List of Publications by Year in descending order

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Μλελνιικι Ινιιι

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

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

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37	Recent advances in metabolic engineering of Corynebacterium glutamicum for bioproduction of value-added aromatic chemicals and natural products. Applied Microbiology and Biotechnology, 2018, 102, 8685-8705.	3.6	64
38	Scanning the Corynebacterium glutamicum R genome for high-efficiency secretion signal sequences. Microbiology (United Kingdom), 2009, 155, 741-750.	1.8	61
39	DivS, a novel SOSâ€inducible cellâ€division suppressor in <i>Corynebacterium glutamicum</i> . Molecular Microbiology, 2008, 67, 597-608.	2.5	60
40	Production of para-aminobenzoate by genetically engineered Corynebacterium glutamicum and non-biological formation of an N-glucosyl byproduct. Metabolic Engineering, 2016, 38, 322-330.	7.0	56
41	Metabolic engineering of 1,2-propanediol pathways in Corynebacterium glutamicum. Applied Microbiology and Biotechnology, 2011, 90, 1721-1729.	3.6	55
42	The ptsl Gene Encoding Enzyme I of the Phosphotransferase System of Corynebacterium glutamicum. Biochemical and Biophysical Research Communications, 2001, 289, 1307-1313.	2.1	53
43	Manipulating Corynebacteria, from Individual Genes to Chromosomes. Applied and Environmental Microbiology, 2005, 71, 7633-7642.	3.1	53
44	High yield secretion of heterologous proteins in Corynebacterium glutamicum using its own Tat-type signal sequence. Applied Microbiology and Biotechnology, 2011, 91, 677-687.	3.6	53
45	Isolation and characterization of IS 31831, a transposable element from Corynebacterium glutamicum. Molecular Microbiology, 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. Applied and Environmental Microbiology, 2008, 74, 5146-5152.	3.1	52
47	Regulation of the expression of phosphoenolpyruvate : carbohydrate phosphotransferase system (PTS) genes in Corynebacterium glutamicum R. Microbiology (United Kingdom), 2008, 154, 264-274.	1.8	51
48	Regulation of Expression of Genes Involved in Quinate and Shikimate Utilization in <i>Corynebacterium glutamicum</i> . Applied and Environmental Microbiology, 2009, 75, 3461-3468.	3.1	50
49	Efficient markerless gene replacement in Corynebacterium glutamicum using a new temperature-sensitive plasmid. Journal of Microbiological Methods, 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 Corynebacterium glutamicum. Journal of Bacteriology, 2011, 193, 4123-4133.	2.2	50
51	Efficient induction of formate hydrogen lyase of aerobically grown Escherichia coli in a three-step biohydrogen production process. Applied Microbiology and Biotechnology, 2007, 74, 754-760.	3.6	49
52	Overexpression of the phosphofructokinase encoding gene is crucial for achieving high production of D-lactate in Corynebacterium glutamicum under oxygen deprivation. Applied Microbiology and Biotechnology, 2015, 99, 4679-4689.	3.6	49
53	Cre/loxP-mediated deletion system for large genome rearrangements in Corynebacterium glutamicum. Applied Microbiology and Biotechnology, 2005, 67, 225-233.	3.6	48
