Poster # P-II_0566

Protein–RNA crosslinking combined with MS becomes quantitative at peptide and amino-acid level

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Abstract

Purpose: Develop complete data processing workflows for quantification of Protein-RNA crosslinked samples

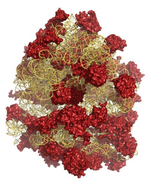
Methods: *E. coli* ribosomes were exposed to UV or chemical crosslinkers and/or labeled with TMT6plex. Separation was achieved using Thermo Scientific™ Vanquish™ Neo LC system and crosslinked samples were detected on Thermo Scientific™ Orbitrap Exploris™ 480 or Thermo Scientific™ Astral™ mass spectrometers and data was analyzed using using the NuXL node in Thermo Scientific™ Proteome Discoverer™ v3.1 software.

Results: TMT quantitation and LFQ can be achieved accurately using the NuXL node in Proteome Discoverer v3.1 software for UV- or chemically-induced crosslinks.

Introduction

Mass Spectrometry can resolve UV- and chemically induced protein-RNA crosslinking at the peptide and amino-acid level. Our search engine NuXL[4] improves the identification of protein-RNA UV/chemical crosslinks at amino-acid resolution, irrespective of sample complexity (isolated complexes or cellular entities). Yet the quantification of crosslinks remains a challenge for sensitive and precise detection of abundance changes among peptides crosslinked under different cellular conditions/states. UV crosslinks various amino acids to mainly uracil, whereas chemical crosslinking connects specific amino acids to guanosine and adenosine. Accurate MS-based quantification requires monitoring of the same crosslinked species derived from different states, and this can be hampered by changes in crosslinking patterns. Here, we explored a label-free(LFQ) or Tandem Mass Tags(TMT) quantitation approaches to analyze UV/chemical crosslinks using the NuXL node in Proteome Discoverer (PD) software.

- RNA/DNA protein complexes are essential for many cellular processes like DNA replication, DNA repair, transcription, splicing, RNA maturation, translation control etc.



- Defects in nucleic acid processing proteins are linked to severe diseases.
- Determination of the sites of interactions between proteins and RNA and/or DNA is required.
- Standard methods like X-ray crystallography, NMR, or cryo-EM are the golden standard to study the compositions of RNA and/or DNA protein complexes but can be challenging for large and dynamic complexes and cannot be applied on entire cells.
- Crosslinking mass spectrometry (XL-MS) offers a straightforward method to identify proteins and protein domains, which interact with RNA and/or DNA on the molecular and atomic level not only in isolated complexes but also in entire cellular systems.

Materials and methods

Sample preparation

Different amounts of *E. coli* ribosomes were exposed to UV or chemical crosslinkers. Crosslinked samples were digested, purified using TiO_2 and/or labeled with TMT6plex[3].

LC-MS/MS methods

Liquid chromatography was performed using an Thermo Scientific™ UltiMate™ -3000 RSLC nanosystem or a Vanquish Neo UHPLC system. Peptides were eluted over a 60 min 6-45 or 50% gradient (A: water, 0.1% formic acid; B: 80% acetonitrile, 0.1% formic acid) at 300 nL/min flow rate. The crosslinked samples were analyzed on Orbitrap Exploris 480 MS or Astral mass spectrometers in DDA mode. The following MS settings were used- Exploris 480- MS1 scan range, 350–1600 *m/z*; MS1 resolution, 120,000 FWHM; AGC target MS1, 1E6; maximum injection time MS1, 60 ms; isolation window, 1.6 m/z; collision energy, 30 or 33(TMT)%; charge states, 2+ to 6+; dynamic exclusion, 9 s; Top 20 most abundant precursors were selected for fragmentation; MS2 resolution, 30,000, AGC target MS2, 1e5; maximum injection time MS2, 120 ms. OT Astral: MS1 scan range, 400–1400 *m/z*; MS1 resolution, 180,000 FWHM; AGC target MS1, 500%; maximum injection time MS1, 5 ms; isolation window, 1.6 m/z; collision energy, 32%; charge states, 2+ to 6+; dynamic exclusion, 10 s; Top speed 1 sec for fragmentation; MS2, AGC target MS2, 100%; maximum injection time MS2, 20 ms.

