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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/strain etc.:
* Subcellular compartment/organelle/membrane:
* Protein/peptide modifications:  
  - chemical modifications:  
  - Posttranslational modifications (PTMs):
* Cross-linking (reagent):
* Other information:

**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 SDS-/BN-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 SDS-/BN-PAGE (gel type, MW marker, sample loading scheme, stain):

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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**

* Protein ID (e.g. accession #, UniProt ID):
* Protein sequences (e.g. of bait including tags, antibodies):

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* Specific requirements for sequence database to be used (taxonomy id):
* Further description of (comparative) data analyses:

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