

Yu Kanasaki

List of Publications by Year in descending order

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121
papers

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159585

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124
docs citations

124
times ranked

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#	ARTICLE	IF	CITATIONS
1	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.	3.6	10
2	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.	4.8	5
3	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.	1.6	2
4	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.	0.7	3
5	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.	1.3	4
6	Reacquisition of light-harvesting genes in a marine cyanobacterium confers a broader solar niche. <i>Current Biology</i> , 2021, 31, 1539-1546.e4.	3.9	7
7	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.	3.5	8
8	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, .	0.6	10
9	Genome sequencing of the NIES Cyanobacteria collection with a focus on the heterocyst-forming clade. <i>DNA Research</i> , 2021, 28, .	3.4	12
10	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.	1.4	1
11	Draft Genome Sequence of <i>Lactiplantibacillus plantarum</i> NMZ-1139, Isolated from Whisky Mash. <i>Microbiology Resource Announcements</i> , 2021, 10, e0100821.	0.6	0
12	Genes regulated by branched-chain polyamine in the hyperthermophilic archaeon <i>Thermococcus kodakarensis</i> . <i>Amino Acids</i> , 2020, 52, 287-299.	2.7	4
13	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.	1.3	0
14	<i>Bacillus subtilis</i> Nucleoid-Associated Protein YlxR Is Involved in Bimodal Expression of the Fructoselysine Utilization Operon (<i>frlBONMD-yurI</i>) Promoter. <i>Frontiers in Microbiology</i> , 2020, 11, 2024.	3.5	11
15	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.	9.8	12
16	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.	3.5	4
17	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.	0.7	5
18	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.	3.3	9

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19	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.	2.5	6
20	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.	3.5	14
21	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.	2.5	5
22	Evolutionary Changes in DnaA-Dependent Chromosomal Replication in Cyanobacteria. <i>Frontiers in Microbiology</i> , 2020, 11, 786.	3.5	12
23	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.	2.5	3
24	Integration of a <i>Galdieria</i> plasma membrane sugar transporter enables heterotrophic growth of the obligate photoautotrophic red alga <i>Cyananidioschyzon merolae</i> . <i>Plant Direct</i> , 2019, 3, e00134.	1.9	9
25	Draft Genome Sequence of <i>Zygosaccharomyces mellis</i> CA-7, Isolated from Honey. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
26	Interplay and Targetome of the Two Conserved Cyanobacterial sRNAs Yfr1 and Yfr2 in <i>Prochlorococcus</i> MED4. <i>Scientific Reports</i> , 2019, 9, 14331.	3.3	10
27	Pseudofractophilic <i>Leuconostoc citreum</i> Strain F192-5, Isolated from Satsuma Mandarin Peel. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	7
28	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.	0.7	7
29	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.	3.1	15
30	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, .	0.6	0
31	Capacity for survival in global warming: Adaptation of mesophiles to the temperature upper limit. <i>PLoS ONE</i> , 2019, 14, e0215614.	2.5	18
32	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.	1.3	0
33	Sulfur-Containing Carotenoids from A Marine Coral Symbiont <i>Erythrobacter flavus</i> Strain KJ5. <i>Marine Drugs</i> , 2019, 17, 349.	4.6	29
34	Coordination of Polyploid Chromosome Replication with Cell Size and Growth in a Cyanobacterium. <i>MBio</i> , 2019, 10, .	4.1	37
35	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.	3.5	22
36	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.	2.2	19

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37	Complete Genome Sequence of the Marine Bacterium <i>Erythrobacter flavus</i> Strain KJ5. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4
38	Responses of unicellular predators to cope with the phototoxicity of photosynthetic prey. <i>Nature Communications</i> , 2019, 10, 5606.	12.8	11
39	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.	0.7	11
40	Comparative genome analysis of <i>Aspergillus flavus</i> clinically isolated in Japan. <i>DNA Research</i> , 2019, 26, 95-103.	3.4	11
41	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
42	Complete Genome Sequence of the Nonheterocystous Cyanobacterium <i>Pseudanabaena</i> sp. ABRG5-3. <i>Genome Announcements</i> , 2018, 6, .	0.8	4
43	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.	2.2	8
44	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.	2.8	8
45	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.	0.7	12
46	Identification of the novel <i>hcbB</i> operon catalyzing the dechlorination of pentachlorophenol in the Gram-positive bacterium <i>Nocardiooides</i> sp. strain PD653. <i>Journal of Pesticide Sciences</i> , 2018, 43, 124-131.	1.4	12
47	Transcriptional Activation of Glycogen Catabolism and the Oxidative Pentose Phosphate Pathway by <i>NrrA</i> 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.	3.1	10
48	<i>Actinomyces denticolens</i> as a causative agent of actinomycosis in animals. <i>Journal of Veterinary Medical Science</i> , 2018, 80, 1650-1656.	0.9	2
49	Newly Identified Nucleoid-Associated-Like Protein YlxR Regulates Metabolic Gene Expression in <i>Bacillus subtilis</i> . <i>MSphere</i> , 2018, 3, .	2.9	18
50	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.	2.3	8
51	Non-Destructive Prediction of Transcriptomes from Single-Cell Raman Microscopy. <i>Biophysical Journal</i> , 2018, 114, 390a.	0.5	0
52	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
53	Linear Regression Links Transcriptomic Data and Cellular Raman Spectra. <i>Cell Systems</i> , 2018, 7, 104-117.e4.	6.2	34
54	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.	1.8	6

