



HAL
open science

Metaproteomics for the functional analysis of microbiomes: recent achievements & prospects

Jean Armengaud

► **To cite this version:**

Jean Armengaud. Metaproteomics for the functional analysis of microbiomes: recent achievements & prospects. XVII International Italian Proteomics meeting, Paola Roncada - Italian Proteomics Society, Nov 2023, Roma, Italy. hal-04469787

HAL Id: hal-04469787

<https://hal.inrae.fr/hal-04469787>

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.

**Metaproteomics for the functional analysis of microbiomes:
recent achievements & prospects**

Jean ARMENGAUD

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

Short abstract:

Microorganisms play a major role in human, animal and vegetal health, as well as in key terrestrial geochemical processes. To understand how microbial communities function, how they interact with the host and the risks of dysbiosis, we need to identify the diversity of microorganisms present and quantify the numerous molecular players at work, especially proteins which are the workhorses of biological systems. Metaproteomics is a key technology for such functional studies, as it can provide important answers for these highly complex samples: 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, 4) identification of host biomarkers explaining their global response, and 5) overall functional representation of the biological system. The first important key step in metaproteomics is the selection of the database best suited to the specificities of the sample. Proteotyping of organisms enables us to establish the identity of micro-organisms and their corresponding biomass. Several examples will be presented to demonstrate the power of proteotyping. The challenges of metaproteomics in terms of mass spectrometry, interpretation and exploitation of results will be discussed addressed. Moreover, results from recent technologies such as the Astral tandem mass spectrometer will be presented to demonstrate the new power of next-generation metaproteomics for deep functional analysis of microbiomes.