

Publications

2024

- [131] Sarpong N, **Seifert J**, Bennewitz J, Rodehutscord M, Camarinha-Silva A (2024) Microbial signatures and enterotype clusters in fattening pigs: implications for nitrogen utilization efficiency. *Frontiers in Microbiology*. 15. 10.3389/fmicb.2024.1354537

- [130] Schmid M, Weishaar R, **Seifert J**, Camarinha-Silva A, Rodehutscord M, Bennewitz J (2024) Genomic analyses of nitrogen utilization efficiency, its indicator trait blood urea nitrogen and the relationship to classical growth performance and feed efficiency traits in a Landrace x Piétrain crossbred population. *Journal of Animal Breeding and Genetics*. doi: 10.1111/jbg.12864

- [129] Rios-Galicia B, Sáenz JS, Yergaliyev T, Roth C Camarinha-Silva A, **Seifert J** (2024) Novel taxonomic and functional diversity of eight bacteria from the upper digestive tract of chicken.

International Journal of Systematic and Evolutionary Microbiology. 74(1): 006210. doi: 10.1099/ijsem.0.006210.

2023

- [128] Hau JL, Schleicher L, Herdan S, Simon J, **Seifert J**, Fritz G, Steuber J (2023) Functionality of the Na⁺-translocating NADH:quinone oxidoreductase and quinol:fumarate reductase from *Prevotella bryantii* inferred from homology modeling. *Archives in Microbiology*. 206(1):32. doi: 10.1007/s00203-023-03769-5.

- [127] Dahl S, **Seifert J**, Camarinha-Silva A, Cheng Y-C, Hernández-Arriaga A, Hudler M, Windisch W, König A (2023) Microbiota and nutrient portraits of European roe deer (*Capreolus capreolus*) rumen contents in characteristic southern German habitats. *Microbial Ecology*. 86(4):3082-3096. doi: 10.1007/s00248-023-02308-5

- [126] Berghaus D, Haese E, Weishaar R, Sarpong N, Kurz A, **Seifert J**, Camarinha Silva A, Bennewitz J, Chillon T, Stefanski V, Rodehutscord M (2023) Nitrogen and lysine utilization efficiencies, protein turnover, and blood urea concentrations in crossbred grower pigs at marginal dietary lysine concentration. *Journal of Animal Science*. skad335. doi: 10.1093/jas/skad335

- [125] Dahl S, **Seifert J**, Camarinha-Silva A, Hernández-Arriaga A, Windisch W, König A (2023) "Get the best out of what comes in" – Adaptation of the microbiota of chamois (*Rupicapra rupicapra*) to seasonal forage availability in the Bavarian Alps. *Frontiers in Microbiology*. 14:1238744. doi: 10.3389/fmicb.2023.1238744

- [124] Rios Galicia B, Sáenz JS, Yergaliyev T, Camarinha-Silva A, **Seifert J** (2023) Host specific adaptations of *Ligilactobacillus aviarius* to poultry. *Current Research in Microbial Sciences*. 5. 100199. doi: 10.1016/j.crmicr.2023.100199

- [123] Serrano-Villar S, Tincati C, Raju SC, Sáenz JS, Moreno E, Bargiela R, Cabello A, Sendagorta E, Kurz A, Perez Molina JA, de Benito A, Hov JR, Fernandez-Lopez L, Muriel A, del Campo R, Moreno S, Trøseid M, **Seifert J**, Ferrer M. (2023) Microbiome-derived cobalamin and succinyl-CoA as biomarkers for improved screening of anal cancer.

Nature Medicine. 29. 1738–1749. doi: 10.1038/s41591-023-02407-3

[122] Lazzari G, Münger A, Eggerschwiler L, Borda-Molina D, **Seifert J**, Camarinha-Silva A, Schrade S, Zähner M, Zeyer K, Kreuzer M, Dohme-Meier F. (2023) Effects of *Acacia mearnsii* added to silages differing in nutrient composition and condensed tannins on ruminal and manure-derived methane emissions of dairy cows. Journal of Dairy Science. 106(9). doi: 10.3168/jds.2022-22901

[121] Sáenz JS, Rios-Galicia B, Rehkugler B, **Seifert J.** (2023) Dynamic development of viral and bacterial diversity during grass silage preservation. Viruses. 15(4). 951. doi: 10.3390/v15040951

[120] Amin N, Schwarzkopf S, Tröscher-Mußotter J, Camarinha-Silva A, Dänicke S, Huber K, Frahm J, **Seifert J.** (2023) Host metabolome and faecal microbiome shows potential interactions impacted by age and weaning times in calves. Animal Microbiome. 5. 12. doi: 10.1186/s42523-023-00233-z

[119] Lazzari G, Münger A, Heimo D, **Seifert J**, Camarinha-Silva A, Borda-Molina D, Zähner M, Schrade S, Kreuzer M, Dohme-Meier F. (2023) Effects of tanniferous sainfoin and *Acacia mearnsii* extract on urinary N excretion and ammonia volatilization from the slurry of dairy cows.

Animal Feed Science and Technology. 297. 115577.

doi: 10.1016/j.anifeedsci.2023.115577

[118] Trautmann A, Schleicher L, Koch A, Günther J, Steuber J, **Seifert J.** (2023) A shift towards succinate-producing *Prevotella* in the ruminal microbiome challenged with monensin. Proteomics. 23 (21-22). e2200121. doi: 10.1002/pmic.202200121

2022

[117] Tröscher-Mußotter J, Deusch S, Borda-Molina D, Frahm J, Dänicke S, Camarinha-Silva A, Huber K, **Seifert J.** (2022) Cow's microbiome from antepartum to postpartum: A long-term study covering two physiological challenges. Frontiers in Microbiology 13. doi: 10.3389/fmicb.2022.1000750

[116] Roth C, Sims T, Rodehutscord M, **Seifert J**, Camarinha-Silva A. (2022) The active core microbiota of two high-yielding laying hen breeds fed with different levels of calcium and phosphorus.

