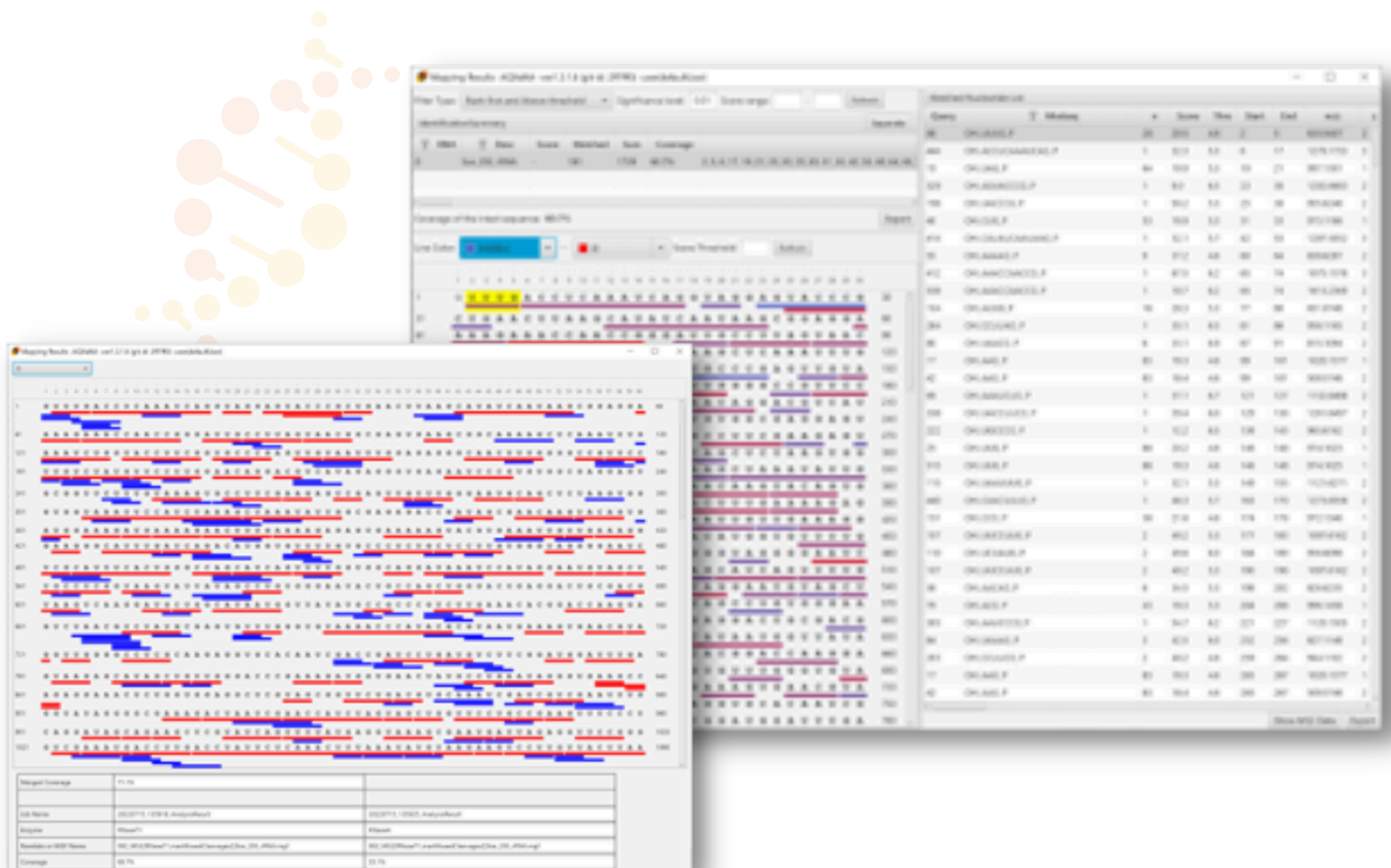


The logo for AQXeNA, featuring a stylized circuit board icon on the left and the text "AQXeNA" in a bold, sans-serif font. The "X" is highlighted with orange and yellow diagonal stripes.

AQXeNA is a powerful analytical platform for the automated identification and quantification of XNA* from the large amounts of mass spectrometric data obtained from LC-MS experiments.

