

Masayuki Inui

List of Publications by Year in descending order

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168
papers

8,073
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44066

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4401
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#	ARTICLE	IF	CITATIONS
1	An efficient succinic acid production process in a metabolically engineered <i>Corynebacterium glutamicum</i> strain. <i>Applied Microbiology and Biotechnology</i> , 2008, 81, 459-464.	3.6	367
2	Expression of <i>Clostridium acetobutylicum</i> butanol synthetic genes in <i>Escherichia coli</i> . <i>Applied Microbiology and Biotechnology</i> , 2008, 77, 1305-1316.	3.6	339
3	Metabolic Analysis of <i>Corynebacterium glutamicum</i> during Lactate and Succinate Productions under Oxygen Deprivation Conditions. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2004, 7, 182-196.	1.0	311
4	Metabolic Engineering of <i>Corynebacterium glutamicum</i> for Fuel Ethanol Production under Oxygen-Deprivation Conditions. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2004, 8, 243-254.	1.0	256
5	Comparative analysis of the <i>Corynebacterium glutamicum</i> group and complete genome sequence of strain R. <i>Microbiology (United Kingdom)</i> , 2007, 153, 1042-1058.	1.8	223
6	Production of organic acids by <i>Corynebacterium glutamicum</i> under oxygen deprivation. <i>Applied Microbiology and Biotechnology</i> , 2005, 68, 475-480.	3.6	221
7	Engineering of a Xylose Metabolic Pathway in <i>Corynebacterium glutamicum</i> . <i>Applied and Environmental Microbiology</i> , 2006, 72, 3418-3428.	3.1	219
8	Production of d-lactic acid by <i>Corynebacterium glutamicum</i> under oxygen deprivation. <i>Applied Microbiology and Biotechnology</i> , 2008, 78, 449-454.	3.6	207
9	Enhanced Hydrogen Production from Formic Acid by Formate Hydrogen Lyase-Overexpressing <i>Escherichia coli</i> Strains. <i>Applied and Environmental Microbiology</i> , 2005, 71, 6762-6768.	3.1	202
10	Bacterial phosphotransferase system (PTS) in carbohydrate uptake and control of carbon metabolism. <i>Journal of Bioscience and Bioengineering</i> , 2001, 92, 502-517.	2.2	183
11	Effect of Lignocellulose-Derived Inhibitors on Growth of and Ethanol Production by Growth-Arrested <i>Corynebacterium glutamicum</i> R. <i>Applied and Environmental Microbiology</i> , 2007, 73, 2349-2353.	3.1	153
12	Enhanced hydrogen production from glucose using <i>ldh</i> - and <i>frd</i> -inactivated <i>Escherichia coli</i> strains. <i>Applied Microbiology and Biotechnology</i> , 2006, 73, 67-72.	3.6	135
13	Anaerobic growth of <i>Corynebacterium glutamicum</i> using nitrate as a terminal electron acceptor. <i>Applied Microbiology and Biotechnology</i> , 2007, 75, 889-897.	3.6	135
14	Transcriptional profiling of <i>Corynebacterium glutamicum</i> metabolism during organic acid production under oxygen deprivation conditions. <i>Microbiology (United Kingdom)</i> , 2007, 153, 2491-2504.	1.8	129
15	Engineering of an l-arabinose metabolic pathway in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2008, 77, 1053-1062.	3.6	128
16	Sugar transporters in efficient utilization of mixed sugar substrates: current knowledge and outlook. <i>Applied Microbiology and Biotechnology</i> , 2010, 85, 471-480.	3.6	124
17	Improvement of the Redox Balance Increases L-Valine Production by <i>Corynebacterium glutamicum</i> under Oxygen Deprivation Conditions. <i>Applied and Environmental Microbiology</i> , 2012, 78, 865-875.	3.1	116
