

Kenji Nakahigashi

List of Publications by Year in descending order

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32
papers

3,386
citations

304743

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454955

30
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docs citations

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times ranked

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citing authors

#	ARTICLE	IF	CITATIONS
1	High-Light-Induced Stress Activates Lipid Deacylation at the <i>Sn</i> -2 Position in the Cyanobacterium <i>Synechocystis</i> Sp. PCC 6803. <i>Plant and Cell Physiology</i> , 2022, 63, 82-91.	3.1	4
2	Alteration of fatty acid chain length of <i>Chlamydomonas reinhardtii</i> by simultaneous expression of medium-chain-specific thioesterase and acyl carrier protein. <i>Phycological Research</i> , 2017, 65, 94-99.	1.6	16
3	Comprehensive identification of translation start sites by tetracycline-inhibited ribosome profiling. <i>DNA Research</i> , 2016, 23, 193-201.	3.4	83
4	GenoBase: comprehensive resource database of <i>Escherichia coli</i> K-12. <i>Nucleic Acids Research</i> , 2015, 43, D606-D617.	14.5	29
5	Effect of codon adaptation on codon-level and gene-level translation efficiency in vivo. <i>BMC Genomics</i> , 2014, 15, 1115.	2.8	48
6	Metabolomic study of Chilean biomining bacteria <i>Acidithiobacillus ferrooxidans</i> strain Wenelen and <i>Acidithiobacillus thiooxidans</i> strain Licanantay. <i>Metabolomics</i> , 2013, 9, 247-257.	3.0	39
7	Metabolic regulation analysis of wild-type and <i>arcA</i> mutant <i>Escherichia coli</i> under nitrate conditions using different levels of omics data. <i>Molecular BioSystems</i> , 2012, 8, 2593.	2.9	39
8	Glycogen is the primary source of glucose during the lag phase of <i>E. coli</i> proliferation. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 1442-1448.	2.3	31
9	Catabolic regulation analysis of <i>Escherichia coli</i> and its <i>crp</i> , <i>mlc</i> , <i>mgsA</i> , <i>pgi</i> and <i>ptsG</i> mutants. <i>Microbial Cell Factories</i> , 2011, 10, 67.	4.0	79
10	¹³ C-metabolic flux analysis for batch culture of <i>Escherichia coli</i> and its <i>pyk</i> and <i>pgi</i> gene knockout mutants based on mass isotopomer distribution of intracellular metabolites. <i>Biotechnology Progress</i> , 2010, 26, 975-992.	2.6	92
11	A systematic survey of in vivo obligate chaperonin-dependent substrates. <i>EMBO Journal</i> , 2010, 29, 1552-1564.	7.8	156
12	Update on the Keio collection of <i>Escherichia coli</i> single-gene deletion mutants. <i>Molecular Systems Biology</i> , 2009, 5, 335.	7.2	226
13	Systematic phenome analysis of <i>Escherichia coli</i> multiple-knockout mutants reveals hidden reactions in central carbon metabolism. <i>Molecular Systems Biology</i> , 2009, 5, 306.	7.2	143
14	Resources for <i>Escherichia coli</i> Systems Biology. , 2009, , 87-97.		0
15	Multiple High-Throughput Analyses Monitor the Response of <i>E. coli</i> to Perturbations. <i>Science</i> , 2007, 316, 593-597.	12.6	694
16	Epigenetic maintenance of the vernalized state in <i>Arabidopsis thaliana</i> requires LIKE HETEROCHROMATIN PROTEIN 1. <i>Nature Genetics</i> , 2006, 38, 706-710.	21.4	309
17	Large-scale identification of protein-protein interaction of <i>Escherichia coli</i> K-12. <i>Genome Research</i> , 2006, 16, 686-691.	5.5	368
18	The <i>Arabidopsis</i> HETEROCHROMATIN PROTEIN1 Homolog (TERMINAL FLOWER2) Silences Genes Within the Euchromatic Region but not Genes Positioned in Heterochromatin. <i>Plant and Cell Physiology</i> , 2005, 46, 1747-1756.	3.1	98

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19	Arabidopsis TERMINAL FLOWER 2 Gene Encodes a Heterochromatin Protein 1 Homolog and Represses both FLOWERING LOCUS T to Regulate Flowering Time and Several Floral Homeotic Genes. <i>Plant and Cell Physiology</i> , 2003, 44, 555-564.	3.1	214
20	Cloning and Sequencing a HemK -family Gene in <i>Porphyromonas gingivalis</i> . <i>DNA Sequence</i> , 2003, 14, 71-74.	0.7	0
21	Heat Shock Proteome of <i>Agrobacterium tumefaciens</i> : Evidence for New Control Systems. <i>Journal of Bacteriology</i> , 2002, 184, 1772-1778.	2.2	40
22	HemK, a class of protein methyl transferase with similarity to DNA methyl transferases, methylates polypeptide chain release factors, and hemK knockout induces defects in translational termination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 1473-1478.	7.1	110
23	Viability of <i>Escherichia coli</i> cells under long-term cultivation in a rich nutrient medium.. <i>Genes and Genetic Systems</i> , 2001, 76, 271-278.	0.7	4
24	Isolation and characterization of a cDNA from soybean and its homolog from <i>Escherichia coli</i> , which both complement the light sensitivity of <i>Escherichia coli</i> hemH mutant strain VS101.. <i>Genes and Genetic Systems</i> , 2001, 76, 327-334.	0.7	3
25	DnaK Chaperone-Mediated Control of Activity of a σ_{32} Homolog (RpoH) Plays a Major Role in the Heat Shock Response of <i>Agrobacterium tumefaciens</i> . <i>Journal of Bacteriology</i> , 2001, 183, 5302-5310.	2.2	20
26	Regulation of the heat-shock response. <i>Current Opinion in Microbiology</i> , 1999, 2, 153-158.	5.1	217
27	Differential and Independent Roles of a σ_{32} Homolog (RpoH) and an HrcA Repressor in the Heat Shock Response of <i>Agrobacterium tumefaciens</i> . <i>Journal of Bacteriology</i> , 1999, 181, 7509-7515.	2.2	48
28	Regulatory Conservation and Divergence of σ_{32} Homologs from Gram-Negative Bacteria: <i>Serratia marcescens</i> , <i>Proteus mirabilis</i> , <i>Pseudomonas aeruginosa</i> , and <i>Agrobacterium tumefaciens</i> . <i>Journal of Bacteriology</i> , 1998, 180, 2402-2408.	2.2	35
29	Regulatory Region C of the <i>E. coli</i> Heat Shock Transcription Factor, σ_{32} , Constitutes a DnaK Binding Site and is Conserved Among Eubacteria. <i>Journal of Molecular Biology</i> , 1996, 256, 829-837.	4.2	118
30	Isolation and characterization of visible light-sensitive mutants of <i>Escherichia coli</i> K12. <i>Journal of Molecular Biology</i> , 1991, 219, 393-398.	4.2	119
31	An <i>E. coli</i> promoter that is sensitive to visible light.. <i>Japanese Journal of Genetics</i> , 1990, 65, 381-386.	1.0	2
32	Functional expression of the mutants of the chloroplast tRNA ^{Lys} gene from the liverwort, <i>Marchantia polymorpha</i> , in <i>Escherichia coli</i> . <i>FEBS Letters</i> , 1990, 265, 59-62.	2.8	2