54	Analyses of the acetate-producing pathways in Corynebacterium glutamicum under oxygen-deprived conditions. Applied Microbiology and Biotechnology, 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 Corynebacterium glutamicum. Applied Microbiology and Biotechnology, 2008, 78, 309-318.	3.6	48
56	Expression of Corynebacterium glutamicum glycolytic genes varies with carbon source and growth phase. Microbiology (United Kingdom), 2007, 153, 2190-2202.	1.8	47
57	Effect of carbon source availability and growth phase on expression of Corynebacterium glutamicum genes involved in the tricarboxylic acid cycle and glyoxylate bypass. Microbiology (United Kingdom), 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> . Journal of Bacteriology, 2009, 191, 968-977.	2.2	46
59	Postgenomic Approaches to Using Corynebacteria as Biocatalysts. Annual Review of Microbiology, 2012, 66, 521-550.	7.3	46
60	Implementing biofuels on a global scale. Nature Biotechnology, 2006, 24, 761-764.	17.5	44
61	Transposon mutagenesis of coryneform bacteria. Molecular Genetics and Genomics, 1994, 245, 397-405.	2.4	42
62	Multiple large segment deletion method for Corynebacterium glutamicum. Applied Microbiology and Biotechnology, 2005, 69, 151-161.	3.6	41
63	Technological Options for Biological Fuel Ethanol. Journal of Molecular Microbiology and Biotechnology, 2008, 15, 16-30.	1.0	40
64	<i>Corynebacterium glutamicum</i> Glyceraldehyde-3-Phosphate Dehydrogenase Isoforms with Opposite, ATP-Dependent Regulation. Journal of Molecular Microbiology and Biotechnology, 2004, 8, 91-103.	1.0	39
65	Transcriptional regulators of multiple genes involved in carbon metabolism in Corynebacterium glutamicum. Journal of Biotechnology, 2011, 154, 114-125.	3.8	39
66	ArnR, a Novel Transcriptional Regulator, Represses Expression of the <i>narKGHJI</i> Operon in <i>Corynebacterium glutamicum</i> . Journal of Bacteriology, 2008, 190, 3264-3273.	2.2	38
67	Transcriptionally regulated adhA gene encodes alcohol dehydrogenase required for ethanol and n-propanol utilization in Corynebacterium glutamicum R. Applied Microbiology and Biotechnology, 2007, 76, 1347-1356.	3.6	37
68	Regulation of Quinone Oxidoreductase by the Redox-sensing Transcriptional Regulator QorR in Corynebacterium glutamicum. Journal of Biological Chemistry, 2009, 284, 16736-16742.	3.4	37
69	Rho and RNase play a central role in FMN riboswitch regulation in Corynebacterium glutamicum. Nucleic Acids Research, 2015, 43, 520-529.	14.5	37
70	Replacement Recombination inCoryneformBacteria: High Efficiency Integration Requirement for Non-methylated Plasmid DNA. Bioscience, Biotechnology and Biochemistry, 1993, 57, 2036-2038.	1.3	36
71	Expression of the gapA gene encoding glyceraldehyde-3-phosphate dehydrogenase of Corynebacterium glutamicum is regulated by the global regulator SugR. Applied Microbiology and Biotechnology, 2008, 81, 291-301.	3.6	36
72	Identification of a Gene Encoding a Transporter Essential for Utilization of C <sub>4</sub> Dicarboxylates in <i>Corynebacterium glutamicum</i> . Applied and Environmental Microbiology, 2008, 74, 5290-5296.	3.1	36

