

# Yasukazu Nakamura, ????

## List of Publications by Year in Descending Order

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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	Genome evolution of a nonparasitic secondary heterotroph, the diatom .. <i>Science Advances</i> , <b>2022</b> , 8, eabi5075	14.7	2
141	Identification of the sex-determining factor in the liverwort <i>Marchantia polymorpha</i> reveals unique evolution of sex chromosomes in a haploid system. <i>Current Biology</i> , <b>2021</b> ,	6.3	5
140	Genome sequencing of the NIES Cyanobacteria collection with a focus on the heterocyst-forming clade. <i>DNA Research</i> , <b>2021</b> , 28,	4.5	5
139	Complete sequence and structure of the genome of the harmful algal bloom-forming cyanobacterium <i>Planktothrix agardhii</i> NIES-204 and detailed analysis of secondary metabolite gene clusters. <i>Harmful Algae</i> , <b>2021</b> , 101, 101942	5.3	2
138	OryzaGenome2.1: Database of Diverse Genotypes in Wild Oryza Species. <i>Rice</i> , <b>2021</b> , 14, 24	5.8	4
137	Chromatin Organization in Early Land Plants Reveals an Ancestral Association between H3K27me3, Transposons, and Constitutive Heterochromatin. <i>Current Biology</i> , <b>2020</b> , 30, 573-588.e7	6.3	72
136	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> , <b>2020</b> , 15, e0239614	3.7	1
135	Reclassification of Biebl and Sprär 2003 as a later heterotypic synonym of Donker 1926 (Approved Lists 1980) emend. Keis . 2001. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2020</b> , 70, 2463-2466	2.2	4
134	subsp. subsp. nov., isolated from rice grain silage. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2020</b> , 70, 3111-3116	2.2	2
133	Generating Publication-Ready Prokaryotic Genome Annotations with DFAST. <i>Methods in Molecular Biology</i> , <b>2019</b> , 1962, 215-226	1.4	5
132	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> , <b>2019</b> , 29, 1495-1505	9.7	18
131	Reclassification of <i>Paenibacillus thermophilus</i> Zhou et al. 2013 as a later heterotypic synonym of <i>Paenibacillus macerans</i> (Schardinger 1905) Ash et al. 1994. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2019</b> , 69, 417-421	2.2	0
130	<i>Lactobacillus salitolerans</i> sp. nov., a novel lactic acid bacterium isolated from spent mushroom substrates. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2019</b> , 69, 964-969	2.2	3
129	DFAST: a flexible prokaryotic genome annotation pipeline for faster genome publication. <i>Bioinformatics</i> , <b>2018</b> , 34, 1037-1039	7.2	371
128	DNA Data Bank of Japan: 30th anniversary. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D30-D35	20.1	38
127	Draft Genome Sequence of the Nitrogen-Fixing and Hormogonia-Inducing Cyanobacterium Strain WK-1, Isolated from the Coralloid Roots of. <i>Genome Announcements</i> , <b>2018</b> , 6,		6
126	<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> , <b>2018</b> , 68, 3512-3517 <sup>2</sup>	17.2	18

125	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> , <b>2018</b> , 8, 16346	4.9	16
124	Plant Genome DataBase Japan (PGDBj). <i>Methods in Molecular Biology</i> , <b>2017</b> , 1533, 45-77	1.4	7
123	Insights into Land Plant Evolution Garnered from the <i>Marchantia polymorpha</i> Genome. <i>Cell</i> , <b>2017</b> , 171, 287-304.e15	56.2	538
122	CyanoBase: a large-scale update on its 20th anniversary. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D551-D554	20.1	64
121	Methods for analyzing next-generation sequencing data IX. Genome annotation, visualization, and registration to DDBJ. <i>Japanese Journal of Lactic Acid Bacteria</i> , <b>2017</b> , 28, 3-11	0	
