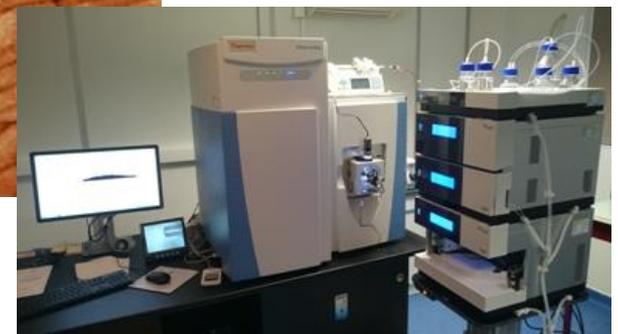
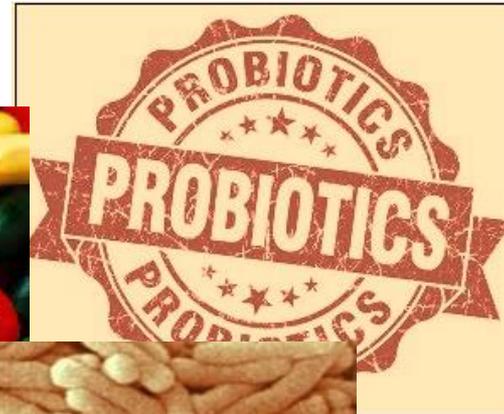
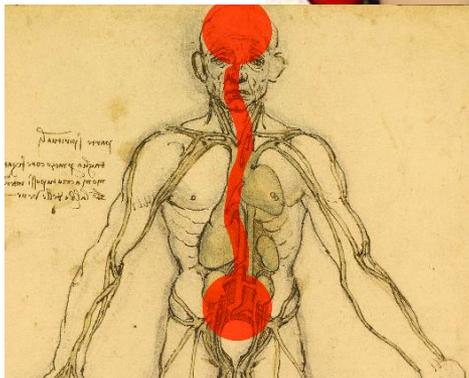


DISCOVERY SERVICES ON HOST AND MICROBIOME



With **PHYLOGENE**,
It's time to think out of the box...



ABOUT PHYLOGENE

A 20 years old ISO 17025 accredited servicing and R&D lab in omics.

MICROBIOTA IS A PART OF US

As now the world discovered that our body has a microbial part, everybody now knows the importance of our microbes for our health.

MICROBIOME UNDERSTANDING RATIONALE

After 10 years of clinical studies to discover diseases and probiotics effects on microbiotas described by **differences based on taxonomy** approaches, few convincing explanations have been brought mechanistically to the microbiotas working.

Using a conjunction of omics techniques, it is possible to discover which **function** is impacted on host and microbiome up to the interactions host/microbiome and the **mechanisms of action** understanding.

WHY WORK WITH PHYLOGENE?

- Extended experience of omics data processing,
- Expertise in proteomics, metaproteomics and bioinformatics,
- Customized prices and time to results optimization,
- Network of trained CROs,
- Integrated process from sample to result delivery,



“Finally, the gut 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.”
Blakeley-Ruiz and all. 2019 Microbiome

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MICROBIOME EXPERTISE

-Metaproteomics comparative study of microbiome by relative quantification LC-MS/MS « shotgun proteomics » and bioinformatics/biostatistics dedicated data processing and analysis for the holobionte : HolXplore™
« *Effects of the product on functions and interactions of host and microbiome simultaneously* »

-Metagenomics comparative study of microbiome by NGS sequencing 16S rDNA and ITS
« *The product/treatment does or does not impact the semi-quantitative composition and microbiome diversity* ».

-Coupling metagenomics and metaproteomics

-Determination of microbial communities diversity and taxonomic composition
-Customization of database queries on impacted taxons

-Follow-up by quantitative PCRs of major species or genus.
« *The product has/does not have an effect on tested genus* »

-HolXplore: A global analysis of the human proteome and the associated microbiota's metaproteome.

- Taxonomic analyses

Analysis of the diversity of the associated microbiota, shift of the microbiota structure at different taxonomic levels, samples dispersion according to the diversity of their microbiota.

- Functional analyses

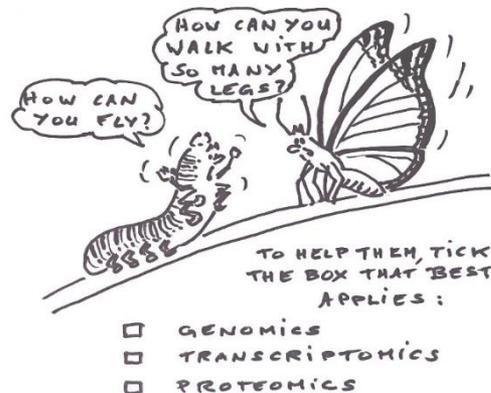
In parallel for 1) *Bacteria*, 2) *Fungi* and 3) *Homo sapiens* taxons:

- Search for orthologs and associated COG functional categories and general processes, determination of potential significant evolutions at different functional levels (terms, functional categories, general processes), involvement of proteins orthologs into KEGG pathways, samples dispersion according to the bacterial, fungal or human proteome.

- Correlations / Claims

-Samples dispersion according to the bacterial, fungal and human proteomes, correlations between different functions and between different functions and taxonomic groups, involvement of bacterial, fungal and human proteins orthologs into KEGG pathways.

-Claims / Possible biological effects on host sample and its microbiota.



“In particular, proteomics appears uniquely positioned to study the interplay of the human immune system with commensurate and pathogenic bacteria at the systems level.”

Grassl et al. 2016. Genome medicine.

