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Proteins annotation of Nano-DESI MSI datasets

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Protocol status: Working

We use this protocol and it's working

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Abstract

Scope:

Annotate protein species detected by Nano-DESI IMS analysis.

Troubleshooting

- 1 Create mass list from the averaged spectrum.
- 2 Calculate the charge state of each multiply charged peaks based on the spacing between the isotopic peaks.
- 3 Calculate the exact mass based on the m/z and charge state.
- 4 Obtain CID data from each sample.
- 5 Assign peaks by matching the exact mass and the CID spectrum to the protein databank.
<http://prospector.ucsf.edu/prospector/cgi-bin/msform.cgi?form=msproduct>