Frontiers in Physiology 13. doi:10.3389/fphys.2022.951350.

[115] Röhm K, Gonzalez-Uarquin F, Harmel RK, Trung MN, Diener M, Fiedler D, Huber K, **Seifert J.** (2022) Investigation of a potential electrogenic transport-system for myo-inositol in the small intestine of laying hens. British Poultry Science 63:91-97; doi.10.1080/00071668.2021.1958301

2021

[114] Van Den Bossche T, Arntzen MØ, Becher D, Benndorf D; Eijsink VGH; Henry C, Jagtap PD, Jehmlich N, Juste C, Kunath BJ, Mesuere B, Muth T, Pope PB, **Seifert J**, Tanca A, Uzzau S, WilmesP, Hettich R, Armengaud J (2021) The Metaproteomics Initiative: a coordinated approach for propelling the functional characterization of microbiomes.

Microbiomes 9(1):243. doi.org/10.1186/s40168-021-01176-w

[113] Kurz A, **Seifert J** (2021) Factors influencing proteolysis and protein utilization in the intestine of pigs: a review.

Animals 11(12):3551; doi.org/10.3390/ani11123551

[112] Schleicher L, Herdan S, Fritz G, Trautmann A, **Seifert J**, Steuber J (2021) Central carbon metabolism, sodium-motive electron transfer and ammonium formation by the vaginal pathogen *Prevotella bivia*.

International Journal of Molecular Sciences 22: 11925; doi.org/10.3390/ijms222111925

[111] Tröscher-Mußotter J, Saenz JS, Grindler S, Meyer J, Kononov SU, Mezger B, Borda-Molina D, Frahm J, Dänicke S, Camarinha-Silva A, Huber K, **Seifert J** (2021) Microbiome clusters disclose physiologic variances in dairy cows challenged by calving and lipopolysaccharides.

mSystems 6(5): e00856-21; doi.org/10.1128/mSystems.00856-21

[110] Trautmann A, Schleicher L, Pfirrmann J, Boldt C, Steuber J, **Seifert J** (2021) Na⁺-coupled respiration and reshaping of extracellular polysaccharide layer counteract monensin-induced cation permeability in *Prevotella bryantii* B14.

International Journal of Molecular Sciences 22: 10202; doi.10.3390/ijms221910202

[109] Schleicher L, Trautmann A, Stegmann D, Fritz G, Gätgens J, Bott M, Hein S, Simon J, **Seifert J**, Steuber J (2021) A sodium-translocating module linking succinate production to formation of a membrane potential in *Prevotella bryantii*.

Applied and Environmental Microbiology; 87(21):e0121121; doi.10.1128/AEM.01211-21

[108] Saenz JS, Kurz A, Ruczizka U, Bünger M, Dippel M, Nagl V, Grenier B, Ladwig A, **Seifert J**, Selberherr E. (2021) Metaproteomics reveals alteration of the gut microbiome in weaned piglets due to the ingestion of the mycotoxins deoxynivalenol and zearalenone.

Toxins 13(8):583; doi.10.3390/toxins13080583

[107] Röhm K, Diener M, Huber K, **Seifert J.** (2021) Characterization of the cecal smooth muscle contraction in laying hens.

Veterinary Sciences 8(6), 91; doi.org/10.3390/vetsci8060091

[106] Amin N, Schwarzkopf S, Kinoshita A, Tröscher-Mußotter J, Dänicke S, Camarinha-Silva A, Huber K, Frahm J, **Seifert J** (2021) Evolution of rumen and oral microbiota in calves is influenced by age and time of weaning.

Animal Microbiome 3:31; doi.org/10.1186/s42523-021-00095-3

[105] Borda-Molina D, Iffland H, Schmid M, Müller R, Schad S, **Seifert J**, Tetens J, Bessei W, Bennewitz J, Camarinha-Silva A (2021) Gut microbial composition and predicted functions are not associated with feather pecking and antagonistic behavior in laying hens.

Life 11(3), 235; doi.org/10.3390/life11030235

[104] Amin N, **Seifert J** (2021) Dynamic progression of the calf's microbiome and its influence on host health.

Computational and Structural Biotechnology Journal 19, 989-1001; doi.org/10.1016/j.csbj.2021.01.035

[103] Meyer J, Kononov SU, Grindler S, Tröscher-Mußotter J, Alaedin MT, Frahm J, Hüther L, Klüss J, Kersten S, von Soosten D, Meyer U, Most E, Eder K, Sauerwein H, **Seifert J**, Huber K, Wegerich A, Rehage J, Dänicke S (2021) Dietary L-carnitine supplementation modifies the lipopolysaccharide-induced acute phase reaction in dairy cows.

Animals 11, 136; doi.org/10.3390/ani11010136

[102] Borda-Molina D, Mátis G, Mackei M, Neogrády Z, Huber K, **Seifert J**, Camarinha-Silva A (2021) Caeca microbial variation in broiler chickens as a result of dietary

combinations using two cereal types, supplementation of crude protein and sodium butyrate.

Frontiers in Microbiology. 11, 617800; doi:10.3389/fmicb.2020.617800

2020

[101] Trautmann A, Schleicher L, Deusch S, Gätgens J, Steuber J, **Seifert J** (2020) Short-chain fatty acids modulate metabolic pathways and membrane lipids in *Prevotella bryantii* B₁₄.

Proteomes. 8, 28; doi:10.3390/proteomes8040028

[100] Sommerfeld V, Omolade Omotoso A, Oster M, Reyer H, Camarinha-Silva A, Hasselmann M, Huber K, Ponsuksili S, **Seifert J**, Stefanski V, Wimmers K, Rodehuts cord M (2020) Phytate degradation, transcellular mineral transporters, and mineral utilization by two strains of laying hens as affected by dietary phosphorus and calcium.

