AQXeNA

Analyze and Quantify Nucleic Acids

"AQXeNA" is a powerful analysis platform for automated identification and quantification of XNA* from the large amounts of mass spectrometric data obtained from LC-MS experiments. AQXeNA can provide the most accurate and confident characterization of XNA more quickly than ever before, achieving beneficial results in Chemical Manufacturing Control and Pharmacokinetics of Oligonucleotide therapeutics.

***XNA: Entire range of nucleic acids including natural DNA/RNA, synthetic nucleic acids and analogues.**

Product features

Various sophisticated algorithm and interfaces are implemented for analysis of XNA using mass spectrometry.

Definition of XNA structures	Registration of target XNA sequence	XNA Identification and Quantification	Analysis and reporting
Easily customizable XNA structure database	User-friendly sequence editor enables users to define XNA sequences	High-throughput peak detection and deconvolution algorithms	Effective reporting of XNA results

Enabled devices and data formats

- **Thermo Fisher Scientific** (.RAW)
- **Waters** (.RAW)
- **Sciex** (.WIFF)
- **Agilent** (.D)
- **Bruker** (.D)
- **Shimadzu** (.LCD)
- **MzML** (.mzML)

Please contact us for the latest information.

Ariadne: Algorithm for Accurate XNA ID from MS^2 data

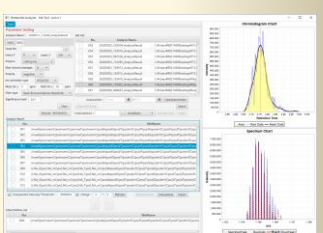


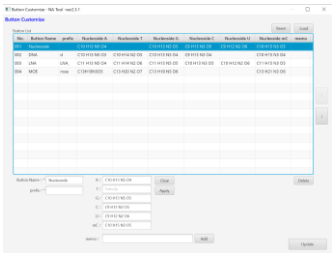
Fig. the workflow of AQXeNA

AQXeNA includes two different technology

- **Ariadne: Accurate XNA Identification algorithm, which is the first in the world.**
- **Ion peak detection algorithm: We have accumulated our knowledge of ion peak detection by development of LipidSearch*.**

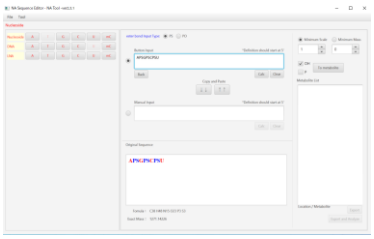
***LipidSearch: analysis software for lipidomics, which is used in more than 300 institutes of 30 countries.**

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 from UVPD can easily be defined in the database.

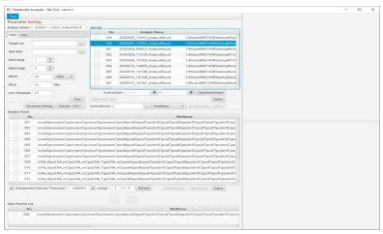
User-friendly sequence editor



- ✓ can define any nucleic acid sequence including hydrosylates by sequence-specific endonucleases or exonucleases.
- ✓ makes it easy to perform the characterization of long mRNAs for vaccines as well as metabolic analyses of antisense and siRNA drugs.

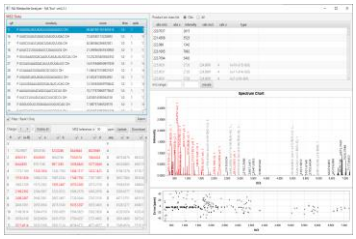
High-throughput peak detection and deconvolution algorithm

AQXeNA provides high accuracy peak detection of charge state, monoisotopic m/z, and peak area using a sophisticated algorithm based on a Gaussian fitting method from large data sets.



Ariadne: Accurate XNA identification algorithm

- ✓ Ariadne, which has been developed by Dr. Nakayama of RIKEN achieves more accurate identification of nucleic acids using MS^2 spectra.
- ✓ It is patented in Japan and the US.



Effective reporting of results

AQXeNA supports reporting results such as multivalent ion deconvolution and comparison between Treatment and Control groups.

【 Contact 】

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※ Ariadne：Database search for RNA identification using tandem mass spectrometry data (https://ariadne.riken.jp/)