

Publications of the IBG-1 research group
“Metabolic Regulation and Engineering”
Heads: Prof. Dr. Michael Bott and Dr. Meike Baumgart

----- 2020 -----

Spielmann A., Brack Y., van Beek H., Flachbart L., Sundermeyer L., Baumgart M. & Bott M., (2020) NADPH biosensor-based identification of an alcohol dehydrogenase variant with improved catalytic properties caused by a single charge reversal at the protein surface. *AMB Express* 10: 14. (<http://dx.doi.org/10.1186/s13568-020-0946-7>)

Wolf N., Bussmann M., Koch-Koerfges A., Katcharava N., Schulte J., Polen T., Hartl J., Vorholt J.A., Baumgart M. & Bott M., (2020) Molecular basis of growth inhibition by acetate of an adenylate cyclase-deficient mutant of *Corynebacterium glutamicum*. *Front. Microbiol.* 11. (<http://dx.doi.org/10.3389/fmicb.2020.00087>)

----- 2019 -----

Davoudi C.F., Ramp P., Baumgart M. & Bott M., (2019) Identification of Surf1 as an assembly factor of the cytochrome *bc₁-aa₃* supercomplex of Actinobacteria. *Biochim Biophys Acta Bioenerg* 1860: 148033. (<http://dx.doi.org/10.1016/j.bbabi.2019.06.005>)

Kallscheuer N., Menezes R., Foito A., da Silva M.H., Braga A., Dekker W., Sevillano D.M., Rosado-Ramos R., Jardim C., Oliveira J., Ferreira P., Rocha I., Silva A.R., Sousa M., Allwood J.W., Bott M., Faria N., Stewart D., Ottens M., Naesby M., Nunes Dos Santos C. & Marienhagen J., (2019) Identification and microbial production of the raspberry phenol salidroside that is active against Huntington's disease. *Plant Physiol.* 179: 969-985. (<http://dx.doi.org/10.1104/pp.18.01074>)

Kortmann M., Baumgart M. & Bott M., (2019) Pyruvate carboxylase from *Corynebacterium glutamicum*: purification and characterization. *Appl. Microbiol. Biotechnol.* 103: 6571-6580. (<http://dx.doi.org/10.1007/s00253-019-09982-x>)

Kortmann M., Mack C., Baumgart M. & Bott M., (2019) Pyruvate carboxylase variants enabling improved lysine production from glucose identified by biosensor-based high-throughput fluorescence-activated cell sorting screening. *ACS Synth. Biol.* 8: 274-281. (<http://dx.doi.org/10.1021/acssynbio.8b00510>)

Kraxner K.J., Polen T., Baumgart M. & Bott M., (2019) The conserved actinobacterial transcriptional regulator FtsR controls expression of *ftsZ* and further target genes and influences growth and cell division in *Corynebacterium glutamicum*. *BMC Microbiol.* 19: 179. (<http://dx.doi.org/10.1186/s12866-019-1553-0>)

Milke L., Ferreira P., Kallscheuer N., Braga A., Vogt M., Kappelmann J., Oliveira J., Silva A.R., Rocha I., Bott M., Noack S., Faria N. & Marienhagen J., (2019) Modulation of the central carbon

metabolism of *Corynebacterium glutamicum* improves malonyl-CoA availability and increases plant polyphenol synthesis. Biotechnol. Bioeng. 116: 1380-1391. (<http://dx.doi.org/10.1002/bit.26939>)

Noack S. & Baumgart M., (2019) Communities of Niche-Optimized Strains: Small-genome organism consortia in bioproduction. Trends Biotechnol. 37: 126-139. (<http://dx.doi.org/10.1016/j.tibtech.2018.07.011>)

2018

Alderwick L.J., Birch H.L., Krumbach K., Bott M., Eggeling L. & Besra G.S., (2018) AftD functions as an alpha1-->5 arabinofuranosyltransferase involved in the biosynthesis of the mycobacterial cell wall core. Cell Surf 1: 2-14. (<http://dx.doi.org/10.1016/j.tcs.2017.10.001>)

Baumgart M., Unthan S., Kloß R., Radek A., Polen T., Tenhaef N., Müller M.F., Küberl A., Siebert D., Brühl N., Marin K., Hans S., Krämer R., Bott M., Kalinowski J., Wiechert W., Seibold G., Frunzke J., Rückert C., Wendisch V.F. & Noack S., (2018) *Corynebacterium glutamicum* chassis C1*: building and testing a novel platform host for synthetic biology and industrial biotechnology. ACS Synth. Biol. 7: 132-144. (<http://dx.doi.org/10.1021/acssynbio.7b00261>)

Cormann K.U., Baumgart M. & Bott M., (2018) Structure-based design of versatile biosensors for small molecules based on the PAS domain of a thermophilic histidine kinase. ACS Synth. Biol. 7: 2888-2897. (<http://dx.doi.org/10.1021/acssynbio.8b00348>)

Dudnik A., Almeida A.F., Andrade R., Avila B., Banados P., Barbay D., Bassard J.E., Benkoulouche M., Bott M., Braga A., Breitel D., Brennan R., Bulteau L., Chanforan C., Costa I., Costa R.S., Doostmohammadi M., Faria N., Feng C.Y., Fernandes A., Ferreira P., Ferro R., Foito A., Freitag S., Garcia G., Gaspar P., Godinho-Pereira J., Hamberger B., Hartmann A., Heider H., Jardim C., Julien-Laferrriere A., Kallscheuer N., Kerbe W., Kuipers O.P., Li S., Love N., Marchetti-Spaccamela A., Marienhagen J., Martin C., Mary A., Mazurek V., Meinhart C., Sevillano D.M., Menezes R., Naesby M., Norholm M.H.H., Okkels F.T., Oliveira J., Ottens M., Parrot D., Pei L., Rocha I., Rosado-Ramos R., Rousseau C., Sagot M.F., dos Santos C.N., Schmidt M., Shelenga T., Shepherd L., Silva A.R., da Silva M.H., Simon O., Stahlhut S.G., Solopova A., Sorokin A., Stewart D., Stougie L., Su S., Thole V., Tikhonova O., Trick M., Vain P., Verissimo A., Vila-Santa A., Vinga S., Vogt M., Wang L.S., Wang L.J., Wei W., Youssef S., Neves A.R. & Forster J., (2018) BacHBerry: BACterial Hosts for production of Bioactive phenolics from bERRY fruits. Phytochem. Rev. 17: 291-326. (<http://dx.doi.org/10.1007/s11101-017-9532-2>)

Kranz A., Busche T., Vogel A., Usadel B., Kalinowski J., Bott M. & Polen T., (2018a) RNAseq analysis of alpha-proteobacterium *Gluconobacter oxydans* 621H. BMC Genomics 19: 24. (<http://dx.doi.org/10.1186/s12864-017-4415-x>)

Kranz A., Steinmann A., Degner U., Mengus-Kaya A., Matamouros S., Bott M. & Polen T., (2018b) Global mRNA decay and 23S rRNA fragmentation in *Gluconobacter oxydans* 621H. BMC Genomics 19: 753. (<http://dx.doi.org/10.1186/s12864-018-5111-1>)

Morosov X., Davoudi C.F., Baumgart M., Brocker M. & Bott M., (2018) The copper-deprivation stimulon of *Corynebacterium glutamicum* comprises proteins for biogenesis of the actinobacterial cytochrome *bc₁-aa₃* supercomplex. J. Biol. Chem. 293: 15628-15640. (<http://dx.doi.org/10.1074/jbc.RA118.004117>)

Spielmann A., Baumgart M. & Bott M., (2018) NADPH-related processes studied with a SoxR-based biosensor in *Escherichia coli*. Microbiologyopen: e785. (<http://dx.doi.org/10.1002/mbo3.785>)

----- 2017 -----

Schulte J., Baumgart M. & Bott M., (2017) Development of a single-cell GlxR-based cAMP biosensor for *Corynebacterium glutamicum*. J. Biotechnol. 258: 33-40. (<http://dx.doi.org/10.1016/j.jbiotec.2017.07.004>)

