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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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Keywords: proteolytic peptide measurement, proteomic analysis of human whole lung tissue, proteomic analysis, reconstituted peptide elution, reconstituted peptide, tandem mass spectrometry, protein lysate, protein identification, human whole lung tissue, using liquid chromatography, protein, liquid chromatography, orbitrap eclipse tribrid mass spectrometer, orbitrap eclipse tribrid mass spectrometer frozen

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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