

## Publication list Prof. Dr. Michael Bott

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197. **Spielmann, A., Baumgart, M. and 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>)
196. **Cormann, K.U., Baumgart, M. and 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>)
195. **Kallscheuer, N., Menezes, R., Foito, A., da Silva, M.H., Braga, A., Decker, W., Sevillano, D.M., Rosado-Ramos, R., Jardim, C., Oliveira, J., Ferreira, P., Rocha, I., Silva, A.R., Sousa, M., Allwood, J., Bott, M., Faria, N., Stewart, D., Ottens, M., Naesby, M., Santos, C. and Marienhagen, J. (2018)** Identification of a phenol against Huntington's disease in raspberries and its microbial production. *Plant Physiol.* (<http://dx.doi.org/10.1104/pp.18.01074>)
194. **Kranz, A., Steinmann, A., Degner, U., Mengus-Kaya, A., Matamouros, S., Bott, M. and Polen, T. (2018)** 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>)
193. **Morosov, X., Davoudi, C., Baumgart, M., Brocker, M., and Bott, M. (2018)** The copper-deprivation stimulon of *Corynebacterium glutamicum* comprises proteins for biogenesis of the actinobacterial cytochrome *bc<sub>1</sub>-aa<sub>3</sub>* supercomplex. *J. Biol. Chem.* 293: 15628-15640 (<http://dx.doi.org/10.1074/jbc.RA118.004117>)
192. **Alderwick, L., Birch, H.L., Krumbach, K., Bott, M., Eggeling, L. and Besra, G.S. (2018)** AftD functions as an a1? 5 arabinofuranosyltransferase involved in the biosynthesis of the mycobacterial cell wall core. *Cell Surface* 1: 2-14 (<http://dx.doi.org/10.1016/j.tcsw.2017.10.001>)
191. **Kranz, A., Busche, T., Vogel, A., Usadel, B., Kalinowski, J., Bott, M. and Polen, T. (2018)** RNAseq analysis of  $\alpha$ -proteobacterium *Gluconobacter oxydans* 621H. *BMC Genomics* 19:24 (<http://dx.doi.org/10.1186/s12864-017-4415-x>)
190. **Dudnik, A., Almeida, A.F., Andrade, R., Avila, B., Bañados, P., Barbay, D., Bassard, J.-E., Benkoulouche, M., Bott, M. et al. (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>)

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189. **Kleine, B., Chattopadhyay, A., Polen, T. Pinto, D., Mascher, T., Bott, M., Brocker, M., and 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>)
188. **Bott, M., Jäger, K.-E., Pietruszka, J., and 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>)
187. **Baumgart, M., Unthan, S., Kloß, R., Radek, A., Polen, T., Tenhaef, N., 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. and Noack, S. (2017)** *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>)

186. **Schulte, J., Baumgart, M., and 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>)
185. **Kallscheuer, N., Polen, T., Bott, M. and Marienhagen, J. (2017)** 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>)
184. **Kircher, M., Bott, M., and Marienhagen, J. (2017)** Die Bedeutung der Biotechnologie für die Bioökonomie. In: Bioökonomie für Einsteiger. J. Pietzsch (ed.), Springer Spektrum, Heidelberg, pp. 105-128 ([http://dx.doi.org/10.1007/978-3-662-53763-3\\_5](http://dx.doi.org/10.1007/978-3-662-53763-3_5))
183. **Kiefler, I., Bringer, S. and Bott, M. (2017)** Metabolic engineering of *Gluconobacter oxydans* 621H for improved biomass yield. Appl. Microbiol. Biotechnol. 101: 5453-5467 (<http://dx.doi.org/10.1007/s00253-017-8308-3>)
182. **Kranz, A., Vogel, A., Degner, U., Kiefler, I., Bott, M., Usadel, B. and 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>)
181. **Kallscheuer, N., Vogt, M., Bott, M., and 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. 258:190-196 (<http://dx.doi.org/10.1016/j.jbiotec.2017.01.006>)
180. **Kallscheuer, N., Gätgens, J., Lübcke, M., Pietruszka, J., Bott, M., and Polen, T. (2017)** Improved production of adipic acid with *Escherichia coli* by reversal of  $\beta$ -oxidation. Appl. Microbiol. Biotechnol. 101: 2371-2382. (<http://dx.doi.org/10.1007/s00253-016-8033-3>)
179. **Bott, M. and Eggeling, L. (2017)** Chapter 13: Novel technologies for optimal strain breeding. In Amino Acid Fermentation. A. Yokota and M. Ikeda (eds.), Advances in Biochemical Engineering/Biotechnology 159: 227-254 ([http://dx.doi.org/10.1007/10\\_2016\\_33](http://dx.doi.org/10.1007/10_2016_33))
178. **Schulte, J., Baumgart, M. and 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>)
177. **Hochheim, J., Kranz, A., Krumbach, K., Sokolowsky, S., Eggeling, L., Noack, S., Bocola, M., Bott, M. and 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>)
176. **Limberg, M.H., Aryani, T., Schulte, J., Mahr, R., Baumgart, M., Bott, M., Wiechert, W. and 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>)

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175. **Vogt, M., Brüsseler, C., van Ooyen, J., Bott, M., and 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>)
174. **Graf, S., Fedotovskaya, O., Kao, W., Hunte, C., Ädelroth, P., Bott, M., von Ballmoos, C. and 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>)

