



CovalX offers a unique Contract Research Organization (CRO) service laboratory specializing in protein and protein interaction analysis by mass spectrometry. Our clients already include many of the largest pharmaceutical companies as well as smaller biotech companies and academic laboratories internationally. CovalX scientists have the know-how and experience to understand your needs in the fields of protein analysis, antibody characterization.

Protein and Protein Interaction Analysis

The use of mass spectrometry allows a much faster, cheaper and more accurate method for studying proteins and protein interactions:

Protein Analysis

- Intact mass determination, determination of the modification.
- Identification of Proteins via peptide mass fingerprint analyzed by nLC-Orbitrap MS/MS.
- N-terminal sequencing by MALDI ToF MS.
- N and O glycosylation analysis by nLC-Orbitrap MS/MS

Protein Interaction Analysis

- Epitope Mapping: Conformational and linear epitope and paratope mapping by mass spectrometry.
- Protein complex analysis: Stoichiometry of the interaction by High-Mass MALDI MS.
- Therapeutic Aggregates analysis analyzed by Size Exclusion Chromatography and High-Mass MALDI MS.
- PEG-Protein conjugate analysis by High-Mass MALDI MS.
- Affinity constant determination (KD) by SPR.

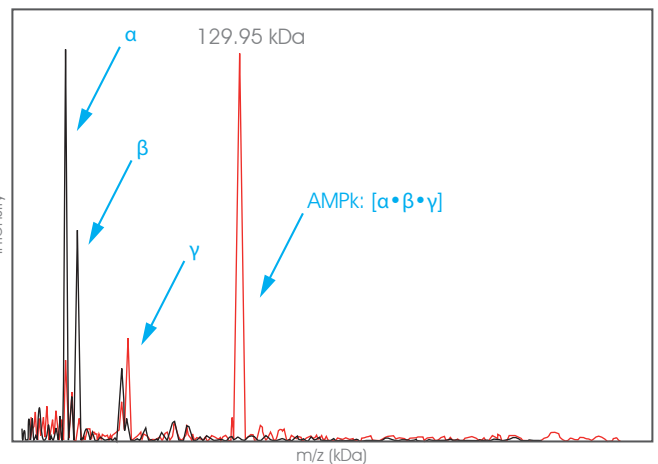


Figure 1. In the spectrum presented, the protein complex AMPK is analyzed by High-Mass MALDI ToF mass spectrometry before cross-linking (black) and after cross-linking (red) with CovalX's K200 MALDI MS Analysis Kit. Before cross-linking, the three subunits α , β and γ of the protein complex are detected with $m=30.22$ kDa, $m=37.38$ kDa and $m=64.97$ kDa. After cross-linking, the intact protein complex corresponding to the stoichiometry $[\alpha\beta\gamma]$ is detected with $m=129.95$ kDa. Riek U et al.; J. Biol. Chem.; 2008.

Our services include:

Unique Epitope Mapping service:

Fast conformational or linear Epitope mapping.
Both Paratope and Epitope characterization.

Antibody characterization:

Multibinding, integrity, Ab/Ag stoichiometry, N and O glycosylation, N-terminal sequencing, affinity constant, aggregation analysis

Antibody Characterization

Antibody-Antigen interactions are largely used in drug discovery, molecular biology, pharmacology and clinical diagnostics. The characterization of monoclonal antibodies of interest is a prerequisite for therapeutic proteins developments, quality control, optimizing detection assays or making sure that the best antibody is selected for a specific project.

CovalX laboratory service for antibody characterization allows:

- **Interaction Analysis:** Characterization of the immuno-complexes; stoichiometry of the binding.
- **Multi-binding experiments:** Sandwich assays.
- **Epitope mapping:** Fast and high resolution conformational epitope and paratope mapping.

