Publications

2018

Atashgahi S, Sánchez Andrea I, Heipieper HJ, van der Meer JR, Stams AJM, Smidt H. Harnessing resistance for bioremediation and detoxification. Science (2018) Submitted.

Feng Y, Stams AJM, Sánchez-Andrea I, de Vos WM. Eubacterium maltovorans sp. nov., a novel human intestinal acetogenic and butyrogenic bacterium with a versatile metabolism. Int J Syst Evol Microbiol (2018) Submitted.

Frank F, Lücker S, Vossen RHAM, Jetten MSM, Hall RJ, Op den Camp HJM, Anvar SY. Resolving the complete genome of Kuenenia stuttgartiensis from a membrane bioreactor enrichment using Single-Molecule Real-Time sequencing. Scientific Reports 8, Article number: 4580 (2018) doi:10.1038/s41598-018-23053-7

Magnabosco C, Timmers P, Lau M, Borgonie G, Linage-Alvarez B, Kuloyo O, Alleva R, Kieft T, Slater G, van Heerden E, Sherwood Lollar B, Onstott T. Fluctuations in populations of subsurface methane oxidizers in coordination with changes in electron acceptor availability. FEMS microbiol ecol (2018) Minor revisions.

Müller N, Timmers P, Plugge CM, Stams AJM, Schink B. Syntrophy in methanogenic degradation. Book chapter in 2nd edition of (Endo)symbiotic methanogenic archaea (2018) Under review.

Roghair M, Hoogstad T, Strik DPBTB, Plugge CM, Timmers PHA, Weusthuis RA, Bruins ME, Buisman CJN. Controlling ethanol use in chain elongation by CO2 loading rate. Environ Sci Technol. 52:1496-150 (2018). https://www.ncbi.nlm.nih.gov/pubmed/29304274

van Kessel MAHJ, Stultiens K, Slegers MFW, Guerrero Cruz S, Jetten MSM, Kartal B, Op den Camp HJM. Current perspectives on the application of N-damo and anammox in wastewater treatment. Curr. Opinion Biotechnol 50: 222–227 (2018). doi.org/10.1016/j.copbio.2018.01.031

Zhu YF, Klompe S, Vlot M, van der Oost J, Staals RHJ. Shooting the messenger: RNA-targeting CRISPR-Cas systems. Biosci Rep. 2018 Jun 29; 38(3) Bioscience Reports (2018) doi: 10.1042/BSR20170788
Sorokin DY, Merkel AY, Abbas B, Makarova KS, Rijpstra WIC, Koenen M, Sinninghe Damsté JS, Galinski EA, Koonin EV, van Loosdrecht MCM. Methanonatronarchaeum thermophilum gen. nov., sp. nov. and 'Candidatus Methanohalarchaeum thermophilum', extremely halo(natrono)philic methyl-reducing methanogens from hypersaline lakes comprising a new euryarchaeal class Methanonatronarchaeia classis nov. Int J Syst Evol Microbiol 68: 2199 2208, doi:10.1099/ijsem.0.002810

Villanueva L. Engineering E. coli to Have a Hybrid Archaeal/Bacterial Membrane. Trends Microbiol 26 (7) 559-560 (2018), https://doi.org/10.1016/j.tim.2018.05.003

Szklany K, Wopereis H, de Waard C, van Wageningen T, An R, van Limpt K, Knol J, Garssen J, Knippels LMJ, Belzer C, Kraneveld AD. Supplementation of dietary non-digestible oligosaccharides from birth

onwards improve social and reduce anxiety-like behaviour in male BALB/c mice. Nutr Neurosci. 2019 Mar 14:1-15. doi: 10.1080/1028415X.2019.1576362

Bekker V, Zwittink RD, Knetsch CW, Sanders IMJG, Berghuis D, Heidt PJ, Vossen JMJJ, de Vos WM, Belzer C, Bredius RGM, Van't Hof PJ, Lankester AC, Kuijper EJ. Dynamics of the Gut Microbiota in Children Receiving Selective or Total Gut Decontamination Treatment during Hematopoietic Stem Cell Transplantation. Biol Blood Marrow Transplant. 2019 Feb 5. pii: S1083-8791(19)30095-3. doi: 10.1016/j.bbmt.2019.01.037

Hildebrand F, Moitinho-Silva L, Blasche S, Jahn MT, Gossmann TI, Heuerta-Cepas J, Hercog R, Luetge M, Bahram M, Pryszlak A, Alves RJ, Waszak SM, Zhu A, Ye L, Costea PI, Aalvink S, Belzer C, Forslund SK, Sunagawa S, Hentschel U, Merten C, Patil KR, Benes V, Bork P. Antibiotics-induced monodominance of a novel gut bacterial order.Gut. 2019 Jan 18. pii: gutjnl-2018-317715. doi: 10.1136/gutjnl-2018-317715

Kleinjans L, Veening-Griffioen DH, Wehkamp T, van Bergenhenegouwen J, Knol J, Garssen J, Knippels LMJ, Belzer C, Jeurink PV. Mice co-administrated with partially hydrolysed whey proteins and prebiotic fibre mixtures show allergen-specific tolerance and a modulated gut microbiota. Benef Microbes. 2019 Mar 13;10(2):165-178. doi: 10.3920/BM2018.0001. Epub 2018 Dec 10

Szopinska JW, Gresse R, van der Marel S, Boekhorst J, Lukovac S, van Swam I, Franke B, Timmerman H, Belzer C, Arias Vasquez A. Reliability of a participant-friendly fecal collection method for microbiome analyses: a step towards large sample size investigation. BMC Microbiol. 2018 Sep 6;18(1):110. doi: 10.1186/s12866-018-1249-x.

Geerlings SY, Kostopoulos I, de Vos WM, Belzer C. Akkermansia muciniphila in the Human Gastrointestinal Tract: When, Where, and How? Microorganisms. 2018 Jul 23;6(3). pii: E75. doi: 10.3390/microorganisms6030075. Review

Elderman M, Hugenholtz F, Belzer C, Boekschoten M, de Haan B, de Vos P, Faas M. Changes in intestinal gene expression and microbiota composition during late pregnancy are mouse strain dependent. Sci Rep. 2018 Jul 3;8(1):10001. doi: 10.1038/s41598-018-28292-2.

Elderman M, Hugenholtz F, Belzer C, Boekschoten M, van Beek A, de Haan B, Savelkoul H, de Vos P, Faas M. Sex and strain dependent differences in mucosal immunology and microbiota composition in mice. Biol Sex Differ. 2018 Jun 18;9(1):26. doi: 10.1186/s13293-018-0186-6.

van der Lugt B, Rusli F, Lute C, Lamprakis A, Salazar E, Boekschoten MV, Hooiveld GJ, Müller M, Vervoort J, Kersten S, Belzer C, Kok DEG, Steegenga WT. Integrative analysis of gut microbiota composition, host colonic gene expression and intraluminal metabolites in aging C57BL/6J mice. Aging (Albany NY). 2018 May 16;10(5):930-950. doi: 10.18632/aging.101439.

Singh R, de Groot PF, Geerlings SE, Hodiamont CJ, Belzer C, Berge IJMT, de Vos WM, Bemelman FJ, Nieuwdorp M. Fecal microbiota transplantation against intestinal colonization by extended spectrum beta-lactamase producing Enterobacteriaceae: a proof of principle study. BMC Res Notes. 2018 Mar 22;11(1):190. doi: 10.1186/s13104-018-3293-x.

