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# **③** Overall protocol for MicroPOTS LCMS top down proteomics of kidney tissue sections

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dx.doi.org/10.17504/protocols.io.eq2lynm1qvx9/v1

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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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Keywords: proteomics of kidney tissue section, proteomics of kidney, micropots lcm, proteomic, overall protocol for micropots Icm, kidney tissue section, micropots platform, proteoform identification, overall workflow for Icm, Icm, tissue functional unit, kidney, functional units from tissue section, selected tissue

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## Abstract

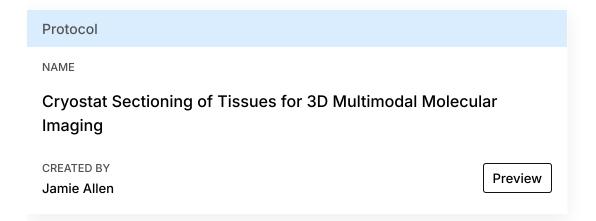
This is the overall workflow for LCMS top down proteomics of kidney functional units from tissue sections using the MicroPOTS platform. The expected outcomes are proteoform identification and quantitation values from selected tissue functional units.

## **Troubleshooting**



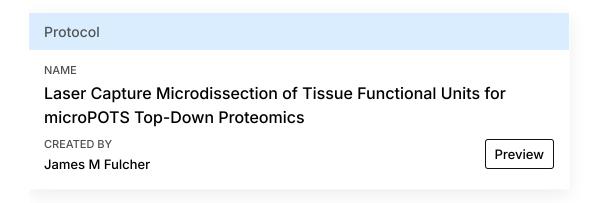
## Tissue collection

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



# Sample preparation

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



# **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** 

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# **Data Analysis**

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** 

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Preview

Preview