Data analysis

The NuXL node in PD 3.1, based on the OpenMS software[1,3] package, is used for analyzing XL-MS data from UV or chemically crosslinked protein–RNA samples. The NuXL node is designed to identify UV- and chemically-induced crosslinks by taking individual MS fragmentation behavior into account. Respective presets (Figure 1) have been assembled based on our own *in vitro* and *in vivo* datasets including human nucleosomes, HeLa cells and *Escherichia coli* cells as well as on published data. We calculate match-odds and subscores and employ semi-supervised score calibration using Percolator. Moreover, entrapment experiments have been employed using manually curated data ensuring proper false discovery rate (FDR) control.

Quantitation of crosslinking data was accomplished using the NuXL node in Proteome Discoverer 3.1 software together with the Reporter Ions Quantifier node (for TMT quantitation) or the Minora Feature Detector node (for LFQ). Detailed templates are shown in Figure 2. LFQ of crosslinked peptide-RNA oligonucleotides was measured by their intensities in MS1.

Results

Workflows in the NuXL node

NuXL robustly identifies crosslinked peptides and amino acids from XL-MS data offering optimized search settings for a broad spectrum of crosslinking agents (UV, 4SU, 6SG, formaldehyde (FA), 1,2:3,4-diepoxybutane (DEB) and mechlorethamine (NM)) for both RNA- and DNA-protein crosslink samples (Table1). Further, combined with other downstream analysis nodes, the NuXL node can provide TMT quantitation and LFQ of crosslinked peptides(Figure 2).

Table 1. Supported protocols.

	UV XL	UV XL (4SU)	UV XL (6SG)	DEB	NM	FA
RNA	√	√	√	√	√	√
DNA	√			√	√	√

DEB: Diepoxybutane, NM: nitrogen mustard (mechlorethamine), 4SU: 4 Thiouridine, 6SG: 6-Thioguanosine, FA: Formaldehyde

Crosslinked peptides are identified by the NuXL search node, regular peptides by the SEQUEST search engine. The Reporter Ions Quantifier node is calculating abundances from TMT labeled peptides. The Minora node is used for LFQ for all the peptides.

Figure 1. Presets available in the NuXL node

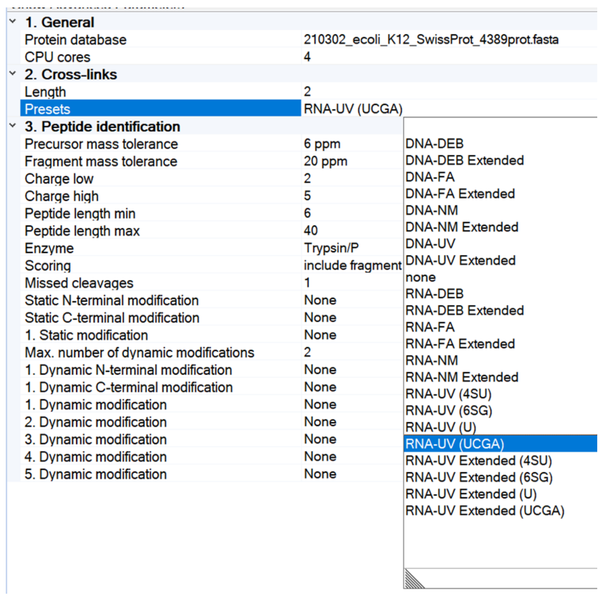
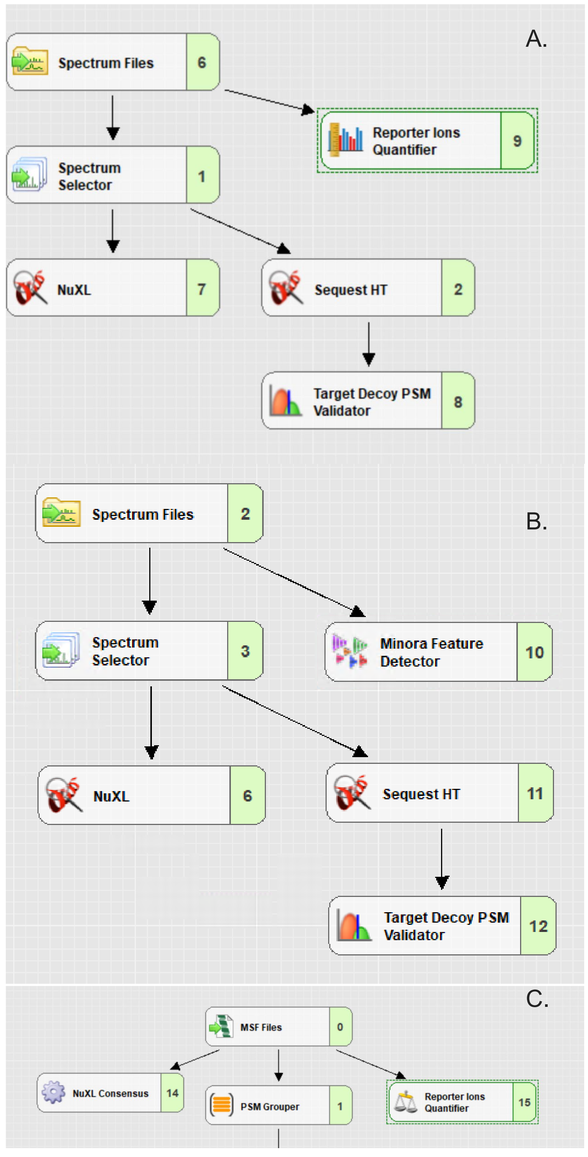


