NEWS:

Microbiotas functional metabolism is revealed with metaproteomics and data processing.

New recent publications on studies on gut and skin microbiotas show the variability at the genome, transcriptome and proteome level but a remarkable stability of metabolic shared functions which is shown with metaproteomics and data processing.

In the gut(2), almost all the functions observed are observed in multiple phyla, these functions are not specific to any one phylum, genus, or species. There is a clear persistence of conserved metabolic functions across time and individuals. The microbiome’s metabolism is not driven by a set of discrete linear pathways but a web of interconnected reactions facilitated by a network of enzymes that connect multiple molecules across multiple pathways. Metaproteomics allows to perform in-depth microbiome analysis up to metabolism understanding in rat and swine. (3)(4)

And now, metaproteome analyses further revealed the capabilities of dietary pre- and probiotics treatments in modulating metabolic pathways and functional activities of gut microbial ecosystem. (5)

Functional studies of the skin microbiota at the metatranscriptomic and proteomic levels illustrate the interactions between the microbiota and the host skin(1).


With Phylogene as well, you can characterize and understand the microbiotas metabolism.

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

PHYLOGENE
62, Route Nationale 113
30620 BERNIS
Tel : +33 4 66 04 77 99
Fax : +33 4 66 04 77 97
e-mail : gskorski@phylogene.com
web : www.phylogene.com
http://ms.phylogene.com