

# Mass Spectrometry Sample Submission Form

## To be filled by MS core facility staff

Project number:

Project submission date:

|                             | Method | Operator | Date of completion |
|-----------------------------|--------|----------|--------------------|
| Protein digestion method:   |        |          |                    |
| Instrument(s):              |        |          |                    |
| FAIMS:                      |        |          |                    |
| MS method / Quantification: |        |          |                    |
| Gradient length:            |        |          |                    |
| Injection volume:           |        |          |                    |
| Data analysis:              |        |          |                    |

## To be filled by customers

|                      |   |
|----------------------|---|
| Name:                |   |
| Group:               |   |
| Project description: |   |
| Number of samples:   |   |
| Organism:            | <input type="checkbox"/> human <input type="checkbox"/> mouse <input type="checkbox"/> rat <input type="checkbox"/> yeast <input type="checkbox"/> <i>E. coli</i> <input type="checkbox"/> other:<br><input type="checkbox"/> recombinant protein*  |
| Protocol contains**: | <input type="checkbox"/> NP-40 <input type="checkbox"/> SDS <input type="checkbox"/> Triton X-100 <input type="checkbox"/> Glycerol <input type="checkbox"/> Digitonin <input type="checkbox"/> CHAPS <input type="checkbox"/> Tween<br><input type="checkbox"/> Brij <input type="checkbox"/> PEG <input type="checkbox"/> other detergent or polymer: |

### Sample type:

- Peptide mixture                       Purified protein                       Co-IP / BioID  
 (sub)Proteome                       Intact cell/organelle/membrane

### Digestion type:

- MS-READY                      clean-up method: \_\_\_\_\_  
 GEL OR GEL BANDS\*                       not alkylated                       alkylated  
 IN-SOLUTION  
 Sample volume: \_\_\_\_\_  
 protein amount: \_\_\_\_\_  
 Buffer composition: \_\_\_\_\_  
 PELLET  
 protein amount: \_\_\_\_\_  
 BEADS                       Co-IP                       BioID                       Agarose                       Magnetic  
 protein amount: \_\_\_\_\_

**Analysis method:**

- PROTEIN IDENTIFICATION
- PROTEIN QUANTIFICATION
  - LFQ       iBAQ       TMT       SILAC       AQUA       other
- number of conditions: \_\_\_\_\_ number of replicates: \_\_\_\_\_
- SPECIAL PTM
  - name: \_\_\_\_\_ residue(s): \_\_\_\_\_ mass: \_\_\_\_\_  fixed  variable
- SPECIAL ENZYMATIC DIGEST
  - name: \_\_\_\_\_ residue(s): \_\_\_\_\_
- CROSS-LINKING
  - name: \_\_\_\_\_
- OTHERS:

**Results to be sent:**

- .RAW files      you run protein search and quantification yourself
- unmodified search engine output      you perform the data analysis yourself
- LFQAnalyst input files      you perform data analysis *partially* by yourself
- full data analysis\*\*\*      you only want to perform data interpretation

**(in case of quantitative proteomics) Experimental design:**

conditions (will appear in RAW file name):

|  |  |  |  |  |  |  |  |  |
|--|--|--|--|--|--|--|--|--|
|  |  |  |  |  |  |  |  |  |
|--|--|--|--|--|--|--|--|--|

comparisons (condition1 vs condition2):

|  |  |  |  |  |  |  |  |
|--|--|--|--|--|--|--|--|
|  |  |  |  |  |  |  |  |
|--|--|--|--|--|--|--|--|

Further information:

\* send annotated gel or protein sequences to [ruwolt@fmp-berlin.de](mailto:ruwolt@fmp-berlin.de) or [stephanowitz@fmp-berlin.de](mailto:stephanowitz@fmp-berlin.de)

\*\* send sample preparation protocol to [ruwolt@fmp-berlin.de](mailto:ruwolt@fmp-berlin.de)

\*\*\* contains e.g. protein identifications, quality control, original and modified data matrices, volcano plots