Christian Diener

Curriculum Vitae

Research Topics

- Niche dynamics in microbial communities
- Shaping of the intestinal environment by the human gut microbiome
- Predicting intervention effects in the gut microbiome
- Computational methods to quantify microbe-host interactions

Career

2024–now **Assistant Professor**, *Medical University of Graz*, Austria

I joined the faculty of the Diagnostic and Research Institute of Hygiene, Microbiology and Environmental Medicine in 2024. Our lab studies the human gut microbiome through an approach that combines ecology, systems biology, and metabolism with the goal of designing targeted precision interventions for microbiome-associated diseases. We are associated with the FWF Cluster of Excellence Microbes drive Planetary Health.

2018–2024 **Senior Research Scientist**, *Institute for Systems Biology*, USA

I started as a Washington Research Foundation Distinguished Postdoctoral Fellow in the Gibbons Lab. I was promoted to a Research Scientist position in 2020 and to a Senior Research Scientist position in 2022. My research is focused on leveraging data from metagenomics, deep phenotyping and wet lab experiments to unravel the functional consequences of compositional shifts in the mammalian gut microbiome. I also worked with environmental samples and long-read sequencing of metagenome samples. In the wet lab, I standardized and performed anaerobic *ex vivo* culturing assays and processed samples for shotgun sequencing, RNA-seq, proteomic, and metabolomic quantification.

2015–2018 **Investigator in Medical Sciences "B"**, *National Institute for Genomic Medicine*, Mexico

I held a position in Dr. Osbaldo Resendis' laboratory of Human Systems Biology. In the first half of my position I studied metabolic alterations in cancer using a variety of data sources such as metabolome, genome and transcriptome data and combined those with mathematical modeling (flux balance analysis). Later I switched my focus to the microbiome where I analyzed 16S amplicon sequencing and metagenomic data sets from various cohorts and modeled the underlying microbial communities.

2012–2014 **Postdoctoral Fellow**, *Universidad Nacional Autónoma de México (UNAM)*, Mexico

I worked as a postdoctoral fellow in the laboratory of Integrative Research of Biological Systems of Dr. Gabriel Del Rio Guerra in the field of Synthetic Biology and Peptide design. During my position at the UNAM I used a combination of machine learning and optimization theory to design multi-functional cell-penetrating and antimicrobial peptides and validated their function in *E. coli* and *S. cerevisiae* using a variety of molecular biology methods.

Education

2008–2012 **Ph.D. in Bioinformatics**, *Freie Universität Berlin*, Germany
Ph.D. with distinction (*summa cum laude*) in Bioinformatics from the Free University of Berlin within the International Max Planck Research School for Computational Biology and Scientific Computing (IMPRS-CBSC).
Thesis: "Localized signaling and communication during yeast mating", supervised by Dr. Edda Klipp and Dr. Martin Vingron.

2007–2008 **preparatory program (M.Sc. equivalent) in Systems Biology**, *Max Planck Institute for Molecular Genetics*, Berlin, Germany
Fast-track program of the International Max Planck Research School for Computational Biology and Scientific Computing (IMPRS-CBSC).

2004–2007 **B.Sc. in Computational Biology**, *Freie Universität Berlin*, Germany

Awards & Funding

07/2022 **Dr. Christine Schaeffer Award for Exemplary Service to STEM Education**, *Institute for Systems Biology*
The award is given to ISB scientists who have taken up the mantle of devoting their time and efforts to improving STEM education.

04/2022 **ISB Innovator Award 2022 (PI)**, *Institute for Systems Biology*
Awarded $55,000 for the project "A Clinical and Experimental Exploration of Gut Microbiome-Statin Interactions".

01/2021 **Precision Nutrition Gaps And Opportunities Workshop Poster Award**, *National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK)*
Awarded for poster titled "Predicting personalized responses to dietary interventions with metagenome-scale metabolic models of the gut microbiota".

04/2019 **ISB Innovator Award 2019 (PI)**, *Institute for Systems Biology*
Awarded $55,000 for the project Integrating genetics, blood proteomics and the gut microbiome to understand transitions from high to lower weights".

05/2017 **Poster prize winner PostDoc**, *Copenhagen Bioscience Conference*
Awarded for best research project in the PostDoc category.

10/2011 **Award of the American Society of Biochemistry and Molecular Biology**, *Cellular Signaling Conference, Mérida México*
Awarded for exceptional research quality.

2011 **Scholarship of the German Academic Exchange Program (DAAD)**, *Universidad Nacional Autónoma de México*
Scholarship for a short research stay.

2007 **Scholarship of the International Max Planck Research School**, *Max Planck Institute for Molecular Genetics*
Full scholarship for pre-doc and Ph.D. studies.

2007 **Young investigator award**, *SYSBIOHEALTH symposium*, Milano, Italy
Awarded for best poster.

Teaching & Mentoring

2024-2025 **Lecturer**, *Medical University of Graz*

Taught and tutored Project-based Learning courses during the academic year 2024/2025 at the Diagnostic and Research Institute of Hygiene, Microbiology and Environmental Medicine.