18	Engineering of pentose transport in <i>Corynebacterium glutamicum</i> to improve simultaneous utilization of mixed sugars. <i>Applied Microbiology and Biotechnology</i> , 2009, 85, 105-115.	3.6	104

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19	Engineering of <i>Corynebacterium glutamicum</i> for High-Yield L-Valine Production under Oxygen Deprivation Conditions. <i>Applied and Environmental Microbiology</i> , 2013, 79, 1250-1257.	3.1	103
20	Metabolic engineering of <i>Corynebacterium glutamicum</i> for shikimate overproduction by growth-arrested cell reaction. <i>Metabolic Engineering</i> , 2016, 38, 204-216.	7.0	101
21	New Multiple-Deletion Method for the <i>Corynebacterium glutamicum</i> Genome, Using a Mutant <i>lox</i> Sequence. <i>Applied and Environmental Microbiology</i> , 2005, 71, 8472-8480.	3.1	96
22	Strain optimization for efficient isobutanol production using <i>Corynebacterium glutamicum</i> under oxygen deprivation. <i>Biotechnology and Bioengineering</i> , 2013, 110, 2938-2948.	3.3	96
23	Simultaneous utilization of d-cellobiose, d-glucose, and d-xylose by recombinant <i>Corynebacterium glutamicum</i> under oxygen-deprived conditions. <i>Applied Microbiology and Biotechnology</i> , 2008, 81, 691-699.	3.6	91
24	Engineering of sugar metabolism of <i>Corynebacterium glutamicum</i> for production of amino acid L-alanine under oxygen deprivation. <i>Applied Microbiology and Biotechnology</i> , 2010, 87, 159-165.	3.6	91
25	High-Throughput Transposon Mutagenesis of <i>Corynebacterium glutamicum</i> and Construction of a Single-Gene Disruptant Mutant Library. <i>Applied and Environmental Microbiology</i> , 2006, 72, 3750-3755.	3.1	89
26	Xylitol production by recombinant <i>Corynebacterium glutamicum</i> under oxygen deprivation. <i>Applied Microbiology and Biotechnology</i> , 2010, 86, 1057-1066.	3.6	88
27	Overexpression of Genes Encoding Glycolytic Enzymes in <i>Corynebacterium glutamicum</i> Enhances Glucose Metabolism and Alanine Production under Oxygen Deprivation Conditions. <i>Applied and Environmental Microbiology</i> , 2012, 78, 4447-4457.	3.1	84
28	Production of isopropanol by metabolically engineered <i>Escherichia coli</i> . <i>Applied Microbiology and Biotechnology</i> , 2008, 77, 1219-1224.	3.6	78
29	Identification and Functional Analysis of the Gene Cluster for L-Arabinose Utilization in <i>Corynebacterium glutamicum</i> . <i>Applied and Environmental Microbiology</i> , 2009, 75, 3419-3429.	3.1	77
30	Regulation of <i>Corynebacterium glutamicum</i> Heat Shock Response by the Extracytoplasmic-Function Sigma Factor SigH and Transcriptional Regulators HspR and HrcA. <i>Journal of Bacteriology</i> , 2009, 191, 2964-2972.	2.2	77
31	Production of 4-Hydroxybenzoic Acid by an Aerobic Growth-Arrested Bioprocess Using Metabolically Engineered <i>Corynebacterium glutamicum</i> . <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	76
32	A single V317A or V317M substitution in Enzyme II of a newly identified Î ² -glucoside phosphotransferase and utilization system of <i>Corynebacterium glutamicum</i> R extends its specificity towards cellobiose. <i>Microbiology (United Kingdom)</i> , 2003, 149, 1569-1580.	1.8	74
33	Metabolic engineering for improved production of ethanol by <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 1165-1172.	3.6	69
34	Thermal and Solvent Stress Cross-Tolerance Conferred to <i>Corynebacterium glutamicum</i> by Adaptive Laboratory Evolution. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2284-2298.	3.1	68
