Sample submission form for proteomics analysis UT PCF

Submission date:

Your name:

E-mail address and phone:

Company/organization:

Billing address:

Value added tax (VAT) number:

Species and strain/cell type (if applicable):
(e.g. Saccharomyces cerevisiae S288c or fibroblasts/keratinocytes/etc.)

Do the samples contain proteins that have sequences differing from the UniProt databases: ◯ No ◯ Yes *(I will send amino acid sequences in a separate file)*

Estimated proteome complexity:
(rough expectation about the nr of different proteins in the samples)
◯ 1-100 ◯ 100-500 ◯ 500-1000 ◯ 1000-2000 ◯ 2000-4000
◯ 4000-6000 ◯ >6000 ◯ Unknown

Assay used to determine protein concentration:
(add concentrations to the sample table on the next page; if not determined, leave blank)

If your samples contain artificially labelled amino acids or other labels, check appropriate boxes:
☐ Lys8 ☐ Lys4 ☐ Arg10 ☐ Arg6
☐ TMT-tag ☐ ^{18}O phosphate ☐ iTRAQ-tag ☐ ^{15}N ☐ Other:

Do your samples need digestion with other proteases than trypsin (*i.e.* default protease):
☐ No *(trypsin only)* ☐ LysC *(cleaves C-term to K)* ☐ ArgC *(cleaves C-term to R)* ☐ LysN *(cleaves N-term to K)*
☐ Chymotrypsin *(cleaves C-term to W, Y, P, L; lower rate at M, A, D, E, H, I)* ☐ AspN *(cleaves N-term to D)* ☐ GluC *(cleaves C-term to E)* ☐ No digestion *(intact analysis only or proteins have been proteolysed)*

Check contaminants your samples may have:
(so we can take necessary steps to minimize interference from them; even if there are trace amounts of contaminants, please indicate it)
☐ Salts ☐ Detergents ☐ Cell culture media
☐ Lipids ☐ DNA/RNA ☐ Radioactive isotopes ☐ Fetal Bovine Serum
☐ Excess single proteins *(e.g. albumin, Igs, streptavidin etc.)* ☐ High M_w PEG polymer(s) ☐ Other: *(Please describe below)*

Does your analysis involve glycosites or glycans: No

Does your analysis involve phosphorylation: No

Are there any other post-translational modifications that are of special interest to you: ◉ No ◯ Yes

What type of quantification does your experiment require: Qualitative analysis (no quantification)

Do you have a specific preference for an instrument to be used: ☐ Q Exactive HF ☐ Q Exactive Plus ☑ I will leave the facility to decide

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)

Which analysis approach would you prefer: ☐ Data-dependent acquisition (DDA)

☐ Data-independent acquisition (DIA) ☐ Targeted acquisition ☑ I don't know, I will let the facility decide

In which format would you like to receive your results:

◉ MaxQuant format
(an automated recommended report in table(s) format for DDA data that is convenient for downstream data processing and analysis e.g. with Excel or R)

○ Raw files only
(such as MS .raw files or peaklists such as .mgf; when you wish to carry out MS spectra processing with your own tools)

○ Skyline format
(choose only for targeted proteomics experiments; the output is tables which contain data about integrated peak areas of peptides and other relevant details)

○ DIA-NN format
(an automated recommended report in table(s) format for DIA data that is convenient for downstream data processing and analysis e.g. with Excel or R)

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

In which form will the samples be handed over:

☐ Proteins/peptides in solution ☐ Gel band ☐ Pelleted cells ☐ Lysate ☐ Pelleted proteins ☐ SPE tips (e.g. StageTips) ☐ (Nano)particles ☐ Tissue

Do you require the leftovers of your samples back: ◉ No ○ Yes

How should your samples be stored: ○ At +4°C ◉ At -20°C ○ At -80°C

List samples to be submitted below (if there are more samples attach the list in a separate Excel table file):

Nr.	Sample group *(e.g. condition 1/2, patient/ctrl, etc.)*	Sample name *(also indicate total protein concentration and volume of solution in microliters if possible)*
1.		
2.		
3.		
4.		
5.		
6.		
7.		
8.		
9.		
10.		
11.		
12.		
13.		
14.		