Chia LW, Hornung BVH, Aalvink S, Schaap PJ, de Vos WM, Knol J, Belzer C. Deciphering the trophic interaction between Akkermansia muciniphila and the butyrogenic gut commensal Anaerostipes caccae

using a metatranscriptomic approach. Antonie Van Leeuwenhoek. 2018 Feb 19. doi: 10.1007/s10482-018-1040-x

Zwittink RD, Renes IB, van Lingen RA, van Zoeren-Grobben D, Konstanti P, Norbruis OF, Martin R, Groot Jebbink LJM, Knol J, Belzer C. Association between duration of intravenous antibiotic administration and early-life microbiota development in late-preterm infants. Eur J Clin Microbiol Infect Dis. 2018 Jan 24. doi: 10.1007/s10096-018-3193-y

van der Ark KCH, Aalvink S, Suarez-Diez M, Schaap PJ, de Vos WM, Belzer C. Model-driven design of a minimal medium for Akkermansia muciniphila confirms mucus adaptation. Microb Biotechnol. 2018 Jan 26. doi: 10.1111/1751-7915.13033

Hester ER, Harpenslager SF, van Diggelen JMH, Lamers LL, Jetten MSM, Lüke C, Lücker S, Welte CU. Linking nitrogen load to the structure and function of wetland soil and rhizosphere microbial communities.

Welte CU. Revival of methane microbiology

in 't Zandt MH, van den Bosch TJM, Rijkers R, van Kessel MAHJ, Jetten MSM, Welte CU. Co-cultivation of the strictly anaerobic methanogen Methanosarcina barkeri with aerobic methanotrophs in an oxygen-limited membrane bioreactor. Appl Microbiol Biotechnol 102: 5685-5694 (2018)

de Jong AEE, in 't Zandt MH, Meisel OH, Jetten MSM, Dean JF, Rasigraf O, Welte CU. Increases in temperature and nutrient availability positively affect methane-cycling microorganisms in Arctic thermokarst lake sediments. Environ Microbiol 20: 4314-4327

Van Vliet DM, Palakawong Na Ayudthaya S, Diop S, Villanueva L, Stams AJM, Sánchez-Andrea I. Anaerobic degradation of sulfated polysaccharides by two novel Kiritimatiellales strains isolated from Black Sea sediment. Front Microbiol 10: 253 (2018), https://dx.doi.org/10.3389/fmicb.2019.00253

D Rush, Z Erdem. Cruise 64PE434: NICO Leg 7 GoMex: R/V Pelagia, 11-03-2018 to 04-04-2018, Philipsburg, Sint Maarten–Nassau, Bahamas (2018) Non-peer reviewed publication. http://www.vliz.be/imisdocs/publications/16/322716.pdf

Cantera S, Sánchez-Andrea I, Lebrero R, Garcia-Encina PA, Stams AJM, Muno R. Multi-production of high added market value metabolites from diluted methane emissions via methanotrophic extremophiles. Bioresour Technol 267, 401-407 (2018) https://doi.org/10.1016/j.resconrec.2015.11.019
Feng Y, Stams AJM, Sánchez-Andrea I, de Vos WM. Eubacterium maltosivorans sp. nov., a novel human intestinal acetogenic and butyrogenic bacterium with a versatile metabolism. Int J Syst Evol Microbiol 68: 3546-3550 (2018)

Florentino AP, Pereira IAC, Boeren S, van der Born, Stams AJM, Sánchez-Andrea I. Insights into sulfur metabolism of Desulfurella amilsii by differential proteomics. Environ Microbiol 21(1), 209–225 (2018).

Atashgahi S, Sánchez-Andrea I, Heipieper HJ, van der Meer Jr, Stams AJM, Smith H. Prospects for harnessing biocide resistance for bioremediation and detoxification. Science 360 (6390), 743-746

Sánchez-Andrea I, Jetten MSM. Editorial overview: Microbial environmental biotechnology. Curr Opin in Biotech 50, vii-ix (2018) doi:10.1016/j.copbio.2018.03.004
Claassens NJ, Sánchez-Andrea I, Sousa DZ, Bar-Even A. Towards sustainable feedstocks: a guide to electron donors for microbial carbon fixation. Curr Opin Biotech 50, 195-205 (2018)

Harris HW, Sánchez-Andrea I, McLean JS, Salas EC, Tran W, El-Naggar MY and Nealson KH. Redox sensing within the genus Shewanella. Front Microbiol 8, 2568 (2018)
J.L. Rombouts, G. Mos, D.G. Weissbrodt, R. Kleerebezem, M.C.M. van Loosdrecht. Diversity and metabolism of xylose and glucose fermenting microbial communities in sequencing batch or continuous culturing. FEMS microbiol ecol 95, 2019

Laura C. Valk, Jeroen Frank, Pilar de la Torre-Cortés, Max van ’t Hof, Antonius J. A. van Maris, Jack T. Pronk,Mark C. M. van Loosdrecht. Galacturonate Metabolism in Anaerobic Chemostat Enrichment Cultures: Combined Fermentation and Acetogenesis by the Dominant sp. nov. “Candidatus Galacturonibacter soehngenii” . Appl Environ Microbiol 84:e01370-18. https://doi.org/10.1128/AEM.01370-18

Marissa Boleij, Martin Pabst, Thomas R. Neu, Mark C. M. van Loosdrecht, and Yuemei Lin. Identification of Glycoproteins Isolated from Extracellular Polymeric Substances of Full-Scale Anammox Granular Sludge. Environ. Sci. Technol., 2018, 52 (22), pp 13127–13135. Published: https://pubs.acs.org/doi/10.1021/acs.est.8b03180

Van Kessel, MAHJ, Stultiens, K, Slegers, MFW, Guerrero Cruz, S, Jetten, MSM, Kartal, B, Op den Camp, HJMCurrent perspectives on the application of N-damo and anammox in wastewater treatment . Current opinion in Biotechnology 50, pp. 222-227. https://doi.org/10.1016/j.copbio.2018.01.031 (submitted in 2017, published in 2018)

Cantera S, Sánchez-Andrea I, Lebrero R, Garcia-Encina PA, Stams AJM, Munoz R . Multi-production of high added market value metabolites from diluted methane emissions via methanotrophic extremophiles. Bioresource Technology, 267, 401-407. https://doi.org/10.1016/j.resconrec.2015.11.019

Feng Y, Stams AJM, Sánchez-Andrea I, de Vos WM . Eubacterium maltosivorans sp. nov., a novel human intestinal acetogenic and butyrogenic bacterium with a versatile metabolism. International Journal of Systematic and Evolutionary Microbiology, 68: 3546-3550.

Florentino AP, Pereira IAC, Boeren S, van den Born M, Stams AJM, Sánchez-Andrea Insights into sulfur metabolism of Desulfurella amilsii by differential proteomics , Environmental Microbiology, 21(1), 209–225.

Atashgahi S, Sánchez-Andrea I, Heipieper HJ, van der Meer Jr, Stams AJM, Smit H . Prospects for harnessing biocide resistance for bioremediation and detoxification. Science 360 (6390), 743-746

Sánchez-Andrea I, Jetten MSM. Editorial overview: Microbial environmental biotechnology. Current Opinion in Biotechnology,50, vii-ix.

Claassens NJ, Sánchez-Andrea I, Sousa DZ. Towards sustainable feedstocks: a guide to electron donors for microbial carbon fixation, Bar-Even A. Current Opinion in Biotechnology, 50, 195-205.