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55	Conserved two-component <i>Hik34</i> <i>Rre1</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.	2.5	17
56	Surface Sensing for <i>Paenibacillus</i> sp. NAIST15-1 Flagellar Gene Expression on Solid Medium. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	2
57	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.	7.1	93
58	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, .	3.1	16
59	Genome Mining of Amino Group Carrier Protein-Mediated Machinery: Discovery and Biosynthetic Characterization of a Natural Product with Unique Hydrazone Unit. <i>ACS Chemical Biology</i> , 2017, 12, 124-131.	3.4	29
60	CyanoBase: A large-scale update on its 20th anniversary. <i>Nucleic Acids Research</i> , 2017, 45, D551-D554.	14.5	95
61	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
62	Control of Cell Nuclear DNA Replication by Chloroplast and Mitochondrion. , 2017, , 195-204.		1
63	Complete Genome Sequence of a Coastal Cyanobacterium, <i>Synechococcus</i> sp. Strain NIES-970. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
64	The 100%-Complete Nuclear and Organellar Genome Sequences of the Ultrasmall Red Algal Species <i>Cyanidioschyzon merolae</i> 10D. , 2017, , 61-72.		0
65	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
66	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
67	Draft Genome Sequence of <i>Microbacterium</i> sp. Strain HM58-2, Which Hydrolyzes Acylhydrazides. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
68	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.	2.2	11
69	Variety of DNA Replication Activity Among Cyanobacteria Correlates with Distinct Respiration Activity in the Dark. <i>Plant and Cell Physiology</i> , 2016, 58, pcw186.	3.1	8
70	Genomic characterization of a fructophilic bee symbiont <i>Lactobacillus kunkeei</i> reveals its niche-specific adaptation. <i>Systematic and Applied Microbiology</i> , 2016, 39, 516-526.	2.8	51
71	Chloroplast-mediated regulation of CO ₂ -concentrating mechanism by Ca ²⁺ -binding protein CAS in the green alga <i>Chlamydomonas reinhardtii</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12586-12591.	7.1	73
72	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

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73	Complete genome sequence of cyanobacterium Fischerella sp. NIES-3754, providing thermoresistant optogenetic tools. Journal of Biotechnology, 2016, 220, 45-46.	3.8	27
74	Complete genome sequence of cyanobacterium Nostoc sp. NIES-3756, a potentially useful strain for phytochrome-based bioengineering. Journal of Biotechnology, 2016, 218, 51-52.	3.8	14
75	Complete Genome Sequence of Cyanobacterium Leptolyngbya sp. NIES-3755. Genome Announcements, 2016, 4, .	0.8	7
76	Diversification of DnaA dependency for DNA replication in cyanobacterial evolution. ISME Journal, 2016, 10, 1113-1121.	9.8	39
77	Genetic Analysis of Collective Motility of Paenibacillus sp. NAIST15-1. PLoS Genetics, 2016, 12, e1006387.	3.5	16
78	Draft Genome Sequence of Bradyrhizobium japonicum Is-1, Which Is Incompatible with Rj 2 Genotype Soybeans. Genome Announcements, 2015, 3, .	0.8	2
79	Microevolution of Virulence-Related Genes in Helicobacter pylori Familial Infection. PLoS ONE, 2015, 10, e0127197.	2.5	23
80	Intensive DNA Replication and Metabolism during the Lag Phase in Cyanobacteria. PLoS ONE, 2015, 10, e0136800.	2.5	44
81	A nitrogen source-dependent inducible and repressible gene expression system in the red alga Cyanidioschyzon merolae. Frontiers in Plant Science, 2015, 6, 657.	3.6	32
82	Identification of genes involved in the phosphate metabolism in Cryptococcus neoformans. Fungal Genetics and Biology, 2015, 80, 19-30.	2.1	26
83	Identification of centromere regions in chromosomes of a unicellular red alga, <i>Cyanidioschyzon merolae</i> . FEBS Letters, 2015, 589, 1219-1224.	2.8	13
84	Genomic analysis of parallel-evolved cyanobacterium Synechocystis sp. PCC 6803 under acid stress. Photosynthesis Research, 2015, 125, 243-254.	2.9	25
85	A Putative Type III Secretion System Effector Encoded by the <i>MA20_12780</i> Gene in Bradyrhizobium japonicum Is-34 Causes Incompatibility with <i>Rj4</i> Genotype Soybeans. Applied and Environmental Microbiology, 2015, 81, 5812-5819.	3.1	25
86	Analysis of spontaneous suppressor mutants from the photomixotrophically grown <i>pmgA</i> -disrupted mutant in the cyanobacterium Synechocystis sp. PCC 6803. Photosynthesis Research, 2015, 126, 465-475.	2.9	3
87	Complete Genome Sequence of Bifidobacterium longum 105-A, a Strain with High Transformation Efficiency. Genome Announcements, 2014, 2, .	0.8	16
88	Draft Genome Sequence of Bradyrhizobium japonicum Is-34, Which Is Incompatible with <i>Rj4</i> Genotype Soybeans. Genome Announcements, 2014, 2, .	0.8	2
89	Draft Genome Sequence of Strain Q-1, an Iodide-Oxidizing Alphaproteobacterium Isolated from Natural Gas Brine Water. Genome Announcements, 2014, 2, .	0.8	9
90	Exopolysaccharide production by a unicellular freshwater cyanobacterium Cyanosphaera sp. isolated from a rice field in Vietnam. Journal of Applied Phycology, 2014, 26, 265-272.	2.8	21

