# Exosomes Proteomics Solutions

Extracellular vesicles are mainly composed of microvesicles, apoptotic vesicles, and exosomes. They have a double-layer membrane structure and are shed from cell membranes or secreted by cells. As one type of small vesicles with a diameter of 40~100 nm and a density of 1.10~1.18 g/ml, exosomes can carry nucleic acid, protein mass and lipid, etc. and exist in various body fluids such as blood, saliva and urine. Exosomes can affect cell functions by transferring substances such as nucleic acids, proteins and lipids between cells. For example, they play an important role in the process of antigen presentation in antigen-presenting cells, in the development of tumor cells, and in signal transduction in nerve cells. The detection and analysis of exosomes can accelerate disease-related basic research, assist in disease diagnosis, drug development, therapeutic research, and drug efficacy evaluation.

Analysis of exosomal protein expression patterns
• Obtain the different protein compositions in exosomes from different sample sources by gel electrophoresis or mass spectrometry. Analyze their potential as biomarkers and identify specific differences in protein composition or expression for clinical applications.
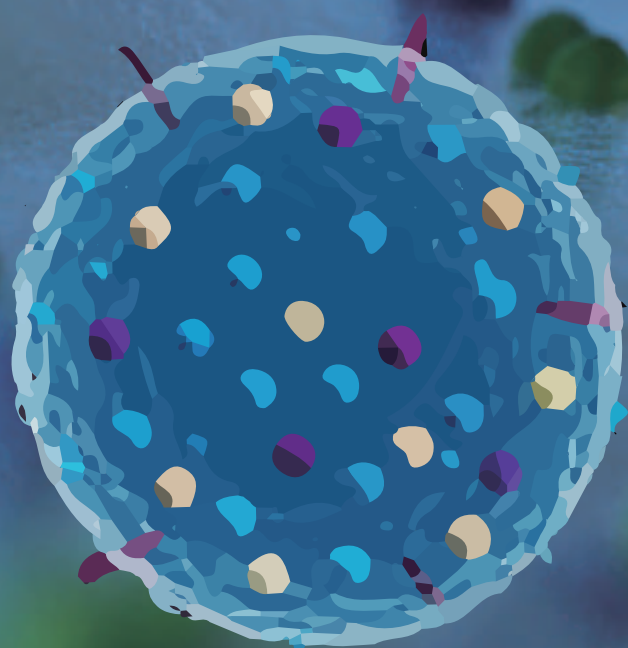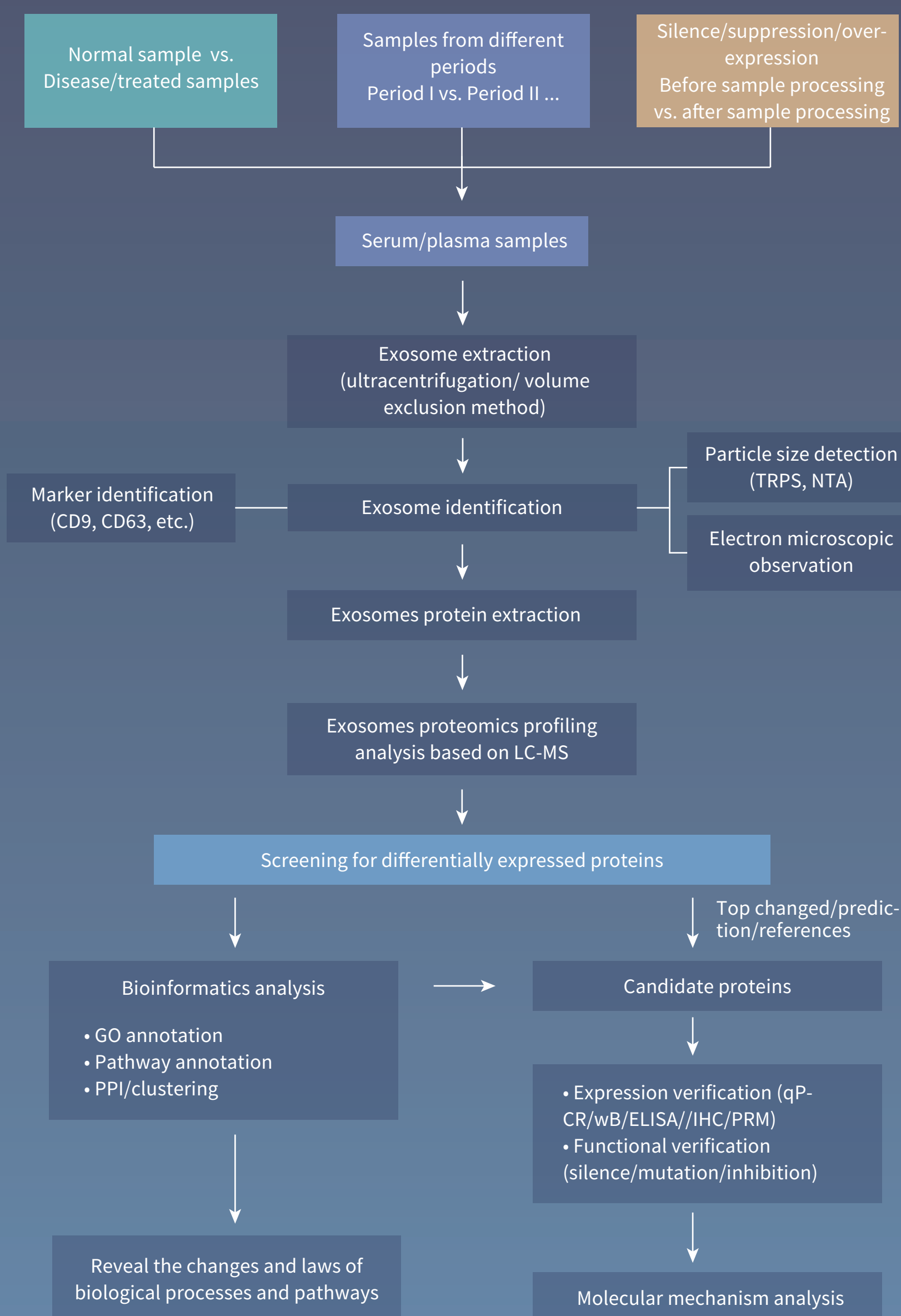
Analysis of exosomal protein function models
• The biological function of exosomal protein in cell supernatant is studied after qualitative analysis.

