

NEWS:

Microbiome :Metaproteomics for human and microbiome interactions.

Oral cavity is one of the most diverse microbiome of the body.

Recent improvements in mass spectrometry-based proteomics allowed to develop a rapid workflow for mapping the saliva proteome quantitatively and at great depth.

3700 quantified human proteins in 100-min gradients or 5500 proteins after simple fractionation and more than 2000 microbial proteins from 50 bacterial genera were found. Co-analysis of the proteomics results with next-generation sequencing data revealed strong agreement and confirms that the oral microbiome differs between individuals and changes drastically upon eating and tooth brushing.

This study shows that metaproteomics is an important addition to the toolbox and appears uniquely positioned to the simultaneous determination of microbial and host activities

Grassl N, 2016. Ultra-deep and quantitative saliva proteome reveals dynamics of the oral microbiome. *Genome Med.* 2016 Apr 21;8(1):44
<http://www.ncbi.nlm.nih.gov/pubmed/27102203>

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

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

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