Michael Bott

List of Publications by Year in Descending Order

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

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

#	Paper	IF	Citations
212	Production of l-arabinonic acid from l-arabinose by the acetic acid bacterium Gluconobacter oxydans. <i>Bioresource Technology Reports</i> , 2022 , 17, 100965	4.1	O
211	A Tetratricopeptide Repeat Scaffold Couples Signal Detection to Odhl Phosphorylation in Metabolic Control by the Protein Kinase PknG. <i>MBio</i> , 2021 , 12, e0171721	7.8	1
210	On the way toward regulatable expression systems in acetic acid bacteria: target gene expression and use cases. <i>Applied Microbiology and Biotechnology</i> , 2021 , 105, 3423-3456	5.7	3
209	FNR-Type Regulator GoxR of the Obligatorily Aerobic Acetic Acid Bacterium Affects Expression of Genes Involved in Respiration and Redox Metabolism. <i>Applied and Environmental Microbiology</i> , 2021 , 87,	4.8	1
208	An energetic profile of Corynebacterium glutamicum underpinned by measured biomass yield on ATP. <i>Metabolic Engineering</i> , 2021 , 65, 66-78	9.7	3
207	Advances in metabolic engineering of Corynebacterium glutamicum to produce high-value active ingredients for food, feed, human health, and well-being. <i>Essays in Biochemistry</i> , 2021 , 65, 197-212	7.6	14
206	Highly tunable TetR-dependent target gene expression in the acetic acid bacterium Gluconobacter oxydans. <i>Applied Microbiology and Biotechnology</i> , 2021 , 105, 6835-6852	5.7	1
205	Metabolic engineering of Pseudomonas putida for production of the natural sweetener 5-ketofructose from fructose or sucrose by periplasmic oxidation with a heterologous fructose dehydrogenase. <i>Microbial Biotechnology</i> , 2021 , 14, 2592-2604	6.3	1
204	Metabolic engineering of Corynebacterium glutamicum for production of scyllo-inositol, a drug candidate against Alzheimerß disease. <i>Metabolic Engineering</i> , 2021 , 67, 173-185	9.7	1
203	A Sodium-Translocating Module Linking Succinate Production to Formation of Membrane Potential in Prevotella bryantii. <i>Applied and Environmental Microbiology</i> , 2021 , 87, e0121121	4.8	3
202	The respiratory supercomplex from C.ட்டுlutamicum Structure, 2021 ,	5.2	1
201	HrrSA orchestrates a systemic response to heme and determines prioritization of terminal cytochrome oxidase expression. <i>Nucleic Acids Research</i> , 2020 , 48, 6547-6562	20.1	1
200	Novel plasmid-free Gluconobacter oxydans strains for production of the natural sweetener 5-ketofructose. <i>Microbial Cell Factories</i> , 2020 , 19, 54	6.4	5
199	Molecular Basis of Growth Inhibition by Acetate of an Adenylate Cyclase-Deficient Mutant of. <i>Frontiers in Microbiology</i> , 2020 , 11, 87	5.7	4
198	The Iron Deficiency Response of Corynebacterium glutamicum and a Link to Thiamine Biosynthesis. <i>Applied and Environmental Microbiology</i> , 2020 , 86,	4.8	5
197	NADPH biosensor-based identification of an alcohol dehydrogenase variant with improved catalytic properties caused by a single charge reversal at the protein surface. <i>AMB Express</i> , 2020 , 10, 14	4.1	2
196	The Importance of Biotechnology for the Bioeconomy 2020 , 105-128		1

(2018-2020)