Baumgart M., Huber I., Abdollahzadeh I., Gensch T. & Frunzke J., (2017) Heterologous expression of the *Halothiobacillus neapolitanus* carboxysomal gene cluster in *Corynebacterium glutamicum*. J. Biotechnol. 258: 126-135. (<http://dx.doi.org/10.1016/j.jbiotec.2017.03.019>)

Bott M. & Eggeling L., (2017) Novel technologies for optimal strain breeding. In: Amino Acid Fermentation. A. Yokota & M. Ikeda (eds). Advances in Biochemical Engineering/ Biotechnology, Springer Berlin Heidelberg, pp. 227-254. (http://dx.doi.org/10.1007/10_2016_33)

Bott M., Jäger K.E., Pietruszka J. & Wiechert W., (2017) 40 Years of biotechnology research at Forschungszentrum Jülich. J. Biotechnol. 258: 1. (<http://dx.doi.org/10.1016/j.jbiotec.2017.08.014>)

Hochheim J., Kranz A., Krumbach K., Sokolowsky S., Eggeling L., Noack S., Bocola M., Bott M. & Marienhagen J., (2017) Mutations in MurE, the essential UDP-N-acetylmuramoylalanine-D-glutamate 2,6-diaminopimelate ligase of *Corynebacterium glutamicum*: effect on L-lysine formation and analysis of systemic consequences. Biotechnol. Lett. 39: 283-288. (<http://dx.doi.org/10.1007/s10529-016-2243-8>)

Kallscheuer N., Gätgens J., Lubcke M., Pietruszka J., Bott M. & Polen T., (2017) Improved production of adipate with *Escherichia coli* by reversal of beta-oxidation. Appl. Microbiol. Biotechnol. 101: 2371-2382. (<http://dx.doi.org/10.1007/s00253-016-8033-3>)

Kallscheuer N., Vogt M., Bott M. & Marienhagen J., (2017) Functional expression of plant-derived O-methyltransferase, flavanone 3-hydroxylase, and flavonol synthase in *Corynebacterium glutamicum* for production of pterostilbene, kaempferol, and quercetin. J. Biotechnol. In press. <http://dx.doi.org/10.1016/j.jbiotec.2017.01.006>

- Kallscheuer N., Polen T., Bott M. & Marienhagen J., (2017b) Reversal of beta-oxidative pathways for the microbial production of chemicals and polymer building blocks. *Metab. Eng.* 42: 33-42. (<http://dx.doi.org/10.1016/j.ymben.2017.05.004>)
- Kiefler I., Bringer S. & Bott M., (2017) Metabolic engineering of *Gluconobacter oxydans* 621H for increased biomass yield. *Appl. Microbiol. Biotechnol.* 101: 5453-5467. (<http://dx.doi.org/10.1007/s00253-017-8308-3>)
- Kleine B., Chattopadhyay A., Polen T., Pinto D., Mascher T., Bott M., Bocker M. & Freudl R., (2017) The three-component system EsrISR regulates a cell envelope stress response in *Corynebacterium glutamicum*. *Mol. Microbiol.* 106: 719-741. (<http://dx.doi.org/10.1111/mmi.13839>)
- Kranz A., Vogel A., Degner U., Kiefler I., Bott M., Usadel B. & Polen T., (2017) High precision genome sequencing of engineered *Gluconobacter oxydans* 621H by combining long nanopore and short accurate Illumina reads. *J. Biotechnol.* 258: 197-205. (<http://dx.doi.org/10.1016/j.jbiotec.2017.04.016>)
- Limberg M.H., Schulte J., Aryani T., Mahr R., Baumgart M., Bott M., Wiechert W. & Oldiges M., (2017) Metabolic profile of 1,5-diaminopentane producing *Corynebacterium glutamicum* under scale-down conditions: Blueprint for robustness to bioreactor inhomogeneities. *Biotechnol. Bioeng.* 114: 560-575. (<http://dx.doi.org/10.1002/bit.26184>)
- Schulte J., Baumgart M. & Bott M., (2017) Identification of the cAMP phosphodiesterase CpdA as novel key player in cAMP-dependent regulation in *Corynebacterium glutamicum*. *Mol. Microbiol.* 103: 534-552. (<http://dx.doi.org/10.1111/mmi.13574>)

2016

- Vogt M., Brüsseler C., van Ooyen J., Bott M. & Marienhagen J., (2016) Production of 2-methyl-1-butanol and 3-methyl-1-butanol in engineered *Corynebacterium glutamicum*. *Metab. Eng.* 38: 436-445. (<http://dx.doi.org/10.1016/j.ymben.2016.10.007>)
- Pfeifer E., Hünnefeld M., Popa O., Polen T., Kohlheyer D., Baumgart M. & Frunzke J., (2016) Silencing of cryptic prophages in *Corynebacterium glutamicum*. *Nucleic Acids Res.* 44: 10117-10131. (<http://dx.doi.org/10.1093/nar/gkw692>)
- Pahlke J., Dostalova H., Holatko J., Degner U., Bott M., Patek M. & Polen T., (2016) The small 6C RNA of *Corynebacterium glutamicum* is involved in the SOS response. *RNA Biol.* 13: 848-860. (<http://dx.doi.org/10.1080/15476286.2016.1205776>)
- Nguyen G.T.T., Erlenkamp G., Jack O., Küberl A., Bott M., Fiorani F., Gohlke H. & Groth G., (2016) Chalcone-based Selective Inhibitors of a C₄ Plant Key Enzyme as Novel Potential Herbicides. *Sci. Rep.* 6: 27333. (<http://dx.doi.org/10.1038/srep27333>)

Küberl A., Polen T. & Bott M., (2016) The pupylation machinery is involved in iron homeostasis by targeting the iron storage protein ferritin. *Proc. Natl. Acad. Sci. USA* 113: 4806-4811. (<http://dx.doi.org/10.1073/pnas.1514529113>)

Kao W.C., Kleinschroth T., Nitschke W., Baymann F., Neehaul Y., Hellwig P., Richers S., Vonck J., Bott M. & Hunte C., (2016) The obligate respiratory supercomplex from Actinobacteria. *Biochim. Biophys. Acta Bioenergetics* 1857: 1705-1714. (<http://dx.doi.org/10.1016/j.bbabi.2016.07.009>)

Kallscheuer N., Vogt M., Stenzel A., Gätgens J., Bott M. & Marienhagen J., (2016) Construction of a *Corynebacterium glutamicum* platform strain for the production of stilbenes and (2S)-flavanones. *Metab. Eng.* 38: 47-55. (<http://dx.doi.org/10.1016/j.ymben.2016.06.003>)

Kallscheuer N., Vogt M., Kappelmann J., Krumbach K., Noack S., Bott M. & Marienhagen J., (2016) Identification of the phd gene cluster responsible for phenylpropanoid utilization in *Corynebacterium glutamicum*. *Appl. Microbiol. Biotechnol.* 100: 1871-1881. (<http://dx.doi.org/10.1007/s00253-015-7165-1>)

Graf S., Fedotovskaya O., Kao W.C., Hunte C., Adelroth P., Bott M., von Ballmoos C. & Brzezinski P., (2016) Rapid Electron Transfer within the III-IV Supercomplex in *Corynebacterium glutamicum*. *Sci. Rep.* 6: 34098. (<http://dx.doi.org/10.1038/srep34098>)

Bringer S. & Bott M., (2016) Central carbon metabolism and respiration in *Gluconobacter oxydans*. In: Acetic acid bacteria: ecology and physiology. K. Matsushita, H. Toyama, N. Tonouchi & A. Kainuma (eds). Springer Verlag Berlin, Heidelberg, New York, pp. 235-253. (http://dx.doi.org/10.1007/978-4-431-55933-7_11)

Baumgart M., Schubert K., Bramkamp M. & Frunzke J., (2016) Impact of LytR-CpsA-Psr proteins on cell wall biosynthesis in *Corynebacterium glutamicum*. *J. Bacteriol.* 198: 3045-3059. (<http://dx.doi.org/10.1128/JB.00406-16>)

2015

Witthoff S., Schmitz K., Niedenfuhr S., Nöh K., Noack S., Bott M. & Marienhagen J., (2015) Metabolic engineering of *Corynebacterium glutamicum* for methanol metabolism. *Appl. Environ. Microbiol.* 81: 2215-2225. (<http://dx.doi.org/10.1128/AEM.03110-14>)