Figure 2. Processing workflow including (A)TMT Quantitation and (B) Label Free Quantitation (LFQ) and NuXL Consensus workflow(C).

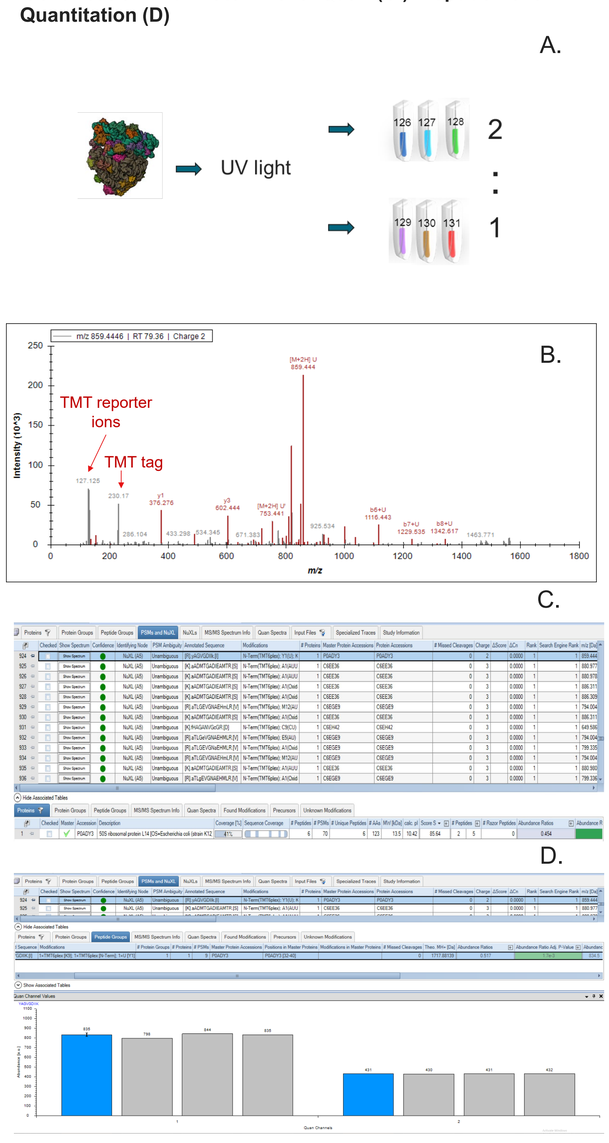


Results

TMT quantitation

We investigated the feasibility of quantitative UV XL-MS with different amounts of E. coli ribosomes. Samples were exposed to UV light and then split in 2:1 ratio , labeled with TMT6plex in triplicates (Figure 3A). Crosslinked samples were analyzed on OT Exploris 480 (Figure 3B-D).

