**  **

Mass spectrometry sample submission form

Please read the mass spectrometry guidelines on our home page (<http://cores.imp.ac.at/protein-chemistry/policy>) carefully before preparing your first samples. For instance, use mass spectrometry compatible buffers, high-quality solvents and appropriate plastic-ware, which prevent adherence of proteins and peptides. Avoid keratin contamination. In case of in-solution samples, use only highest quality HPLC grade solutions. Additionally, detergents must not be present in the submitted sample, as these substances interfere with successful peptide identification. All reagents should be highest grade (e.g. ultra grade or MS compatible). Provide a gel picture even in case of in-solution samples. For gel samples use mass spectrometry compatible staining.

**The use of radioactive isotopes is strictly forbidden!**

**Agarose beads for in-solution digests or on-bead digests should not be frozen prior to the digest, but stored at +4°C. Please plan your experiments accordingly. The best timeframe for submission is Monday to Thursday.**

It is absolutely essential to contact Karl Mechtler (IMBA, tel.ext. 4280, mechtler@imp.ac.at) before submitting your samples for MS. In case Karl is absent, please contact Elisabeth Roitinger (IMBA, tel.ext. 4298, elisabeth.roitinger@imba.oeaw.ac.at).

Please fill in this form, save it and send it to us (proteomics@imp.ac.at).

Contact information of sample owner Date Click here to enter a date.

Name Click here to enter text.

Group Click here to enter text.

Telephone Click here to enter text.

Email Click here to enter text.

## Contact information of the GROUP/PROJECT leader

Name Click here to enter text.

Telephone Click here to enter text.

Email Click here to enter text.

## The group/project leader is informed about this sample submission and approves

[ ]  Yes

[ ]  No

## Sample names with estimated total volume (µl) and amount (g)

Controls

Click here to enter text.

Samples

Click here to enter text.

## Sample background information

Experiment performed to generate your samples (please provide a short description)

Click here to enter text.

Protein(s) of interest

Click here to enter text.

Protein sequence is derived from the following organism

Click here to enter text.

Samples are derived from the following organism

Click here to enter text.

Protein tag(s) used

Click here to enter text.

*If sequence information (including any tag) or accessions are available, please send an email to Otto Hudecz (Otto.Hudecz@imp.ac.at) and Richard Imre (**richard.imre@imp.ac.at**).*

## Aim of analysis

[ ]  Protein identification

[ ]  Analysis of protein modifications

Please indicate which proteins should be analysed for modifications:

 Click here to enter text.

Please state which modifications should be searched for:

 Click here to enter text.

[ ]  Protein quantification

[ ]  Other Click here to enter text.

You will be provided with the mass spec results in form of Excel tables and additional figures, dependent on your experimental question.

We will keep the mass spec raw data for long term storage on our servers.

Do you nevertheless want to have a copy of the mass spec raw data?

[ ] Yes[x] No

### If the material is derived from an immune precipitation experiment, please specify:

Bait protein

 Click here to enter text.

Antibody is derived from (rabbit, mouse, …): Click here to enter text.

## Antibody

[ ]  Polyclonal, antigen (eg. peptide derived from human APC3)

Click here to enter text.

[ ]  Monoclonal, antigen

Click here to enter text.

[ ]  Crude serum

[ ]  Protein A/G purified (=IgG fraction)

[ ]  Affinity purified

## Type of beads or chromatographic resin used

[ ]  Magnetic

[ ]  Agarose

[ ]  Sepharose

[ ]  Protein A

[ ]  Protein G

[ ]  Other Click here to enter text.

Beads or resin supplier and catalog # Click here to enter text.

## Antibody cross linked to beads

[ ]  Yes, how: Click here to enter text.

[ ]  No

## Current state of the submitted sample

SDS-PAGE –Gel → proceed to **A.**

In-solution → proceed to **B**.

Bound to beads → proceed to **C.**

# A. SDS-PAGE-Gel

## Type of gel used

[ ]  Polyacrylamide (self cast)

[ ]  Precast by a company. Please specify: Click here to enter text.

[ ]  Other: Click here to enter text.

Buffers used to run the gel

Click here to enter text.

*Refer to silver/coomassie staining protocols listed on our homepage.*

Staining method used to visualize proteins

Click here to enter text.

*Store gel after staining in 1 % acetic acid in a fresh plastic box, tissue culture dish or glass ware. Please provide a picture of the gel and copy/insert your gel image into the field at the end of this document.*

# B. In-solution sample

*Provide a picture of a gel loaded with a small amount of sample. Please copy/insert your gel image into the field at the end of this document.*

*Samples should not contain high amounts of salt (>100 mM), they should be free of non-volatile buffer components (e.g. phosphate buffer) and of detergents (e.g. SDS, Triton, Tween**, NP-40). Additionally, the sample volume should be as small as possible (opt. 20 – 100 µl) and the pH of the sample should be neutral. Use 1M TRIS buffer (pH 8.0) to neutralize your sample prepared by yourself.*

Composition of the solution that contains your sample

Click here to enter text.

### If the material is derived from an immune precipitation experiment, please specify:

*It is important to follow the washing conditions described on our homepage, especially a sufficient number of non-detergent washing steps!*

Wash buffer (may include detergents and inhibitors)

Click here to enter text.

No of washing steps performed plus total volume used

Click here to enter text.

Final wash buffer for mass spec analysis (no detergents, no inhibitors)

 Click here to enter text.

No. of washing steps performed plus total volume used

Click here to enter text.

Elution buffer

[ ]  100mM glycine pH 2.0 – 2.5

[ ]  Other: Click here to enter text.

 Volume (µl): Click here to enter text.

Eluates neutralized

 [ ]  Yes, buffer used and volume:Click here to enter text.

 [ ]  No

**C. Samples bound to beads**

## Condition beads are submitted

 [ ]  Frozen

 [ ]  +4°C (wet ice)

[ ]  Dry

[ ]  In suspension, please state composition: Click here to enter text.

Bead volume submitted (µl): Click here to enter text.

### If the material is derived from an immune precipitation experiment, please specify:

 *It is important to follow the washing conditions described on our homepage, especially a sufficient number of non-detergent washing steps!*

Wash buffer (may include detergents and inhibitors)

Click here to enter text.

No of washing steps performed plus total volume used

Click here to enter text.

Final wash buffer for mass spec analysis (no detergents, no inhibitors)

Click here to enter text.

No. of washing steps performed plus total volume used

 Click here to enter text.

## Image of your gel

Please click the center icon to place your image, or copy/paste it to the image placeholder.



Mass spectrometry sample submission form version 7, Susanne Opravil, Elisabeth Roitinger

(February 2018)