Vogt M., Krumbach K., Bang W.G., van Ooyen J., Noack S., Klein B., Bott M. & Eggeling L., (2015) The contest for precursors: channelling L-isoleucine synthesis in *Corynebacterium glutamicum* without byproduct formation. *Appl. Microbiol. Biotechnol.* 99: 791-800. (<http://dx.doi.org/10.1007/s00253-014-6109-5>)

Vogt M., Haas S., Polen T., van Ooyen J. & Bott M., (2015) Production of 2-ketoisocaproate with *Corynebacterium glutamicum* strains devoid of plasmids and heterologous genes. *Microb. Biotechnol.* 8: 351-360. (<http://dx.doi.org/10.1111/1751-7915.12237>)

- Unthan S., Baumgart M., Radek A., Herbst M., Siebert D., Brühl N., Bartsch A., Bott M., Wiechert W., Marin K., Hans S., Krämer R., Seibold G., Frunzke J., Kalinowski J., Rückert C., Wendisch V.F. & Noack S., (2015) Chassis organism from *Corynebacterium glutamicum* - a top-down approach to identify and delete irrelevant gene clusters. *Biotechnol. J.* 10: 290-301. (<http://dx.doi.org/10.1002/biot.201400041>)
- Otten A., Brocker M. & Bott M., (2015) Metabolic engineering of *Corynebacterium glutamicum* for the production of itaconate. *Metab. Eng.* 30: 156-165. (<http://dx.doi.org/10.1016/j.ymben.2015.06.003>)
- Ostermann S., Richhardt J., Bringer S., Bott M., Wiechert W. & Oldiges M., (2015) ¹³C Tracers for Glucose Degrading Pathway Discrimination in *Gluconobacter oxydans* 621H. *Metabolites* 5: 455-474. (<http://dx.doi.org/10.3390/metabo5030455>)
- Mustafi N., Bott M. & Frunzke J., (2015) Genetically encoded biosensors for strain development and single-cell analysis of *Corynebacterium glutamicum*. In: *Corynebacterium glutamicum: from systems biology to biotechnological applications*. A. Burkovski (ed). Norfolk, UK: Caister Academic Press, pp. 179-196. (<http://dx.doi.org/10.21775/9781910190050.12>)
- Michel A., Koch-Koerfges A., Krumbach K., Brocker M. & Bott M., (2015) Anaerobic growth of *Corynebacterium glutamicum* via mixed-acid fermentation. *Appl. Environ. Microbiol.* 81: 7496-7508. (<http://dx.doi.org/10.1128/AEM.02413-15>)
- Küberl A., Polen T. & Bott M., (2015) Pupylierung—ein bakterielles Pendant zur Ubiquitylierung. *Biospektrum* 21: 158-160. (<http://dx.doi.org/10.1007/s12268-015-0553-3>)
- Kortmann M., Kuhl V., Klaffl S. & Bott M., (2015) A chromosomally encoded T7 RNA polymerase-dependent gene expression system for *Corynebacterium glutamicum*: construction and comparative evaluation at the single-cell level. *Microb. Biotechnol.* 8: 253-265. (<http://dx.doi.org/10.1111/1751-7915.12236>)
- Kim E.M., Um Y., Bott M. & Woo H.M., (2015) Engineering of *Corynebacterium glutamicum* for growth and succinate production from levoglucosan, a pyrolytic sugar substrate. *FEMS Microbiol. Lett.* 362. (<http://dx.doi.org/10.1093/femsle/fnv161>)
- Kiefler I., Bringer S. & Bott M., (2015) SdhE-dependent formation of a functional *Acetobacter pasteurianus* succinate dehydrogenase in *Gluconobacter oxydans* - a first step toward a complete tricarboxylic acid cycle. *Appl. Microbiol. Biotechnol.* 99: 9147-9160. (<http://dx.doi.org/10.1007/s00253-015-6972-8>)
- Kallscheuer N., Bott M., van Ooyen J. & Polen T., (2015) Single-Domain Peptidyl-Prolyl cis/trans Isomerase FkpA from *Corynebacterium glutamicum* Improves the Biomass Yield at Increased Growth Temperatures. *Appl. Environ. Microbiol.* 81: 7839-7850. (<http://dx.doi.org/10.1128/AEM.02113-15>)

- Eikmanns B. & Bott M., (2015) Engineering *Corynebacterium glutamicum* for the production of organic acids and alcohols. In: *Corynebacterium glutamicum: from systems biology to biotechnological applications*. Norfolk, UK: Caister Academic Press, pp. 111-137. (<http://dx.doi.org/10.21775/9781910190050.08>)
- Eggeling L., Bott M. & Marienhagen J., (2015) Novel screening methods-biosensors. *Curr. Opin. Biotechnol.* 35C: 30-36. (<http://dx.doi.org/10.1016/j.copbio.2014.12.021>)
- Eggeling L. & Bott M., (2015) A giant market and a powerful metabolism: L-lysine provided by *Corynebacterium glutamicum*. *Appl. Microbiol. Biotechnol.* 99: 3387-3394. (<http://dx.doi.org/10.1007/s00253-015-6508-2>)
- Bott M., (2015) Need for speed - finding productive mutations using transcription factor-based biosensors, fluorescence-activated cell sorting and recombineering. *Microb. Biotechnol.* 8: 8-10. (<http://dx.doi.org/10.1111/1751-7915.12248>)
- Baumgart M. & Frunzke J., (2015) The manganese-responsive regulator MntR represses transcription of a predicted ZIP family metal ion transporter in *Corynebacterium glutamicum*. *FEMS Microbiol. Lett.* 362: 1-10. (<http://dx.doi.org/10.1093/femsle/fnu001>)

2014

- Zahoor A., Otten A. & Wendisch V.F., (2014) Metabolic engineering of *Corynebacterium glutamicum* for glycolate production. *J. Biotechnol.* 192 Pt B: 366-375. (<http://dx.doi.org/10.1016/j.jbiotec.2013.12.020>)
- Vogt M., Haas S., Klaffl S., Polen T., Eggeling L., van Ooyen J. & Bott M., (2014) Pushing product formation to its limit: metabolic engineering of *Corynebacterium glutamicum* for L-leucine overproduction. *Metab. Eng.* 22: 40-52. (<http://dx.doi.org/10.1016/j.ymben.2013.12.001>)
- Townsend P.D., Jungwirth B., Pojer F., Bussmann M., Money V.A., Cole S.T., Pühler A., Tauch A., Bott M., Cann M.J. & Pohl E., (2014) 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* 9: e113265. (<http://dx.doi.org/10.1371/journal.pone.0113265>)
- Siedler S., Schendzielorz G., Binder S., Eggeling L., Bringer S. & Bott M., (2014) SoxR as a single-cell biosensor for NADPH-consuming enzymes in *Escherichia coli*. *ACS Synth. Biol.* 3: 41-47. (<http://dx.doi.org/10.1021/sb400110j>)
- Siedler S., Bringer S., Polen T. & Bott M., (2014) NADPH-dependent reductive biotransformation with *Escherichia coli* and its *pfkA* deletion mutant: influence on global gene expression and role of oxygen supply. *Biotechnol. Bioeng.* 111: 2067-2075. (<http://dx.doi.org/10.1002/bit.25271>)