195	A tunable L-arabinose-inducible expression plasmid for the acetic acid bacterium Gluconobacter oxydans. <i>Applied Microbiology and Biotechnology</i> , 2020 , 104, 9267-9282	5.7	8
194	Improved pEKEx2-derived expression vectors for tightly controlled production of recombinant proteins in Corynebacterium glutamicum. <i>Plasmid</i> , 2020 , 112, 102540	3.3	11
193	Regulation of EAminobutyrate (GABA) Utilization in by the PucR-Type Transcriptional Regulator GabR and by Alternative Nitrogen and Carbon Sources. <i>Frontiers in Microbiology</i> , 2020 , 11, 544045	5.7	5
192	Relevance of NADH Dehydrogenase and Alternative Two-Enzyme Systems for Growth of With Glucose, Lactate, and Acetate. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 621213	5.8	2
191	Library Selection with a Randomized Repertoire of (PBarrel Enzymes Results in Unexpected Induction of Gene Expression. <i>Biochemistry</i> , 2019 , 58, 4207-4217	3.2	
190	Modulation of the central carbon metabolism of Corynebacterium glutamicum improves malonyl-CoA availability and increases plant polyphenol synthesis. <i>Biotechnology and Bioengineering</i> , 2019 , 116, 1380-1391	4.9	22
189	Pyruvate Carboxylase Variants Enabling Improved Lysine Production from Glucose Identified by Biosensor-Based High-Throughput Fluorescence-Activated Cell Sorting Screening. <i>ACS Synthetic Biology</i> , 2019 , 8, 274-281	5.7	25
188	Identification of Surf1 as an assembly factor of the cytochrome bc-aa supercomplex of Actinobacteria. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2019 , 1860, 148033	4.6	7
187	Pyruvate carboxylase from Corynebacterium glutamicum: purification and characterization. <i>Applied Microbiology and Biotechnology</i> , 2019 , 103, 6571-6580	5.7	3
186	The conserved actinobacterial transcriptional regulator FtsR controls expression of ftsZ and further target genes and influences growth and cell division in Corynebacterium glutamicum. <i>BMC Microbiology</i> , 2019 , 19, 179	4.5	6
185	Identification and Microbial Production of the Raspberry Phenol Salidroside that Is Active against Huntington Disease. <i>Plant Physiology</i> , 2019 , 179, 969-985	6.6	17
184	NADPH-related processes studied with a SoxR-based biosensor in Escherichia coli. <i>MicrobiologyOpen</i> , 2018 , 8, e785	3.4	3
183	AftD functions as an 🛘 -🌣 arabinofuranosyltransferase involved in the biosynthesis of the mycobacterial cell wall core. <i>Cell Surface</i> , 2018 , 1, 2-14	4.8	10
182	BacHBerry: BACterial Hosts for production of Bioactive phenolics from bERRY fruits. <i>Phytochemistry Reviews</i> , 2018 , 17, 291-326	7.7	12
181	RNAseq analysis of Eproteobacterium Gluconobacter oxydans 621H. <i>BMC Genomics</i> , 2018 , 19, 24	4.5	9
180	Corynebacterium glutamicum Chassis C1*: Building and Testing a Novel Platform Host for Synthetic Biology and Industrial Biotechnology. <i>ACS Synthetic Biology</i> , 2018 , 7, 132-144	5.7	43
179	Structure-Based Design of Versatile Biosensors for Small Molecules Based on the PAS Domain of a Thermophilic Histidine Kinase. <i>ACS Synthetic Biology</i> , 2018 , 7, 2888-2897	5.7	2
178	Global mRNA decay and 23S rRNA fragmentation in Gluconobacter oxydans 621H. <i>BMC Genomics</i> , 2018 , 19, 753	4.5	2

177	The copper-deprivation stimulon of comprises proteins for biogenesis of the actinobacterial cytochrome - supercomplex. <i>Journal of Biological Chemistry</i> , 2018 , 293, 15628-15640	5.4	12
176	Functional expression of plant-derived O-methyltransferase, flavanone 3-hydroxylase, and flavonol synthase in Corynebacterium glutamicum for production of pterostilbene, kaempferol, and quercetin. <i>Journal of Biotechnology</i> , 2017 , 258, 190-196	3.7	42
175	Metabolic engineering of Gluconobacter oxydans 621H for increased biomass yield. <i>Applied Microbiology and Biotechnology</i> , 2017 , 101, 5453-5467	5.7	17
174	Die Bedeutung der Biotechnologie f∃die Biolonomie 2017 , 105-128		1
173	High precision genome sequencing of engineered Gluconobacter oxydans 621H by combining long nanopore and short accurate Illumina reads. <i>Journal of Biotechnology</i> , 2017 , 258, 197-205	3.7	15
172	Reversal of Ebxidative pathways for the microbial production of chemicals and polymer building blocks. <i>Metabolic Engineering</i> , 2017 , 42, 33-42	9.7	33
171	Improved production of adipate with Escherichia coli by reversal of Ebxidation. <i>Applied Microbiology and Biotechnology</i> , 2017 , 101, 2371-2382	5.7	16
170	Novel Technologies for Optimal Strain Breeding. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2017 , 159, 227-254	1.7	2
169	The three-component system EsrISR regulates a cell envelope stress response in Corynebacterium glutamicum. <i>Molecular Microbiology</i> , 2017 , 106, 719-741	4.1	10
168	Development of a single-cell GlxR-based cAMP biosensor for Corynebacterium glutamicum. <i>Journal of Biotechnology</i> , 2017 , 258, 33-40	3.7	14
167	Identification of the cAMP phosphodiesterase CpdA as novel key player in cAMP-dependent regulation in Corynebacterium glutamicum. <i>Molecular Microbiology</i> , 2017 , 103, 534-552	4.1	11
166	Mutations in MurE, the essential UDP-N-acetylmuramoylalanyl-D-glutamate 2,6-diaminopimelate ligase of Corynebacterium glutamicum: effect on L-lysine formation and analysis of systemic consequences. <i>Biotechnology Letters</i> , 2017 , 39, 283-288	3	7
165	Metabolic profile of 1,5-diaminopentane producing Corynebacterium glutamicum under scale-down conditions: Blueprint for robustness to bioreactor inhomogeneities. <i>Biotechnology and Bioengineering</i> , 2017 , 114, 560-575	4.9	34
164	The obligate respiratory supercomplex from Actinobacteria. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2016 , 1857, 1705-14	4.6	37
163	Production of 2-methyl-1-butanol and 3-methyl-1-butanol in engineered Corynebacterium glutamicum. <i>Metabolic Engineering</i> , 2016 , 38, 436-445	9.7	30
162	Rapid Electron Transfer within the III-IV Supercomplex in Corynebacterium glutamicum. <i>Scientific Reports</i> , 2016 , 6, 34098	4.9	18
161	Chalcone-based Selective Inhibitors of a C4 Plant Key Enzyme as Novel Potential Herbicides. <i>Scientific Reports</i> , 2016 , 6, 27333	4.9	6
160	Central Carbon Metabolism and Respiration in Gluconobacter oxydans 2016 , 235-253		3

