Michael Bott

List of Publications by Citations

212 papers	10,291 citations	60 h-index	92 g-index
220 ext. papers	11,447 ext. citations	4.8 avg, IF	6.38 L-index

#	Paper	IF	Citations
212	The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins. *Journal of Biotechnology*, **2003**, 104, 5-25	3.7	750
211	Metabolic engineering of Escherichia coli and Corynebacterium glutamicum for biotechnological production of organic acids and amino acids. *Current Opinion in Microbiology*, **2006**, 9, 268-74	7.9	224
210	A high-throughput approach to identify genomic variants of bacterial metabolite producers at the single-cell level. *Genome Biology*, **2012**, 13, R40	18.3	185
209	Toward biotechnological production of adipic acid and precursors from biorenewables. *Journal of Biotechnology*, **2013**, 167, 75-84	3.7	183
208	The development and application of a single-cell biosensor for the detection of l-methionine and branched-chain amino acids. *Metabolic Engineering*, **2012**, 14, 449-57	9.7	170
207	Toward homosuccinate fermentation: metabolic engineering of Corynebacterium glutamicum for anaerobic production of succinate from glucose and formate. *Applied and Environmental Microbiology*, **2012**, 78, 3325-37	4.8	170
206	Corynebacterial protein kinase G controls 2-oxoglutarate dehydrogenase activity via the phosphorylation status of the OdhI protein. *Journal of Biological Chemistry*, **2006**, 281, 12300-7	5.4	168
205	Metabolic engineering of microorganisms for the synthesis of plant natural products. *Journal of Biotechnology*, **2013**, 163, 166-78	3.7	162
204	The respiratory chain of Corynebacterium glutamicum. *Journal of Biotechnology*, **2003**, 104, 129-53	3.7	160
203	Molecular analysis of the cytochrome bc1-aa3 branch of the Corynebacterium glutamicum respiratory chain containing an unusual diheme cytochrome c1. *Archives of Microbiology*, **2001**, 175, 282-94	2	148
202	A giant market and a powerful metabolism: L-lysine provided by Corynebacterium glutamicum. *Applied Microbiology and Biotechnology*, **2015**, 99, 3387-94	5.7	142
201	Deletion of the genes encoding the MtrA-MtrB two-component system of Corynebacterium glutamicum has a strong influence on cell morphology, antibiotics susceptibility and expression of genes involved in osmoprotection. *Molecular Microbiology*, **2004**, 54, 420-38	4.1	139
200	Towards a phosphoproteome map of Corynebacterium glutamicum. *Proteomics*, **2003**, 3, 1637-46	4.8	139
199	Bio-based production of organic acids with Corynebacterium glutamicum. *Microbial Biotechnology*, **2013**, 6, 87-102	6.3	135
198	Anaerobic citrate metabolism and its regulation in enterobacteria. *Archives of Microbiology*, **1997**, 167, 78-88	3	128
197	The phosphate starvation stimulon of Corynebacterium glutamicum determined by DNA microarray analyses. *Journal of Bacteriology*, **2003**, 185, 4519-29	3.5	126
196	Co-ordinated regulation of gluconate catabolism and glucose uptake in Corynebacterium glutamicum by two functionally equivalent transcriptional regulators, GntR1 and GntR2. *Molecular Microbiology*, **2008**, 67, 305-22	4.1	123

195	Recombineering in Corynebacterium glutamicum combined with optical nanosensors: a general strategy for fast producer strain generation. *Nucleic Acids Research*, **2013**, 41, 6360-9	20.1	120
194	clpC and clpP1P2 gene expression in Corynebacterium glutamicum is controlled by a regulatory network involving the transcriptional regulators ClgR and HspR as well as the ECF sigma factor sigmaH. *Molecular Microbiology*, **2004**, 52, 285-302	4.1	119