120	DNA Data Bank of Japan. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D25-D31	20.1	58
119	Genome-wide association study and genomic prediction in citrus: Potential of genomics-assisted breeding for fruit quality traits. <i>Scientific Reports</i> , <b>2017</b> , 7, 4721	4.9	69
118	Genomic characterization reconfirms the taxonomic status of. <i>Bioscience of Microbiota, Food and Health</i> , <b>2017</b> , 36, 129-134	3.2	1
117	Draft Sequencing of the Heterozygous Diploid Genome of Satsuma ( Marc.) Using a Hybrid Assembly Approach. <i>Frontiers in Genetics</i> , <b>2017</b> , 8, 180	4.5	36
116	Complete Genome Sequence of a Coastal Cyanobacterium, sp. Strain NIES-970. <i>Genome Announcements</i> , <b>2017</b> , 5,		2
115	DNAPod: DNA polymorphism annotation database from next-generation sequence read archives. <i>PLoS ONE</i> , <b>2017</b> , 12, e0172269	3.7	2
114	Methods for analyzing next-generation sequencing data VII. long-read assembly. <i>Japanese Journal of Lactic Acid Bacteria</i> , <b>2016</b> , 27, 101-110	0	
113	Methods for analyzing next-generation sequencing data VIII. Post-assembly analysis. <i>Japanese Journal of Lactic Acid Bacteria</i> , <b>2016</b> , 27, 187-195	0	
112	Methods for analyzing next-generation sequencing data VI. genome assembly. <i>Japanese Journal of Lactic Acid Bacteria</i> , <b>2016</b> , 27, 41-52	0	
111	Genome sequence and overview of Shr3 in the eighth class of the phylum. <i>Standards in Genomic Sciences</i> , <b>2016</b> , 11, 90		6
110	Complete genome sequence of cyanobacterium <i>Fischerella</i> sp. NIES-3754, providing thermoresistant optogenetic tools. <i>Journal of Biotechnology</i> , <b>2016</b> , 220, 45-6	3.7	17
109	OryzaGenome: Genome Diversity Database of Wild <i>Oryza</i> Species. <i>Plant and Cell Physiology</i> , <b>2016</b> , 57, e1	4.9	26
108	Complete genome sequence of cyanobacterium <i>Nostoc</i> sp. NIES-3756, a potentially useful strain for phytochrome-based bioengineering. <i>Journal of Biotechnology</i> , <b>2016</b> , 218, 51-2	3.7	11

107	The Naming of Names: Guidelines for Gene Nomenclature in Marchantia. <i>Plant and Cell Physiology</i> , <b>2016</b> , 57, 257-61	4.9	38
106	DNA data bank of Japan (DDBJ) progress report. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D51-7	20.1	58
105	Complete Genome Sequence of Cyanobacterium Leptolyngbya sp. NIES-3755. <i>Genome Announcements</i> , <b>2016</b> , 4,		5
104	Hybrid Origins of Citrus Varieties Inferred from DNA Marker Analysis of Nuclear and Organelle Genomes. <i>PLoS ONE</i> , <b>2016</b> , 11, e0166969	3.7	55
103	Be happy with your Perl scripts. <i>Ikushugaku Kenkyu</i> , <b>2016</b> , 18, 27-33	0.1	
102	Complete Genome Sequence of Aurantimicrobium minutum Type Strain KNCT, a Planktonic Ultramicrobacterium Isolated from River Water. <i>Genome Announcements</i> , <b>2016</b> , 4,		13
101	DFAST and DAGA: web-based integrated genome annotation tools and resources. <i>Bioscience of Microbiota, Food and Health</i> , <b>2016</b> , 35, 173-184	3.2	117
100	Complete genome sequence and analysis of Lactobacillus hokkaidonensis LOOC260(T), a psychrotrophic lactic acid bacterium isolated from silage. <i>BMC Genomics</i> , <b>2015</b> , 16, 240	4.5	26
99	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> , <b>2015</b> , 83, 1114-22	6.9	2
98	The DDBJ Japanese Genotype-phenotype Archive for genetic and phenotypic human data. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D18-22	20.1	45
97	Loss of cytochrome cM stimulates cyanobacterial heterotrophic growth in the dark. <i>Plant and Cell Physiology</i> , <b>2015</b> , 56, 334-45	4.9	21