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159	Construction of a Corynebacterium glutamicum platform strain for the production of stilbenes and (2S)-flavanones. <i>Metabolic Engineering</i> , 2016 , 38, 47-55	9.7	116
158	Identification of the phd gene cluster responsible for phenylpropanoid utilization in Corynebacterium glutamicum. <i>Applied Microbiology and Biotechnology</i> , 2016 , 100, 1871-1881	5.7	62
157	The small 6C RNA of Corynebacterium glutamicum is involved in the SOS response. <i>RNA Biology</i> , 2016 , 13, 848-60	4.8	4
156	The pupylation machinery is involved in iron homeostasis by targeting the iron storage protein ferritin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 480	6-1115	34
155	Recombineering and biosensor-guided FACS screening for strain development of Corynebacterium glutamicum. <i>New Biotechnology</i> , 2016 , 33, S66	6.4	1
154	Novel screening methodsbiosensors. <i>Current Opinion in Biotechnology</i> , 2015 , 35, 30-6	11.4	110
153	Metabolic engineering of Corynebacterium glutamicum for methanol metabolism. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 2215-25	4.8	71
152	Chassis organism from Corynebacterium glutamicuma top-down approach to identify and delete irrelevant gene clusters. <i>Biotechnology Journal</i> , 2015 , 10, 290-301	5.6	87
151	Metabolic engineering of Corynebacterium glutamicum for the production of itaconate. <i>Metabolic Engineering</i> , 2015 , 30, 156-165	9.7	67
150	A giant market and a powerful metabolism: L-lysine provided by Corynebacterium glutamicum. <i>Applied Microbiology and Biotechnology</i> , 2015 , 99, 3387-94	5.7	142
149	The contest for precursors: channelling L-isoleucine synthesis in Corynebacterium glutamicum without byproduct formation. <i>Applied Microbiology and Biotechnology</i> , 2015 , 99, 791-800	5.7	29
148	Production of 2-ketoisocaproate with Corynebacterium glutamicum strains devoid of plasmids and heterologous genes. <i>Microbial Biotechnology</i> , 2015 , 8, 351-60	6.3	25
147	Engineering of Corynebacterium glutamicum for growth and succinate production from levoglucosan, a pyrolytic sugar substrate. <i>FEMS Microbiology Letters</i> , 2015 , 362,	2.9	23
146	Single-Domain Peptidyl-Prolyl cis/trans Isomerase FkpA from Corynebacterium glutamicum Improves the Biomass Yield at Increased Growth Temperatures. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 7839-50	4.8	1
145	Anaerobic growth of Corynebacterium glutamicum via mixed-acid fermentation. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 7496-508	4.8	30
144	SdhE-dependent formation of a functional Acetobacter pasteurianus succinate dehydrogenase in Gluconobacter oxydansa first step toward a complete tricarboxylic acid cycle. <i>Applied Microbiology and Biotechnology</i> , 2015 , 99, 9147-60	5.7	7
143	(13)C Tracers for Glucose Degrading Pathway Discrimination in Gluconobacter oxydans 621H. <i>Metabolites</i> , 2015 , 5, 455-74	5.6	
142	Need for speed - finding productive mutations using transcription factor-based biosensors, fluorescence-activated cell sorting and recombineering. <i>Microbial Biotechnology</i> , 2015 , 8, 8-10	6.3	6

