

Dr. Sabine Kleinsteuber: Publications since 1995

Publications in peer-reviewed scientific journals

- Bonatelli ML, T Rohwerder, D Popp, Y Liu, C Akay, C Schultz, K-P Liao, C Ding, T Reemtsma, L Adrian, and **S Kleinsteuber**. **2023**. Recently evolved combination of unique sulfatase and amidase genes enables bacterial degradation of the wastewater micropollutant acesulfame worldwide. *Front Microbiol* 14:1223838. doi: 10.3389/fmicb.2023.1223838
- Liu B, H Sträuber, F Centler, H Harms, UN da Rocha, and **S Kleinsteuber**. **2023**. Functional redundancy secures resilience of chain elongation communities upon pH shifts in closed bioreactor ecosystems. *Environ Sci Technol*. doi: 10.1021/acs.est.2c09573
- Logroño W, **S Kleinsteuber**, J Kretzschmar, F Harnisch, J De Vrieze, and M Nikolausz. **2023**. The microbiology of Power-to-X applications. *FEMS Microbiol Rev* 47:fuad013. doi: 10.1093/femsre/fuad013
- Baleeiro FCF, L Varchmin, **S Kleinsteuber**, H Sträuber, and A Neumann. **2023**. Formate-induced CO tolerance and methanogenesis inhibition in fermentation of syngas and plant biomass for carboxylate production. *Biotechnol Biofuels Bioprod* 16:26. doi: 10.1186/s13068-023-02271-w
- Baleeiro FCF, J Raab, **S Kleinsteuber**, A Neumann, and H Sträuber. **2023**. Microtrophic chain elongation with syngas and lactate as electron donors. *Microb Biotechnol* 16:322-336. doi: 10.1111/1751-7915.14163
- Becker D, D Popp, F Bonk, **S Kleinsteuber**, H Harms, and F Centler. **2023**. Metagenomic analysis of anaerobic microbial communities degrading short-chain fatty acids as sole carbon sources. *Microorganisms* 11:420. doi: 10.3390/microorganisms11020420
- Logroño W, P Kluge, **S Kleinsteuber**, H Harms, and M Nikolausz. **2022**. Effect of inoculum microbial diversity in ex situ biomethanation of hydrogen. *Bioengineering* 9:678. doi:10.3390/bioengineering9110678
- Bachmann M, M Wensch-Dorendorf, C Kuhnitzsch, **S Kleinsteuber**, D Popp, A Thierbach, SD Martens, O Steinhöfel, and A Zeyner. **2022**. Changes in composition and diversity of epiphytic microorganisms on field pea seeds, partial crop peas, and whole crop peas during maturation and ensiling with or without lactic acid inoculant. *Microbiol Spectrum* 10:e00953-22. doi:10.1128/spectrum.00953-22
- Xiong B, **S Kleinsteuber**, H Sträuber, C Dusny, H Harms, and LY Wick. **2022**. Impact of fungal hyphae on growth and dispersal of obligate anaerobic bacteria in aerated habitats. *mBio* 13:e00769-22. doi:10.1128/mbio.00769-22
- Baleeiro FCF, **S Kleinsteuber**, and H Sträuber. **2022**. Recirculation of H₂, CO₂, and ethylene improves carbon fixation and carboxylate yields in anaerobic fermentation. *ACS Sus Chem Eng* 10:4073-4081. doi:10.1021/acssuschemeng.1c05133
- Logroño W, M Nikolausz, H Harms, and **S Kleinsteuber**. **2022**. Physiological effects of 2-bromoethanesulfonate on hydrogenotrophic pure and mixed cultures. *Microorganisms* 10:355. doi:10.3390/microorganisms10020355
- Eziuzor SC, F Borim Corrêa, S Peng, J Schultz, **S Kleinsteuber**, UN da Rocha, L Adrian, and C Vogt. **2022**. Structure and functional capacity of a benzene-mineralizing, nitrate-reducing microbial community. *J Appl Microbiol* 132:2795-2811. doi:10.1111/jam.15443
- Liu B, H Sträuber, J Saraiva, H Harms, SG Silva, JC Kasmanas, **S Kleinsteuber**, and UN da Rocha. **2022**. Machine learning-assisted identification of bioindicators predicts medium-chain carboxylate production performance of an anaerobic mixed culture. *Microbiome* 10:48. doi:10.1186/s40168-021-01219-2
- Baleeiro FCF, MS Ardila, **S Kleinsteuber**, and H Sträuber. **2021**. Effect of oxygen contamination on propionate and caproate formation in anaerobic fermentation. *Front Bioeng Biotechnol* 9:725443. doi:10.3389/fbioe.2021.725443
- Baleeiro FCF, **S Kleinsteuber**, and H Sträuber. **2021**. Hydrogen as a co-electron donor for chain elongation with complex communities. *Front Bioeng Biotechnol* 9:650631. doi:10.3389/fbioe.2021.650631
- Logroño W, D Popp, M Nikolausz, P Kluge, H Harms, and **S Kleinsteuber**. **2021**. Microbial communities in flexible biomethanation of hydrogen are functionally resilient upon starvation. *Front Microbiol* 12:619632. doi:10.3389/fmicb.2021.619632

