

Yu Kanasaki

List of Publications by Year in descending order

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120
papers

4,215
citations

159358

30
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123241

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124
all docs

124
docs citations

124
times ranked

4186
citing authors

#	ARTICLE	IF	CITATIONS
1	Salt Stress and Hyperosmotic Stress Regulate the Expression of Different Sets of Genes in <i>Synechocystis</i> sp. PCC 6803. <i>Biochemical and Biophysical Research Communications</i> , 2002, 290, 339-348.	1.0	273
2	Salt Stress Inhibits the Repair of Photodamaged Photosystem II by Suppressing the Transcription and Translation of psbA Genes in <i>Synechocystis</i> A. <i>Plant Physiology</i> , 2002, 130, 1443-1453.	2.3	246
3	The pathway for perception and transduction of low-temperature signals in <i>Synechocystis</i> . <i>EMBO Journal</i> , 2000, 19, 1327-1334.	3.5	238
4	Cold-regulated genes under control of the cold sensor Hik33 in <i>Synechocystis</i> . <i>Molecular Microbiology</i> , 2001, 40, 235-244.	1.2	238
5	The histidine kinase Hik33 perceives osmotic stress and cold stress in <i>Synechocystis</i> sp. PCC 6803. <i>Molecular Microbiology</i> , 2002, 46, 905-915.	1.2	185
6	Identification of histidine kinases that act as sensors in the perception of salt stress in <i>Synechocystis</i> sp. PCC 6803. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 9061-9066.	3.3	170
7	Positive Regulation of Sugar Catabolic Pathways in the Cyanobacterium <i>Synechocystis</i> sp. PCC 6803 by the Group 2 σ Factor SigE. <i>Journal of Biological Chemistry</i> , 2005, 280, 30653-30659.	1.6	159
8	Identical Hik-Rre Systems Are Involved in Perception and Transduction of Salt Signals and Hyperosmotic Signals but Regulate the Expression of Individual Genes to Different Extents in <i>Synechocystis</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 21531-21538.	1.6	144
9	Gene Expression Profiling Reflects Physiological Processes in Salt Acclimation of <i>Synechocystis</i> sp. Strain PCC 6803. <i>Plant Physiology</i> , 2004, 136, 3290-3300.	2.3	131
10	Gene-engineered Rigidification of Membrane Lipids Enhances the Cold Inducibility of Gene Expression in <i>Synechocystis</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 12191-12198.	1.6	127
11	Five Histidine Kinases Perceive Osmotic Stress and Regulate Distinct Sets of Genes in <i>Synechocystis</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 53078-53086.	1.6	120
12	Identification of Substrain-Specific Mutations by Massively Parallel Whole-Genome Resequencing of <i>Synechocystis</i> sp. PCC 6803. <i>DNA Research</i> , 2012, 19, 67-79.	1.5	119
13	R2R3-type MYB transcription factor, CmMYB1, is a central nitrogen assimilation regulator in <i>Cyanidioschyzon merolae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12548-12553.	3.3	112
14	Tetrapyrrole signal as a cell-cycle coordinator from organelle to nuclear DNA replication in plant cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 803-807.	3.3	103
15	CyanoBase: A large-scale update on its 20th anniversary. <i>Nucleic Acids Research</i> , 2017, 45, D551-D554.	6.5	95
16	Acidophilic green algal genome provides insights into adaptation to an acidic environment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E8304-E8313.	3.3	93
17	The Histidine Kinase Hik34 Is Involved in Thermotolerance by Regulating the Expression of Heat Shock Genes in <i>Synechocystis</i> . <i>Plant Physiology</i> , 2005, 138, 1409-1421.	2.3	89
18	Histidine kinases play important roles in the perception and signal transduction of hydrogen peroxide in the cyanobacterium, <i>Synechocystis</i> sp. PCC 6803. <i>Plant Journal</i> , 2007, 49, 313-324.	2.8	89

