augment the cold tolerance genetic mechanisms of Oryza sativa by network complementation. Scientific Reports, 2018, 8, 16346. | 3.3 | 32 |
| 90 | The DBCLS BioHackathon: standardization and interoperability for bioinformatics web services and workflows. Journal of Biomedical Semantics, 2010, 1, 8. | 1.6 | 31 |

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| 91 | Gene organization of human NOTCH4 and (CTG)n polymorphism in this human counterpart gene of mouse proto-oncogene Int3. Gene, 1997, 189, 235-244. | 2.2 | 30 |
| 92 | Complete Genome Structure of the Thermophilic Cyanobacterium Thermosynechococcus elongatus BP-1 (Supplement). DNA Research, 2002, 9, 135-148. | 3.4 | 29 |
| 93 | Loss of Cytochrome cM Stimulates Cyanobacterial Heterotrophic Growth in the Dark. Plant and Cell Physiology, 2015, 56, 334-345. | 3.1 | 28 |
| 94 | Distinctive Features of Plant Organs Characterized by Global Analysis of Gene Expression in Arabidopsis. DNA Research, 2004, 11, 11-25. | 3.4 | 27 |
| 95 | Complete genome sequence of cyanobacterium Fischerella sp. NIES-3754, providing thermoresistant optogenetic tools. Journal of Biotechnology, 2016, 220, 45-46. | 3.8 | 27 |
| 96 | Codon-Anticodon Assignment and Detection of Codon Usage Trends in Seven Microbial Genomes. Microbial & Comparative Genomics, 1997, 2, 299-312. | 0.4 | 25 |
| 97 | Structural Analysis of a Lotus japonicus Genome. III. Sequence Features and Mapping of Sixty-two TAC Clones Which Cover the 6.7 Mb Regions of the Genome. DNA Research, 2003, 10, 27-33. | 3.4 | 25 |
| 98 | Establishment of publicly available cDNA material and information resource of Chlamydomonas reinhardtii (Chlorophyta) to facilitate gene function analysis. Phycologia, 2004, 43, 722-726. | 1.4 | 24 |
| 99 | Complete nucleotide sequence of the mitochondrial DNA from a liverwort,Marchantia polymorpha. Plant Molecular Biology Reporter, 1992, 10, 105-163. | 1.8 | 23 |
| 100 | Extension of CyanoBase. CyanoMutants: repository of mutant information on Synechocystis sp. strain PCC6803. Nucleic Acids Research, 1999, 27, 66-68. | 14.5 | 23 |
| 101 | Mudi, a web tool for identifying mutations by bioinformatics analysis of wholeâ€genome sequence. Genes To Cells, 2014, 19, 517-527. | 1.2 | 21 |
| 102 | Detection of genes in Escherichia coli sequences determined by genome projects and prediction of protein production levels, based on multivariate diversity in codon usage. Bioinformatics, 1996, 12, 213-225. | 4.1 | 19 |
| 103 | Promoter trapping in Lotus japonicus reveals novel root and nodule GUS expression domains. Plant and Cell Physiology, 2005, 46, 1202-1212. | 3.1 | 19 |
| 104 | The 2nd DBCLS BioHackathon: interoperable bioinformatics Web services for integrated applications. Journal of Biomedical Semantics, 2011, 2, 4. | 1.6 | 19 |
| 105 | Commonalities and Differences among Symbiosis Islands of Three &lt;i&gt;Mesorhizobium loti&lt;/i&gt; Strains. Microbes and Environments, 2013, 28, 275-278. | 1.6 | 17 |
| 106 | Complete Genome Sequence of Aurantimicrobium minutum Type Strain KNC [T] , a Planktonic Ultramicrobacterium Isolated from River Water. Genome Announcements, 2016, 4, . | 0.8 | 17 |
| 107 | OryzaGenome2.1: Database of Diverse Genotypes in Wild Oryza Species. Rice, 2021, 14, 24. | 4.0 | 17 |
| 108 | Lactobacillus buchneri subsp. silagei subsp. nov., isolated from rice grain silage. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3111-3116. | 1.7 | 17 |

