

Yasukazu Nakamura, ????

List of Publications by Citations

Source: <https://exaly.com/author-pdf/5641713/yasukazu-nakamura-publications-by-citations.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

142
papers

20,099
citations

55
h-index

141
g-index

152
ext. papers

23,149
ext. citations

10
avg, IF

7.46
L-index

#	Paper	IF	Citations
142	Analysis of the genome sequence of the flowering plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000 , 408, 796-815	50.4	7262
141	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012 , 485, 635-41	50.4	2138
140	Plant recognition of symbiotic bacteria requires two LysM receptor-like kinases. <i>Nature</i> , 2003 , 425, 585-92	50.4	893
139	Complete genomic sequence of nitrogen-fixing symbiotic bacterium <i>Bradyrhizobium japonicum</i> USDA110. <i>DNA Research</i> , 2002 , 9, 189-97	4.5	637
138	Genome structure of the legume, <i>Lotus japonicus</i> . <i>DNA Research</i> , 2008 , 15, 227-39	4.5	558
137	Gene organization deduced from the complete sequence of liverwort <i>Marchantia polymorpha</i> mitochondrial DNA. A primitive form of plant mitochondrial genome. <i>Journal of Molecular Biology</i> , 1992 , 223, 1-7	6.5	545
136	Insights into Land Plant Evolution Garnered from the <i>Marchantia polymorpha</i> Genome. <i>Cell</i> , 2017 , 171, 287-304.e15	56.2	538
135	DFAST: a flexible prokaryotic genome annotation pipeline for faster genome publication. <i>Bioinformatics</i> , 2018 , 34, 1037-1039	7.2	371
134	<i>Klebsormidium flaccidum</i> genome reveals primary factors for plant terrestrial adaptation. <i>Nature Communications</i> , 2014 , 5, 3978	17.4	362
133	A nucleoporin is required for induction of Ca ²⁺ spiking in legume nodule development and essential for rhizobial and fungal symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 359-64	11.5	317
132	Complete genome structure of the thermophilic cyanobacterium <i>Thermosynechococcus elongatus</i> BP-1. <i>DNA Research</i> , 2002 , 9, 123-30	4.5	255
131	Complete genome structure of <i>Gloeobacter violaceus</i> PCC 7421, a cyanobacterium that lacks thylakoids. <i>DNA Research</i> , 2003 , 10, 137-45	4.5	209
130	Complete genomic structure of the bloom-forming toxic cyanobacterium <i>Microcystis aeruginosa</i> NIES-843. <i>DNA Research</i> , 2007 , 14, 247-56	4.5	202
129	Role of the putative membrane-bound endo-1,4-beta-glucanase KORRIGAN in cell elongation and cellulose synthesis in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2001 , 42, 251-63	4.9	178
128	The sulfate transporter <i>SST1</i> is crucial for symbiotic nitrogen fixation in <i>Lotus japonicus</i> root nodules. <i>Plant Cell</i> , 2005 , 17, 1625-36	11.6	173
127	Expression profiling-based identification of CO ₂ -responsive genes regulated by CCM1 controlling a carbon-concentrating mechanism in <i>Chlamydomonas reinhardtii</i> . <i>Plant Physiology</i> , 2004 , 135, 1595-607	6.6	163
126	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 <i>Lotus japonicus</i> . <i>Plant Physiology</i> , 2003 , 131, 941-51	6.6	156

