Empowering Life Science with Precision

Jotbody provides professional service for Extracellular Vesicles

1. About us

Established in 2020, Jotbody (HK) Limited is a state-of-the-art biotechnology company specializing in extracellular vesicles (EVs) and nanobody research based in in Hong Kong Science and Technology Park.

Our team, comprising experienced scientists and dedicated board members, is committed to advancing global research and development. Since 2014, we have been deeply involved in EV research, collaborating with industry and academic partners. Furthermore, we were honored with a place on Forbes ASIA 100 to watch in 2023.

Our expertise lies in EV functionalization for therapeutic applications, which has been proven across various disease models, including a number of pre-clinical models of human deseases like cancer, neurodegenerative disorders, cardiovascular diseases, and inflammatory conditions.

Within the realm of EVs, we offer comprehensive services tailored to meet the evolving needs of researchers worldwide. Our services encompass:

- Isolation.
- Purification.
- Characterization.
- Omics analysis.
- Functionalization.
- CDMO solutions.

Our vision is clear: to elevate life science with precision through the incredible potential of extracellular vesicles. We are dedicated to fostering collaboration, igniting innovation, and upholding the highest standards of quality in all our EV-focused initiatives. By spearheading EV research and technology, we aim to be the reliable partner for researchers striving to unravel the complexities of intercellular communication and harness the therapeutic benefits of EVs.

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2. DIA Proteomics/ Phosphoproteomics Service

Introduction

DIA (Data-independent acquisition) is a new mass spectrometry technique developed in recent years and belongs to the non-labeled proteomics methods. With data-independent scanning mode, it divides the entire scanning range of the mass spectrum into several windows, and then detects all the ions in each window, so it can obtain the information of all the ions in the samples without any omission or discrepancy. This technique can reduce the number of missing values in the sample assay while improving quantitative accuracy and reproducibility, enabling highly stable and accurate proteomic quantification in large sample queues.

We can provide 3 kinds of DIA services including Direct-DIA, GPF-DIA, and Fractionated DDA-base DIA. Samples provided for analysis include and are not limited to cells, tissues, paraffin sections, exosomes, etc. We also provide Proteomics Preprocessing Kit (#EV01-03-01) and Phosphopeptide Enrichment Kit (#EV01-05-01) for your proteomics experiments.

Procedure

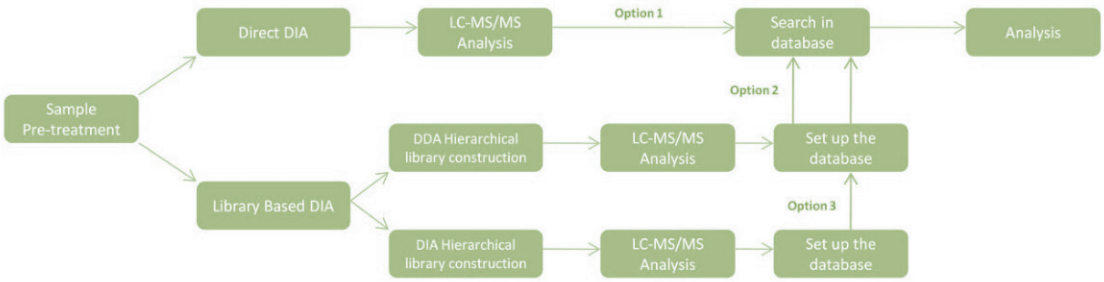

FIGURE 1. THE FLOWCHART OF THE 3 DIA DETECTION TECHNIQUES

Advantages

- Full Scan Mode: a non-dependent data acquisition mode that greatly reduces high abundance interference and comprehensively acquires high and low abundance signals, improving data coverage by nearly 40 %.
- High reproducibility and strong stability: nearly 40% increase in repetition for identifying large number of samples, nearly 1X increase in quantitative precision.
- High quantitative accuracy: quantitative power is closed to the gold standard (SRM/MRM targeting technology).

Application

It can be applied to build up the information base of biological samples, discover biomarkers and etc. in various biological fields, such as biotechnology, agriculture, forestry, husbandry and medicine.

3. Label free Proteomics

Introduction

Label-Free shotgun is an isotope labeling-independent technique for non-labeled proteome quantification. It can analyze peptide fragments of proteins by LC-MS/MS, without the need to use expensive stable isotope tags as internal standards, but only need to analyze mass spectrometry data generated during large-scale identification of proteins, and compare the signal intensities of peptide fragments in different samples, so as to quantify the corresponding proteins of peptides. Label Free quantitative analysis technology can directly obtain the relative quantitative information of the protein represented by a peptide by comparing the peak area of the same peptide in the mass spectrometry.

