Differentially expressed proteins are proteins whose abundance levels vary significantly between different biological conditions or samples. These proteins play a crucial role in understanding various biological processes, disease mechanisms, and identifying potential biomarkers or therapeutic targets.

The identification of differentially expressed proteins is typically accomplished through techniques such as mass spectrometry-based proteomics or protein microarrays. These methods allow for the quantification of protein levels across different samples, enabling researchers to compare and analyze their expression patterns.

The analysis of differentially expressed proteins involves statistical approaches to determine which proteins exhibit significant changes in abundance. Common statistical tests include the t-test, analysis of variance (ANOVA), and more advanced methods like the linear models for microarray data (limma) or the edgeR package. The choice of statistical method depends on the experimental design and the nature of the data.

Once differentially expressed proteins are identified, further analysis is performed to gain insights into their functional roles, interactions, and pathways. Functional enrichment analysis, such as gene ontology (GO) analysis or pathway analysis, helps identify the biological processes, cellular components, and molecular functions associated with the differentially expressed proteins. This information aids in understanding the underlying biological mechanisms and pathways involved.

Moreover, integrating different omics data, such as genomics or transcriptomics, with proteomic data can provide a more comprehensive view of the biological system under study. This integrative analysis helps identify regulatory mechanisms, transcriptional changes, and potential protein-protein interactions associated with the differentially expressed proteins.

Differentially expressed proteins have numerous applications in various fields. In disease research, they can serve as potential diagnostic markers or therapeutic targets. Comparative proteomic studies between healthy and diseased samples can identify proteins that are specifically dysregulated in a disease state, providing insights into disease mechanisms and potential treatment strategies. In drug development, differentially expressed proteins can be used to assess drug efficacy and monitor treatment response.

It is important to note that the identification of differentially expressed proteins is just the initial step in understanding their functional significance. Further experimental validation and functional studies are typically required to confirm their roles and elucidate their molecular mechanisms in the context of specific biological systems.

Ju et al. identified 148 up-regulated proteins and 82 down-regulated proteins, which are potential biomarkers for clinical hydrocephalus diagnosis and arachnoid cyst. Functional enrichment analysis revealed that the Differentially expressed proteins (DEPs) were significantly enriched in the cancer hallmark pathways and immune-related pathways. In addition, network analysis uncovered that DEPs were more likely to be located in the central regions of the human PPIs network, suggesting DEPs may be proteins that play important roles in human PPIs. Finally, they calculated the overlap of drug targets and the DEPs based on drug-target interaction to identify the potential therapeutic drugs of hydrocephalus. The comprehensive proteomic analyses provided valuable resources for investigating the molecular pathways in hydrocephalus, and uncovered potential biomarkers for clinical diagnosis and therapy [1)].

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Ju Y, Wan Z, Zhang Q, Li S, Wang B, Qiu J, Zheng S, Gu S. Proteomic analyses reveal functional pathways and potential targets in pediatric hydrocephalus. Curr Gene Ther. 2023 Jun 13. doi: 10.2174/1566523223666230613144056. Epub ahead of print. PMID: 37317915.