

Tomoya Baba

List of Publications by Year in descending order

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52
papers

15,933
citations

147801

31
h-index

189892

50
g-index

52
all docs

52
docs citations

52
times ranked

18252
citing authors

#	ARTICLE	IF	CITATIONS
1	Highly Precise and Sensitive Polymerase Chain Reaction Using Mesoporous Silica-Immobilized Enzymes. ACS Applied Materials & Interfaces, 2022, 14, 29483-29490.	8.0	3
2	Numerical Simulation of Fine Particle Deposition in Layering Granulation. Tetsu-To-Hagane/Journal of the Iron and Steel Institute of Japan, 2021, 107, 394-402.	0.4	0
3	Batch-Learning Self-Organizing Map Identifies Horizontal Gene Transfer Candidates and Their Origins in Entire Genomes. Frontiers in Microbiology, 2020, 11, 1486.	3.5	8
4	Minimal Genomes: How Many Genes Does a Cell Require To Be Viable. Journal of Geography (Chigaku) Tj ETQq0 0 0,rgBT /Overlock 10 T	0.5	3
5	Essential cellular modules for the proliferation of the primitive cell. Geoscience Frontiers, 2018, 9, 1155-1161.	8.4	6
6	Complete Genome Sequence of Aurantimicrobium minutum Type Strain KNC ^T, a Planktonic Ultramicrobacterium Isolated from River Water. Genome Announcements, 2016, 4, .	0.8	17
7	Genome sequence and overview of Oligoflexus tunisiensis Shr3T in the eighth class Oligoflexia of the phylum Proteobacteria. Standards in Genomic Sciences, 2016, 11, 90.	1.5	12
8	Identification of Essential Genes and Synthetic Lethal Gene Combinations in Escherichia coli K-12. Methods in Molecular Biology, 2015, 1279, 45-65.	0.9	23
9	Aurantimicrobium minutum gen. nov., sp. nov., a novel ultramicrobacterium of the family Microbacteriaceae, isolated from river water. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 4072-4079.	1.7	32
10	Nanoporous scaffold for DNA polymerase: pore-size optimisation of mesoporous silica for DNA amplification. RSC Advances, 2014, 4, 25920-25923.	3.6	6
11	Diversity of RuBisCO gene responsible for CO2 fixation in an Antarctic moss pillar. Polar Biology, 2012, 35, 1641-1650.	1.2	11
12	Eukaryotic phlotypes in aquatic moss pillars inhabiting a freshwater lake in East Antarctica, based on 18S rRNA gene analysis. Polar Biology, 2012, 35, 1495-1504.	1.2	27
13	Microflorae of aquatic moss pillars in a freshwater lake, East Antarctica, based on fatty acid and 16S rRNA gene analyses. Polar Biology, 2012, 35, 425-433.	1.2	36
14	Direct PCR amplification of the 16S rRNA gene from single microbial cells isolated from an Antarctic iceberg using laser microdissection microscopy. Polar Science, 2011, 5, 375-382.	1.2	6
15	ENVIRONMENTAL DEPENDENCY OF GENE KNOCKOUTS ON PHENOTYPE MICROARRAY ANALYSIS IN ESCHERICHIA COLI. Journal of Bioinformatics and Computational Biology, 2010, 08, 83-99.	0.8	10
16	Complete genome sequence and comparative analysis of Shewanella violacea, a psychrophilic and piezophilic bacterium from deep sea floor sediments. Molecular BioSystems, 2010, 6, 1216.	2.9	42
17	Glutathione production by efficient ATP-regenerating<i> Escherichia coli</i> mutants. FEMS Microbiology Letters, 2009, 297, 217-224.	1.8	25
18	Systematic genome-wide scanning for genes involved in ATP generation in Escherichia coli. Metabolic Engineering, 2009, 11, 1-7.	7.0	26

