

Masayuki Inui

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169
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#	Paper	IF	Citations
165	An efficient succinic acid production process in a metabolically engineered <i>Corynebacterium glutamicum</i> strain. <i>Applied Microbiology and Biotechnology</i> , 2008 , 81, 459-64	5.7	332
164	Expression of <i>Clostridium acetobutylicum</i> butanol synthetic genes in <i>Escherichia coli</i> . <i>Applied Microbiology and Biotechnology</i> , 2008 , 77, 1305-16	5.7	309
163	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, 182-96	0.9	291
162	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, 243-54	0.9	243
161	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	2.9	212
160	Production of organic acids by <i>Corynebacterium glutamicum</i> under oxygen deprivation. <i>Applied Microbiology and Biotechnology</i> , 2005 , 68, 475-80	5.7	202
159	Engineering of a xylose metabolic pathway in <i>Corynebacterium glutamicum</i> . <i>Applied and Environmental Microbiology</i> , 2006 , 72, 3418-28	4.8	193
158	Enhanced hydrogen production from formic acid by formate hydrogen lyase-overexpressing <i>Escherichia coli</i> strains. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 6762-8	4.8	180
157	Production of D-lactic acid by <i>Corynebacterium glutamicum</i> under oxygen deprivation. <i>Applied Microbiology and Biotechnology</i> , 2008 , 78, 449-54	5.7	179
156	Bacterial phosphotransferase system (PTS) in carbohydrate uptake and control of carbon metabolism. <i>Journal of Bioscience and Bioengineering</i> , 2001 , 92, 502-517	3.3	135
155	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, 2349-53	4.8	131
154	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	2.9	123
153	Engineering of an L-arabinose metabolic pathway in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2008 , 77, 1053-62	5.7	118
152	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	5.7	115
151	Anaerobic growth of <i>Corynebacterium glutamicum</i> using nitrate as a terminal electron acceptor. <i>Applied Microbiology and Biotechnology</i> , 2007 , 75, 889-97	5.7	107
150	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, 865-75	4.8	97
149	Sugar transporters in efficient utilization of mixed sugar substrates: current knowledge and outlook. <i>Applied Microbiology and Biotechnology</i> , 2010 , 85, 471-80	5.7	97

148	Engineering of <i>Corynebacterium glutamicum</i> for high-yield L-valine production under oxygen deprivation conditions. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 1250-7	4.8	92
147	Engineering of pentose transport in <i>Corynebacterium glutamicum</i> to improve simultaneous utilization of mixed sugars. <i>Applied Microbiology and Biotechnology</i> , 2009 , 85, 105-15	5.7	90
146	Strain optimization for efficient isobutanol production using <i>Corynebacterium glutamicum</i> under oxygen deprivation. <i>Biotechnology and Bioengineering</i> , 2013 , 110, 2938-48	4.9	86
145	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, 3750-5	4.8	82
144	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, 159-65	5.7	81
143	New multiple-deletion method for the <i>Corynebacterium glutamicum</i> genome, using a mutant lox sequence. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 8472-80	4.8	81
142	Xylitol production by recombinant <i>Corynebacterium glutamicum</i> under oxygen deprivation. <i>Applied Microbiology and Biotechnology</i> , 2010 , 86, 1057-66	5.7	80
141	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, 691-9	5.7	75
140	A single V317A or V317M substitution in Enzyme II of a newly identified beta-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	2.9	71
139	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, 4447-57	4.8	70
138	Production of isopropanol by metabolically engineered <i>Escherichia coli</i> . <i>Applied Microbiology and Biotechnology</i> , 2008 , 77, 1219-24	5.7	68
137	Metabolic engineering of <i>Corynebacterium glutamicum</i> for shikimate overproduction by growth-arrested cell reaction. <i>Metabolic Engineering</i> , 2016 , 38, 204-216	9.7	66
136	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, 2964-72	3.5	63
135	Large-scale engineering of the <i>Corynebacterium glutamicum</i> genome. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 3369-72	4.8	62
134	Metabolic engineering for improved production of ethanol by <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2015 , 99, 1165-72	5.7	61
133	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, 3419-29	4.8	61
132	Thermal and solvent stress cross-tolerance conferred to <i>Corynebacterium glutamicum</i> by adaptive laboratory evolution. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 2284-98	4.8	57
131	OxyR acts as a transcriptional repressor of hydrogen peroxide-inducible antioxidant genes in <i>Corynebacterium glutamicum</i> R. <i>FEBS Journal</i> , 2013 , 280, 3298-312	5.7	53