96	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> , <b>2014</b> , 81, 36-43	5.4	7
95	SABRE2: a database connecting plant EST/full-length cDNA clones with Arabidopsis information. <i>Plant and Cell Physiology</i> , <b>2014</b> , 55, e5	4.9	6
94	Klebsormidium flaccidum genome reveals primary factors for plant terrestrial adaptation. <i>Nature Communications</i> , <b>2014</b> , 5, 3978	17.4	362
93	CyanoBase and RhizoBase: databases of manually curated annotations for cyanobacterial and rhizobial genomes. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D666-70	20.1	53
92	Draft Genome Sequence of Lactobacillus oryzae Strain SG293T. <i>Genome Announcements</i> , <b>2014</b> , 2,		1
91	Toward richer metadata for microbial sequences: replacing strain-level NCBI taxonomy taxids with BioProject, BioSample and Assembly records. <i>Standards in Genomic Sciences</i> , <b>2014</b> , 9, 1275-7		26
90	DDBJ progress report: a new submission system for leading to a correct annotation. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D44-9	20.1	32

89	Complete Genome Sequence of <i>Bifidobacterium longum</i> 105-A, a Strain with High Transformation Efficiency. <i>Genome Announcements</i> , <b>2014</b> , 2,		15
88	Mudi, a web tool for identifying mutations by bioinformatics analysis of whole-genome sequence. <i>Genes To Cells</i> , <b>2014</b> , 19, 517-27	2.3	14
87	Plant Genome DataBase Japan (PGDBj): a portal website for the integration of plant genome-related databases. <i>Plant and Cell Physiology</i> , <b>2014</b> , 55, e8	4.9	30
86	Draft Genome Sequence of <i>Weissella oryzae</i> SG25T, Isolated from Fermented Rice Grains. <i>Genome Announcements</i> , <b>2014</b> , 2,		7
85	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> , <b>2014</b> , 55, 445-54	4.9	49
84	DDBJ read annotation pipeline: a cloud computing-based pipeline for high-throughput analysis of next-generation sequencing data. <i>DNA Research</i> , <b>2013</b> , 20, 383-90	4.5	63
83	The International Nucleotide Sequence Database Collaboration. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D21-4	20.1	98
82	H2DB: a heritability database across multiple species by annotating trait-associated genomic loci. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D880-4	20.1	5
81	Commonalities and differences among symbiosis islands of three <i>Mesorhizobium loti</i> strains. <i>Microbes and Environments</i> , <b>2013</b> , 28, 275-8	2.6	13
80	DDBJ new system and service refactoring. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D25-9	20.1	26
79	Complete genome sequence of <i>Bradyrhizobium</i> sp. S23321: insights into symbiosis evolution in soil oligotrophs. <i>Microbes and Environments</i> , <b>2012</b> , 27, 306-15	2.6	46
78	The International Nucleotide Sequence Database Collaboration. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D33-7	20.1	86
77	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , <b>2012</b> , 485, 635-41	50.4	2138
76	The DNA Data Bank of Japan launches a new resource, the DDBJ Omics Archive of functional genomics experiments. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D38-42	20.1	39
75	The integral membrane protein SEN1 is required for symbiotic nitrogen fixation in <i>Lotus japonicus</i> nodules. <i>Plant and Cell Physiology</i> , <b>2012</b> , 53, 225-36	4.9	76
74	Survey of the genetic information carried in the genome of <i>Eucalyptus camaldulensis</i> . <i>Plant Biotechnology</i> , <b>2011</b> , 28, 471-480	1.3	27
73	The genomic standards consortium: bringing standards to life for microbial ecology. <i>ISME Journal</i> , <b>2011</b> , 5, 1565-7	11.9	48