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19	The Construction of Systematic In-Frame, Single-Gene Knockout Mutant Collection in <i>Escherichia coli</i> K-12. <i>Methods in Molecular Biology</i> , 2008, 416, 171-181.	0.9	45
20	Genome Structure of the Legume, <i>Lotus japonicus</i> . <i>DNA Research</i> , 2008, 15, 227-239.	3.4	691
21	The Applications of Systematic In-Frame, Single-Gene Knockout Mutant Collection of <i>Escherichia coli</i> K-12. <i>Methods in Molecular Biology</i> , 2008, 416, 183-194.	0.9	38
22	Multiple High-Throughput Analyses Monitor the Response of <i>E. coli</i> to Perturbations. <i>Science</i> , 2007, 316, 593-597.	12.6	694
23	Highly accurate genome sequences of <i>Escherichia coli</i> K12 strains MG1655 and W3110. <i>Molecular Systems Biology</i> , 2006, 2, 2006.0007.	7.2	409
24	High-throughput Fluorescence Labelling of Full-length cDNA Products Based on a Reconstituted Translation System. <i>Journal of Biochemistry</i> , 2006, 141, 19-24.	1.7	6
25	Construction of <i>Escherichia coli</i> K12 in-frame, single-gene knockout mutants: the Keio collection. <i>Molecular Systems Biology</i> , 2006, 2, 2006.0008.	7.2	6,537
26	<i>Escherichia coli</i> proteome chips for detecting protein-protein interactions. <i>Proteomics</i> , 2006, 6, 6433-6436.	2.2	12
27	Comparative Analysis of <i>argK-tox</i> Clusters and Their Flanking Regions in Phaseolotoxin-Producing <i>Pseudomonas syringae</i> Pathovars. <i>Journal of Molecular Evolution</i> , 2006, 63, 401-414.	1.8	35
28	Experimental and Computational Assessment of Conditionally Essential Genes in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2006, 188, 8259-8271.	2.2	237
29	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
30	Functional analysis of 1440 <i>Escherichia coli</i> genes using the combination of knock-out library and phenotype microarrays. <i>Metabolic Engineering</i> , 2005, 7, 318-327.	7.0	47
31	Ribosome binding proteins YhbH and YfiA have opposite functions during 100S formation in the stationary phase of <i>Escherichia coli</i> . <i>Genes To Cells</i> , 2005, 10, 1103-1112.	1.2	126
32	The map-based sequence of the rice genome. <i>Nature</i> , 2005, 436, 793-800.	27.8	3,365
33	Global metabolic response of <i>Escherichia coli</i> to <i>gnd</i> or <i>zwf</i> gene-knockout, based on 13 C-labeling experiments and the measurement of enzyme activities. <i>Applied Microbiology and Biotechnology</i> , 2004, 64, 91-98.	3.6	98
34	Effect of <i>zwf</i> gene knockout on the metabolism of <i>Escherichia coli</i> grown on glucose or acetate. <i>Metabolic Engineering</i> , 2004, 6, 164-174.	7.0	97
35	Identification of the Two Missing Bacterial Genes Involved in Thiamine Salvage: Thiamine Pyrophosphokinase and Thiamine Kinase. <i>Journal of Bacteriology</i> , 2004, 186, 3660-3662.	2.2	55
36	Analysis of <i>Escherichia coli</i> anaplerotic metabolism and its regulation mechanisms from the metabolic responses to altered dilution rates and phosphoenolpyruvate carboxykinase knockout. <i>Biotechnology and Bioengineering</i> , 2003, 84, 129-144.	3.3	124

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37	Analysis of metabolic and physiological responses to gnd knockout in <i>Escherichia coli</i> by using C-13 tracer experiment and enzyme activity measurement. <i>FEMS Microbiology Letters</i> , 2003, 220, 295-301.	1.8	54
38	Systematic characterization of <i>Escherichia coli</i> genes/ORFs affecting biofilm formation. <i>FEMS Microbiology Letters</i> , 2003, 225, 107-114.	1.8	42
39	Responses of the Central Metabolism in <i>Escherichia coli</i> to Phosphoglucose isomerase and Glucose-6-Phosphate Dehydrogenase Knockouts. <i>Journal of Bacteriology</i> , 2003, 185, 7053-7067.	2.2	173
40	The genome sequence and structure of rice chromosome 1. <i>Nature</i> , 2002, 420, 312-316.	27.8	519
41	A physical map with yeast artificial chromosome (YAC) clones covering 63% of the 12 rice chromosomes. <i>Genome</i> , 2001, 44, 32-37.	2.0	50
42	Antisense Expression of a Rice Sucrose Transporter OsSUT1 in Rice (<i>Oryza sativa</i> L.). <i>Plant and Cell Physiology</i> , 2001, 42, 1181-1185.	3.1	82
43	Rice Genomics: Current Status of Genome Sequencing. <i>Novartis Foundation Symposium</i> , 2001, 236, 28-45.	1.1	4
44	A physical map with yeast artificial chromosome (YAC) clones covering 63% of the 12 rice chromosomes. <i>Genome</i> , 2001, 44, 32-37.	2.0	44
45	Hd1, a Major Photoperiod Sensitivity Quantitative Trait Locus in Rice, Is Closely Related to the Arabidopsis Flowering Time Gene CONSTANS. <i>Plant Cell</i> , 2000, 12, 2473-2483.	6.6	1,417
46	Construction of a Contiguous 874-kb Sequence of the <i>Escherichia coli</i> K12 Genome Corresponding to 50.0-68.8 min on the Linkage Map and Analysis of Its Sequence Features. <i>DNA Research</i> , 1997, 4, 91-95.	3.4	50
47	Alkaline and Thermophilic Amylases of Industrial Use. <i>Annals of the New York Academy of Sciences</i> , 1996, 799, 332-340.	3.8	0
48	A 570-kb DNA Sequence of the <i>Escherichia coli</i> K-12 Genome Corresponding to the 28.0-40.1 min Region on the Linkage Map. <i>DNA Research</i> , 1996, 3, 363-377.	3.4	41
49	A 460-kb DNA Sequence of the <i>Escherichia coli</i> K-12 Genome Corresponding to the 40.1-50.0 min Region on the Linkage Map. <i>DNA Research</i> , 1996, 3, 379-392.	3.4	48
50	A 718-kb DNA Sequence of the <i>Escherichia coli</i> K-12 Genome Corresponding to the 12.7-28.0 min Region on the Linkage Map. <i>DNA Research</i> , 1996, 3, 137-155.	3.4	76
51	Identification and characterization of clustered genes for thermostable xylan-degrading enzymes, beta-xylosidase and xylanase, of <i>Bacillus stearothermophilus</i> 21. <i>Applied and Environmental Microbiology</i> , 1994, 60, 2252-2258.	3.1	53
52	Crosslinked polymers with increased affinity for methyl orange. <i>Die Makromolekulare Chemie Rapid Communications</i> , 1988, 9, 553-558.	1.1	3