- Müller C, K Knöller, R Lucas, **S Kleinsteuber**, R Trubitsch, H Weiß, R Stollberg, HH Richnow, and C Vogt. **2021**. Benzene degradation in contaminated aquifers: Enhancing natural attenuation by injecting nitrate. *J Contam Hydrol* 238:103759. doi: 10.1016/j.jconhyd.2020.103759
- Liu B, D Popp, N Müller, H Sträuber, H Harms, and **S Kleinsteuber**. **2020**. Three novel *Clostridia* isolates produce *n*-caproate and *iso*-butyrate from lactate: comparative genomics of chain-elongating bacteria. *Microorganisms* 8:1970. doi:10.3390/microorganisms8121970
- Liu B, D Popp, H Sträuber, H Harms, and **S Kleinsteuber**. **2020**. Draft genome sequences of three *Clostridia* isolates involved in lactate-based chain elongation. *Microbiol Resour Announc* 9:e00679-20. doi:10.1128/MRA.00679-20
- Logroño W, D Popp, **S Kleinsteuber**, H Sträuber, H Harms, and M Nikolausz. **2020**. Microbial resource management for ex situ biomethanation at alkaline pH. *Microorganisms* 8:614. doi:10.3390/microorganisms8040614
- Liu B, **S Kleinsteuber**, F Centler, H Harms, and H Sträuber. **2020**. Competition between butyrate fermenters and chain-elongating bacteria limits the efficiency of medium-chain carboxylate production. *Front Microbiol* 11:336. doi:10.3389/fmicb.2020.00336
- Krause JL, SS Schaepe, K Fritz-Wallace, B Engelmann, U Rolle-Kampczyk, **S Kleinsteuber**, F Schattenberg, Z Liu, S Mueller, N Jehmlich, M von Bergen, and G Herberth. **2020**. Following the community development of SIHUMix – a new intestinal *in vitro* model for bioreactor use. *Gut Microbes* 11:1116-1129. doi:10.1080/19490976.2019.1702431
- Özbayram EG, **S Kleinsteuber**, and M Nikolausz. **2020**. Biotechnological utilization of animal gut microbiota for valorization of lignocellulosic biomass. *Appl Microbiol Biotechnol* 104:489-508. doi:10.1007/s00253-019-10239-w
- Kasmaei KM, D Schlosser, H Sträuber, and **S Kleinsteuber**. **2020**. Does glucose affect the de-esterification of methyl ferulate by *Lactobacillus buchneri*? *Microbiology Open* 9:e971. doi:10.1002/mbo3.971
- Kleinsteuber S**, T Rohwerder, U Lohse, B Seiwert, and T Reemtsma. **2019**. Sated by a zero-calorie sweetener – Wastewater bacteria can feed on acesulfame. *Front Microbiol* 10:2606. doi:10.3389/fmicb.2019.02606
- Chowdhury R, S Ghosh, D Manna, S Das, S Dutta, **S Kleinsteuber**, H Sträuber, MK Hassan, S Kuitinen, and A Pappinen. **2019**. Hybridization of sugar-carboxylate-syngas platforms for the production of bio-alcohols from lignocellulosic biomass (LCB) - A state-of-the-art review and recommendations. *Energy Convers Manag* 200:112111. doi:10.1016/j.enconman.2019.112111
- Baleeiro FCF, **S Kleinsteuber**, A Neumann, and H Sträuber. **2019**. Syngas-aided anaerobic fermentation for medium-chain carboxylate and alcohol production: the case for microbial communities. *Appl Microbiol Biotechnol*. doi:10.1007/s00253-019-10086-9
- Lambrecht J, N Cichocki, F Schattenberg, **S Kleinsteuber**, H Harms, S Müller, and H Sträuber. **2019**. Key sub-community dynamics of medium-chain carboxylate production. *Microb Cell Fact* 18:92. doi:10.1186/s12934-019-1143-8
- Ziganshin AM, B Wintsche, J Seifert, M Carstensen, J Born, and **S Kleinsteuber**. **2019**. Spatial separation of metabolic stages in a tube anaerobic baffled reactor: reactor performance and microbial community dynamics. *Appl Microbiol Biotechnol* 103:3915-3929. doi:10.1007/s00253-019-09767-2
- Bonk F, D Popp, S Weinrich, H Sträuber, D Becker, **S Kleinsteuber**, H Harms, and F Centler. **2019**. Determination of microbial maintenance in acetogenesis and methanogenesis by experimental and modeling techniques. *Front Microbiol* 10:166. doi:10.3389/fmicb.2019.00166
- Lv Z, AF Leite, H Harms, K Glaser, J Liebetrau, **S Kleinsteuber**, and M Nikolausz. **2019**. Microbial community shifts in biogas reactors upon complete or partial ammonia inhibition. *Appl Microbiol Biotechnol* 103:519-533. doi:10.1007/s00253-018-9444-0
- Bonk F, D Popp, S Weinrich, H Sträuber, **S Kleinsteuber**, H Harms, and F Centler. **2018**. Ammonia inhibition of anaerobic volatile fatty acid degrading microbial communities. *Front Microbiol* 9:2921. doi:10.3389/fmicb.2018.02921