Procedure

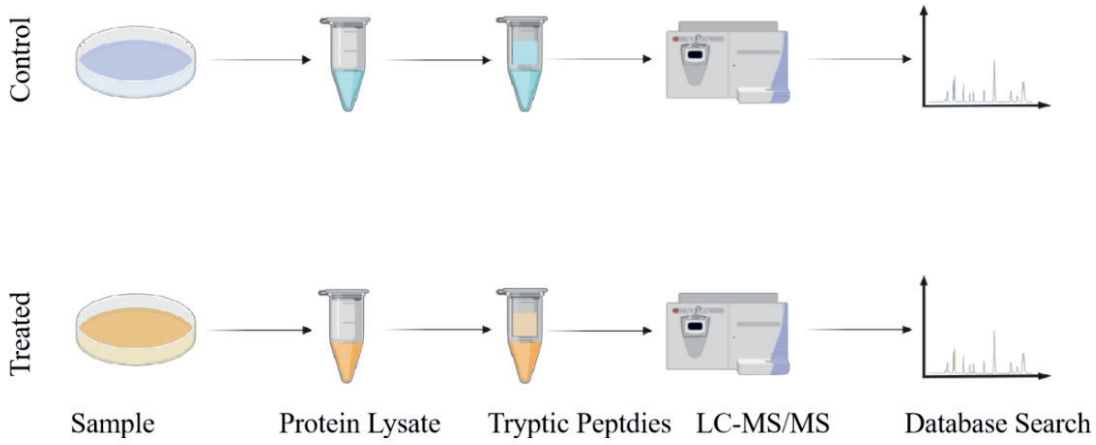

FIGURE 2. THE FLOWCHART OF LABEL FREE TECHNOLOGY (CREATED WITH MED PEER (WWW.MEDPEER.CN))

Advantages

- Cost-effective: no need for expensive isotope labeling reagents and short experimental cycles.
- Widely applicable: The "presence or absence of differential proteins" can be compared between species.
- Flexible and convenient: Unlimited number of samples, flexible and convenient.

Application

It can be applied for protein identification and quantification, screening and identification of differential proteins in various fields, such as agriculture, forestry, husbandry, basic medicine and clinical diagnosis and biomedicine.

4. Identification of interacting proteins

Introduction

LC-MS/MS protein identification technology can be used to identify proteins in purified solution samples, such as IP, Co-IP, pull-down, etc., and obtain a series of proteins interacting with the target protein.

Proteins are first digested into peptides by trypsin, and the peptides are ionized in the mass spectrometer to carry a certain amount of charge, which can be analyzed by the detector to obtain the mass-to-charge ratio (m/z) of each peptide (Primary mass spectrometry). To obtain more detailed sequence information of the peptides, some of the peptides were fragmented and analyzed again to produce secondary mass spectrometry. Finally, the mass spectrometry search software was used to select the appropriate protein database, and all the mass spectrometry data obtained were analyzed, while the identified proteins were sorted in the form of scores.

We also provide Co-IP kit (#EV 03-01-02) and one-stop service from sample preparation, IP enrichment, pretreatment and mass spectrometry.

Procedure

FIGURE 3. THE FLOWCHART FOR LC-MS/MS PROTEIN IDENTIFICATION

Advantages

- Widely applicable: It 's suitable for protein identification of complex samples, can identify multiple proteins simultaneously.
- High sensitivity and high accuracy: It can capture comprehensive and detailed peptide information.

Application

It is applied for the identification of protein solutions prepared by IP, Co-IP, and pull-down methods in a variety of basic research in biotechnology, agriculture, forestry, husbandry, and medicine.

5. SDS-PAGE enzymatic assay

Introduction

It can identify proteins by LC-MS/MS for glue spot samples (2D glue dug spots), glue strip samples (SDS-PAGE samples), and WB membrane samples.

First, the protein bands were digested into peptide mixtures with enzyme, which were separated by HPLC to obtain a number of simpler fractions that were analyzed in a high-resolution mass spectrometer. Based on the secondary mass spectrometry information and the corresponding database, the software can obtain the exact sequence of peptides by combining match scoring and mismatch filtering, and then stitch the complete sequence to realize the identification of proteins.

Procedure

FIGURE 4. THE FLOWCHART OF SDS- PAGE ENZYMATIC ASSAY

Advantages

- Easy and fast: 2D glue spot detection is fast and sample pre-treatment is easy.
- High requirement for samples: protein need to be pure or relatively homogenous.

Application

It is applied to the identification of SDS-PAGE adhesive strips prepared by IP, Co-IP, and pull-down methods in a variety of basic research in biotechnology, agriculture, forestry, husbandry, and medicine.

