## **NEWS:**

## Proteomic and metaproteomic approaches to understand host-microbe interactions

Advances in next generation sequencing technologies have been transformational to our understanding of the microbiome and its link to health or disease. However, genomics studies alone are not sufficient to determine the interactions that are occurring between host and microbe.

Recent improvements in model systems, including *ex vivo* culture systems that more fully approximate the microbiome and host components, and in technology that facilitates deeper metaproteome analysis, have made it possible for MS-based proteomics and metaproteomics studies to provide complementary information to elucidate the **functional microbiome**.

Metaproteomics has benefited from advances in the proteomics field, and is an important tool in understanding the functional microbiome and the complex interplay which exists between the microbiome and its host.

In the future, a true integration with other–omic technologies, including genomics, viromics, epigenomics, lipidomics and metabolomics will probably be necessary for a complete comprehension of these fields

Proteomic and metaproteomic approaches to understand host-microbe interactions. Starr AE and all 2017 <a href="https://www.ncbi.nlm.nih.gov/pubmed/29061041">https://www.ncbi.nlm.nih.gov/pubmed/29061041</a>

With Phylogene, you can also characterize and understand the microbiome effects.

Bacterial 16s rDNA and fungal ITS sequencing with OTUbased estimation to investigate microbial communities diversity and determine taxonomic composition High-resolution nano LC-MS/MS quantitative proteomics and CORAVALID™ / MicroXplore™ data processing: The efficient tool for discovery

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