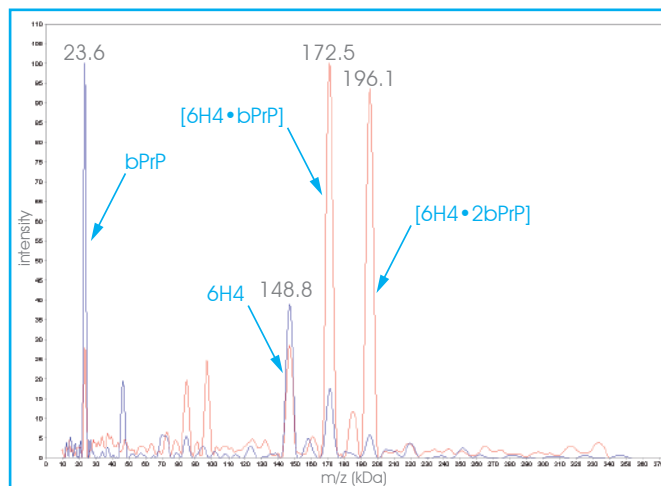


Figure 2. Analysis of the complex formed by the bovine prion protein (bPrP) and a monoclonal antibody anti-bPrP (6H4). The complexes are analyzed before (blue) and after cross-linking (red).

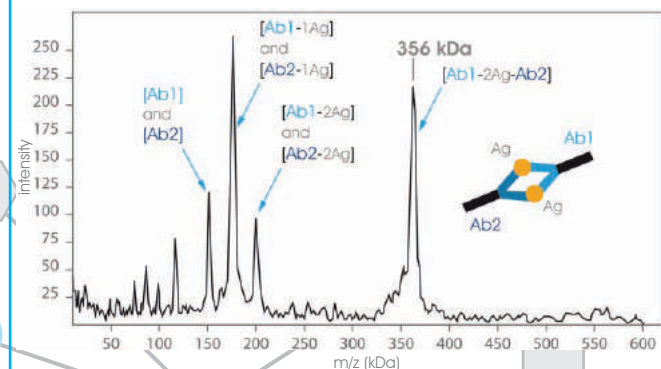


Figure 3. Multiplexing experiments. Two monoclonal antibodies against the prion protein 6H4 and 3B8 are incubated in the presence of the bovine prion protein. The sandwich complex 6H4-2bPrP-3B8 is observed at $m/z = 356$ kDa. This verifies the two antibodies are able to bind the same antigen at the same time, enhancing assay performance.

Bich et al. Anal. Biochem, 2008, 375:35-45
Nazabal et al. Anal. Chem. 2006, 78(11), 3562-3570

Therapeutic Protein Aggregates Characterization

The analysis of the aggregation phenomenon of therapeutic proteins is of crucial importance as more and more pharmaceutical products are proteins or peptides. CovalX introduces a unique tool for the direct characterization of therapeutic protein samples based on High-Mass MALDI mass spectrometry.

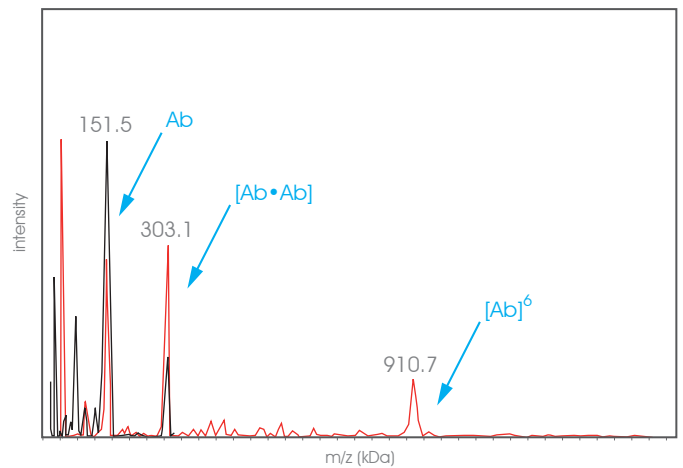


Figure 4. High Mass MALDI ToF analysis of an aggregated sample of therapeutic protein Hab42 before (black) and after (red) cross-linking.

For more details concerning protein and protein interaction analysis, feel free to contact our protein scientists: email cro@covalx.com.