193	The structure of the periplasmic ligand-binding domain of the sensor kinase CitA reveals the first extracellular PAS domain. *Journal of Biological Chemistry*, **2003**, 278, 39189-96	5.4	118
192	A high-resolution reference map for cytoplasmic and membrane-associated proteins of Corynebacterium glutamicum. *Electrophoresis*, **2001**, 22, 4404-22	3.6	118
191	Regulation of anaerobic citrate metabolism in Klebsiella pneumoniae. *Molecular Microbiology*, **1995**, 18, 533-46	4.1	117
190	Construction of a Corynebacterium glutamicum platform strain for the production of stilbenes and (2S)-flavanones. *Metabolic Engineering*, **2016**, 38, 47-55	9.7	116
189	Novel screening methods--biosensors. *Current Opinion in Biotechnology*, **2015**, 35, 30-6	11.4	110
188	Construction of a prophage-free variant of Corynebacterium glutamicum ATCC 13032 for use as a platform strain for basic research and industrial biotechnology. *Applied and Environmental Microbiology*, **2013**, 79, 6006-15	4.8	110
187	Expression of the Escherichia coli pntAB genes encoding a membrane-bound transhydrogenase in Corynebacterium glutamicum improves L-lysine formation. *Applied Microbiology and Biotechnology*, **2007**, 75, 47-53	5.7	110
186	Improved L-lysine production with Corynebacterium glutamicum and systemic insight into citrate synthase flux and activity. *Biotechnology and Bioengineering*, **2012**, 109, 2070-81	4.9	107
185	Taking control over control: use of product sensing in single cells to remove flux control at key enzymes in biosynthesis pathways. *ACS Synthetic Biology*, **2014**, 3, 21-9	5.7	105
184	Efficient aerobic succinate production from glucose in minimal medium with Corynebacterium glutamicum. *Microbial Biotechnology*, **2012**, 5, 116-28	6.3	104
183	Purification of a cytochrome bc-aa3 supercomplex with quinol oxidase activity from Corynebacterium glutamicum. Identification of a fourth subunity of cytochrome aa3 oxidase and mutational analysis of diheme cytochrome c1. *Journal of Biological Chemistry*, **2003**, 278, 4339-46	5.4	101
182	SoxR as a single-cell biosensor for NADPH-consuming enzymes in Escherichia coli. *ACS Synthetic Biology*, **2014**, 3, 41-7	5.7	99
181	A ligand-induced switch in the periplasmic domain of sensor histidine kinase CitA. *Journal of Molecular Biology*, **2008**, 377, 512-23	6.5	99
180	Glutamate production by Corynebacterium glutamicum: dependence on the oxoglutarate dehydrogenase inhibitor protein OdhI and protein kinase PknG. *Applied Microbiology and Biotechnology*, **2007**, 76, 691-700	5.7	98
179	Identification of RamA, a novel LuxR-type transcriptional regulator of genes involved in acetate metabolism of Corynebacterium glutamicum. *Journal of Bacteriology*, **2006**, 188, 2554-67	3.5	97
178	Pushing product formation to its limit: metabolic engineering of Corynebacterium glutamicum for L-leucine overproduction. *Metabolic Engineering*, **2014**, 22, 40-52	9.7	95

177	Genetic analysis of the cytochrome c-aa3 branch of the Bradyrhizobium japonicum respiratory chain. *Molecular Microbiology*, **1990**, 4, 2147-57	4.1	95
176	Offering surprises: TCA cycle regulation in Corynebacterium glutamicum. *Trends in Microbiology*, **2007**, 15, 417-25	12.4	94
175	Proteome analysis of Corynebacterium glutamicum. *Electrophoresis*, **2001**, 22, 1712-23	3.6	94
174	Emerging Corynebacterium glutamicum systems biology. *Journal of Biotechnology*, **2006**, 124, 74-92	3.7	93
173	The AraC-type regulator RipA represses aconitase and other iron proteins from Corynebacterium under iron limitation and is itself repressed by DtxR. *Journal of Biological Chemistry*, **2005**, 280, 40500-8	5.4	90
