Ikuo Uchiyama

List of Publications by Year
in descending order

48	4,623	172457	206112
papers	citations	29	48
		h-index	g-index

51	51	51	6018
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Molecular phylogeny of fucoxanthin–chlorophyll *a*/*c* proteins from *Chaetoceros gracilis* and Lhcq/Lhcf diversity. Physiologia Plantarum, 2022, 174, e13598.	5.2	12
2	A simple and practical workflow for genotyping of CRISPR–Cas9–based knockout phenotypes using multiplexed amplicon sequencing. Genes To Cells, 2020, 25, 498-509.	1.2	11
3	BioHackathon 2015: Semantics of data for life sciences and reproducible research. F1000Research, 2020, 9, 136.	1.6	5
4	Structural basis for energy harvesting and dissipation in a diatom PSII–FCPII supercomplex. Nature Plants, 2019, 5, 890-901.	9.3	92
5	MBGD update 2018: microbial genome database based on hierarchical orthology relations covering closely related and distantly related comparisons. Nucleic Acids Research, 2019, 47, D382-D389.	14.5	34
6	A comprehensive reference transcriptome resource for the Iberian ribbed newt Pleurodeles waltl, an emerging model for developmental and regeneration biology. DNA Research, 2019, 26, 217-229.	3.4	45
7	An acid-tolerant ammonia-oxidizing γ-proteobacterium from soil. ISME Journal, 2017, 11, 1130-1141.	9.8	123
8	Complete genome sequence and expression profile of the commercial lytic enzyme producerLysobacter enzymogenesM497-1. DNA Research, 2017, 24, dsw055.	3.4	12
9	Artificial acceleration of mammalian cell reprogramming by bacterial proteins. Genes To Cells, 2017, 22, 918-928.	1.2	4
10	A Novel Approach to Helicobacter pylori Pan-Genome Analysis for Identification of Genomic Islands. PLoS ONE, 2016, 11, e0159419.	2.5	24
11	Genome-wide survey of codons under diversifying selection in a highly recombining bacterial species,*Helicobacter pylori*. DNA Research, 2016, 23, 135-143.	3.4	8
12	Construction of an Ortholog Database Using the Semantic Web Technology for Integrative Analysis of Genomic Data. PLoS ONE, 2015, 10, e0122802.	2.5	11
13	Low frequency of endospore–specific genes in subseafloor sedimentary metagenomes. Environmental Microbiology Reports, 2015, 7, 341-350.	2.4	11
14	MBGD update 2015: microbial genome database for flexible ortholog analysis utilizing a diverse set of genomic data. Nucleic Acids Research, 2015, 43, D270-D276.	14.5	70
15	Epigenetic modification maintains intrinsic limb-cell identity in Xenopus limb bud regeneration. Developmental Biology, 2015, 406, 271-282.	2.0	32
16	Diofenolan induces male offspring production through binding to the juvenile hormone receptor in Daphnia magna. Aquatic Toxicology, 2015, 159, 44-51.	4.0	32
17	Functional Classification of Uncultured "Candidatus Caldiarchaeum subterraneum"Using the Maple System. PLoS ONE, 2015, 10, e0132994.	2.5	29
18	High frequency of phylogenetically diverse reductive dehalogenase-homologous genes in deep subseafloor sedimentary metagenomes. Frontiers in Microbiology, 2014, 5, 80.	3.5	61