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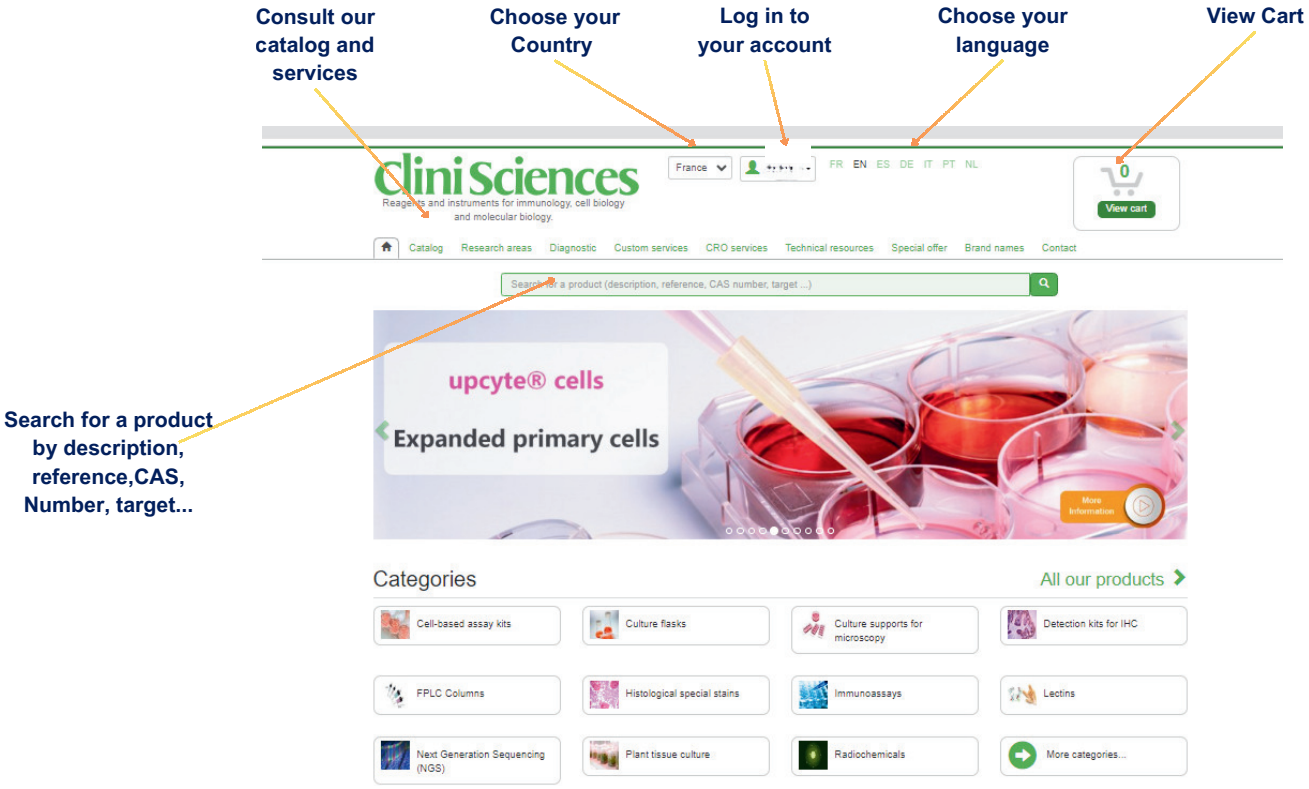

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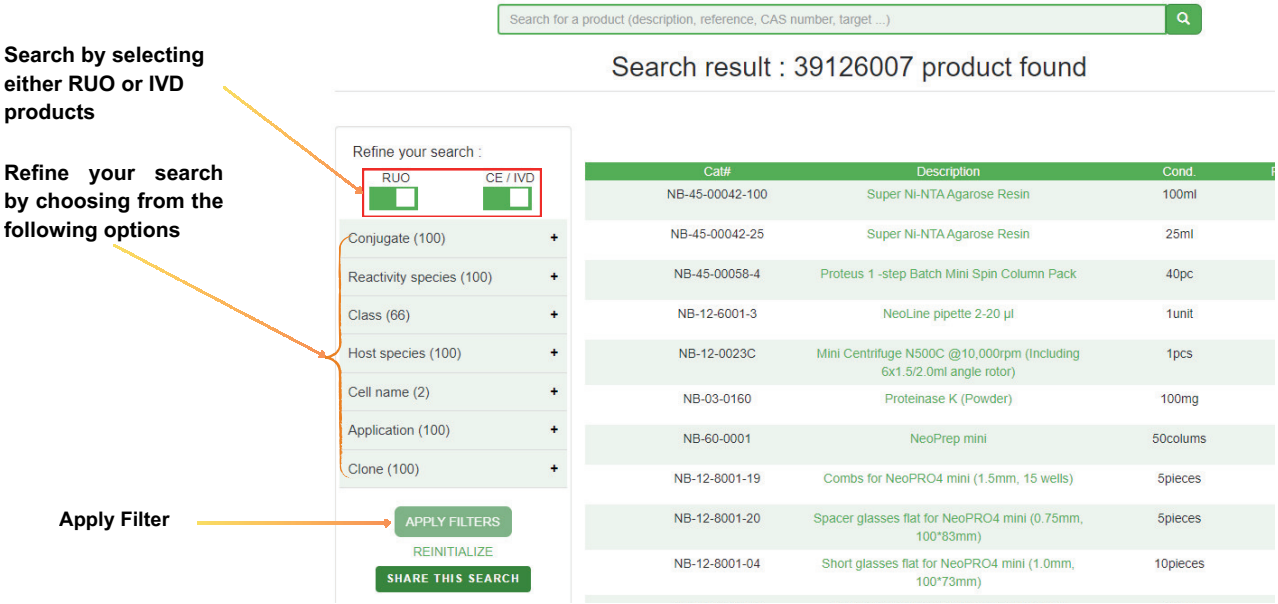

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