Animals 10, 1736; doi:10.3390/ani10101736

[99] Sommerfeld V, Huber K, Bennewitz J, Camarinha-Silva A, Hasselmann M, Ponsuksili S, **Seifert J**, Stefanski V, Wimmers K, Rodehuts cord M (2020) Phytate degradation, myo-inositol release, and utilization of phosphorus and calcium by two strains of laying hens in five production periods.

Poultry Science 99 (12) 6797-6808; doi.org/10.1016/j.psj.2020.08.064

[98] Meyer J, Daniels SU, Grindler S, Tröscher-Mußotter J, Alaedin MT, Frahm J, Hüther L, Klüss J, Kersten S, von Soosten D, Meyer U, Most E, Eder K, Sauerwein H, **Seifert J**, Huber K, Rehage J, Dänicke S (2020) Effects of a dietary L-carnitine supplementation for dairy cows on performance, energy metabolism and recovery from calving.

Animals 10, 342; doi.org/10.3390/ani10020342

[97] Rosenfelder-Kuon P, Klein N, Zegowitz G, Thuringer L, Schollenberger M, Kühn I, **Seifert J**, Rodehuts cord M (2020) Phytate degradation cascade in pigs as affected by phytase supplementation and rapeseed cake inclusion in corn-soybean meal-based diets.

Journal of Animal Science 98 (3), skaa053. doi: 10.1093/jas/skaa053

[96] Schleicher L, Fritz G, **Seifert J**, Steuber J (2020) Anoxic cell rupture of *Prevotella bryantii* by high-pressure homogenization protects the Na⁺-translocating NADH:quinone oxidoreductase from oxidative damage.

Archive of Microbiology 202, 1263–1266, doi: 10.1007/s00203-019-01805-x

2019

[95] Deusch S, Bok E, Schleicher L, **Seifert J**, Steuber J (2019) Occurrence and function of the Na⁺-translocating NADH:Quinone oxidoreductase in *Prevotella* spp. Microorganisms 7(5), 117, doi.org/10.3390/microorganisms7050117

[94] Ziganshin AM, Wintsche B, **Seifert J**, Carstensen M, Born J, Kleinsteuber S (2019) Spatial separation of metabolic stages in a tube anaerobic baffled reactor: Reactor performance and microbial community dynamics.

Applied Microbiology and Biotechnology 103(9), 3915-3929, doi: 10.1007/s00253-019-09767-2

[93] Pankoke H, Maus I, Loh G, Hüser A, **Seifert J**, Tilker A, Hark S, Scyrba A, Pelzer S, Kleinböltig J (2019) Evaluation of commercially available DNA extraction kits for the analysis of the broiler chicken cecal microbiota.

FEMS Microbiol. Letters, doi: 10.1093/femsle/fnz033.

[92] Heyer CME, Schmucker S, Burbach K, Weiss E, Eklund M, Aumiller T, Capezzone F, Steuber J, Rodehutscord M, Hoelzle LE, **Seifert J**, Mosenthin R, Stefanski V (2019) Phytate degradation, intestinal microbiota, microbial metabolites, and immune values are changed in growing pigs fed diets with varying calcium-phosphorus concentration and fermentable substrates.
Journal of Animal Physiology and Animal Nutrition. 103(4):1185-1197

[91] **Seifert J**, Muth T (2019) Editorial for Special Issue: Metaproteomics.
Proteomes. 7(1), 9, doi:10.3390/proteomes7010009

[90] Tröscher-Mußotter J, Tilocca B, Stefanski V, **Seifert J** (2019) Analysis of the bacterial and host proteins along and across the porcine gastrointestinal tract.
Proteomes. 7(1), 4; doi:10.3390/proteomes7010004

2018

[89] Deusch S, Serrano-Villar S, Rojo D, Martínez-Martínez M, Bargiela R, Vázquez-Castellano JF, Sainz T, Barbas C, Moya A, Moreno S, Gosalbese MJ, Estrada V, **Seifert J**, Ferrer M (2018) Effects of HIV, ART and prebiotics on the active fraction of the gut microbiota.
AIDS. 32/10: 1229-1237

[88] Borda-Molina D, **Seifert J**, Camarinha-Silva A (2018) Current perspectives of the chicken gastrointestinal tract and its microbiome.
Computational and Structural Biotechnology Journal. 16:131-139.

[87] Heinritz S, Weiss E, **Seifert J**, Mosenthin R, Kuß S, Degenhardt AG, Koch TJ (2018) Effect of cellobiose supplementation on *in vitro* fermentation activity and bacterial numbers of porcine inocula
Journal of Animal Physiology and Animal Nutrition. 102(2):474-482.

[86] Zecchin S, Mueller R, **Seifert J**, Stingl U, Anantharaman K, von Bergen M, Calvalca L, Pester M (2018) Rice paddy *Nitrospirae* encode and express genes related to sulfate respiration: proposal of the new genus *Candidatus Sulfobium*
Applied and Environmental Microbiology. 84(5). pii: e02224-172017

2017

[85] Burbach K, Strang EJB, Mosenthin R, Camarinha-Silva A, **Seifert J** (2017) Porcine intestinal microbiota is shaped by diet composition based on rye or triticale
Journal of Applied Microbiology. 123:1571-1583

[84] Tilocca B, Burbach K, Heyer CME, Mosenthin R, Hoelzle LE, Stefanski V, Camarinha-Silva A, **Seifert J** (2017) Dietary changes in nutritional studies shape the structural and functional composition of the pigs fecal microbiome – from days to weeks
Microbiome. 5:144. doi: 10.1186/s40168-017-0362-7

[83] Deusch S, Camarinha-Silva A, Conrad J, Beifuss U, Rodehutscord M, **Seifert J** (2017) A structural and functional elucidation of the rumen microbiome influenced by various diets and microenvironments
Frontiers in Microbiology. 8:1605. doi: 10.3389/fmicb.2017.01605