141	Pupylierung lein bakterielles Pendant zur Ubiquitinylierung. <i>BioSpektrum</i> , 2015 , 21, 158-160	0.1	
140	A chromosomally encoded T7 RNA polymerase-dependent gene expression system for Corynebacterium glutamicum: construction and comparative evaluation at the single-cell level. <i>Microbial Biotechnology</i> , 2015 , 8, 253-65	6.3	51
139	Genetically-encoded Biosensors for Strain Development and Single Cell Analysis of Corynebacterium glutamicum 2015 , 179-196		2
138	The Genus Corynebacterium 2015 , 487-504		
137	Succinate production from COEgrown microalgal biomass as carbon source using engineered Corynebacterium glutamicum through consolidated bioprocessing. <i>Scientific Reports</i> , 2014 , 4, 5819	4.9	33
136	Role of flavohaemoprotein Hmp and nitrate reductase NarGHJI of Corynebacterium glutamicum for coping with nitrite and nitrosative stress. <i>FEMS Microbiology Letters</i> , 2014 , 350, 239-48	2.9	9
135	Pushing product formation to its limit: metabolic engineering of Corynebacterium glutamicum for L-leucine overproduction. <i>Metabolic Engineering</i> , 2014 , 22, 40-52	9.7	95
134	Acyl-CoA sensing by FasR to adjust fatty acid synthesis in Corynebacterium glutamicum. <i>Journal of Biotechnology</i> , 2014 , 192 Pt A, 96-101	3.7	13
133	Engineering of Corynebacterium glutamicum for minimized carbon loss during utilization of D-xylose containing substrates. <i>Journal of Biotechnology</i> , 2014 , 192 Pt A, 156-60	3.7	65
132	Phosphatase activity of the histidine kinases ensures pathway specificity of the ChrSA and HrrSA two-component systems in Corynebacterium glutamicum. <i>Molecular Microbiology</i> , 2014 , 92, 1326-42	4.1	13
131	Combinatorial optimization of synthetic operons for the microbial production of monolignols in Escherichia coli. <i>New Biotechnology</i> , 2014 , 31, S158	6.4	
130	SoxR as a single-cell biosensor for NADPH-consuming enzymes in Escherichia coli. <i>ACS Synthetic Biology</i> , 2014 , 3, 41-7	5.7	99
129	Synthetic biology platform of CoryneBrick vectors for gene expression in Corynebacterium glutamicum and its application to xylose utilization. <i>Applied Microbiology and Biotechnology</i> , 2014 , 98, 5991-6002	5.7	47
128	NADPH-dependent reductive biotransformation with Escherichia coli and its pfkA deletion mutant: influence on global gene expression and role of oxygen supply. <i>Biotechnology and Bioengineering</i> , 2014 , 111, 2067-75	4.9	3
127	Succinic Acid 2014 , 435-472		13
126	Interaction of 2-oxoglutarate dehydrogenase OdhA with its inhibitor OdhI in Corynebacterium glutamicum: Mutants and a model. <i>Journal of Biotechnology</i> , 2014 , 191, 99-105	3.7	22
125	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. <i>PLoS ONE</i> , 2014 , 9, e113265	3.7	21
124	Pupylated proteins in Corynebacterium glutamicum revealed by MudPIT analysis. <i>Proteomics</i> , 2014 , 14, 1531-42	4.8	27

Subtilase SprP exerts pleiotropic effects in Pseudomonas aeruginosa. MicrobiologyOpen, 2014, 3, 89-1033.4 123 11 Taking control over control: use of product sensing in single cells to remove flux control at key 122 5.7 105 enzymes in biosynthesis pathways. ACS Synthetic Biology, 2014, 3, 21-9 Glycerol as a substrate for aerobic succinate production in minimal medium with Corynebacterium 121 6.3 47 glutamicum. Microbial Biotechnology, 2013, 6, 189-95 Reductive whole-cell biotransformation with Corynebacterium glutamicum: improvement of NADPH generation from glucose by a cyclized pentose phosphate pathway using pfkA and gapA 120 5.7 33 deletion mutants. Applied Microbiology and Biotechnology, 2013, 97, 143-52 Combined fluxomics and transcriptomics analysis of glucose catabolism via a partially cyclic pentose phosphate pathway in Gluconobacter oxydans 621H. Applied and Environmental 119 4.8 49 Microbiology, 2013, 79, 2336-48 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 118 4.8 110 Microbiology, **2013**, 79, 6006-15 Evidence for a key role of cytochrome bo3 oxidase in respiratory energy metabolism of 117 3.5 43 Gluconobacter oxydans. Journal of Bacteriology, 2013, 195, 4210-20 Metabolic engineering of microorganisms for the synthesis of plant natural products. Journal of 116 3.7 162 Biotechnology, **2013**, 163, 166-78 Bio-based production of organic acids with Corynebacterium glutamicum. Microbial Biotechnology, 6.3 115 135 2013, 6, 87-102 Toward biotechnological production of adipic acid and precursors from biorenewables. Journal of 183 114 3.7 Biotechnology, 2013, 167, 75-84 TCA Cycle and Glyoxylate Shunt of Corynebacterium glutamicum. Microbiology Monographs, 2013, 281-3638 113 4 Conversion of Corynebacterium glutamicum from an aerobic respiring to an aerobic fermenting bacterium by inactivation of the respiratory chain. Biochimica Et Biophysica Acta - Bioenergetics, 112 4.6 2013, 1827, 699-708 Role of the pentose phosphate pathway and the Entner-Doudoroff pathway in glucose metabolism 111 5.7 34 of Gluconobacter oxydans 621H. Applied Microbiology and Biotechnology, 2013, 97, 4315-23 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 110 3.5 49 glutamicum. Journal of Bacteriology, 2013, 195, 4283-96 Recombineering in Corynebacterium glutamicum combined with optical nanosensors: a general 109 20.1 120 strategy for fast producer strain generation. Nucleic Acids Research, 2013, 41, 6360-9 Crystal and solution studies reveal that the transcriptional regulator AcnR of Corynebacterium 108 glutamicum is regulated by citrate-Mg2+ binding to a non-canonical pocket. Journal of Biological 8 5.4 Chemistry, **2013**, 288, 15800-12 Secretory production of an FAD cofactor-containing cytosolic enzyme (sorbitol-xylitol oxidase from Streptomyces coelicolor) using the twin-arginine translocation (Tat) pathway of Corynebacterium 107 6.3 19 glutamicum. Microbial Biotechnology, 2013, 6, 202-6 Proline addition increases the efficiency of l-lysine production byCorynebacterium glutamicum. 106 3.4 Engineering in Life Sciences, 2013, 13, 393-398

