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

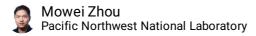
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ABSTRACT

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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1

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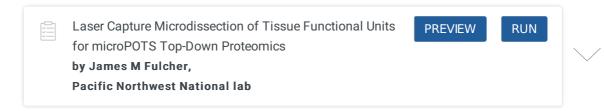
Tissue collection

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



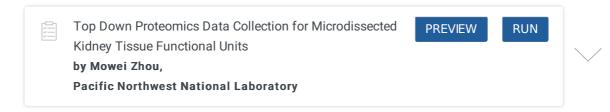
Sample preparation

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:



Data Analysis

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