72	The 2nd DBCLS BioHackathon: interoperable bioinformatics Web services for integrated applications. <i>Journal of Biomedical Semantics</i> , <b>2011</b> , 2, 4	2.2	15

71	DDBJ progress report. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D22-7	20.1	34
70	The International Nucleotide Sequence Database Collaboration. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D15-8	20.1	75
69	Autocatalytic differentiation of epigenetic modifications within the Arabidopsis genome. <i>EMBO Journal</i> , <b>2010</b> , 29, 3496-506	13	102
68	DDBJ launches a new archive database with analytical tools for next-generation sequence data. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D33-8	20.1	63
67	CyanoBase: the cyanobacteria genome database update 2010. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D379-81	20.1	128
66	Complete genomic structure of the cultivated rice endophyte <i>Azospirillum</i> sp. B510. <i>DNA Research</i> , <b>2010</b> , 17, 37-50	4.5	136
65	SNP discovery and linkage map construction in cultivated tomato. <i>DNA Research</i> , <b>2010</b> , 17, 381-91	4.5	81
64	Biological databases at DNA Data Bank of Japan in the era of next-generation sequencing technologies. <i>Advances in Experimental Medicine and Biology</i> , <b>2010</b> , 680, 125-35	3.6	10
63	Meeting Report: "Metagenomics, Metadata and Meta-analysis" (M3) Workshop at the Pacific Symposium on Biocomputing 2010. <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 357-60		2
62	An interspecific linkage map of SSR and intronic polymorphism markers in tomato. <i>Theoretical and Applied Genetics</i> , <b>2010</b> , 121, 731-9	6	81
61	The DBCLS BioHackathon: standardization and interoperability for bioinformatics web services and workflows. The DBCLS BioHackathon Consortium*. <i>Journal of Biomedical Semantics</i> , <b>2010</b> , 1, 8	2.2	24
60	Development of a bacterial cell enrichment method and its application to the community analysis in soybean stems. <i>Microbial Ecology</i> , <b>2009</b> , 58, 703-14	4.4	85
59	Host plant genome overcomes the lack of a bacterial gene for symbiotic nitrogen fixation. <i>Nature</i> , <b>2009</b> , 462, 514-7	50.4	77
58	A large scale analysis of protein-protein interactions in the nitrogen-fixing bacterium <i>Mesorhizobium loti</i> . <i>DNA Research</i> , <b>2008</b> , 15, 13-23	4.5	63
57	Genome structure of the legume, <i>Lotus japonicus</i> . <i>DNA Research</i> , <b>2008</b> , 15, 227-39	4.5	558
56	Construction of signature-tagged mutant library in <i>Mesorhizobium loti</i> as a powerful tool for functional genomics. <i>DNA Research</i> , <b>2008</b> , 15, 297-308	4.5	32
55	Characterization of the soybean genome using EST-derived microsatellite markers. <i>DNA Research</i> , <b>2007</b> , 14, 271-81	4.5	110
54	Complete genomic structure of the bloom-forming toxic cyanobacterium <i>Microcystis aeruginosa</i> NIES-843. <i>DNA Research</i> , <b>2007</b> , 14, 247-56	4.5	202

53	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> , <b>2007</b> , 48, 1821-5	4.9	129
52	A large-scale protein protein interaction analysis in <i>Synechocystis</i> sp. PCC6803. <i>DNA Research</i> , <b>2007</b> , 14, 207-16	4.5	149
51	Genome-wide analyses of the structural gene families involved in the legume-specific 5-deoxyisoflavonoid biosynthesis of <i>Lotus japonicus</i> . <i>DNA Research</i> , <b>2007</b> , 14, 25-36	4.5	38
50	Genome sequencing and genome resources in model legumes. <i>Plant Physiology</i> , <b>2007</b> , 144, 588-93	6.6	50
49	A nucleoporin is required for induction of Ca <sup>2+</sup> 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> , <b>2006</b> , 103, 359-64	11.5	317