105	C1 metabolism in Corynebacterium glutamicum: an endogenous pathway for oxidation of methanol to carbon dioxide. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 6974-83	4.8	43
104	Visualization of imbalances in sulfur assimilation and synthesis of sulfur-containing amino acids at the single-cell level. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 6730-6	4.8	8
103	Efficient aerobic succinate production from glucose in minimal medium with Corynebacterium glutamicum. <i>Microbial Biotechnology</i> , 2012 , 5, 116-28	6.3	104
102	Engineering yield and rate of reductive biotransformation in Escherichia coli by partial cyclization of the pentose phosphate pathway and PTS-independent glucose transport. <i>Applied Microbiology and Biotechnology</i> , 2012 , 93, 1459-67	5.7	29
101	A high-throughput approach to identify genomic variants of bacterial metabolite producers at the single-cell level. <i>Genome Biology</i> , 2012 , 13, R40	18.3	185
100	Physiology and global gene expression of a Corynebacterium glutamicum E (1)F(O)-ATP synthase mutant devoid of oxidative phosphorylation. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2012 , 1817, 370-80	4.6	35
99	Lrp of Corynebacterium glutamicum controls expression of the brnFE operon encoding the export system for L-methionine and branched-chain amino acids. <i>Journal of Biotechnology</i> , 2012 , 158, 231-41	3.7	67
98	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. <i>Journal of Biotechnology</i> , 2012 , 157, 359-72	3.7	39
97	The development and application of a single-cell biosensor for the detection of l-methionine and branched-chain amino acids. <i>Metabolic Engineering</i> , 2012 , 14, 449-57	9.7	170
96	Corynebacterium glutamicum harbours a molybdenum cofactor-dependent formate dehydrogenase which alleviates growth inhibition in the presence of formate. <i>Microbiology (United Kingdom)</i> , 2012 , 158, 2428-2439	2.9	15
95	Specific association of lectin LecB with the surface of Pseudomonas aeruginosa: role of outer membrane protein OprF. <i>PLoS ONE</i> , 2012 , 7, e46857	3.7	30
94	Toward homosuccinate fermentation: metabolic engineering of Corynebacterium glutamicum for anaerobic production of succinate from glucose and formate. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 3325-37	4.8	170
93	Improved L-lysine production with Corynebacterium glutamicum and systemic insight into citrate synthase flux and activity. <i>Biotechnology and Bioengineering</i> , 2012 , 109, 2070-81	4.9	107
92	Expressionsoptimierung in Mikroorganismen. <i>BioSpektrum</i> , 2012 , 18, 449-451	0.1	
91	Two-component signal transduction in Corynebacterium glutamicum and other corynebacteria: on the way towards stimuli and targets. <i>Applied Microbiology and Biotechnology</i> , 2012 , 94, 1131-50	5.7	25
90	The two-component system ChrSA is crucial for haem tolerance and interferes with HrrSA in haem-dependent gene regulation in Corynebacterium glutamicum. <i>Microbiology (United Kingdom)</i> , 2012 , 158, 3020-3031	2.9	18
89	Mutational analysis of the pentose phosphate and Entner-Doudoroff pathways in Gluconobacter oxydans reveals improved growth of a Ødd Øda mutant on mannitol. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 6975-86	4.8	42
88	The two-component signal transduction system CopRS of Corynebacterium glutamicum is required for adaptation to copper-excess stress. <i>PLoS ONE</i> , 2011 , 6, e22143	3.7	29

(2009-2011)

