High Resolution Imaging Mass Spectrometry Analysis using Bruker Daltonics Platforms

Elizabeth Neumann[1], Jamie Allen[1], David Anderson[1], Danielle Gutierrez[1], Jeff Spraggins[1]

[1]Vanderbilt University

Sep 20, 2019

1 *Works for me* dx.doi.org/10.17504/protocols.io.7gdhjs6

VU Biomolecular Multimodal Imaging Center

Human BioMolecular Atlas Program (HuBMAP) Method Development Community

Jamie Allen

ABSTRACT

Scope:

Acquire 10 µm spatial resolution imaging mass spectrometry (IMS) datasets of ~ 5mm^2 regions of tissue.

Expected Outcome:

A series of ion images that can be used to visualize the distribution of lipids localizing to physiological regions within the human kidney.

MATERIALS TEXT

Slide Adapter for Instrument
Bruker MALDI timsTOF Flex

BEFORE STARTING

Prepare tissue by following protocols for sectioning and matrix application.

1 Scann a 3200 dpi image of the matrix coated tissue section in the MTP slide adapter 2 with sufficient contrast to visualize the tissue boundaries.

2 Choose a method that has "height correct" initiated upon sample docking.

3 Insert the slide adapter plate into the instrument airlock. Then press "load."

4 While the height correct profile is being generated, open FlexImaging and follow the prompts to designate sample file name, method, pitch, scanned image of the slide, etc.

5 Once the height correct profile has been generated, train the target position with three teaching points following the instructions within FlexImaging.

6 Draw a measurement region around the tissue for IMS analysis.

7 Go to an area off of the tissue and ensure the focus of the laser is adequate for 10 µm spatial resolution imaging.

8 Start the acquisition.