OCT 07, 2020

OPEN ACCESS

DOI:
dx.doi.org/10.17504/protocols.io.bmwik7ce

Protocol Citation: yang1832, Julia Laskin 2020. Nano-DESI Mass Spectrometry Imaging kidney characterization pipeline for tissues collected by Vanderbilt University.
protocols.io
<https://dx.doi.org/10.17504/protocols.io.bmwik7ce>

License: This is an open access protocol distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

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

Created: Sep 30, 2020

Last Modified: Oct 07, 2020

PROTOCOL integer ID:
 42666

Nano-DESI Mass Spectrometry Imaging kidney characterization pipeline for tissues collected by Vanderbilt University

yang1832¹, Julia Laskin¹

¹Purdue University

Human BioMolecular Atlas Program (HuBMAP) Method Development Community

NanoDESI MSI Julia Laskin group

yang1832

ABSTRACT

Our goal is to map the biological tissues with Nano-DESI Mass Spectrometry Imaging and build an atlas of human kidney.

Scope:

Provide an overview of the sample preparation steps used by the Vanderbilt Tissue Mapping Center and Nano-DESI MSI workflow used by Julia Laskin's group as part of the Human Biomolecular Atlas Program (HuBMAP, NIH Common Fund).

- 1 Collection of post-surgical tissue by Vanderbilt.
Collection: dx.doi.org/10.17504/protocols.io.7gehjte
- 2 Stabilize and freeze tissues by Vanderbilt
Freezing Tissue: dx.doi.org/10.17504/protocols.io.6wghfbw
- 3 Initial Rapid Pathology Assessment of Kidney Tissue by Vanderbilt.
Staining: dx.doi.org/10.17504/protocols.io.4qngvve
Assessment: dx.doi.org/10.17504/protocols.io.9dph25n
- 4 Cryosection tissues into micrometer thick sections, alternating between thaw mounting onto indium tin-oxide and positively charged glass

slides (proceed to step 4), or collecting several tissue sections within an microcentrifuge tube for proteomics analysis by Vanderbilt.
Cryosectioning: [dx.doi.org/10.17504/protocols.io.7ethjen](https://doi.org/10.17504/protocols.io.7ethjen)

- 5** Perform autofluorescence microscopy on all tissue sections before IMS (step 5) by Vanderbilt.
Autofluorescence: [dx.doi.org/10.17504/protocols.io.7e3hjgn](https://doi.org/10.17504/protocols.io.7e3hjgn)
- 6** Perform high resolution IMS lipidomics and metabolomics analysis of tissue sections.
IMS: [dx.doi.org/10.17504/protocols.io.bmw7k7de](https://doi.org/10.17504/protocols.io.bmw7k7de)
- 7** Delipid the tissue section.
Sample preparation: [dx.doi.org/10.17504/protocols.io.bmw6k7he](https://doi.org/10.17504/protocols.io.bmw6k7he)
- 8** Perform high resolution IMS proteomics analysis of tissue sections.
IMS: [dx.doi.org/10.17504/protocols.io.bm2nk8de](https://doi.org/10.17504/protocols.io.bm2nk8de)
- 9** Annotation of Lipids from IMS Data
Annotation: [dx.doi.org/10.17504/protocols.io.bm2qk8dw](https://doi.org/10.17504/protocols.io.bm2qk8dw)
- 10** Annotation of proteins from IMS data.
Annotation: [dx.doi.org/10.17504/protocols.io.bm2rk8d6](https://doi.org/10.17504/protocols.io.bm2rk8d6)
- 11** Match the autofluorescence images from IMS sections with the ion images to visualize the correlation between molecules distribution and biological pathology.
- 12** Nano-DESI imaging mass spectrometry data processing.
Data processing: [dx.doi.org/10.17504/protocols.io.bm2sk8ee](https://doi.org/10.17504/protocols.io.bm2sk8ee)