125	Sequence and analysis of chromosome 3 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000 , 408, 820-2	50.4	153
124	CyanoBase, a www database containing the complete nucleotide sequence of the genome of <i>Synechocystis</i> sp. strain PCC6803. <i>Nucleic Acids Research</i> , 1998 , 26, 63-7	20.1	152
123	A large-scale protein protein interaction analysis in <i>Synechocystis</i> sp. PCC6803. <i>DNA Research</i> , 2007 , 14, 207-16	4.5	149
122	Sequence and analysis of chromosome 5 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000 , 408, 823-6	50.4	137
121	Complete genomic structure of the cultivated rice endophyte <i>Azospirillum</i> sp. B510. <i>DNA Research</i> , 2010 , 17, 37-50	4.5	136
120	Gain-of-function phenotypes of chemically synthetic CLAVATA3/ESR-related (CLE) peptides in <i>Arabidopsis thaliana</i> and <i>Oryza sativa</i> . <i>Plant and Cell Physiology</i> , 2007 , 48, 1821-5	4.9	129
119	CyanoBase: the cyanobacteria genome database update 2010. <i>Nucleic Acids Research</i> , 2010 , 38, D379-81	20.1	128
118	Comprehensive structural analysis of the genome of red clover (<i>Trifolium pratense</i> L.). <i>DNA Research</i> , 2005 , 12, 301-64	4.5	120
117	DFAST and DAGA: web-based integrated genome annotation tools and resources. <i>Bioscience of Microbiota, Food and Health</i> , 2016 , 35, 173-184	3.2	117
116	Characterization of the soybean genome using EST-derived microsatellite markers. <i>DNA Research</i> , 2007 , 14, 271-81	4.5	110
115	Autocatalytic differentiation of epigenetic modifications within the <i>Arabidopsis</i> genome. <i>EMBO Journal</i> , 2010 , 29, 3496-506	13	102
114	Structural analysis of four large plasmids harboring in a unicellular cyanobacterium, <i>Synechocystis</i> sp. PCC 6803. <i>DNA Research</i> , 2003 , 10, 221-8	4.5	100
113	The International Nucleotide Sequence Database Collaboration. <i>Nucleic Acids Research</i> , 2013 , 41, D21-4	20.1	98
112	Generation of expressed sequence tags from low-CO ₂ and high-CO ₂ adapted cells of <i>Chlamydomonas reinhardtii</i> . <i>DNA Research</i> , 2000 , 7, 305-7	4.5	92
111	COMPARISON OF RNA EXPRESSION PROFILES BETWEEN THE TWO GENERATIONS OF PORPHYRA YEZOENSIS (RHODOPHYTA), BASED ON EXPRESSED SEQUENCE TAG FREQUENCY ANALYSIS. <i>Journal of Phycology</i> , 2003 , 39, 923-930	3	90
110	The International Nucleotide Sequence Database Collaboration. <i>Nucleic Acids Research</i> , 2012 , 40, D33-7	20.1	86
109	Development of a bacterial cell enrichment method and its application to the community analysis in soybean stems. <i>Microbial Ecology</i> , 2009 , 58, 703-14	4.4	85
108	SNP discovery and linkage map construction in cultivated tomato. <i>DNA Research</i> , 2010 , 17, 381-91	4.5	81

107	An interspecific linkage map of SSR and intronic polymorphism markers in tomato. <i>Theoretical and Applied Genetics</i> , 2010 , 121, 731-9	6	81
106	Host plant genome overcomes the lack of a bacterial gene for symbiotic nitrogen fixation. <i>Nature</i> , 2009 , 462, 514-7	50.4	77
105	The integral membrane protein SEN1 is required for symbiotic nitrogen fixation in <i>Lotus japonicus</i> nodules. <i>Plant and Cell Physiology</i> , 2012 , 53, 225-36	4.9	76
104	Codon usage tabulated from the international DNA sequence databases. <i>Nucleic Acids Research</i> , 1997 , 25, 244-5	20.1	76
103	Generation of 7137 non-redundant expressed sequence tags from a legume, <i>Lotus japonicus</i> . <i>DNA Research</i> , 2000 , 7, 127-30	4.5	76
102	The International Nucleotide Sequence Database Collaboration. <i>Nucleic Acids Research</i> , 2011 , 39, D15-8	20.1	75
101	Chromatin Organization in Early Land Plants Reveals an Ancestral Association between H3K27me3, Transposons, and Constitutive Heterochromatin. <i>Current Biology</i> , 2020 , 30, 573-588.e7	6.3	72
100	Codon usage tabulated from the international DNA sequence databases; its status 1999. <i>Nucleic Acids Research</i> , 1999 , 27, 292	20.1	72
99	Gene clusters for ribosomal proteins in the mitochondrial genome of a liverwort, <i>Marchantia polymorpha</i> . <i>Nucleic Acids Research</i> , 1992 , 20, 3199-205	20.1	71
98	Genome-wide association study and genomic prediction in citrus: Potential of genomics-assisted breeding for fruit quality traits. <i>Scientific Reports</i> , 2017 , 7, 4721	4.9	69
97	CyanoBase: a large-scale update on its 20th anniversary. <i>Nucleic Acids Research</i> , 2017 , 45, D551-D554	20.1	64
96	DDBJ read annotation pipeline: a cloud computing-based pipeline for high-throughput analysis of next-generation sequencing data. <i>DNA Research</i> , 2013 , 20, 383-90	4.5	63
95	DDBJ launches a new archive database with analytical tools for next-generation sequence data. <i>Nucleic Acids Research</i> , 2010 , 38, D33-8	20.1	63
94	A large scale analysis of protein-protein interactions in the nitrogen-fixing bacterium <i>Mesorhizobium loti</i> . <i>DNA Research</i> , 2008 , 15, 13-23	4.5	63
93	Codon usage tabulated from the international DNA sequence databases. <i>Nucleic Acids Research</i> , 1998 , 26, 334	20.1	63
92	Genome-wide analysis of ATP-binding cassette (ABC) proteins in a model legume plant, <i>Lotus japonicus</i> : comparison with <i>Arabidopsis</i> ABC protein family. <i>DNA Research</i> , 2006 , 13, 205-28	4.5	62
91	Complete genomic sequence of nitrogen-fixing symbiotic bacterium <i>Bradyrhizobium japonicum</i> USDA110 (supplement). <i>DNA Research</i> , 2002 , 9, 225-56	4.5	61
90	DNA Data Bank of Japan. <i>Nucleic Acids Research</i> , 2017 , 45, D25-D31	20.1	58