[82] Kaewtapee C, Burbach K, Tomforde G, Hartinger T, Camarinha-Silva A, Heinritz S, **Seifert J**, Wiltafsky M, Mosenthin R, Rosenfelder-Kuon P (2017) Effect of *Bacillus subtilis* and *Bacillus licheniformis* supplementation in diets with low- and high-protein content on ileal crude protein and amino acid digestibility and intestinal microbiota composition of growing pigs
Journal of Animal Science and Biotechnology. 8:37

[81] Oberbach A, Haange SB, Schlichting N, Heinrich M, Lehmann S, Till H, Hugenholtz F, Kullnick Y, Smidt H, Frank K, **Seifert J**, Jehmlich N, von Bergen M (2017) Metabolic in vivo labelling highlights differences of metabolically active microbes from the mucosal gastrointestinal microbiome between high fat and normal chow diet.
Journal of Proteome Research. 16:1593-1604

2016

[80] Tilocca B, Witzig M, Rodehutscord M, **Seifert J**. (2016) Variations of phosphorous accessibility causing changes in microbiome functions in the gastrointestinal tract of chickens
Plos One 1(10): e0164735. doi:10.1371/journal.pone.0164735

[79] Heyer CME, Schmucker S, Aumiller T, Föll A, Uken K, Rodehutscord M, Hoelzle LE, **Seifert J**, Stefanski V, Mosenthin R, Eklund M, Weiss E (2016) The impact of dietary phosphorus and calcium on the intestinal microbiota and mitogen-induced proliferation of mesenteric lymph node lymphocytes in pigs
Journal of Animal Science. 94:373–376

[78] Serrano-Villar S, Rojo D, Martínez-Martínez M, Deusch S, Vázquez-Castellanos JF, Bargiela R, Sainz T, Vera M, Moreno S, Estrada V, Gosalbes MJ, Latorre A, **Seifert J**, Barbas C, Moya A, Ferrer M (2016) Gut bacteria metabolism impacts immune recovery in HIV-infected individuals
eBioMedicine 8:203-216

[77] Serrano-Villar S, Rojo D, Martínez-Martínez M, Deusch S, Vázquez-Castellanos JF, Sainz T, Vera M, Moreno S, Estrada V, Gosalbes MJ, Latorre A, **Seifert J**, Barbas C, Moya A, Ferrer M (2016) HIV infection results in metabolic alterations in the gut microbiota different than those induced by other diseases.
Scientific Reports 6:26192

[76] Heinritz S, Weiss E, Eklund M, Aumiller T, Louis S, Rings A, Messner S, Camarinha-Silva A, **Seifert J**, Bischoff SC, Mosenthin R. (2016) Intestinal microbiota and microbial metabolites are changed in a pig model fed a high-fat/low-fiber or a low-fat/high-fiber diet.
Plos One 11(4): e0154329.

[75] Starke R, Keller A, Jehmlich N, Vogt C, Richnow HH, Kleinsteuber S, von Bergen M, **Seifert J**. (2016) Pulsed ¹³C₂-acetate protein-SIP unveils *Epsilonproteobacteria* as dominant acetate utilizers in a sulfate-reducing microbial community mineralizing benzene.
Microbial Ecology 71:901-911

[74] Starke R, Kermer R, Ullmann-Zeunert L, Baldwin I, **Seifert J**, Bastida F, von Bergen M, Jehmlich N. (2016) Bacteria dominate the short-term assimilation of plant-derived N in soil.
Soil Biology & Biochemistry 96:30-38

[73] Schiffmann CL, Otto W, Hansen R, Nielsen PH, Adrian L, **Seifert J**, von Bergen M, Jehmlich N. (2016) Proteomic dataset of the organohalide-respiring bacterium *Dehalococcoides mccartyi* strain CBDB1 grown on hexachlorobenzene as electron acceptor.
Data in Brief 22:7:253-256

[72] Vogt C, Lueders T, Richnow HH, Krüger M, von Bergen M, **Seifert J** (2016) Stable isotope probing approaches to study anaerobic hydrocarbon degradation and degraders

Journal of Molecular Microbiology and Biotechnology 26(1-3):195-210

[71] Rabus R, Boll M, Heider J, Meckenstock RU, Buckel W, Einsle O, Ermler U, Golding BT, Gunsalus RP, Kroneck PM, Krüger M, Lueders T, Martins BM, Musat F, Richnow HH, Schink B, **Seifert J**, Szaleńiec M, Treude T, Ullmann GM, Vogt C, von Bergen M, Wilkes H. (2016) Anaerobic microbial degradation of hydrocarbons: from enzymatic reactions to the environment.

Journal of Molecular Microbiology and Biotechnology 26(1-3):5-28

[70] Herbst FA, Lünsmann V, Kjeldal H, Jehmlich N, Tholey A, von Bergen M, Nielsen JL, Hettich RL, **Seifert J**, Nielsen PH (2016) Enhancing Metaproteomics - The value of models and defined environmental microbial systems. Proteomics. 16(5):783-798.

[69] Burbach K, **Seifert J**, Pieper DH, Camarinha-Silva A (2016) Evaluation of DNA extraction kits and phylogenetic diversity of the porcine gastrointestinal tract based on Illumina sequencing of two hypervariable regions MicrobiologyOpen 5:70-82

2015

[68] Witzig M, Camarinha-Silva A, Green-Engert R, Hözle K, Zeller E, **Seifert J**, Hözle LE, Rodehutscord, M (2015) Spatial variation of the gut microbiota in broiler chickens as affected by dietary available phosphorus and assessed by T-RFLP analysis and 454 pyrosequencing Plos One 10(11):e0143442.

[67] Bargiela R, Herbst FA, Martínez-Martínez M, **Seifert J**, Rojo D, Cappello S, Genovese M, Crisafi F, Denaro R, Chernikova TN, Barbas C, von Bergen M, Yakimov MM, Ferrer M, Golyshin PN (2015) Metaproteomics and metabolomics analyses of three chronically petroleum-polluted sites reveal the importance of general anaerobic processes uncoupled with degradation Proteomics 15(20):3508-3520.