48	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> , <b>2006</b> , 13, 205-28	4.5	62
47	The sulfate transporter SST1 is crucial for symbiotic nitrogen fixation in <i>Lotus japonicus</i> root nodules. <i>Plant Cell</i> , <b>2005</b> , 17, 1625-36	11.6	173
46	Comprehensive structural analysis of the genome of red clover ( <i>Trifolium pratense</i> L.). <i>DNA Research</i> , <b>2005</b> , 12, 301-64	4.5	120
45	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> , <b>2005</b> , 18, 487-98	3.6	54
44	Activation tagging approach in a model legume, <i>Lotus japonicus</i> . <i>Journal of Plant Research</i> , <b>2005</b> , 118, 391-9	2.6	31
43	Promoter trapping in <i>Lotus japonicus</i> reveals novel root and nodule GUS expression domains. <i>Plant and Cell Physiology</i> , <b>2005</b> , 46, 1202-12	4.9	17
42	Expression profiling-based identification of CO <sub>2</sub> -responsive genes regulated by CCM1 controlling a carbon-concentrating mechanism in <i>Chlamydomonas reinhardtii</i> . <i>Plant Physiology</i> , <b>2004</b> , 135, 1595-607	6.6	163
41	Distinctive features of plant organs characterized by global analysis of gene expression in <i>Arabidopsis</i> . <i>DNA Research</i> , <b>2004</b> , 11, 11-25	4.5	23
40	Characteristics of the <i>Lotus japonicus</i> gene repertoire deduced from large-scale expressed sequence tag (EST) analysis. <i>Plant Molecular Biology</i> , <b>2004</b> , 54, 405-14	4.6	58
39	Establishment of publicly available cDNA material and information resource of <i>Chlamydomonas reinhardtii</i> (Chlorophyta) to facilitate gene function analysis. <i>Phycologia</i> , <b>2004</b> , 43, 722-726	2.7	22
38	Structural analysis of a <i>Lotus japonicus</i> 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> , <b>2003</b> , 10, 27-33	4.5	25
37	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> , <b>2003</b> , 39, 923-930	3	90
36	Plant recognition of symbiotic bacteria requires two LysM receptor-like kinases. <i>Nature</i> , <b>2003</b> , 425, 585-92	5.4	893



35	Structural analysis of four large plasmids harboring in a unicellular cyanobacterium, <i>Synechocystis</i> sp. PCC 6803. <i>DNA Research</i> , <b>2003</b> , 10, 221-8	4.5	100
34	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> , <b>2003</b> , 131, 941-51	6.6	156
33	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> , <b>2003</b> , 10, 277-85	4.5	46
32	Complete genome structure of <i>Gloeobacter violaceus</i> PCC 7421, a cyanobacterium that lacks thylakoids (supplement). <i>DNA Research</i> , <b>2003</b> , 10, 181-201	4.5	39
31	Complete genome structure of <i>Gloeobacter violaceus</i> PCC 7421, a cyanobacterium that lacks thylakoids. <i>DNA Research</i> , <b>2003</b> , 10, 137-45	4.5	209
30	Structural analysis of a <i>Lotus japonicus</i> 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> , <b>2003</b> , 10, 115-22	4.5	32
29	Analysis of gene expression in <i>Arabidopsis thaliana</i> by array hybridization with genomic DNA fragments aligned along chromosomal regions. <i>Plant Journal</i> , <b>2002</b> , 30, 247-55	6.9	7
28	Complete genomic sequence of nitrogen-fixing symbiotic bacterium <i>Bradyrhizobium japonicum</i> USDA110. <i>DNA Research</i> , <b>2002</b> , 9, 189-97	4.5	637
27	Complete genome structure of the thermophilic cyanobacterium <i>Thermosynechococcus elongatus</i> BP-1. <i>DNA Research</i> , <b>2002</b> , 9, 123-30	4.5	255
26	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> , <b>2002</b> , 9, 63-70	4.5	48
25	Complete genome structure of the thermophilic cyanobacterium <i>Thermosynechococcus elongatus</i> BP-1 (supplement). <i>DNA Research</i> , <b>2002</b> , 9, 135-48	4.5	27