2022 **Mentor**, *Institute for Systems Biology*

I mentored two undergrad students from Cornell and Notre Dam University within the ISB Summer Undergraduate Research Experience.

2021 **Research Consultant**, *Institute for Systems Biology*

I collaborated with community college educators from Washington state in developing classroom modules for the NSF funded Biological Data Literacy Program within the ISB Education program. The designed activities were implemented in classrooms in 2022.

2020–2022 **Lead Instructor**, *Institute for Systems Biology*, http://isbscience/microbiome2022

I designed teaching materials and acted as a lead instructor for the ISB Microbiome Series, a recurring freely available online course teaching microbiome data analysis and metabolic modeling. The three iterations of the course were attended by more than 3000 international registrants.

2019 **Mentor**, *Institute for Systems Biology*

I mentored two high school students from Washington state within the ISB Internship program.

2017–2018 **Instructor**, *Desafío LatAm*, Mexico City

Developed and gave classes in a Developer Bootcamp Program for professionals in Big Data Engineering (5h/week). Topics: Data Science with Python, Statistics and Visualization, Machine Learning, Apache Spark, Streaming Data, Deep Learning, Deployment of Machine Learning Solutions.

2013 **Teaching Assistant**, *Universidad Nacional Autónoma de México*

Taught classes, designed and graded exercises and exams to students in the Bioengineering program. Courses: Introduction to Machine Learning.

2008–2012 **Teaching Assistant**, *Humboldt University of Berlin*

Prepared lectures, designed exercises and exams and provided tutoring to students in the Biophysics program. Courses: Introduction to Systems Biology, Statistical Physics, Introduction to Databases in Bioinformatics.

Languages

English	fluent
Spanish	fluent
German	native speaker

Publications

[1] Christian Diener et al. “**Metagenomic estimation of dietary intake from human stool**”. In: *Nature metabolism* (2025), pp. 1–14.

[2] Nick Quinn-Bohmann et al. “Moving from genome-scale to community-scale metabolic models for the human gut microbiome”. In: *Nature Microbiology* (2025), pp. 1–12.

[3] Audrey Byrne et al. “Neonates exposed to HIV but uninfected exhibit an altered gut microbiota and inflammation associated with impaired breast milk antibody function”. In: *Microbiome* 12.1 (2024), p. 261.

[4] Johannes P Johnson-Martínez et al. “Aberrant bowel movement frequencies coincide with increased microbe-derived blood metabolites associated with reduced organ function”. In: *Cell Reports Medicine* 5.7 (2024).

[5] Nick Quinn-Bohmann, Jose A Freixas-Coutin, et al. “Meta-analysis of the human upper respiratory tract microbiome reveals robust taxonomic associations with health and disease”. In: *BMC biology* 22.1 (2024), p. 93.

[6] Nick Quinn-Bohmann, Tomasz Wilmanski, et al. “**Microbial community-scale metabolic modelling predicts personalized short-chain fatty acid production profiles in the human gut**”. In: *Nature Microbiology* (2024), pp. 1–13.

[7] Katherine Ramos Sarmiento et al. “Island biogeography theory provides a plausible explanation for why larger vertebrates and taller humans have more diverse gut microbiomes”. In: *The ISME Journal* 18.1 (2024), wrae114.

[8] Jordy E. Sulaiman et al. “Elucidating human gut microbiota interactions that robustly inhibit diverse Clostridioides difficile strains across different nutrient landscapes”. In: *Nature Communications* 15.1 (2024), p. 7416.

[9] Christian Diener and Sean M Gibbons. “Coarse graining the human gut microbiome”. In: *Cell Host & Microbe* 31.7 (2023), pp. 1076–1078.

[10] Christian Diener and Sean M Gibbons. “**More is different: metabolic modeling of diverse microbial communities**”. In: *Msystems* 8.2 (2023), e01270–22.

[11] Anna-Ursula Happel et al. “Bifidobacterium infantis supplementation versus placebo in early life to improve immunity in infants exposed to HIV: a protocol for a randomized trial”. In: *BMC Complementary Medicine and Therapies* 23.1 (2023), p. 367.

[12] Joe J Lim et al. “Growth phase estimation for abundant bacterial populations sampled longitudinally from human stool metagenomes”. In: *Nature Communications* 14.1 (2023), p. 5682.

[13] Vanessa R Marcelino et al. “Disease-specific loss of microbial cross-feeding interactions in the human gut”. In: *Nature Communications* 14.1 (2023), p. 6546.

[14] Kengo Watanabe et al. “Multiomic signatures of body mass index identify heterogeneous health phenotypes and responses to a lifestyle intervention”. In: *Nature medicine* 29.4 (2023), pp. 996–1008.

[15] Christian Diener et al. “**Genome–microbiome interplay provides insight into the determinants of the human blood metabolome**”. In: *Nature metabolism* 4.11 (2022), pp. 1560–1572.

[16] Rachel H Ng et al. “Constraint-based reconstruction and analyses of metabolic models: open-source python tools and applications to cancer”. In: *Frontiers in oncology* 12 (2022), p. 914594.

