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

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Human BioMolecular Atlas Program (HuBMAP) Method Development Community

PNNL-TTD

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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.

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PROTOCOL CITATION

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Tissue collection

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

Cryostat Sectioning of Tissues for 3D Multimodal Molecular Imaging
by Jamie Allen,
Vanderbilt University

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Sample preparation

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

Laser Capture Microdissection of Tissue Functional Units for microPOTS Top-Down Proteomics
by James M Fulcher,
Pacific Northwest National lab

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Data Acquisition

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

Top Down Proteomics Data Collection for Microdissected Kidney Tissue Functional Units
by Mowei Zhou,
Pacific Northwest National Laboratory

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Data Analysis

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

Proteoform Identification and Quantitation with TopPIC and TDPortal for Human Tissues

by Mowei Zhou,

Pacific Northwest National Laboratory

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