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

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91	Identification of a HAD superfamily phosphatase, HdpA, involved in 1,3â€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 <sup>H</sup> in Corynebacterium glutamicum. Journal of Bacteriology, 2015, 197, 483-496.	2.2	23
93	Protocatechuate overproduction by Corynebacterium glutamicum 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 Corynebacterium glutamicum 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 Corynebacterium glutamicum 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 Corynebacterium glutamicum. Applied and Environmental Microbiology, 2010, 76, 5488-5495.	3.1	21
98	Diversity of metabolic shift in response to oxygen deprivation in Corynebacterium glutamicum 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 <i>14751</i> , 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 Corynebacterium glutamicum. Microbiology (United Kingdom), 2015, 161, 254-263.	1.8	19
103	Enhanced Glucose Consumption and Organic Acid Production by Engineered Corynebacterium glutamicum Based on Analysis of a <i>pfkB1</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 Corynebacterium glutamicum protein secretion. Applied Microbiology and Biotechnology, 2013, 97, 4917-4926.	3.6	18
106	Biorefinery Applications of Corynebacterium glutamicum. Microbiology Monographs, 2013, , 149-172.	0.6	18
107	Glucose consumption rate critically depends on redox state in Corynebacterium glutamicum under oxygen deprivation. Applied Microbiology and Biotechnology, 2015, 99, 5573-5582.	3.6	18
108	The extracytoplasmic function σ factor σ <sup>C</sup> 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 Corynebacterium casei and development of stable corynebacterial cloning vector. Applied Microbiology and Biotechnology, 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. Journal of Bacteriology, 2011, 193, 1327-1333.	2.2	17
111	Regulation of the nitrate reductase operon narKGHJI by the cAMP-dependent regulator GlxR in Corynebacterium glutamicum. Microbiology (United Kingdom), 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 Corynebacterium glutamicum. Journal of Bacteriology, 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 Corynebacterium glutamicum under oxygen-deprived conditions. Applied Microbiology and Biotechnology, 2015, 99, 1427-1433.	3.6	16
114	Living cell reaction process forl-isoleucine andl-valine production. Journal of Industrial Microbiology, 1990, 5, 289-293.	0.9	15
115	Identification of a second β-glucoside phosphoenolpyruvate : carbohydrate phosphotransferase system in Corynebacterium glutamicum R. Microbiology (United Kingdom), 2009, 155, 3652-3660.	1.8	15
116	Functional Characterization of Corynebacterium alkanolyticum β-Xylosidase and Xyloside ABC Transporter in Corynebacterium glutamicum. Applied and Environmental Microbiology, 2015, 81, 4173-4183.	3.1	15
117	Depression of by-product formation during l-isoleucine production by a living-cell reaction process. Applied Microbiology and Biotechnology, 1991, 35, 348-351.	3.6	14
118	Antisense-RNA-mediated plasmid copy number control in pCG1-family plasmids, pCGR2 and pCG1, in Corynebacterium glutamicum. Microbiology (United Kingdom), 2010, 156, 3609-3623.	1.8	14
119	<i>CorynebacteriumÂglutamicum </i> <scp>Z</scp> ur acts as a zincâ€sensing transcriptional repressor of both zincâ€inducible and zincâ€repressible genes involved in zinc homeostasis. FEBS Journal, 2012, 279, 4385-4397.	4.7	14
120	Enhanced production of d-lactate from mixed sugars in Corynebacterium glutamicum by overexpression of glycolytic genes encoding phosphofructokinase and triosephosphate isomerase. Journal of Bioscience and Bioengineering, 2019, 127, 288-293.	2.2	13
121	Introduction of Glyoxylate Bypass Increases Hydrogen Gas Yield from Acetate and <scp>l</scp> -Glutamate in <i>Rhodobacter sphaeroides</i> . Applied and Environmental Microbiology, 2019, 85, .	3.1	13
122	Alternative technologies for biotechnological fuel ethanol manufacturing. Journal of Chemical Technology and Biotechnology, 2007, 82, 693-697.	3.2	12
123	Characterization of a 24-kb plasmid pCGR2 newly isolated from Corynebacterium glutamicum. Applied Microbiology and Biotechnology, 2010, 87, 1855-1866.	3.6	12
124	<i>Corynebacterium glutamicum</i> CsoR Acts as a Transcriptional Repressor of Two Copper/Zinc-Inducible P <sub>1B</sub> -Type ATPase Operons. Bioscience, Biotechnology and Biochemistry, 2012, 76, 1952-1958.	1.3	12
125	The physiological role of riboflavin transporter and involvement of FMN-riboswitch in its gene expression in Corynebacterium glutamicum. Applied Microbiology and Biotechnology, 2014, 98, 4159-4168.	3.6	12
126	Coexistence of the Entner–Doudoroff and Embden–Meyerhof–Parnas pathways enhances glucose consumption of ethanol-producing Corynebacterium glutamicum. Biotechnology for Biofuels, 2021, 14. 45.	6.2	12