Parshina SN, Strepis N, Aalvink S, Nozhevnikova AN, Stams AJM, Sousa DZ . Trichococcus shcherbakoviae sp. nov. isolated from a laboratory-scale anaerobic EGSB bioreactor operated at low temperature. Int J Syst Evol Microbiol 69(2):529-534. https://doi.org/10.1099/ijsem.0.003193

Salvador AF, Cavaleiro AF, Paulo AMS, Silva SA, Guedes AP, Pereira MA, Stams AJM, Souza DZ Alves MM. Inhibition studies with 2-bromoethane-sulfonate reveal a novel syntrophic relationship in anaerobic oleate degradation. Appl Environ Microbiol 9;85(2). https://doi.org/10.1128/AEM.01733-18

Hidalgo CA, Nobu MK, Narihiro T, Tamaki H, Liu WT, Kamagata Y, Stams AJM, Imachi H, Sousa DZ . Novel energy conservation strategies and behavior of Pelotomaculum schinkii driving syntrophic propionate catabolism. Environ Microbiol. 20(12):4503-4511. https://doi.org/10.1111/1462-2920.14388.

Sousa DZ, Visser M, Pieterse MM, Pinkse MWH, Verhaert PDEM, van Gelder AH, Vogt C, Franke S, Kümmel S, Stams AJM . The deep subsurface sulfate reducer Desulfotomaculum kuznetsovii employs two methanol degrading pathways. Nat Commun 16;9(1):239. https://doi.org/10.1038/s41467-017-02518-9.

Ziels RM, Sousa DZ, Stensel HD, Beck DAC . DNA-SIP based genome-centric metagenomics identifies key long-chain fatty acid-degrading populations in anaerobic digesters with different feeding frequencies, ISME J 12(1):112-123. https://doi.org/10.1038/ismej.2017

P Dalcin Martins, RE Danczak, S Roux, J Frank, MA Borton, RA Wolfe, MN Burris, MJ Wilkins. Viral and Metabolic Controls on High Rates of Microbial Sulfur and Carbon Cycling in Wetland Ecosystems. Microbiome, 6(1): 138. https://doi.org/10.1186/s40168-018-0522-4

AG Grottoli, P Dalcin Martins, MJ Wilkins, MD Johnston, ME Warner, WJ Cai, TF Melman, KD Hoadley, DT Pettay, S Levas, V Schoepf . Coral physiology and microbiome dynamics under combined warming and ocean acidification. PLOS ONE, 13(1): e0191156 https://doi.org/10.1371/journal.pone.0191156

HJ de Vries, F Beyer, M Jarzembowska, J Lipińska, P van den Brink, A. Zwijnenburg, PHA Timmers, AJM Stams, CM Plugge. Isolation and characterization of Sphingomonadaceae from fouled membranes npj Biofilms and Microbiomes 5 (1), 6 2019

C Magnabosco, PHA Timmers, MCY Lau, G Borgonie, B Linage-Alvarez, et al. Fluctuations in populations of subsurface methane oxidizers in coordination with changes in electron acceptor availability FEMS microbiology ecology 2018, 94 (7), fiy089

M Roghair, T Hoogstad, DP Strik, CM Plugge, PHA Timmers, et al.. Controlling Ethanol Use in Chain Elongation by CO2 Loading Rate. Environmental science & technology 2018, 52 (3), 1496-1505

PHA Timmers, CD Vavourakis, R Kleerebezem, JS Sinninghe Damste, G Muyzer, AJM Stams, DY Sorokin, CM Plugge . Metabolism and occurrence of methanogenic and sulfate-reducing syntrophic acetate oxidizing communities in haloalkaline environments. Frontiers in microbiology 2018, 9, 3039

N Müller, PHA Timmers, CM Plugge, AJM Stams, B Schink . Syntrophy in methanogenic degradation In: Hackstein J. (eds) (Endo)symbiotic Methanogenic Archaea. Microbiology Monographs, vol 19. Springer, Cham, Switzerland; pp 153-192

Sharon Y. Geerlings, Ioannis Kostopoulos, Willem M. De Vos and Clara Belzer. Akkermansia muciniphila in the Human Gastrointestinal Tract: When, Where, and How? Microorganisms 6.3 (2018): 75. Published: https://doi.org/10.3390/microorganisms6030075

Atashgahi S, MG Liebensteiner MG, Janssen DB, Smidt H, Stams A, Sipkema D. Microbial synthesis and transformation of inorganic and organic chlorine compounds. Frontiers in Microbiology 9, 3079https://www.frontiersin.org/articles/10.3389/fmicb.2018.03079/full

Atashgahi S, Shetty SS, Smidt H, De Vos WM. Flux, impact and fate of halogenated xenobiotic compounds in the gut. Frontiers in Physiology 9, 888. https://www.frontiersin.org/articles/10.3389/fphys.2018.00888/full

Atashgahi S, Sánchez Andrea I, Heipieper HJ, van der Meer JR, Stams FJM, Smidt H. Prospects for harnessing biocide resistance for bioremediation and detoxification. Science 360 (6390), 743-746. http://science.sciencemag.org/content/360/6390/743

Ferrer, Sorokin et al. Proteomic analysis of Methanonatronarchaeum thermophilum AMET1, a representative of a putative new class of Euryarchaeota, Methanonatronarchaeia. Gene, 2019, 9:article 28

Sorokin et al. Methanonatronarchaeum thermophilum gen. nov., sp. nov, and 'Candidatus Methanohalarchaeum thermophilum' - extremely halo(natrono)philic methyl-reducing methanogens from hypersaline lakes representing a novel euryarchaeal class Methanonatronarchaeia classis nov. IJSEM, 2018, 68:2199-2208.

Sorokin et al. Sulfur respiration in a group of facultatively anaerobic natronoarchaea ubiquitous in hypersaline soda lakes. Front Microbiol, 2018, 9: article 2359.

Vavourakis, Sorokin et al. A metagenomics roadmap to the uncultured genome diversity in hypersaline soda lake sediments. Microbiome, 2018, 6:article 168 Front Microbiol.

Timmers, Sorokin et al. Metabolism and occurrence of methanogenic and sulfate-reducing syntrophic acetate oxidizing communities in haloalkaline environments . 2018, 9: article 3039

Namsaraev, Sorokin et al. Effect of salinity on diazotrophic activity and microbial composition of phototrophic communities from Bitter-1 soda lake (Kulunda Steppe, Russia). Extremophiles, 2018, 22:651:663.

de Graaff D. R., Felz S., Neu T.R., Pronk M., van Loosdrecht M.C.M., Lin Y.M. Sialic Acids in the Extracellular Polymeric Substances of Seawater-Adapted Aerobic Granular Sludge. Water Res. 2019 May 15;155:343-351. doi: 10.1016/j.watres.2019.02.040

Felz S., Vermeulen P., van Loosdrecht M. C. M., Lin Y. M. Chemical characterization methods for the analysis of structural extracellular polymeric substances (EPS) in aerobic granular sludge. Water research, accepted

Seviour T., Dueholm M. S., Lotti T., Derlon N., Neuhauser E., Paul E., Neu T. R., Nerenberg R., Flemming H.C., Horn H., Malpei F., Yu H., van Loosdrecht M.C.M., Lin Y.M.. EPS in the water sector: suffering from an identity crisis. Water Res. Water Research doi.org/10.1016/j.watres.2018.11.020

Boleij M., Pabst M., Neu T.R., van Loosdrecht M.C.M., Lin Y. M. Identification of Glycoproteins Isolated from Extracellular Polymeric Substances of Full-Scale Anammox Granular Sludge. Environ Sci Technol. Oct 30. doi: 10.1021/acs.est.8b03180

2017

Arantes AL, Alves JI, **Stams AJM**, Alves MM, **Sousa DZ**. Enrichment of syngas-converting communities from a multi-orifice baffled bioreactor. Microb Biotechnol (2017). https://doi.org/10.1111/1751 7915.12864

Arshad A, Dalcin Martins P, **Frank J**, **Jetten MSM**, Op den Camp HJM, **Welte CU**. Mimicking microbial interactions under nitrate reducing conditions in an anoxic bioreactor: enrichment of novel Nitrospirae bacteria distantly related to Thermodesulfovibrio. Env Microbiol 19: 4965-4977 (2017). doi.org/10.1111/1462-2920.13977. This article was featured on the cover of Environmental Microbiology.

