

# Chapter 1

## General

Steen, A. D., *et al.* (2019). High proportions of bacteria and archaea across most biomes remain uncultured. *The ISME Journal* **13**, 3126–3130. <https://doi.org/10.1038/s41396-019-0484-y>

## Diversity

Baker, B. J., *et al.* (2020). Diversity, ecology and evolution of Archaea. *Nature Microbiology*. **5**(7), 887-900. <https://doi.org/10.1038/s41564-020-0715-z>

Dion, M. B., *et al.* (2020). Phage diversity, genomics and phylogeny. *Nature Reviews Microbiology* **18**(3), 125-138. <https://doi.org/10.1038/s41579-019-0311-5>

## Ecology and Geomicrobiology

Evans, C. R., *et al.* (in press). Metabolic heterogeneity and cross-feeding in bacterial multicellular systems. *Trends in Microbiology*. <https://doi.org/10.1016/j.tim.2020.03.008>

## Evolution

## Genomics

## Extreme environments

## Human microbiome

Alavi, S., *et al.* (in press). Interpersonal gut microbiome variation drives susceptibility and resistance to cholera infection. *Cell*. <https://doi.org/10.1016/j.cell.2020.05.036>

- Alessi, A. M., *et al.* (2020).  $\beta$ -Glucan is a major growth substrate for human gut bacteria related to *Coprococcus eutactus*. *Environmental Microbiology* **22**(6), 2150-2164. <https://sfamjournals.onlinelibrary.wiley.com/doi/abs/10.1111/1462-2920.14977>
- Andreo-Martínez, P., *et al.* (2020). An approach to gut microbiota profile in children with autism spectrum disorder. *Environmental Microbiology Reports* **12**(2), 115-135. <https://sfamjournals.onlinelibrary.wiley.com/doi/abs/10.1111/1758-2229.12810>
- Anhê, F. F., *et al.* (2020). Type 2 diabetes influences bacterial tissue compartmentalisation in human obesity. *Nature Metabolism* **2**(3), 233-242. <https://doi.org/10.1038/s42255-020-0178-9>
- Badia, J. & Baldomà, L. (2020). Membrane vesicles from the gut microbiota and their interactions with the host. *Bacterial Membrane Vesicles: Biogenesis, Functions and Applications*. M. Kaparakis-Liaskos and T. A. Kufer (Ed). Cham, Springer International Publishing: 189-217. [https://doi.org/10.1007/978-3-030-36331-4\\_9](https://doi.org/10.1007/978-3-030-36331-4_9)
- Bellone, M., *et al.* (2020). Microbiota-propelled T helper 17 cells in inflammatory diseases and cancer. *Microbiology & Molecular Biology Reviews* **84**(2), e00064-19. <https://mmbr.asm.org/content/mmbr/84/2/e00064-19.full.pdf>
- Bittinger, K., *et al.* (2020). Bacterial colonization reprograms the neonatal gut metabolome. *Nature Microbiology* **5**(6), 838-847. <https://doi.org/10.1038/s41564-020-0694-0>
- Burberry, A., *et al.* (2020). *C9orf72* suppresses systemic and neural inflammation induced by gut bacteria. *Nature* **582**(7810), 89-94. <https://doi.org/10.1038/s41586-020-2288-7>
- Campbell, C., *et al.* (2020). Bacterial metabolism of bile acids promotes generation of peripheral regulatory T cells. *Nature* **581**(7809), 475-479. <https://doi.org/10.1038/s41586-020-2193-0>
- Deehan, E. C., *et al.* (2020). Precision microbiome modulation with discrete dietary fiber structures directs short-chain fatty acid production. *Cell Host & Microbe* **27**(3), 389-404.e6. <https://doi.org/10.1016/j.chom.2020.01.006>