[17] Tomasz Wilmanski et al. “**Heterogeneity in statin responses explained by variation in the human gut microbiome**”. In: *Med* 3.6 (2022), pp. 388–405.

[18] Jessica A Day et al. “Lettuce (Lactuca sativa) productivity influenced by microbial inocula under nitrogen-limited conditions in aquaponics”. In: *PLoS One* 16.2 (2021), e0247534.

[19] Christian Diener, Anna CH Hoge, et al. “Non-responder phenotype reveals apparent microbiome-wide antibiotic tolerance in the murine gut”. In: *Communications Biology* 4.1 (2021), p. 316.

[20] Christian Diener, Shizhen Qin, et al. “Baseline gut metagenomic functional gene signature associated with variable weight loss responses following a healthy lifestyle intervention in humans”. In: *Msystems* 6.5 (2021), pp. 10–1128.

[21] Christian Diener, María de Lourdes Reyes-Escogido, et al. “**Progressive shifts in the gut microbiome reflect prediabetes and diabetes development in a treatment-naive Mexican cohort**”. In: *Frontiers in endocrinology* 11 (2021), p. 602326.

[22] Melissa C Kordahi et al. “Genomic and functional characterization of a mucosal symbiont involved in early-stage colorectal cancer”. In: *Cell host & microbe* 29.10 (2021), pp. 1589–1598.

[23] Tomasz Wilmanski, Christian Diener, et al. “**Gut microbiome pattern reflects healthy ageing and predicts survival in humans**”. In: *Nature metabolism* 3.2 (2021), pp. 274–286.

[24] Tomasz Wilmanski, Noa Rappaport, et al. “From taxonomy to metabolic output: what factors define gut microbiome health?” In: *Gut microbes* 13.1 (2021), p. 1907270.

[25] Christian Diener, Sean M Gibbons, and Osbaldo Resendis-Antonio. “**MICOM: metagenome-scale modeling to infer metabolic interactions in the gut microbiota**”. In: *MSystems* 5.1 (2020), pp. 10–1128.

[26] Christian Lieven et al. “MEMOTE for standardized genome-scale metabolic model testing”. In: *Nature biotechnology* 38.3 (2020), pp. 272–276.

[27] Erika A Peláez Coyotl et al. “Antimicrobial peptide against mycobacterium tuberculosis that activates autophagy is an effective treatment for tuberculosis”. In: *Pharmaceutics* 12.11 (2020), p. 1071.

[28] Evan Bolyen et al. “**Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2**”. In: *Nature biotechnology* 37.8 (2019), pp. 852–857.

[29] Alex Carr et al. “Use and abuse of correlation analyses in microbial ecology”. In: *The ISME journal* 13.11 (2019), pp. 2647–2655.

[30] Vanessa L Hale, Patricio Jeraldo, Jun Chen, et al. “Distinct microbes, metabolites, and ecologies define the microbiome in deficient and proficient mismatch repair colorectal cancers”. In: *Genome medicine* 10 (2018), pp. 1–13.

[31] Vanessa L Hale, Patricio Jeraldo, Michael Mundy, et al. “Synthesis of multi-omic data and community metabolic models reveals insights into the role of hydrogen sulfide in colon cancer”. In: *Methods* 149 (2018), pp. 59–68.

[32] Christian Diener, Georgina Garza Ramos Martínez, et al. “Effective design of multifunctional peptides by combining compatible functions”. In: *PLoS Computational Biology* 12.4 (2016), e1004786.

[33] Christian Diener, Felipe Muñoz-Gonzalez, et al. “The space of enzyme regulation in HeLa cells can be inferred from its intracellular metabolome”. In: *Scientific reports* 6.1 (2016), p. 28415.

[34] Christian Diener and Osbaldo Resendis-Antonio. “Personalized prediction of proliferation rates and metabolic liabilities in cancer biopsies”. In: *Frontiers in physiology* 7 (2016), p. 644.

[35] Christian Diener et al. “Yeast mating and image-based quantification of spatial pattern formation”. In: *PLoS computational biology* 10.6 (2014), e1003690.

[36] Jonathan G Rodriguez Plaza et al. “Cell penetrating peptides and cationic antibacterial peptides: two sides of the same coin”. In: *Journal of Biological Chemistry* 289.21 (2014), pp. 14448–14457.

[37] Florian Rubelt et al. “Onset of immune senescence defined by unbiased pyrosequencing of human immunoglobulin mRNA repertoires”. In: *PloS one* 7.11 (2012), e49774.

[38] Matteo Barberis et al. “A low number of SIC1 mRNA molecules ensures a low noise level in cell cycle progression of budding yeast”. In: *Molecular BioSystems* 7.10 (2011), pp. 2804–2812.

[39] Thomas W Spiesser et al. “What influences DNA replication rate in budding yeast?” In: *PloS one* 5.4 (2010), e10203.

Key publications shown in **bold**. A full list of scientific works and citations can be found on Google Scholar.