

## Abstract

- ⇒ Chemical cross-linking combined with mass spectrometry (CXMS) is an established method in protein chemistry to explain low-resolution 3D protein structures and interactions in protein complexes.
- ⇒ Interpretation of CXMS data is challenging due to two-fold identification problem. The first challenge is to identify interacting peptides from non-interacting peptides and the second is to determine the site of interactions.
- ⇒ We developed an algorithm X-Link Peptide Mapping (XLPM) to analyze and interpret CXMS data.
- ⇒ VisInt-X is a tool to visualize interpreted CXMS results. VisInt-X visualizes the results of the analysis including 2D information representations of interacting partners, scores and sites of interactions, while 3D structural modeling representation maps interactions onto protein structures.
- ⇒ VisInt-X is the first tool for comprehensive visualization of CXMS analysis.

## Visualization and Visual Elements

- ⇒ VizInt-X is a visualization tool for results of cross-linking experiments.
- ⇒ Figure 1 shows a complete visualization of results in VizInt-X.
- ⇒ The visualization is divided into two parts. The top panel shows 3D visualization of protein structures, while the bottom panel shows 2D visualization of cross-linking results.
- ⇒ VizInt-X asks for PDB files or PDB id, protein sequences in fasta format and results of cross-linking experiments.
- ⇒ After processing of the results the first level of visualization is shown. First level is a heat map. It gives a complete view of interaction between two proteins. Intensity of blue color is according to cross-linked interaction scores. Proteins are divided into completely digested tryptic peptides. Mouse over to one of the cells in heat map shows peptide and scores represented by that cell. (figure 2)
- ⇒ Clicking on one of the cells in level 1 opens level 2 visualization. Level 2 visualization is a tree map showing all mass spectra representing selected peptide pair in level 1. While level 1 shows completely digested tryptic peptides, level 2 includes mis-cleaved trptic peptides as well. Mouse over on a cell in level 2 gives additional details about that mass spectra including charge, m/z and mass. (figure 3)
- ⇒ Selecting one of the cell in level 2 opens a level 3 visualization, which is again a heat map. Level 3 heat map shows interactions between individual residues of the peptide pair.
- ⇒ The results in 2D visualization is mapped onto protein 3D structure for better analysis. The blue colored residues in the protein structure shows all residues of the selected peptide in level2, while brown colored residues are residues selected in level 3 visualization.
- ⇒ While scores in cross-link results analysis gives a quantitative confidence level of a particular interaction, their mapping onto protein 3D structure gives a physical assessment of interactions.
- ⇒ Currently, VizInt-X can be accessed through a website.
- ⇒ In future, we will make an offline software available for VizInt-X.
- ⇒ We are also developing a virtual reality solution for VizInt-X.