89	DNA data bank of Japan (DDBJ) progress report. <i>Nucleic Acids Research</i> , 2016 , 44, D51-7	20.1	58
88	Characteristics of the <i>Lotus japonicus</i> gene repertoire deduced from large-scale expressed sequence tag (EST) analysis. <i>Plant Molecular Biology</i> , 2004 , 54, 405-14	4.6	58
87	Hybrid Origins of Citrus Varieties Inferred from DNA Marker Analysis of Nuclear and Organelle Genomes. <i>PLoS ONE</i> , 2016 , 11, e0166969	3.7	55
86	Comparison of the transcript profiles from the root and the nodulating root of the model legume <i>Lotus japonicus</i> by serial analysis of gene expression. <i>Molecular Plant-Microbe Interactions</i> , 2005 , 18, 487-98	3.6	54
85	CyanoBase and RhizoBase: databases of manually curated annotations for cyanobacterial and rhizobial genomes. <i>Nucleic Acids Research</i> , 2014 , 42, D666-70	20.1	53
84	Genome sequencing and genome resources in model legumes. <i>Plant Physiology</i> , 2007 , 144, 588-93	6.6	50
83	Genome-wide analysis of intraspecific DNA polymorphism in Micro-Tomp, a model cultivar of tomato (<i>Solanum lycopersicum</i>). <i>Plant and Cell Physiology</i> , 2014 , 55, 445-54	4.9	49
82	The genomic standards consortium: bringing standards to life for microbial ecology. <i>ISME Journal</i> , 2011 , 5, 1565-7	11.9	48
81	Structural analysis of a <i>Lotus japonicus</i> genome. II. Sequence features and mapping of sixty-five TAC clones which cover the 6.5-mb regions of the genome. <i>DNA Research</i> , 2002 , 9, 63-70	4.5	48
80	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. <i>Nucleic Acids Research</i> , 1993 , 21, 1297-305	20.1	48
79	Complete genome sequence of <i>Bradyrhizobium</i> sp. S23321: insights into symbiosis evolution in soil oligotrophs. <i>Microbes and Environments</i> , 2012 , 27, 306-15	2.6	46
78	Structural analysis of a <i>Lotus japonicus</i> genome. V. Sequence features and mapping of sixty-four TAC clones which cover the 6.4 mb regions of the genome. <i>DNA Research</i> , 2003 , 10, 277-85	4.5	46
77	Transfer RNA genes in the mitochondrial genome from a liverwort, <i>Marchantia polymorpha</i> : the absence of chloroplast-like tRNAs. <i>Nucleic Acids Research</i> , 1992 , 20, 3773-7	20.1	46
76	The DDBJ Japanese Genotype-phenotype Archive for genetic and phenotypic human data. <i>Nucleic Acids Research</i> , 2015 , 43, D18-22	20.1	45
75	Codon usage tabulated from the international DNA sequence databases. <i>Nucleic Acids Research</i> , 1996 , 24, 214-5	20.1	44
74	The DNA Data Bank of Japan launches a new resource, the DDBJ Omics Archive of functional genomics experiments. <i>Nucleic Acids Research</i> , 2012 , 40, D38-42	20.1	39
73	Complete genome structure of <i>Gloeobacter violaceus</i> PCC 7421, a cyanobacterium that lacks thylakoids (supplement). <i>DNA Research</i> , 2003 , 10, 181-201	4.5	39
72	DNA Data Bank of Japan: 30th anniversary. <i>Nucleic Acids Research</i> , 2018 , 46, D30-D35	20.1	38

