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| --- | --- | --- | --- |
| 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.:

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* Labeling: No

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

- SILAC amino acids used:

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

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

Yes

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

Yes

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

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

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**C. Control**

included

not included

short description of the control:

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

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

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