- Bonk F, D Popp, S Weinrich, H Sträuber, **S Kleinsteuber**, H Harms, and F Centler. **2018**. Intermittent fasting for microbes: how discontinuous feeding increases functional stability in anaerobic digestion. *Biotechnol Biofuels* 11:274. doi:10.1186/s13068-018-1279-5
- Günther S, D Becker, T Hübschmann, S Reinert, **S Kleinsteuber**, S Müller, and C Wilhelm. **2018**. Long-term biogas production from glycolate by diverse and highly dynamic communities. *Microorganisms* 6:103. doi:10.3390 / microorganisms6040103
- Sträuber H, F Bühligen, **S Kleinsteuber**, and M Dittrich-Zechendorf. **2018**. Carboxylic acid production from ensiled crops in anaerobic solid-state fermentation - trace elements as pH controlling agents support microbial chain elongation with lactic acid. *Eng Life Sci* 18:447-458. doi: 10.1002/elsc.201700186
- Özbayram EG, **S Kleinsteuber**, M Nikolausz, B Ince, and O Ince. **2018**. Bioaugmentation of anaerobic digesters treating lignocellulosic feedstock by enriched microbial consortia. *Eng Life Sci* 18:440-446. doi:10.1002/elsc.201700199
- Wintsche B, N Jehmlich, D Popp, H Harms, and **S Kleinsteuber**. **2018**. Metabolic adaptation of methanogens in anaerobic digesters upon trace element limitation. *Front Microbiol* 9:405. doi:10.3389/fmicb.2018.00405
- Kahl S, **S Kleinsteuber**, J Nivala, M van Afferden, and T Reemtsma. **2018**. Emerging biodegradation of the previously persistent artificial sweetener acesulfame in biological wastewater treatment. *Environ Sci Technol* 52:2717-2725. doi:10.1021/acs.est.7b05619
- Özbayram EG, O Ince, B Ince, H Harms, and **S Kleinsteuber**. **2018**. Comparison of rumen and manure microbiomes and implications for the inoculation of anaerobic digesters. *Microorganisms* 6:15. doi:10.3390 / microorganisms6010015
- Özbayram EG, **S Kleinsteuber**, M Nikolausz, B Ince, and O Ince. **2018**. Enrichment of lignocellulose-degrading microbial communities from natural and engineered methanogenic environments. *Appl Microbiol Biotechnol* 102:1035-1043. doi:10.1007/s00253-017-8632-7
- Keller AH, **S Kleinsteuber**, and C Vogt. **2018**. Anaerobic benzene mineralization by nitrate-reducing and sulfate-reducing microbial consortia enriched from the same site: Comparison of community composition and degradation characteristics. *Microb Ecol* 75:941-953. doi:10.1007/s00248-017-1100-1
- Popp D, CM Plugge, **S Kleinsteuber** , H Harms, and H Sträuber. **2017**. Inhibitory effect of coumarin on syntrophic fatty acid oxidizing and methanogenic cultures and biogas reactor microbiomes. *Appl Environ Microbiol* 83:e00438-17. doi:10.1128/AEM.00438-17
- Özbayram EG, **S Kleinsteuber**, M Nikolausz, B Ince, and O Ince. **2017**. Effect of bioaugmentation by cellulolytic bacteria enriched from sheep rumen on methane production from wheat straw. *Anaerobe* 46:122-130. doi:10.1016/j.anaerobe.2017.03.013
- Lucas R, J Groeneveld, H Harms, K Johst, K Frank, and **S Kleinsteuber**. **2017**. A critical evaluation of ecological indices for the comparative analysis of microbial communities based on molecular datasets. *FEMS Microbiol Ecol* 93:fiw209. doi:10.1093/femsec/fiw209
- Wintsche B, K Glaser, H Sträuber, F Centler, J Liebetrau, H Harms, and **S Kleinsteuber**. **2016**. Trace elements induce predominance among methanogenic activity in anaerobic digestion. *Front Microbiol* 7:2034. doi:10.3389/fmicb.2016.02034
- Ziganshin AM, EE Ziganshina, **S Kleinsteuber**, and M Nikolausz. **2016**. Comparative analysis of methanogenic communities in different laboratory-scale anaerobic digesters. *Archaea*. doi:10.1155/2016/3401272
- Bühligen F, R Lucas, M Nikolausz, and **S Kleinsteuber**. **2016**. A T-RFLP database for the rapid profiling of methanogenic communities in anaerobic digesters. *Anaerobe* 39:114-116. doi:10.1016/j.anaerobe.2016.03.013
- Ziganshin AM, T Schmidt, Z Lv, J Liebetrau , HH Richnow , **S Kleinsteuber**, and M Nikolausz. **2016**. Reduction of the hydraulic retention time at constant high organic loading rate to reach the microbial limits of anaerobic digestion in various reactor systems. *Bioresour Technol* 217:62-71. doi:10.1016/j.biortech.2016.01.096
- Starke R, A Keller, N Jehmlich, C Vogt, HH Richnow, **S Kleinsteuber**, M von Bergen, and J Seifert. **2016**. Pulsed ¹³C₂-acetate protein-SIP unveils *Epsilonproteobacteria* as dominant acetate utilizers in a sulfate-reducing microbial community mineralizing benzene. *Microb Ecol* 71:901-911. doi:10.1007/s00248-016-0731-y