24	Complete genomic sequence of nitrogen-fixing symbiotic bacterium <i>Bradyrhizobium japonicum</i> USDA110 (supplement). <i>DNA Research</i> , <b>2002</b> , 9, 225-56	4.5	61
23	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> , <b>2001</b> , 42, 251-63	4.9	178
22	Sequence and analysis of chromosome 5 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , <b>2000</b> , 408, 823-6	50.4	137
21	Analysis of the genome sequence of the flowering plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , <b>2000</b> , 408, 796-815	50.4	7262
20	Sequence and analysis of chromosome 3 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , <b>2000</b> , 408, 820-2	50.4	153
19	Generation of 7137 non-redundant expressed sequence tags from a legume, <i>Lotus japonicus</i> . <i>DNA Research</i> , <b>2000</b> , 7, 127-30	4.5	76
18	Generation of expressed sequence tags from low-CO <sub>2</sub> and high-CO <sub>2</sub> adapted cells of <i>Chlamydomonas reinhardtii</i> . <i>DNA Research</i> , <b>2000</b> , 7, 305-7	4.5	92



17	Codon usage tabulated from the international DNA sequence databases; its status 1999. <i>Nucleic Acids Research</i> , <b>1999</b> , 27, 292	20.1	72
16	Extension of CyanoBase. CyanoMutants: repository of mutant information on <i>Synechocystis</i> sp. strain PCC6803. <i>Nucleic Acids Research</i> , <b>1999</b> , 27, 66-8	20.1	21
15	Structural analysis of <i>Arabidopsis thaliana</i> 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> , <b>1998</b> , 5, 203-16	4.5	9
14	CyanoBase, a www database containing the complete nucleotide sequence of the genome of <i>Synechocystis</i> sp. strain PCC6803. <i>Nucleic Acids Research</i> , <b>1998</b> , 26, 63-7	20.1	152
13	Codon usage tabulated from the international DNA sequence databases. <i>Nucleic Acids Research</i> , <b>1998</b> , 26, 334	20.1	63
12	Codon usage tabulated from the international DNA sequence databases. <i>Nucleic Acids Research</i> , <b>1997</b> , 25, 244-5	20.1	76
11	Codon-anticodon assignment and detection of codon usage trends in seven microbial genomes. <i>Microbial &amp; Comparative Genomics</i> , <b>1997</b> , 2, 299-312		18
10	Gene organization of human NOTCH4 and (CTG) <sub>n</sub> polymorphism in this human counterpart gene of mouse proto-oncogene Int3. <i>Gene</i> , <b>1997</b> , 189, 235-44	3.8	24
9	Codon usage tabulated from the international DNA sequence databases. <i>Nucleic Acids Research</i> , <b>1996</b> , 24, 214-5	20.1	44
8	Detection of genes in <i>Escherichia coli</i> sequences determined by genome projects and prediction of protein production levels, based on multivariate diversity in codon usage. <i>Bioinformatics</i> , <b>1996</b> , 12, 213-25 <sup>2</sup>	7.2	8
7	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> , <b>1993</b> , 21, 1297-305	20.1	48
6	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> , <b>1992</b> , 20, 3773-7	20.1	46
5	Gene clusters for ribosomal proteins in the mitochondrial genome of a liverwort, <i>Marchantia polymorpha</i> . <i>Nucleic Acids Research</i> , <b>1992</b> , 20, 3199-205	20.1	71
4	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> , <b>1992</b> , 223, 1-7	6.5	545
3	Complete nucleotide sequence of the mitochondrial DNA from a liverwort, <i>Marchantia polymorpha</i> . <i>Plant Molecular Biology Reporter</i> , <b>1992</b> , 10, 105-163	1.7	22
2	Gene Encoding a Putative Zinc Finger Protein in <i>Synechocystis</i> PCC6803.. <i>Agricultural and Biological Chemistry</i> , <b>1991</b> , 55, 2259-2264		5
1	AnAms1.0: A high-quality chromosome-scale assembly of a domestic cat <i>Felis catus</i> of American Shorthair breed		2