

Yasukazu Nakamura, ä, -æ'ä;ä, €

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5641713/publications.pdf>

Version: 2024-02-01

145
papers

25,443
citations

20797

60
h-index

9854

141
g-index

152
all docs

152
docs citations

152
times ranked

25636
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome evolution of a nonparasitic secondary heterotroph, the diatom <i>Nitzschia putrida</i> . Science Advances, 2022, 8, eabi5075.	4.7	9
2	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, .	3.3	16
3	Mitochondrial genome of <i>Garcinia mangostana</i> L. variety Mesta. Scientific Reports, 2022, 12, .	1.6	6
4	Complete sequence and structure of the genome of the harmful algal bloom-forming cyanobacterium <i>Planktothrix agardhii</i> NIES-204T and detailed analysis of secondary metabolite gene clusters. Harmful Algae, 2021, 101, 101942.	2.2	5
5	OryzaGenome2.1: Database of Diverse Genotypes in Wild <i>Oryza</i> Species. Rice, 2021, 14, 24.	1.7	17
6	Genome sequencing of the NIES Cyanobacteria collection with a focus on the heterocyst-forming clade. DNA Research, 2021, 28, .	1.5	12
7	Identification of the sex-determining factor in the liverwort <i>Marchantia polymorpha</i> reveals unique evolution of sex chromosomes in a haploid system. Current Biology, 2021, 31, 5522-5532.e7.	1.8	36
8	Chromatin Organization in Early Land Plants Reveals an Ancestral Association between H3K27me3, Transposons, and Constitutive Heterochromatin. Current Biology, 2020, 30, 573-588.e7.	1.8	160
9	Reclassification of <i>Clostridium diolis</i> Biebl and Spr�nger 2003 as a later heterotypic synonym of <i>Clostridium beijerinckii</i> Donker 1926 (Approved Lists 1980) emend. Keis et al. 2001. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2463-2466.	0.8	12
10	<i>Lactobacillus buchneri</i> subsp. <i>silagei</i> subsp. nov., isolated from rice grain silage. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3111-3116.	0.8	17
11	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.	1.1	1
12	Large-scale genome analysis of bovine commensal <i>Escherichia coli</i> reveals that bovine-adapted <i>E. coli</i> lineages are serving as evolutionary sources of the emergence of human intestinal pathogenic strains. Genome Research, 2019, 29, 1495-1505.	2.4	39
13	Generating Publication-Ready Prokaryotic Genome Annotations with DFAST. Methods in Molecular Biology, 2019, 1962, 215-226.	0.4	7
14	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. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 417-421.	0.8	7
15	<i>Lactobacillus salitolerans</i> sp. nov., a novel lactic acid bacterium isolated from spent mushroom substrates. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 964-969.	0.8	14
16	Plant and Cell Physiology's 2018 Database Issue and Beyond. Plant and Cell Physiology, 2018, 59, 1-2.	1.5	8
17	DFAST: a flexible prokaryotic genome annotation pipeline for faster genome publication. Bioinformatics, 2018, 34, 1037-1039.	1.8	775
18	DNA Data Bank of Japan: 30th anniversary. Nucleic Acids Research, 2018, 46, D30-D35.	6.5	51