- Sträuber H., R Lucas, and **S Kleinsteuber**. 2016. Metabolic and microbial community dynamics during the anaerobic digestion of maize silage in a two-phase process. *Appl Microbiol Biotechnol* 100:479–491. doi:10.1007/s00253-015-6996-0
- Akyol Ç, EG Özbayram, O Ince, **S Kleinsteuber**, and B Ince. 2016. Anaerobic co-digestion of cow manure and barley: Effect of cow manure to barley ratio on methane production and digestion stability. *Environ Prog Sustainable Energy* 35:589-595. doi:10.1002/ep.12250
- Keller AH, KM Schleinitz, R Starke, S Bertilsson, C Vogt, and **S Kleinsteuber**. 2015. Metagenome-based metabolic reconstruction reveals the ecophysiological function of *Epsilonproteobacteria* in a hydrocarbon-contaminated sulfidic aquifer. *Front Microbiol* 6:1396. doi:10.3389/fmicb.2015.01396
- Popp D, S Schrader, **S Kleinsteuber**, H Harms, and H Sträuber. 2015. Biogas production from coumarin-rich plants – inhibition by coumarin and recovery by adaptation of the bacterial community. *FEMS Microbiol Ecol* 91:fiv103. doi:10.1093/femsec/fiv103
- Sträuber H, F Bühligen, **S Kleinsteuber**, M Nikolausz, and K Porsch. 2015. Improved anaerobic fermentation of wheat straw by alkaline pre-treatment and addition of alkali-tolerant microorganisms. *Bioengineering* 2:66-93. doi:10.3390/bioengineering2020066
- Lucas R, A Kuchenbuch, I Fetzer, H Harms, and **S Kleinsteuber**. 2015. Long-term monitoring reveals stable and remarkably similar microbial communities in parallel full-scale biogas reactors digesting energy crops. *FEMS Microbiol Ecol* 91:fiv004 . doi:10.1093/femsec/fiv004
- Bozinovski D, M Taubert, **S Kleinsteuber**, H-H Richnow, M von Bergen, C Vogt, and J Seifert. 2014. Metaproteogenomic analysis of a sulfate-reducing enrichment culture reveals genomic organization of key enzymes in *m*-xylene degradation pathway and metabolic activity of proteobacteria. *Syst Appl Microbiol* 37:448-501. doi:10.1016/j.syapm.2014.07.005
- Schmidt T, AM Ziganshin, M Nikolausz, F Scholwin, M Nelles, **S Kleinsteuber**, and J Pröter. 2014. Effects of the reduction of the hydraulic retention time to 1.5 days at constant organic loading in CSTR, ASBR, and fixed-bed reactors – Performance and methanogenic community composition. *Biomass Bioenergy* 69:241-248. doi:10.1016/j.biombioe.2014.07.021
- Poser A, C Vogt, K Knöllner, J Ahlheim, H Weiss, **S Kleinsteuber**, and H-H Richnow. 2014. Stable sulfur and oxygen isotope fractionation of anoxic sulfide oxidation by two different enzymatic pathways. *Environ Sci Technol* 48:9094-9102. doi:10.1021/es404808r
- Dorer C, C Vogt, **S Kleinsteuber**, AJ Stams, and H-H Richnow. 2014. Compound-specific isotope analysis as a tool to characterize biodegradation of ethylbenzene. *Environ Sci Technol* 48:9122-9132. doi:10.1021/es500282t
- Kuppardt A, **S Kleinsteuber**, C Vogt, T Lüders, H Harms, and A Chatzinotas. 2014. Phylogenetic and functional diversity within toluene-degrading, sulphate-reducing consortia enriched from a contaminated aquifer. *Microb Ecol* 68:222-234. doi:10.1007/s00248-014-0403-8
- Tischer K, **S Kleinsteuber**, KM Schleinitz, I Fetzer, O Spott, F Stange, U Lohse, J Franz, F Neumann, S Gerling, C Schmidt, E Hasselwander, H Harms, and A Wendeborg. 2013. Microbial communities along biogeochemical gradients in a hydrocarbon-contaminated aquifer. *Environ Microbiol* 15:2603-2615. doi:10.1111/1462-2920.12168
- Ziganshin AM, J Liebetrau, J Pröter, and **S Kleinsteuber**. 2013. Microbial community structure and dynamics during anaerobic digestion of various agricultural waste materials. *Appl Microbiol Biotechnol* 97:5161-5174. doi:10.1007/s00253-013-4867-0
- Wagner A, L Segler, **S Kleinsteuber**, G Sawers, H Smidt, and U Lechner. 2013. Regulation of reductive dehalogenase gene transcription in *Dehalococcoides mccartyi*. *Phil Trans R Soc B* 368:20120317. doi:10.1098/rstb.2012.0317
- Nikolausz M, RFH Walter, H Sträuber, J Liebetrau, T Schmidt, **S Kleinsteuber**, F Bratfisch, U Günther, and HH Richnow. 2013. Evaluation of stable isotope fingerprinting techniques for the assessment of the predominant methanogenic pathways in anaerobic digesters. *Appl Microbiol Biotechnol* 97:2251-2262. doi:10.1007/s00253-012-4657-0
- Leibelung S, MB Maeß, F Centler, **S Kleinsteuber**, M von Bergen, M Thullner, H Harms, and RH Müller. 2013. Posttranslational oxidative modification of (*R*)-2-(2,4-dichlorophenoxy)propionate/ α -ketoglutarate-dependent