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19	Chloroplast-mediated regulation of CO ₂ -concentrating mechanism by Ca ²⁺ -binding protein CAS in the green alga <i>Chlamydomonas reinhardtii</i> . Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12586-12591.	3.3	73
20	Whole-genome resequencing shows numerous genes with nonsynonymous SNPs in the Japanese native cattle Kuchinoshima-Ushi. BMC Genomics, 2011, 12, 103.	1.2	72
21	Structure-Activity Relationship of the Free-Radical-Scavenging Reaction by Vitamin E (Î±-, Î²-, Î³-, Î´-) Tj ETQq1 1 0.784314 rgBT /Overl... 2007, 111, 652-662.	1.2	69
22	Light-dependent and asynchronous replication of cyanobacterial multi-copy chromosomes. Molecular Microbiology, 2012, 83, 856-865.	1.2	68
23	Genomic characterization of a fructophilic bee symbiont <i>Lactobacillus kunkeei</i> reveals its niche-specific adaptation. Systematic and Applied Microbiology, 2016, 39, 516-526.	1.2	51
24	Intensive DNA Replication and Metabolism during the Lag Phase in Cyanobacteria. PLoS ONE, 2015, 10, e0136800.	1.1	44
25	Genomic Structure of the Cyanobacterium <i>Synechocystis</i> sp. PCC 6803 Strain GT-S. DNA Research, 2011, 18, 393-399.	1.5	42
26	Diversification of DnaA dependency for DNA replication in cyanobacterial evolution. ISME Journal, 2016, 10, 1113-1121.	4.4	39
27	Coordination of Polyploid Chromosome Replication with Cell Size and Growth in a Cyanobacterium. MBio, 2019, 10, .	1.8	37
28	Iodide Oxidation by a Novel Multicopper Oxidase from the Alphaproteobacterium Strain Q-1. Applied and Environmental Microbiology, 2012, 78, 3941-3949.	1.4	35
29	Stopped-Flow Kinetic Study of the Aroxyl Radical-Scavenging Action of Catechins and Vitamin C in Ethanol and Micellar Solutions. Journal of Agricultural and Food Chemistry, 2008, 56, 4406-4417.	2.4	34
30	Linear Regression Links Transcriptomic Data and Cellular Raman Spectra. Cell Systems, 2018, 7, 104-117.e4.	2.9	34
31	An RNA helicase, CrhR, regulates the low-temperature-inducible expression of heat-shock genes groES, groEL1 and groEL2 in <i>Synechocystis</i> sp. PCC 6803. Microbiology (United Kingdom), 2010, 156, 442-451.	0.7	32
32	A nitrogen source-dependent inducible and repressible gene expression system in the red alga <i>Cyanidioschyzon merolae</i> . Frontiers in Plant Science, 2015, 6, 657.	1.7	32
33	Genome Mining of Amino Group Carrier Protein-Mediated Machinery: Discovery and Biosynthetic Characterization of a Natural Product with Unique Hydrazone Unit. ACS Chemical Biology, 2017, 12, 124-131.	1.6	29
34	Sulfur-Containing Carotenoids from A Marine Coral Symbiont <i>Erythrobacter flavus</i> Strain KJ5. Marine Drugs, 2019, 17, 349.	2.2	29
35	Complete genome sequence of cyanobacterium <i>Fischerella</i> sp. NIES-3754, providing thermoresistant optogenetic tools. Journal of Biotechnology, 2016, 220, 45-46.	1.9	27
36	Identification of genes involved in the phosphate metabolism in <i>Cryptococcus neoformans</i> . Fungal Genetics and Biology, 2015, 80, 19-30.	0.9	26

