

### Publication accepted at *Science*




Our manuscript describing the first reconstruction of natural products from ancient microbiomes has been accepted for publication in the prestigious journal *Science*. In this transdisciplinary project between the Warinner and Stallforth labs, we investigated the dental calculus of 12 Neanderthals and 52 anatomically modern humans spanning 100,000 years to the present. We were able to reconstruct the genomes of bacteria and a previously uncharacterized biosynthetic gene cluster (BGC). Based on a combination of bioinformatics analyses and molecular biology approaches, we recreated a previously unknown group of metabolites that we named paleofurans. This is the first account of a natural product being generated from ancient DNA up to 100,000 years old. This major breakthrough will enable us gain insight into how microorganisms of the past interacted with each other. We will further pursue our approach to identify ancient natural products with potent bioactivities.

Our work has been selected as *First Release* article (publication date May 4<sup>th</sup> 2023) by *Science* as the editors recognized the timeliness and importance of our research.

### WSS Colloquium

The first Werner Siemens-Colloquium was held on March 20<sup>th</sup> 2023 at the Leibniz-HKI. We hosted international experts of microbial genomics, computational biology, natural product chemistry, and paleogenomics to explore and imagine the future of microbial paleogenomic research and the emerging field of paleobiotechnology. The panel speakers were: Dr. Katerina Guschanski (Edinburgh), Prof. Nadine Ziemert (Tübingen), and Dr. Antonio Fernandez-Guerra (Copenhagen). This symposium was highly successful and enabled students and senior researchers to discuss their research in both an interdisciplinary and truly interactive fashion. Due to the success of this event, we will organize further WSS Colloquia on a regular basis.




WERNER SIEMENS-STIFTUNG  
PALEOBIOTECHNOLOGY KOLLOQUIUM

#### Microbiome functional evolution: past to present

**Topic** Advances in high-throughput sequencing and computational metagenomics are opening up dramatic new opportunities for understanding the structure and complex functions of diverse microbiomes. At the same time, the rise of paleogenomics is enabling the study of microbial communities deeper and deeper into the past. It is now possible, for the first time, to combine these advances to investigate microbiome functional evolution over the past 100,000 years in high resolution. This colloquium brings together diverse experts in microbial genomics, computational biology, natural product chemistry, and archaeology to explore and imagine the future of microbial paleogenomic research and the emerging field of paleobiotechnology.

**Date and Location** *Monday 20th March, 13:00-15:00*


**Open Lecture** *Dorothy Hodgkins Seminar Room*  
(registration-required) *Biotech Center, Leibniz Hans Knöll Institute*  
*Hermann-Löns-Str. 70, 07745 Jena*




**Panel**



Prof. Nadine  
Ziemert  
Institute of Microbiology and Infection Medicine (IMI),  
Institute for Bioinformatics and Medical Informatics (IBMI),  
University of Tübingen, DE




Dr. Katerina  
Guschanski  
University of Edinburgh, UK  
Vrije Universiteit, NL



Dr. Antonio  
Fernandez-Guerra  
Lundbeck Foundation Genomics Center,  
Globe Institute,  
University of Copenhagen, DK

**More Information and registration, scan the QR code or visit:**  
<https://www.leibniz-hki.de/en/event/microbiome-functional-evolution-past-to-present.html>



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## WSS Retreat

The groups of Christina Warinner and Pierre Stallforth met for a three-day retreat at the Rittergut Positz, Thuringia (March 15 – 17<sup>th</sup> 2023). The main focus was to discuss current and new projects in a cross-disciplinary fashion. Team-building activities allowed all team members – in particular new ones – to get to know each other.



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## WSS Summer School on Ancient Metagenomics (online)



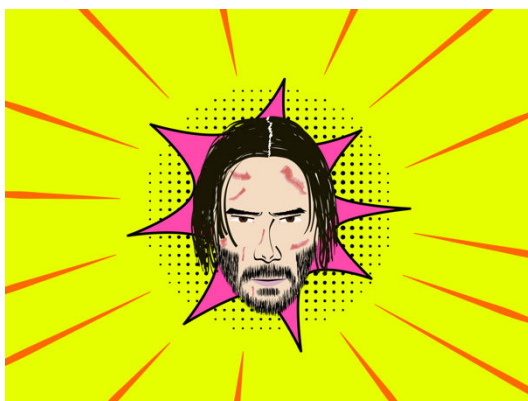
After a very successful summer school in the summer of 2022 (112 applicants to only 30 places), a second course will take place beginning of August 2023. The aim of the practical course is to provide masters and early PhD students a grounding in the steps of the latest ancient metagenomic bioinformatic workflows, from familiarizing students with the command line, to demonstrating how to process next-generation-sequencing (NGS) data, and all the way to how to perform *de novo* metagenomic assembly. Focusing on host-associated ancient metagenomics, the course consists of a combination of lectures and hands-on exercises with a range of