- Schendzielorz G., Dippong M., Grünberger A., Kohlheyer D., Yoshida A., Binder S., Nishiyama C., Nishiyama M., Bott M. & Eggeling L., (2014) Taking control over control: use of product sensing in single cells to remove flux control at key enzymes in biosynthesis pathways. *ACS Synth. Biol.* 3: 21-29. (<http://dx.doi.org/10.1021/sb400059y>)
- Radek A., Krumbach K., Gätgens J., Wendisch V.F., Wiechert W., Bott M., Noack S. & Marienhagen J., (2014) Engineering of *Corynebacterium glutamicum* for minimized carbon loss during utilization of D-xylose containing substrates. *J. Biotechnol.* 192: 156-160. (<http://dx.doi.org/10.1016/j.jbiotec.2014.09.026>)
- Raasch K., Bocola M., Labahn J., Leitner A., Eggeling L. & Bott M., (2014) Interaction of 2-oxoglutarate dehydrogenase OdhA with its inhibitor OdhI in *Corynebacterium glutamicum*: Mutants and a model. *J. Biotechnol.* 191: 99-105. (<http://dx.doi.org/10.1016/j.jbiotec.2014.05.023>)
- Platzen L., Koch-Koerfges A., Weil B., Brocker M. & Bott M., (2014) Role of flavohaemoprotein Hmp and nitrate reductase NarGHJ of *Corynebacterium glutamicum* for coping with nitrite and nitrosative stress. *FEMS Microbiol. Lett.* 350: 239-248. (<http://dx.doi.org/10.1111/1574-6968.12318>)
- Pelzer A., Polen T., Funken H., Rosenau F., Wilhelm S., Bott M. & Jaeger K.E., (2014) Subtilase SprP exerts pleiotropic effects in *Pseudomonas aeruginosa*. *MicrobiologyOpen* 3: 89-103. (<http://dx.doi.org/10.1002/mbo3.150>)
- Litsanov B., Brocker M., Oldiges M. & Bott M., (2014) Succinic acid. In: Bioprocessing of renewable resources to commodity bioproducts. A. Kondo & V. Bisaria (eds). Hoboken, NJ, USA: John Wiley & Sons, Inc., pp. 437-474. (<http://dx.doi.org/10.1002/9781118845394.ch16>)
- Lee J., Sim S.J., Bott M., Um Y., Oh M.K. & Woo H.M., (2014) Succinate production from CO₂-grown microalgal biomass as carbon source using engineered *Corynebacterium glutamicum* through consolidated bioprocessing. *Sci. Rep.* 4: 5819. (<http://dx.doi.org/10.1038/srep05819>)
- Küberl A., Fränzel B., Eggeling L., Polen T., Wolters D.A. & Bott M., (2014) Pupylated proteins in *Corynebacterium glutamicum* revealed by MudPIT analysis. *Proteomics* 14: 1531-1542. (<http://dx.doi.org/10.1002/pmic.201300531>)
- Kang M.K., Lee J., Um Y., Lee T.S., Bott M., Park S.J. & Woo H.M., (2014) Synthetic biology platform of CoryneBrick vectors for gene expression in *Corynebacterium glutamicum* and its application to xylose utilization. *Appl. Microbiol. Biotechnol.* 98: 5991-6002. (<http://dx.doi.org/10.1007/s00253-014-5714-7>)
- Irzik K., van Ooyen J., Gätgens J., Krumbach K., Bott M. & Eggeling L., (2014) Acyl-CoA sensing by FasR to adjust fatty acid synthesis in *Corynebacterium glutamicum*. *J. Biotechnol.* 192: 96-101. (<http://dx.doi.org/10.1016/j.jbiotec.2014.10.031>)

Hentschel E., Mack C., Gätgens C., Bott M., Brocker M. & Frunzke J., (2014) Phosphatase activity of the histidine kinases ensures pathway specificity of the ChrSA and HrrSA two-component systems in *Corynebacterium glutamicum*. Mol. Microbiol. 92: 1326-1342. (<http://dx.doi.org/10.1111/mmi.12633>)

Hentschel E., Mack C., Gätgens C., Bott M., Brocker M. & Frunzke J., (2014) Phosphatase activity of the histidine kinases ensures pathway specificity of the ChrSA and HrrSA two-component systems in *Corynebacterium glutamicum*. Mol. Microbiol. 92: 1326-1342. (<http://dx.doi.org/10.1111/mmi.12633>)

2013

Witthoff S., Mühlroth A., Marienhagen J. & Bott M., (2013) C1 metabolism in *Corynebacterium glutamicum*: an endogenous pathway for oxidation of methanol to carbon dioxide. Appl. Environ. Microbiol. 79: 6974-6983. (<http://dx.doi.org/10.1128/AEM.02705-13>)

Wieschalka S., Blombach B., Bott M. & Eikmanns B.J., (2013) Bio-based production of organic acids with *Corynebacterium glutamicum*. Microb. Biotechnol. 6: 87-102. (<http://dx.doi.org/10.1111/1751-7915.12013>)

Siedler S., Lindner S.N., Bringer S., Wendisch V.F. & Bott M., (2013) 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. Appl. Microbiol. Biotechnol. 97: 143-152. (<http://dx.doi.org/10.1007/s00253-012-4314-7>)

Scheele S., Oertel D., Bongaerts J., Evers S., Hellmuth H., Maurer K.H., Bott M. & Freudl R., (2013) 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*. Microb. Biotechnol. 6: 202-206. (<http://dx.doi.org/10.1111/1751-7915.12005>)

Richhardt J., Luchterhand B., Bringer S., Buchs J. & Bott M., (2013) Evidence for a key role of cytochrome *bo₃* oxidase in respiratory energy metabolism of *Gluconobacter oxydans*. J. Bacteriol. 195: 4210-4220. (<http://dx.doi.org/10.1128/JB.00470-13>)

Richhardt J., Bringer S. & Bott M., (2013) Role of the pentose phosphate pathway and the Entner-Doudoroff pathway in glucose metabolism of *Gluconobacter oxydans* 621H. Appl. Microbiol. Biotechnol. 97: 4315-4323. (<http://dx.doi.org/10.1007/s00253-013-4707-2>)

Polen T., Spelberg M. & Bott M., (2013) Toward biotechnological production of adipic acid and precursors from biorenewables. J. Biotechnol. 167: 75-84. (<http://dx.doi.org/10.1016/j.jbiotec.2012.07.008>)

- Marienhagen J. & Bott M., (2013) Metabolic engineering of microorganisms for the synthesis of plant natural products. *J. Biotechnol.* 163: 166-178.
(<http://dx.doi.org/10.1016/j.jbiotec.2012.06.001>)
- Litsanov B., Brocker M. & Bott M., (2013) Glycerol as a substrate for aerobic succinate production in minimal medium with *Corynebacterium glutamicum*. *Microb. Biotechnol.* 6: 189-195.
(<http://dx.doi.org/10.1111/j.1751-7915.2012.00347.x>)
- Koch-Koerfges A., Pfler N., Platzen L., Oldiges M. & Bott M., (2013) Conversion of *Corynebacterium glutamicum* from an aerobic respiring to an aerobic fermenting bacterium by inactivation of the respiratory chain. *Biochim. Biophys. Acta Bioenergetics* 1827: 699-708.
(<http://dx.doi.org/10.1016/j.bbabi.2013.02.004>)
- Klaffl S., Brocker M., Kalinowski J., Eikmanns B.J. & Bott M., (2013) 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*. *J. Bacteriol.* 195: 4283-4296. (<http://dx.doi.org/10.1128/JB.00265-13>)
- Hoffmann K., Grünberger A., Lausberg F., Bott M. & Eggeling L., (2013) Visualization of imbalances in sulfur assimilation and synthesis of sulfur-containing amino acids at the single-cell level. *Appl. Environ. Microbiol.* 79: 6730-6736. (<http://dx.doi.org/10.1128/AEM.01804-13>)
- Hanke T., Nöh K., Noack S., Polen T., Bringer S., Sahm H., Wiechert W. & Bott M., (2013) Combined fluxomics and transcriptomics analysis of glucose catabolism via a partially cyclic pentose phosphate pathway in *Gluconobacter oxydans* 621H. *Appl. Environ. Microbiol.* 79: 2336-2348.
(<http://dx.doi.org/10.1128/AEM.03414-12>)
- Garcia-Nafria J., Baumgart M., Turkenburg J.P., Wilkinson A.J., Bott M. & Wilson K.S., (2013) Crystal and solution studies reveal that the transcriptional regulator AcnR of *Corynebacterium glutamicum* is regulated by citrate-Mg²⁺ binding to a non-canonical pocket. *J. Biol. Chem.* 288: 15800-15812. (<http://dx.doi.org/10.1074/jbc.M113.462440>)
- Bott M. & Eikmanns B.J., (2013) TCA cycle and glyoxylate shunt of *Corynebacterium glutamicum*. In: *Biology and Biotechnology of Corynebacterium glutamicum*. H. Yukawa & M. Inui (eds). Berlin, Heidelberg: Springer Verlag, pp. 281 - 313. (http://dx.doi.org/10.1007/978-3-642-29857-8_10)
- Binder S., Siedler S., Marienhagen J., Bott M. & Eggeling L., (2013) Recombineering in *Corynebacterium glutamicum* combined with optical nanosensors: a general strategy for fast producer strain generation. *Nucleic Acids Res.* 41: 6360-6369. (<http://dx.doi.org/10.1093/nar/gkt312>)
- Baumgart M., Unthan S., Rückert C., Sivalingam J., Grünberger A., Kalinowski J., Bott M., Noack S. & Frunzke J., (2013) Construction of a prophage-free variant of *Corynebacterium glutamicum* ATCC 13032 for use as a platform strain for basic research and industrial biotechnology. *Appl. Environ. Microbiol.* 79: 6006-6015. (<http://dx.doi.org/10.1128/AEM.01634-13>)