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|---|---------|----|-----------|
| 109 | Complete Genome Sequence of Bifidobacterium longum 105-A, a Strain with High Transformation Efficiency. Genome Announcements, 2014, 2, . | 0.8 | 16 |
| 110 | Repeated translocation of a supergene underlying rapid sex chromosome turnover in <i>Takifugu</i> pufferfish. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, . | 7.1 | 16 |
| 111 | Biological Databases at DNA Data Bank of Japan in the Era of Next-Generation Sequencing Technologies. Advances in Experimental Medicine and Biology, 2010, 680, 125-135. | 1.6 | 14 |
| 112 | Complete genome sequence of cyanobacterium Nostoc sp. NIES-3756, a potentially useful strain for phytochrome-based bioengineering. Journal of Biotechnology, 2016, 218, 51-52. | 3.8 | 14 |
| 113 | Lactobacillus salitolerans sp. nov., a novel lactic acid bacterium isolated from spent mushroom substrates. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 964-969. | 1.7 | 14 |
| 114 | Genome sequence and overview of Oligoflexus tunisiensis Shr3T in the eighth class Oligoflexia of the phylum Proteobacteria. Standards in Genomic Sciences, 2016, 11, 90. | 1.5 | 12 |
| 115 | Reclassification of Clostridium diolis Biebl and SprÃ¶er 2003 as a later heterotypic synonym of Clostridium beijerinckii Donker 1926 (Approved Lists 1980) emend. Keis et al. 2001. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2463-2466. | 1.7 | 12 |
| 116 | Genome sequencing of the NIES Cyanobacteria collection with a focus on the heterocyst-forming clade. DNA Research, 2021, 28, . | 3.4 | 12 |
| 117 | Draft Genome Sequence of Weissella oryzae SG25 T , Isolated from Fermented Rice Grains. Genome Announcements, 2014, 2, . | 0.8 | 11 |
| 118 | Plant Genome DataBase Japan (PGDBj). Methods in Molecular Biology, 2017, 1533, 45-77. | 0.9 | 10 |
| 119 | Draft Genome Sequence of the Nitrogen-Fixing and Hormogonia-Inducing Cyanobacterium <i>Nostoc cycadae</i> Strain WK-1, Isolated from the Coralloid Roots of <i>Cycas revoluta</i>. Genome Announcements, 2018, 6, . | 0.8 | 10 |
| 120 | Structural Analysis ofArabidopsis thaliana Chromosome 5. VI. Sequence Features of the Regions of 1,367,185 bp Covered by 19 Physically Assigned P1 and TAC Clones. DNA Research, 1998, 5, 203-216. | 3.4 | 9 |
| 121 | Sll0939 is induced by Slr0967 in the cyanobacterium Synechocystis sp. PCC6803 and is essential for growth under various stress conditions. Plant Physiology and Biochemistry, 2014, 81, 36-43. | 5.8 | 9 |
| 122 | Genome evolution of a nonparasitic secondary heterotroph, the diatom <i>Nitzschia putrida</i>. Science Advances, 2022, 8, eabi5075. | 10.3 | 9 |
| 123 | Plant and Cell Physiologyâ€™s 2018 Database Issue and Beyond. Plant and Cell Physiology, 2018, 59, 1-2. | 3.1 | 8 |
| 124 | Analysis of gene expression inArabidopsis thalianaby array hybridization with genomic DNA fragments aligned along chromosomal regions. Plant Journal, 2002, 30, 247-255. | 5.7 | 7 |
| 125 | SABRE2: A Database Connecting Plant EST/Full-Length cDNA Clones with Arabidopsis Information. Plant and Cell Physiology, 2014, 55, e5-e5. | 3.1 | 7 |
| 126 | Complete Genome Sequence of Cyanobacterium Leptolyngbya sp. NIES-3755. Genome Announcements, 2016, 4, . | 0.8 | 7 |