35	OxyR acts as a transcriptional repressor of hydrogen peroxide-inducible antioxidant genes in <i>Corynebacterium glutamicum</i> . <i>FEBS Journal</i> , 2013, 280, 3298-3312.	4.7	66
36	Large-Scale Engineering of the <i>Corynebacterium glutamicum</i> Genome. <i>Applied and Environmental Microbiology</i> , 2005, 71, 3369-3372.	3.1	65

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37	Recent advances in metabolic engineering of <i>Corynebacterium glutamicum</i> for bioproduction of value-added aromatic chemicals and natural products. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 8685-8705.	3.6	64
38	Scanning the <i>Corynebacterium glutamicum</i> R genome for high-efficiency secretion signal sequences. <i>Microbiology (United Kingdom)</i> , 2009, 155, 741-750.	1.8	61
39	DivS, a novel SOS-inducible cell-division suppressor in <i>Corynebacterium glutamicum</i> . <i>Molecular Microbiology</i> , 2008, 67, 597-608.	2.5	60
40	Production of para-aminobenzoate by genetically engineered <i>Corynebacterium glutamicum</i> and non-biological formation of an N-glucosyl byproduct. <i>Metabolic Engineering</i> , 2016, 38, 322-330.	7.0	56
41	Metabolic engineering of 1,2-propanediol pathways in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2011, 90, 1721-1729.	3.6	55
42	The ptsI Gene Encoding Enzyme I of the Phosphotransferase System of <i>Corynebacterium glutamicum</i> . <i>Biochemical and Biophysical Research Communications</i> , 2001, 289, 1307-1313.	2.1	53
43	Manipulating <i>Corynebacteria</i> , from Individual Genes to Chromosomes. <i>Applied and Environmental Microbiology</i> , 2005, 71, 7633-7642.	3.1	53
44	High yield secretion of heterologous proteins in <i>Corynebacterium glutamicum</i> using its own Tat-type signal sequence. <i>Applied Microbiology and Biotechnology</i> , 2011, 91, 677-687.	3.6	53
45	Isolation and characterization of IS 31831, a transposable element from <i>Corynebacterium glutamicum</i> . <i>Molecular Microbiology</i> , 1994, 11, 739-746.	2.5	52
46	Group 2 Sigma Factor SigB of <i>Corynebacterium glutamicum</i> Positively Regulates Glucose Metabolism under Conditions of Oxygen Deprivation. <i>Applied and Environmental Microbiology</i> , 2008, 74, 5146-5152.	3.1	52
47	Regulation of the expression of phosphoenolpyruvate-carbohydrate phosphotransferase system (PTS) genes in <i>Corynebacterium glutamicum</i> R. <i>Microbiology (United Kingdom)</i> , 2008, 154, 264-274.	1.8	51
48	Regulation of Expression of Genes Involved in Quinate and Shikimate Utilization in <i>Corynebacterium glutamicum</i> . <i>Applied and Environmental Microbiology</i> , 2009, 75, 3461-3468.	3.1	50
49	Efficient markerless gene replacement in <i>Corynebacterium glutamicum</i> using a new temperature-sensitive plasmid. <i>Journal of Microbiological Methods</i> , 2011, 85, 155-163.	1.6	50
50	Genome-Wide Identification of <i>In Vivo</i> Binding Sites of GlxR, a Cyclic AMP Receptor Protein-Type Regulator in <i>Corynebacterium glutamicum</i> . <i>Journal of Bacteriology</i> , 2011, 193, 4123-4133.	2.2	50
51	Efficient induction of formate hydrogen lyase of aerobically grown <i>Escherichia coli</i> in a three-step biohydrogen production process. <i>Applied Microbiology and Biotechnology</i> , 2007, 74, 754-760.	3.6	49
52	Overexpression of the phosphofructokinase encoding gene is crucial for achieving high production of D-lactate in <i>Corynebacterium glutamicum</i> under oxygen deprivation. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 4679-4689.	3.6	49