172	The DtxR regulon of Corynebacterium glutamicum. *Journal of Bacteriology*, **2006**, 188, 2907-18	3.5	89
171	Carbonic anhydrase activity in acetate grown Methanosarcina barkeri. *Archives of Microbiology*, **1989**, 151, 137-142	3	88
170	Chassis organism from Corynebacterium glutamicum--a top-down approach to identify and delete irrelevant gene clusters. *Biotechnology Journal*, **2015**, 10, 290-301	5.6	87
169	The Escherichia coli citrate carrier CitT: a member of a novel eubacterial transporter family related to the 2-oxoglutarate/malate translocator from spinach chloroplasts. *Journal of Bacteriology*, **1998**, 180, 4160-5	3.5	85
168	The periplasmic domain of the histidine autokinase CitA functions as a highly specific citrate receptor. *Molecular Microbiology*, **1999**, 33, 858-72	4.1	83
167	Genetic and biochemical analysis of the serine/threonine protein kinases PknA, PknB, PknG and PknL of Corynebacterium glutamicum: evidence for non-essentiality and for phosphorylation of OdhI and FtsZ by multiple kinases. *Molecular Microbiology*, **2009**, 74, 724-41	4.1	81
166	Formation of several bacterial c-type cytochromes requires a novel membrane-anchored protein that faces the periplasm. *Molecular Microbiology*, **1993**, 9, 729-40	4.1	78
165	Coupling of carbon monoxide oxidation to CO2 and H2 with the phosphorylation of ADP in acetate-grown Methanosarcina barkeri. *FEBS Journal*, **1986**, 159, 393-8		78
164	Global expression profiling and physiological characterization of Corynebacterium glutamicum grown in the presence of L-valine. *Applied and Environmental Microbiology*, **2003**, 69, 2521-32	4.8	77
163	The Bradyrhizobium japonicum cycM gene encodes a membrane-anchored homolog of mitochondrial cytochrome c. *Journal of Bacteriology*, **1991**, 173, 6766-72	3.5	75
162	Klebsiella pneumoniae genes for citrate lyase and citrate lyase ligase: localization, sequencing, and expression. *Molecular Microbiology*, **1994**, 14, 347-56	4.1	74
161	Metabolic engineering of Corynebacterium glutamicum for methanol metabolism. *Applied and Environmental Microbiology*, **2015**, 81, 2215-25	4.8	71
160	Metabolic engineering of Corynebacterium glutamicum for the production of itaconate. *Metabolic Engineering*, **2015**, 30, 156-165	9.7	67

159	Lrp of Corynebacterium glutamicum controls expression of the brnFE operon encoding the export system for L-methionine and branched-chain amino acids. *Journal of Biotechnology*, **2012**, 158, 231-41	3.7	67
158	Engineering of Corynebacterium glutamicum for minimized carbon loss during utilization of D-xylose containing substrates. *Journal of Biotechnology*, **2014**, 192 Pt A, 156-60	3.7	65
157	Proton translocation coupled to the oxidation of carbon monoxide to CO2 and H2 in Methanosarcina barkeri. *FEBS Journal*, **1989**, 179, 469-72		63
156	Identification of the phd gene cluster responsible for phenylpropanoid utilization in Corynebacterium glutamicum. *Applied Microbiology and Biotechnology*, **2016**, 100, 1871-1881	5.7	62
155	Two-component systems of Corynebacterium glutamicum: deletion analysis and involvement of the PhoS-PhoR system in the phosphate starvation response. *Journal of Bacteriology*, **2006**, 188, 724-32	3.5	62
154	Metabolic engineering of Gluconobacter oxydans for improved growth rate and growth yield on glucose by elimination of gluconate formation. *Applied and Environmental Microbiology*, **2010**, 76, 4369-76	4.8	60