173. **Kao, W.-C., Kleinschroth, T., Nitschke, W., Baymann, F., Neehaul, Y., Hellwig, P., Richers, S., Vonck, J., Bott, M. and Hunte, C. (2015)** The obligate respiratory supercomplex from Actinobacteria. *BBA Bioenergetics* 1857: 1705-1714 (<http://dx.doi.org/10.1016/j.bbabi.2016.07.009>)
172. **Pahlke, J., Dostálová, H., Holátko, J., Degner, U., Bott, M., Pátek, M., and Polen, T. (2016)** The small 6C RNA of *Corynebacterium glutamicum* is involved in the SOS response. *RNA Biology* 13: 848-860 (<http://dx.doi.org/10.1080/15476286.2016.1205776>)
171. **Bringer, S. and Bott, M. (2016)** Central carbon metabolism and respiration in *Gluconobacter oxydans*. In: *Acetic acid bacteria: ecology and physiology*. K. Matsushita, H. Toyama, N. Tonouchi, and A. Kainuma (eds.). Chapter 11, pp. 235-253. Springer-Verlag, Berlin, Heidelberg, New York ([http://dx.doi.org/10.1007/978-4-431-55933-7\\_11](http://dx.doi.org/10.1007/978-4-431-55933-7_11))
170. **Kallscheuer, N., Vogt, M., Stenzel, A., Gätgens, J., Bott, M. and 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>)
169. **Nguyen, G.T.T., Erlenkamp, G., Jäck, O., Küberl, A., Bott, M., Fiorani, F., Gohlke, H., and Groth, G. (2016)** Chalcone-based selective inhibitors of a C<sub>4</sub> plant key enzyme as novel potential herbicides. *Sci. Rep.* 6, 27333 (<http://dx.doi.org/10.1038/srep27333>)
168. **Küberl, A., Polen, T. and 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>)
167. **Kallscheuer, N., Vogt, M., Kappelmann, J., Noack, S., Bott, M. and Marienhagen, J. (2016)** Identification of the *phd* gene cluster involved in phenylpropanoid utilization in *Corynebacterium glutamicum*. *Appl. Microbiol. Biotechnol.* 100: 1871-1881 (<http://dx.doi.org/10.1007/s00253-015-7165-1>)
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166. **Kim, E., Um, Y., Bott, M. and Woo, H. M. (2015)** Engineering of *Corynebacterium glutamicum* for growth and succinate production from levoglucosan as a pyrolytic sugar substrate. *FEMS Microbiol. Lett.* 362: fnv161
165. **Kiefler, I., Bringer, S. and 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
164. **Kallscheuer, N., Bott, M., van Ooyen, J. and Polen, T. (2015)** Single-domain FkpA from *Corynebacterium glutamicum* exhibits PPIase as well as chaperone activity and improves growth at increased temperature. *Appl. Environ. Microbiol.* 81: 7839-7850
163. **Michel, A., Koch-Koerfges, A., Krumbach, K., Brocker, M. and Bott, M. (2015)** Anaerobic growth of *Corynebacterium glutamicum* via mixed-acid fermentation. *Appl. Environ. Microbiol.* 81:7496 –7508
162. **Ostermann, S., Richhardt, J., Bringer, S., Bott, M., Wiechert, W., and Oldiges, M. (2015)** <sup>13</sup>C tracers for glucose degrading pathway discrimination in *Gluconobacter oxydans* 621H. *Metabolites* 5, 455-474
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158. **Küberl, A., Polen, T., and Bott, M. (2015)** Pupylierung – ein bakterielles Pendant zur Ubiquitinylierung. BIOSpektrum 02-2015,158-160
157. **Mustafi, N., Bott, M., and Frunzke, J. (2015)** Development and application of genetically-encoded biosensors for strain development and single cell analysis of *Corynebacterium glutamicum*. In: *Corynebacterium glutamicum: systems biology, biotechnological applications and control*. A. Burkovski (ed.), Caister Academic Press, Norfolk, UK, chapter 12, pp. 179-196
156. **Eikmanns, B.J. and Bott, M. (2015)** Engineering *Corynebacterium glutamicum* for production of organic acids and alcohols. In: *Corynebacterium glutamicum: systems biology, biotechnological applications and control*. A. Burkovski (ed.), Caister Academic Press, Norfolk, UK, chapter 8, pp. 111-137
155. **Witthoff, S., Schmitz, K., Niedenführ, S., Nöh, K., Noack, S., Bott, M. and Marienhagen, J. (2015)** Metabolic engineering of *Corynebacterium glutamicum* for the metabolization of methanol. Appl. Environm. Microbiol. 81: 2215-2225
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153. **Kortmann, M., Kuhl, V., Klaffl, S. and 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
152. **Unthan, S., Baumgart, M., Radek, A., Herbst, M., Siebert, D., Brühl, N., Bott, M., Wiechert, W., Marin, K., Hans, S., Krämer, R., Seibold, G., Frunzke, J., Kalinowski, J., Rückert, C., Wendisch, V.F. and Noack, S. (2015)** Top-down towards a chassis organism – Identification and deletion of irrelevant gene clusters from *Corynebacterium glutamicum*. Biotechnol. J. 10: 290-301
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150. **Bott, M. (2015)** Need for speed – finding productive mutations using transcription factor-based biosensors, FACS, and recombineering. Microb. Biotechnol. 8: 8-10
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