## Publication record (peer-reviewed, chronological order)

### In review

Brändel SD, Melville DW, Wilhelm K, Sarapak J, Haeckh F, Corman VM, Page R, Drosten C, Tschapka M, Sommer S, Wasimuddin. Astrovirus infection alters gut microbial communities in a widespread Neotropical bat across human-modified landscapes.

Carranco AS, Romo D, de Lourdes Torres M, Wilhelm K, Sommer S. From nest to hatchling: nidobiome assembly and host selection in oviparous vertebrates without parental care.

Fleischer R, Hanifen KE, Mallory ML, Provencher J, Sommer S. Microbial shifts and reduced condition with microplastic ingestion in wild seabirds.

Jetter K, Jani K, Wilhelm K, Stehle U, Chamedjeu RR, Riedel C, Sommer S, Wilfert L, Schäfer P. Effects of pig slurry fertilization history on grassland microbiomes: Insights from field and mesocosm experiments.

Meyer M, Schindler M, Wilhelm K, Gruber J, Schillinger A, Hiller C, Jani K, Jetter K, Carranco AS, Vesely K, Bruck M, ? S, Frötscher H, Schneeweihs S, Baumgartner C, Sommer S. Nests of the endangered European pond turtle leave a biogeochemical and microbial imprint on floodplain soils.

Mikkelsen AJ, Radchuk V, Ratovonamana YR, Eatrefene F, Kasola C, Odilon NG, Rasoanaivo FH, Razafindrazanaka BE, Razafindraibe H, Sommer S, Ganzhorn JU. Population dynamics of the carnivoran *Galidictis fasciata grandidieri* under hypervariable rainfall in the spiny forest of Madagascar.

### 2026

Carranco AS, Romo D, de Lourdes Torres M, Wilhelm K, Gillingham MAF, **Sommer S** (2026) Egg microbiome of the yellow-spotted Amazon river turtle (*Podocnemis unifilis*) modulates fusariosis fungal infection and hatching success. *Communications Biology***.**

Menke S, Fackelmann G, Vucetich LM, Vucetich JA, Forbey JS, **Sommer S** (2026) Forage quality shapes physiological and gut microbial responses in moose (*Alces alces*) of Isle Royale National Park. *Scientific Reports*, 16, 3724. https://doi.org/10.1038/s41598-026-35555-w.

Olayemi A, Sarapak J, Wilhelm K, Günther S, **Sommer S,** Fichet-Calvet E, Melville DW (2026) Regional Lassa virus lineages select for divergent MHC-I repertoires in *Mastomys natalensis rodents*. PLoS Pathogens, 22(4) e1014121. https://doi.org/10.1371/journal.ppat.1014121.

Víquez-R L, Speer K, Wilhelm K, Perkins S, Simmons NB, Medellín RA, **Sommer S**, Tschapka M (2026) Tequila Bats (Phyllostomidae: *Leptonycteris yerbabuenae*) and their associated bat flies: disentangling the effects of physical proximity and organism source as predictors of microbiota dissimilarities. *Journal of Mammalogy*. https://doi.org/10.1093/jmammal/gyaf080.

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151. Chamedjeu RR**,** Jani K**,** Jetter K, Wilhelm K, Schäfer P, Wilfert L, **Sommer S**, Riedel C (2025) Impact of fertilization on the bacterial core microbiome of grassland soils: Abundance in the field and growth *in vitro. Environmental Microbiology Reports*, 17:e70235. https://doi.org/10.1111/1758-2229.70235.
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**2024**

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(2023), Non-structural genes of novel lemur adenoviruses reveal codivergence of virus and host. *Virus Evolution*, 9:1. https://doi.org/10.1093/ve/vead024.

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