153	Characterization of citrate utilization in Corynebacterium glutamicum by transcriptome and proteome analysis. *FEMS Microbiology Letters*, **2007**, 273, 109-19	2.9	58
152	Identification of AcnR, a TetR-type repressor of the aconitase gene acn in Corynebacterium glutamicum. *Journal of Biological Chemistry*, **2005**, 280, 585-95	5.4	58
151	Citrate utilization by Corynebacterium glutamicum is controlled by the CitAB two-component system through positive regulation of the citrate transport genes citH and tctCBA. *Journal of Bacteriology*, **2009**, 191, 3869-80	3.5	54
150	Role of cytochrome bd oxidase from Corynebacterium glutamicum in growth and lysine production. *Applied and Environmental Microbiology*, **2007**, 73, 861-8	4.8	52
149	A chromosomally encoded T7 RNA polymerase-dependent gene expression system for Corynebacterium glutamicum: construction and comparative evaluation at the single-cell level. *Microbial Biotechnology*, **2015**, 8, 253-65	6.3	51
148	Identification of genes and proteins necessary for catabolism of acyclic terpenes and leucine/isovalerate in Pseudomonas aeruginosa. *Applied and Environmental Microbiology*, **2006**, 72, 4819-28	4.8	51
147	Combined fluxomics and transcriptomics analysis of glucose catabolism via a partially cyclic pentose phosphate pathway in Gluconobacter oxydans 621H. *Applied and Environmental Microbiology*, **2013**, 79, 2336-48	4.8	49
146	Complex regulation of the phosphoenolpyruvate carboxykinase gene pck and characterization of its GntR-type regulator IolR as a repressor of myo-inositol utilization genes in Corynebacterium glutamicum. *Journal of Bacteriology*, **2013**, 195, 4283-96	3.5	49
145	Corynebacterium glutamicum as a host for synthesis and export of D-Amino Acids. *Journal of Bacteriology*, **2011**, 193, 1702-9	3.5	48
144	Genes for a second terminal oxidase in Bradyrhizobium japonicum. *Archives of Microbiology*, **1992**, 158, 335-43	3	48
143	Proton-motive-force-driven formation of CO from CO2 and H2 in methanogenic bacteria. *FEBS Journal*, **1987**, 168, 407-12		48
142	Synthetic biology platform of CoryneBrick vectors for gene expression in Corynebacterium glutamicum and its application to xylose utilization. *Applied Microbiology and Biotechnology*, **2014**, 98, 5991-6002	5.7	47

141	Glycerol as a substrate for aerobic succinate production in minimal medium with Corynebacterium glutamicum. *Microbial Biotechnology*, **2013**, 6, 189-95	6.3	47
140	The transcriptional activator ClgR controls transcription of genes involved in proteolysis and DNA repair in Corynebacterium glutamicum. *Molecular Microbiology*, **2005**, 57, 576-91	4.1	46
139	Increased NADPH availability in Escherichia coli: improvement of the product per glucose ratio in reductive whole-cell biotransformation. *Applied Microbiology and Biotechnology*, **2011**, 92, 929-37	5.7	45
138	RosR (Cg1324), a hydrogen peroxide-sensitive MarR-type transcriptional regulator of Corynebacterium glutamicum. *Journal of Biological Chemistry*, **2010**, 285, 29305-18	5.4	45
137	The nonphosphorylative Entner-Doudoroff pathway in the thermoacidophilic euryarchaeon Picrophilus torridus involves a novel 2-keto-3-deoxygluconate- specific aldolase. *Journal of Bacteriology*, **2010**, 192, 964-74	3.5	45
136	Transcriptional control of the succinate dehydrogenase operon sdhCAB of Corynebacterium glutamicum by the cAMP-dependent regulator GlxR and the LuxR-type regulator RamA. *Journal of Biotechnology*, **2009**, 143, 173-82	3.7	45
135	Evidence for a key role of cytochrome bo3 oxidase in respiratory energy metabolism of Gluconobacter oxydans. *Journal of Bacteriology*, **2013**, 195, 4210-20	3.5	43