Baumgart M., Luder K., Grover S., Gätgens C., Besra G.S. & Frunzke J., (2013) IpsA, a novel LacI-type regulator, is required for inositol-derived lipid formation in *Corynebacteria* and *Mycobacteria*. BMC Biol. 11: 122 (<http://dx.doi.org/10.1186/1741-7007-11-122>)

----- 2012 -----

Witthoff S., Eggeling L., Bott M. & Polen T., (2012) *Corynebacterium glutamicum* harbours a molybdenum cofactor-dependent formate dehydrogenase which alleviates growth inhibition in the presence of formate. Microbiology 158: 2428-2439. (<http://dx.doi.org/10.1099/mic.0.059196-0>)

van Ooyen J., Noack S., Bott M., Reth A. & Eggeling L., (2012) Improved L-lysine production with *Corynebacterium glutamicum* and systemic insight into citrate synthase flux and activity. Biotechnol. Bioeng. 109: 2070-2081. (<http://dx.doi.org/10.1002/bit.24486>)

Siedler S., Bringer S., Blank L.M. & Bott M., (2012) Engineering yield and rate of reductive biotransformation in *Escherichia coli* by partial cyclization of the pentose phosphate pathway and PTS-independent glucose transport. Appl. Microbiol. Biotechnol. 93: 1459-1467. (<http://dx.doi.org/10.1007/s00253-011-3626-3>)

Richhardt J., Bringer S. & Bott M., (2012) Mutational analysis of the pentose phosphate and Entner-Doudoroff pathways in *Gluconobacter oxydans* reveals improved growth of a $\Delta edd \Delta eda$ mutant on mannitol. Appl. Environ. Microbiol. 78: 6975-6986. (<http://dx.doi.org/10.1128/AEM.01166-12>)

Mustafi N., Grünberger A., Kohlheyer D., Bott M. & Frunzke J., (2012) The development and application of a single-cell biosensor for the detection of L-methionine and branched-chain amino acids. Metab. Eng. 14: 449-457. (<http://dx.doi.org/10.1016/j.ymben.2012.02.002>)

Litsanov B., Kabus A., Brocker M. & Bott M., (2012) Efficient aerobic succinate production from glucose in minimal medium with *Corynebacterium glutamicum*. Microb. Biotechnol. 5: 116-128. (<http://dx.doi.org/10.1111/j.1751-7915.2011.00310.x>)

Litsanov B., Brocker M. & Bott M., (2012) Toward homosuccinate fermentation: metabolic engineering of *Corynebacterium glutamicum* for anaerobic production of succinate from glucose and formate. Appl. Environ. Microbiol. 78: 3325-3337. (<http://dx.doi.org/10.1128/AEM.07790-11>)

Lange C., Mustafi N., Frunzke J., Kennerknecht N., Wessel M., Bott M. & Wendisch V.F., (2012) Lrp of *Corynebacterium glutamicum* controls expression of the brnFE operon encoding the export system for L-methionine and branched-chain amino acids. J. Biotechnol. 158: 231-241. (<http://dx.doi.org/10.1016/j.jbiotec.2011.06.003>)

Koch-Koerfges A., Kabus A., Ochrombel I., Marin K. & Bott M., (2012) Physiology and global gene expression of a *Corynebacterium glutamicum* ΔF_1F_0 -ATP synthase mutant devoid of oxidative

phosphorylation. Biochim. Biophys. Acta Bioenergetics 1817: 370-380.
(<http://dx.doi.org/10.1016/j.bbambio.2011.10.006>)

Heyer A., Gätgens C., Hentschel E., Kalinowski J., Bott M. & Frunzke J., (2012) The two-component system ChrSA is crucial for haem tolerance and interferes with HrrSA in haem-dependent gene regulation in *Corynebacterium glutamicum*. Microbiology 158: 3020-3031.
(<http://dx.doi.org/10.1099/mic.0.062638-0>)

Hanke T., Richhardt J., Polen T., Sahm H., Bringer S. & Bott M., (2012) Influence of oxygen limitation, absence of the cytochrome *bc₁* complex and low pH on global gene expression in *Gluconobacter oxydans* 621H using DNA microarray technology. J. Biotechnol. 157: 359-372.
(<http://dx.doi.org/10.1016/j.jbiotec.2011.12.020>)

Funken H., Bartels K.M., Wilhelm S., Brocker M., Bott M., Bains M., Hancock R.E., Rosenau F. & Jaeger K.E., (2012) Specific association of lectin LecB with the surface of *Pseudomonas aeruginosa*: Role of outer membrane protein OprF. PLoS One 7: e46857.
(<http://dx.doi.org/10.1371/journal.pone.0046857>)

Bott M. & Brocker M., (2012) Two-component signal transduction in *Corynebacterium glutamicum* and other corynebacteria: on the way towards stimuli and targets. Appl. Microbiol. Biotechnol. 94: 1131-1150. (<http://dx.doi.org/10.1007/s00253-012-4060-x>)

Binder S., Schendzielorz G., Stäbler N., Krumbach K., Hoffmann K., Bott M. & Eggeling L., (2012) A high-throughput approach to identify genomic variants of bacterial metabolite producers at the single-cell level. Genome Biol. 13: R40. (<http://dx.doi.org/10.1186/gb-2012-13-5-r40>)

----- 2011 -----

van Ooyen J., Emer D., Bussmann M., Bott M., Eikmanns B.J. & Eggeling L., (2011) Citrate synthase in *Corynebacterium glutamicum* is encoded by two *gltA* transcripts which are controlled by RamA, RamB, and GlxR. J. Biotechnol. 154: 140-148.

Stäbler N., Oikawa T., Bott M. & Eggeling L., (2011) *Corynebacterium glutamicum* as a host for synthesis and export of D-Amino Acids. J. Bacteriol. 193: 1702-1709.

Siedler S., Bringer S. & Bott M., (2011) Increased NADPH availability in *Escherichia coli*: improvement of the product per glucose ratio in reductive whole-cell biotransformation. Appl. Microbiol. Biotechnol. 92: 929-937.

Schelder S., Zaade D., Litsanov B., Bott M. & Brocker M., (2011) The two-component signal transduction system CopRS of *Corynebacterium glutamicum* is required for adaptation to copper-excess stress. PLoS One 6: e22143.

Frunzke J., Gätgens C., Brocker M. & Bott M., (2011) Control of heme homeostasis in *Corynebacterium glutamicum* by the two-component system HrrSA. J. Bacteriol. 193: 1212-1221.

Brocker M., Mack C. & Bott M., (2011) Target genes, consensus binding site, and role of phosphorylation for the response regulator MtrA of *Corynebacterium glutamicum*. J. Bacteriol. 193: 1237-1349.

Baumgart M., Mustafi N., Krug A. & Bott M., (2011) Deletion of the aconitase gene in *Corynebacterium glutamicum* causes strong selection pressure for secondary mutations inactivating citrate synthase. J. Bacteriol. 193: 6864-6873.

Baumgart M. & Bott M., (2011) Biochemical characterisation of aconitase from *Corynebacterium glutamicum*. J. Biotechnol. 154: 163-170.