Belzer C, Chia LW, **Aalvink S**, Chamlagain B, Piironen V, Knol J, **de Vos WM**. Microbial Metabolic Networks at the Mucus Layer Lead to Diet-Independent Butyrate and Vitamin B12 Production by Intestinal Symbionts. MBio. Sep 19;8(5). pii: e00770-17 (2017) doi:10.1128/mBio.00770-17.

Berger S, **Frank J**, Dalcin Martins P, **Jetten MSM, Welte CU**. High quality draft genome sequence of 'Candidatus *Methanoperedens BLZ2*', a nitrate-reducing anaerobic methane-oxidizing archaeon enriched in an anoxic bioreactor. Genome Announcements 5 pii: e01159-17 (2017) doi.org/10.1128/genomeA.01159- 17

de Groot PF, **Belzer C,** Aydin Ö, Levin E, Levels JH, **Aalvink S**, Boot F, Holleman F, van Raalte DH, Scheithauer TP, Simsek S, Schaap FG, Olde Damink SWM, Roep BO, Hoekstra JB, **de Vos WM**, Nieuwdorp M. Distinct fecal and oral microbiota composition in human type 1 diabetes, an observational study. PLoS One. Dec 6;12(12):e0188475 (2017). doi: 10.1371/journal.pone.0188475"

Diender M, Uhl PS, Bitter JH, **Stams AJM, Sousa DZ**. High rate biomethanation of carbon monoxide rich gases via a thermophilic synthetic co-culture. ACS Sustain Chem Eng (2017). 10.1021/acssuschemeng.7b03601

Elderman M, Sovran B, Hugenholtz F, Graversen K, Huijskes M, Houtsma E, **Belzer C**, Boekschoten M, de Vos P, Dekker J, Wells J, Faas M. The effect of age on the intestinal mucus thickness, microbiota composition and immunity in relation to sex in mice. PLoS One. Sep 12;12(9):e0184274 (2017) doi: 10.1371/journal.pone.0184274

Feng Y, Stams AJM, de Vos W, Sánchez-Andrea I. Enrichment of sulfidogenic bacteria from the human intestinal tract. FEMS Microbiol Lett (4) 364 (2017). https://doi.org/10.1093/femsle/fnx028

Florentino AP, **Stams AJM**, **Sánchez-Andrea I**. Genome sequence of Desulfurella amilsii strain TR1 and comparative genomics of Desulfurellaceae family. Front Microbiol 8, 222 (2017). https://doi.org/10.3389/fmicb.2017.00222

Gagliano MC, Ismail SB, **Stams AJM**, Plugge CM, Temmink H, Van Lier JB. Biofilm formation and granule properties in anaerobic digestion at high salinity. Water Res 121: 61-71 (2017). https://doi.org/10.1016/j.watres.2017.05.016
Hänninen A, Toivonen R, Pöysti S, **Belzer C**, Plovier H, Ouwerkerk JP, Emani R, Cani PD, **De Vos WM**. *Akkermansia muciniphila* induces gut microbiota remodelling and controls islet autoimmunity in NOD mice. Gut pii: gutjnl-2017-314508 (2017) doi: 10.1136/gutjnl-2017-314508

in 't Zandt MH, Beckmann S, Rijkers R, **Jetten MSM**, Manefield M, **Welte CU.** Nutrient and acetate amendment leads to acetoclastic methane production and microbial community change in a non producing Australian coal well. Microb Biotechnol, in press (2017). Doi: 10.1111/1751-7915.12853
Kopejtka K, Tomasch J, ZengY, Tichý M, **Sorokin DY**, Koblížek M. Genome analysis suggests a regressive evolution of photo-trophy among haloalkaliphilic *Rhodobacterales*. Gen Biol Evol 9: 1950 1962 (2017). 10.1093/gbe/evx141

Korpela K, Zijlmans MA, Kuitunen M, Kukkonen K, Savilahti E, Salonen A, de Weerth C, **de Vos WM** (2017) Childhood BMI in relation to microbiota in infancy and lifetime antibiotic use. Microbiome. Mar 3;5(1):26. doi: 10.1186/s40168-017-0245-y.

Lankelma JM, Birnie E, Weehuizen TAF, Scicluna BP, **Belzer C**, Houtkooper RH, Roelofs JJTH, de Vos AF, van der Poll T, Budding AE, Wiersinga WJ. The gut microbiota as a modulator of innate immunity during melioidosis. PLoS Negl Trop Dis. Apr 19;11(4):e0005548 (2017) doi: 10.1371/journal.pntd.0005548

Melton ED, **Sorokin DY**, Overmars L, Lapidus AL, Pillay M, Ivanova N, del Rio TG, Kyrpides NC, Woyke T, Muyzer G. Draft genome sequence of *Dethiobacter alkaliphilus* strain AHT1T, a gram-positive sulfidogenic polyextremophile. Stand Genom Sci 12: article 57 (2017). 10.1186/s40793-017-0268-9

Milani C, Duranti S, Bottacini F, Casey E, Turroni F, Mahony J, **Belzer C,** Delgado Palacio S, Arboleya Montes S, Mancabelli L, Lugli GA, Rodriguez JM, Bode L, **de Vos W**, Gueimonde M, Margolles A, van Sinderen D, Ventura M. The First Microbial Colonizers of the Human Gut: Composition, Activities, and Health Implications of the Infant Gut Microbiota. Microbiol Mol Biol Rev. Nov 8;81(4). pii: e00036-17 (2017) doi: 10.1128/MMBR.00036-17

Ottman N, Davids M, Suarez-Diez M, Boeren S, Schaap PJ, Martins Dos Santos VAP, Smidt H, **Belzer C, de**
Vos WM. Genome-scale model and omics analysis of metabolic capacities of *Akkermansia muciniphila* reveal a preferential mucin-degrading lifestyle. Appl Environ Microbiol. Jul 7. pii: AEM.01014-17 (2017) doi: 10.1128/AEM.01014-17

Ottman N, **Geerlings SY, Aalvink S, de Vos WM, Belzer C**. Action and function of *Akkermansia muciniphila* in microbiome ecology, health and disease. Best Practice & Research Clinical Gastroenterology (2017) https://doi.org/10.1016/j.bpg.2017.10.001

Ottman N, Reunanen J, Meijerink M, Pietilä TE, Kainulainen V, Klievink J, Huuskonen L, **Aalvink S**, Skurnik M, Boeren S, Satokari R, Mercenier A, Palva A, Smidt H, **de Vos WM, Belzer C.** Pili-like proteins of *Akkermansia muciniphila* modulate host immune responses and gut barrier function. PLoS One. Mar 1;12(3):e0173004 (2017) doi:10.1371/journal.pone.0173004

Ouwerkerk JP, **Aalvink S, Belzer C, De Vos WM**. Preparation and preservation of viable *Akkermansia muciniphila* cells for therapeutic interventions. Benef Microbes. Apr 26;8(2):163-169 (2017) doi: 10.3920/BM2016.0096

Ouwerkerk JP, Koehorst JJ, Schaap PJ, Ritari J, Paulin L, **Belzer C, de Vos WM**. Complete Genome Sequence of *Akkermansia glycaniphila* Strain PytT, a Mucin-Degrading Specialist of the Reticulated Python Gut. Genome Announc. Jan 5;5(1). pii: e01098-16 (2017) doi: 10.1128/genomeA.01098-16.