130	Scanning the <i>Corynebacterium glutamicum</i> R genome for high-efficiency secretion signal sequences. <i>Microbiology (United Kingdom)</i> , 2009 , 155, 741-750	2.9	53
129	Metabolic engineering of 1,2-propanediol pathways in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2011 , 90, 1721-9	5.7	48
128	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, 5146-52	4.8	48
127	Manipulating corynebacteria, from individual genes to chromosomes. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 7633-42	4.8	48
126	The ptsI gene encoding enzyme I of the phosphotransferase system of <i>Corynebacterium glutamicum</i> . <i>Biochemical and Biophysical Research Communications</i> , 2001 , 289, 1307-13	3.4	48
125	Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> . <i>Molecular Microbiology</i> , 1994 , 11, 739-46	4.1	48
124	DivS, a novel SOS-inducible cell-division suppressor in <i>Corynebacterium glutamicum</i> . <i>Molecular Microbiology</i> , 2008 , 67, 597-608	4.1	47
123	Analyses of the acetate-producing pathways in <i>Corynebacterium glutamicum</i> under oxygen-deprived conditions. <i>Applied Microbiology and Biotechnology</i> , 2007 , 77, 853-60	5.7	47
122	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	2.9	46
121	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,	4.8	45
120	Genome-wide identification of in vivo binding sites of GlxR, a cyclic AMP receptor protein-type regulator in <i>Corynebacterium glutamicum</i> . <i>Journal of Bacteriology</i> , 2011 , 193, 4123-33	3.5	45
119	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, 309-18	5.7	44
118	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, 677-87	5.7	43
117	Regulation of expression of genes involved in quinate and shikimate utilization in <i>Corynebacterium glutamicum</i> . <i>Applied and Environmental Microbiology</i> , 2009 , 75, 3461-8	4.8	43
116	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, 4679-89	5.7	42
115	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, 754-60	5.7	42
114	Expression of <i>Corynebacterium glutamicum</i> glycolytic genes varies with carbon source and growth phase. <i>Microbiology (United Kingdom)</i> , 2007 , 153, 2190-2202	2.9	42
113	Cre/loxP-mediated deletion system for large genome rearrangements in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2005 , 67, 225-33	5.7	41

112	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	5.7	40
111	Involvement of the LuxR-type transcriptional regulator RamA in regulation of expression of the gapA gene, encoding glyceraldehyde-3-phosphate dehydrogenase of <i>Corynebacterium glutamicum</i> . <i>Journal of Bacteriology</i> , 2009 , 191, 968-77	3.5	40
110	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	2.9	40
109	Efficient markerless gene replacement in <i>Corynebacterium glutamicum</i> using a new temperature-sensitive plasmid. <i>Journal of Microbiological Methods</i> , 2011 , 85, 155-63	2.8	38
108	Multiple large segment deletion method for <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2005 , 69, 151-61	5.7	38
107	Transcriptionally regulated adhA 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, 1347-56	5.7	37
106	<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	0.9	37
105	Postgenomic approaches to using corynebacteria as biocatalysts. <i>Annual Review of Microbiology</i> , 2012 , 66, 521-50	17.5	35
104	Transcriptional regulators of multiple genes involved in carbon metabolism in <i>Corynebacterium glutamicum</i> . <i>Journal of Biotechnology</i> , 2011 , 154, 114-25	3.7	35
103	ArnR, a novel transcriptional regulator, represses expression of the narKGHJI operon in <i>Corynebacterium glutamicum</i> . <i>Journal of Bacteriology</i> , 2008 , 190, 3264-73	3.5	34
102	Expression of the gapA 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	5.7	34
101	Replacement Recombination in Coryneform Bacteria: High Efficiency Integration Requirement for Non-methylated Plasmid DNA. <i>Bioscience, Biotechnology and Biochemistry</i> , 1993 , 57, 2036-2038	2.1	34
100	Transposon mutagenesis of coryneform bacteria. <i>Molecular Genetics and Genomics</i> , 1994 , 245, 397-405		34
99	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	9.7	34
98	Molecular mechanism of SugR-mediated sugar-dependent expression of the ldhA gene encoding L-lactate dehydrogenase in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2009 , 83, 315-27	5.7	33
97	The ldhA gene, encoding fermentative L-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, 4251-8	3.5	33
96	Technological options for biological fuel ethanol. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2008 , 15, 16-30	0.9	33
95	Identification of a gene encoding a transporter essential for utilization of C4 dicarboxylates in <i>Corynebacterium glutamicum</i> . <i>Applied and Environmental Microbiology</i> , 2008 , 74, 5290-6	4.8	33