dioxygenases (RdpA) leads to improved degradation of 2,4-dichlorophenoxyacetate (2,4-D). *Eng Life Sci* 13:278-291. doi:10.1002/elsc.201100093

Ziganshin AM, EE Ziganshina, **S Kleinsteuber**, J Pröter, and ON Ilinskaya. **2012**. Methanogenic community dynamics during anaerobic utilization of agricultural wastes. *Acta Naturae* 4:91-97.

Sträuber H, M Schröder, and **S Kleinsteuber**. **2012**. Metabolic and microbial community dynamics during the hydrolytic and acidogenic fermentation in a leach-bed process. *Energy, Sustainability and Society* 2:13. doi:10.1186/2192-0567-2-13

Taubert M, C Vogt, T Wubet, **S Kleinsteuber**, MT Tarkka, H Harms, F Buscot, H-H Richnow, M von Bergen, and J Seifert. **2012**. Protein-SIP enables time-resolved analysis of the carbon flux in a sulfate-reducing, benzene-degrading microbial consortium. *ISME J* 6:2291-2301. doi:10.1038/ismej.2012.68

Müller S, T Hübschmann, **S Kleinsteuber**, and C Vogt. **2012**. High resolution single cell analytics to follow microbial community dynamics in anaerobic ecosystems. *Methods* 57:338-349. doi:10.1016/j.ymeth.2012.04.001

Kleinsteuber S, KM Schleinitz, and C Vogt. **2012**. Key players and team play: anaerobic microbial communities in hydrocarbon-contaminated aquifers. *Appl Microbiol Biotechnol* 94:851-873

Vogt C, **S Kleinsteuber**, and H-H Richnow. **2011**. Anaerobic benzene degradation by bacteria. *Microb Biotechnol* 4:710-724. doi:10.1111/j.1751-7915.2011.00260.x

Ziganshin, AM, T Schmidt, F Scholwin, ON Il'inskaya, H Harms, and **S Kleinsteuber**. **2011**. Bacteria and archaea involved in anaerobic digestion of distillers grains with solubles. *Appl Microbiol Biotechnol* 89:2039-2052. doi:10.1007/s00253-010-2981-9

Bombach P, T Hübschmann, I Fetzer, **S Kleinsteuber**, R Geyer, H Harms, and S Müller. **2011**. Resolution of natural microbial community dynamics by community fingerprinting, flow cytometry and trend interpretation analysis. *Adv Biochem Eng Biotechnol* 124:151-81. doi:10.1007/10_2010_82

Witzig M, J Boguhn, **S Kleinsteuber**, I Fetzer, and M Rodehutsord. **2010**. Influence of the maize silage to grass silage ratio and feed particle size of rations for ruminants on the community structure of ruminal *Firmicutes in vitro*. *J Appl Microbiol* 109:1998-2010. doi:10.1111/j.1365-2672.2010.04829.x

Schleinitz KM, T Vallaëys, and **S Kleinsteuber**. **2010**. Structural characterisation of ISCR8, ISCR2 and ISCR23, subgroups of IS91-like insertion elements. *Antimicrob Agents Chemother* 54:4321-4328. doi:10.1128/AAC.00006-10

Jehmlich N, **S Kleinsteuber**, C Vogt, D Benndorf, H Harms, F Schmidt, M von Bergen, and J Seifert. **2010**. Phylogenetic and proteomic analysis of an anaerobic toluene degrading community. *J Appl Microbiol* 109:1937-1945. doi:10.1111/j.1365-2672.2010.04823.x

Wick LY, F Buchholz, I Fetzer, **S Kleinsteuber**, C Härtig, L Shi, A Miltner, H Harms, and GN Pucci. **2010**. Responses of soil microbial communities to weak electric fields. *Sci Total Environ* 408:4886-4893. doi:10.1016/j.scitotenv.2010.06.048

Witzig M, J Boguhn, **S Kleinsteuber**, I Fetzer, and M Rodehutsord. **2010**. Effect of the corn silage to grass silage ratio and feed particle size of rations for ruminants on the ruminal *Bacteroides-Prevotella* community *in vitro*. *Anaerobe* 16:412-419. doi:10.1016/j.anaerobe.2010.05.002

Koschorreck M, W Geller, T Neu, **S Kleinsteuber**, T Kunze, A Trosiener, and K Wendt-Potthoff. **2010**. Structure and function of the microbial community in an *in situ* reactor to treat an acidic mine pit lake. *FEMS Microbiol Ecol* 73:385-395. doi:10.1111/j.1574-6941.2010.00886.x

Herrmann S, **S Kleinsteuber**, A Chatzinotas, S Kuppardt, T Lueders, H-H Richnow, and C Vogt. **2010**. Functional characterization of an anaerobic benzene-degrading enrichment culture by DNA stable isotope probing. *Environ Microbiol* 12:4012-411. doi:10.1111/j.1462-2920.2009.02077.x

