

# Ikuo Uchiyama

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6796569/publications.pdf>

Version: 2024-02-01

48  
papers

4,623  
citations

172457

29  
h-index

206112

48  
g-index

51  
all docs

51  
docs citations

51  
times ranked

6018  
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole genome sequencing of meticillin-resistant <i>Staphylococcus aureus</i> . <i>Lancet</i> , The, 2001, 357, 1225-1240.	13.7	1,835
2	Comparative genomics of <i>Physcomitrella patens</i> gametophytic transcriptome and <i>Arabidopsis thaliana</i> : Implication for land plant evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 8007-8012.	7.1	341
3	Thermoadaptation trait revealed by the genome sequence of thermophilic <i>Geobacillus kaustophilus</i> . <i>Nucleic Acids Research</i> , 2004, 32, 6292-6303.	14.5	186
4	The Whole-genome Sequencing of the Obligate Intracellular Bacterium <i>Orientia tsutsugamushi</i> Revealed Massive Gene Amplification During Reductive Genome Evolution. <i>DNA Research</i> , 2008, 15, 185-199.	3.4	166
5	A Deeply Branching Thermophilic Bacterium with an Ancient Acetyl-CoA Pathway Dominates a Subsurface Ecosystem. <i>PLoS ONE</i> , 2012, 7, e30559.	2.5	161
6	An acid-tolerant ammonia-oxidizing $\beta$ -proteobacterium from soil. <i>ISME Journal</i> , 2017, 11, 1130-1141.	9.8	123
7	Shaping the genome "restriction" modification systems as mobile genetic elements. <i>Current Opinion in Genetics and Development</i> , 1999, 9, 649-656.	3.3	114
8	MBGD: microbial genome database for comparative analysis. <i>Nucleic Acids Research</i> , 2003, 31, 58-62.	14.5	113
9	Complete Genome Sequence of <i>Macrococcus caseolyticus</i> Strain JSCS5402, Reflecting the Ancestral Genome of the Human-Pathogenic <i>Staphylococci</i> . <i>Journal of Bacteriology</i> , 2009, 191, 1180-1190.	2.2	111
10	Structural basis for energy harvesting and dissipation in a diatom PSII-FCPII supercomplex. <i>Nature Plants</i> , 2019, 5, 890-901.	9.3	92
11	Chromosome Painting In Silico in a Bacterial Species Reveals Fine Population Structure. <i>Molecular Biology and Evolution</i> , 2013, 30, 1454-1464.	8.9	87
12	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 <i>Pyrococcus abyssi</i> . <i>Nucleic Acids Research</i> , 2005, 33, e112-e112.	14.5	84
13	Diversity of restriction modification gene homologues in <i>Helicobacter pylori</i> . <i>Gene</i> , 2000, 259, 89-98.	2.2	81
14	Hierarchical clustering algorithm for comprehensive orthologous-domain classification in multiple genomes. <i>Nucleic Acids Research</i> , 2006, 34, 647-658.	14.5	74
15	Insertion with long target duplication: a mechanism for gene mobility suggested from comparison of two related bacterial genomes. <i>Gene</i> , 2000, 259, 99-108.	2.2	70
16	MBGD update 2015: microbial genome database for flexible ortholog analysis utilizing a diverse set of genomic data. <i>Nucleic Acids Research</i> , 2015, 43, D270-D276.	14.5	70
17	Genetic Diversity of <i>Staphylocoagulase</i> Genes ( <i>coa</i> ): Insight into the Evolution of Variable Chromosomal Virulence Factors in <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , 2009, 4, e5714.	2.5	67
18	Genome Comparison In Silico in <i>Neisseria</i> Suggests Integration of Filamentous Bacteriophages by their Own Transposase. <i>DNA Research</i> , 2005, 12, 389-401.	3.4	63

