# F-M Kerckhof

## List of Publications by Year
## in descending order

Source: https://exaly.com/author-pdf/4536898/publications.pdf

Version: 2024-02-01

| | | | |
|---|---|---|---|
| 53<br>papers | 3,112<br>citations | 201385<br>27<br>h-index | 168136<br>53<br>g-index |
| 59<br>all docs | 59<br>docs citations | 59<br>times ranked | 5527<br>citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Cocultivating aerobic heterotrophs and purple bacteria for microbial protein in sequential photo- and chemotrophic reactors. Bioresource Technology, 2021, 319, 124192. | 4.8 | 28 |
| 2 | Electrochemical and phylogenetic comparisons of oxygen-reducing electroautotrophic communities. Biosensors and Bioelectronics, 2021, 171, 112700. | 5.3 | 2 |
| 3 | Cytometric fingerprints of gut microbiota predict Crohnâ€™s disease state. ISME Journal, 2021, 15, 354-358. | 4.4 | 19 |
| 4 | PhenoGMM: Gaussian Mixture Modeling of Cytometry Data Quantifies Changes in Microbial Community Structure. MSphere, 2021, 6, . | 1.3 | 21 |
| 5 | Low microbial biomass within the reproductive tract of mid-lactation dairy cows: A study approach. Journal of Dairy Science, 2021, 104, 6159-6174. | 1.4 | 6 |
| 6 | Root-Associated Bacterial Community Shifts in Hydroponic Lettuce Cultured with Urine-Derived Fertilizer. Microorganisms, 2021, 9, 1326. | 1.6 | 8 |
| 7 | From Biogas and Hydrogen to Microbial Protein Through Co-Cultivation of Methane and Hydrogen Oxidizing Bacteria. Frontiers in Bioengineering and Biotechnology, 2021, 9, 733753. | 2.0 | 17 |
| 8 | Gut Microbiota of Migrating Wild Rabbit Fish (Siganus guttatus) Larvae Have Low Spatial and Temporal Variability. Microbial Ecology, 2020, 79, 539-551. | 1.4 | 25 |
| 9 | Discriminating Bacterial Phenotypes at the Population and Singleâ€Cell Level: A Comparison of Flow Cytometry and Raman Spectroscopy Fingerprinting. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2020, 97, 713-726. | 1.1 | 16 |
| 10 | Microbial protein production from methane via electrochemical biogas upgrading. Chemical Engineering Journal, 2020, 391, 123625. | 6.6 | 31 |
| 11 | Bacterial mock communities as standards for reproducible cytometric microbiome analysis. Nature Protocols, 2020, 15, 2788-2812. | 5.5 | 26 |
| 12 | A prebiotic-enhanced lipid-based nutrient supplement (LNSp) increases Bifidobacterium relative abundance and enhances short-chain fatty acid production in simulated colonic microbiota from undernourished infants. FEMS Microbiology Ecology, 2020, 96, . | 1.3 | 10 |
| 13 | Microbial Protein out of Thin Air: Fixation of Nitrogen Gas by an Autotrophic Hydrogen-Oxidizing Bacterial Enrichment. Environmental Science &amp; Technology, 2020, 54, 3609-3617. | 4.6 | 35 |
| 14 | Gut microbiota generation of protein-bound uremic toxins and related metabolites is not altered at different stages of chronic kidney disease. Kidney International, 2020, 97, 1230-1242. | 2.6 | 125 |
| 15 | Future prospects for dissecting inter-individual variability in the absorption, distribution and elimination of plant bioactives of relevance for cardiometabolic endpoints. European Journal of Nutrition, 2019, 58, 21-36. | 1.8 | 34 |
| 16 | Enriched hydrogen-oxidizing microbiomes show a high diversity of co-existing hydrogen-oxidizing bacteria. Applied Microbiology and Biotechnology, 2019, 103, 8241-8253. | 1.7 | 24 |
| 17 | Learning Singleâ€Cell Distances from Cytometry Data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2019, 95, 782-791. | 1.1 | 4 |
| 18 | Determining stoichiometry and kinetics of two thermophilic nitrifying communities as a crucial step in the development of thermophilic nitrogen removal. Water Research, 2019, 156, 34-45. | 5.3 | 8 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 19 | A unified framework for unconstrained and constrained ordination of microbiome read count data. PLoS ONE, 2019, 14, e0205474. | 1.1 | 14 |
| 20 | Oxygen-reducing microbial cathodes monitoring toxic shocks in tap water. Biosensors and Bioelectronics, 2019, 132, 115-121. | 5.3 | 53 |
| 21 | Reduced TCA cycle rates at high hydrostatic pressure hinder hydrocarbon degradation and obligate oil degraders in natural, deep-sea microbial communities. ISME Journal, 2019, 13, 1004-1018. | 4.4 | 14 |
| 22 | Characterization of spoilage markers in modified atmosphere packaged iceberg lettuce. International Journal of Food Microbiology, 2018, 279, 1-13. | 2.1 | 29 |
| 23 | Initial evenness determines diversity and cell density dynamics in synthetic microbial ecosystems. Scientific Reports, 2018, 8, 340. | 1.6 | 12 |
| 24 | Flow cytometric fingerprinting for microbial strain discrimination and physiological characterization. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2018, 93, 201-212. | 1.1 | 43 |
| 25 | Pinpointing wastewater and process parameters controlling the AOB to NOB activity ratio in sewage treatment plants. Water Research, 2018, 138, 37-46. | 5.3 | 34 |
| 26 | Microbiological, chemical and sensory spoilage analysis of raw Atlantic cod (Gadus morhua) stored under modified atmospheres. Food Microbiology, 2018, 70, 232-244. | 2.1 | 90 |
| 27 | Mucin degradation niche as a driver of microbiome composition and Akkermansia muciniphila abundance in a dynamic gut model is donor independent. FEMS Microbiology Ecology, 2018, 94, . | 1.3 | 51 |
| 28 | Chronic rhinosinusitis with nasal polyps is characterized by dysbacteriosis of the nasal microbiota. Scientific Reports, 2018, 8, 7926. | 1.6 | 67 |
| 29 | Label-free Raman characterization of bacteria calls for standardized procedures. Journal of Microbiological Methods, 2018, 151, 69-75. | 0.7 | 38 |
| 30 | Interâ€individual differences determine the outcome of wheat bran colonization by the human gut microbiome. Environmental Microbiology, 2017, 19, 3251-3267. | 1.8 | 88 |
| 31 | Effect of Operational Parameters in the Continuous Anaerobic Fermentation of Cheese Whey on Titers, Yields, Productivities, and Microbial Community Structures. ACS Sustainable Chemistry and Engineering, 2017, 5, 1400-1407. | 3.2 | 55 |
| 32 | Efficient molasses fermentation under high salinity by inocula of marine and terrestrial origin. Biotechnology for Biofuels, 2017, 10, 23. | 6.2 | 19 |
| 33 | Absolute quantification of microbial taxon abundances. ISME Journal, 2017, 11, 584-587. | 4.4 | 273 |
| 34 | Reconciliation between operational taxonomic units and species boundaries. FEMS Microbiology Ecology, 2017, 93, . | 1.3 | 71 |
| 35 | In vitro Increased Respiratory Activity of Selected Oral Bacteria May Explain Competitive and Collaborative Interactions in the Oral Microbiome. Frontiers in Cellular and Infection Microbiology, 2017, 7, 235. | 1.8 | 9 |
| 36 | Biotic Interactions in Microbial Communities as Modulators of Biogeochemical Processes: Methanotrophy as a Model System. Frontiers in Microbiology, 2016, 7, 1285. | 1.5 | 95 |

