

Publications

Senne de Oliveira Lino F^{*}, Garg S^{*}, Li SS, Misiakou MA, Kang K, Labate Vale da Costa B, Svend-Aage Beyer-Pedersen T, Guerra Giaccon T, Basso TO, Panagiotou G, Sommer MOA[#] (2024) Strain dynamics of contaminating bacteria modulate the yield of ethanol biorefineries. *Nat Commun* 15(1), 5323.

Barber AE^{*}, Sae-Ong T^{*}, Kang K, Seelbinder S, Li J, Walther G, Panagiotou G[#] & Kurzai O[#] (2021) *Aspergillus fumigatus* pan-genome analysis identifies genetic variants associated with human infection. *Nat Microbiol* 6(12), 1526-1536.

Kang K, Imamovic L, Misiakou M, Sørensen MB, Heshiki Y, Ni Y, Zheng T, Li J, Ellabaan MMH, Colomer-Lluch M, Rode AA, Bytzer P, Panagiotou G[#], Sommer MOA (corresponding author[#]) (2021) Expansion and persistence of antibiotic-specific resistance genes following antibiotic treatment. *Gut Microbes* 13(1), 1-19.

Barber AE, Riedel J, Sae-Ong T, Kang K, Brabetz W, Panagiotou G, Deising HB, Kurzai O (2020) Effects of agricultural fungicide use on *Aspergillus fumigatus* abundance, antifungal susceptibility, and population structure. *mBio* 11(6), e02213-20.

Haange SB, Jehmlich N, Krügel U, Hintschich C, Wehrmann D, Hankir M, Seyfried F, Froment J, Hübschmann T, Müller S, Wissenbach DK, Kang K, Buettner C, Panagiotou G, Noll M, Rolle-Kampczyk U, Fenske W, von Bergen M (2020) Gastric bypass surgery in a rat model alters the community structure and functional composition of the intestinal microbiota independently of weight loss. *Microbiome* 8(1), 13.

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.

Kang K, Bergdahl B, Machado D, Dato L, Han TL, Li J, Villas-Boas S, Herrgård MJ, Förster J, Panagiotou G (2019) Linking genetic, metabolic and phenotypic diversity among *S. cerevisiae* strains using multi-omics associations *Gigascience* 8(4), giz015.

Zheng T, Li J, Ni Y, Kang K, Misiakou MA, Imamovic L, Chow BKC, Rode AA, Bytzer P, Sommer M, Panagiotou G^{**} (2019) Mining, analyzing, and integrating viral signals from metagenomic data. *Microbiome* 7(1), 42.

Kang K, Ni Y, Li J, Imamovic L, Sarkar C, Kobler MD, Heshiki Y, Zheng T, Kumari S, Wong JCY, Archana A, Wong CWM, Dingle C, Denizen S, Baker DM, Sommer MOA, Webster CJ, Panagiotou G^{**} (2018) The environmental exposures and inner- and intercity traffic flows of the metro system may contribute to the human skin microbiome and resistome. *Cell Reports* 24(5), 1190-1202.

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