71	The Naming of Names: Guidelines for Gene Nomenclature in Marchantia. <i>Plant and Cell Physiology</i> , 2016 , 57, 257-61	4.9	38
70	Genome-wide analyses of the structural gene families involved in the legume-specific 5-deoxyisoflavonoid biosynthesis of Lotus japonicus. <i>DNA Research</i> , 2007 , 14, 25-36	4.5	38
69	Draft Sequencing of the Heterozygous Diploid Genome of Satsuma (Marc.) Using a Hybrid Assembly Approach. <i>Frontiers in Genetics</i> , 2017 , 8, 180	4.5	36
68	DDBJ progress report. <i>Nucleic Acids Research</i> , 2011 , 39, D22-7	20.1	34
67	DDBJ progress report: a new submission system for leading to a correct annotation. <i>Nucleic Acids Research</i> , 2014 , 42, D44-9	20.1	32
66	Construction of signature-tagged mutant library in Mesorhizobium loti as a powerful tool for functional genomics. <i>DNA Research</i> , 2008 , 15, 297-308	4.5	32
65	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. <i>DNA Research</i> , 2003 , 10, 115-22	4.5	32
64	Activation tagging approach in a model legume, Lotus japonicus. <i>Journal of Plant Research</i> , 2005 , 118, 391-9	2.6	31
63	Plant Genome DataBase Japan (PGDBj): a portal website for the integration of plant genome-related databases. <i>Plant and Cell Physiology</i> , 2014 , 55, e8	4.9	30
62	Survey of the genetic information carried in the genome of Eucalyptus camaldulensis. <i>Plant Biotechnology</i> , 2011 , 28, 471-480	1.3	27
61	Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1 (supplement). <i>DNA Research</i> , 2002 , 9, 135-48	4.5	27
60	Complete genome sequence and analysis of Lactobacillus hokkaidonensis LOOC260(T), a psychrotrophic lactic acid bacterium isolated from silage. <i>BMC Genomics</i> , 2015 , 16, 240	4.5	26
59	OryzaGenome: Genome Diversity Database of Wild Oryza Species. <i>Plant and Cell Physiology</i> , 2016 , 57, e1	4.9	26
58	Toward richer metadata for microbial sequences: replacing strain-level NCBI taxonomy taxids with BioProject, BioSample and Assembly records. <i>Standards in Genomic Sciences</i> , 2014 , 9, 1275-7		26
57	DDBJ new system and service refactoring. <i>Nucleic Acids Research</i> , 2013 , 41, D25-9	20.1	26
56	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. <i>DNA Research</i> , 2003 , 10, 27-33	4.5	25
55	The DBCLS BioHackathon: standardization and interoperability for bioinformatics web services and workflows. The DBCLS BioHackathon Consortium*. <i>Journal of Biomedical Semantics</i> , 2010 , 1, 8	2.2	24
54	Gene organization of human NOTCH4 and (CTG) _n polymorphism in this human counterpart gene of mouse proto-oncogene Int3. <i>Gene</i> , 1997 , 189, 235-44	3.8	24