members from the SPAAM community of ancient metagenomics researchers (<https://spaam-community.github.io/>), allowing participants to become familiar with the types of questions and particularities of ancient DNA data that ancient metagenomic researchers work with. Round table discussions with experts at each stage of the workflow will be held to allow participants to get advice on their own projects and research.

By the end of the course, participants will understand how to effectively carry out the major bioinformatic components of an ancient metagenomic project in an open and transparent manner.

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## Keanumycin



The Department of Paleobiotechnology isolated a novel antifungal from a bacterial strain that is effective against various fungal pathogens that can attack crops. Because the newly discovered substance is so lethal, the researchers decided to name it after the action hero Keanu Reeves. This work was published in the prestigious *Journal of the American Chemical Society* (*J. Am. Chem. Soc.* 2023, 145, 4, 2342–2353). Furthermore, our study generated a tremendous amount of media coverage (New York Times, Washington Post, New York Post, CNN, The Independent, and others)

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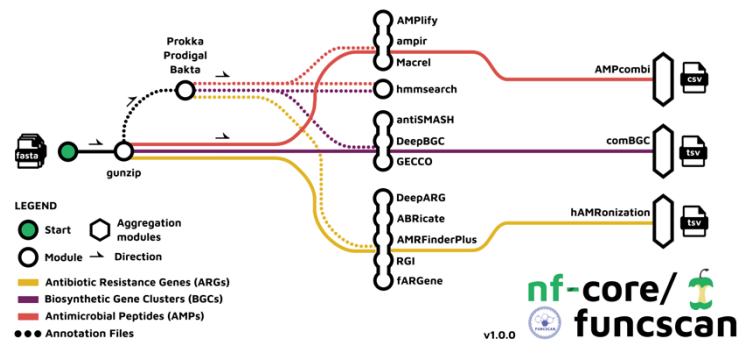
## nf-core/Funcscan

The Stallforth and Warinner Groups released an open-source and community-driven bioinformatics pipeline, nf-core/funcscan (<https://nf-co.re/funcscan>).

Developed within the nf-core initiative for bioinformatics pipelines, the pipeline enables high-throughput screening of nucleotide sequences such as assembled contigs for functional genes.

It currently features a range of tools that allow mining for antimicrobial peptides, antibiotic resistance genes and biosynthetic gene clusters, as well as dedicated tools for standardizing the output of each gene type.

nf-core/funcscan provides for a highly automated, parallelized, reproducible framework in the search for genes in microbial genomes and metagenomes for the production of natural products that will enable us to find novel biosynthetic genes in ancient DNA in a streamlined fashion.



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## Other News

- Pierre Stallforth became member of the Executive Board of the Excellence Cluster *Balance of the Microverse* in 2023.
- The Stallforth lab was awarded the 2022 Cozzarelli prize for a publication in the *Proceedings of the National Academy of Sciences USA (PNAS, 2021, 118, e2013759118)*
- Pierre Stallforth became Liaison Professor (Vertrauensdozent) for the German Academic Merit Foundation (Studienstiftung des deutschen Volkes) in December 2022.
- Christina Warinner's research article, "Understanding the microbial biogeography of ancient human dentitions to guide study design and interpretation", published in *FEMS Microbes* in 2022 (<https://www.doi.org/10.1093/femsmc/xtac006>) was named a winner of the 2022 Federation of European Microbiological Societies (FEMS) Article Awards. Selected by editorial boards and select editors-in-chief, the Article Awards recognize the year's best scientific papers published by FEMS Journals and Oxford University Press. See: <https://news.harvard.edu/gazette/story/newsplus/anthropology-professor-nabs-award-for-best-scientific-paper/>
- Christina Warinner was recently featured as a guest scientist speaking on the topic of the evolution of the microbiome on National Public Radio's Science Friday on April 14, 2023. Science Friday is a nationally syndicated weekly call-in talk show on public radio stations that aims to educate the public about current scientific topics. It has a weekly audience of more than 2 million listeners (radio listeners and podcast downloads). See <https://www.sciencefriday.com/segments/lactose-intolerance-gut-microbiome/>