#	ARTICLE	IF	CITATIONS
19	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
20	High frequency of phylogenetically diverse reductive dehalogenase-homologous genes in deep seafloor sedimentary metagenomes. Frontiers in Microbiology, 2014, 5, 80.	3.5	61
21	Comparison between <i>Pyrococcus horikoshii</i> and <i>Pyrococcus abyssi</i> genome sequences reveals linkage of restriction modification genes with large genome polymorphisms. Gene, 2000, 259, 109-121.	2.2	56
22	Domain Movement within a Gene: A Novel Evolutionary Mechanism for Protein Diversification. PLoS ONE, 2011, 6, e18819.	2.5	50
23	A comprehensive reference transcriptome resource for the Iberian ribbed newt <i>Pleurodeles waltl</i> , an emerging model for developmental and regeneration biology. DNA Research, 2019, 26, 217-229.	3.4	45
24	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
25	Molecular impact of juvenile hormone agonists on neonatal <i>Daphnia magna</i> . Journal of Applied Toxicology, 2014, 34, 537-544.	2.8	35
26	Genome-Wide Survey of Mutual Homologous Recombination in a Highly Sexual Bacterial Species. Genome Biology and Evolution, 2012, 4, 628-640.	2.5	34
27	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
28	Evolution of Paralogous Genes: Reconstruction of Genome Rearrangements Through Comparison of Multiple Genomes Within <i>Staphylococcus aureus</i> . Molecular Biology and Evolution, 2006, 23, 1269-1285.	8.9	32
29	Epigenetic modification maintains intrinsic limb-cell identity in <i>Xenopus</i> limb bud regeneration. Developmental Biology, 2015, 406, 271-282.	2.0	32
30	Diofenolan induces male offspring production through binding to the juvenile hormone receptor in <i>Daphnia magna</i> . Aquatic Toxicology, 2015, 159, 44-51.	4.0	32
31	Construction and analysis of a profile library characterizing groups of structurally known proteins. Protein Science, 1996, 5, 1991-1999.	7.6	31
32	Functional Classification of Uncultured <i>Candidatus Caldiarchaeum subterraneum</i> Using the Maple System. PLoS ONE, 2015, 10, e0132994.	2.5	29
33	A Novel Approach to <i>Helicobacter pylori</i> Pan-Genome Analysis for Identification of Genomic Islands. PLoS ONE, 2016, 11, e0159419.	2.5	24
34	How genomes rearrange: Genome comparison within bacteria <i>Neisseria</i> suggests roles for mobile elements in formation of complex genome polymorphisms. Gene, 2006, 383, 52-63.	2.2	21
35	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
36	Development of New PCR Primers by Comparative Genomics for the Detection of <i>Helicobacter suis</i> in Gastric Biopsy Specimens. Helicobacter, 2014, 19, 260-271.	3.5	19

#	ARTICLE	IF	CITATIONS
37	Characterization of a 1200-kb Genomic Segment of Chromosome 3p22-p21.3. <i>DNA Research</i> , 1999, 6, 37-44.	3.4	16
38	Complete genome sequence and expression profile of the commercial lytic enzyme producer <i>Lysobacter enzymogenes</i> M497-1. <i>DNA Research</i> , 2017, 24, dsw055.	3.4	12
39	Molecular phylogeny of fucoxanthin-chlorophyll <i>a</i> / <i>c</i> proteins from <i>Chaetoceros gracilis</i> and Lhcq/Lhcf diversity. <i>Physiologia Plantarum</i> , 2022, 174, e13598.	5.2	12
40	Construction of an Ortholog Database Using the Semantic Web Technology for Integrative Analysis of Genomic Data. <i>PLoS ONE</i> , 2015, 10, e0122802.	2.5	11
41	Low frequency of endospore-specific genes in subseafloor sedimentary metagenomes. <i>Environmental Microbiology Reports</i> , 2015, 7, 341-350.	2.4	11
42	A simple and practical workflow for genotyping of CRISPR-Cas9 based knockout phenotypes using multiplexed amplicon sequencing. <i>Genes To Cells</i> , 2020, 25, 498-509.	1.2	11
43	<i>Helicobacter suis</i> 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. <i>Microbes and Infection</i> , 2011, 13, 697-708.	1.9	10
44	Genome-wide survey of codons under diversifying selection in a highly recombining bacterial species, <i>Helicobacter pylori</i> . <i>DNA Research</i> , 2016, 23, 135-143.	3.4	8
45	BioHackathon 2015: Semantics of data for life sciences and reproducible research. <i>F1000Research</i> , 2020, 9, 136.	1.6	5
46	Artificial acceleration of mammalian cell reprogramming by bacterial proteins. <i>Genes To Cells</i> , 2017, 22, 918-928.	1.2	4
47	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. <i>DNA Research</i> , 1999, 6, 227-233.	3.4	0
48	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. <i>F1000Research</i> , 0, 8, 1677.	1.6	0