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Data Article

Data for the identification of proteins and post-translational modifications of proteins associated to histones H3 and H4 in *S. cerevisiae*, using tandem affinity purification coupled with mass spectrometry

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ABSTRACT

Tandem affinity purification method (TAP) allows the efficient purification of native protein complexes which incorporate a target protein fused with the TAP tag. Purified multiprotein complexes can then be subjected to diverse types of proteomic analyses. Here we describe the data acquired after applying the TAP strategy on histones H3 and H4 coupled with mass spectrometry to identify associated proteins and protein post-translational modifications in the budding yeast, *Saccharomyces cerevisiae*. The mass spectrometry dataset described here consists of 14 files generated from four different analyses in a 5600 Triple TOF (Sciex) by information-dependent acquisition (IDA) LC–MS/MS. The above files contain information about protein identification, protein relative abundance, and PTMs identification. The instrumental raw data from these files has been also uploaded to the ProteomeXchange Consortium via the PRIDE partner repository, with the dataset identifier

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PRIDE: PXD002671 and http://dx.doi.org/10.6019/PXD002671. These data are discussed and interpreted in http://dx.doi.org/10.1016/j.jprot.2016.01.004. Valero et al. (2016) [1].

Specifications Table

Subject area	Biology
More specific subject area	Proteomics, protein-protein interactions, post-translational modifications
Type of data	Tables and MS spectra
How data was acquired	LC–MS/MS nanoESI qQTOF Mass spectrometer (5600 Triple TOF, Sciex)
Data format	Analyzed and filtered
Experimental factors	Recombinant yeast cells expressing TAP-tagged histone H3 or H4 were generated. Whole-cell extracts from these cells, grown to $OD_{600} \cong 2.0$, were prepared and subjected to the tandem affinity purification procedure.
Experimental features	Original tandem affinity purification protocol was applied to whole extracts prepared with two buffers with distinct harsh properties.Affinity purified multiprotein complexes were digested by trypsin and LC–MS/MS analyzed (5600 Triple TOF spectrometer). Proteins and post-translational modifications were identified.
Data source location	Burjassot (València), Spain
Data accessibility	Data are within the article and also on ProteomeXchange Consortium, dataset identifier PRIDE: PXD002671; http://dx.doi.org/10.6019/PXD002671.

Value of the data

- The original tandem affinity purification (TAP) method combined with LC–MS/MS analysis can be applied efficiently to histone proteins H3 and H4 in the budding yeast to identify escort proteins and their post-translational modifications.
- Among around 400 proteins associated to H3 and H4, most of them are involved in chromatin dynamics, and H3, H4, H2B and H2A histones, Rtt106p, Spt16p, Pob3p and Psh1p were the most abundant.
- Multiple protein post-translational modifications (PTMs) can be identified on the purified proteins, being some of them new ubiquitination sites.
- Data indicate that serine and threonine residues of yeast histones are also targets of ubiquitination.
- The conditions for MS analyses employed in this work prevent artifacts due to overalkylation by iodoacetamide (IAM).

1. 1. Data

Proteins co-purifying with yeast TAP-tagged histones H3 and H4 under two different extraction conditions were analyzed by mass spectrometry using LC–MS/MS in IDA mode [1]. The resulting data are presented as lists of proteins and PTMs obtained for each tagged histone and each extraction condition. Spectra of peptides to validate ubiquitination sites are also included. Additionally, results of