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37	External Light Conditions and Internal Cell Cycle Phases Coordinate Accumulation of Chloroplast and Mitochondrial Transcripts in the Red Alga <i>Cyanidioschyzon merolae</i> . <i>DNA Research</i> , 2012, 19, 289-303.	1.5	25
38	Genomic analysis of parallel-evolved cyanobacterium <i>Synechocystis</i> sp. PCC 6803 under acid stress. <i>Photosynthesis Research</i> , 2015, 125, 243-254.	1.6	25
39	A Putative Type III Secretion System Effector Encoded by the <i>MA20_12780</i> Gene in <i>Bradyrhizobium japonicum</i> Is-34 Causes Incompatibility with <i>Rj4</i> Genotype Soybeans. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5812-5819.	1.4	25
40	Microevolution of Virulence-Related Genes in <i>Helicobacter pylori</i> Familial Infection. <i>PLoS ONE</i> , 2015, 10, e0127197.	1.1	23
41	Complete Genome Sequence of 3-Chlorobenzoate-Degrading Bacterium <i>Cupriavidus necator</i> NH9 and Reclassification of the Strains of the Genera <i>Cupriavidus</i> and <i>Ralstonia</i> Based on Phylogenetic and Whole-Genome Sequence Analyses. <i>Frontiers in Microbiology</i> , 2019, 10, 133.	1.5	22
42	Exopolysaccharide production by a unicellular freshwater cyanobacterium <i>Cyanothece</i> sp. isolated from a rice field in Vietnam. <i>Journal of Applied Phycology</i> , 2014, 26, 265-272.	1.5	21
43	DNA replication depends on photosynthetic electron transport in cyanobacteria. <i>FEMS Microbiology Letters</i> , 2013, 344, 138-144.	0.7	19
44	Identification of metabolic engineering targets for improving glycerol assimilation ability of <i>Saccharomyces cerevisiae</i> based on adaptive laboratory evolution and transcriptome analysis. <i>Journal of Bioscience and Bioengineering</i> , 2019, 128, 162-169.	1.1	19
45	Newly Identified Nucleoid-Associated-Like Protein YlxR Regulates Metabolic Gene Expression in <i>Bacillus subtilis</i> . <i>MSphere</i> , 2018, 3, .	1.3	18
46	Capacity for survival in global warming: Adaptation of mesophiles to the temperature upper limit. <i>PLoS ONE</i> , 2019, 14, e0215614.	1.1	18
47	Conserved two-component <i>Hik34</i> module directly activates heat stress inducible transcription of major chaperone and other genes in <i>Synechococcus elongatus</i> PCC 7942. <i>Molecular Microbiology</i> , 2017, 104, 260-277.	1.2	17
48	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
49	Identification of the <i>hcb</i> Gene Operon Involved in Catalyzing Aerobic Hexachlorobenzene Dechlorination in <i>Nocardioides</i> sp. Strain PD653. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	16
50	Genetic Analysis of Collective Motility of <i>Paenibacillus</i> sp. NAIST15-1. <i>PLoS Genetics</i> , 2016, 12, e1006387.	1.5	16
51	Algal Protein Kinase, Triacylglycerol Accumulation Regulator 1, Modulates Cell Viability and Gametogenesis in Carbon/Nitrogen-Imbalanced Conditions. <i>Plant and Cell Physiology</i> , 2019, 60, 916-930.	1.5	15
52	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
53	Fpr1, a primary target of rapamycin, functions as a transcription factor for ribosomal protein genes cooperatively with Hmo1 in <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2020, 16, e1008865.	1.5	14
54	Identification of centromere regions in chromosomes of a unicellular red alga, <i>Cyanidioschyzon merolae</i> . <i>FEBS Letters</i> , 2015, 589, 1219-1224.	1.3	13

