

# Masayuki Inui

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/456369/masayuki-inui-publications-by-year.pdf>

**Version:** 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

165  
papers

6,921  
citations

45  
h-index

77  
g-index

169  
ext. papers

7,551  
ext. citations

4.7  
avg, IF

5.84  
L-index

#	Paper	IF	Citations
165	Regulation of Ribonuclease J Expression in .. <i>Journal of Bacteriology</i> , <b>2022</b> , e0005322	3.5	0
164	Identification and Molecular Characterization of the Operon Required for L-Asparagine Utilization in <i>Corynebacterium glutamicum</i> . <i>Microorganisms</i> , <b>2022</b> , 10, 1002	4.9	
163	The Gene Encoding Fermentative l-Lactate Dehydrogenase in Is Positively Regulated by the Global Regulator GlxR. <i>Microorganisms</i> , <b>2021</b> , 9,	4.9	1
162	Protocatechuate overproduction by <i>Corynebacterium glutamicum</i> via simultaneous engineering of native and heterologous biosynthetic pathways. <i>Metabolic Engineering</i> , <b>2021</b> , 65, 232-242	9.7	5
161	Coexistence of the Entner-Doudoroff and Embden-Meyerhof-Parnas pathways enhances glucose consumption of ethanol-producing <i>Corynebacterium glutamicum</i> . <i>Biotechnology for Biofuels</i> , <b>2021</b> , 14, 45	7.8	2
160	History-Driven Genetic Modification Design Technique Using a Domain-Specific Lexical Model for the Acceleration of DBTL Cycles for Microbial Cell Factories. <i>ACS Synthetic Biology</i> , <b>2021</b> , 10, 2308-2317	5.7	1
159	Anaerobic glucose consumption is accelerated at non-proliferating elevated temperatures through upregulation of a glucose transporter gene in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , <b>2020</b> , 104, 6719-6729	5.7	1
158	Aromatic Compound Catabolism in <i>Corynebacterium glutamicum</i> . <i>Microbiology Monographs</i> , <b>2020</b> , 323-338	3.7	1
157	Aromatic Compound Production by <i>Corynebacterium glutamicum</i> . <i>Microbiology Monographs</i> , <b>2020</b> , 339-370	3.7	1
156	Global Transcriptional Regulators Involved in Carbon, Nitrogen, Phosphorus, and Sulfur Metabolisms in <i>Corynebacterium glutamicum</i> . <i>Microbiology Monographs</i> , <b>2020</b> , 113-147	0.8	2
155	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> , <b>2020</b> , 59, 24-35	9.7	16
154	Metabolic engineering of <i>Corynebacterium glutamicum</i> for hyperproduction of polymer-grade L- and D-lactic acid. <i>Applied Microbiology and Biotechnology</i> , <b>2019</b> , 103, 3381-3391	5.7	15
153	Engineering the transcriptional activator NifA for the construction of <i>Rhodobacter sphaeroides</i> strains that produce hydrogen gas constitutively. <i>Applied Microbiology and Biotechnology</i> , <b>2019</b> , 103, 9739-9749	5.7	5
152	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> , <b>2019</b> , 125, 13-20	3.8	16
151	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> , <b>2019</b> , 127, 288-293	3.3	11
150	Introduction of Glyoxylate Bypass Increases Hydrogen Gas Yield from Acetate and l-Glutamate in. <i>Applied and Environmental Microbiology</i> , <b>2019</b> , 85,	4.8	8
149	Efficient construction of xenogeneic genomic libraries by circumventing restriction-modification systems that restrict methylated DNA. <i>Journal of Microbiological Methods</i> , <b>2018</b> , 146, 13-15	2.8	