Bartels K.M., Funken H., Knapp A., Brocker M., Bott M., Wilhelm S., Jaeger K.E. & Rosenau F., (2011) Glycosylation is required for outer membrane localization of the lectin LecB in *Pseudomonas aeruginosa*. J. Bacteriol. 193: 1107-1113.

2010

Zhang Z., Buitenhuis J., Cukkemane A., Brocker M., Bott M. & Dhont J.K., (2010) Charge reversal of the rodlike colloidal fd virus through surface chemical modification. Langmuir 26: 10593-10599.

Woo H.M., Noack S., Seibold G.M., Willbold S., Eikmanns B.J. & Bott M., (2010) Link between phosphate starvation and glycogen metabolism in *Corynebacterium glutamicum*, revealed by metabolomics. Appl. Environ. Microbiol. 76: 6910-6919.

Rehm N., Georgi T., Hiery E., Degner U., Schmiedl A., Burkovski A. & Bott M., (2010) L-Glutamine as a nitrogen source for *Corynebacterium glutamicum*: derepression of the AmtR regulon and implications for nitrogen sensing. Microbiology 156: 3180-3193.

Reher M., Fuhrer T., Bott M. & Schonheit P., (2010) The nonphosphorylative Entner-Doudoroff pathway in the thermoacidophilic euryarchaeon *Picrophilus torridus* involves a novel 2-keto-3-deoxygluconate- specific aldolase. J. Bacteriol. 192: 964-974.

Manilla-Perez E., Reers C., Baumgart M., Hetzler S., Reichelt R., Malkus U., Kalscheuer R., Wältermann M. & Steinbüchel A., (2010) Analysis of lipid export in hydrocarbonoclastic bacteria of the genus *Alcanivorax*: identification of lipid export-negative mutants of *Alcanivorax borkumensis* SK2 and *Alcanivorax jadensis* T9. J. Bacteriol. 192: 643-656.

Krawczyk S., Raasch K., Schultz C., Hoffelder M., Eggeling L. & Bott M., (2010) The FHA domain of OdhI interacts with the carboxyterminal 2-oxoglutarate dehydrogenase domain of OdhA in *Corynebacterium glutamicum*. FEBS Lett. 584: 1463-1468.

- Krajewski V., Simic P., Mouncey N.J., Bringer S., Sahm H. & Bott M., (2010) Metabolic engineering of *Gluconobacter oxydans* for improved growth rate and growth yield on glucose by elimination of gluconate formation. *Appl. Environ. Microbiol.* 76: 4369-4376.
- Garcia-Nafria J., Baumgart M., Bott M., Wilkinson A.J. & Wilson K.S., (2010) The *Corynebacterium glutamicum* aconitase repressor: scratching around for crystals. *Acta Crystallogr. Sect. F* 66: 1074-1077.
- Bussmann M., Baumgart M. & Bott M., (2010) RosR (Cg1324), a hydrogen peroxide-sensitive MarR-type transcriptional regulator of *Corynebacterium glutamicum*. *J. Biol. Chem.* 285: 29305-29318.
- Boulahya K.A., Guedon E., Delaunay S., Schultz C., Boudrant J., Bott M. & Goergen J.L., (2010) OdhI dephosphorylation kinetics during different glutamate production processes involving *Corynebacterium glutamicum*. *Appl. Microbiol. Biotechnol.* 87: 1867-1874.
- Bott M., Bringer-Meyer S., Brocker M., Eggeling L., Freudl R., Frunzke J. & Polen T., (2010) Systemische Mikrobiologie – Etablierung bakterieller Produktionsplattformen für die Weiße Biotechnologie In: *Jahrbuch der Heinrich-Heine-Universität Düsseldorf 2008/2009*. H. Süssmuth (ed). Düsseldorf: Düsseldorf University Press, pp. 227-242.
- Bott M., (2010) Signal transduction by serine/threonine protein kinases in bacteria. In: *Bacterial Signaling*. R. Krämer & K. Jung (eds). Weinheim: Wiley-VCH Verlag, pp. 427-447.

2009

- Schultz C., Niebisch A., Schwaiger A., Viets U., Metzger S., Bramkamp M. & Bott M., (2009) 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. *Mol. Microbiol.* 74: 724-741.
- Russo S., Schweitzer J.E., Polen T., Bott M. & Pohl E., (2009) Crystal structure of the caseinolytic protease gene regulator, a transcriptional activator in actinomycetes. *J. Biol. Chem.* 284: 5208-5216.
- Emer D., Krug A., Eikmanns B.J. & Bott M., (2009) Complex expression control of the *Corynebacterium glutamicum* aconitase gene: identification of RamA as a third transcriptional regulator besides AcnR and RipA. *J. Biotechnol.* 140: 92-98.
- Eggeling L. & Bott M., (2009) The genus *Corynebacterium*. In: *Practical Handbook of Microbiology*. E. Goldman & L. H. Green (eds). Boca Raton: CRC Press, Taylor & Francis Group, pp. 355-373.

Busmann M., Emer D., Hasenbein S., Degraf S., Eikmanns B.J. & Bott M., (2009) Transcriptional control of the succinate dehydrogenase operon *sdhCAB* of *Corynebacterium glutamicum* by the cAMP-dependent regulator GlxR and the LuxR-type regulator RamA. J. Biotechnol. 143: 173-182.

Brocker M., Schaffer S., Mack C. & Bott M., (2009) Citrate utilization by *Corynebacterium glutamicum* is controlled by the CitAB two-component system through positive regulation of the citrate transport genes *citH* and *tctCBA*. J. Bacteriol. 191: 3869-3880.

2008

Wendisch V.F. & Bott M., (2008) Phosphorus metabolism and its regulation. In: *Corynebacteria: genomics and molecular biology*. A. Burkovski (ed). Norfolk, UK: Caister Academic Press, pp. 203-216.

Sevvana M., Vijayan V., Zweckstetter M., Reinelt S., Madden D.R., Herbst-Irmer R., Sheldrick G.M., Bott M., Griesinger C. & Becker S., (2008) A ligand-induced switch in the periplasmic domain of sensor histidine kinase CitA. J. Mol. Biol. 377: 512-523.

Frunzke J., Engels V., Hasenbein S., Gätgens C. & Bott M., (2008) Co-ordinated regulation of gluconate catabolism and glucose uptake in *Corynebacterium glutamicum* by two functionally equivalent transcriptional regulators, GntR1 and GntR2. Mol. Microbiol. 67: 305-322.

Frunzke J., Bramkamp M., Schweitzer J.E. & Bott M., (2008) Population heterogeneity in *Corynebacterium glutamicum* ATCC 13032 caused by prophage CGP3. J. Bacteriol. 190: 5111-5119.

Frunzke J. & Bott M., (2008) Regulation of iron homeostasis in *Corynebacterium glutamicum*. In: *Corynebacteria: genomics and molecular biology*. A. Burkovski (ed). Norfolk, UK: Caister Academic Press, pp. 241-266.

2007

Steinbüchel A., Bott M. & Eikmanns B., (2007) Dedication to Professor Dr. Hermann Sahm on the occasion of his 65th birthday. Appl. Microbiol. Biotechnol. 76: 483-484.

Schultz C., Niebisch A., Gebel L. & Bott M., (2007) Glutamate production by *Corynebacterium glutamicum*: dependence on the oxoglutarate dehydrogenase inhibitor protein OdhI and protein kinase PknG. Appl. Microbiol. Biotechnol. 76: 691-700.

Schaaf S. & Bott M., (2007) Target genes and DNA-binding sites of the response regulator PhoR from *Corynebacterium glutamicum*. J. Bacteriol. 189: 5002-5011.

Polen T., Schluesener D., Poetsch A., Bott M. & Wendisch V.F., (2007) Characterization of citrate utilization in *Corynebacterium glutamicum* by transcriptome and proteome analysis. FEMS Microbiol. Lett. 273: 109-119.

Kabus A., Niebisch A. & Bott M., (2007) Role of cytochrome *bd* oxidase from *Corynebacterium glutamicum* in growth and lysine production. Appl. Environ. Microbiol. 73: 861-868.