53	Distinctive features of plant organs characterized by global analysis of gene expression in <i>Arabidopsis</i> . <i>DNA Research</i> , 2004 , 11, 11-25	4.5	23
52	Establishment of publicly available cDNA material and information resource of <i>Chlamydomonas reinhardtii</i> (Chlorophyta) to facilitate gene function analysis. <i>Phycologia</i> , 2004 , 43, 722-726	2.7	22
51	Complete nucleotide sequence of the mitochondrial DNA from a liverwort, <i>Marchantia polymorpha</i> . <i>Plant Molecular Biology Reporter</i> , 1992 , 10, 105-163	1.7	22
50	Loss of cytochrome cM stimulates cyanobacterial heterotrophic growth in the dark. <i>Plant and Cell Physiology</i> , 2015 , 56, 334-45	4.9	21
49	Extension of CyanoBase. CyanoMutants: repository of mutant information on <i>Synechocystis</i> sp. strain PCC6803. <i>Nucleic Acids Research</i> , 1999 , 27, 66-8	20.1	21
48	Large-scale genome analysis of bovine commensal reveals that bovine-adapted lineages are serving as evolutionary sources of the emergence of human intestinal pathogenic strains. <i>Genome Research</i> , 2019 , 29, 1495-1505	9.7	18
47	Codon-anticodon assignment and detection of codon usage trends in seven microbial genomes. <i>Microbial & Comparative Genomics</i> , 1997 , 2, 299-312		18
46	<i>Lactobacillus paragasseri</i> sp. nov., a sister taxon of <i>Lactobacillus gasseri</i> , based on whole-genome sequence analyses. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018 , 68, 3512-3517 ²		18
45	Complete genome sequence of cyanobacterium <i>Fischerella</i> sp. NIES-3754, providing thermoresistant optogenetic tools. <i>Journal of Biotechnology</i> , 2016 , 220, 45-6	3.7	17
44	Promoter trapping in <i>Lotus japonicus</i> reveals novel root and nodule GUS expression domains. <i>Plant and Cell Physiology</i> , 2005 , 46, 1202-12	4.9	17
43	Potential of <i>Oryza officinalis</i> to augment the cold tolerance genetic mechanisms of <i>Oryza sativa</i> by network complementation. <i>Scientific Reports</i> , 2018 , 8, 16346	4.9	16
42	Complete Genome Sequence of <i>Bifidobacterium longum</i> 105-A, a Strain with High Transformation Efficiency. <i>Genome Announcements</i> , 2014 , 2,		15
41	The 2nd DBCLS BioHackathon: interoperable bioinformatics Web services for integrated applications. <i>Journal of Biomedical Semantics</i> , 2011 , 2, 4	2.2	15
40	Mudi, a web tool for identifying mutations by bioinformatics analysis of whole-genome sequence. <i>Genes To Cells</i> , 2014 , 19, 517-27	2.3	14
39	Commonalities and differences among symbiosis islands of three <i>Mesorhizobium loti</i> strains. <i>Microbes and Environments</i> , 2013 , 28, 275-8	2.6	13
38	Complete Genome Sequence of <i>Aurantimicrobium minutum</i> Type Strain KNCT, a Planktonic Ultramicrobacterium Isolated from River Water. <i>Genome Announcements</i> , 2016 , 4,		13
37	Complete genome sequence of cyanobacterium <i>Nostoc</i> sp. NIES-3756, a potentially useful strain for phytochrome-based bioengineering. <i>Journal of Biotechnology</i> , 2016 , 218, 51-2	3.7	11
36	Biological databases at DNA Data Bank of Japan in the era of next-generation sequencing technologies. <i>Advances in Experimental Medicine and Biology</i> , 2010 , 680, 125-35	3.6	10

35	Structural analysis of Arabidopsis thaliana chromosome 5. VI. Sequence features of the regions of 1,367,185 bp covered by 19 physically assigned P1 and TAC clones. <i>DNA Research</i> , 1998 , 5, 203-16	4.5	9
34	Detection of genes in Escherichia coli sequences determined by genome projects and prediction of protein production levels, based on multivariate diversity in codon usage. <i>Bioinformatics</i> , 1996 , 12, 213-25 ²	7.2	8
33	Plant Genome DataBase Japan (PGDBj). <i>Methods in Molecular Biology</i> , 2017 , 1533, 45-77	1.4	7
32	Sll0939 is induced by Slr0967 in the cyanobacterium Synechocystis sp. PCC6803 and is essential for growth under various stress conditions. <i>Plant Physiology and Biochemistry</i> , 2014 , 81, 36-43	5.4	7
31	Draft Genome Sequence of Weissella oryzae SG25T, Isolated from Fermented Rice Grains. <i>Genome Announcements</i> , 2014 , 2,		7
30	Analysis of gene expression in Arabidopsis thaliana by array hybridization with genomic DNA fragments aligned along chromosomal regions. <i>Plant Journal</i> , 2002 , 30, 247-55	6.9	7
29	Genome sequence and overview of Shr3 in the eighth class of the phylum. <i>Standards in Genomic Sciences</i> , 2016 , 11, 90		6
28	Draft Genome Sequence of the Nitrogen-Fixing and Hormogonia-Inducing Cyanobacterium Strain WK-1, Isolated from the Coralloid Roots of. <i>Genome Announcements</i> , 2018 , 6,		6
27	SABRE2: a database connecting plant EST/full-length cDNA clones with Arabidopsis information. <i>Plant and Cell Physiology</i> , 2014 , 55, e5	4.9	6
26	Generating Publication-Ready Prokaryotic Genome Annotations with DFAST. <i>Methods in Molecular Biology</i> , 2019 , 1962, 215-226	1.4	5
25	Complete Genome Sequence of Cyanobacterium Leptolyngbya sp. NIES-3755. <i>Genome Announcements</i> , 2016 , 4,		5
24	H2DB: a heritability database across multiple species by annotating trait-associated genomic loci. <i>Nucleic Acids Research</i> , 2013 , 41, D880-4	20.1	5
23	Gene Encoding a Putative Zinc Finger Protein in Synechocystis PCC6803.. <i>Agricultural and Biological Chemistry</i> , 1991 , 55, 2259-2264		5
22	Identification of the sex-determining factor in the liverwort Marchantia polymorpha reveals unique evolution of sex chromosomes in a haploid system. <i>Current Biology</i> , 2021 ,	6.3	5
21	Genome sequencing of the NIES Cyanobacteria collection with a focus on the heterocyst-forming clade. <i>DNA Research</i> , 2021 , 28,	4.5	5
20	Reclassification of Biebl and Spröer 2003 as a later heterotypic synonym of Donker 1926 (Approved Lists 1980) emend. Keis . 2001. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020 , 70, 2463-2466	2.2	4
19	OryzaGenome2.1: Database of Diverse Genotypes in Wild Oryza Species. <i>Rice</i> , 2021 , 14, 24	5.8	4
18	Lactobacillus salitolerans sp. nov., a novel lactic acid bacterium isolated from spent mushroom substrates. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019 , 69, 964-969	2.2	3