#	ARTICLE	IF	CITATIONS
37	Genome sequence and overview of <i>Oligoflexus tunisiensis</i> Shr3T in the eighth class Oligoflexia of the phylum Proteobacteria. <i>Standards in Genomic Sciences</i> , 2016, 11, 90.	1.5	12
38	Complete genome sequence of cyanobacterium <i>Fischerella</i> sp. NIES-3754, providing thermoresistant optogenetic tools. <i>Journal of Biotechnology</i> , 2016, 220, 45-46.	1.9	27
39	OryzaGenome: Genome Diversity Database of Wild <i>Oryza</i> Species. <i>Plant and Cell Physiology</i> , 2016, 57, e1-e1.	1.5	34
40	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, 51-52.	1.9	14
41	The Naming of Names: Guidelines for Gene Nomenclature in <i>Marchantia</i> . <i>Plant and Cell Physiology</i> , 2016, 57, 257-261.	1.5	60
42	DNA data bank of Japan (DDBJ) progress report. <i>Nucleic Acids Research</i> , 2016, 44, D51-D57.	6.5	76
43	Complete Genome Sequence of Cyanobacterium <i>Leptolyngbya</i> sp. NIES-3755. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
44	Hybrid Origins of Citrus Varieties Inferred from DNA Marker Analysis of Nuclear and Organelle Genomes. <i>PLoS ONE</i> , 2016, 11, e0166969.	1.1	76
45	Be happy with your Perl scripts. <i>Ikushugaku Kenkyu</i> , 2016, 18, 27-33.	0.1	0
46	The Arabidopsis TAC Position Viewer: a high-resolution map of transformation-competent artificial chromosome (TAC) clones aligned with the <i>Arabidopsis thaliana</i> Columbia genome. <i>Plant Journal</i> , 2015, 83, 1114-1122.	2.8	4
47	The DDBJ Japanese Genotype-phenotype Archive for genetic and phenotypic human data. <i>Nucleic Acids Research</i> , 2015, 43, D18-D22.	6.5	57
48	Loss of Cytochrome cM Stimulates Cyanobacterial Heterotrophic Growth in the Dark. <i>Plant and Cell Physiology</i> , 2015, 56, 334-345.	1.5	28
49	Complete genome sequence and analysis of <i>Lactobacillus hokkaidonensis</i> LOOC260T, a psychrotrophic lactic acid bacterium isolated from silage. <i>BMC Genomics</i> , 2015, 16, 240.	1.2	44
50	DDBJ progress report: a new submission system for leading to a correct annotation. <i>Nucleic Acids Research</i> , 2014, 42, D44-D49.	6.5	36
51	Complete Genome Sequence of <i>Bifidobacterium longum</i> 105-A, a Strain with High Transformation Efficiency. <i>Genome Announcements</i> , 2014, 2, .	0.8	16
52	Mudi, a web tool for identifying mutations by bioinformatics analysis of whole-genome sequence. <i>Genes To Cells</i> , 2014, 19, 517-527.	0.5	21
53	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-e8.	1.5	38
54	Draft Genome Sequence of <i>Weissella oryzae</i> SG25 T, Isolated from Fermented Rice Grains. <i>Genome Announcements</i> , 2014, 2, .	0.8	11

#	ARTICLE	IF	CITATIONS
55	Genome-Wide Analysis of Intraspecific DNA Polymorphism in "Micro-Tom"™, a Model Cultivar of Tomato (<i>Solanum lycopersicum</i>). <i>Plant and Cell Physiology</i> , 2014, 55, 445-454.	1.5	69
56	Sll0939 is induced by Slr0967 in the cyanobacterium <i>Synechocystis</i> sp. PCC6803 and is essential for growth under various stress conditions. <i>Plant Physiology and Biochemistry</i> , 2014, 81, 36-43.	2.8	9
57	SABRE2: A Database Connecting Plant EST/Full-Length cDNA Clones with Arabidopsis Information. <i>Plant and Cell Physiology</i> , 2014, 55, e5-e5.	1.5	7
58	<i>Klebsormidium flaccidum</i> genome reveals primary factors for plant terrestrial adaptation. <i>Nature Communications</i> , 2014, 5, 3978.	5.8	532
59	CyanoBase and RhizoBase: databases of manually curated annotations for cyanobacterial and rhizobial genomes. <i>Nucleic Acids Research</i> , 2014, 42, D666-D670.	6.5	56
60	Draft Genome Sequence of <i>Lactobacillus oryzae</i> Strain SG293 ^T. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
61	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, 1275-1277.	1.5	38
62	DDBJ Read Annotation Pipeline: A Cloud Computing-Based Pipeline for High-Throughput Analysis of Next-Generation Sequencing Data. <i>DNA Research</i> , 2013, 20, 383-390.	1.5	68
63	The International Nucleotide Sequence Database Collaboration. <i>Nucleic Acids Research</i> , 2013, 41, D21-D24.	6.5	110
64	H2DB: a heritability database across multiple species by annotating trait-associated genomic loci. <i>Nucleic Acids Research</i> , 2013, 41, D880-D884.	6.5	5
65	Commonalities and Differences among Symbiosis Islands of Three <i>Mesorhizobium loti</i> Strains. <i>Microbes and Environments</i> , 2013, 28, 275-278.	0.7	17
66	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-D42.	6.5	43
67	DDBJ new system and service refactoring. <i>Nucleic Acids Research</i> , 2012, 41, D25-D29.	6.5	37
68	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, 225-236.	1.5	95
69	Complete Genome Sequence of <i>Bradyrhizobium</i> sp. S23321: Insights into Symbiosis Evolution in Soil Oligotrophs. <i>Microbes and Environments</i> , 2012, 27, 306-315.	0.7	76
70	The International Nucleotide Sequence Database Collaboration. <i>Nucleic Acids Research</i> , 2012, 40, D33-D37.	6.5	327
71	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	13.7	2,860
72	Survey of the genetic information carried in the genome of <i>Eucalyptus camaldulensis</i> . <i>Plant Biotechnology</i> , 2011, 28, 471-480.	0.5	33