Paulo AMS, Aydin TR, Dimitrov MR, Vreeling H, Cavaleiro AJ, García-Encina PA, **Stams AJM**, Plugge CM (2017) Sodium lauryl ether sulfate (SLES) degradation by nitrate-reducing bacteria. Appl Microbiol Biotechnol (on-line) doi: 10.1007/s00253-017-8212-x

Paulo LM, Ramiro-Garcia J, van Mourik S, **Stams AJM**, **Sousa DZ**. Effect of nickel and cobalt on methanogenic enrichment cultures and role of biogenic sulfide in metal toxicity attenuation. Front Microbiol 8:1341 (2017). https://doi.org/10.3389/fmicb.2017.01341

Peng P, Zheng Y, Koehorst JJ, Schaap PJ, **Stams AJM**, Smidt H, **Atashgahi S**. Concurrent haloalkanoate degradation and chlorate reduction by Pseudomonas chloritidismutans AW-1T. Appl Environ Microbiol 83(12) e00325-17 (2017). https://doi.org/10.1128/AEM.00325-17

Plovier H, Everard A, Druart C, Depommier C, Van Hul M, Geurts L, Chilloux J, Ottman N, Duparc T, Lichtenstein L, Myridakis A, Delzenne NM, Klievink J, Bhattacharjee A, **van der Ark KC**, **Aalvink S**, Martinez LO, Dumas ME, Maiter D, Loumaye A, Hermans MP, Thissen JP, **Belzer C**, **de Vos WM**, Cani PD (2017) A purified membrane protein from *Akkermansia muciniphila* or the pasteurized bacterium improves metabolism in obese and diabetic mice. Nat Med. Jan;23(1):107-113. doi: 10.1038/nm.4236. Epub 2016 Nov 28. PMID: 27892954

Pronk M, Neu TR, **van Loosdrecht MCM, Lin YM**. The acid soluble extracellular polymeric substance of aerobic granular sludge dominated by *Defluviicoccus* sp. Water Res Oct 1;122:148-158 (2017). 10.1016/j.watres.2017.05.068

Redl S*, **Diender M***, Jensen TØ, Sousa D, Nielsen AT. Exploiting the potential of gas fermentation. Ind Crops Prod (2017). 10.1016/j.indcrop.2016.11.015

Reed DC, Deemer BR, **van Grinsven S**, Harrison JA. Are elusive anaerobic pathways key methane sinks in eutrophic lakes and reservoirs? Biogeochemistry 134: 29 (2017). https://doi.org/10.1007/s10533 017-0356-3

Rush D, **Sinninghe Damsté J** (2017) Lipids as paleomarkers to constrain the marine nitrogen cycle. Environ Microbiol, in press. doi: 10.1111/1462-2920.13682

Shetty SA, Hugenholtz H, Lahti L, Smidt H, **De Vos WM**. Intestinal microbiome landscaping: insight in community assemblage and implications for microbial modulation strategies. FEMS Microbiol Rev fuw045, 41, 182–199 (2017). https://academic.oup.com/femsre/article/41/2/182/2979411

Shetty SA, Ritari J, Paulin L, Smidt H, **De Vos WM**. Complete genome sequence of *Eubacterium hallii* strain L2-7. Genome Announc 5:e01167-17 (2017) https://doi.org/10.1128/genomeA.01167-17

Sorokin DY, Chernyh N. *Desulfonatronospira sulfatiphila* sp. nov., and *Desulfitispora elongata* sp. nov., the two novel haloalkaliphilic sulfidogenic bacteria from soda lakes. Int J Syst Evol Microbiol 67: 396-401 (2017). DOI:10.1099/ijsem.0.001640

Sorokin DY, Makarova KS, Abbas B, Ferrer M, Golyshin PN, Galinski EA, Ciordia S, Mena MC, Merkel AY, Wolf YI, **van Loosdrecht MCM**, Koonin EV. Discovery of extremely halophilic, methyl-reducing euryarchaea provides insights into the evolutionary origin of methanogenesis. Nat Microbiol 2: article 17081 (2017). 10.1038/nmicrobiol.2017.81

Sorokin DY, Messina E, Smedile F, Roman P, **Sinninghe Damsté JS**, Ciordia S, Mena MC, Ferrer M, Golyshin PN, Kublanov IV, Samarov NI, Toshchakov SV, La Cono V, Yakimov MM. Discovery of the anaerobic lithoheterotrophic haloarchaea, ubiquitous in hypersaline habitats. ISME J 11: 1245–1260 (2017). doi: 10.1038/ismej.2016.203

Sorokin DY, Yakimov MM, Kublanov IV, Oren A. Genus *Halanaeroarchaeum*. Bergey's Manual of Systematic of Bacteria and Archaea (2017). 10.1002/9781118960608.gbm01496

Sorokin DY. Haloalkaliphilic anaerobes. Encyclopedia Life Science (2017). 10.1002/9780470015902.a0027654

Sousa JAB, Bijmans MFM, **Stams AJM**, Plugge CM. Thiosulfate conversion to sulfide by a haloalkaliphilic microbial community in a bioreactor fed with H2 gas. Environ Sci Technol 51: 914-923 (2017). https://doi.org/10.1021/acs.est.6b04497

Speth D, Lagkouvardos I, Wang Y, Qian P, Dutilh B, **Jetten M** (2017) Draft genome of *Scalindua rubra*, obtained from the interface above the discovery deep brine in the Red Sea, sheds light on potential salt adaptation strategies in anammox Bacteria. Microb Ecol. doi:10.1007/s00248-017-0929-7

Swarts DC#, Szczepaniak M#, Sheng G#, Chandradoss SD, **Zhu YF**, Timmers EM, Zhang Y, Zhao HT, Lou JZ, Wang YL, Joo C, van der Oost J. Autonomous generation and loading of DNA guides by bacterial Argonaute. Molecular Cell 65(6): 985-998 (2017)
https://doi.org/10.1016/j.molcel.2017.01.033

Tian WD, Ma C, **Lin YM, Welles L**, Lopez-Vazquez C, **van Loosdrecht MCM**. Enrichment and characterization of a psychrophilic '*Candidatus* Accumulibacter phosphatis' culture. Int Biodeterior Biodegradation 124:267-275 (2017). https://doi.org/10.1016/j.ibiod.2017.03.030

Timmers PHA, Welte CU, Koehorst JJ, Plugge CM**, Jetten MSM, Stams AJM**. Reverse methanogenesis and respiration in methanotrophic archaea. Archaea, 1654237 (2017)
https://www.hindawi.com/journals/archaea/2017/1654237/

Timmers PHA, Widjaja-Greefkes HCA, Plugge CM, **Stams AJM**. Evaluation and optimization of PCR primers for selective and quantitative detection of marine ANME subclusters involved in sulfate dependent anaerobic methane oxidation. Applied Microbiol Biotechnol, 101: 5847–5859 (2017). https://link.springer.com/article/10.1007/s00253-017-8338-x

