NEWS

Our microbial communities living on surfaces inside and outside the body have been investigated by high-throughput sequencing technologies. Several millions of genes have been discovered close to our own tens of thousands genes. Recent improvements in protein and peptide separation efficiencies and highly accurate mass spectrometers have promoted the field of metaproteomics (1), the study of the collective proteome of microbial communities. Now, the effects of cosmetics or drugs on microbiomes can be directly investigated by label-free relative quantitative LC-MS/MS

 Metaproteomics of our microbiome - developing insight in function and activity in man and model systems. Kolmeder CA and all. 2014 <u>http://www.ncbi.nlm.nih.gov/pubmed/23707234</u>

High-resolution nano LC-MS/MS quantitative proteomics and CORAVALID[™] data processing: The efficient tool

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