87	Increased NADPH availability in Escherichia coli: improvement of the product per glucose ratio in reductive whole-cell biotransformation. <i>Applied Microbiology and Biotechnology</i> , 2011 , 92, 929-37	5.7	45	
86	Corynebacterium glutamicum as a host for synthesis and export of D-Amino Acids. <i>Journal of Bacteriology</i> , 2011 , 193, 1702-9	3.5	48	
85	Biochemical characterisation of aconitase from Corynebacterium glutamicum. <i>Journal of Biotechnology</i> , 2011 , 154, 163-70	3.7	20	
84	Citrate synthase in Corynebacterium glutamicum is encoded by two gltA transcripts which are controlled by RamA, RamB, and GlxR. <i>Journal of Biotechnology</i> , 2011 , 154, 140-8	3.7	42	
83	Glycosylation is required for outer membrane localization of the lectin LecB in Pseudomonas aeruginosa. <i>Journal of Bacteriology</i> , 2011 , 193, 1107-13	3.5	18	
82	Control of heme homeostasis in Corynebacterium glutamicum by the two-component system HrrSA. <i>Journal of Bacteriology</i> , 2011 , 193, 1212-21	3.5	35	
81	Target genes, consensus binding site, and role of phosphorylation for the response regulator MtrA of Corynebacterium glutamicum. <i>Journal of Bacteriology</i> , 2011 , 193, 1237-49	3.5	30	
80	Deletion of the aconitase gene in Corynebacterium glutamicum causes strong selection pressure for secondary mutations inactivating citrate synthase. <i>Journal of Bacteriology</i> , 2011 , 193, 6864-73	3.5	23	
79	Link between phosphate starvation and glycogen metabolism in Corynebacterium glutamicum, revealed by metabolomics. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 6910-9	4.8	24	
78	RosR (Cg1324), a hydrogen peroxide-sensitive MarR-type transcriptional regulator of Corynebacterium glutamicum. <i>Journal of Biological Chemistry</i> , 2010 , 285, 29305-18	5.4	45	
77	The nonphosphorylative Entner-Doudoroff pathway in the thermoacidophilic euryarchaeon Picrophilus torridus involves a novel 2-keto-3-deoxygluconate- specific aldolase. <i>Journal of Bacteriology</i> , 2010 , 192, 964-74	3.5	45	
76	L-Glutamine as a nitrogen source for Corynebacterium glutamicum: derepression of the AmtR regulon and implications for nitrogen sensing. <i>Microbiology (United Kingdom)</i> , 2010 , 156, 3180-3193	2.9	18	
75	Metabolic engineering of Gluconobacter oxydans for improved growth rate and growth yield on glucose by elimination of gluconate formation. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 4369-	Æ ⁸	60	
74	Charge reversal of the rodlike colloidal fd virus through surface chemical modification. <i>Langmuir</i> , 2010 , 26, 10593-9	4	18	
73	OdhI dephosphorylation kinetics during different glutamate production processes involving Corynebacterium glutamicum. <i>Applied Microbiology and Biotechnology</i> , 2010 , 87, 1867-74	5.7	17	
72	The FHA domain of OdhI interacts with the carboxyterminal 2-oxoglutarate dehydrogenase domain of OdhA in Corynebacterium glutamicum. <i>FEBS Letters</i> , 2010 , 584, 1463-8	3.8	24	
71	The Corynebacterium glutamicum aconitase repressor: scratching around for crystals. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1074-7		3	
70	Signal Transduction by Serine/Threonine Protein Kinases in Bacteria 2009 , 427-447			

69	Crystal structure of the caseinolytic protease gene regulator, a transcriptional activator in actinomycetes. <i>Journal of Biological Chemistry</i> , 2009 , 284, 5208-16	5.4	12
68	Citrate utilization by Corynebacterium glutamicum is controlled by the CitAB two-component system through positive regulation of the citrate transport genes citH and tctCBA. <i>Journal of Bacteriology</i> , 2009 , 191, 3869-80	3.5	54
67	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. <i>Molecular Microbiology</i> , 2009 , 74, 724-41	4.1	81
66	Complex expression control of the Corynebacterium glutamicum aconitase gene: identification of RamA as a third transcriptional regulator besides AcnR and RipA. <i>Journal of Biotechnology</i> , 2009 , 140, 92-8	3.7	29
65	Transcriptional control of the succinate dehydrogenase operon sdhCAB of Corynebacterium glutamicum by the cAMP-dependent regulator GlxR and the LuxR-type regulator RamA. <i>Journal of Biotechnology</i> , 2009 , 143, 173-82	3.7	45
64	A ligand-induced switch in the periplasmic domain of sensor histidine kinase CitA. <i>Journal of Molecular Biology</i> , 2008 , 377, 512-23	6.5	99
63	Population Heterogeneity in Corynebacterium glutamicum ATCC 13032 caused by prophage CGP3. <i>Journal of Bacteriology</i> , 2008 , 190, 5111-9	3.5	40
62	Co-ordinated regulation of gluconate catabolism and glucose uptake in Corynebacterium glutamicum by two functionally equivalent transcriptional regulators, GntR1 and GntR2. <i>Molecular Microbiology</i> , 2008 , 67, 305-22	4.1	123
61	Characterization of citrate utilization in Corynebacterium glutamicum by transcriptome and proteome analysis. <i>FEMS Microbiology Letters</i> , 2007 , 273, 109-19	2.9	58
60	Expression of the Escherichia coli pntAB genes encoding a membrane-bound transhydrogenase in Corynebacterium glutamicum improves L-lysine formation. <i>Applied Microbiology and Biotechnology</i> , 2007 , 75, 47-53	5.7	110
59	Glutamate production by Corynebacterium glutamicum: dependence on the oxoglutarate dehydrogenase inhibitor protein Odhl and protein kinase PknG. <i>Applied Microbiology and Biotechnology</i> , 2007 , 76, 691-700	5.7	98
58	Dedication to Professor Dr. Hermann Sahm on the occasion of his 65th birthday. <i>Applied Microbiology and Biotechnology</i> , 2007 , 76, 483-4	5.7	
57	Target genes and DNA-binding sites of the response regulator PhoR from Corynebacterium glutamicum. <i>Journal of Bacteriology</i> , 2007 , 189, 5002-11	3.5	39
56	Role of cytochrome bd oxidase from Corynebacterium glutamicum in growth and lysine production. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 861-8	4.8	52
55	RamB, the transcriptional regulator of acetate metabolism in Corynebacterium glutamicum, is subject to regulation by RamA and RamB. <i>Journal of Bacteriology</i> , 2007 , 189, 1145-9	3.5	38
54	Offering surprises: TCA cycle regulation in Corynebacterium glutamicum. <i>Trends in Microbiology</i> , 2007 , 15, 417-25	12.4	94
53	Komplexe Regulation des Citrat-Zyklus in Corynebacterium glutamicum. <i>Chemie-Ingenieur-Technik</i> , 2006 , 78, 1429-1429	0.8	
52	Two-component systems of Corynebacterium glutamicum: deletion analysis and involvement of the PhoS-PhoR system in the phosphate starvation response. <i>Journal of Bacteriology</i> , 2006 , 188, 724-32	3.5	62