Kabus A., Georgi T., Wendisch V.F. & Bott M., (2007) Expression of the *Escherichia coli* *pntAB* genes encoding a membrane-bound transhydrogenase in *Corynebacterium glutamicum* improves L-lysine formation. Appl. Microbiol. Biotechnol. 75: 47-53.

Cramer A., Auchter M., Frunzke J., Bott M. & Eikmanns B.J., (2007) RamB, the transcriptional regulator of acetate metabolism in *Corynebacterium glutamicum*, is subject to regulation by RamA and RamB. J. Bacteriol. 189: 1145-1149.

Bott M., (2007) Offering surprises: TCA cycle regulation in *Corynebacterium glutamicum*. Trends Microbiol. 15: 417-425.

Bott M., (2007) Corynebacteria: the good guys and the bad guys. Microbiology today May 2007: 74-77.

2006

Wennerhold J. & Bott M., (2006) The DtxR regulon of *Corynebacterium glutamicum*. J. Bacteriol. 188: 2907-2918.

Wendisch V.F., Bott M., Kalinowski J., Oldiges M. & Wiechert W., (2006) Emerging *Corynebacterium glutamicum* systems biology. J. Biotechnol. 124: 74-92.

Wendisch V.F., Bott M. & Eikmanns B.J., (2006) Metabolic engineering of *Escherichia coli* and *Corynebacterium glutamicum* for biotechnological production of organic acids and amino acids. Curr. Opin. Microbiol. 9: 268-274.

Reher M., Bott M. & Schönheit P., (2006) Characterization of glycerate kinase (2-phosphoglycerate forming), a key enzyme of the nonphosphorylative Entner-Doudoroff pathway, from the thermoacidophilic euryarchaeon *Picrophilus torridus*. FEMS Microbiol. Lett. 259: 113-119.

Niebisch A., Kabus A., Schultz C., Weil B. & Bott M., (2006) Corynebacterial protein kinase G controls 2-oxoglutarate dehydrogenase activity via the phosphorylation status of the OdhI protein. J. Biol. Chem. 281: 12300-12307.

Kocan M., Schaffer S., Ishige T., Sorger-Herrmann U., Wendisch V.F. & Bott M., (2006) Two-component systems of *Corynebacterium glutamicum*: Deletion analysis and involvement of the PhoS-PhoR system in the phosphate starvation response. J. Bacteriol. 188: 724-732.

Förster-Fromme K., Höschle B., Mack C., Bott M., Armbruster W. & Jendrossek D., (2006) Identification of genes and proteins necessary for catabolism of acyclic terpenes and leucine/isovalerate in *Pseudomonas aeruginosa*. Appl. Environm. Microbiol. 72: 4819-4828.

Cramer A., Gerstmeir R., Schaffer S., Bott M. & Eikmanns B.J., (2006) Identification of RamA, a novel LuxR-type transcriptional regulator of genes involved in acetate metabolism of *Corynebacterium glutamicum*. J. Bacteriol. 188: 2554-2567.

Brocker M. & Bott M., (2006) Evidence for activator and repressor functions of the response regulator MtrA from *Corynebacterium glutamicum*. FEMS Microbiol. Lett. 264: 205-212.

2005

Wennerhold J., Krug A. & Bott M., (2005) The AraC-type regulator RipA represses aconitase and other iron proteins from *Corynebacterium* under iron limitation and is itself repressed by DtxR. J. Biol. Chem. 280: 40500-40508.

Wendisch V.F. & Bott M., (2005) Phosphorus metabolism. In: Handbook of *Corynebacterium glutamicum*. L. Eggeling & M. Bott (eds). Boca Raton, Florida, USA: CRC Press, Taylor & Francis Group, pp. 377-396.

Krug A., Wendisch V.F. & Bott M., (2005) Identification of AcnR, a TetR-type repressor of the aconitase gene *acn* in *Corynebacterium glutamicum*. J. Biol. Chem. 280: 585-595.

Engels S., Ludwig C., Schweitzer J.E., Mack C., Bott M. & Schaffer S., (2005) The transcriptional activator ClgR controls transcription of genes involved in proteolysis and DNA repair in *Corynebacterium glutamicum*. Mol. Microbiol. 57: 576-591.

Eggeling L. & Bott M., (2005) Handbook of *Corynebacterium glutamicum*. Boca Raton, Florida, USA: CRC Press, Taylor & Francis Group.

Bott M. & Niebisch A., (2005) Respiratory energy metabolism. In: Handbook of *Corynebacterium glutamicum*. L. Eggeling & M. Bott (eds). Boca Raton, Florida, USA: CRC Press, Taylor & Francis Group, pp. 307-334.

2004

Möker N., Brocker M., Schaffer S., Krämer R., Morbach S. & Bott M., (2004) 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. Mol. Microbiol. 54: 420-438.

Heinz D., Bott M., Kalinowski J., Niefind K., Takors R. & Wendisch V.F., (2004) Die gläserne Zelle. In: Biotechnologie 2020 - von der gläsernen Zelle zum maßgeschneiderten Prozess. Frankfurt: DECHEMA e.V., pp. 6-13.

Engels S., Schweitzer J.E., Ludwig C., Bott M. & Schaffer S., (2004) *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 σ^H . Mol. Microbiol. 52: 285-302.

2003

Zelic B., Gerharz T., Bott M., Vasic-Racki B., Wandrey C. & Takors R., (2003) Fed-batch process for pyruvate production by recombinant *Escherichia coli* YVC202 strain. Eng. Life Sci. 3: 299-305.

Takors R., Zelić B., Gerharz T. & Bott M., (2003) Pyruvat-Produktion aus Glucose mit rekombinanten *Escherichia coli*-Stämmen. In: Transkript. pp. 96-99.

Reinelt S., Hofmann E., Gerharz T., Bott M. & Madden D.R., (2003) The structure of the periplasmic ligand-binding domain of the sensor kinase CitA reveals the first extracellular PAS domain. J. Biol. Chem. 278: 39189-39196.

Reinelt S., Hofmann E., Bott M., Gerharz T. & Madden D.R., (2003) Crystal structure of the ligand binding domain of the sensor kinase CitA. Biophys J 84: 355a-355a.

Niebisch A. & Bott M., (2003) Purification of a cytochrome *bc₁-aa₃* supercomplex with quinol oxidase activity from *Corynebacterium glutamicum* - Identification of a fourth subunit of cytochrome *aa₃* oxidase and mutational analysis of diheme cytochrome *c₁*. J. Biol. Chem. 278: 4339-4346.

Lange C., Rittmann D., Wendisch V.F., Bott M. & Sahm H., (2003) Global expression profiling and physiological characterization of *Corynebacterium glutamicum* grown in the presence of L-valine. Appl. Environm. Microbiol. 69: 2521-2532.

Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M., Burkovski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat L., Goesmann A., Hartmann M., Huthmacher K., Kramer R., Linke B., McHardy A.C., Meyer F., Mockel B., Pfefferle W., Puhler A., Rey D.A., Ruckert C., Rupp O., Sahm H., Wendisch V.F., Wiegrabe I. & Tauch A., (2003) The complete *Corynebacterium glutamicum*

ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins. J. Biotechnol. 104: 5-25.

Ishige T., Krause M., Bott M., Wendisch V.F. & Sahm H., (2003) The phosphate starvation stimulon of *Corynebacterium glutamicum* determined by DNA microarray analyses. J. Bacteriol. 185: 4519-4529.

Gerharz T., Reinelt S., Kaspar S., Scapozza L. & Bott M., (2003) Identification of basic amino acid residues important for citrate binding by the periplasmic receptor domain of the sensor kinase CitA. Biochemistry 42: 5917-5924.

Bott M. & Niebisch A., (2003) The respiratory chain of *Corynebacterium glutamicum*. J. Biotechnol. 104: 129-153.

Bott M., (2003) Muster des Lebens - die Analyse des Proteoms. Forschen in Jülich 1/2003: 12-13.

Bendt A.K., Burkovski A., Schaffer S., Bott M., Farwick M. & Hermann T., (2003) Towards a phosphoproteome map of *Corynebacterium glutamicum*. Proteomics 3: 1637-1646.