Müller S, C Vogt, M Laube, H Harms, and **S Kleinsteuber**. **2009**. Community dynamics within a bacterial consortium during growth on toluene under sulfate-reducing conditions. *FEMS Microbiol Ecol* 70:586-596. doi:10.1111/j.1574-6941.2009.00768.x

Schleinitz, KM, S Schmeling, N Jehmlich, M von Bergen, H Harms, **S Kleinsteuber**, C Vogt, and G Fuchs. **2009**. Phenol degradation in the strictly anaerobic iron reducing bacterium *Geobacter metallireducens* GS15. *Appl Environ Microbiol* 75:3912-3919. doi:10.1128/AEM.01525-08

- Porsch K, J Meier, **S Kleinsteuber**, and K Wendt-Potthoff. **2009**. Importance of different physiological groups of iron reducing microorganisms in an acidic mining lake remediation experiment. *Microb Ecol* 57:701-717. doi:10.1007/s00248-009-9505-0
- Wagner A, L Adrian, **S Kleinsteuber**, JJ Andreesen, and U Lechner. **2009**. Transcription analysis of genes encoding homologues of reductive dehalogenases in "*Dehalococcoides*" sp. strain CBDB1 using terminal restriction fragment length polymorphism and quantitative PCR. *Appl Environ Microbiol* 75:1876-1884. doi:10.1128/AEM.01042-08
- Günther S, M Trutnau, **S Kleinsteuber**, G Hause, T Bley, I Röske, H Harms, and S Müller. **2009**. Dynamics of polyphosphate accumulating bacteria in waste water treatment plant communities detected via DAPI and tetracycline labeling. *Appl Environ Microbiol* 75:2111-2121. doi:10.1128/AEM.01540-08
- Kleinsteuber S**, KM Schleinitz, J Breitfeld, H Harms, H-H Richnow, and C Vogt. **2008**. Molecular characterization of bacterial communities mineralizing benzene under sulfate-reducing conditions. *FEMS Microbiol Ecol* 66:143-157. doi:10.1111/j.1574-6941.2008.00536.x
- Herrmann S, **S Kleinsteuber**, T Neu, H-H Richnow, and C Vogt. **2008**. Enrichment of anaerobic benzene degrading microorganisms by *in situ* microcosms. *FEMS Microbiol Ecol* 63:94-106. doi:10.1111/j.1574-6941.2007.00401.x
- Kleinsteuber S**, F-D Müller, A Chatzinotas, K Wendt-Potthoff, and H Harms. **2008**. Diversity and *in situ* quantification of *Acidobacteria* subdivision 1 in an acidic mining lake. *FEMS Microbiol. Ecol.* 63:107-117. doi:10.1111/j.1574-6941.2007.00402.x
- Kiesel B, RH Müller, and **S Kleinsteuber**. **2007**. Adaptive potential of alkaliphilic bacteria towards chloroaromatic substrates assessed by a *gfp*-tagged 2,4-D degradation plasmid. *Eng Life Sci* 7:361-372. doi:10.1002/elsc.200720200