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91	DNA replication depends on photosynthetic electron transport in cyanobacteria. FEMS Microbiology Letters, 2013, 344, 138-144.	1.8	19
92	Identification of Substrain-Specific Mutations by Massively Parallel Whole-Genome Resequencing of <i>Synechocystis</i> sp. PCC 6803. DNA Research, 2012, 19, 67-79.	3.4	119
93	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> .. Journal of Biological Chemistry, 2012, 287, 2269.	3.4	0
94	Five histidine kinases perceive osmotic stress and regulate distinct sets of genes in <i>Synechocystis</i> .. Journal of Biological Chemistry, 2012, 287, 2269.	3.4	0
95	Iodide Oxidation by a Novel Multicopper Oxidase from the Alphaproteobacterium Strain Q-1. Applied and Environmental Microbiology, 2012, 78, 3941-3949.	3.1	35
96	External Light Conditions and Internal Cell Cycle Phases Coordinate Accumulation of Chloroplast and Mitochondrial Transcripts in the Red Alga <i>Cyanidioschyzon merolae</i> . DNA Research, 2012, 19, 289-303.	3.4	25
97	Light-dependent and asynchronous replication of cyanobacterial multi-copy chromosomes. Molecular Microbiology, 2012, 83, 856-865.	2.5	68
98	Whole-genome resequencing shows numerous genes with nonsynonymous SNPs in the Japanese native cattle Kuchinoshima-Ushi. BMC Genomics, 2011, 12, 103.	2.8	72
99	Genomic Structure of the Cyanobacterium <i>Synechocystis</i> sp. PCC 6803 Strain GT-S. DNA Research, 2011, 18, 393-399.	3.4	42
100	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.	1.8	32
101	Correction for Imamura et al., R2R3-type MYB transcription factor, CmMYB1, is a central nitrogen assimilation regulator in <i>Cyanidioschyzon merolae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 14180-14180.	7.1	2
102	Tetrapyrrole signal as a cell-cycle coordinator from organelle to nuclear DNA replication in plant cells. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 803-807.	7.1	103
103	Mg-Protoporphyrin IX Signaling in <i>Cyanidioschyzon merolae</i> . Plant Signaling and Behavior, 2009, 4, 1190-1192.	2.4	9
104	R2R3-type MYB transcription factor, CmMYB1, is a central nitrogen assimilation regulator in <i>Cyanidioschyzon merolae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12548-12553.	7.1	112
105	Sensors and Signal Transducers of Environmental Stress in Cyanobacteria. , 2009, , 15-31.		1
106	Comparison between the free-radical-scavenging activities with vitamin E and ubiquinol in biological systems based on their reaction rates: A research account. BioFactors, 2008, 32, 49-58.	5.4	5
107	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.	5.2	34
108	Structure-Activity Relationship of the Free-Radical-Scavenging Reaction by Vitamin E (Î±-, Î²-, Î³-, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2007, 111, 652-662.	2.6	69

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109	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.	5.7	89
110	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.	4.8	89
111	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.	3.4	159
112	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.	3.4	144
113	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.	4.8	131
114	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.	3.4	120
115	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.	3.4	127
116	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.	7.1	170
117	Salt Stress Inhibits the Repair of Photodamaged Photosystem II by Suppressing the Transcription and Translation of <i>psbA</i> Genes in <i>Synechocystis</i> A. <i>Plant Physiology</i> , 2002, 130, 1443-1453.	4.8	246
118	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.	2.1	273
119	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.	2.5	185
120	Cold-regulated genes under control of the cold sensor Hik33 in <i>Synechocystis</i> . <i>Molecular Microbiology</i> , 2001, 40, 235-244.	2.5	238
121	The pathway for perception and transduction of low-temperature signals in <i>Synechocystis</i> . <i>EMBO Journal</i> , 2000, 19, 1327-1334.	7.8	238