134	C1 metabolism in Corynebacterium glutamicum: an endogenous pathway for oxidation of methanol to carbon dioxide. *Applied and Environmental Microbiology*, **2013**, 79, 6974-83	4.8	43
133	Corynebacterium glutamicum Chassis C1*: Building and Testing a Novel Platform Host for Synthetic Biology and Industrial Biotechnology. *ACS Synthetic Biology*, **2018**, 7, 132-144	5.7	43
132	Functional expression of plant-derived O-methyltransferase, flavanone 3-hydroxylase, and flavonol synthase in Corynebacterium glutamicum for production of pterostilbene, kaempferol, and quercetin. *Journal of Biotechnology*, **2017**, 258, 190-196	3.7	42
131	Citrate synthase in Corynebacterium glutamicum is encoded by two gltA transcripts which are controlled by RamA, RamB, and GlxR. *Journal of Biotechnology*, **2011**, 154, 140-8	3.7	42
130	Mutational analysis of the pentose phosphate and Entner-Doudoroff pathways in Gluconobacter oxydans reveals improved growth of a Δedd Δeda mutant on mannitol. *Applied and Environmental Microbiology*, **2012**, 78, 6975-86	4.8	42
129	In vitro binding of the response regulator CitB and of its carboxy-terminal domain to A + T-rich DNA target sequences in the control region of the divergent citC and citS operons of Klebsiella pneumoniae. *Journal of Molecular Biology*, **1997**, 269, 719-31	6.5	40
128	Population Heterogeneity in Corynebacterium glutamicum ATCC 13032 caused by prophage CGP3. *Journal of Bacteriology*, **2008**, 190, 5111-9	3.5	40
127	Influence of oxygen limitation, absence of the cytochrome bc(1) complex and low pH on global gene expression in Gluconobacter oxydans 621H using DNA microarray technology. *Journal of Biotechnology*, **2012**, 157, 359-72	3.7	39
126	Target genes and DNA-binding sites of the response regulator PhoR from Corynebacterium glutamicum. *Journal of Bacteriology*, **2007**, 189, 5002-11	3.5	39
125	Fed-Batch Process for Pyruvate Production by Recombinant Escherichia coli YYC202 Strain. *Engineering in Life Sciences*, **2003**, 3, 299-305	3.4	39
124	Identification of basic amino acid residues important for citrate binding by the periplasmic receptor domain of the sensor kinase CitA. *Biochemistry*, **2003**, 42, 5917-24	3.2	39

123	RamB, the transcriptional regulator of acetate metabolism in Corynebacterium glutamicum, is subject to regulation by RamA and RamB. *Journal of Bacteriology*, **2007**, 189, 1145-9	3.5	38
122	The sensor kinase CitA (DpiB) of Escherichia coli functions as a high-affinity citrate receptor. *Archives of Microbiology*, **2002**, 177, 313-21	3	38
121	The obligate respiratory supercomplex from Actinobacteria. *Biochimica Et Biophysica Acta - Bioenergetics*, **2016**, 1857, 1705-14	4.6	37
120	Physiology and global gene expression of a Corynebacterium glutamicum (1)F(O)-ATP synthase mutant devoid of oxidative phosphorylation. *Biochimica Et Biophysica Acta - Bioenergetics*, **2012**, 1817, 370-80	4.6	35
119	Control of heme homeostasis in Corynebacterium glutamicum by the two-component system HrrSA. *Journal of Bacteriology*, **2011**, 193, 1212-21	3.5	35
118	Biosynthesis of the prosthetic group of citrate lyase. *Biochemistry*, **2000**, 39, 9438-50	3.2	35
117	Metabolic profile of 1,5-diaminopentane producing Corynebacterium glutamicum under scale-down conditions: Blueprint for robustness to bioreactor inhomogeneities. *Biotechnology and Bioengineering*, **2017**, 114, 560-575	4.9	34
116	Role of the pentose phosphate pathway and the Entner-Doudoroff pathway in glucose metabolism of Gluconobacter oxydans 621H. *Applied Microbiology and Biotechnology*, **2013**, 97, 4315-23	5.7	34