#	ARTICLE	IF	CITATIONS
73	The genomic standards consortium: bringing standards to life for microbial ecology. ISME Journal, 2011, 5, 1565-1567.	4.4	59
74	The 2nd DBCLS BioHackathon: interoperable bioinformatics Web services for integrated applications. Journal of Biomedical Semantics, 2011, 2, 4.	0.9	19
75	DDBJ progress report. Nucleic Acids Research, 2011, 39, D22-D27.	6.5	42
76	The International Nucleotide Sequence Database Collaboration. Nucleic Acids Research, 2011, 39, D15-D18.	6.5	92
77	Meeting Report: "Metagenomics, Metadata and Meta-analysis"(M3) Workshop at the Pacific Symposium on Biocomputing 2010. Standards in Genomic Sciences, 2010, 2, 357-360.	1.5	2
78	An interspecific linkage map of SSR and intronic polymorphism markers in tomato. Theoretical and Applied Genetics, 2010, 121, 731-739.	1.8	92
79	The DBCLS BioHackathon: standardization and interoperability for bioinformatics web services and workflows. Journal of Biomedical Semantics, 2010, 1, 8.	0.9	31
80	Autocatalytic differentiation of epigenetic modifications within the Arabidopsis genome. EMBO Journal, 2010, 29, 3496-3506.	3.5	127
81	DDBJ Sequence Read Archive / DDBJ Omics Archive. Nature Precedings, 2010, , .	0.1	2
82	DDBJ launches a new archive database with analytical tools for next-generation sequence data. Nucleic Acids Research, 2010, 38, D33-D38.	6.5	86
83	CyanoBase: the cyanobacteria genome database update 2010. Nucleic Acids Research, 2010, 38, D379-D381.	6.5	142
84	Complete Genomic Structure of the Cultivated Rice Endophyte Azospirillum sp. B510. DNA Research, 2010, 17, 37-50.	1.5	148
85	SNP Discovery and Linkage Map Construction in Cultivated Tomato. DNA Research, 2010, 17, 381-391.	1.5	87
86	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.	0.8	14
87	Development of a Bacterial Cell Enrichment Method and its Application to the Community Analysis in Soybean Stems. Microbial Ecology, 2009, 58, 703-714.	1.4	108
88	Host plant genome overcomes the lack of a bacterial gene for symbiotic nitrogen fixation. Nature, 2009, 462, 514-517.	13.7	103
89	A Large Scale Analysis of Protein-Protein Interactions in the Nitrogen-fixing Bacterium Mesorhizobium loti. DNA Research, 2008, 15, 13-23.	1.5	73
90	Genome Structure of the Legume, Lotus japonicus. DNA Research, 2008, 15, 227-239.	1.5	691