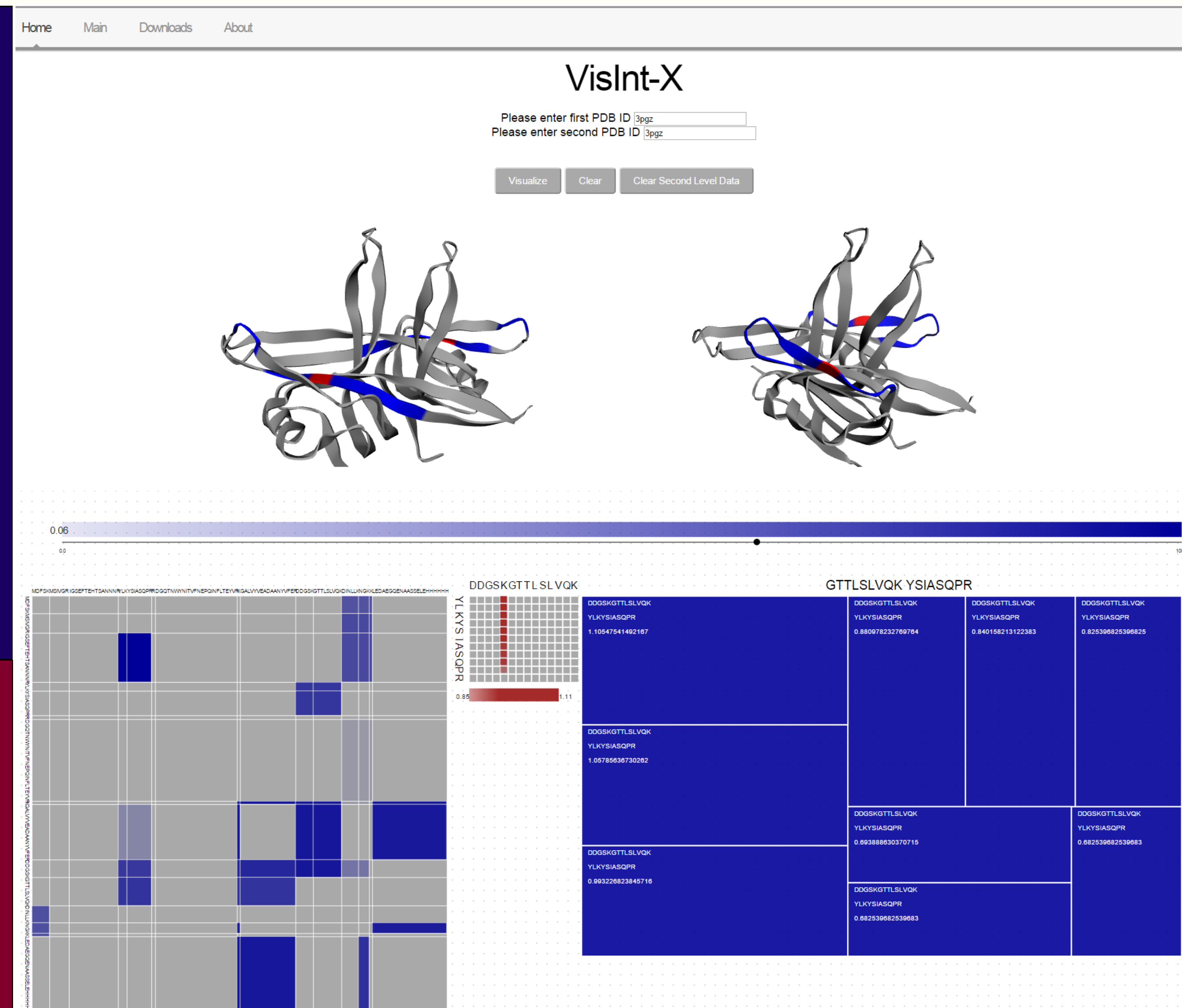


Figure 1: VisInt-X screen. Top panel shows protein 3-D structures. Bottom panel shows results of a cross-linking experiments. Left: Heat map showing first level of visualization, Middle: heat map showing third level of visualization, Right: Tree map showing second level of visualization. First level describes protein wide interactions from a cross-linking experiment. Second level shows all peptide pairs identified for a selected interaction. Third level shows residue level interaction for a peptide pair selected in level 2. Blue colored residues in protein structures show all interacting residues, while brown colored residues show selection in the third level visualization.

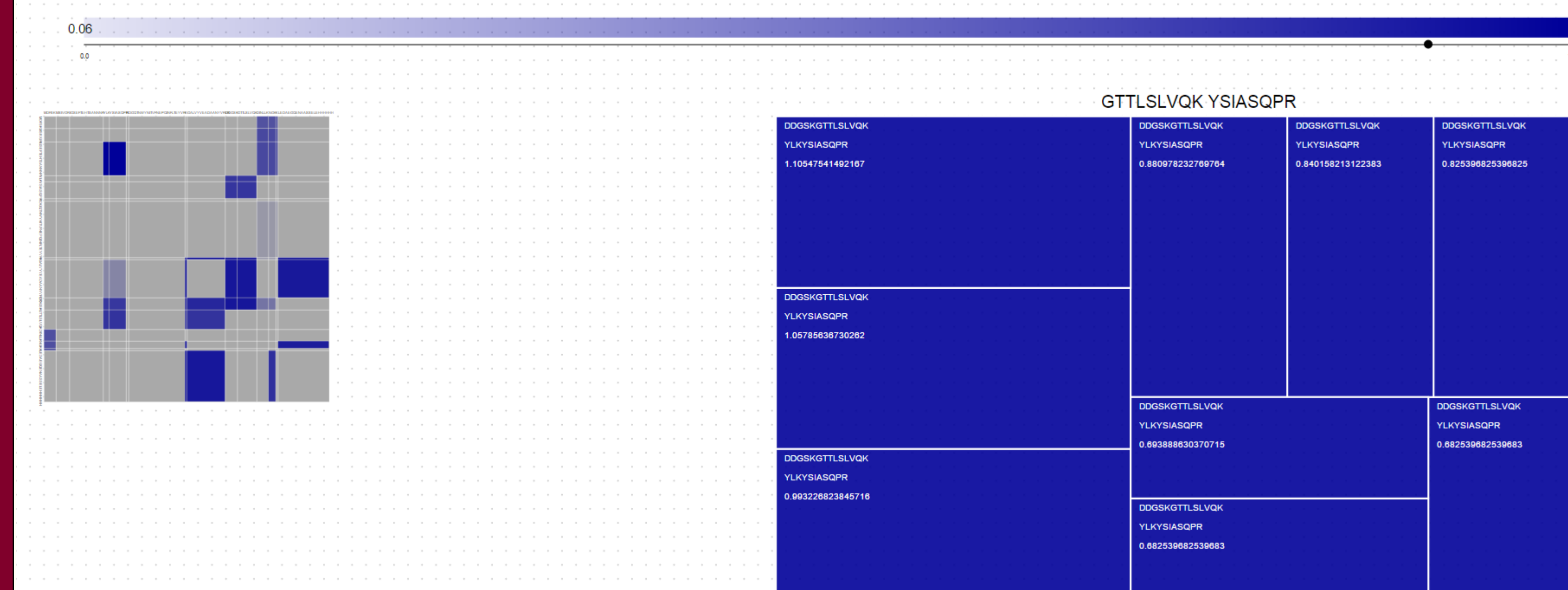


Figure 3: Level 2 visualization. When a peptide pair is selected in level 1 visualization, level 2 tree map opens on the right corner. The tree map is arranged from left to right top to bottom. Mouse over a block in tree map shows additional details of that peptide pair.

## Conclusion

- ⇒ VizInt-X is the first attempt at visualization of chemical cross-linking mass spectrometry (CXMS) data.
- ⇒ The three level visualization describes details of all the matched spectra and entire protein.
- ⇒ Heat map in the first level gives a profile of interaction between a pair of proteins on a single page.
- ⇒ The second level gives in depth details of all spectra representing the interaction between a pair of peptides and the third level heat map for the residues interaction.
- ⇒ Mapping of results onto protein tertiary structure gives a physical view of the interaction and better analytical capability.
- ⇒ An offline package and virtual reality solution will add to usability of VizInt-X in future.

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## References

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