115	Defective formation and/or utilization of carbon monoxide in H2/CO2 fermenting methanogens dependent on acetate as carbon source. *Archives of Microbiology*, **1985**, 143, 266-269	3	34
114	The pupylation machinery is involved in iron homeostasis by targeting the iron storage protein ferritin. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 4806-11	11.5	34
113	Reversal of oxidative pathways for the microbial production of chemicals and polymer building blocks. *Metabolic Engineering*, **2017**, 42, 33-42	9.7	33
112	Succinate production from CO grown microalgal biomass as carbon source using engineered Corynebacterium glutamicum through consolidated bioprocessing. *Scientific Reports*, **2014**, 4, 5819	4.9	33
111	Reductive whole-cell biotransformation with Corynebacterium glutamicum: improvement of NADPH generation from glucose by a cyclized pentose phosphate pathway using pfkA and gapA deletion mutants. *Applied Microbiology and Biotechnology*, **2013**, 97, 143-52	5.7	33
110	Conversion of Corynebacterium glutamicum from an aerobic respiring to an aerobic fermenting bacterium by inactivation of the respiratory chain. *Biochimica Et Biophysica Acta - Bioenergetics*, **2013**, 1827, 699-708	4.6	31
109	Anaerobic growth of Corynebacterium glutamicum via mixed-acid fermentation. *Applied and Environmental Microbiology*, **2015**, 81, 7496-508	4.8	30
108	Production of 2-methyl-1-butanol and 3-methyl-1-butanol in engineered Corynebacterium glutamicum. *Metabolic Engineering*, **2016**, 38, 436-445	9.7	30
107	Specific association of lectin LecB with the surface of Pseudomonas aeruginosa: role of outer membrane protein OprF. *PLoS ONE*, **2012**, 7, e46857	3.7	30
106	Target genes, consensus binding site, and role of phosphorylation for the response regulator MtrA of Corynebacterium glutamicum. *Journal of Bacteriology*, **2011**, 193, 1237-49	3.5	30

105	Catabolite repression of the citrate fermentation genes in Klebsiella pneumoniae: evidence for involvement of the cyclic AMP receptor protein. *Journal of Bacteriology*, **2001**, 183, 5248-56	3.5	30
104	The contest for precursors: channelling L-isoleucine synthesis in Corynebacterium glutamicum without byproduct formation. *Applied Microbiology and Biotechnology*, **2015**, 99, 791-800	5.7	29
103	Engineering yield and rate of reductive biotransformation in Escherichia coli by partial cyclization of the pentose phosphate pathway and PTS-independent glucose transport. *Applied Microbiology and Biotechnology*, **2012**, 93, 1459-67	5.7	29
102	The two-component signal transduction system CopRS of Corynebacterium glutamicum is required for adaptation to copper-excess stress. *PLoS ONE*, **2011**, 6, e22143	3.7	29
101	Complex expression control of the Corynebacterium glutamicum aconitase gene: identification of RamA as a third transcriptional regulator besides AcnR and RipA. *Journal of Biotechnology*, **2009**, 140, 92-8	3.7	29
100	Evidence for activator and repressor functions of the response regulator MtrA from Corynebacterium glutamicum. *FEMS Microbiology Letters*, **2006**, 264, 205-12	2.9	29
99	Bradyrhizobium japonicum cytochrome c550 is required for nitrate respiration but not for symbiotic nitrogen fixation. *Journal of Bacteriology*, **1995**, 177, 2214-7	3.5	28
98	Purification of two active fusion proteins of the Na(+)-dependent citrate carrier of Klebsiella pneumoniae. *FEBS Letters*, **1994**, 347, 37-41	3.8	28
