



Sep 08, 2022

Sample submission for LC-MS BioMS core facility at the University of Manchester

In 1 collection

ronan.ocualain1

¹University of Manchester

1 Works for me



dx.doi.org/10.17504/protocols.io.dm6gpb4qdlzp/v1



ABSTRACT

Submitting samples to the BioMS core facility.

DOI

dx.doi.org/10.17504/protocols.io.dm6gpb4qdlzp/v1

PROTOCOL CITATION

ronan.ocualain 2022. Sample submission for LC-MS BioMS core facility at the University of Manchester. **protocols.io**

https://protocols.io/view/sample-submission-for-lc-ms-bioms-core-facility-at-cfirtkd6

COLLECTIONS (1)



Researcher led sample preparation for LC-MS using the BioMS research core facility

KEYWORDS

sample submission, LC-MS, proteomics

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

CREATED

Aug 19, 2022

LAST MODIFIED

Sep 08, 2022



1

PROTOCOL INTEGER ID

68913

PARENT PROTOCOLS

Part of collection

Researcher led sample preparation for LC-MS using the BioMS research core facility

GUIDELINES

Peptides should be dried down, use the speed vac in lab B2075 for this purpose. Instructions are <u>here</u>

MATERIALS TEXT

Locate a plastic bag, or box to place your dried down peptides in. Use a black or blue pen to enter details.

These are currently located in the top drawer of lab B2075 as you enter, on the left.



SAFETY WARNINGS

none

BEFORE STARTING

Peptides should be dried down, use the speed vac in lab B2075 for this purpose. Instructions are here

1 Place the dried down peptides into the drawer in B2071, either in a labelled bag (<20), or box if you are submitting a large batch of samples.

On the label, you must include

- PPMS order number (not project),
- number of samples,
- and any other important details, such as run length,
- sample manifest (i.e. which order you wish the data to be acquired in, if minimization of carryover is important),
- and whether the samples have been prepared in S-trap lysis buffer, or another buffer (e.g. urea, triton etc).

Don't forget to include your lab group/PI, as this is the folder within which your data files will be stored on the server.

Manifests: Go to PPMS, and prepare a manifest relating to the samples, pay particular attention to the run order that you would like.

Any analytical technique will suffer from a degree of sample carryover, LC-MS is no different.

For example, if you have knockdown/knockout samples, it is recommended that you run these before your WT/control samples.

Add in the position of the blanks/standards that you would like to see in the acquisition of your data, we usually add these between every five to six samples.