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High resolution Nano-DESI mass spectrometry imaging of proteomics of tissue

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

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Abstract

Scope:
Acquire imaging mass spectrometry (IMS) datasets of proteins on human kidney tissue with ~12µm spatial resolution.

Expected Outcome:
Visualize the proteins distribution localizing to physiological regions within the human kidney by generating ion images of multiply charged protein peaks.

1 Scanned the tissue section with PathScan Enabler IV to visuslize the morphology in optical image.

2 Calibrate the instrument with Agilent tune mix.

3 Set up the appropriate method for proteins.

4 Add protein standards into ACN:H_2O:acetic acid=65:34:1 solvent as the extracting solvent. Add extracting solvent into the syringe.

5 Place the slide on the slide holder and set up the primary capillary and secondary capillary and the solvent flow rate until there is liquid bridge between the two capillaries when land on the tissue surface. Direct the secondary capillary to the mass spectrometry inlet and clamp the capillary voltage on the syringe, adjust the positions of the capillaries untill there are stable and intensive signals in the spectrum.

6 Using the Labview software to train the shear force probe until it can appropriately recognize the sample surface from the air.

7 Place the shear force probe close to the liquid bridge so that it can lead the moving of the capillaries and enable the liquid bridge landing on the sample surface without scratching the tissue.

8 Set the start point and the end point of the scanning region.

9 Set up the worklist.

10 Start the acquisition.