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127	Random genome deletion methods applicable to prokaryotes. Applied Microbiology and Biotechnology, 2008, 79, 519-526.	3.6	11
128	Coordinated Regulation of <i>gnd</i> , Which Encodes 6-Phosphogluconate Dehydrogenase, by the Two Transcriptional Regulators GntR1 and RamA in Corynebacterium glutamicum. Journal of Bacteriology, 2012, 194, 6527-6536.	2.2	11
129	Corynebacterium glutamicum ArnR Controls Expression of Nitrate Reductase Operon narKGHJI and Nitric Oxide (NO)-Detoxifying Enzyme Gene hmp in an NO-Responsive Manner. Journal of Bacteriology, 2014, 196, 60-69.	2.2	11
130	A new insertion sequence, IS14999, from Corynebacterium glutamicum. Microbiology (United) Tj ETQq0 0 0 rgBT	/Oyerlock 1.8	10 Tf 50 62 10
131	Translation Efficiency of Antiterminator Proteins Is a Determinant for the Difference in Glucose Repression of Two Î <sup>2</sup> -Glucoside Phosphotransferase System Gene Clusters in <i>Corynebacterium glutamicum</i> R. Journal of Bacteriology, 2011, 193, 349-357.	2.2	10
132	Genome-Wide Analysis of the Role of Global Transcriptional Regulator GntR1 in Corynebacterium glutamicum. Journal of Bacteriology, 2014, 196, 3249-3258.	2.2	10
133	NdnR is an NAD-responsive transcriptional repressor of the ndnR operon involved in NAD de novo biosynthesis in Corynebacterium glutamicum. Microbiology (United Kingdom), 2012, 158, 975-982.	1.8	9
134	Engineering the transcriptional activator NifA for the construction of Rhodobacter sphaeroides strains that produce hydrogen gas constitutively. Applied Microbiology and Biotechnology, 2019, 103, 9739-9749.	3.6	9
135	Advanced Fermentation Technologies. , 0, , 311-330.		7
136	Metabolic engineering of bacteria for utilization of mixed sugar substrates for improved production of chemicals and fuel ethanol. Biofuels, 2011, 2, 303-313.	2.4	7
137	Copper homeostasis-related genes in three separate transcriptional units regulated by CsoR in Corynebacterium glutamicum. Applied Microbiology and Biotechnology, 2015, 99, 3505-3517.	3.6	7
138	Bioenergy and Biorefinery. Biotechnology Journal, 2019, 14, e1900160.	3.5	7
139	AraR, an <scp>l</scp> -Arabinose-Responsive Transcriptional Regulator in Corynebacterium glutamicum ATCC 31831, Exerts Different Degrees of Repression Depending on the Location of Its Binding Sites within the Three Target Promoter Regions. Journal of Bacteriology, 2015, 197, 3788-3796.	2.2	6
140	Polynucleotide Phosphorylase, RNase E/G, and YbeY Are Involved in the Maturation of 4.5S RNA in Corynebacterium glutamicum. Journal of Bacteriology, 2017, 199, .	2.2	6
141	The Biotechnological Potential of Corynebacterium glutamicum, from Umami to Chemurgy. Microbiology Monographs, 2013, , 1-49.	0.6	6
142	Genomes and Genome-Level Engineering of Amino Acid-Producing Bacteria. , 2006, , 349-401.		5
143	Regulation of genes involved in sugar uptake, glycolysis and lactate production inCorynebacterium glutamicum. Future Microbiology, 2010, 5, 1475-1481.	2.0	5
144	Trehalose acts as a uridine 5â€2â€diphosphoglucoseâ€competitive inhibitor of trehalose 6â€phosphate synthase in <i>CorynebacteriumÂglutamicum</i> . FEBS Journal, 2017, 284, 4298-4313.	4.7	5

