

# Publications

Loos D<sup>\*</sup>, Pereira da Costa Filho A<sup>\*</sup>, Dutilh B E, Barber AE<sup>#</sup>, Panagiotou G<sup>#</sup> (2024) A global survey of host, aquatic, and soil microbiomes reveals shared abundance and genomic features between bacterial and fungal generalists. *Cell Rep* 43(4), 114046.

Loos D<sup>\*</sup>, Zhang L, Beemelmans C, Kurzai O, Panagiotou G<sup>#</sup> (2021) DAnIEL: A user-friendly web server for fungal ITS amplicon sequencing data. *Front Microbiol* 12, 720513.

Mirhakkak M, Schäuble S, Klassert T, Brunke S, Brandt P, Loos D, Uribe R, de Oliveira Lino FS, Ni Y, Vylkova S, Slevogt H, Hube B, Weiss G, Sommer M, Panagiotou G<sup>#</sup> (2021) Metabolic modeling predicts specific gut bacteria as key determinants for *Candida albicans* colonization levels. *ISME J* 15(5), 1257-1270.

Seelbinder B, Chen J, Brunke S, Vazquez-Urbe R, Santhanam R, Meyer AC, de Oliveira Lino FS, Chan KF, Loos D, Imamovic L, Tsang CC, Lam RP, Sridhar S, Kang K, Hube B, Woo PCY, Sommer MOA, Panagiotou G (2020) Antibiotics create a shift from mutualism to competition in human gut communities with a longer-lasting impact on fungi than bacteria. *Microbiome* 8(1), 133.

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