148	Production of 4-Hydroxybenzoic Acid by an Aerobic Growth-Arrested Bioprocess Using Metabolically Engineered <i>Corynebacterium glutamicum</i> . <i>Applied and Environmental Microbiology</i> , <b>2018</b> , 84,	4.8	45
147	Glutamine-rich toxic proteins GrtA, GrtB and GrtC together with the antisense RNA AsgR constitute a toxin-antitoxin-like system in <i>Corynebacterium glutamicum</i> . <i>Molecular Microbiology</i> , <b>2018</b> , 108, 578-594	4.1	1
146	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> , <b>2018</b> , 102, 8685-8705	5.7	40
145	Extracytoplasmic function sigma factor $\sigma^{24}$ confers resistance to environmental stress by enhancing mycolate synthesis and modifying peptidoglycan structures in <i>Corynebacterium glutamicum</i> . <i>Molecular Microbiology</i> , <b>2018</b> , 107, 312-329	4.1	13
144	Polynucleotide Phosphorylase, RNase E/G, and YbeY Are Involved in the Maturation of 4.5S RNA in <i>Corynebacterium glutamicum</i> . <i>Journal of Bacteriology</i> , <b>2017</b> , 199,	3.5	6
143	Functional analysis of arabinofuranosidases and a xylanase of <i>Corynebacterium alkanolyticum</i> for arabinoxylan utilization in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , <b>2017</b> , 101, 5019-5032	5.7	3
142	Increasing Diversity of the Bio-Based Chemicals Produced by <i>Corynebacterium glutamicum</i> . <i>Kagaku To Seibutsu</i> , <b>2017</b> , 55, 690-698	0	
141	Trehalose acts as a uridine 5Sdiphosphoglucose-competitive inhibitor of trehalose 6-phosphate synthase in <i>Corynebacterium glutamicum</i> . <i>FEBS Journal</i> , <b>2017</b> , 284, 4298-4313	5.7	4
140	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> , <b>2017</b> , 83,	4.8	15
139	Metabolic engineering of <i>Corynebacterium glutamicum</i> for shikimate overproduction by growth-arrested cell reaction. <i>Metabolic Engineering</i> , <b>2016</b> , 38, 204-216	9.7	66
138	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> , <b>2016</b> , 99, 1149-66	4.1	15
137	The extracytoplasmic function $\sigma$ factor $\sigma^{24}$ regulates expression of a branched quinol oxidation pathway in <i>Corynebacterium glutamicum</i> . <i>Molecular Microbiology</i> , <b>2016</b> , 100, 486-509	4.1	12
136	Regulons of global transcription factors in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , <b>2016</b> , 100, 45-60	5.7	18
135	Production of para-aminobenzoate by genetically engineered <i>Corynebacterium glutamicum</i> and non-biological formation of an N-glucosyl byproduct. <i>Metabolic Engineering</i> , <b>2016</b> , 38, 322-330	9.7	34
134	Thermal and solvent stress cross-tolerance conferred to <i>Corynebacterium glutamicum</i> by adaptive laboratory evolution. <i>Applied and Environmental Microbiology</i> , <b>2015</b> , 81, 2284-98	4.8	57
133	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> , <b>2015</b> , 99, 1427-33	5.7	12
132	Glucose consumption rate critically depends on redox state in <i>Corynebacterium glutamicum</i> under oxygen deprivation. <i>Applied Microbiology and Biotechnology</i> , <b>2015</b> , 99, 5573-82	5.7	16
131	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> , <b>2015</b> , 99, 4679-89	5.7	42