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55	Characterization of mycosporine-like amino acids in the cyanobacterium <i>Nostoc verrucosum</i> . <i>Journal of General and Applied Microbiology</i> , 2018, 64, 203-211.	0.4	12
56	Identification of the novel <i>hcbB</i> operon catalyzing the dechlorination of pentachlorophenol in the Gram-positive bacterium <i>Nocardioides</i> sp. strain PD653. <i>Journal of Pesticide Sciences</i> , 2018, 43, 124-131.	0.8	12
57	Changes in the transcriptome, ploidy, and optimal light intensity of a cryptomonad upon integration into a kleptoplastic dinoflagellate. <i>ISME Journal</i> , 2020, 14, 2407-2423.	4.4	12
58	Evolutionary Changes in DnaA-Dependent Chromosomal Replication in Cyanobacteria. <i>Frontiers in Microbiology</i> , 2020, 11, 786.	1.5	12
59	Genome sequencing of the NIES Cyanobacteria collection with a focus on the heterocyst-forming clade. <i>DNA Research</i> , 2021, 28, .	1.5	12
60	Identification of the Three Genes Involved in Controlling Production of a Phytotoxin Tropolone in <i>Burkholderia plantarii</i> . <i>Journal of Bacteriology</i> , 2016, 198, 1604-1609.	1.0	11
61	Responses of unicellular predators to cope with the phototoxicity of photosynthetic prey. <i>Nature Communications</i> , 2019, 10, 5606.	5.8	11
62	Physiological properties and genetic analysis related to exopolysaccharide (EPS) production in the fresh-water unicellular cyanobacterium <i>Aphanothece sacrum</i> (Suizenji Nori). <i>Journal of General and Applied Microbiology</i> , 2019, 65, 39-46.	0.4	11
63	Comparative genome analysis of <i>Aspergillus flavus</i> clinically isolated in Japan. <i>DNA Research</i> , 2019, 26, 95-103.	1.5	11
64	<i>Bacillus subtilis</i> Nucleoid-Associated Protein YlxR Is Involved in Bimodal Expression of the Fructoselysine Utilization Operon (<i>friBONMD-yurI</i>) Promoter. <i>Frontiers in Microbiology</i> , 2020, 11, 2024.	1.5	11
65	Transcriptional Activation of Glycogen Catabolism and the Oxidative Pentose Phosphate Pathway by NrrA Facilitates Cell Survival Under Nitrogen Starvation in the Cyanobacterium <i>Synechococcus</i> sp. Strain PCC 7002. <i>Plant and Cell Physiology</i> , 2018, 59, 1225-1233.	1.5	10
66	Draft Genome Sequence of the Nitrogen-Fixing and Hormogonia-Inducing Cyanobacterium <i>Nostoc cycadae</i> Strain WK-1, Isolated from the Coralloid Roots of <i>Cycas revoluta</i> . <i>Genome Announcements</i> , 2018, 6, .	0.8	10
67	Interplay and Targetome of the Two Conserved Cyanobacterial sRNAs Yfr1 and Yfr2 in <i>Prochlorococcus</i> MED4. <i>Scientific Reports</i> , 2019, 9, 14331.	1.6	10
68	16S rRNA Gene Amplicon Sequencing of Gut Microbiota in Three Species of Deep-Sea Fish in Suruga Bay, Japan. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	10
69	Evolutionary Adaptation by Repetitive Long-Term Cultivation with Gradual Increase in Temperature for Acquiring Multi-Stress Tolerance and High Ethanol Productivity in <i>Kluyveromyces marxianus</i> DMKU 3-1042. <i>Microorganisms</i> , 2022, 10, 798.	1.6	10
70	Mg-Protoporphyrin IX Signaling in <i>Cyanidioschyzon merolae</i> . <i>Plant Signaling and Behavior</i> , 2009, 4, 1190-1192.	1.2	9
71	Draft Genome Sequence of Strain Q-1, an Iodide-Oxidizing Alphaproteobacterium Isolated from Natural Gas Brine Water. <i>Genome Announcements</i> , 2014, 2, .	0.8	9
72	Integration of a <i>Galdieria</i> plasma membrane sugar transporter enables heterotrophic growth of the obligate photoautotrophic red alga <i>Cyanidioschyzon merolae</i> . <i>Plant Direct</i> , 2019, 3, e00134.	0.8	9