53	Cre/loxP-mediated deletion system for large genome rearrangements in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2005, 67, 225-233.	3.6	48
54	Analyses of the acetate-producing pathways in <i>Corynebacterium glutamicum</i> under oxygen-deprived conditions. <i>Applied Microbiology and Biotechnology</i> , 2007, 77, 853-860.	3.6	48

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55	Regulation of expression of general components of the phosphoenolpyruvate: carbohydrate phosphotransferase system (PTS) by the global regulator SugR in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2008, 78, 309-318.	3.6	48
56	Expression of <i>Corynebacterium glutamicum</i> glycolytic genes varies with carbon source and growth phase. <i>Microbiology (United Kingdom)</i> , 2007, 153, 2190-2202.	1.8	47
57	Effect of carbon source availability and growth phase on expression of <i>Corynebacterium glutamicum</i> genes involved in the tricarboxylic acid cycle and glyoxylate bypass. <i>Microbiology (United Kingdom)</i> , 2008, 154, 3073-3083.	1.8	46
58	Involvement of the LuxR-Type Transcriptional Regulator RamA in Regulation of Expression of the <i>gapA</i> Gene, Encoding Glyceraldehyde-3-Phosphate Dehydrogenase of <i>Corynebacterium glutamicum</i> . <i>Journal of Bacteriology</i> , 2009, 191, 968-977.	2.2	46
59	Postgenomic Approaches to Using <i>Corynebacteria</i> as Biocatalysts. <i>Annual Review of Microbiology</i> , 2012, 66, 521-550.	7.3	46
60	Implementing biofuels on a global scale. <i>Nature Biotechnology</i> , 2006, 24, 761-764.	17.5	44
61	Transposon mutagenesis of coryneform bacteria. <i>Molecular Genetics and Genomics</i> , 1994, 245, 397-405.	2.4	42
62	Multiple large segment deletion method for <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2005, 69, 151-161.	3.6	41
63	Technological Options for Biological Fuel Ethanol. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2008, 15, 16-30.	1.0	40
64	<i>Corynebacterium glutamicum</i> Glyceraldehyde-3-Phosphate Dehydrogenase Isoforms with Opposite, ATP-Dependent Regulation. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2004, 8, 91-103.	1.0	39
65	Transcriptional regulators of multiple genes involved in carbon metabolism in <i>Corynebacterium glutamicum</i> . <i>Journal of Biotechnology</i> , 2011, 154, 114-125.	3.8	39
66	ArnR, a Novel Transcriptional Regulator, Represses Expression of the <i>narKGHJ</i> Operon in <i>Corynebacterium glutamicum</i> . <i>Journal of Bacteriology</i> , 2008, 190, 3264-3273.	2.2	38
67	Transcriptionally regulated <i>adhA</i> gene encodes alcohol dehydrogenase required for ethanol and n-propanol utilization in <i>Corynebacterium glutamicum</i> R. <i>Applied Microbiology and Biotechnology</i> , 2007, 76, 1347-1356.	3.6	37
68	Regulation of Quinone Oxidoreductase by the Redox-sensing Transcriptional Regulator QorR in <i>Corynebacterium glutamicum</i> . <i>Journal of Biological Chemistry</i> , 2009, 284, 16736-16742.	3.4	37
69	Rho and RNase play a central role in FMN riboswitch regulation in <i>Corynebacterium glutamicum</i> . <i>Nucleic Acids Research</i> , 2015, 43, 520-529.	14.5	37
70	Replacement Recombination in Coryneform Bacteria: High Efficiency Integration Requirement for Non-methylated Plasmid DNA. <i>Bioscience, Biotechnology and Biochemistry</i> , 1993, 57, 2036-2038.	1.3	36
71	Expression of the <i>gapA</i> gene encoding glyceraldehyde-3-phosphate dehydrogenase of <i>Corynebacterium glutamicum</i> is regulated by the global regulator SugR. <i>Applied Microbiology and Biotechnology</i> , 2008, 81, 291-301.	3.6	36