#	ARTICLE	IF	CITATIONS
91	Construction of Signature-tagged Mutant Library in <i>Mesorhizobium loti</i> as a Powerful Tool for Functional Genomics. <i>DNA Research</i> , 2008, 15, 297-308.	1.5	41
92	Complete Genomic Structure of the Bloom-forming Toxic Cyanobacterium <i>Microcystis aeruginosa</i> NIES-843. <i>DNA Research</i> , 2007, 14, 247-256.	1.5	253
93	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, 1821-1825.	1.5	142
94	A Large-scale Protein-protein Interaction Analysis in <i>Synechocystis</i> sp. PCC6803. <i>DNA Research</i> , 2007, 14, 207-216.	1.5	170
95	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> , 2007, 14, 25-36.	1.5	41
96	Genome Sequencing and Genome Resources in Model Legumes. <i>Plant Physiology</i> , 2007, 144, 588-593.	2.3	53
97	Characterization of the Soybean Genome Using EST-derived Microsatellite Markers. <i>DNA Research</i> , 2007, 14, 271-281.	1.5	133
98	From The Cover: 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, 359-364.	3.3	361
99	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, 205-228.	1.5	71
100	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, 487-498.	1.4	57
101	Activation tagging approach in a model legume, <i>Lotus japonicus</i> . <i>Journal of Plant Research</i> , 2005, 118, 391-399.	1.2	32
102	Promoter trapping in <i>Lotus japonicus</i> reveals novel root and nodule GUS expression domains. <i>Plant and Cell Physiology</i> , 2005, 46, 1202-1212.	1.5	19
103	The Sulfate Transporter SST1 Is Crucial for Symbiotic Nitrogen Fixation in <i>Lotus japonicus</i> Root Nodules. <i>Plant Cell</i> , 2005, 17, 1625-1636.	3.1	227
104	Comprehensive Structural Analysis of the Genome of Red Clover (<i>Trifolium pratense</i> L.). <i>DNA Research</i> , 2005, 12, 301-364.	1.5	145
105	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, 1595-1607.	2.3	188
106	Distinctive Features of Plant Organs Characterized by Global Analysis of Gene Expression in <i>Arabidopsis</i> . <i>DNA Research</i> , 2004, 11, 11-25.	1.5	27
107	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, 405-414.	2.0	63
108	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.	0.6	24

#	ARTICLE	IF	CITATIONS
109	COMPARISON OF RNA EXPRESSION PROFILES BETWEEN THE TWO GENERATIONS OF <i>PORPHYRA YEZOENSIS</i> (RHODOPHYTA), BASED ON EXPRESSED SEQUENCE TAG FREQUENCY ANALYSIS. <i>Journal of Phycology</i> , 2003, 39, 923-930.	1.0	99
110	Plant recognition of symbiotic bacteria requires two LysM receptor-like kinases. <i>Nature</i> , 2003, 425, 585-592.	13.7	1,092
111	Structural Analysis of Four Large Plasmids Harboring in a Unicellular Cyanobacterium, <i>Synechocystis</i> sp. PCC 6803. <i>DNA Research</i> , 2003, 10, 221-228.	1.5	124
112	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, 941-951.	2.3	181
113	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, 277-285.	1.5	46
114	Complete Genome Structure of <i>Gloeobacter violaceus</i> PCC 7421, a Cyanobacterium that Lacks Thylakoids (Supplement). <i>DNA Research</i> , 2003, 10, 181-201.	1.5	42
115	Complete Genome Structure of <i>Gloeobacter violaceus</i> PCC 7421, a Cyanobacterium that Lacks Thylakoids. <i>DNA Research</i> , 2003, 10, 137-145.	1.5	269
116	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> , 2003, 10, 115-122.	1.5	62
117	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> , 2003, 10, 27-33.	1.5	25
118	Complete Genomic Sequence of Nitrogen-fixing Symbiotic Bacterium <i>Bradyrhizobium japonicum</i> USDA110. <i>DNA Research</i> , 2002, 9, 189-197.	1.5	768
119	Complete Genome Structure of the Thermophilic Cyanobacterium <i>Thermosynechococcus elongatus</i> BP-1. <i>DNA Research</i> , 2002, 9, 123-130.	1.5	312
120	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.	1.5	50
121	Complete Genome Structure of the Thermophilic Cyanobacterium <i>Thermosynechococcus elongatus</i> BP-1 (Supplement). <i>DNA Research</i> , 2002, 9, 135-148.	1.5	29
122	Complete Genomic Sequence of Nitrogen-fixing Symbiotic Bacterium <i>Bradyrhizobium japonicum</i> USDA110 (Supplement). <i>DNA Research</i> , 2002, 9, 225-256.	1.5	76
123	Analysis of gene expression in <i>Arabidopsis thaliana</i> by array hybridization with genomic DNA fragments aligned along chromosomal regions. <i>Plant Journal</i> , 2002, 30, 247-255.	2.8	7
124	Role of the Putative Membrane-Bound Endo-1,4-β-Glucanase KORRIGAN in Cell Elongation and Cellulose Synthesis in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2001, 42, 251-263.	1.5	185
125	Sequence and analysis of chromosome 5 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 823-826.	13.7	175
126	Analysis of the genome sequence of the flowering plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 796-815.	13.7	8,336