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145	The ldhA Gene Encoding Fermentative l-Lactate Dehydrogenase in Corynebacterium Glutamicum Is Positively Regulated by the Global Regulator GlxR. Microorganisms, 2021, 9, 550.	3.6	5
146	The Lacl-Type Transcriptional Regulator AraR Acts as an l -Arabinose-Responsive Repressor of l -Arabinose Utilization Genes in Corynebacterium glutamicum ATCC 31831. Journal of Bacteriology, 2014, 196, 2242-2254.	2.2	4
147	Regulation of the Expression of De Novo Pyrimidine Biosynthesis Genes in Corynebacterium glutamicum. Journal of Bacteriology, 2015, 197, 3307-3316.	2.2	4
148	Genome Engineering of Corynebacterium glutamicum. Microbiology Monographs, 2013, , 89-105.	0.6	4
149	Microorganisms for Xylitol Production: Focus on Strain Improvement. , 2012, , 109-131.		3
150	Identification of a gene involved in plasmid structural instability in Corynebacterium glutamicum. Applied Microbiology and Biotechnology, 2013, 97, 8219-8226.	3.6	3
151	pCGR2 copy number depends on the par locus that forms a ParC-ParB-DNA partition complex in Corynebacterium glutamicum. Journal of Applied Microbiology, 2013, 115, 495-508.	3.1	3
152	Functional analysis of arabinofuranosidases and a xylanase of Corynebacterium alkanolyticum for arabinoxylan utilization in Corynebacterium glutamicum. Applied Microbiology and Biotechnology, 2017, 101, 5019-5032.	3.6	3
153	Global Transcriptional Regulators Involved in Carbon, Nitrogen, Phosphorus, and Sulfur Metabolisms in Corynebacterium glutamicum. Microbiology Monographs, 2020, , 113-147.	0.6	3
154	Regulation of Sugar Uptake, Glycolysis, and the Pentose Phosphate Pathway in Corynebacterium glutamicum. Microbiology Monographs, 2013, , 263-279.	0.6	3
155	Hydrogen production based on the heterologous expression of NAD+-reducing [NiFe]-hydrogenase from Cupriavidus necator in different genetic backgrounds of Escherichia coli strains. International Journal of Hydrogen Energy, 2022, 47, 22010-22021.	7.1	3
156	Construction of a Rhodobacter sphaeroides Strain That Efficiently Produces Hydrogen Gas from Acetate without Poly(β-Hydroxybutyrate) Accumulation: Insight into the Role of PhaR in Acetate Metabolism. Applied and Environmental Microbiology, 2022, 88, .	3.1	3
157	Cyclic adenosine 3′,5′-monophosphate and coryneform bacteria. FEMS Microbiology Letters, 1995, 133, 239-244.	1.8	2
158	Development of Growth-Arrested Bioprocesses with Corynebacterium glutamicum for Cellulosic Ethanol Production from Complex Sugar Mixtures. , 2014, , 121-139.		2
159	Anaerobic glucose consumption is accelerated at non-proliferating elevated temperatures through upregulation of a glucose transporter gene in Corynebacterium glutamicum. Applied Microbiology and Biotechnology, 2020, 104, 6719-6729.	3.6	2
160	History-Driven Genetic Modification Design Technique Using a Domain-Specific Lexical Model for the Acceleration of DBTL Cycles for Microbial Cell Factories. ACS Synthetic Biology, 2021, 10, 2308-2317.	3.8	2
161	Aromatic Compound Catabolism in Corynebacterium glutamicum. Microbiology Monographs, 2020, , 323-337.	0.6	2
162	Glutamineâ€rich toxic proteins GrtA, GrtB and GrtC together with the antisense RNA AsgR constitute a toxin–antitoxinâ€like system in <i>Corynebacterium glutamicum</i> . Molecular Microbiology, 2018, 108, 578-594.	2.5	1

#	Article	IF	CITATIONS
163	Aromatic Compound Production by Corynebacterium glutamicum. Microbiology Monographs, 2020, , 339-370.	0.6	1
164	Regulation of Ribonuclease J Expression in <i>Corynebacterium glutamicum</i> . Journal of Bacteriology, 2022, 204, e0005322.	2.2	1
165	Identification and Molecular Characterization of the Operon Required for L-Asparagine Utilization in Corynebacterium glutamicum. Microorganisms, 2022, 10, 1002.	3.6	1
166	Increasing Diversity of the Bio-Based Chemicals Produced by <i>Corynebacterium glutamicum</i> . Kagaku To Seibutsu, 2017, 55, 690-698.	0.0	0
167	Efficient construction of xenogeneic genomic libraries by circumventing restriction-modification systems that restrict methylated DNA. Journal of Microbiological Methods, 2018, 146, 13-15.	1.6	0
168	Toward Realization of New Biorefinery Industries Using Corynebacterium glutamicum. , 2014, , 253-262.		0