72	Identification of a Gene Encoding a Transporter Essential for Utilization of C ₄ Dicarboxylates in <i>Corynebacterium glutamicum</i> . <i>Applied and Environmental Microbiology</i> , 2008, 74, 5290-5296.	3.1	36

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73	The <i>ldhA</i> Gene, Encoding Fermentative α -Lactate Dehydrogenase of <i>Corynebacterium glutamicum</i> , Is under the Control of Positive Feedback Regulation Mediated by LldR. <i>Journal of Bacteriology</i> , 2009, 191, 4251-4258.	2.2	36
74	Carbohydrate-binding property of a cell wall integrity and stress response component (WSC) domain of an alcohol oxidase from the rice blast pathogen <i>Pyricularia oryzae</i> . <i>Enzyme and Microbial Technology</i> , 2019, 125, 13-20.	3.2	35
75	Deletion of cgR_1596 and cgR_2070, Encoding NlpC/P60 Proteins, Causes a Defect in Cell Separation in <i>Corynebacterium glutamicum</i> . <i>Journal of Bacteriology</i> , 2008, 190, 8204-8214.	2.2	33
76	Molecular mechanism of SugR-mediated sugar-dependent expression of the <i>ldhA</i> gene encoding α -lactate dehydrogenase in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2009, 83, 315-327.	3.6	33
77	A novel redox-sensing transcriptional regulator <i>CyeR</i> controls expression of an Old Yellow Enzyme family protein in <i>Corynebacterium glutamicum</i> . <i>Microbiology (United Kingdom)</i> , 2010, 156, 1335-1341.	1.8	31
78	Identification of mannose uptake and catabolism genes in <i>Corynebacterium glutamicum</i> and genetic engineering for simultaneous utilization of mannose and glucose. <i>Applied Microbiology and Biotechnology</i> , 2011, 89, 1905-1916.	3.6	31
79	Reactions upstream of glycerate-1,3-bisphosphate drive <i>Corynebacterium glutamicum</i> d-lactate productivity under oxygen deprivation. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 6693-6703.	3.6	31
80	Random segment deletion based on IS31831 and Cre/loxP excision system in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2007, 74, 1333-1341.	3.6	29
81	Characterization of shikimate dehydrogenase homologues of <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 8139-8149.	3.6	29
82	Chorismate-dependent transcriptional regulation of quinate/shikimate utilization genes by <i>LysR</i> -type transcriptional regulator <i>QsuR</i> in <i>Corynebacterium glutamicum</i> : carbon flow control at metabolic branch point. <i>Molecular Microbiology</i> , 2014, 92, 356-368.	2.5	28
83	Isolation and Molecular Characterization of pMG160, a Mobilizable Cryptic Plasmid from <i>Rhodobacter blasticus</i> . <i>Applied and Environmental Microbiology</i> , 2003, 69, 725-733.	3.1	27
84	Identification of new secreted proteins and secretion of heterologous amylase by <i>C. glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2009, 82, 491-500.	3.6	27
85	Characterization of the mannitol catabolic operon of <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2011, 91, 1375-1387.	3.6	27
86	Electroporation-transformation system for coryneform bacteria by auxotrophic complementation.. <i>Agricultural and Biological Chemistry</i> , 1990, 54, 443-447.	0.3	26
87	Regulons of global transcription factors in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 45-60.	3.6	26
88	Extracytoplasmic function sigma factor σ^D confers resistance to environmental stress by enhancing mycolate synthesis and modifying peptidoglycan structures in <i>Corynebacterium glutamicum</i> . <i>Molecular Microbiology</i> , 2018, 107, 312-329.	2.5	26