130	AraR, an l-Arabinose-Responsive Transcriptional Regulator in <i>Corynebacterium glutamicum</i> ATCC 31831, Exerts Different Degrees of Repression Depending on the Location of Its Binding Sites within the Three Target Promoter Regions. <i>Journal of Bacteriology</i> , <b>2015</b> , 197, 3788-96	3.5	5
129	Engineering the glycolytic pathway: A potential approach for improvement of biocatalyst performance. <i>Bioengineered</i> , <b>2015</b> , 6, 328-34	5.7	14
128	Regulation of the Expression of De Novo Pyrimidine Biosynthesis Genes in <i>Corynebacterium glutamicum</i> . <i>Journal of Bacteriology</i> , <b>2015</b> , 197, 3307-16	3.5	3
127	Expanding the regulatory network governed by the extracytoplasmic function sigma factor $\sigma^H$ in <i>Corynebacterium glutamicum</i> . <i>Journal of Bacteriology</i> , <b>2015</b> , 197, 483-96	3.5	22
126	Rho and RNase play a central role in FMN riboswitch regulation in <i>Corynebacterium glutamicum</i> . <i>Nucleic Acids Research</i> , <b>2015</b> , 43, 520-9	20.1	30
125	Metabolic engineering for improved production of ethanol by <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , <b>2015</b> , 99, 1165-72	5.7	61
124	Functional Characterization of <i>Corynebacterium alkanolyticum</i> $\beta$ -Xylosidase and Xyloside ABC Transporter in <i>Corynebacterium glutamicum</i> . <i>Applied and Environmental Microbiology</i> , <b>2015</b> , 81, 4173-83 <sup>4.8</sup>		15
123	Copper homeostasis-related genes in three separate transcriptional units regulated by CsoR in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , <b>2015</b> , 99, 3505-17	5.7	7
122	Identification and expression analysis of a gene encoding a shikimate transporter of <i>Corynebacterium glutamicum</i> . <i>Microbiology (United Kingdom)</i> , <b>2015</b> , 161, 254-263	2.9	10
121	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> , <b>2014</b> , 98, 4159-68	5.7	11
120	The LacI-Type transcriptional regulator AraR acts as an L-arabinose-responsive repressor of L-arabinose utilization genes in <i>Corynebacterium glutamicum</i> ATCC 31831. <i>Journal of Bacteriology</i> , <b>2014</b> , 196, 2242-54	3.5	3
119	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> , <b>2014</b> , 92, 356-68	4.1	22
118	Genome-wide analysis of the role of global transcriptional regulator GntR1 in <i>Corynebacterium glutamicum</i> . <i>Journal of Bacteriology</i> , <b>2014</b> , 196, 3249-58	3.5	10
117	<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> , <b>2014</b> , 196, 60-9	3.5	8
116	Development of Growth-Arrested Bioprocesses with <i>Corynebacterium glutamicum</i> for Cellulosic Ethanol Production from Complex Sugar Mixtures <b>2014</b> , 121-139		1
115	Toward Realization of New Biorefinery Industries Using <i>Corynebacterium glutamicum</i> <b>2014</b> , 253-262		
114	Identification of a gene involved in plasmid structural instability in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , <b>2013</b> , 97, 8219-26	5.7	3
113	Characterization of shikimate dehydrogenase homologues of <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , <b>2013</b> , 97, 8139-49	5.7	18

112	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> , <b>2013</b> , 195, 1718-26	3.5	14
111	Influence of SigB inactivation on <i>Corynebacterium glutamicum</i> protein secretion. <i>Applied Microbiology and Biotechnology</i> , <b>2013</b> , 97, 4917-26	5.7	17
110	OxyR acts as a transcriptional repressor of hydrogen peroxide-inducible antioxidant genes in <i>Corynebacterium glutamicum</i> R. <i>FEBS Journal</i> , <b>2013</b> , 280, 3298-312	5.7	53
109	Biorefinery Applications of <i>Corynebacterium glutamicum</i> . <i>Microbiology Monographs</i> , <b>2013</b> , 149-172	0.8	17
108	Reactions upstream of glycerate-1,3-bisphosphate drive <i>Corynebacterium glutamicum</i> (D)-lactate productivity under oxygen deprivation. <i>Applied Microbiology and Biotechnology</i> , <b>2013</b> , 97, 6693-703	5.7	27
107	Engineering of <i>Corynebacterium glutamicum</i> for high-yield L-valine production under oxygen deprivation conditions. <i>Applied and Environmental Microbiology</i> , <b>2013</b> , 79, 1250-7	4.8	92
106	Strain optimization for efficient isobutanol production using <i>Corynebacterium glutamicum</i> under oxygen deprivation. <i>Biotechnology and Bioengineering</i> , <b>2013</b> , 110, 2938-48	4.9	86
105	pCGR2 copy number depends on the par locus that forms a ParC-ParB-DNA partition complex in <i>Corynebacterium glutamicum</i> . <i>Journal of Applied Microbiology</i> , <b>2013</b> , 115, 495-508	4.7	3
104	The Biotechnological Potential of <i>Corynebacterium glutamicum</i> , from Umami to Chemurgy. <i>Microbiology Monographs</i> , <b>2013</b> , 1-49	0.8	4
103	Genome Engineering of <i>Corynebacterium glutamicum</i> . <i>Microbiology Monographs</i> , <b>2013</b> , 89-105	0.8	4
102	Regulation of Sugar Uptake, Glycolysis, and the Pentose Phosphate Pathway in <i>Corynebacterium glutamicum</i> . <i>Microbiology Monographs</i> , <b>2013</b> , 263-279	0.8	3
101	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> , <b>2012</b> , 586, 4228-32	3.8	18
100	<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> , <b>2012</b> , 76, 1952-8	2.1	10
99	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> , <b>2012</b> , 78, 4447-57	4.8	70
98	<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> , <b>2012</b> , 279, 4385-97	5.7	14
97	Postgenomic approaches to using corynebacteria as biocatalysts. <i>Annual Review of Microbiology</i> , <b>2012</b> , 66, 521-50	17.5	35
96	Microorganisms for Xylitol Production: Focus on Strain Improvement <b>2012</b> , 109-131		2
95	NdnR is an NAD-responsive transcriptional repressor of the ndnR operon involved in NAD de novo biosynthesis in <i>Corynebacterium glutamicum</i> . <i>Microbiology (United Kingdom)</i> , <b>2012</b> , 158, 975-982	2.9	8

