# Mass Spectrometry Sample Submission Form

## To be filled by MS core facility staff

<table>
<thead>
<tr>
<th>Method</th>
<th>Operator</th>
<th>Date of completion</th>
</tr>
</thead>
<tbody>
<tr>
<td>Protein digestion method:</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Instrument(s):</td>
<td></td>
<td></td>
</tr>
<tr>
<td>FAIMS:</td>
<td></td>
<td></td>
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<tr>
<td>MS method / Quantification:</td>
<td></td>
<td></td>
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<tr>
<td>Gradient length:</td>
<td></td>
<td></td>
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<tr>
<td>Injection volume:</td>
<td></td>
<td></td>
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<tr>
<td>Data analysis:</td>
<td></td>
<td></td>
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</tbody>
</table>

## To be filled by customers

<table>
<thead>
<tr>
<th>Name:</th>
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<tbody>
<tr>
<td>Group:</td>
<td></td>
</tr>
<tr>
<td>Project description:</td>
<td></td>
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</tbody>
</table>

<table>
<thead>
<tr>
<th>Number of samples:</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Organism:</td>
<td>human</td>
</tr>
<tr>
<td>Protocol contains**:</td>
<td>NP-40</td>
</tr>
<tr>
<td></td>
<td>Brij</td>
</tr>
</tbody>
</table>

### Sample type:

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

### Digestion type:

- [ ] MS-READY
- [ ] GEL OR GEL BANDS*
  - [ ] not alkylated
  - [ ] alkylated
- [ ] IN-SOLUTION
  - Sample volume: ________________________________
  - Protein amount: ________________________________
  - Buffer composition: ________________________________
- [ ] PELLET
  - Protein amount: ________________________________
- [ ] BEADS
  - Protein amount: ________________________________
**Analysis method:**

- [ ] PROTEIN IDENTIFICATION
- [x] 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: ______________
- [ ] 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

**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 or stephanowitz@fmp-berlin.de
** send sample preparation protocol to ruwolt@fmp-berlin.de
*** contains e.g. protein identifications, quality control, original and modified data matrices, volcano plots