Udayappan SD, Kovatcheva-Datchary P, Bakker GJ, Havik SR, Herrema H, Cani PD, Bouter KE, **Belzer C**, Witjes JJ, Vrieze A, de Sonnaville N, Chaplin A, van Raalte DH, **Aalvink S**, Dallinga-Thie GM, Heilig HGHJ, Bergström G, van der Meij S, van Wagensveld BA, Hoekstra JBL, Holleman F, Stroes ESG, Groen AK, Bäckhed F, **de Vos WM**, Nieuwdorp M. Intestinal *Ralstonia pickettii* augments glucose intolerance in obesity. PLoS One. Nov 22;12(11):e0181693 (2017) doi: 10.1371/journal.pone.0181693. eCollection 2017.
Vaksmaa A, **Jetten M**, Ettwig K, Lüke C (2017) McrA primers for the detection and quantification of the anaerobic archaeal methanotroph 'Candidatus *Methanoperedens nitroreducens*'. Appl Microbiol Biotechnol. Feb 101(4):1631-1641. doi: 10.1007/s00253-016-8065-8. PMID: 28084539

van den Bosch TJM, **Welte CU.** Detoxifying symbionts in agriculturally important pest insects. Microb Biotechnol 10: 531-40 (2017)

van der Ark KCH, Nugroho ADW, Berton-Carabin C, Wang C, **Belzer C, de Vos WM**, Schroen K. Encapsulation of the therapeutic microbe *Akkermansia muciniphila* in a double emulsion enhances survival in simulated gastric conditions. Food Res Int. Dec;102:372-379 (2017) doi: 10.1016/j.foodres.2017.09.004. Epub 2017 Sep 9

van der Ark KCH, van Heck RGA, Martins Dos Santos VAP, **Belzer C, de Vos WM**. More than just a gut feeling: constraint-based genome-scale metabolic models for predicting functions of human intestinal microbes. Microbiome. Jul 14;5(1):78 (2017) doi: 10.1186/s40168-017-0299-x.

Van Herreweghen F, Van den Abbeele P, De Mulder T, De Weirdt R, Geirnaert A, Hernandez-Sanabria E, Vilchez-Vargas R, Jauregui R, Pieper DH, **Belzer C**, **De Vos WM**, Van de Wiele T

(2017) In vitro colonisation of the distal colon by *Akkermansia muciniphila* is largely mucin and pH dependent. Benef Microbes. Feb 7;8(1):81-96. doi: 10.3920/BM2016.0013. Epub 2016

Villanueva L, Schouten S, **Sinninghe Damsté J** (2017) Phylogenomic analysis of lipid biosynthetic genes of Archaea shed light on the 'lipid divide'. Environ Microbiol. Jan;19(1):54-69. doi: 10.1111/1462-2920.13361

Wegh CAM, Schoterman MHC, Vaughan EE, **Belzer C***, Benninga MA*. The effect of fiber and prebiotics on children's gastrointestinal disorders and microbiome. Expert Rev Gastroenterol Hepatol. Jul 24 (2017) doi: 10.1080/17474124.2017.1359539

Zwittink RD, van Zoeren-Grobben D, Martin R, van Lingen RA, Groot Jebbink LJ, Boeren S, Renes IB, van Elburg RM, **Belzer C***, Knol J*. Metaproteomics reveals functional differences in intestinal microbiota development of preterm infants. Mol Cell Proteomics. Jul 6. pii: mcp.000102.2017 (2017) doi: 10.1074/mcp.RA117.000102

2016

Buntin N, Hongpattarakere T, Ritari J, Douillard FP, Paulin L, Boeren S, Shetty SA, de Vos WM (2016) An inducible operon is involved in inulin utilization in lactobacillus plantarum Strains, as revealed by comparative proteogenomics and metabolic profiling. Appl Environ Microbiol. Dec 30;83(2). pii: e02402-16. doi: 10.1128/AEM.02402-16. Print 2017 Jan 15. PMID: 27815279

Alves J, Alves M, Plugge C, Stams A,Sousa D(2016) Comparative analysis of carbon monoxide tolerance among Thermoanaerobacter species. Front Microbiol 7: 1330. doi: 10.3389/fmicb.2016.01330

Bhattacharjee A, Motlagh A, Jetten M, Goel R (2016) Methane dependent denitrification-from ecosystem to laboratory-scale enrichment for engineering applications. Wat Res 99, 244-252 Collaboration University of Utah USA

Cavaleiro A, Pereira M, Guedes A, Stams A, Alves M, Sousa D (2016) First steps of unsaturated LCFA biodegradation can occur uncoupled from methanogenesis in anaerobic bioreactors. Environ Sci Technol 50: 3082-3090. Epub: 10.1021/acs.est.5b03204

Claassens NJ, Sousa DZ, Martins dos Santos VAP, de Vos WM, van der Oost J (2016) Harnessing the power of microbial autotrophy. Nature Rev. Microbiol. 14: 692-706. doi:10.1038/nrmicro.2016.130

Derrien M, Belzer C, de Vos W (2016) Akkermansia muciniphila and its role in regulating host functions. Microb Pathog. 15 : 30178-30179.Diender M, Stams A, Sousa D (2016) Production of medium-chain fatty acids and higher alcohols by a synthetic co-culture grown on carbon monoxide or syngas. Biotechnol Biofuels 2;9:82

Diender M, Pereira R, Wessels H, Stams A, Sousa D (2016) Proteomic analysis of the hydrogen and carbon monoxide metabolism of Methanothermobacter marburgensis. Front Microbiol 7:1049. doi: 10.3389/fmicb.2016.01049

Felz S, Al-Zuhairy S, Aarstad O, van Loosdrecht M & Lin Y (2016). Extraction of Structural Extracellular Polymeric Substances from Aerobic Granular Sludge. Journal of Visualized Experiments: JoVE, 115:54534 doi: 10.3791/54534

Florentino A, Brienza C, Stams A and Sánchez-Andrea I (2016) Desulfurella amilsii sp. nov., a novel acidotolerant sulfur-respiring bacterium isolated from acidic river sediments. Int J Syst Evol Microbiol 66: 1249-1253

Fuentes S, de Vos W (2016) How to Manipulate the Microbiota: Fecal Microbiota Transplantation. Adv Exp Med Biol. 902:143-53.

Geelhoed J, Henstra A, Stams A (2016) Carbon monoxide as electron donor for fumarate reduction by Geobacter sulfurreducens employing an NADP-dependent pathway. Appl Microbiol Biotechnol 100: 997-1007 (Epub: doi: 10.1007/s00253-015-7033-z)

Jarzembowska M, Sousa D, Beyer F, Zwijnenburg A, Plugge C, Stams A (2016) Lachnotalea glycerini gen. nov., sp. nov., a new glycerol-degrading bacterium isolated from deep anoxic groundwater. Int J Syst Evol Microbiol 66: 774–779 (Epub: doi: 10.1099/ijsem.0.000791

Jung M.-Y., Kim J.-G., Sinninghe Damsté J.S., Madsen E.L., Kim S.-J., Hong H.-J., Si O.-J., Rhee S.-K. (2016) A hydrophobic ammonia-oxidizing archaeon of the Nitrosocosmicus clade isolated from a coal tar-contaminated sediment. Environm Microbiol Lett. 8, 983-992.

Korpela K, Salonen A, Virta L, Kekkonen R, Forslund K, Bork P, de Vos W (2016) Intestinal microbiome is related to lifetime antibiotic use in Finnish pre-school children. Nature Commun 7:10410.