[66] Deusch S, **Seifert J** (2015) Catching the tip of the iceberg – evaluation of sample preparation protocols for metaproteomic studies of the rumen microbiota Proteomics 15(20):3590-3595. doi: 10.1002/pmic.201400556

[65] Goris T, Schiffmann CL, Gadkari J, Schubert T, **Seifert J**, Jehmlich N, von Bergen M, Diekert G (2015) Proteomics of the organohalide-respiring epsilonproteobacterium *Sulfurospirillum multivorans* adapted to tetrachloroethene and other energy substrates Scientific Reports. 5: 13794

[64] Witzig M, Boghun J, Zeder M, **Seifert J**, Rodehutscord M (2015) Effect of donor animal species and their feeding on the composition of the microbial community establishing in a rumen simulation Journal of Applied Microbiology 119: 33-46.

[63] Tobalina L, Bargiela R, Pey J, Herbst FA, Lores I, Rojo D, Barbas C, Peláez AI, Sánchez J, von Bergen M, **Seifert J**, Ferrer M, Planes FJ (2015) Context-specific metabolic network reconstruction of a naphthalene degrading bacterial community guided by metaproteomic data. Bioinformatics. 31(11): 1771-1779

[62] Kümmel S, Herbst FA, Bahr A, Duarte M, Pieper DH, Jehmlich N, **Seifert J**, von Bergen M, Bombach P, Richnow HH, Vogt C. (2015) Anaerobic naphthalene degradation by sulfate-reducing Desulfobacteraceae from various anoxic aquifers.

FEMS Microbiology Ecology. 91(3): fiv006

[61] Sachsenberg T, Herbst FA, Taubert K, Kermer R, Jehmlich N, von Bergen M, **Seifert J**, Kohlbacher O. (2015) MetaProSIP: automated inference of stable isotope incorporation rates in proteins for functional metaproteomics. Journal of Proteome Research. 14(2):619-627. doi: 10.1021/pr500245w

[60] Deusch S, Tilocca B, Camarinha-Silva A, **Seifert J**. (2015) News in livestock research - use of Omics-technologies to study the microbiota in the gastrointestinal tract of farm animals.

Computational and Structural Biotechnology Journal. 13: 55-63

[59] Pöritz M, Schiffmann C, Hause G, Heinemann U, **Seifert J**, Jehmlich N, von Bergen M, Nijenhuis I, Lechner U. (2015) *Dehalococcoides mccartyi* strain DCMB5 respires a broad spectrum of chlorinated aromatic compounds.

Applied and Environmental Microbiology. 81(2): 587-596

2014

[58] Bozinovski D, Taubert M, Kleinsteuber S, Richnow HH, von Bergen M, Vogt C, **Seifert J** (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.

Systematic and Applied Microbiology. 37(7):488-501

[57] Kleindienst S, Herbst FA, Stagars M, von Netzer F, von Bergen M, **Seifert J**, Peplies J, Amann R, Musat F, Lueders T, Knittel K (2014) Diverse sulfate-reducing bacteria of the *Desulfosarcina/Desulfococcus* clade are the key alkane degraders at marine seeps.

ISME Journal. 8(10): 2029-2044

[56] Lieder S, Jahn M, **Seifert J**, von Bergen M, Müller S, Takors R (2014) Subpopulation-proteomics reveal growth rate, but not cell cycling, as a major impact on protein composition in *Pseudomonas putida* KT2440
AMB express. 09/2014; 4(71):<http://www.amb-express.com/content/4/1/71>.

[55] Marozava S, Röling WF, **Seifert J**, Küffner R, von Bergen M, Meckenstock RU. (2014) Physiology of *Geobacter metallireducens* under excess and limitation of electron donors. Part I. Batch cultivation with excess of carbon sources.
Systematic and Applied Microbiology. 37(4): 277–286

[54] Marozava S, Röling WF, **Seifert J**, Küffner R, von Bergen M, Meckenstock RU. (2014) Physiology of *Geobacter metallireducens* under excess and limitation of electron donors. Part II. Mimicking environmental conditions during cultivation in retentostats.
Systematic and Applied Microbiology. 37(4): 287-295

[53] Schiffmann C, Jehmlich N, Otto W, Hansen R, Nielsen PH, Adrian L, **Seifert J**, von Bergen M. (2014) Proteome profile and proteogenomics of the organohalide-respiring bacterium *Dehalococcoides mccartyi* strain CBDB1 grown on hexachlorobenzene as electron acceptor.

Journal of Proteomics 98: 59-64

[52] Schiffmann C, Hansen R, Baumann S, Kublik A, Nielsen PH, Adrian L, von Bergen M, Jehmlich N, **Seifert J**. (2014) Comparison of targeted peptide quantification assays for reductive dehalogenases by selective reaction monitoring (SRM) and precursor reaction monitoring (PRM).

Analytical and Bioanalytical Chemistry 406:283–291

2013

[51] Bodelier P, Meima-Franke M, Hordijk C, Steenbergh A, Hefting M, Bodrossy L, von Bergen M, **Seifert J.** (2013) Microbial minorities modulate methane consumption through niche partitioning.

ISME Journal 7(11):2214-2228

[50] Siegert M, Taubert M, **Seifert J.**, von Bergen M, Basen M, Bastida F, Gehre M, Richnow HH, Krüger M. (2013) The nitrogen cycle in anaerobic methanotrophic mats of the Black Sea is linked to sulfate reduction and biomass decomposition.

FEMS Microbiology Ecology 86(2):231-245

[49] Pérez-Cobas AE, Gosalbes MJ, Friedrichs A, Knecht H, Artacho A, Eismann K, Otto W, Rojo D, Bargiela R, von Bergen M, Neulinger SC, Däumer C, Heinzen FA, Latorre A, Barbas C, **Seifert J.**, Martins dos Santos V, Ott SJ, Ferrer M, Moya A. (2013) Gut microbiota disturbance during antibiotic therapy: a multi-omic approach.

