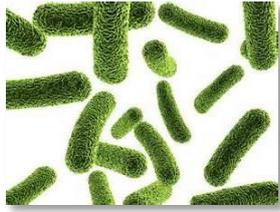


NEWS:



Would you like to know what your organism is doing with the proposed substrates? Try label-free comparative LC-MS/MS analysis with pathways analysis

Usually, a limited number of parameters are followed which are chosen and targeted by experience with what is known on the process. Comparative relative quantification "label-free" proteomics allows to get a fold change between thousands of non-targeted identified proteins. Then, by further bioinformatics/biostatistics analysis you can get a precise picture of the working pathways. So, you will know the positive as well as the negative effects of your parameter change.

For example, see :

Mangiapane E and all. Ten years of subproteome investigations in lactic acid bacteria: A key for food starter and probiotic typing. J Proteomics. 2015 May 6.

<http://www.ncbi.nlm.nih.gov/pubmed/25957532>

Tian X. and all. Quantitative proteomics reveals dynamic responses of Synechocystis sp. PCC 6803 to next-generation biofuel butanol
Journal of proteomics 78 (2013) 326-345

<http://www.ncbi.nlm.nih.gov/pubmed/23079071> and

Tang X. and all. Comparative proteomics analysis of engineered Saccharomyces cerevisiae with enhanced biofuel precursor production. PLoS One. 2013 Dec 23;8(12):e84661. <http://www.ncbi.nlm.nih.gov/pubmed/24376832>

About the cost ? How long will you try to get the expected yield if you don't know how resources are used by your organisms?

High-resolution nano LC-MS/MS quantitative proteomics and CORAVALID™ data processing: The efficient discovery tool
High-resolution SRM LC-MS/MS quantitative proteomics: The efficient multiplex confirmatory method

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