



**HAL**  
open science

## Disentangling microbiota functions with metaproteomics

Jean Armengaud

► **To cite this version:**

Jean Armengaud. Disentangling microbiota functions with metaproteomics. European Society of Applied Biocatalysis ESAB webinar, Jennifer Littlechild - ESAB, Jul 2023, Exeter, United Kingdom. hal-04469805

**HAL Id: hal-04469805**

**<https://hal.inrae.fr/hal-04469805v1>**

Submitted on 21 Feb 2024

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

# European Society of Applied Biocatalysis ESAB webminar

July 28<sup>th</sup>, 2023

## Disentangling microbiota functions with metaproteomics

Jean ARMENGAUD

*Laboratory «Innovative technologies for Detection and Diagnostics»,  
ProGénoMix IBISA platform  
CEA, Bagnols-sur-Cèze, France*

### Short abstract:

Microbial ecosystems play a major role in biogeochemical cycles, plant development and animal health. How microorganisms interact with each other, with their hosts, and with their environment are key questions. Understanding the functioning of microbial communities requires identifying the diversity of microorganisms present and quantifying the numerous molecular players in action. Proteins are the workhorses of biological systems. Metaproteomics is a key technology for such functional studies as it can provide for these particularly complex samples four types of answers: 1) identification of the taxa present, 2) quantification of the biomass of these organisms, 3) identification of the proteins of these taxa and their function, and 4) overall functional representation of the biological system. Challenges in terms of mass spectrometry, interpretation and mining of results will be addressed.