Li S, Zhu A, Benes V, Costa P, Hercog H, Hilderbrand F, Huerta-Cepas J, Nieuwdorp M Salojarvi J, Voigt A, Zeller G, Sunagaw S, De Vos W & Bork P (2016) Durable coexistence of donor and recipient strains after fecal microbiota transplantion. Science 352; 586-589

Liebensteiner M, Oosterkamp M, Stams A (2016) Microbial respiration with chlorine oxyanions: diversity, and physiological and biochemical properties of chlorate- and perchlorate-reducing micro-organisms. Ann New York Acad Sci 1365: 59-72 (Epub: doi: 10.1111/nyas.12806)

Lüke C, Speth D, Kox MAR, Villanueva L, Jetten MSM (2016) Metagenomic analysis of nitrogen and methane cycling in the Arabian Sea oxygen minimum zone. PeerJ4:e1924. doi.org/10.7717/peerj.1924

Mehboob F, Oosterkamp MJ, Farrakh S, Boeren S, Veuskens T, Plugge CM, de Vos WM, Schraa G, Stams AJM, Schaap PJ (2016) Genome and proteome analysis of Pseudomonas chloritidismutans AW-1T that grow with n-decane with chlorate or oxygen as electron acceptor. Environ. Microbiol. 18:3247 – 3257. Epub: doi: 10.1111/1462-2920.12880

Ottman N, Huuskonen L, Reunanen J, Boeren S, Klievink J, Smidt H, Belzer C, de Vos W (2016) Characterization of Outer Membrane Proteome of Akkermansia muciniphila Reveals Sets of Novel Proteins Exposed to the Human Intestine. Front Microbiol. 2016 Jul 26;7:1157.

Ouwerkerk J, Aalvink S, Belzer C, de Vos W (2016). Akkermansia glycaniphilasp. nov.: an anaerobic mucin-degrading bacterium isolated from reticulated python faeces. Int J Syst Evol Microbiol. 2016 Aug 5.

Ouwerkerk J, van der Ark K, Davids M, Claassens N, Robert Finestra T, de Vos W, Belzer C (2016) Adaptation of Akkermansia muciniphilato the oxic-anoxic interface of the mucus layer. Appl Environ Microbiol. 2016 Sep 23. pii: AEM.01641-16. [Epub ahead of print]

Palakawong N, Pristaš P, Hrehová L, Javorský P, Stams A, Plugge CM (2016) Actinomyces succiniciruminis sp. nov. and Actinomyces glycerinitolerans sp. nov., two novel organic acid-producing bacteria isolated from rumen. Syst Appl Microbiol 39: 445-452. doi: 10.1016/j.syapm.2016.08.001

Plouvier, H, Everard A, Druart C, Depommier C, van Hul M, Geurts L. Chilloux J, Ottman N, Duparc T, Lichtenstein L, Myrikadis A, Delzene N, Klievink J, Battacharjee A, van der Ark K, Aalvink S, Martinez L, Dumas M, Maitero D, Loumaye A, Hermans M, Thissen J, Belzer C, de Vos WM & Cani P (2016) A purified membrane protein from Akkermansia muciniphilaor the pasteurized bacterium improves metabolism in obese and diabetic mice. Nature Med. Nov 20 2016, doi:10.1038/nm.4236

Richter H, Molitor B, Diender M, Sousa D, Angenent LT (2016) A narrow pH range supports butanol, hexanol, and octanol production from syngas in a continuous co-culture of Clostridium ljungdahlii and Clostridium kluyveri with in-line product extraction. Front Microbiol ;7:1773. doi: 10.3389/fmicb.2016.01773

Sánchez-Andrea I, Stams A, Weijma J, Gonzalez Contreras P, Dijkman H, Rozendal R, Johnson D (2016) A case in support of implementing innovative bio-processes in the metal mining industry. FEMS Microbiol Lett 363: 11. pii: fnw106. doi: 10.1093/femsle/fnw106.

Sorokin D and Chernyh N (2016) 'Candidatus Desulfonatronobulbus propionicus': a first haloalkaliphilic member of the order Syntrophobacterales from soda lakes. Extremophiles 20:895-901 DOI 10.1007/s00792-016-0881-3

Sorokin DY, Kublanov IV, Yakimov MM, Rijpstra WIC & Sinninghe Damsté JS(2016). Halanaeroarchaeum sulfurireducens gen. nov., sp. nov., the first obligately anaerobic sulfur-respiring haloarchaeon, isolated from a hypersaline lake. Int. J. Syst. Evol. Microbiol. 66(6), 2377-2381. doi: 10.1099/ijsem.0.001041

Sorokin DY, Rakitin AL, Gumerov VM, Beletsky AV, Sinninghe Damsté JS, Mardanov AV & Ravin NV (2016). Phenotypic and genomic properties of Chitinispirillum alkaliphilum gen. nov., sp. nov., a haloalkaliphilic anaerobic chitinolytic bacterium representing a novel class in the Phylum Fibrobacteres. Front. Microbiol. 7. doi:10.3389/fmicb.2016.00407

Strepis N, Sánchez-Andrea I, van Gelder A, van Kruistum H, Shapiro N, Kyrpides N, Göker M, Klenk H, Schaap P, Stams A, Sousa D(2016) Description of Trichococcus ilyis sp. nov. by combined physiological and in silico genome hybridization analyses. Int J Syst Evol Microbiol 66: 3957-3963. doi: 10.1099/ijsem.0.001294.

Timmers P, Suarez-Zuluaga D, van Rossem M, Diender M, Stams A, Plugge C (2016) Anaerobic oxidation of methane associated with sulfate reduction in a natural freshwater gas source. ISME J 10: 1400-1412. doi:10.1038/ismej.2015.213)

Tytgat H, Douillard F, Laine P, Paulin L, Willems R, de Vos W (2016) Complete Genome Sequence of Enterococcus faeciumCommensal Isolate E1002. Genome Announc. 4(2). Tytgat H & de Vos W (2016) Sugar Coating the Envelope: Glycoconjugates For Microbe - Host Crosstalk. Trends in Microbiol. 2016 Jun 30

Tytgat H, Douillard F, Reunanen J, Rasinkangas P, Hendrickx A, Laine P, Paulin L, Satokari R, de Vos W (2016) Lactobacillus rhamnosus GG Outcompetes Enterococcus faeciumby Mucus-Binding Pili - Evidence for a Novel Probiotic Mechanism on a Distance. Appl Environ Microbiol. 2016 Jul 15.

Udayappan S, Manneras-Holm L, Chaplin-Scott A, Belzer C, Herrema H, Dallinga-Thie G, Duncan S, Stroes E, Groen A, Flint H, Backhed F, de Vos W & Nieuwdorp M (2016) Oral treatment with Eubacterium hallii improves insulin sensitivity in db/db mice. NPJ Biofilms and Microbiomes 2, 16009

Vaksmaa A, Lüke C, van Alen T, Valè G, Lupotto E, Jetten M, Ettwig K (2016) Distribution and activity of the anaerobic methanotrophic community in a nitrogen-fertilized Italian paddy soil. FEMS Microbiol Ecol. pii: fiw181.

van den Nieuwboer M, van Hemert S, Claassen E, de Vos W (2016) Lactobacillus plantarumWCFS1 and its host interaction: a dozen years after the genome. Microb Biotechnol. 2016 May 27.

Visser M, Pieterse M, Pinkse MWH, Nijsse B, Verhaert PDEM, de Vos WM, Schaap PJ and Stams AJM (2016) Unravelling the one-carbon metabolism of the acetogen Sporomusa strain An4 by genome and proteome analysis. Environ. Microbiol. 18:2843-2855. doi: 10.1111/1462-2920.12973

Visser M, Stams A, Frutschi M, Bernier-Latmani R (2016) Phylogenetic comparison of Desulfotomaculum species of subgroup 1a and description of Desulfotomaculum reducens sp.nov. Int J Syst Evol Microbiol 66: 762–767 (Epub: doi: 10.1099/ijsem.0.000786)

Welte C (2016) A microbial route from coal to gas. Science 354 (6309), 184. doi: 10.1126/science.aai8101

Welte C, Rasigraf O, Vaksmaa A, Versantvoort W, Arshad A, Op den Camp H, Jetten M, Lüke C, Reimann J (2016) Nitrate and nitrite dependent anaerobic oxidation of methane. Environ Microbiol Rep doi: 10.1111/1758-2229.12487.