17	The Arabidopsis TAC Position Viewer: a high-resolution map of transformation-competent artificial chromosome (TAC) clones aligned with the Arabidopsis thaliana Columbia-0 genome. <i>Plant Journal</i> , 2015 , 83, 1114-22	6.9	2
16	Meeting Report: "Metagenomics, Metadata and Meta-analysis" (M3) Workshop at the Pacific Symposium on Biocomputing 2010. <i>Standards in Genomic Sciences</i> , 2010 , 2, 357-60		2
15	Complete Genome Sequence of a Coastal Cyanobacterium, sp. Strain NIES-970. <i>Genome Announcements</i> , 2017 , 5,		2
14	DNApod: DNA polymorphism annotation database from next-generation sequence read archives. <i>PLoS ONE</i> , 2017 , 12, e0172269	3.7	2
13	AnAms1.0: A high-quality chromosome-scale assembly of a domestic cat Felis catus of American Shorthair breed		2
12	subsp. subsp. nov., isolated from rice grain silage. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020 , 70, 3111-3116	2.2	2
11	Complete sequence and structure of the genome of the harmful algal bloom-forming cyanobacterium Planktothrix agardhii NIES-204 and detailed analysis of secondary metabolite gene clusters. <i>Harmful Algae</i> , 2021 , 101, 101942	5.3	2
10	Genome evolution of a nonparasitic secondary heterotroph, the diatom .. <i>Science Advances</i> , 2022 , 8, eabi5075	5.0	2
9	Draft Genome Sequence of Lactobacillus oryzae Strain SG293T. <i>Genome Announcements</i> , 2014 , 2,		1
8	Genomic characterization reconfirms the taxonomic status of. <i>Bioscience of Microbiota, Food and Health</i> , 2017 , 36, 129-134	3.2	1
7	Whole-exome sequencing of 79 xenografts as a potential approach for the identification of genetic variants associated with sensitivity to cytotoxic anticancer drugs. <i>PLoS ONE</i> , 2020 , 15, e0239614	3.7	1
6	Reclassification of Paenibacillus thermophilus Zhou et al. 2013 as a later heterotypic synonym of Paenibacillus macerans (Schardinger 1905) Ash et al. 1994. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019 , 69, 417-421	2.2	0
5	Methods for analyzing next-generation sequencing data IX.Genome annotation, visualization, and registration to DDBJ . <i>Japanese Journal of Lactic Acid Bacteria</i> , 2017 , 28, 3-11	0	
4	Methods for analyzing next-generation sequencing data VII. long-read assembly . <i>Japanese Journal of Lactic Acid Bacteria</i> , 2016 , 27, 101-110	0	
3	Methods for analyzing next-generation sequencing data VIII. Post-assembly analysis. <i>Japanese Journal of Lactic Acid Bacteria</i> , 2016 , 27, 187-195	0	
2	Methods for analyzing next-generation sequencing dataVI. genome assembly . <i>Japanese Journal of Lactic Acid Bacteria</i> , 2016 , 27, 41-52	0	
1	Be happy with your Perl scripts. <i>Ikushugaku Kenkyu</i> , 2016 , 18, 27-33	0.1	