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

📁 In 1 collection

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ronan.ocualain¹

¹University of Manchester

BioMS CRF, UoM



ronan o'cualain

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Protocol status: Working

We use this protocol and it's working

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Abstract

Submitting samples to the BioMS core facility.

Guidelines

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

Instructions are **here**

Materials

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 start

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.

Note

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.