PRODUCT FEATURES

- **Easily customizable XNA structure database**
- **in silico generation of related substances**
- **High-throughput peak detection and deconvolution algorithm**
- **Analysis of sequences consisting of thousands of bases, such as mRNA**
- **Effective reporting of results**



Easily customizable XNA structure database

- XNA structures such as nucleosides, linkers, 5'/3' ends, modification groups, and MS/MS dissociation profiles generated not only by CID/HCD but also by UVPD can be easily defined in the database.
- Contains a wide range of modified nucleic acids. Users can register new nucleic acid structures.
- Intuitive editing and management of nucleic acid sequences using the components found in the database.

in silico generation of related substances

- truncations at internal and ends of sequences, modifications to nucleosides and linkers, are automatically considered

High-throughput peak detection and deconvolution algorithm

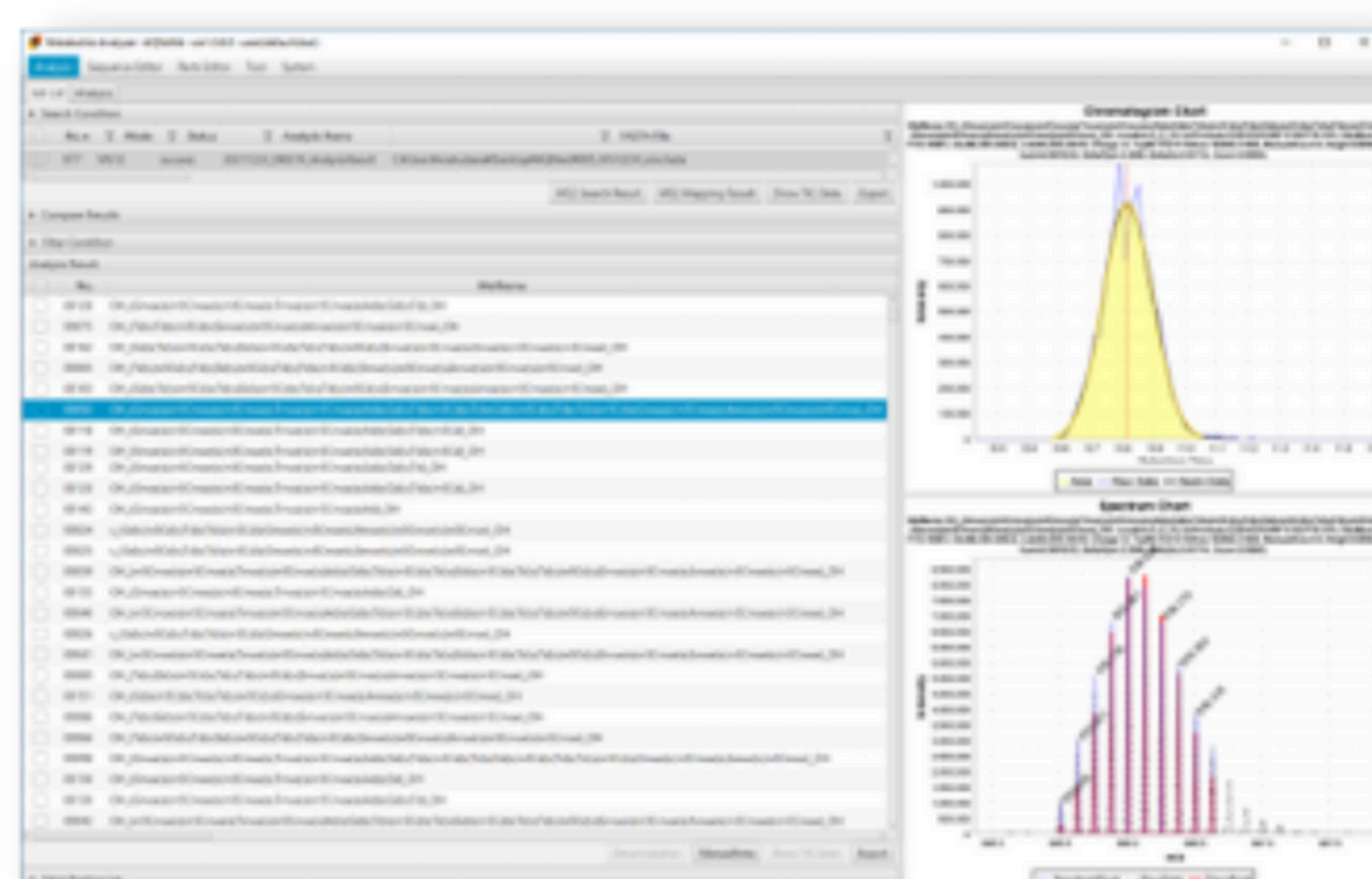
- Ariadne: Accurate algorithmic identification of fragment ions from XNA, the world's first.
- High-throughput peak detection and deconvolution

Analysis of sequences consisting of thousands of bases, such as mRNA

- Automatic extraction of nuclease digestion peaks allows analysis of long-chain sequences spanning thousands of bases.
- Visualization features through coverage calculation and mapping, with the ability to extract only unique digestions. Improved coverage through merged mapping of analysis results using different digestion enzymes.

Effective reporting of results

Treat/control comparisons between groups using identified data and multivalent ion deconvolution.
Bubble plots for LC-MS/MS visualization



Contact