94	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	5.4	32
93	Implementing biofuels on a global scale. <i>Nature Biotechnology</i> , 2006 , 24, 761-4	44.5	32
92	Rho and RNase play a central role in FMN riboswitch regulation in <i>Corynebacterium glutamicum</i> . <i>Nucleic Acids Research</i> , 2015 , 43, 520-9	20.1	30
91	Deletion of cgR_1596 and cgR_2070, encoding NlpC/P60 proteins, causes a defect in cell separation in <i>Corynebacterium glutamicum</i> R. <i>Journal of Bacteriology</i> , 2008 , 190, 8204-14	3.5	29
90	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, 6693-703	5.7	27
89	Electroporation-transformation system for coryneform bacteria by auxotrophic complementation.. <i>Agricultural and Biological Chemistry</i> , 1990 , 54, 443-447		25
88	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, 1905-16	5.7	24
87	Random segment deletion based on IS31831 and Cre/loxP excision system in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2007 , 74, 1333-41	5.7	24
86	Isolation and molecular characterization of pMG160, a mobilizable cryptic plasmid from <i>Rhodobacter blasticus</i> . <i>Applied and Environmental Microbiology</i> , 2003 , 69, 725-33	4.8	23
85	Expanding the regulatory network governed by the extracytoplasmic function sigma factor Σ in <i>Corynebacterium glutamicum</i> . <i>Journal of Bacteriology</i> , 2015 , 197, 483-96	3.5	22
84	Chorismate-dependent transcriptional regulation of quinate/shikimate utilization genes by LysR-type transcriptional regulator QsuR in <i>Corynebacterium glutamicum</i> : carbon flow control at metabolic branch point. <i>Molecular Microbiology</i> , 2014 , 92, 356-68	4.1	22
83	Characterization of the mannitol catabolic operon of <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2011 , 91, 1375-87	5.7	22
82	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	5.7	22
81	Vectors for Genetic Engineering of <i>Corynebacteria</i> . <i>ACS Symposium Series</i> , 2003 , 175-191	0.4	22
80	A novel redox-sensing transcriptional regulator CyeR controls expression of an Old Yellow Enzyme family protein in <i>Corynebacterium glutamicum</i> . <i>Microbiology (United Kingdom)</i> , 2010 , 156, 1335-1341	2.9	21
79	Diversity of metabolic shift in response to oxygen deprivation in <i>Corynebacterium glutamicum</i> and its close relatives. <i>Applied Microbiology and Biotechnology</i> , 2011 , 90, 1051-61	5.7	20
78	Regulation of the expression of genes involved in NAD de novo biosynthesis in <i>Corynebacterium glutamicum</i> . <i>Applied and Environmental Microbiology</i> , 2010 , 76, 5488-95	4.8	20
77	Site-directed integration system using a combination of mutant lox sites for <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2007 , 77, 871-8	5.7	20

76	Regulons of global transcription factors in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2016 , 100, 45-60	5.7	18
75	Characterization of shikimate dehydrogenase homologues of <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2013 , 97, 8139-49	5.7	18
74	Identification of a HAD superfamily phosphatase, HdpA, involved in 1,3-dihydroxyacetone production during sugar catabolism in <i>Corynebacterium glutamicum</i> . <i>FEBS Letters</i> , 2012 , 586, 4228-32	3.8	18
73	Transcriptional regulation of <i>Corynebacterium glutamicum</i> methionine biosynthesis genes in response to methionine supplementation under oxygen deprivation. <i>Applied Microbiology and Biotechnology</i> , 2008 , 81, 505-13	5.7	18
72	Isolation and characterization of a native composite transposon, Tn14751, carrying 17.4 kilobases of <i>Corynebacterium glutamicum</i> chromosomal DNA. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 407-16	4.8	18
71	Influence of SigB inactivation on <i>Corynebacterium glutamicum</i> protein secretion. <i>Applied Microbiology and Biotechnology</i> , 2013 , 97, 4917-26	5.7	17
70	Biorefinery Applications of <i>Corynebacterium glutamicum</i> . <i>Microbiology Monographs</i> , 2013 , 149-172	0.8	17
69	Glucose consumption rate critically depends on redox state in <i>Corynebacterium glutamicum</i> under oxygen deprivation. <i>Applied Microbiology and Biotechnology</i> , 2015 , 99, 5573-82	5.7	16
68	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, 1107-15	5.7	16
67	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, 1327-33	3.5	16
66	Isobutanol production in <i>Corynebacterium glutamicum</i> : Suppressed succinate by-production by pckA inactivation and enhanced productivity via the Entner-Doudoroff pathway. <i>Metabolic Engineering</i> , 2020 , 59, 24-35	9.7	16
65	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	3.8	16
64	Metabolic engineering of <i>Corynebacterium glutamicum</i> for hyperproduction of polymer-grade L- and D-lactic acid. <i>Applied Microbiology and Biotechnology</i> , 2019 , 103, 3381-3391	5.7	15
63	RNase III mediated cleavage of the coding region of mraZ mRNA is required for efficient cell division in <i>Corynebacterium glutamicum</i> . <i>Molecular Microbiology</i> , 2016 , 99, 1149-66	4.1	15
62	Enhanced Glucose Consumption and Organic Acid Production by Engineered <i>Corynebacterium glutamicum</i> Based on Analysis of a pfkB1 Deletion Mutant. <i>Applied and Environmental Microbiology</i> , 2017 , 83,	4.8	15
61	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, 4173-83 ^{4.8}		15
60	Identification of a second beta-glucoside phosphoenolpyruvate: carbohydrate phosphotransferase system in <i>Corynebacterium glutamicum</i> R. <i>Microbiology (United Kingdom)</i> , 2009 , 155, 3652-3660	2.9	15
59	Regulation of the nitrate reductase operon narKGHJl by the cAMP-dependent regulator GlxR in <i>Corynebacterium glutamicum</i> . <i>Microbiology (United Kingdom)</i> , 2011 , 157, 21-28	2.9	15