94	Coordinated regulation of <i>gnd</i> , which encodes 6-phosphogluconate dehydrogenase, by the two transcriptional regulators GntR1 and RamA in <i>Corynebacterium glutamicum</i> . <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 6527-36	3.5	11
93	Improvement of the redox balance increases L-valine production by <i>Corynebacterium glutamicum</i> under oxygen deprivation conditions. <i>Applied and Environmental Microbiology</i> , <b>2012</b> , 78, 865-75	4.8	97
92	Efficient markerless gene replacement in <i>Corynebacterium glutamicum</i> using a new temperature-sensitive plasmid. <i>Journal of Microbiological Methods</i> , <b>2011</b> , 85, 155-63	2.8	38
91	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> , <b>2011</b> , 89, 1905-16	5.7	24
90	Diversity of metabolic shift in response to oxygen deprivation in <i>Corynebacterium glutamicum</i> and its close relatives. <i>Applied Microbiology and Biotechnology</i> , <b>2011</b> , 90, 1051-61	5.7	20
89	Metabolic engineering of 1,2-propanediol pathways in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , <b>2011</b> , 90, 1721-9	5.7	48
88	High yield secretion of heterologous proteins in <i>Corynebacterium glutamicum</i> using its own Tat-type signal sequence. <i>Applied Microbiology and Biotechnology</i> , <b>2011</b> , 91, 677-87	5.7	43
87	Characterization of the mannitol catabolic operon of <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , <b>2011</b> , 91, 1375-87	5.7	22
86	Transcriptional regulators of multiple genes involved in carbon metabolism in <i>Corynebacterium glutamicum</i> . <i>Journal of Biotechnology</i> , <b>2011</b> , 154, 114-25	3.7	35
85	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> , <b>2011</b> , 193, 1327-33	3.5	16
84	Metabolic engineering of bacteria for utilization of mixed sugar substrates for improved production of chemicals and fuel ethanol. <i>Biofuels</i> , <b>2011</b> , 2, 303-313	2	6
83	Regulation of the nitrate reductase operon <i>narKGHJI</i> by the cAMP-dependent regulator GlxR in <i>Corynebacterium glutamicum</i> . <i>Microbiology (United Kingdom)</i> , <b>2011</b> , 157, 21-28	2.9	15
82	Translation efficiency of antiterminator proteins is a determinant for the difference in glucose repression of two $\beta$ -glucoside phosphotransferase system gene clusters in <i>Corynebacterium glutamicum</i> R. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 349-57	3.5	10
81	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> , <b>2011</b> , 193, 4123-33	3.5	45
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> , <b>2010</b> , 156, 1335-1341	2.9	21
79	Antisense-RNA-mediated plasmid copy number control in pCG1-family plasmids, pCGR2 and pCG1, in <i>Corynebacterium glutamicum</i> . <i>Microbiology (United Kingdom)</i> , <b>2010</b> , 156, 3609-3623	2.9	12
78	Regulation of the expression of genes involved in NAD de novo biosynthesis in <i>Corynebacterium glutamicum</i> . <i>Applied and Environmental Microbiology</i> , <b>2010</b> , 76, 5488-95	4.8	20
77	Regulation of genes involved in sugar uptake, glycolysis and lactate production in <i>Corynebacterium glutamicum</i> . <i>Future Microbiology</i> , <b>2010</b> , 5, 1475-81	2.9	5

