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Overall protocol for MicroPOTS LCMS top down proteomics of kidney tissue sections

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Human BioMolecular Atl... PNNL-TTD

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Protocol status: Working
We use this protocol and it's working

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Abstract

This is the overall workflow for LCMS top down proteomics of kidney functional units from tissue sections using the MicroPOTS platform. The expected outcomes are proteoform identification and quantitation values from selected tissue functional units.

Troubleshooting

Tissue collection

1 The tissue sections were prepared and shipped from Vanderbilt-TMC following the protocol below:

Protocol

NAME

Cryostat Sectioning of Tissues for 3D Multimodal Molecular Imaging

CREATED BY

Jamie Allen

Preview

Sample preparation

2 Functional units (glomerulus, medullary, tubule) were dissected and collected into the microPOTS platform using the method below:

Protocol

NAME

Laser Capture Microdissection of Tissue Functional Units for microPOTS Top-Down Proteomics

CREATED BY

James M Fulcher

Preview

Data Acquisition

3 The samples were analyzed by LCMS top down proteomics as described below:

Protocol

NAME

Top Down Proteomics Data Collection for Microdissected Kidney Tissue Functional Units

CREATED BY

Mowei Zhou

Preview

Data Analysis

4 LCMS datasets were analyzed for proteoform identification and quantitation. The final results are reported.

Protocol

NAME

Proteoform Identification and Quantitation with TopPIC and TDPortal for Human Tissues

CREATED BY

Mowei Zhou

Preview