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| 127 | Generating Publication-Ready Prokaryotic Genome Annotations with DFAST. Methods in Molecular Biology, 2019, 1962, 215-226. | 0.9 | 7 |
| 128 | Reclassification of Paenibacillus thermophilus Zhou et al. 2013 as a later heterotypic synonym of Paenibacillus macerans (Schardinger 1905) Ash et al. 1994. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 417-421. | 1.7 | 7 |
| 129 | Mitochondrial genome of Garcinia mangostana L. variety Mesta. Scientific Reports, 2022, 12, . | 3.3 | 6 |
| 130 | Gene Encoding a Putative Zinc Finger Protein in Synechocystis PCC6803.. Agricultural and Biological Chemistry, 1991, 55, 2259-2264. | 0.3 | 5 |
| 131 | H2DB: a heritability database across multiple species by annotating trait-associated genomic loci. Nucleic Acids Research, 2013, 41, D880-D884. | 14.5 | 5 |
| 132 | Complete sequence and structure of the genome of the harmful algal bloom-forming cyanobacterium Planktothrix agardhii NIES-204T and detailed analysis of secondary metabolite gene clusters. Harmful Algae, 2021, 101, 101942. | 4.8 | 5 |
| 133 | The Arabidopsis TAC Position Viewer: a highâ€resolution map of transformationâ€competent artificial chromosome (<scp>TAC</scp>) clones aligned with the <i>Arabidopsis thaliana</i> Columbiaâ€0 genome. Plant Journal, 2015, 83, 1114-1122. | 5.7 | 4 |
| 134 | Complete Genome Sequence of a Coastal Cyanobacterium, <i>Synechococcus</i> sp. Strain NIES-970. Genome Announcements, 2017, 5, . | 0.8 | 3 |
| 135 | Meeting Report: â€œMetagenomics, Metadata and Meta-analysisâ€•(M3) Workshop at the Pacific Symposium on Biocomputing 2010. Standards in Genomic Sciences, 2010, 2, 357-360. | 1.5 | 2 |
| 136 | DDBJ Sequence Read Archive / DDBJ Omics Archive. Nature Precedings, 2010, , . | 0.1 | 2 |
| 137 | Genomic characterization reconfirms the taxonomic status of &lt;i&gt;Lactobacillus parakefiri&lt;/i&gt;. Bioscience of Microbiota, Food and Health, 2017, 36, 129-134. | 1.8 | 2 |
| 138 | DNApod: DNA polymorphism annotation database from next-generation sequence read archives. PLoS ONE, 2017, 12, e0172269. | 2.5 | 2 |
| 139 | Draft Genome Sequence of Lactobacillus oryzae Strain SG293 <sup>T</sup>. Genome Announcements, 2014, 2, . | 0.8 | 1 |
| 140 | Whole-exome sequencing of 79 xenografts as a potential approach for the identification of genetic variants associated with sensitivity to cytotoxic anticancer drugs. PLoS ONE, 2020, 15, e0239614. | 2.5 | 1 |
| 141 | <b><i>Methods for analyzing next-generation sequencing data </i></b><b><i>VII. long-read assembly </i></b>. Japanese Journal of Lactic Acid Bacteria, 2016, 27, 101-110. | 0.1 | 0 |
| 142 | <b>Methods for analyzing next-generation sequencing data VIII. Post-assembly analysis</b>. Japanese Journal of Lactic Acid Bacteria, 2016, 27, 187-195. | 0.1 | 0 |
| 143 | <b>Methods for analyzing next-generation sequencing dataVI. genome assembly </b>. Japanese Journal of Lactic Acid Bacteria, 2016, 27, 41-52. | 0.1 | 0 |
| 144 | <b>Methods for analyzing next-generation sequencing data IX.Genome annotation, visualization, and registration to DDBJ </b>. Japanese Journal of Lactic Acid Bacteria, 2017, 28, 3-11. | 0.1 | 0 |

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|---|---------|----|-----------|
| 145 | Be happy with your Perl scripts. Ikushugaku Kenkyu, 2016, 18, 27-33. | 0.3 | 0 |