The website Covid 19

Mass spectrometry Coalition

<https://covid19-msc.org/>

The Idea

Take 1000 sample with different range of severity.

Collecting proteomic and metabolomic data.

We must make the repository with all data and link the data with the metadata.

Create a dashboard where is possible to collect again the raw data and reprocess everything.

Work package 3.

Flask for the database in the backend.

We want to connect pride - metabolomic

From <https://covid19-msc.org/action-plan/> I considered the point 5:

5.      Open data repositories

Critical to our collective effort is how we manage the data. We suggest that for omics data you use a data repository (ideally PRIDE for proteomics datasets, as part of ProteomeXchange), and that you tell us the accession number. PRIDE enables the inclusion of the submitted datasets in the EMBL-EBI COVID-19 data portal (<https://www.covid19dataportal.org/>). After deposition we will record these along with the requisite metadata to identify the datasets. We will soon be updating the website with a dedicated page where you can submit this information. The website will also be updated regularly so that many researchers can access the processed data. It is through this that we will gain the most and most quickly.  For native data on recombinant viral antigens get in touch as we will make the data repository and we will curate that data for all to examine and to compare to data from patient samples.

What the best way to connect these data (metadata are necessary)

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7264033/>

37.5 hours in the week

Not before september.

Only the UK people got the grant.

(Consortium in Manchestaer - metadata - Liverpool part of the consortium)