Gut 62(11):1591-1601

[48] **Seifert J.**, Herbst FA, Nielsen P, Planes F, Ferrer M, von Bergen M. (2013) Bioinformatic progress and applications in metaproteogenomics for bridging the gap between genomic sequences and metabolic functions in microbial communities.

Proteomics 13(18-19):2786-2804

[47] Herbst FA; Bahr A, Duarte M, Pieper DH, Richnow HH, von Bergen M, **Seifert J.**, Bombach P. (2013) Elucidation of in situ polycyclic aromatic hydrocarbon degradation by functional metaproteomics (protein-SIP).

Proteomics 13(18-19):2910-2920

[46] Herbst FA, Taubert M, Jehmlich N, Behr T, Schmidt F, von Bergen M, **Seifert J.** (2013) Sulfur-34S stable isotope labeling of amino acids for quantification (SULAQ34) of proteomic changes in *Pseudomonas fluorescens* during naphthalene degradation.

Molecular & Cellular Proteomics 12(8):2060-2069

[45] Hernández E, Bargiela R, Suárez Diez M, Friedrichs A, Pérez-Cobas AE, Gosalbes MJ, Knecht H, Martínez-Martínez M, **Seifert J.**, von Bergen M, Artacho A, Ruiz A, Campoy C, Latorre A, Ott SJ, Moya A, Suárez A, Martins dos Santos VAP, Ferrer M. (2013) Functional consequences of microbial shifts in the human gastrointestinal tract linked to antibiotic treatment and obesity.

Gut Microbes 4(4):306-315

[44] von Bergen M, Jehmlich N, Taubert M, Vogt C, Bastida F, Herbst FA, Schmidt F, Richnow HH, **Seifert J.** (2013) Insights from quantitative metaproteomics and protein stable isotope probing into microbial ecology.

ISME Journal 7(10):1877-1885

[43] Jahn M, **Seifert J.**, Hübschmann, T, von Bergen M, Harms H, Müller S. (2013) Comparison of preservation methods for bacterial cells in cytomics and proteomics.

Journal of Integrated OMICS 3(1): 25-33

[42] Kung J, **Seifert J.**, von Bergen M, Boll M. (2013) Cyclohexanecarboxyl-CoA and cyclohex-1-ene-1-carboxyl-CoA dehydrogenases - two enzymes involved in the fermentation of benzoate and crotonate in *Syntrophus aciditrophicus*.

Journal of Bacteriology 195(14):3193-3200

- [41] Jechalke S, Franchini AG, Bastida F, Bombach P, Rosell M, **Seifert J**, von Bergen M, Vogt C, Richnow HH. (2013) Analysis of structure, function and activity of a benzene degrading microbial community. *FEMS Microbiology Ecology* 85(1):14-26
- [40] Eberlein C, Estelmann S, **Seifert J**, von Bergen M, Müller M, Meckenstock R, Boll M. (2013) Identification and characterization of 2-naphthoyl-coenzyme A reductase, the prototype of a novel class of dearomatizing reductases. *Molecular Microbiology* 88 (5):1032-1039
- [39] Taubert M, von Bergen M, **Seifert J**. (2013) Limitations in detection of ¹⁵N incorporation by mass spectrometry in protein-based stable isotope probing (protein-SIP) *Analytical and Bioanalytical Chemistry* 405 (12):3989-3996
- [38] Schipp CJ, Marco-Urrea E, Kublick A, **Seifert J**, Adrian L. (2013) Organic cofactors in the metabolisms of Dehalococcoides mccartyi strains. *Philos. Trans. R. Soc. B-Biol. Sci.* 368 (1616): 20120321
- [37] Jahn M, **Seifert J**, von Bergen M, Schmid A, Bühler B, Müller S. (2013) Subpopulation-proteomics in prokaryotic populations. *Current Opinion in Biotechnology* 24 (1), 79-97
- [36] Tang S, Chan WWM, Fletcher KE, Liang X, **Seifert J**, Löfller FE, Edwards EA, Adrian L. (2013) Functional characterization of reductive dehalogenases using blue native polyacrylamide gel electrophoresis *Applied and Environmental Microbiology* 79 (3), 974-981
- [35] Ferrer M, Ruiz A, Lanza F, Haange SB, Oberbach A, Till H, Campoy C, Segura MT, Richter M, Bargiela R, von Bergen M, **Seifert J**, Suarez A. (2013) Microbiota from the distal guts of lean and obese adolescents exhibit partial functional redundancy besides clear differences in community structure. *Environmental Microbiology* 15 (1), 211-226
- [34] Guazzaroni ME, Herbst FA, Lores I, Tamames J, Peláez AI, López-Cortés N, Alcaide M, Del Pozo MV, Vieites JM, von Bergen M, Gallego JLR, Bargiela R, López-López A, Pieper DH, Rosseló-Móra R, Sánchez J, **Seifert J**, Ferrer M. (2013) Metaproteogenomics insights beyond bacterial response to naphthalene exposure and bio-stimulation. *ISME Journal* 7 (1), 122-136
- 2012
- [33] Taubert M, Vogt C, Wubet T, Kleinstuber S, Tarkka MT, Harms H, Buscot F, Richnow HH, von Bergen M, **Seifert J**. (2012) Protein-SIP enables time-resolved analysis of the carbon flux in a sulfate-reducing, benzene-degrading microbial consortium. *ISME Journal* 6 (12), 2291 – 2301. doi: 10.1038/ismej.2012.68
- [32] Haange SB, Oberbach A, Schlichting N, Hugenholtz F, Smidt H, von Bergen M, Till H, **Seifert J**. (2012) Metaproteome analysis and molecular genetics of rat intestinal microbiota reveals section and localization resolved species distribution and enzymatic functionalities. *Journal of Proteome Research* 11 (11), 5406-5417
- [31] **Seifert J**, Taubert M, Jehmlich N, Schmidt F, Völker U, Vogt C, Richnow HH, von Bergen M (2012) Protein-based stable isotope probing in functional metaproteomics. *Mass Spectrometry Reviews* 31 (6), 683-697

[30] Reinhold A, Westermann M, **Seifert J**, von Bergen M, Schubert T, Diekert G. (2012) Impact of vitamin B12 on the formation of the tetrachloroethene reductive dehalogenase in *Desulfitobacterium hafniense* strain Y51.