- Kleinsteuber S**, V Riis, I Fetzner, H Harms, and S Müller. **2006**. Population dynamics within a microbial consortium during growth on diesel fuel in saline environments. *Appl Environ Microbiol* 72:3531-3542. doi:10.1128/AEM.72.5.3531-3542.2006
- Vogt C, A Lösche, **S Kleinsteuber**, and S Müller. **2005**. Population profiles of a stable, commensalistic bacterial culture grown with toluene under sulphate-reducing conditions. *Cytometry Part A* 66A:91-102. doi:10.1002/cyto.a.20158
- Schleinitz KM, **S Kleinsteuber**, T Vallaey, and W Babel. **2004**. Localization and characterization of two novel genes encoding stereospecific 2(2,4-dichlorophenoxy)propionate cleavage in *Delftia acidovorans* MC1. *Appl Environ Microbiol* 70:5357-5365. doi:10.1128/AEM.70.9.5357-5365.2004
- Maskow T and **S Kleinsteuber**. **2004**. Carbon and energy fluxes during haloadaptation of *Halomonas* sp. EF11 growing on phenol. *Extremophiles* 8:133-141. doi:10.1007/s00792-003-0372-1
- Riis V, **S Kleinsteuber**, and W Babel. **2003**. Influence of high salinities on the degradation of diesel fuel by bacterial consortia. *Can. J Microbiol* 49:713-721. doi:10.1139/W03-083
- Hoffmann D, **S Kleinsteuber**, RH Müller, and W Babel. **2003**. A transposon encoding the complete 2,4-dichlorophenoxyacetic acid degradation pathway in the alkali-tolerant strain *Delftia acidovorans* P4a. *Microbiology* 149:2545-2556. doi:10.1099/mic.0.26260-0
- Müller, RH, **S Kleinsteuber**, and W Babel. **2001**. Physiological and genetic characteristics of two bacterial strains utilizing phenoxypropionate- and phenoxyacetate herbicides. *Microbiol Res* 156:121-131. doi:10.1078/0944-5013-00089
- Kleinsteuber S**, RH Müller, and W Babel. **2001**. Expression of the 2,4-D degradative pathway of pJP4 in an alkaliphilic, moderately halophilic soda lake isolate, *Halomonas* sp. EF43. *Extremophiles* 5:375-384. doi:10.1007/s007920100202
- Hoffmann D, **S Kleinsteuber**, RH Müller, and W Babel. **2001**. Development and application of PCR primers for the detection of the *tfp* genes in *Delftia acidovorans* P4a involved in the degradation of 2,4-D. *Acta Biotechnol* 21:321-331. doi:10.1002/1521-3846(200111)21:4<321::AID-ABIO321>3.0.CO;2-I
- Müller RH, S Jorks, **S Kleinsteuber**, and W Babel. **1999**. *Comamonas acidovorans* strain MC1: a new isolate capable of degrading the chiral herbicides dichlorprop and mecoprop and the herbicides 2,4-D and MCPA. *Microbiol Res* 154:241-246. doi:10.1016/S0944-5013(99)80021-4