76	Sugar transporters in efficient utilization of mixed sugar substrates: current knowledge and outlook. <i>Applied Microbiology and Biotechnology</i> , <b>2010</b> , 85, 471-80	5.7	97
75	Xylitol production by recombinant <i>Corynebacterium glutamicum</i> under oxygen deprivation. <i>Applied Microbiology and Biotechnology</i> , <b>2010</b> , 86, 1057-66	5.7	80
74	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> , <b>2010</b> , 87, 159-65	5.7	81
73	Characterization of a 24-kb plasmid pCGR2 newly isolated from <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , <b>2010</b> , 87, 1855-66	5.7	12
72	Regulation of expression of genes involved in quinate and shikimate utilization in <i>Corynebacterium glutamicum</i> . <i>Applied and Environmental Microbiology</i> , <b>2009</b> , 75, 3461-8	4.8	43
71	Regulation of quinone oxidoreductase by the redox-sensing transcriptional regulator QorR in <i>Corynebacterium glutamicum</i> . <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 16736-16742	5.4	32
70	Identification and functional analysis of the gene cluster for L-arabinose utilization in <i>Corynebacterium glutamicum</i> . <i>Applied and Environmental Microbiology</i> , <b>2009</b> , 75, 3419-29	4.8	61
69	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> , <b>2009</b> , 191, 2964-72	3.5	63
68	Scanning the <i>Corynebacterium glutamicum</i> R genome for high-efficiency secretion signal sequences. <i>Microbiology (United Kingdom)</i> , <b>2009</b> , 155, 741-750	2.9	53
67	Identification of a second beta-glucoside phosphoenolpyruvate: carbohydrate phosphotransferase system in <i>Corynebacterium glutamicum</i> R. <i>Microbiology (United Kingdom)</i> , <b>2009</b> , 155, 3652-3660	2.9	15
66	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> , <b>2009</b> , 81, 1107-15	5.7	16
65	Identification of new secreted proteins and secretion of heterologous amylase by <i>C. glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , <b>2009</b> , 82, 491-500	5.7	22
64	Molecular mechanism of SugR-mediated sugar-dependent expression of the <i>ldhA</i> gene encoding L-lactate dehydrogenase in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , <b>2009</b> , 83, 315-27	5.7	33
63	Engineering of pentose transport in <i>Corynebacterium glutamicum</i> to improve simultaneous utilization of mixed sugars. <i>Applied Microbiology and Biotechnology</i> , <b>2009</b> , 85, 105-15	5.7	90
62	The <i>ldhA</i> gene, encoding fermentative L-lactate dehydrogenase of <i>Corynebacterium glutamicum</i> , is under the control of positive feedback regulation mediated by <i>LldR</i> . <i>Journal of Bacteriology</i> , <b>2009</b> , 191, 4251-8	3.5	33
61	Involvement of the LuxR-type transcriptional regulator <i>RamA</i> 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> , <b>2009</b> , 191, 968-77	3.5	40
60	<i>DivS</i> , a novel SOS-inducible cell-division suppressor in <i>Corynebacterium glutamicum</i> . <i>Molecular Microbiology</i> , <b>2008</b> , 67, 597-608	4.1	47
59	Technological options for biological fuel ethanol. <i>Journal of Molecular Microbiology and Biotechnology</i> , <b>2008</b> , 15, 16-30	0.9	33