- Diener, C., *et al.* (2020). MICOM: Metagenome-scale modeling to Infer metabolic interactions in the gut microbiota. *mSystems* **5**(1), e00606-19. <https://msystems.asm.org/content/msys/5/1/e00606-19.full.pdf>
- Flint, H. J. (2020). The gut microbiome: essential symbionts or unwelcome guests? *Why Gut Microbes Matter: Understanding Our Microbiome*. Cham, Springer International Publishing: 9-14. [https://doi.org/10.1007/978-3-030-43246-1\\_2](https://doi.org/10.1007/978-3-030-43246-1_2)
- Funabashi, M., *et al.* (2020). A metabolic pathway for bile acid dehydroxylation by the gut microbiome. *Nature* **582**(7813), 566-570. <https://doi.org/10.1038/s41586-020-2396-4>
- Gaike, A. H., *et al.* (2020). The gut microbial diversity of newly diagnosed diabetics but not of prediabetics is significantly different from that of healthy nondiabetics. *mSystems* **5**(2), e00578-19. <https://msystems.asm.org/content/msys/5/2/e00578-19.full.pdf>
- Ganal-Vonarburg, S. C., *et al.* (2020). Microbial–host molecular exchange and its functional consequences in early mammalian life. *Science* **368**(6491), 604-607. <https://science.sciencemag.org/content/sci/368/6491/604.full.pdf>
- Illiano, P., *et al.* (2020). The mutual interplay of gut microbiota, diet and human disease. *The FEBS Journal* **287**(5), 833-855. <https://febs.onlinelibrary.wiley.com/doi/abs/10.1111/febs.15217>
- Kazemian, N., *et al.* (2020). Gut microbiota and cardiovascular disease: opportunities and challenges. *Microbiome* **8**(1), 36. <https://doi.org/10.1186/s40168-020-00821-0>
- Kim, S., *et al.* (2020). *Akkermansia muciniphila* prevents fatty liver disease, decreases serum triglycerides, and maintains gut homeostasis. *Applied & Environmental Microbiology* **86**(7), e03004-19. <https://aem.asm.org/content/aem/86/7/e03004-19.full.pdf>
- Kosti, I., *et al.* (2020). Meta-analysis of vaginal microbiome data provides new insights into preterm birth. *Frontiers in Microbiology* **11**, 476. <https://www.frontiersin.org/article/10.3389/fmicb.2020.00476>
- Melo, L. D. R., *et al.* (2020). Phage therapy efficacy: a review of the last 10 years of preclinical studies. *Critical Reviews in Microbiology* **46** (1), 78-99.

<https://doi.org/10.1080/1040841X.2020.1729695>

Mendez, R., *et al.* (2020). Gut microbial dysbiosis in individuals with Sjögren's syndrome. *Microbial Cell Factories* **19**(1), 90. <https://doi.org/10.1186/s12934-020-01348-7>

Meng, X., *et al.* (in press). Gut dysbacteriosis and intestinal disease: mechanism and treatment. *Journal of Applied Microbiology*. <https://sfamjournals.onlinelibrary.wiley.com/doi/abs/10.1111/jam.14661>

Nakajima, A., *et al.* (2020). A soluble fiber diet increases *Bacteroides fragilis* group abundance and immunoglobulin A production in the gut. *Applied & Environmental Microbiology* **86**(13), e00405-20. <https://aem.asm.org/content/aem/86/13/e00405-20.full.pdf>

Nejman, D., *et al.* (2020). The human tumor microbiome is composed of tumor type-specific intracellular bacteria. *Science* **368**(6494), 973-980. <https://science.sciencemag.org/content/sci/368/6494/973.full.pdf>

Nemet, I., *et al.* (2020). A cardiovascular disease-linked gut microbial metabolite acts via adrenergic receptors. *Cell* **180**(5), 862-877.e822. <https://doi.org/10.1016/j.cell.2020.02.016>

Neugent, M. L., *et al.* (2020). Advances in understanding the human urinary microbiome and its potential role in urinary tract infection. *mBio* **11**(2), e00218-20. <https://mbio.asm.org/content/mbio/11/2/e00218-20.full.pdf>

Newton, I. L. G. & Rice, D. W. (2020). The Jekyll and Hyde symbiont: Could *Wolbachia* be a nutritional mutualist? *Journal of Bacteriology* **202**(4), e00589-19. <https://jb.asm.org/content/jb/202/4/e00589-19.full.pdf>

Norouzi-Beirami, M. H., *et al.* (2020). Beyond taxonomic analysis of microbiomes: A functional approach for revisiting microbiome changes in colorectal cancer. *Frontiers in Microbiology* **10**, 3117. <https://www.frontiersin.org/article/10.3389/fmicb.2019.03117>

Selber-Hnatiw, S., *et al.* (2020). Metabolic networks of the human gut microbiota. *Microbiology* **166**(2), 96-119. <https://doi.org/10.1099/mic.0.000853>

- Strandwitz, P., *et al.* (2019). GABA-modulating bacteria of the human gut microbiota. *Nature Microbiology* **4**(3), 396-403. <https://doi.org/10.1038/s41564-018-0307-3>
- Ternes, D., *et al.* (2020). Microbiome in colorectal cancer: How to get from meta-omics to mechanism? *Trends in Microbiology* **28**(5), 401-423. <https://doi.org/10.1016/j.tim.2020.01.001>
- Thiele, I., *et al.* (2020). Personalized whole-body models integrate metabolism, physiology, and the gut microbiome. *Molecular Systems Biology* **16**(5), e8982. <https://www.embopress.org/doi/abs/10.15252/msb.20198982>
- Timm, C. M., *et al.* (2020). Isolation and characterization of diverse microbial representatives from the human skin microbiome. *Microbiome* **8**(1), 58. <https://doi.org/10.1186/s40168-020-00831-y>
- Zhang, F., *et al.* (2020). Bioavailability based on the gut microbiota: a new perspective. *Microbiology & Molecular Biology Reviews* **84**(2), e00072-19. <https://mmbr.asm.org/content/mmbr/84/2/e00072-19.full.pdf>