97	Pupylated proteins in Corynebacterium glutamicum revealed by MudPIT analysis. *Proteomics*, **2014**, 14, 1531-42	4.8	27
96	Pyruvate Carboxylase Variants Enabling Improved Lysine Production from Glucose Identified by Biosensor-Based High-Throughput Fluorescence-Activated Cell Sorting Screening. *ACS Synthetic Biology*, **2019**, 8, 274-281	5.7	25
95	Production of 2-ketoisocaproate with Corynebacterium glutamicum strains devoid of plasmids and heterologous genes. *Microbial Biotechnology*, **2015**, 8, 351-60	6.3	25
94	Two-component signal transduction in Corynebacterium glutamicum and other corynebacteria: on the way towards stimuli and targets. *Applied Microbiology and Biotechnology*, **2012**, 94, 1131-50	5.7	25
93	A membrane-bound NAD(P)+-reducing hydrogenase provides reduced pyridine nucleotides during citrate fermentation by Klebsiella pneumoniae. *Journal of Bacteriology*, **1999**, 181, 241-5	3.5	25
92	Link between phosphate starvation and glycogen metabolism in Corynebacterium glutamicum, revealed by metabolomics. *Applied and Environmental Microbiology*, **2010**, 76, 6910-9	4.8	24
91	The FHA domain of OdhI interacts with the carboxyterminal 2-oxoglutarate dehydrogenase domain of OdhA in Corynebacterium glutamicum. *FEBS Letters*, **2010**, 584, 1463-8	3.8	24
90	Engineering of Corynebacterium glutamicum for growth and succinate production from levoglucosan, a pyrolytic sugar substrate. *FEMS Microbiology Letters*, **2015**, 362,	2.9	23
89	Deletion of the aconitase gene in Corynebacterium glutamicum causes strong selection pressure for secondary mutations inactivating citrate synthase. *Journal of Bacteriology*, **2011**, 193, 6864-73	3.5	23
88	Methylmalonyl-CoA decarboxylase from Propionigenium modestum--cloning and sequencing of the structural genes and purification of the enzyme complex. *FEBS Journal*, **1997**, 250, 590-9		23

87	Modulation of the central carbon metabolism of Corynebacterium glutamicum improves malonyl-CoA availability and increases plant polyphenol synthesis. *Biotechnology and Bioengineering*, **2019**, 116, 1380-1391	4.9	22
86	Interaction of 2-oxoglutarate dehydrogenase OdhA with its inhibitor OdhI in Corynebacterium glutamicum: Mutants and a model. *Journal of Biotechnology*, **2014**, 191, 99-105	3.7	22
85	Identification of a gene cluster in Klebsiella pneumoniae which includes citX, a gene required for biosynthesis of the citrate lyase prosthetic group. *Journal of Bacteriology*, **2002**, 184, 2439-46	3.5	22
84	The crystal structures of apo and cAMP-bound GlxR from Corynebacterium glutamicum reveal structural and dynamic changes upon cAMP binding in CRP/FNR family transcription factors. *PLoS ONE*, **2014**, 9, e113265	3.7	21
83	Biochemical characterisation of aconitase from Corynebacterium glutamicum. *Journal of Biotechnology*, **2011**, 154, 163-70	3.7	20
82	Secretory production of an FAD cofactor-containing cytosolic enzyme (sorbitol-xylitol oxidase from Streptomyces coelicolor) using the twin-arginine translocation (Tat) pathway of Corynebacterium glutamicum. *Microbial Biotechnology*, **2013**, 6, 202-6	6.3	19
81	Characterization of glycerate kinase (2-phosphoglycerate forming), a key enzyme of the nonphosphorylative Entner-Doudoroff pathway, from the thermoacidophilic euryarchaeon Picrophilus torridus. *FEMS Microbiology Letters*, **2006**, 259, 113-9	2.9	19
80	Rapid Electron Transfer within the III-IV Supercomplex in Corynebacterium glutamicum. *Scientific Reports*, **2016**, 6, 34098	4.9	18
79	L-Glutamine as a nitrogen source for Corynebacterium glutamicum: derepression of the AmtR regulon and implications for nitrogen sensing. *Microbiology (United Kingdom)*, **2010**, 156, 3180-3193	2.9	18
