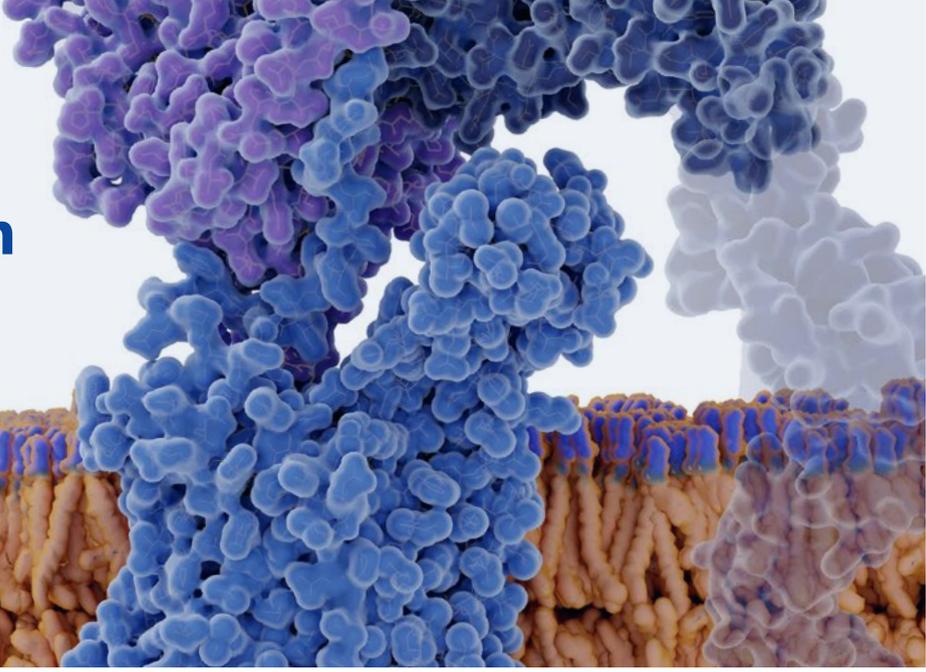


Label-Free Quantification



Label-free quantification is an important mass spectrometry method that requires no specific sample labeling. Instead, it utilizes MS/MS generated signals of specific peptides for comparison to define protein expression modifications between samples. Two alternative label-free quantification strategies are frequently used, Spectra Count (SC) and peptide ion intensities measurements (a.k.a., XIC, extracted ion chromatography), with the latter being more accurate and widely used. Label-free quantification requires highly stable and reproducible liquid chromatography with tandem mass spectrometry (LC-MS-MS) and has no requirement for expensive isotopes for labeling.

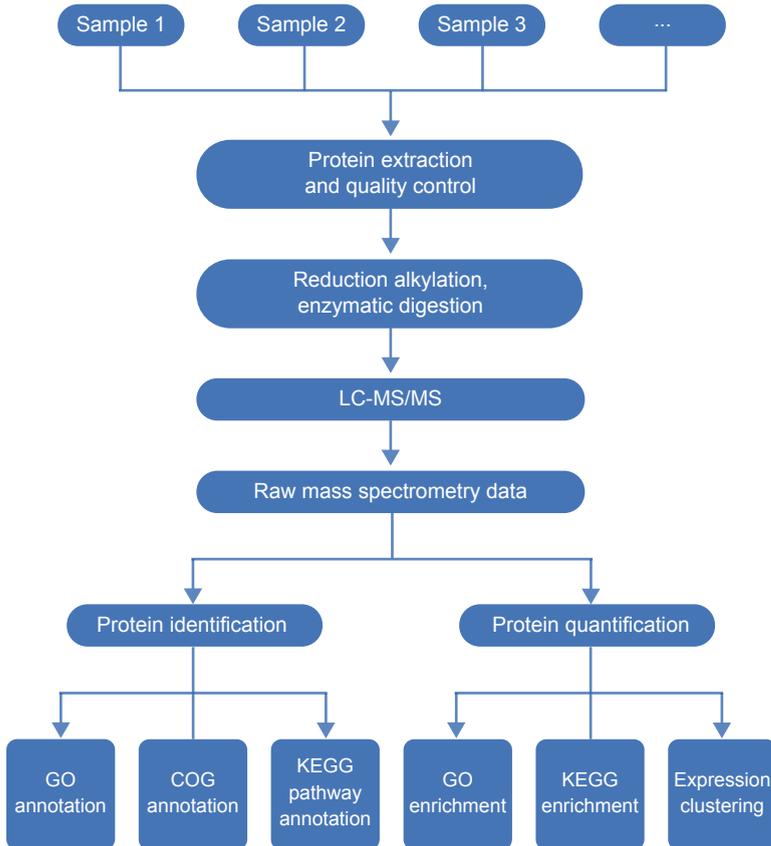
Label-free based quantitative proteomic analysis can be applied to analyze almost all regular biological samples (cells, tissues, biofluids, feces, plant samples, etc.), especially for large quantity sample comparison.

Application Areas

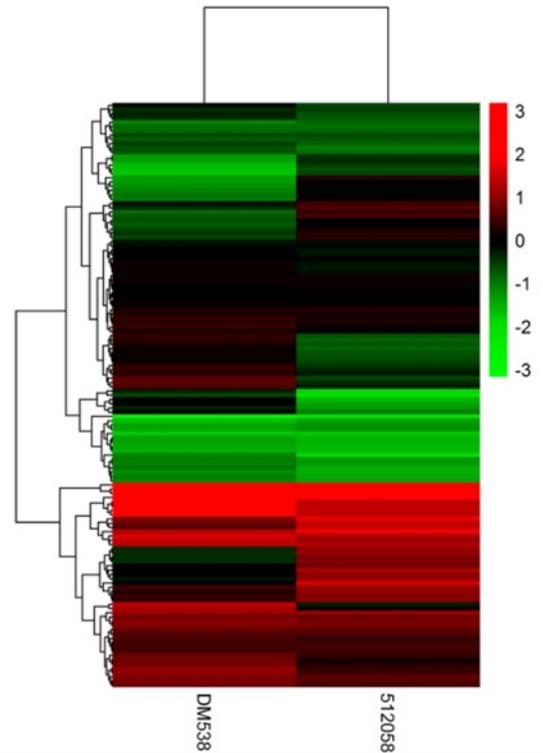


- ✓ Disease biomarker research
- ✓ Drug efficacy evaluation
- ✓ Plant growth and development research
- ✓ Plant disease resistance and insect resistance research
- ✓ Microbial stress and adversity physiology research
- ✓ Food component and quality identification
- ✓ Environmental risk assessment
- ✓ Special behavior mechanism and food/medicinal value research

Workflow of Label-Free Quantitative Proteomics



Demo Results



Hierarchical clustering based on label-free proteome quantification.

Highlights

- ✔ Cost-effective experiment – no need for expensive isotope labels as internal standards
- ✔ Minimal sample manipulation – reducing sample loss and preventing biological characteristics alterations
- ✔ Efficient – Overcomes shortcomings of labeled quantification in quantifying multiple samples regardless of sample conditions
- ✔ Wide dynamic range – detectable peptides can reach over 4 orders of magnitude, improving the overall accuracy and detection efficiency for low abundance proteins
- ✔ High operational stability and reproducibility – require at least 3 technical or biological replicates

Scope of Application

- ✔ Suitable for quantitative comparison of large sample volume
- ✔ Suitable for experimental designs that require no label attachment
- ✔ Suitable for experiments that require protein reference database, EST sequence (transcriptome), or genome annotation information