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73	RNase E-dependent degradation of <i>tnaA</i> mRNA encoding tryptophanase is prerequisite for the induction of acid resistance in <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2020, 10, 7128.	1.6	9
74	Variety of DNA Replication Activity Among Cyanobacteria Correlates with Distinct Respiration Activity in the Dark. <i>Plant and Cell Physiology</i> , 2016, 58, pcw186.	1.5	8
75	Mutations responsible for alcohol tolerance in the mutant of <i>Synechococcus elongatus</i> PCC 7942 (SY1043) obtained by single-cell screening system. <i>Journal of Bioscience and Bioengineering</i> , 2018, 125, 572-577.	1.1	8
76	In vitro and in silico characterisation of <i>Lactobacillus paraplantarum</i> D2-1, a starter culture for soymilk fermentation. <i>International Journal of Food Sciences and Nutrition</i> , 2018, 69, 857-869.	1.3	8
77	Intracellular free flavin and its associated enzymes participate in oxygen and iron metabolism in <i>Amphibacillus xylanus</i> lacking a respiratory chain. <i>FEBS Open Bio</i> , 2018, 8, 947-961.	1.0	8
78	Identification of Transcription Factors and the Regulatory Genes Involved in Triacylglycerol Accumulation in the Unicellular Red Alga <i>Cyanidioschyzon merolae</i> . <i>Plants</i> , 2021, 10, 971.	1.6	8
79	Complete Genome Sequence of Cyanobacterium <i>Leptolyngbya</i> sp. NIES-3755. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
80	Pseudofructophilic <i>Leuconostoc citreum</i> Strain F192-5, Isolated from Satsuma Mandarin Peel. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	7
81	Free flavins accelerate release of ferrous iron from iron storage proteins by both free flavin-dependent and -independent ferric reductases in <i>Escherichia coli</i> . <i>Journal of General and Applied Microbiology</i> , 2019, 65, 308-315.	0.4	7
82	Reacquisition of light-harvesting genes in a marine cyanobacterium confers a broader solar niche. <i>Current Biology</i> , 2021, 31, 1539-1546.e4.	1.8	7
83	Draft Genome Sequence of <i>Oceanobacillus picturae</i> Heshi-B3, Isolated from Fermented Rice Bran in a Traditional Japanese Seafood Dish. <i>Genome Announcements</i> , 2016, 4, .	0.8	6
84	Draft Genome Sequence of <i>Paenibacillus amylolyticus</i> Heshi-A3, Isolated from Fermented Rice Bran in a Japanese Fermented Seafood Dish. <i>Genome Announcements</i> , 2016, 4, .	0.8	6
85	The CRP-family transcriptional regulator DevH regulates expression of heterocyst-specific genes at the later stage of differentiation in the cyanobacterium <i>Anabaena</i> sp. strain PCC 7120. <i>Molecular Microbiology</i> , 2020, 114, 553-562.	1.2	6
86	ParA-like protein influences the distribution of multi-copy chromosomes in cyanobacterium <i>Synechococcus elongatus</i> PCC 7942. <i>Microbiology (United Kingdom)</i> , 2018, 164, 45-56.	0.7	6
87	Comparison between the free radical scavenging activities with vitamin E and ubiquinol in biological systems based on their reaction rates: A research account. <i>BioFactors</i> , 2008, 32, 49-58.	2.6	5
88	Acclimation process of the chlorophyll <i>a</i> -bearing cyanobacterium <i>Acaryochloris marina</i> to an orange light environment revealed by transcriptomic analysis and electron microscopic observation. <i>Journal of General and Applied Microbiology</i> , 2020, 66, 106-115.	0.4	5
89	Novel (p)ppGpp0 suppressor mutations reveal an unexpected link between methionine catabolism and GTP synthesis in <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 2020, 113, 1155-1169.	1.2	5
90	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. <i>Harmful Algae</i> , 2021, 101, 101942.	2.2	5

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91	Draft Genome Sequence of <i>Microbacterium</i> sp. Strain HM58-2, Which Hydrolyzes Acylhydrazides. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
92	Complete Genome Sequence of the Nonheterocystous Cyanobacterium <i>Pseudanabaena</i> sp. ABRG5-3. <i>Genome Announcements</i> , 2018, 6, .	0.8	4
93	Complete Genome Sequence of the Marine Bacterium <i>Erythrobacter flavus</i> Strain KJ5. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	4
94	Genes regulated by branched-chain polyamine in the hyperthermophilic archaeon <i>Thermococcus kodakarensis</i> . <i>Amino Acids</i> , 2020, 52, 287-299.	1.2	4
95	H-NS Family Proteins Drastically Change Their Targets in Response to the Horizontal Transfer of the Catabolic Plasmid pCAR1. <i>Frontiers in Microbiology</i> , 2020, 11, 1099.	1.5	4
96	Transcriptome differences between <i>Cupriavidus necator</i> NH9 grown with 3-chlorobenzoate and that grown with benzoate. <i>Bioscience, Biotechnology and Biochemistry</i> , 2021, 85, 1546-1561.	0.6	4
97	Analysis of spontaneous suppressor mutants from the photomixotrophically grown <i>pmgA</i> -disrupted mutant in the cyanobacterium <i>Synechocystis</i> sp. PCC 6803. <i>Photosynthesis Research</i> , 2015, 126, 465-475.	1.6	3
98	Draft Genome Sequences of <i>Bradyrhizobium elkanii</i> Strains BLY3-8 and BLY6-1, Which Are Incompatible with Rj 3 Genotype Soybean Cultivars. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
99	Physiological and genomic analysis of newly-isolated polysaccharide synthesizing cyanobacterium <i>Chroococcus</i> sp. FPU101 and chemical analysis of the exopolysaccharide. <i>Journal of General and Applied Microbiology</i> , 2021, 67, 207-213.	0.4	3
100	Complete Genome Sequence of a Coastal Cyanobacterium, <i>Synechococcus</i> sp. Strain NIES-970. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
101	Transcriptome profile of carbon catabolite repression in an efficient l-(+)-lactic acid-producing bacterium <i>Enterococcus mundtii</i> QU25 grown in media with combinations of cellobiose, xylose, and glucose. <i>PLoS ONE</i> , 2020, 15, e0242070.	1.1	3
102	Draft Genome Sequence of <i>Bradyrhizobium japonicum</i> Is-34, Which Is Incompatible with Rj4 Genotype Soybeans. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
103	Draft Genome Sequence of <i>Bradyrhizobium japonicum</i> Is-1, Which Is Incompatible with Rj 2 Genotype Soybeans. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
104	Surface Sensing for <i>Paenibacillus</i> sp. NAIST15-1 Flagellar Gene Expression on Solid Medium. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	2
105	Whole-Genome Sequences of Two Closely Related Bacteria, <i>Actinomyces</i> sp. Strain Chiba101 and <i>Actinomyces denticolens</i> DSM 20671 T. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
106	Draft Genome Sequence of <i>Bacillus licheniformis</i> Heshi-B2, Isolated from Fermented Rice Bran in a Japanese Fermented Seafood Dish. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
107	<i>Actinomyces denticolens</i> as a causative agent of actinomycosis in animals. <i>Journal of Veterinary Medical Science</i> , 2018, 80, 1650-1656.	0.3	2
108	Draft Genome Sequence of <i>Zygosaccharomyces mellis</i> CA-7, Isolated from Honey. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2

