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

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

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1 Works for me

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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 pancreas 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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<https://protocols.io/view/overall-protocol-for-micropots-lcms-top-down-prote-cfi4tkgw>



FORK NOTE

FORK FROM

Forked from Overall protocol for MicroPOTS LCMS top down proteomics of kidney tissue sections, Mowei Zhou

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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**

Sample preparation

- 2 Functional units (islet and acinar) 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

PREVIEW

RUN



Data Acquisition

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



Top Down Proteomics Data Collection for Microdissected
Pancreas Tissue Functional Units

by Mowei Zhou,

Pacific Northwest National Laboratory

PREVIEW

RUN



Data Analysis

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



Proteoform Identification and Quantitation with Combined
TopPIC and TDPortal Results

by Mowei Zhou,

Pacific Northwest National Laboratory

PREVIEW

RUN