Applied and Environmental Microbiology 78 (22), 8025-8032

[29] Wagner A, Cooper M, Ferdi S, **Seifert J**, Adrian L. (2012) Growth of *Dehalococcoides* sp. strain CBDB1 by reductive dehalogenation of brominated benzenes to benzene.

Environmental Science & Technology 46 (16), 8960-8968

[28] Baumgarten T, Sperling S, **Seifert J**, von Bergen M, Steiniger F, Wick LY, Heipieper HJ. (2012) Membrane vesicle formation as a multiple-stress response mechanism enhances *Pseudomonas putida* DOT-T1E cell surface hydrophobicity and biofilm formation.

Applied and Environmental Microbiology 78 (17), 6217-6224

[27] Marco-Urrea E, **Seifert J**, von Bergen M, Lorenz A. (2012) Stable isotope peptide mass spectrometry to decipher amino acid metabolism in *Dehalococcoides* strain CBDB1.

Journal of Bacteriology 194 (16), 4169-4177

[26] Kermer R, Hedrich S, Taubert M, Baumann S, Schlömann M, Johnson DB, von Bergen M, **Seifert J** (2012) Elucidation of carbon transfer in a mixed culture of *Acidiphilum cryptum* and *Acidithiobacillus ferrooxidans* using protein-based stable isotope probing.

Journal of Integrated OMICS 2 (1), 37-45

[25] Bozinovski D, Herrmann S, Richnow HH, von Bergen M, **Seifert J**, Vogt C (2012) Functional analysis of an anaerobic m-xylene degrading enrichment culture using protein-based stable isotope probing.

FEMS Microbiology Ecology 81 (1), 134-144

[24] Sultana M, Vogler S, Zargar K, Schmidt AC, Saltikov C, **Seifert J**, Schlömann M (2012) New Clusters of Arsenite Oxidase and Unusual Bacterial Groups in Enrichments from Arsenic-Contaminated Soil.

Archives in Microbiology 194 (7), 623-635

[23] Morris BEL, Herbst FA, Bastida F, **Seifert J**, von Bergen M, Richnow HH, Suflita J (2012) Microbial interactions during residual oil and n-fatty acid metabolism by a methanogenic consortium.

Environmental Microbiology Reports 4 (3), 297-306

[22] Oberender J, Kung J, **Seifert J**, von Bergen M, Boll M (2012) Identification and characterization of a succinyl-CoA:benzoate CoA transferase in *Geobacter metallireducens*.

Journal of Bacteriology 194 (10), 2501-2508

[21] Jehmlich N, Kopinke FD, Lenhard S, Herbst FA, **Seifert J**, Lissner U, Völker U, Schmidt F, von Bergen M. (2012) Sulphur-36S stable isotope labeling of amino acids for quantification (SULAQ).

Proteomics 12 (1), 37-42

2011

[20] Kuntze K, Kiefer P, Baumann S, **Seifert J**, von Bergen M, Vorholt JA, Boll M (2011) Enzymes involved in the anaerobic degradation of meta-substituted halobenzoates.

Molecular Microbiology 82 (3), 758-769

[19] Marco-Urrea E, Paul S, Khodaverdi V, **Seifert J**, von Bergen M, Kretzschmar U, Adrian L (2011) Identification and characterization of a re-citrate synthase in *Dehalococcoides* strain CBDB1. Journal of Bacteriology 193 (19), 5117-5178

[18] Hedrich S, Lünsdorf H, Kleeberg G, Heide G, **Seifert J**, Schlömann M (2011) Schwertmannite formation adjacent to bacterial cells in a mine water treatment plant and in pure cultures of '*Ferrovum myxofaciens*'.

Environmental Science & Technology 45 (18), 7685-7692

[17] Taubert M, Baumann S, von Bergen M, **Seifert J** (2011) Exploring the limits of robust detection of incorporation of ¹³C by mass spectrometry in protein-based stable isotope probing (protein-SIP).

Analytical and Bioanalytical Chemistry 401 (6), 1975-1982

[16] Bastida F, Jechalke S, Bombach P, Franchini AG, **Seifert J**, von Bergen M, Vogt C, Richnow HH (2011) Assimilation of benzene carbon through multiple trophic levels traced by different stable isotope probing methodologies.

FEMS Microbiology Ecology 77 (2), 357-369

[15] Taubert M, Jehmlich N, Schmidt F, Vogt C, Richnow HH, von Bergen M, **Seifert J** (2011) Time resolved protein-based stable isotope probing (Protein-SIP) analysis allows quantification of induced proteins in substrate shift experiments.

Proteomics 11 (11), 2265-2274

[14] Georgieva D, **Seifert J**, Öhler M, von Bergen M, Spencer P, Arni R, Genov N, Betzel C (2011) *Pseudechis australis* venom: Adaptation for a defense against microbial pathogens and recruitment of body transferrin.

Journal of Proteome Research 10 (5), 2440-2464

[13] Sultana M, Härtig C, Planer-Friedrich B, **Seifert J**, Schlömann M (2011) Bacterial Communities in Bangladesh Aquifers Differing in Aqueous Arsenic Concentration.

Geomicrobiology Journal 28 (3), 198 – 211

2010

[12] Jehmlich N, Schmidt F, Taubert M, **Seifert J**, Bastida F, von Bergen M, Richnow HH, Vogt C (2010) Protein-stable isotope probing (Protein-SIP).

Nature Protocols 5 (12), 1957-1966

[11] Jehmlich N, Kleinstuber S, Vogt C, Benndorf D, Harms H, Schmidt F, von Bergen M, **Seifert J** (2010) Phylogenetic and proteomic analysis of an anaerobic toluene-degrading community.