78	Charge reversal of the rodlike colloidal fd virus through surface chemical modification. *Langmuir*, **2010**, 26, 10593-9	4	18
77	Glycosylation is required for outer membrane localization of the lectin LecB in Pseudomonas aeruginosa. *Journal of Bacteriology*, **2011**, 193, 1107-13	3.5	18
76	The two-component system ChrSA is crucial for haem tolerance and interferes with HrrSA in haem-dependent gene regulation in Corynebacterium glutamicum. *Microbiology (United Kingdom)*, **2012**, 158, 3020-3031	2.9	18
75	Identification of triphosphoribosyl-dephospho-CoA as precursor of the citrate lyase prosthetic group. *FEBS Letters*, **2000**, 483, 165-8	3.8	18
74	The active species of "CO2" formed by carbon monoxide dehydrogenase from Peptostreptococcus productus. *Zeitschrift Fur Naturforschung - Section C Journal of Biosciences*, **1989**, 44, 392-6	1.7	18
73	Metabolic engineering of Gluconobacter oxydans 621H for increased biomass yield. *Applied Microbiology and Biotechnology*, **2017**, 101, 5453-5467	5.7	17
72	OdhI dephosphorylation kinetics during different glutamate production processes involving Corynebacterium glutamicum. *Applied Microbiology and Biotechnology*, **2010**, 87, 1867-74	5.7	17
71	Identification and Microbial Production of the Raspberry Phenol Salidroside that Is Active against Huntington's Disease. *Plant Physiology*, **2019**, 179, 969-985	6.6	17
70	Improved production of adipate with Escherichia coli by reversal of β-oxidation. *Applied Microbiology and Biotechnology*, **2017**, 101, 2371-2382	5.7	16

69	High precision genome sequencing of engineered Gluconobacter oxydans 621H by combining long nanopore and short accurate Illumina reads. *Journal of Biotechnology*, **2017**, 258, 197-205	3.7	15
68	Corynebacterium glutamicum harbours a molybdenum cofactor-dependent formate dehydrogenase which alleviates growth inhibition in the presence of formate. *Microbiology (United Kingdom)*, **2012**, 158, 2428-2439	2.9	15
67	Development of a single-cell GlxR-based cAMP biosensor for Corynebacterium glutamicum. *Journal of Biotechnology*, **2017**, 258, 33-40	3.7	14
66	Advances in metabolic engineering of Corynebacterium glutamicum to produce high-value active ingredients for food, feed, human health, and well-being. *Essays in Biochemistry*, **2021**, 65, 197-212	7.6	14
65	Acyl-CoA sensing by FasR to adjust fatty acid synthesis in Corynebacterium glutamicum. *Journal of Biotechnology*, **2014**, 192 Pt A, 96-101	3.7	13
64	Phosphatase activity of the histidine kinases ensures pathway specificity of the ChrSA and HrrSA two-component systems in Corynebacterium glutamicum. *Molecular Microbiology*, **2014**, 92, 1326-42	4.1	13
63	Succinic Acid **2014**, 435-472		13
62	BacHBerry: BACterial Hosts for production of Bioactive phenolics from bERRY fruits. *Phytochemistry Reviews*, **2018**, 17, 291-326	7.7	12
61	Crystal structure of the caseinolytic protease gene regulator, a transcriptional activator in actinomycetes. *Journal of Biological Chemistry*, **2009**, 284, 5208-16	5.4	12
60	The copper-deprivation stimulon of comprises proteins for biogenesis of the actinobacterial cytochrome - supercomplex. *Journal of Biological Chemistry*, **2018**, 293, 15628-15640	5.4	12
59	Identification of the cAMP phosphodiesterase CpdA as novel key player in cAMP-dependent regulation in Corynebacterium glutamicum. *Molecular Microbiology*, **2017**, 103, 534-552	4.1	11
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