51	Identification of RamA, a novel LuxR-type transcriptional regulator of genes involved in acetate metabolism of Corynebacterium glutamicum. <i>Journal of Bacteriology</i> , 2006 , 188, 2554-67	3.5	97
50	The DtxR regulon of Corynebacterium glutamicum. <i>Journal of Bacteriology</i> , 2006 , 188, 2907-18	3.5	89
49	Identification of genes and proteins necessary for catabolism of acyclic terpenes and leucine/isovalerate in Pseudomonas aeruginosa. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 4819	9 -2 8	51
48	Corynebacterial protein kinase G controls 2-oxoglutarate dehydrogenase activity via the phosphorylation status of the Odhl protein. <i>Journal of Biological Chemistry</i> , 2006 , 281, 12300-7	5.4	168
47	Emerging Corynebacterium glutamicum systems biology. <i>Journal of Biotechnology</i> , 2006 , 124, 74-92	3.7	93
46	Metabolic engineering of Escherichia coli and Corynebacterium glutamicum for biotechnological production of organic acids and amino acids. <i>Current Opinion in Microbiology</i> , 2006 , 9, 268-74	7.9	224
45	Characterization of glycerate kinase (2-phosphoglycerate forming), a key enzyme of the nonphosphorylative Entner-Doudoroff pathway, from the thermoacidophilic euryarchaeon Picrophilus torridus. <i>FEMS Microbiology Letters</i> , 2006 , 259, 113-9	2.9	19
44	Evidence for activator and repressor functions of the response regulator MtrA from Corynebacterium glutamicum. <i>FEMS Microbiology Letters</i> , 2006 , 264, 205-12	2.9	29
43	The transcriptional activator ClgR controls transcription of genes involved in proteolysis and DNA repair in Corynebacterium glutamicum. <i>Molecular Microbiology</i> , 2005 , 57, 576-91	4.1	46
42	The AraC-type regulator RipA represses aconitase and other iron proteins from Corynebacterium under iron limitation and is itself repressed by DtxR. <i>Journal of Biological Chemistry</i> , 2005 , 280, 40500-8	5.4	90
41	Identification of AcnR, a TetR-type repressor of the aconitase gene acn in Corynebacterium glutamicum. <i>Journal of Biological Chemistry</i> , 2005 , 280, 585-95	5.4	58
40	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. <i>Molecular Microbiology</i> , 2004 , 52, 285-302	4.1	119
39	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. <i>Molecular Microbiology</i> , 2004 , 54, 420-38	4.1	139
38	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. <i>Journal of Biological Chemistry</i> , 2003 , 278, 4339-46	5.4	101
37	Fed-Batch Process for Pyruvate Production by Recombinant Escherichia coli YYC202 Strain. <i>Engineering in Life Sciences</i> , 2003 , 3, 299-305	3.4	39
36	Towards a phosphoproteome map of Corynebacterium glutamicum. <i>Proteomics</i> , 2003 , 3, 1637-46	4.8	139
35	The respiratory chain of Corynebacterium glutamicum. <i>Journal of Biotechnology</i> , 2003 , 104, 129-53	3.7	160
34	The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins. <i>Journal of Biotechnology</i> , 2003 , 104, 5-25	3.7	75 ⁰

