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High Resolution Imaging Mass Spectrometry Analysis using Bruker Daltonics Platforms

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Protocol status: Working

We use this protocol and it's working

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Protocol Integer ID: 27877

Keywords: HuBMAP, BIOMIC, Kidney, Imaging, MALDI, Chemistry, Mass Spectrometry, Imaging Mass Spectrometry, Vanderbilt, MSRC

Abstract

Scope:

Acquire 10 μm spatial resolution imaging mass spectrometry (IMS) datasets of $\sim 5\text{mm}^2$ 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

Slide Adapter for Instrument

Bruker MALDI timsTOF Flex

Before start

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 μ m spatial resolution imaging.
- 8 Start the acquisition.