#	ARTICLE	IF	CITATIONS
127	Sequence and analysis of chromosome 3 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 820-823.	13.7	188
128	Generation of 7137 Non-redundant Expressed Sequence Tags from a Legume, <i>Lotus japonicus</i> . <i>DNA Research</i> , 2000, 7, 127-130.	1.5	80
129	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, 305-307.	1.5	107
130	Codon usage tabulated from the international DNA sequence databases; its status 1999. <i>Nucleic Acids Research</i> , 1999, 27, 292-292.	6.5	81
131	Extension of CyanoBase. CyanoMutants: repository of mutant information on <i>Synechocystis</i> sp. strain PCC6803. <i>Nucleic Acids Research</i> , 1999, 27, 66-68.	6.5	23
132	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> , 1998, 5, 203-216.	1.5	9
133	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, 63-67.	6.5	174
134	Codon usage tabulated from the international DNA sequence databases. <i>Nucleic Acids Research</i> , 1998, 26, 334-334.	6.5	74
135	Codon usage tabulated from the international DNA sequence databases. <i>Nucleic Acids Research</i> , 1997, 25, 244-245.	6.5	83
136	Codon-Anticodon Assignment and Detection of Codon Usage Trends in Seven Microbial Genomes. <i>Microbial & Comparative Genomics</i> , 1997, 2, 299-312.	0.6	25
137	Gene organization of human NOTCH4 and (CTG) _n polymorphism in this human counterpart gene of mouse proto-oncogene <i>Int3</i> . <i>Gene</i> , 1997, 189, 235-244.	1.0	30
138	Codon usage tabulated from the international DNA sequence databases. <i>Nucleic Acids Research</i> , 1996, 24, 214-215.	6.5	114
139	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> , 1996, 12, 213-225.	1.8	19
140	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, 1297-1305.	6.5	53
141	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, 3773-3777.	6.5	54
142	Gene clusters for ribosomal proteins in the mitochondrial genome of a liverwort, <i>Marchantia polymorpha</i> . <i>Nucleic Acids Research</i> , 1992, 20, 3199-3205.	6.5	79
143	Gene organization deduced from the complete sequence of liverwort <i>Marchantia polymorpha</i> mitochondrial DNA. <i>Journal of Molecular Biology</i> , 1992, 223, 1-7.	2.0	602
144	Complete nucleotide sequence of the mitochondrial DNA from a liverwort, <i>Marchantia polymorpha</i> . <i>Plant Molecular Biology Reporter</i> , 1992, 10, 105-163.	1.0	23

#	ARTICLE	IF	CITATIONS
145	Gene Encoding a Putative Zinc Finger Protein in Synechocystis PCC6803.. Agricultural and Biological Chemistry, 1991, 55, 2259-2264.	0.3	5