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19	Development of New <scp>PCR</scp> Primers by Comparative Genomics for the Detection of <i><scp>H</scp>elicobacter suis</i> in Gastric Biopsy Specimens. Helicobacter, 2014, 19, 260-271.	3.5	19
20	Molecular impact of juvenile hormone agonists on neonatal <i>Daphnia magna</i>. Journal of Applied Toxicology, 2014, 34, 537-544.	2.8	35
21	Chromosome Painting In Silico in a Bacterial Species Reveals Fine Population Structure. Molecular Biology and Evolution, 2013, 30, 1454-1464.	8.9	87
22	Genome-Wide Survey of Mutual Homologous Recombination in a Highly Sexual Bacterial Species. Genome Biology and Evolution, 2012, 4, 628-640.	2.5	34
23	A Deeply Branching Thermophilic Bacterium with an Ancient Acetyl-CoA Pathway Dominates a Subsurface Ecosystem. PLoS ONE, 2012, 7, e30559.	2.5	161
24	Domain Movement within a Gene: A Novel Evolutionary Mechanism for Protein Diversification. PLoS ONE, 2011, 6, e18819.	2.5	50
25	Helicobacter suis KB1 derived from pig gastric lymphoid follicles induces the formation of gastric lymphoid follicles in mice through the activation of B cells and CD4 positive cells. Microbes and Infection, 2011, 13, 697-708.	1.9	10
26	Birth and death of genes linked to chromosomal inversion. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1501-1506.	7.1	62
27	Complete Genome Sequence of <i>Macrococcus caseolyticus</i> Strain JSCS5402, Reflecting the Ancestral Genome of the Human-Pathogenic Staphylococci. Journal of Bacteriology, 2009, 191, 1180-1190.	2.2	111
28	Genetic Diversity of Staphylocoagulase Genes (coa): Insight into the Evolution of Variable Chromosomal Virulence Factors in Staphylococcus aureus. PLoS ONE, 2009, 4, e5714.	2.5	67
29	The Whole-genome Sequencing of the Obligate Intracellular Bacterium Orientia tsutsugamushi Revealed Massive Gene Amplification During Reductive Genome Evolution. DNA Research, 2008, 15, 185-199.	3.4	166
30	How genomes rearrange: Genome comparison within bacteria Neisseria suggests roles for mobile elements in formation of complex genome polymorphisms. Gene, 2006, 383, 52-63.	2.2	21
31	Evolution of Paralogous Genes: Reconstruction of Genome Rearrangements Through Comparison of Multiple Genomes Within Staphylococcus aureus. Molecular Biology and Evolution, 2006, 23, 1269-1285.	8.9	32
32	Hierarchical clustering algorithm for comprehensive orthologous-domain classification in multiple genomes. Nucleic Acids Research, 2006, 34, 647-658.	14.5	74
33	Genome Comparison In Silico in Neisseria Suggests Integration of Filamentous Bacteriophages by their Own Transposase. DNA Research, 2005, 12, 389-401.	3.4	63
34	Discovery of a novel restriction endonuclease by genome comparison and application of a wheat-germ-based cell-free translation assay: PabI (5'-GTA/C) from the hyperthermophilic archaeon Pyrococcus abyssi. Nucleic Acids Research, 2005, 33, e112-e112.	14.5	84
35	Thermoadaptation trait revealed by the genome sequence of thermophilic Geobacillus kaustophilus. Nucleic Acids Research, 2004, 32, 6292-6303.	14.5	186
36	Comparative genomics of Physcomitrella patens gametophytic transcriptome and Arabidopsis thaliana: Implication for land plant evolution. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8007-8012.	7.1	341

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37	MBGD: microbial genome database for comparative analysis. Nucleic Acids Research, 2003, 31, 58-62.	14.5	113
38	Whole genome sequencing of meticillin-resistant Staphylococcus aureus. Lancet, The, 2001, 357, 1225-1240.	13.7	1,835
39	Diversity of restriction–modification gene homologues in Helicobacter pylori. Gene, 2000, 259, 89-98.	2.2	81
40	Comparison between Pyrococcus horikoshii and Pyrococcus abyssi genome sequences reveals linkage of restriction–modification genes with large genome polymorphisms. Gene, 2000, 259, 109-121.	2.2	56
41	Insertion with long target duplication: a mechanism for gene mobility suggested from comparison of two related bacterial genomes. Gene, 2000, 259, 99-108.	2.2	70
42	Characterization of a 1200-kb Genomic Segment of Chromosome 3p22-p21.3. DNA Research, 1999, 6, 37-44.	3.4	16
43	Significant Differences in the Frequency of Transcriptional Units, Types and Numbers of Repetitive Elements, GC Content, and the Number of CpG Islands Between a 1010-kb G-band Genomic Segment on Chromosome 9q31.3 and a 1200-kb R-band Genomic Segment on Chromosome 3p21.3. DNA Research, 1999, 6, 227-233.	3.4	0
44	Shaping the genome – restriction–modification systems as mobile genetic elements. Current Opinion in Genetics and Development, 1999, 9, 649-656.	3.3	114
45	Construction of a Normalized Directionally Cloned cDNA Library from Adult Heart and Analysis of 3040 Clones by Partial Sequencing. Genomics, 1996, 35, 231-235.	2.9	20
46	Construction and analysis of a profile library characterizing groups of structurally known proteins. Protein Science, 1996, 5, 1991-1999.	7.6	31
47	Construction of a dictionary of sequence motifs that characterize groups of related proteins. Protein Engineering, Design and Selection, 1992, 5, 479-488.	2.1	39
48	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. F1000Research, 0, 8, 1677.	1.6	0