58	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> , <b>2008</b> , 154, 3073-3083	2.9	40
57	Regulation of the expression of phosphoenolpyruvate: carbohydrate phosphotransferase system (PTS) genes in <i>Corynebacterium glutamicum</i> R. <i>Microbiology (United Kingdom)</i> , <b>2008</b> , 154, 264-274	2.9	46
56	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> , <b>2008</b> , 74, 5146-52	4.8	48
55	Transcription of <i>Corynebacterium glutamicum</i> genes involved in tricarboxylic acid cycle and glyoxylate cycle. <i>Journal of Molecular Microbiology and Biotechnology</i> , <b>2008</b> , 15, 264-76	0.9	13
54	Identification of a gene encoding a transporter essential for utilization of C4 dicarboxylates in <i>Corynebacterium glutamicum</i> . <i>Applied and Environmental Microbiology</i> , <b>2008</b> , 74, 5290-6	4.8	33
53	ArnR, a novel transcriptional regulator, represses expression of the narKGHJI operon in <i>Corynebacterium glutamicum</i> . <i>Journal of Bacteriology</i> , <b>2008</b> , 190, 3264-73	3.5	34
52	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> , <b>2008</b> , 190, 8204-14	3.5	29
51	Engineering of an L-arabinose metabolic pathway in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , <b>2008</b> , 77, 1053-62	5.7	118
50	Production of isopropanol by metabolically engineered <i>Escherichia coli</i> . <i>Applied Microbiology and Biotechnology</i> , <b>2008</b> , 77, 1219-24	5.7	68
49	Expression of <i>Clostridium acetobutylicum</i> butanol synthetic genes in <i>Escherichia coli</i> . <i>Applied Microbiology and Biotechnology</i> , <b>2008</b> , 77, 1305-16	5.7	309
48	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> , <b>2008</b> , 78, 309-18	5.7	44
47	Production of D-lactic acid by <i>Corynebacterium glutamicum</i> under oxygen deprivation. <i>Applied Microbiology and Biotechnology</i> , <b>2008</b> , 78, 449-54	5.7	179
46	Random genome deletion methods applicable to prokaryotes. <i>Applied Microbiology and Biotechnology</i> , <b>2008</b> , 79, 519-26	5.7	6
45	An efficient succinic acid production process in a metabolically engineered <i>Corynebacterium glutamicum</i> strain. <i>Applied Microbiology and Biotechnology</i> , <b>2008</b> , 81, 459-64	5.7	332
44	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> , <b>2008</b> , 81, 291-301	5.7	34
43	Transcriptional regulation of <i>Corynebacterium glutamicum</i> methionine biosynthesis genes in response to methionine supplementation under oxygen deprivation. <i>Applied Microbiology and Biotechnology</i> , <b>2008</b> , 81, 505-13	5.7	18
42	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> , <b>2008</b> , 81, 691-9	5.7	75
41	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> , <b>2007</b> , 73, 2349-53	4.8	131

40	Transcriptional profiling of <i>Corynebacterium glutamicum</i> metabolism during organic acid production under oxygen deprivation conditions. <i>Microbiology (United Kingdom)</i> , <b>2007</b> , 153, 2491-2504	2.9	123
39	Alternative technologies for biotechnological fuel ethanol manufacturing. <i>Journal of Chemical Technology and Biotechnology</i> , <b>2007</b> , 82, 693-697	3.5	9
38	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> , <b>2007</b> , 74, 754-60	5.7	42
37	Random segment deletion based on IS31831 and Cre/loxP excision system in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , <b>2007</b> , 74, 1333-41	5.7	24
36	Anaerobic growth of <i>Corynebacterium glutamicum</i> using nitrate as a terminal electron acceptor. <i>Applied Microbiology and Biotechnology</i> , <b>2007</b> , 75, 889-97	5.7	107
35	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> , <b>2007</b> , 76, 1347-56	5.7	37
34	Analyses of the acetate-producing pathways in <i>Corynebacterium glutamicum</i> under oxygen-deprived conditions. <i>Applied Microbiology and Biotechnology</i> , <b>2007</b> , 77, 853-60	5.7	47
33	Site-directed integration system using a combination of mutant lox sites for <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , <b>2007</b> , 77, 871-8	5.7	20
32	Comparative analysis of the <i>Corynebacterium glutamicum</i> group and complete genome sequence of strain R. <i>Microbiology (United Kingdom)</i> , <b>2007</b> , 153, 1042-1058	2.9	212
31	Expression of <i>Corynebacterium glutamicum</i> glycolytic genes varies with carbon source and growth phase. <i>Microbiology (United Kingdom)</i> , <b>2007</b> , 153, 2190-2202	2.9	42
30	Genomes and Genome-Level Engineering of Amino Acid-Producing Bacteria <b>2006</b> , 349-401		5
29	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> , <b>2006</b> , 73, 67-72	5.7	115
28	Engineering of a xylose metabolic pathway in <i>Corynebacterium glutamicum</i> . <i>Applied and Environmental Microbiology</i> , <b>2006</b> , 72, 3418-28	4.8	193
27	High-throughput transposon mutagenesis of <i>Corynebacterium glutamicum</i> and construction of a single-gene disruptant mutant library. <i>Applied and Environmental Microbiology</i> , <b>2006</b> , 72, 3750-5	4.8	82
26	Implementing biofuels on a global scale. <i>Nature Biotechnology</i> , <b>2006</b> , 24, 761-4	44.5	32
25	A new insertion sequence, IS14999, from <i>Corynebacterium glutamicum</i> . <i>Microbiology (United Kingdom)</i> , <b>2005</b> , 151, 501-508	2.9	9
24	Cre/loxP-mediated deletion system for large genome rearrangements in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , <b>2005</b> , 67, 225-33	5.7	41
23	Production of organic acids by <i>Corynebacterium glutamicum</i> under oxygen deprivation. <i>Applied Microbiology and Biotechnology</i> , <b>2005</b> , 68, 475-80	5.7	202