89	Isobutanol production in <i>Corynebacterium glutamicum</i> : Suppressed succinate by-production by <i>pckA</i> inactivation and enhanced productivity via the Entner-Doudoroff pathway. <i>Metabolic Engineering</i> , 2020, 59, 24-35.	7.0	26
90	Site-directed integration system using a combination of mutant lox sites for <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2007, 77, 871-878.	3.6	24

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91	Identification of a HAD superfamily phosphatase, HdpA, involved in 1,3-dihydroxyacetone production during sugar catabolism in <i>Corynebacterium glutamicum</i> . FEBS Letters, 2012, 586, 4228-4232.	2.8	23
92	Expanding the Regulatory Network Governed by the Extracytoplasmic Function Sigma Factor σ^H in <i>Corynebacterium glutamicum</i> . Journal of Bacteriology, 2015, 197, 483-496.	2.2	23
93	Protocatechuate overproduction by <i>Corynebacterium glutamicum</i> via simultaneous engineering of native and heterologous biosynthetic pathways. Metabolic Engineering, 2021, 65, 232-242.	7.0	23
94	Vectors for Genetic Engineering of Corynebacteria. ACS Symposium Series, 2003, , 175-191.	0.5	22
95	Transcriptional regulation of <i>Corynebacterium glutamicum</i> methionine biosynthesis genes in response to methionine supplementation under oxygen deprivation. Applied Microbiology and Biotechnology, 2008, 81, 505-513.	3.6	22
96	Metabolic engineering of <i>Corynebacterium glutamicum</i> for hyperproduction of polymer-grade l- and d-lactic acid. Applied Microbiology and Biotechnology, 2019, 103, 3381-3391.	3.6	22
97	Regulation of the Expression of Genes Involved in NAD De Novo Biosynthesis in <i>Corynebacterium glutamicum</i> . Applied and Environmental Microbiology, 2010, 76, 5488-5495.	3.1	21
98	Diversity of metabolic shift in response to oxygen deprivation in <i>Corynebacterium glutamicum</i> and its close relatives. Applied Microbiology and Biotechnology, 2011, 90, 1051-1061.	3.6	21
99	RNase III mediated cleavage of the coding region of <i>mraZ</i> mRNA is required for efficient cell division in <i>Corynebacterium glutamicum</i> . Molecular Microbiology, 2016, 99, 1149-1166.	2.5	21
100	Engineering the glycolytic pathway: A potential approach for improvement of biocatalyst performance. Bioengineered, 2015, 6, 328-334.	3.2	20
101	Isolation and Characterization of a Native Composite Transposon, Tn 14751, Carrying 17.4 Kilobases of <i>Corynebacterium glutamicum</i> Chromosomal DNA. Applied and Environmental Microbiology, 2005, 71, 407-416.	3.1	19
102	Identification and expression analysis of a gene encoding a shikimate transporter of <i>Corynebacterium glutamicum</i> . Microbiology (United Kingdom), 2015, 161, 254-263.	1.8	19
103	Enhanced Glucose Consumption and Organic Acid Production by Engineered <i>Corynebacterium glutamicum</i> Based on Analysis of a <i>prfB1</i> Deletion Mutant. Applied and Environmental Microbiology, 2017, 83, .	3.1	19
104	Transcription of <i>Corynebacterium glutamicum</i> Genes Involved in Tricarboxylic Acid Cycle and Glyoxylate Cycle. Journal of Molecular Microbiology and Biotechnology, 2008, 15, 264-276.	1.0	18
105	Influence of SigB inactivation on <i>Corynebacterium glutamicum</i> protein secretion. Applied Microbiology and Biotechnology, 2013, 97, 4917-4926.	3.6	18
106	Biorefinery Applications of <i>Corynebacterium glutamicum</i> . Microbiology Monographs, 2013, , 149-172.	0.6	18
107	Glucose consumption rate critically depends on redox state in <i>Corynebacterium glutamicum</i> under oxygen deprivation. Applied Microbiology and Biotechnology, 2015, 99, 5573-5582.	3.6	18