33	Identification of basic amino acid residues important for citrate binding by the periplasmic receptor domain of the sensor kinase CitA. <i>Biochemistry</i> , 2003 , 42, 5917-24	3.2	39
32	Global expression profiling and physiological characterization of Corynebacterium glutamicum grown in the presence of L-valine. <i>Applied and Environmental Microbiology</i> , 2003 , 69, 2521-32	4.8	77
31	The structure of the periplasmic ligand-binding domain of the sensor kinase CitA reveals the first extracellular PAS domain. <i>Journal of Biological Chemistry</i> , 2003 , 278, 39189-96	5.4	118
30	The phosphate starvation stimulon of Corynebacterium glutamicum determined by DNA microarray analyses. <i>Journal of Bacteriology</i> , 2003 , 185, 4519-29	3.5	126
29	The sensor kinase CitA (DpiB) of Escherichia coli functions as a high-affinity citrate receptor. <i>Archives of Microbiology</i> , 2002 , 177, 313-21	3	38
28	Identification of a gene cluster in Klebsiella pneumoniae which includes citX, a gene required for biosynthesis of the citrate lyase prosthetic group. <i>Journal of Bacteriology</i> , 2002 , 184, 2439-46	3.5	22
27	Molecular analysis of the cytochrome bc1-aa3 branch of the Corynebacterium glutamicum respiratory chain containing an unusual diheme cytochrome c1. <i>Archives of Microbiology</i> , 2001 , 175, 282	-94	148
26	Proteome analysis of Corynebacterium glutamicum. <i>Electrophoresis</i> , 2001 , 22, 1712-23	3.6	94
25	A high-resolution reference map for cytoplasmic and membrane-associated proteins of Corynebacterium glutamicum. <i>Electrophoresis</i> , 2001 , 22, 4404-22	3.6	118
24	Catabolite repression of the citrate fermentation genes in Klebsiella pneumoniae: evidence for involvement of the cyclic AMP receptor protein. <i>Journal of Bacteriology</i> , 2001 , 183, 5248-56	3.5	30
23	Identification of triphosphoribosyl-dephospho-CoA as precursor of the citrate lyase prosthetic group. <i>FEBS Letters</i> , 2000 , 483, 165-8	3.8	18
22	Biosynthesis of the prosthetic group of citrate lyase. <i>Biochemistry</i> , 2000 , 39, 9438-50	3.2	35
21	The periplasmic domain of the histidine autokinase CitA functions as a highly specific citrate receptor. <i>Molecular Microbiology</i> , 1999 , 33, 858-72	4.1	83
20	A membrane-bound NAD(P)+-reducing hydrogenase provides reduced pyridine nucleotides during citrate fermentation by Klebsiella pneumoniae. <i>Journal of Bacteriology</i> , 1999 , 181, 241-5	3.5	25
19	The Escherichia coli citrate carrier CitT: a member of a novel eubacterial transporter family related to the 2-oxoglutarate/malate translocator from spinach chloroplasts. <i>Journal of Bacteriology</i> , 1998 , 180, 4160-5	3.5	85
18	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. <i>Journal of Molecular Biology</i> , 1997 , 269, 719-31	6.5	40
17	Methylmalonyl-CoA decarboxylase from Propionigenium modestumcloning and sequencing of the structural genes and purification of the enzyme complex. <i>FEBS Journal</i> , 1997 , 250, 590-9		23
16	Anaerobic citrate metabolism and its regulation in enterobacteria. <i>Archives of Microbiology</i> , 1997 , 167, 78-88	3	128

LIST OF PUBLICATIONS

15	Regulation of anaerobic citrate metabolism in Klebsiella pneumoniae. <i>Molecular Microbiology</i> , 1995 , 18, 533-46	4.1	117	
14	Bradyrhizobium japonicum cytochrome c550 is required for nitrate respiration but not for symbiotic nitrogen fixation. <i>Journal of Bacteriology</i> , 1995 , 177, 2214-7	3.5	28	
13	Klebsiella pneumoniae genes for citrate lyase and citrate lyase ligase: localization, sequencing, and expression. <i>Molecular Microbiology</i> , 1994 , 14, 347-56	4.1	74	
12	Purification of two active fusion proteins of the Na(+)-dependent citrate carrier of Klebsiella pneumoniae. <i>FEBS Letters</i> , 1994 , 347, 37-41	3.8	28	
11	Formation of several bacterial c-type cytochromes requires a novel membrane-anchored protein that faces the periplasm. <i>Molecular Microbiology</i> , 1993 , 9, 729-40	4.1	78	
10	Genes for a second terminal oxidase in Bradyrhizobium japonicum. <i>Archives of Microbiology</i> , 1992 , 158, 335-43	3	48	
9	The Bradyrhizobium japonicum cycM gene encodes a membrane-anchored homolog of mitochondrial cytochrome c. <i>Journal of Bacteriology</i> , 1991 , 173, 6766-72	3.5	75	
8	Genetic analysis of the cytochrome c-aa3 branch of the Bradyrhizobium japonicum respiratory chain. <i>Molecular Microbiology</i> , 1990 , 4, 2147-57	4.1	95	
7	The active species of "CO2" formed by carbon monoxide dehydrogenase from Peptostreptococcus productus. <i>Zeitschrift Fur Naturforschung - Section C Journal of Biosciences</i> , 1989 , 44, 392-6	1.7	18	
6	Proton translocation coupled to the oxidation of carbon monoxide to CO2 and H2 in Methanosarcina barkeri. <i>FEBS Journal</i> , 1989 , 179, 469-72		63	
5	Carbonic anhydrase activity in acetate grown Methanosarcina barkeri. <i>Archives of Microbiology</i> , 1989 , 151, 137-142	3	88	
4	Proton-motive-force-driven formation of CO from CO2 and H2 in methanogenic bacteria. <i>FEBS Journal</i> , 1987 , 168, 407-12		48	
3	Coupling of carbon monoxide oxidation to CO2 and H2 with the phosphorylation of ADP in acetate-grown Methanosarcina barkeri. <i>FEBS Journal</i> , 1986 , 159, 393-8		78	
2	Defective formation and/or utilization of carbon monoxide in H2/CO2 fermenting methanogens dependent on acetate as carbon source. <i>Archives of Microbiology</i> , 1985 , 143, 266-269	3	34	
1	The respiratory supercomplex from C. glutamicum		2	