22	Multiple large segment deletion method for <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , <b>2005</b> , 69, 151-61	5.7	38
21	Large-scale engineering of the <i>Corynebacterium glutamicum</i> genome. <i>Applied and Environmental Microbiology</i> , <b>2005</b> , 71, 3369-72	4.8	62
20	Manipulating corynebacteria, from individual genes to chromosomes. <i>Applied and Environmental Microbiology</i> , <b>2005</b> , 71, 7633-42	4.8	48
19	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> , <b>2005</b> , 71, 407-16	4.8	18
18	Enhanced hydrogen production from formic acid by formate hydrogen lyase-overexpressing <i>Escherichia coli</i> strains. <i>Applied and Environmental Microbiology</i> , <b>2005</b> , 71, 6762-8	4.8	180
17	New multiple-deletion method for the <i>Corynebacterium glutamicum</i> genome, using a mutant lox sequence. <i>Applied and Environmental Microbiology</i> , <b>2005</b> , 71, 8472-80	4.8	81
16	Metabolic analysis of <i>Corynebacterium glutamicum</i> during lactate and succinate productions under oxygen deprivation conditions. <i>Journal of Molecular Microbiology and Biotechnology</i> , <b>2004</b> , 7, 182-96	0.9	291
15	<i>Corynebacterium glutamicum</i> glyceraldehyde-3-phosphate dehydrogenase isoforms with opposite, ATP-dependent regulation. <i>Journal of Molecular Microbiology and Biotechnology</i> , <b>2004</b> , 8, 91-103	0.9	37
14	Metabolic engineering of <i>Corynebacterium glutamicum</i> for fuel ethanol production under oxygen-deprivation conditions. <i>Journal of Molecular Microbiology and Biotechnology</i> , <b>2004</b> , 8, 243-54	0.9	243
13	Vectors for Genetic Engineering of Corynebacteria. <i>ACS Symposium Series</i> , <b>2003</b> , 175-191	0.4	22
12	Isolation and molecular characterization of pMG160, a mobilizable cryptic plasmid from <i>Rhodobacter blasticus</i> . <i>Applied and Environmental Microbiology</i> , <b>2003</b> , 69, 725-33	4.8	23
11	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> , <b>2003</b> , 149, 1569-1580	2.9	71
10	Bacterial phosphotransferase system (PTS) in carbohydrate uptake and control of carbon metabolism. <i>Journal of Bioscience and Bioengineering</i> , <b>2001</b> , 92, 502-517	3.3	135
9	The ptsI gene encoding enzyme I of the phosphotransferase system of <i>Corynebacterium glutamicum</i> . <i>Biochemical and Biophysical Research Communications</i> , <b>2001</b> , 289, 1307-13	3.4	48
8	Cyclic adenosine 3',5'-monophosphate and coryneform bacteria. <i>FEMS Microbiology Letters</i> , <b>1995</b> , 133, 239-244	2.9	2
7	Transposon mutagenesis of coryneform bacteria. <i>Molecular Genetics and Genomics</i> , <b>1994</b> , 245, 397-405		34
6	Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> . <i>Molecular Microbiology</i> , <b>1994</b> , 11, 739-46	4.1	48
5	Replacement Recombination in Coryneform Bacteria: High Efficiency Integration Requirement for Non-methylated Plasmid DNA. <i>Bioscience, Biotechnology and Biochemistry</i> , <b>1993</b> , 57, 2036-2038	2.1	34

4	Depression of by-product formation during L: -isoleucine production by a living-cell reaction process. <i>Applied Microbiology and Biotechnology</i> , <b>1991</b> , 35, 348-351	5-7	12
3	Electroporation-transformation system for coryneform bacteria by auxotrophic complementation.. <i>Agricultural and Biological Chemistry</i> , <b>1990</b> , 54, 443-447		25
2	Living cell reaction process for l-isoleucine and l-valine production. <i>Journal of Industrial Microbiology</i> , <b>1990</b> , 5, 289-293		14
1	Advanced Fermentation Technologies	311-330	7