108	The extracytoplasmic function σ factor σ^C regulates expression of a branched quinol oxidation pathway in <i>Corynebacterium glutamicum</i> . Molecular Microbiology, 2016, 100, 486-509.	2.5	18

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109	Characterization of a new 2.4-kb plasmid of <i>Corynebacterium casei</i> and development of stable corynebacterial cloning vector. <i>Applied Microbiology and Biotechnology</i> , 2009, 81, 1107-1115.	3.6	17
110	Gene Expression Profiling of <i>Corynebacterium glutamicum</i> during Anaerobic Nitrate Respiration: Induction of the SOS Response for Cell Survival. <i>Journal of Bacteriology</i> , 2011, 193, 1327-1333.	2.2	17
111	Regulation of the nitrate reductase operon narKGHIJ by the cAMP-dependent regulator GlxR in <i>Corynebacterium glutamicum</i> . <i>Microbiology (United Kingdom)</i> , 2011, 157, 21-28.	1.8	17
112	Involvement of Regulatory Interactions among Global Regulators GlxR, SugR, and RamA in Expression of <i>ramA</i> in <i>Corynebacterium glutamicum</i> . <i>Journal of Bacteriology</i> , 2013, 195, 1718-1726.	2.2	16
113	Promiscuous activity of (S,S)-butanediol dehydrogenase is responsible for glycerol production from 1,3-dihydroxyacetone in <i>Corynebacterium glutamicum</i> under oxygen-deprived conditions. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 1427-1433.	3.6	16
114	Living cell reaction process for l-isoleucine and l-valine production. <i>Journal of Industrial Microbiology</i> , 1990, 5, 289-293.	0.9	15
115	Identification of a second β -glucoside phosphoenolpyruvate-4-epimerase-carbohydrate phosphotransferase system in <i>Corynebacterium glutamicum</i> R. <i>Microbiology (United Kingdom)</i> , 2009, 155, 3652-3660.	1.8	15
116	Functional Characterization of <i>Corynebacterium alkanolyticum</i> β -Xylosidase and Xyloside ABC Transporter in <i>Corynebacterium glutamicum</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 4173-4183.	3.1	15
117	Depression of by-product formation during l-isoleucine production by a living-cell reaction process. <i>Applied Microbiology and Biotechnology</i> , 1991, 35, 348-351.	3.6	14
118	Antisense-RNA-mediated plasmid copy number control in pCG1-family plasmids, pCGR2 and pCG1, in <i>Corynebacterium glutamicum</i> . <i>Microbiology (United Kingdom)</i> , 2010, 156, 3609-3623.	1.8	14
119	<i>Corynebacterium glutamicum</i> Zur acts as a zinc-sensing transcriptional repressor of both zinc-inducible and zinc-repressible genes involved in zinc homeostasis. <i>FEBS Journal</i> , 2012, 279, 4385-4397.	4.7	14
120	Enhanced production of d-lactate from mixed sugars in <i>Corynebacterium glutamicum</i> by overexpression of glycolytic genes encoding phosphofructokinase and triosephosphate isomerase. <i>Journal of Bioscience and Bioengineering</i> , 2019, 127, 288-293.	2.2	13
121	Introduction of Glyoxylate Bypass Increases Hydrogen Gas Yield from Acetate and α -Ketoglutarate in <i>Rhodobacter sphaeroides</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	13
122	Alternative technologies for biotechnological fuel ethanol manufacturing. <i>Journal of Chemical Technology and Biotechnology</i> , 2007, 82, 693-697.	3.2	12
123	Characterization of a 24-kb plasmid pCGR2 newly isolated from <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2010, 87, 1855-1866.	3.6	12
124	<i>Corynebacterium glutamicum</i> CsoR Acts as a Transcriptional Repressor of Two Copper/Zinc-Inducible P _{1B} -Type ATPase Operons. <i>Bioscience, Biotechnology and Biochemistry</i> , 2012, 76, 1952-1958.	1.3	12
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