

Sample submission form for proteomic analysis

UT PCF



Submission date:

Your name:

E-mail address and phone:

Company/organization:

Billing address:

Value added tax (VAT) number:

Species of origin, cell or tissue type, and strain or cell line, if applicable:

- e.g. mouse brain; *S. cerevisiae* S288 strain; human HEK293 cells

Do your samples contain any foreign proteins or protein sequences:

- e.g. affinity or fluorescent tags etc., or additionally expressed proteins from different species

No

Yes (please send us the relevant amino acid sequences, or Uniprot IDs, or protein names with species of origin)

Sample complexity:

- approximate number of different proteins

1-10

10-100

100-1000

1000-5000

>5000

Unknown or not sure

Were your samples labelled:

¹⁸O phosphate

Lys4

Lys8

Arg10

Arg6

¹⁵N

iTRAQ-tag

TMT-tag

Other:

What protease to use:

Trypsin with LysC pre-treatment works the best and is our standard protocol

Trypsin

LysC

ArgC

LysN

(cleaves C-term to K)

(cleaves C-term to R)

(cleaves N-term to K)

Chymotrypsin

AspN

GluC

No digestion

(cleaves C-term to W, Y, P, L; lower rate at M, A, D, E, H, I)

(cleaves N-term to D)

(cleaves C-term to E)

(intact analysis only or proteins are already proteolysed)

Contaminants your samples may have:

- please indicate even if only in trace amounts

- please list any other potentially problematic contaminants not shown in this form and any other relevant details in the box below; if samples come in buffer, please include its composition

Salts

Detergents

Cell culture media

Fetal Bovine Serum

Lipids

DNA/RNA

Excess single proteins

(e.g. albumin, Igs, streptavidin etc.)

High M_w PEG

polymer(s)

Other (please describe in the box below)

In which form will the samples be handed over:

Tissue

Cell pellet

Cell lysate

EVs or other vesicles

Proteins bound to affinity beads

Protein or peptide solution

Protein pellet

Peptides on SPE tips

Do you require the leftovers of your samples:

Yes

No

Do you know the amount of total protein in your samples:

(please add the values to the sample list table at the end of this form)

Yes

No

Describe briefly what information you wish to obtain from the analysis:

(also mention if previous analysis conditions should be repeated and reference a relevant date)

What type of quantification does your experiment require

What analysis method would you prefer:

Data-dependent acquisition (DDA)

Targeted acquisition

Data-independent acquisition (DIA)

I will let the facility to decide

Does your analysis involve mapping of post-translational modifications (PTMs)?

Yes

-please indicate which PTMs in the box on right

No

In what format do you wish to receive your results?

MaxQuant format

(the standard output for DDA data by MaxQuant software, consisting of identified protein and peptide tables with parameters enabling the downstream label-free quantification or other processing and statistical analysis e.g. with Excel, Perseus, or R)

Raw MS files only

(if you wish to carry out MS spectra processing yourself)

Dia-NN format

(the standard output for DIA data by Dia-NN software, consisting of identified protein and peptide tables with parameters enabling the downstream label-free quantification or other processing and statistical analysis e.g. with Excel, Perseus, or R)

Custom report

(i.e. not generated by automated data analysis; please provide details on the format and consider additional costs)

Sample list:

Sample group

e.g. control, condition 1/2, strain A/B etc.

Sample name

Sample info

please indicate the total protein amount, if known, and volume of the sample, if applicable, as well as any other relevant info

- 1.
- 2.
- 3.
- 4.
- 5.
- 6.
- 7.
- 8.
- 9.
- 10.

In case of more than ten samples, or if it's more convenient, please send the sample list as a separate Excel file