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Proteomic Analysis of Human Whole Lung Tissue Using Liquid Chromatography-Tandem Mass Spectrometry (LC-MS/MS) Acquisition by Data-Independent Acquisition (DIA) on an Orbitrap Eclipse Tribrid Mass Spectrometer

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We use this protocol and it's working

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Abstract

Frozen human whole lung tissues were homogenized using a urea-based buffer and bead mill homogenizer to isolate protein. The protein lysate was subjected to tryptic digestion using S-trap Spin columns. The reconstituted peptide elution was desalted with C18 hydrophilic-lipophilic balance (HLB) cartridges. The final reconstituted peptides were diluted with 2% ACN and 0.1% FA. Proteolytic peptide measurement was completed using liquid chromatography-tandem mass spectrometry (LC-MS/MS) acquisition by Data-Independent Acquisition (DIA) on an Orbitrap Eclipse Tribrid mass spectrometer for peptide/protein identification and quantification.

Protocol references

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