|  |  |  |  |
| --- | --- | --- | --- |
| Name: |  | Date: |  |
| Research Group: |  | Phone: |  |
| Project: |  |
| Aim of the experiment: |  |
| Sample description: |  |
| Date of sample generation: |  |
| Number of samples: |  |

**Sample Information**

**A. Sample material**

* Organism:
* Tissue/cell line/yeast strain (incl. auxotrophy) etc.:
* Subcellular compartment/organelle/membrane:
* Protein/peptide modifications:
- chemical modification/derivatization:
- identification of PTMs (phosphorylation, acetylation etc.):
* Cross-linking (reagent):
* Other:

**B. Sample preparation**

* Sample preparation/enrichment/purification strategy incl. tag/antibody (for IP) etc.:

|  |
| --- |
|  |

|  |
| --- |
|  |
|  |

* Labeling: No

 Yes - method (SILAC, 15N, others):

 - SILAC amino acids used:

|  |
| --- |
|  |

|  |
| --- |
|  |

* Sample separated via 1D-/2D-PAGE: No Yes

|  |
| --- |
|  |
|  |

* Gel image (annotated) is provided as pdf, jpg, tiff, pptx: No

 Yes

|  |
| --- |
|  |
|  |

* if applicable: WB image (annotated) included: No

 Yes

Information about 1D-/2D-PAGE (gel type, MW marker, sample loading scheme, stain etc.):

|  |
| --- |
|  |

* Sample in solution or lyophilized – volume and sample composition (buffer, reagents such as proteases/phosphatase inhibitors, detergents etc.)

|  |
| --- |
|  |

|  |
| --- |
|  |
|  |

**C. Control**

included

 not included

short description of the control:

|  |
| --- |
|  |

**Additional information on data analysis (if applicable)**

* Protein ID (e.g. accession #, IPI or SwissProt #):
* Protein sequence:
* Specific requirements for database used:
* Other, comments:

|  |
| --- |
|  |