Figure 3. TMT quantitation of UV crosslinked -*E.coli* ribosomes : Experimental set up (A). PD Analysis of 50S L14 Y(U)AGVGDIIK peptide Annotated MS2 spectrum (B) Identification and Protein Level Quan (C). Peptide Level Quantitation (D)



Label-Free quantitation

We investigated the feasibility of LFQ (Figure 4) using the NuXL node with UV- or chemical crosslinking of *E.coli* ribosomes. Samples were analyzed on OT Astral using DDA approach in duplicates (Figures 5&6).

Figure 4. PD result file showing the LFQ of two technical replicates of UV induced RNA-peptide crosslink.

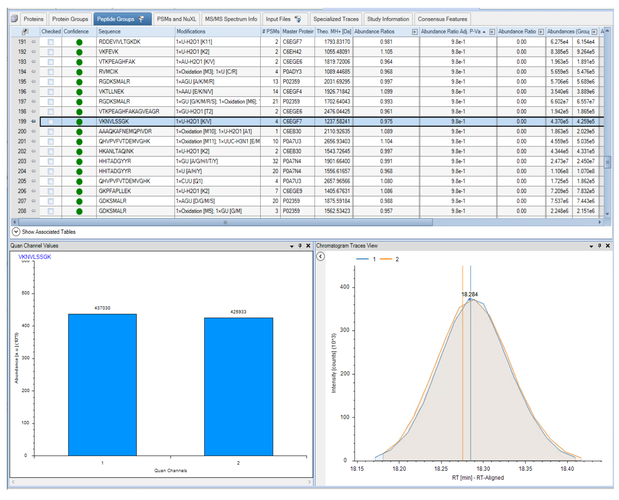


Figure 5. Venn diagram showing the overlap of unique identified RNA crosslinks in duplicates from (A) UV- or (B) NM samples in OT Astral DDA runs

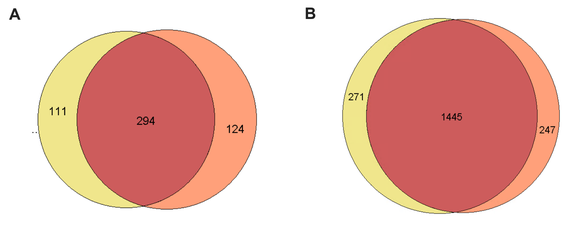
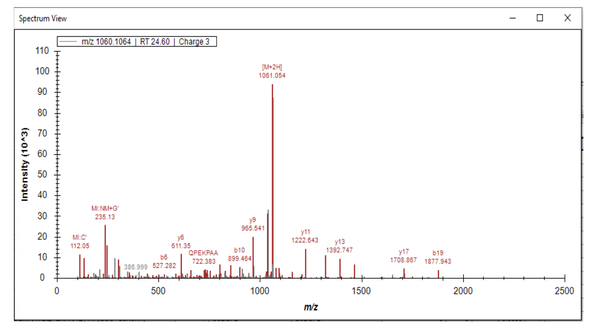


Figure 6. Example of Annotated MS2 spectrum of a NM induced RNA-peptide crosslink from OT-Astral.

The MS2 spectrum view in Proteome Discoverer of the peptide GEILGGmAAVEQPEKPAAQPK crosslinked with CGU+C5H9N1



Conclusions

- The NuXL node embedded in PD 3.0 or 3.1 enables analysis of DNA-/RNA-protein UV- and chemically-induced crosslink data.
- TMT and label-free quantitation of crosslinked peptide-RNA/DNA oligonucleotide can be achieved accurately and reproducibly using precursor or reporter ion quantification PD nodes.
- All major *E.coli* ribosomes proteins and RNA-protein crosslinked peptides were quantified using TMT6plex at expected ratio of 2.1 at amino-acid resolution.
- Proteome Discoverer 3.0/3.1 software with NuXL node was able to confidently identify and quantify peptides using precursor based LFQ. Its performance was validated using UV or chemical crosslinker *E.coli* ribosome.

Availability

The NuXL node is released for Proteome Discoverer 3.0 and 3.1. The binary installer, documentation, and example data are available at https://openms.de/applications/nuxl/.

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