Journal of Applied Microbiology 109(6), 1937-1945

[10] Fetzer I, Jehmlich N, Vogt C, Richnow HH, **Seifert J**, Harms H, von Bergen M, Schmidt F (2010) Calculation of partial isotope incorporation into peptides measured by mass spectrometry.

BMC Research Notes Jun 24;3(1), 178.

[9] Bastida F, Rosell M, Franchini AG, **Seifert J**, Finsterbusch S, Jehmlich J, Jechalke S, von Bergen M, Richnow HH (2010) Elucidating MTBE degradation in a mixed consortium using a multidisciplinary approach.

FEMS Microbiology Ecology 73(2), 370-384

[8] Öhler M, Georgieva D, **Seifert J**, von Bergen M, Arni R, Genov N, Betzel C (2010) The Venomic of Bothrops alternatus is a Pool of Acidic Proteins with Predominant Hemorrhagic and Coagulopathic Activities.
Journal of Proteome Research 9 (5), 2422-2437

[7] Georgieva D, Öhler M, **Seifert J**, von Bergen M, Arni RK, Genov N, Betzel C (2010) Snake Venomic of Crotalus durissus terrificus-Correlation with Pharmacological Activities.
Journal of Proteome Research 9(5), 2302-2316

[6] Jehmlich N, Fetzer I, **Seifert J**, Mattow J, Vogt C, Harms H, Thiede B, Richnow HH, von Bergen M, Schmidt F (2010) Decimal place slope: a fast and precise method for quantifying ¹³C incorporation levels for detecting the metabolic activity of microbial species.
Molecular & Cellular Proteomics. 9 (6), 1221-1227

2009

[5] Jehmlich N, Schmidt F, Taubert M, **Seifert J**, von Bergen M, Richnow HH, Vogt C (2009) Comparison of methods for simultaneous identification of bacterial species and determination of metabolic activity by protein-based stable isotope probing (Protein-SIP) experiments.
Rapid Communication in Mass Spectrometry 23 (12), 1871-1878

[4] Ehinger S, **Seifert J**, Kassahun A, Schmalz L, Hoth N, Schlömann M (2009) Predominance of Methanolobus spp. and Methanoculleus spp. in the Archaeal Communities of Saline Gas Field Formation Fluids.
Geomicrobiology Journal 26, 326-338

[3] Heinzel E, Janneck E, Glombitza F, Schlömann M, **Seifert J** (2009) Population dynamics of iron-oxidizing communities in pilot plants for the treatment of acid mine waters.
Environmental Science and Technology 43 (16), 6138-6144

[2] Heinzel E, Hedrich S, Janneck E, Glombitza F, **Seifert J**, Schlömann M (2009) Bacterial diversity in a plant for mine water treatment.
Applied and Environmental Microbiology 75 (3), 858-861

2005

[1] Ferraroni M, **Seifert J**, Travkin VM, Thiel M, Kaschabek S, Scozzafava A, Golovleva L, Schlömann M, Briganti F (2005) Crystal structure of the hydroxyquinol 1,2-dioxygenase from Nocardioides simplex 3E, a key enzyme involved in polychlorinated aromatics biodegradation.
Journal of Biological Chemistry 280 (22), 21144-21154

Publications in book sections

2021

Deusch S, **Seifert J** (2021)

Metaproteomics in Nutrition. In: Cifuentes, A. (Ed.), Comprehensive Foodomics, vol. 1. Elsevier, pp. 730–741. ISBN: 9780128163955

2019

Seifert J, Tilocca B (2019)

Omics technologies for connecting host responses with poultry gut function. In: Improving gut health in poultry. S.C.Ricke (eds). Burleigh Dodds Science Publishing. ISBN-13: 9781786763044

2011

Jehmlich N, **Seifert J**, Taubert M, Schmidt F, Vogt C, Richnow HH, von Bergen M (2011) Protein Stable Isotope Probing. In: Murrell JC, Whiteley AS (eds) Stable isotope probing and related technologies. ASM Press, Washington

2008

Seifert J, Erler B, Seibt K, Rohrbach N, Arnold J, Schlömann M, Kassahun A, Jenk U (2008) Characterization of the microbial diversity in the abandoned uranium mine Königstein. In Uranium, Mining and Hydrogeology, pp. 733-742. Edited by B. Merkel & A. Hasche-Berger. Berlin: Springer. ISBN:978-3-540-87745-5.

Wagner S, Bilek F, Schaarschmidt T, **Seifert J**, Gniese C, Schlömann M (2008) Identifikation des limitierenden Faktors der biologischen Sulfatreduktion in zwei Technikumsversuchen. In Wissenschaftliche Mitteilungen der Technischen Universität Bergakademie Freiberg 37/2008, Behandlungstechnologien für bergbaubeeinflusste Wässer. Edited by B. Merkel, H. Schaeben & A. Hasche-Berger. Freiberg.

2007

Heinzel E, Hedrich S, **Seifert J**, Schlömann M (2007)

Microbial diversity in a pilot plant for producing iron hydroxysulfates. S. 527-530. In A. Schippers, W. Sand, F. Glombitza und S. Willscher (Hrsg.) Biohydrometallurgy: From the single cell to the environment (IBS 2007). Advanced Materials Research Bd. 20-21. Trans Tech Publications, Stafa-Zürich.

2006

Heinzel E, Hedrich S, Rätzel G, Wolf M, Janneck E, **Seifert J**, Glombitza F, Schlömann M (2006) Bakterielle Diversität in einer Wasserbehandlungsanlage zur Reinigung saurer Grundwässer. S. 61-67. In B. Merkel, H. Schaeben, C. Wolkersdorfer und A. Hasche-Berger (Hrsg.) Behandlungstechnologien für bergbaubeeinflusste Wässer. GIS - Geowissenschaftliche Anwendungen und Entwicklungen. Technische Universität, Institut für Geologie, Wissenschaftliche Mitteilungen 31.