Analysis of exosomal protein post-translational modifications
• Include glycosylation, phosphorylation, ubiquitination, quasi-ubiquitination, methylation, oxidation, nitrosylation, palmitoylation, carboxyacylation, farnesylation, etc.

Exosomes Proteomics Approaches

Normal sample vs. Disease/treated samples

Samples from different periods
Period I vs. Period II ...

Silence/suppression/over-expression
Before sample processing vs. after sample processing

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Serum/plasma samples

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Exosome extraction (ultracentrifugation/ volume exclusion method)

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Marker identification (CD9, CD63, etc.) — Exosome identification — Particle size detection (TRPS, NTA)

Electron microscopic observation

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Exosomes protein extraction

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Exosomes proteomics profiling analysis based on LC-MS

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Screening for differentially expressed proteins

↓   Top changed/prediction/references

Bioinformatics analysis   →   Candidate proteins

• GO annotation
• Pathway annotation
• PPI/clustering

• Expression verification (qP-CR/wB/ELISA//IHC/PRM)
• Functional verification (silence/mutation/inhibition)

↓   ↓

Reveal the changes and laws of biological processes and pathways

Molecular mechanism analysis

Based on advanced mass spectrometry platforms such as the Q Exactive Hybrid Quadrupole-Orbitrap and Agilent 6540 Q-TOF high performance mass spectrometer, Creative Proteomics can provide customers with a one-stop shop for exosome proteomics, aiming to provide a comprehensive analysis of exosomes from a holistic perspective.

Contact Us

CP Creative Proteomics