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109	The Rubisco small subunits in the green algal genus <i>Chloromonas</i> provide insights into evolutionary loss of the eukaryotic carbon-concentrating organelle, the pyrenoid. <i>Bmc Ecology and Evolution</i> , 2021, 21, 11.	0.7	2
110	Sensors and Signal Transducers of Environmental Stress in Cyanobacteria. , 2009, , 15-31.		1
111	Control of Cell Nuclear DNA Replication by Chloroplast and Mitochondrion. , 2017, , 195-204.		1
112	RNA-seq analysis identified glucose-responsive genes and YqfO as a global regulator in <i>Bacillus subtilis</i> . <i>BMC Research Notes</i> , 2021, 14, 450.	0.6	1
113	Identical Hik-Rre systems are involved in perception and transduction of salt signals and hyperosmotic signals but regulate the expression of individual genes to different extents in <i>Synechocystis</i> .. <i>Journal of Biological Chemistry</i> , 2012, 287, 2269.	1.6	0
114	Five histidine kinases perceive osmotic stress and regulate distinct sets of genes in <i>Synechocystis</i> .. <i>Journal of Biological Chemistry</i> , 2012, 287, 2269.	1.6	0
115	Non-Destructive Prediction of Transcriptomes from Single-Cell Raman Microscopy. <i>Biophysical Journal</i> , 2018, 114, 390a.	0.2	0
116	Complete Genome Sequence of <i>Enterococcus faecium</i> QU50, a Thermophilic Lactic Acid Bacterium Capable of Metabolizing Xylose. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
117	Ubr1p-Cup9p-Ptr2p pathway involves in the sensitivity to readthrough compounds negamycin derivatives in budding yeast. <i>Bioscience, Biotechnology and Biochemistry</i> , 2019, 83, 1889-1892.	0.6	0
118	Characteristics of physiology of and genomic mutations in aggregation-enhanced mutants of <i>Methanothermobacter</i> sp. CaT2. <i>Bioscience, Biotechnology and Biochemistry</i> , 2020, 84, 1047-1055.	0.6	0
119	The 100%-Complete Nuclear and Organellar Genome Sequences of the Ultrasmall Red Algal Species <i>Cyanidioschyzon merolae</i> 10D. , 2017, , 61-72.		0
120	Draft Genome Sequence of <i>Lactiplantibacillus plantarum</i> NMZ-1139, Isolated from Whisky Mash. <i>Microbiology Resource Announcements</i> , 2021, 10, e0100821.	0.3	0