

Biosketch

Assist.-Prof. Christian Diener, PhD

Position in CoE: Key Researcher

Personal Details

Place of birth	Berlin, Germany
Nationality	German
Children	-
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Profile	-
List of publications	ORCID: 0000-0002-7476-0868
Academic age	12 years since PhD



Academic Career and Positions Held

I obtained my **Bachelor's degree** in Bioinformatics and my **PhD** from the **Free University of Berlin**. During this time I joined the International **Max Planck Research School (IMPRS-CBSC)** at the **Max Planck Institute for Molecular Genetics**, where I studied the intracellular signaling in haploid yeast populations using a variety of computational techniques. I held a **postdoctoral fellowship** at the **National Autonomous University of Mexico** from 2012-2014 within the Institute of Cellular Physiology where I developed my wet lab skills to design and test novel multifunctional signaling peptides. In 2015 I joined the **National Institute of Genomic Medicine in Mexico** as **Medical Researcher** where I started my research on the human gut microbiome and its influence on human metabolic diseases with an emphasis on type 2 diabetes. This was followed by a move to Seattle, USA in 2018 for a position at the **Institute for Systems Biology** where I was promoted to **Senior Research Scientist** with a research focus on the human gut microbiome. In 2024, I joined the **Medical University of Graz** as an **Assistant Professor of Computational Microbiome Science** within the Cluster of Excellence.

Scientific Achievements and Scientific Contribution to the CoE

Scientific Achievements. My major contributions to the field have been to establish **interactions between the human gut microbiome and human metabolism**. I led projects that identified connections between the human gut microbiome and the human blood metabolome and its effects during **weights loss** and the **onset of type 2 diabetes**. I also participated in large interinstitutional projects that demonstrated the association of the human gut microbiome with **aging, metabolic health, and the efficacy of commonly prescribed drugs** (specifically statins). During this research I led and collaborated on development of several methods and software tools such as COBRAPY, MICOM, QIIME2, and MEMOTE, which are now all widely used in the field. I have authored more than **40 peer-reviewed publications** which have been cited more than 15,000 times (Google Scholar 2024, h-index: 21). I have participated as Senior Researcher on **several NIH R01 grants** and was the Principal Investigator on **two ISB Innovator Award grants**.

Scientific Contribution to the CoE. Our lab will contribute to the CoE by participating in WPs studying the small intestinal microbiome and fecal microbiota transplants (FMTs). Additionally, we will take a role in the synthesis module by suggesting **standardized analysis strategies and core mechanisms** that can be applied across work packages as well as providing **expertise in metagenomic data analysis and metabolic modeling of complex microbial communities** in diverse environments.

10 Most Important Publications (*relevant for the CoE)

1. *Watanabe, K; Wilmanski, T; **Diener, C**; Earls, JC; Zimmer, A; Lincoln, B; Hadlock, JJ; Lovejoy, JC; Gibbons, SM; Magis, AT; Hood, L; Price, ND; Rappaport, N. Multiomic signatures of body mass index identify heterogeneous health phenotypes and responses to a lifestyle intervention. *Nat Med.* **2023**, 29(4):996-1008. <https://doi.org/10.1038/s41591-023-02248-0>.
2. *Marcelino, VR; Welsh, C; **Diener, C**; Gulliver, EL; Rutten, EL; Young, RB; Giles, EM; Gibbons, SM; Greening, C; Forster, SC. Disease-specific loss of microbial cross-feeding interactions in the human gut. *Nat Commun.* **2023**, 14(1):6546. <https://doi.org/10.1038/s41467-023-42112-w>.
3. ***Diener, C**; Dai, CL; Wilmanski, T; Baloni, P; Smith, B; Rappaport, N; Hood, L; Magis, AT; Gibbons, SM. Genome-microbiome interplay provides insight into the determinants of the human blood metabolome. *Nat Metab.* **2022**, 4(11):1560-1572. <https://doi.org/10.1038/s42255-022-00670-1>.
4. *Wilmanski, T; Kornilov, SA; **Diener, C**; Conomos, MP; Lovejoy, JC; Sebastiani, P; Orwoll, ES; Hood, L; Price, ND; Rappaport, N; Magis, AT; Gibbons, SM. Heterogeneity in statin responses explained by variation in the human gut microbiome. *Med.* **2022**, 3(6):388-405.e6. <https://doi.org/10.1016/j.medj.2022.04.007>.
5. *Wilmanski, T; **Diener, C**; ...; Price, ND. Gut microbiome pattern reflects healthy ageing and predicts survival in humans. *Nat Metab.* **2021**, (2):274-286. <https://doi.org/10.1038/s42255-021-00348-0>.
6. ***Diener, C**; Qin, S; Zhou, Y; Patwardhan, S; Tang, L; Lovejoy, JC; Magis, AT; Price, ND; Hood, L; Gibbons, SM. Baseline Gut Metagenomic Functional Gene Signature Associated with Variable Weight Loss Responses following a Healthy Lifestyle Intervention in Humans. *mSystems.* **2021**, 6(5):e0096421. <https://doi.org/10.1128/msystems.00964-21>.
7. ***Diener, C**; Reyes-Escogido, ML; Jimenez-Ceja, LM; Matus, M; Gomez-Navarro, CM; Chu, ND; Zhong, V; Tejero, ME; Alm, E; Resendis-Antonio, O; Guardado-Mendoza, R. Progressive Shifts in the Gut Microbiome Reflect Prediabetes and Diabetes Development in a Treatment-Naive Mexican Cohort. *Front Endocrinol (Lausanne).* **2021**, 11:602326. <https://doi.org/10.3389/fendo.2020.602326>.
8. Lieven, C; Beber, ME; Olivier, BG; Bergmann, FT; Ataman, M; Babaei, P; Bartell, JA; Blank, LM; Chauhan, S; Correia, K; **Diener, C**; ...; Zhang, C. MEMOTE for standardized genome-scale metabolic model testing. *Nat Biotechnol.* **2020**, 38(3):272-276. <https://doi.org/10.1038/s41587-020-0446-y>.
9. ***Diener, C**; Gibbons, SM; Resendis-Antonio, O. MICOM: Metagenome-Scale Modeling To Infer Metabolic Interactions in the Gut Microbiota. *mSystems.* **2020**, 5(1):e00606-19. <https://doi.org/10.1128/msystems.00606-19>
10. Bolyen, E; Rideout, JR; Dillon, MR; Bokulich, NA; Abnet, CC; Al-Ghalith, GA; Alexander, H; Alm, EJ; Arumugam, M; Asnicar, F; Bai, Y; Bisanz, JE; Bittinger, K; Brejnrod, A; Brislawn, CJ; Brown, CT; Callahan, BJ; Caraballo-Rodríguez, AM; Chase, J; Cope, EK; Da Silva, R; **Diener, C**; ...; Caporaso, JG. Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nat Biotechnol.* **2019**, 37(8):852-857. <https://doi.org/10.1038/s41587-019-0209-9>.