| # | Article | IF | Citations |
|---|---|---|---|
| 37 | Chronic cigarette smoke exposure induces microbial and inflammatory shifts and mucin changes in the murine gut. Environmental Microbiology, 2016, 18, 1352-1363. | 1.8 | 149 |
| 38 | Community structure, population dynamics and diversity of fungi in a full-scale membrane bioreactor (MBR) for urban wastewater treatment. Water Research, 2016, 105, 507-519. | 5.3 | 60 |
| 39 | New <i>Methyloceanibacter</i> diversity from North Sea sediments includes methanotroph containing solely the soluble methane monooxygenase. Environmental Microbiology, 2016, 18, 4523-4536. | 1.8 | 81 |
| 40 | Bacillus cereus NVH 0500/00 Can Adhere to Mucin but Cannot Produce Enterotoxins during Gastrointestinal Simulation. Applied and Environmental Microbiology, 2016, 82, 289-296. | 1.4 | 12 |
| 41 | Bacterial Exchange in Household Washing Machines. Frontiers in Microbiology, 2015, 6, 1381. | 1.5 | 64 |
| 42 | <i>Bacillus cereus</i>Adhesion to Simulated Intestinal Mucus Is Determined by Its Growth on Mucin, Rather Than Intestinal Environmental Parameters. Foodborne Pathogens and Disease, 2015, 12, 904-913. | 0.8 | 10 |
| 43 | Exploring methane-oxidizing communities for the co-metabolic degradation of organic micropollutants. Applied Microbiology and Biotechnology, 2015, 99, 3609-3618. | 1.7 | 35 |
| 44 | Optimized Cryopreservation of Mixed Microbial Communities for Conserved Functionality and Diversity. PLoS ONE, 2014, 9, e99517. | 1.1 | 74 |
| 45 | Microbial Odor Profile of Polyester and Cotton Clothes after a Fitness Session. Applied and Environmental Microbiology, 2014, 80, 6611-6619. | 1.4 | 102 |
| 46 | Development of an oral mucosa model to study host-microbiome interactions during wound healing. Applied Microbiology and Biotechnology, 2014, 98, 6831-6846. | 1.7 | 21 |
| 47 | Exploration and prediction of interactions between methanotrophs and heterotrophs. Research in Microbiology, 2013, 164, 1045-1054. | 1.0 | 57 |
| 48 | Conceptualizing functional traits and ecological characteristics of methaneâ€•oxidizing bacteria as life strategies. Environmental Microbiology Reports, 2013, 5, 335-345. | 1.0 | 225 |
| 49 | Barcoded pyrosequencing analysis of the microbial community in a simulator of the human gastrointestinal tract showed a colon region-specific microbiota modulation for two plant-derived polysaccharide blends. Antonie Van Leeuwenhoek, 2013, 103, 409-420. | 0.7 | 19 |
| 50 | Butyrate-producing <i>Clostridium</i> cluster XIVa species specifically colonize mucins in an <i>in vitro</i> gut model. ISME Journal, 2013, 7, 949-961. | 4.4 | 501 |
| 51 | Characterization of Staphylococcus and Corynebacterium Clusters in the Human Axillary Region. PLoS ONE, 2013, 8, e70538. | 1.1 | 74 |
| 52 | Strain-Specific Transfer of Antibiotic Resistance from an Environmental Plasmid to Foodborne Pathogens. Journal of Biomedicine and Biotechnology, 2012, 2012, 1-8. | 3.0 | 29 |
| 53 | Conversion of Biogas to Bioproducts by Algae and Methane Oxidizing Bacteria. Environmental Science &amp; Technology, 2012, 46, 13425-13431. | 4.6 | 78 |