Welte C, Rosengarten J, de Graaf R, Jetten M (2016) SaxA-mediated isothiocyanate metabolism in phytopathogenic pectobacteria. Appl Environ Microbiol 82. doi: 10.1128/AEM.04054-15This article was featured on the cover of AEM

2015

Arshad A, Speth D, Graaf R de, Op den Camp H, Jetten M, Welte C (2015) A metagenomics-based metabolic model of nitrate-dependent anaerobic oxidation of methane by Methanoperedens-like archaea. Front Microbiol 6:1423. doi: 10.3389/fmicb.2015.01423

Bui N., Ritari, J., Boeren, S., de Waard, P., Plugge, C.M., & de Vos, W.M. (2015) Production of butyrate from lysine and the Amadori product fructoselysine by a human gut commensal. Nature Comm. 6:10062. epub: doi:10.1038/ncomms10062

Diender M, Stams A, Sousa D (2015) Pathways and bioenergetics of anaerobic carbon monoxide fermentation. Front Microbiol 19;6:1275

Egger M, Rasigraf O, Sapart CJ, Jilbert T, Jetten M, Röckmann T, van der Veen C, Banda N, Kartal B, Ettwig K, Slomp C (2015) Iron-mediated anaerobic oxidation of methane in brackish coastal sediments. Environ Scie & Technol 49 (1): 277-283. doi: 10.1021/es503663z

Florentino A, Weijma J, Stams A and Sánchez-Andrea I (2015) Sulfur reduction in acid rock drainage environments. Environ Sci Technol 49: 11746–11755

Kulichevskaya I, Ivanova A, Detkova E, Rijpstra W, Sinninghe Damsté J, Dedysh S (2015). Planctomicrobium piriforme gen. nov., sp. nov., a stalked planctomycete from a littoral wetland of a boreal lake. Int J Syst Evol Microbiol 65(5): 1659-1665. dx.doi.org/10.1099/ijs.0.000154

Liebensteiner M, Pinkse M, Nijsse B, Verhaert P, Stams A, Lomans B (2015) Perchlorate and chlorate reduction by the Crenarchaeon Aeropyrum pernix and two thermophilic Firmicutes. Environ Microbiol Rep 7: 936–945 (Epub: doi: 10.1111/1758-2229.12335)

Lin Y, Nierop K, Girbal-Neuhauser E, Adriaanse M & Van Loosdrecht M (2015). Sustainable polysaccharide-based biomaterial recovered from waste aerobic granular sludge as a surface coating material. Sustainable Materials and Technologies, 4, 24-29. Doi: 10.1016/j.susmat.2015.06.002

Oosterkamp M, Boeren S, Atashgahi S, Plugge C, Schaap P, Stams A (2015) Proteomic analysis of nitrate-dependent acetone degradation by Alicycliphilus denitrificans strain BC. FEMS Microbiol Lett 362: 11 fnv080 (Epub: doi: 10.1093/femsle/fnv080)

Moore EK, Hopmans EC, Rijpstra WIC, Sánchez-Andrea I, Villanueva L, Wienk H, Schoutsen F, Stams AJM, Sinninghe Damsté JS (2015). Lysine and novel hydroxylysine lipids in soil bacteria: amino acid membrane lipid response to temperature and pH in Pseudopedobacter saltans. Front. Microbiol. 6: 637. dx.doi.org/10.3389/fmicb.2015.00637

Moore E, Villanueva L, Hopmans E, Rijpstra W, Mets A, Dedysh S, Sinninghe Damsté J (2015). Abundant trimethylornithinelipids and specific gene sequences are indicative of planctomycete importance at the oxic/anoxic interface in Sphagnum-dominated northern wetlands. Appl Environ Microbiol 81(18): 6333-6344. dx.doi.org/10.1128/AEM.00324-15

Sánchez-Andrea I, Stams A, Hedrich S, Nancucheo I, Johnson D (2015) Desulfosporosinus acididurans sp. nov., an acidophilic sulfate-reducing bacterium isolated from acidic sediments. Extremophiles 19: 39-47 (Epub: doi 10.1007/s00792-014-0701-6)

Sorokin DY, Abbas B, Merkel AY, Rijpstra WIC, Sinninghe Damsté JS, Sukhacheva MV, van Loosdrecht MCM(2015). Methanosalsum natronophilumsp. nov., and Methanocalculus alkaliphilus sp. nov., haloalkaliphilic methanogens from hypersaline soda lakes. Int. J. Syst. Evol. Microbiol. 65: 3739-3745. dx.doi.org/10.1099/ijsem.0.000488

Tailford L, Owen C, Walshaw J, Crost E, Hardy-Goddard J, Le Gall G, de Vos W, Taylor G, Juge N (2015) Discovery of intramolecular trans-sialidases in human gut microbiota suggests novel mechanisms of mucosal adaptation. Nat Commun. 2015 Jul 8;6:7624

Timmers P, Gieteling J, Aura Widjaja-Greefkes H, Plugge C, Stams A, Lens P, Meulepas R (2015) Growth of anaerobic methane oxidizing archaea and sulfate reducing bacteria in a high pressure membrane-capsule bioreactor. Appl Environ Microbiol 81: 1286-1296 (Epub: 10.1128/AEM.03255-14)

Timmers P, Widjaja-Greefkes H, Ramiro Garcia J, Plugge C, Stams A (2015) Growth and activity of ANME subclades with different sulfate and sulfide concentrations and with and without methane. Front Microbiol 6: 988 (Epub: doi: 10.3389/fmicb.2015.00988)

Villanueva L, Schouten S,Sinninghe Damsté J (2015). Depth-related distribution of a key gene of the tetraether lipid biosynthetic pathway in marine Thaumarchaeota. Environ Microbiol 17(10): 3527–3539. dx.doi.org/10.1111/1462-2920.12508

Welte C, de Graaf R, van den Bosch T, Op den Camp H, van Dam N, Jetten M (2015) Plasmids from the gut microbiome of cabbage root fly larvae encode SaxA that catalyzes the conversion of the plant toxin 2-phenylethyl isothiocyanate. Environ Microbiol, in press (doi: 10.1111/1462-2920.12997)
Welte C, Jetten M (2015) Fortunate those that are starting now Environ Microbiol Rep. 2015 Feb;7(1):23-5. doi: 10.1111/1758-2229.12229

2014

Dalla Vecchia E, Visser M, Stams A, Bernier-Latmani R (2014) Investigation of sporulation in the Desulfotomaculum genus: a genomic comparison with the genera Bacillus and Clostridium. Environ Microbiol 6: 756–766 (Epub: doi:10.1111/1758-2229.12200)

Lahti L, Salojarvi J, Salonen A, Scheffer M, de VosW (2014) Tipping elements in the human intestinal ecosystem. Nature Comm July 2014 8;5:4344.

Liebensteiner M, Tsesmetzis N,Stams A, Lomans B (2014) Microbial redox processes in deep subsurface environments and the potential application of (per)chlorate in oil reservoirs. Front Microbiol 5: 428 (Epub: doi: 10.3389/fmicb.2014.00428)

Rajilić-Stojanović M, de Vos W (2014) The first 1000 cultured species of the human gastrointestinal microbiota. FEMS Microbiol Rev 38: 996-1047.

Sánchez-Andrea I,
Sanz J, Stams A (2014) Microbacter margulisiaegen. nov., sp. nov., a novel propionigenic bacterium isolated from sediments of an acid rock drainage pond. Int J Syst Evol Microbio 64: 3936–3942 (Epub: doi 10.1099/ijs.0.066241-0)