Müller RH, S Jorks, **S Kleinsteuber**, and W Babel. **1998**. Degradation of various chlorophenols under alkaline conditions by Gram-negative bacteria closely related to *Ochrobactrum anthropi*. *J Basic Microbiol* 38:269-281. doi:10.1002/(SICI)1521-4028(199809)38:4<269::AID-JOBM269>3.0.CO;2-P

Kleinsteuber S, D Hoffmann, RH Müller, and W Babel. **1998**. Detection of chlorocatechol 1,2-dioxygenase genes in proteobacteria by PCR and gene probes. *Acta Biotechnol* 18:231-240. doi:10.1002/abio.370180306

Quiñones A, G Wandt, **S Kleinsteuber**, and W Messer. **1997**. DnaA protein stimulates *polA* gene expression in *Escherichia coli*. *Mol Microbiol* 23:1193-1202. doi:10.1046/j.1365-2958.1997.2961658.x

Kleinsteuber S and A Quiñones. **1995**. Expression of the *dnaB* gene of *Escherichia coli* is inducible by replication-blocking DNA damage in a *recA*-independent manner. *Mol Gen Genet* 248:695-702. doi:10.1007/bf02191709

Book chapters

Popp D, F Bonk, D Becker, and **S Kleinsteuber**. **2020**. Nucleic acid based molecular biology tests. In: Liebetrau J, Pfeiffer D (Eds.) Collection of Methods for Biogas – Methods to determine parameters for analysis purposes and parameters that describe processes in the biogas sector. Series „Biomass energy use” Vol 07, 2nd ed., DBFZ, Leipzig, Germany. ISBN 978-3-946629-47-4, ISSN (online): 2698-9190, p. 232 - 244

Kleinsteuber S. **2018**. Metagenomics of methanogenic communities in anaerobic digesters. In: AJM Stams, DZ Sousa (eds.), Biogenesis of Hydrocarbons, *Handbook of Hydrocarbon and Lipid Microbiology*, Springer Nature. doi:10.1007/978-3-319-53114-4_16-1

Robles C, RB Nair, **S Kleinsteuber**, M Nikolausz, and I Sárvári Horváth. **2018**. Biogas production: microbiological aspects. In: M Tabatabaei, H Ghanavati (eds.) *Biogas, Biofuel and Biorefinery Technologies Vol. 6*. Springer Nature, p. 163 – 198. doi:10.1007/978-3-319-77335-3_7