Date: Click or tap here to enter text.

**Service Request Form**

# Customer Details:

* First Name: Click or tap here to enter text.
* Last Name: Click or tap here to enter text.
* Group (First & Last name of PI):Click or tap here to enter text.
* Affiliated institute/firm: Click or tap here to enter text.
* Address of affiliation: Click or tap here to enter text.
* Email: Click or tap here to enter text.
* Phone: Click or tap here to enter text.

# Details on sample(s):

* Nature of sample: Choose an item.
* Species/ species of expressed proteins (write *Homo sapiens*, *SF21, Plasmodium falciparum*): Click or tap here to enter text.
* Expression host (please write the species name, e.g. *Escherichia coli*, *Homo sapiens*, if not applicable write NA): Click or tap here to enter text.

# Type of analysis: Choose an item.

* Performed protein determination: [ ]  yes [ ]  no [ ]  not feasible
* If yes:
	+ Which assay did you use? Choose an item.
	+ Measured concentration (µg/µl) for in-solution samples: Click or tap here to enter text.
	+ I adjusted the protein concentration for all samples equally: [ ]  yes

**Please note:** If possible, provide us with 20 µg protein in 60 µL buffer for in-solution samples.

* Are there any detergents (even low amounts count) in your sample?

[ ]  Yes (Please indicate which in buffer composition) [ ]  No!

* Buffer composition: Click or tap here to enter text.
* pH of buffer: [ ]  acidic [ ]  neutral [ ]  basic
* **Additional information:** (e.g., expected contaminants, purification history, fusion proteins, known PTMs, truncation, mutation, etc., if you have nothing to mention here, please write NA): Click or tap here to enter text.
* Please paste here the **name of the protein** and the corresponding **amino acid sequence(s)** of your protein(s) in FASTA format (not DNA/RNA sequences), please highlight [in color] the tags, mutations and cleavage sites. Give the Uniprot identifier(s) of your tagged protein(s), if not applicable, write NA): Click or tap here to enter text.

**Example** for protein fasta header & sequence:

>sp|Q6EEV6|SUMO4\_HUMAN

MANEKPTEEVKTENNNHINLKVAGQDGSVVQFKIKRQTPLSKLMKAYCEPRGLSVKQIRFRFGGQPISGTDKPAQLEMEDEDTIDVFQQPTGGVY

For **gel samples only:**

* Molecular weight (kDa): Click or tap here to enter text.
* Do you have a gel image? (if so, please send it to us) [ ]  Yes [ ]  No
* If yes, have all bands for analysis been assigned in the gel image with a number! (Tick for 'Yes', if not, please do so!)

[ ]  Yes, I labelled all bands that I want to have analyzed

**Please label the marker bands with the respective size!**

# Other details:

Describe what you want to know about your sample:

Click or tap here to enter text.

Please be aware our default protease is Trypsin (cleaves C-terminally of K, R).

If you need a different protease or if you are not sure, please write this here and discuss with us: Click or tap here to enter text.

# Data analysis:

For **quantitative experiments** (e.g., TMT, iBAQ, LFQ/DIA, SILAC): Please indicate here which **ratio comparisons** you would like to have in the end and in which order you want to have them in the plots. State the **controls**, please. For IP’s, name the **bait protein** here.

Click or tap here to enter text.

# Table for sample overview and tube labeling:

Please **label the tubes only with** **your initials and number** and give a description in the following table. Indicate the control condition with “yes or no” in the table!

For the conditions, please keep the naming short, avoid spaces, special characters and repetitions, give more explanation in the description column!

Total number of samples: Click or tap here to enter text.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Tube | Condition | Replicate (e.g. rep1) | Control condition (yes/no) | Description/Comments |
| 1 |  |  |  |  |
| 2 |  |  |  |  |
| 3 |  |  |  |  |
| 4 |  |  |  |  |
| 5 |  |  |  |  |
| 6 |  |  |  |  |
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|  |  |  |  |  |

**Please note**: We can store the samples only for a limited time (2 months), then we discard the samples after the analysis is completed!