58	Engineering the glycolytic pathway: A potential approach for improvement of biocatalyst performance. <i>Bioengineered</i> , 2015 , 6, 328-34	5.7	14
57	Involvement of regulatory interactions among global regulators GlxR, SugR, and RamA in expression of ramA in <i>Corynebacterium glutamicum</i> . <i>Journal of Bacteriology</i> , 2013 , 195, 1718-26	3.5	14
56	<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, 4385-97	5.7	14
55	Living cell reaction process for L-isoleucine and L-valine production. <i>Journal of Industrial Microbiology</i> , 1990 , 5, 289-293		14
54	Transcription of <i>Corynebacterium glutamicum</i> genes involved in tricarboxylic acid cycle and glyoxylate cycle. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2008 , 15, 264-76	0.9	13
53	Extracytoplasmic function sigma factor σ^{24} 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	4.1	13
52	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, 1427-33	5.7	12
51	The extracytoplasmic function σ factor σ^{24} regulates expression of a branched quinol oxidation pathway in <i>Corynebacterium glutamicum</i> . <i>Molecular Microbiology</i> , 2016 , 100, 486-509	4.1	12
50	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	2.9	12
49	Characterization of a 24-kb plasmid pCGR2 newly isolated from <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2010 , 87, 1855-66	5.7	12
48	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	5.7	12
47	The physiological role of riboflavin transporter and involvement of FMN-riboswitch in its gene expression in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2014 , 98, 4159-68	5.7	11
46	Coordinated regulation of gnd, which encodes 6-phosphogluconate dehydrogenase, by the two transcriptional regulators GntR1 and RamA in <i>Corynebacterium glutamicum</i> . <i>Journal of Bacteriology</i> , 2012 , 194, 6527-36	3.5	11
45	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	3.3	11
44	Genome-wide analysis of the role of global transcriptional regulator GntR1 in <i>Corynebacterium glutamicum</i> . <i>Journal of Bacteriology</i> , 2014 , 196, 3249-58	3.5	10
43	Identification and expression analysis of a gene encoding a shikimate transporter of <i>Corynebacterium glutamicum</i> . <i>Microbiology (United Kingdom)</i> , 2015 , 161, 254-263	2.9	10
42	<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, 1952-8	2.1	10
41	Translation efficiency of antiterminator proteins is a determinant for the difference in glucose repression of two β -glucoside phosphotransferase system gene clusters in <i>Corynebacterium glutamicum</i> R. <i>Journal of Bacteriology</i> , 2011 , 193, 349-57	3.5	10

40	Alternative technologies for biotechnological fuel ethanol manufacturing. <i>Journal of Chemical Technology and Biotechnology</i> , 2007 , 82, 693-697	3.5	9
39	A new insertion sequence, IS14999, from <i>Corynebacterium glutamicum</i> . <i>Microbiology (United Kingdom)</i> , 2005 , 151, 501-508	2.9	9
38	<i>Corynebacterium glutamicum</i> ArnR controls expression of nitrate reductase operon narKGHJI and nitric oxide (NO)-detoxifying enzyme gene hmp in an NO-responsive manner. <i>Journal of Bacteriology</i> , 2014 , 196, 60-9	3.5	8
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