2002

Schneider K., Kästner C.N., Meyer M., Wessel M., Dimroth P. & Bott M., (2002) Identification of a gene cluster in *Klebsiella pneumoniae* which includes *citX*, a gene required for biosynthesis of the citrate lyase prosthetic group. J. Bacteriol. 184: 2439-+.

Kaspar S. & Bott M., (2002) The sensor kinase CitA (DpiB) of *Escherichia coli* functions as a high-affinity citrate receptor. Arch. Microbiol. 177: 313-321.

2001

Schaffer S., Weil B., Nguyen V.D., Dongmann G., Günther K., Nickolaus M., Hermann T. & Bott M., (2001) A high-resolution reference map for cytoplasmic and membrane-associated proteins of *Corynebacterium glutamicum*. Electrophoresis 22: 4404-4422.

Niebisch A. & Bott M., (2001) Molecular analysis of the cytochrome *bc₁-aa₃* branch of the *Corynebacterium glutamicum* respiratory chain containing an unusual diheme cytochrome *c₁*. Arch. Microbiol. 175: 282-294.

Meyer M., Dimroth P. & Bott M., (2001) Catabolite repression of the citrate fermentation genes in *Klebsiella pneumoniae*: Evidence for involvement of the cyclic AMP receptor protein. J. Bacteriol. 183: 5248-5256.

Hermann T., Pfefferle W., Baumann C., Busker E., Schaffer S., Bott M., Sahm H., Dusch N., Kalinowski J., Puhler A., Bendt A.K., Kramer R. & Burkovski A., (2001) Proteome analysis of *Corynebacterium glutamicum*. Electrophoresis 22: 1712-1723.

Gerharz T., Zelić B., Takors R. & Bott M., (2001) Produktion von Pyruvat aus Glucose mit *Escherichia coli*. In: Biokatalyse. S. Heiden & R. Erb (eds). Heidelberg: Spektrum Akademischer Verlag, pp. 29-33.

1996-2000

Schneider K., Dimroth P. & Bott M., (2000) Identification of triphosphoribosyl-dephospho-CoA as precursor of the citrate lyase prosthetic group. FEBS Lett. 483: 165-168.

Schneider K., Dimroth P. & Bott M., (2000) Biosynthesis of the prosthetic group of citrate lyase. Biochemistry 39: 9438-9450.

Steuber J., Krebs S., Bott M. & Dimroth P., (1999) A membrane-bound NAD(P)⁺-reducing hydrogenase provides reduced pyridine nucleotides during citrate fermentation by *Klebsiella pneumoniae*. J. Bacteriol. 181: 241-245.

Kaspar S., Perozzo R., Reinelt S., Meyer M., Pfister K., Scapozza L. & Bott M., (1999) The periplasmic domain of the histidine autokinase CitA functions as a highly specific citrate receptor. Mol. Microbiol. 33: 858-872.

Pos K.M., Dimroth P. & Bott M., (1998) The *Escherichia coli* citrate carrier CitT: a member of a novel eubacterial transporter family related to the 2-oxoglutarate/malate translocator from spinach chloroplasts. J. Bacteriol. 180: 4160-4165.

Meyer M., Dimroth P. & Bott M., (1997) *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*. J. Mol. Biol. 269: 719-731.

Bott M., Pfister K., Burda P., Kalbermatter O., Woehlke G. & Dimroth P., (1997) Methylmalonyl-CoA decarboxylase from *Propionigenium modestum*: cloning and sequencing of the structural genes and purification of the enzyme complex. Eur. J. Biochem. 250: 590-599.

Bott M., (1997) Genetics and biochemistry of citrate fermentation and citrate transport in enterobacteria. In: Institute of Microbiology. Zürich: ETH Zürich, pp. 49.

Bott M., (1997) Anaerobic citrate metabolism and its regulation in enterobacteria. Arch. Microbiol. 167: 78-88.

1991-1995

- Bott M., Thonymeyer L., Loferer H., Rossbach S., Tully R.E., Keister D., Appleby C.A. & Hennecke H., (1995) *Bradyrhizobium japonicum* cytochrome c_{550} is required for nitrate respiration but not for symbiotic nitrogen fixation. J. Bacteriol. 177: 2214-2217.
- Bott M., Meyer M. & Dimroth P., (1995) Regulation of anaerobic citrate metabolism in *Klebsiella pneumoniae*. Mol. Microbiol. 18: 533-546.
- Pos K.M., Bott M. & Dimroth P., (1994) Purification of two active fusion proteins of the Na^+ -dependent citrate carrier of *Klebsiella pneumoniae*. FEBS Lett. 347: 37-41.
- Bott M. & Dimroth P., (1994) *Klebsiella pneumoniae* genes for citrate lyase and citrate lyase ligase: localization, sequencing, and expression. Mol. Microbiol. 14: 347-356.
- Ritz D., Bott M. & Hennecke H., (1993) Formation of several bacterial c-type cytochromes requires a novel membrane-anchored protein that faces the periplasm. Mol. Microbiol. 9: 729-740.
- Loferer H., Bott M. & Hennecke H., (1993) *Bradyrhizobium japonicum* TlpA, a novel membrane-anchored thioredoxin-like protein involved in the biogenesis of cytochrome aa_3 and development of symbiosis. EMBO J. 12: 3373-3383.
- Hennecke H., Anthamatten D., Babst M., Bott M., Fischer H.M., Kaspar T., Kullik I., Loferer H., Preisig O., Ritz D. & Weidenhaupt M., (1993) Genetic and physiologic requirements for optimal bacteroid function in the *Bradyrhizobium japonicum*-soybean symbiosis. In: Advances in Molecular Genetics of Plant-Microbe Interactions. E. W. Nester & D. P. S. Verma (eds). Dordrecht: Kluwer Academic Publishers pp. 199-207.
- Bott M., Preisig O. & Hennecke H., (1992) Genes for a second terminal oxidase in *Bradyrhizobium japonicum*. Arch. Microbiol. 158: 335-343.
- Bott M., Ritz D. & Hennecke H., (1991) The *Bradyrhizobium japonicum* *cycM* gene encodes a membrane-anchored homolog of mitochondrial cytochrome c. J. Bacteriol. 173: 6766-6772.

1985-1990

- Hennecke H., Bott M., Ramseier T., Thöny-Meyer L., Fischer H.-M., Anthamatten D., Kullik I. & Thöny B., (1990) A genetic approach to analyze the critical role of oxygen in bacteroid metabolism. In: Nitrogen Fixation: Achievements and Objectives. P. M. Gresshoff, R. L.E., G. Stacey & W. E. Newton (eds). New York, London: Chapman and Hall pp. 293-300.
- Bott M., Bolliger M. & Hennecke H., (1990) Genetic analysis of the cytochrome-c- aa_3 branch of the *Bradyrhizobium japonicum* respiratory chain. Mol. Microbiol. 4: 2147-2157.
- Karrasch M., Bott M. & Thauer R.K., (1989) Carbonic anhydrase activity in acetate-grown *Methanosarcina barkeri*. Arch. Microbiol. 151: 137-142.

- Bott M. & Thauer R.K., (1989) The active species of CO₂ formed by carbon monoxide dehydrogenase from *Peptostreptococcus productus*. Z Naturforsch C 44: 392-396.
- Bott M. & Thauer R.K., (1989) Proton translocation coupled to the oxidation of carbon monoxide to CO₂ and H₂ in *Methanosarcina barkeri*. Eur. J. Biochem. 179: 469-472.
- Bott M. & Thauer R.K., (1987) Proton motive force-driven formation of CO from CO₂ and H₂ in methanogenic bacteria. Eur. J. Biochem. 168: 407-412.
- Bott M., Eikmanns B. & Thauer R.K., (1986) Coupling of carbon monoxide oxidation to CO₂ and H₂ with the phosphorylation of ADP in acetate-grown *Methanosarcina barkeri*. Eur. J. Biochem. 159: 393-398.
- Bott M., Eikmanns B. & Thauer R.K., (1985) Defective formation and or utilization of carbon monoxide in H₂/CO₂-fermenting methanogens dependent on acetate as carbon source. Arch. Microbiol. 143: 266-269.