Molecule Profiler software

Gain better insights on
impurities and biotransformations

SCIEX
The Power of Precision

Achieve accurate and flexible processing

Molecule Profiler software delivers highly accurate and flexible workflows for determining impurities and biotransformations for a wide variety of therapeutic molecules—from small molecules to synthetic peptides and oligonucleotides and lipids used for drug delivery.

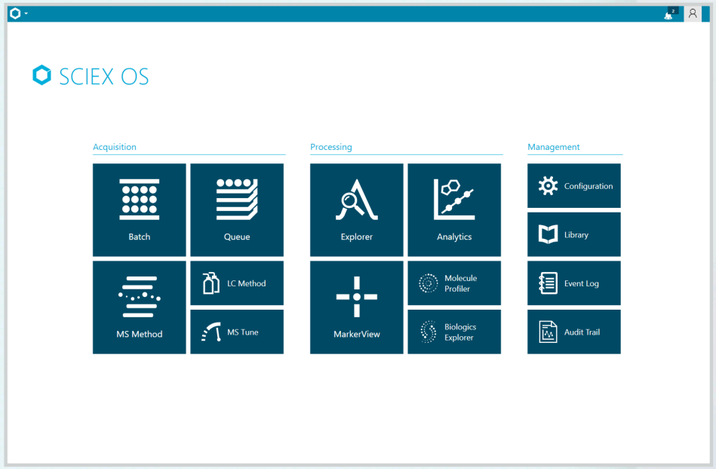
- Acquire data
- Set up processing method from pre-populated list of impurities and metabolites
- Identify impurity or metabolite based on accurate mass data
- Group charge states (for oligonucleotides or peptides)
- Confirm identity and structure with automated fragment ion assignment
- Report relevant results

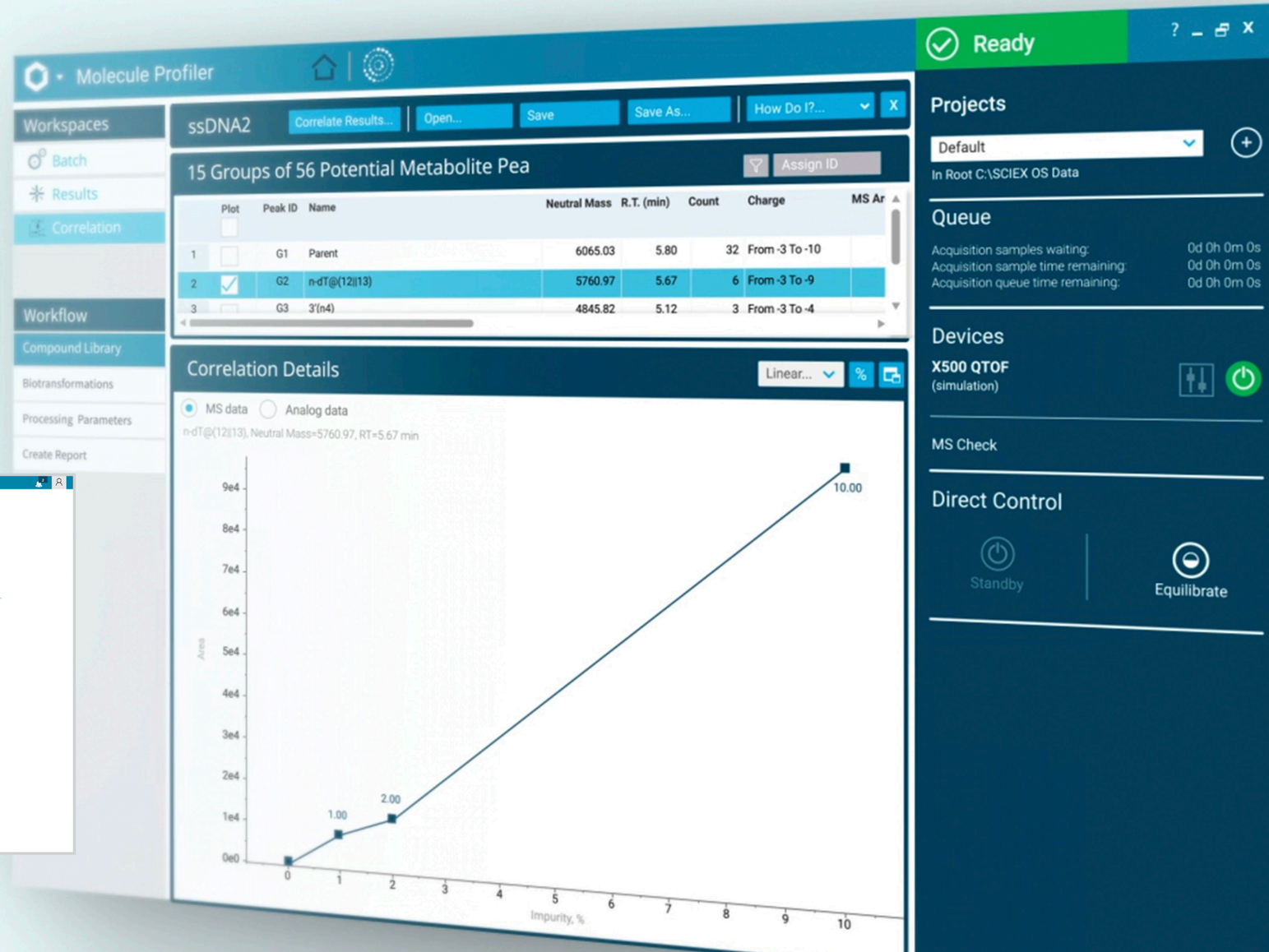
Discover the ease of integration

Having many different software products generally requires you to jump around from application to application, which can take time and increase training requirements.

Molecule Profiler software is seamlessly integrated with SCIEX OS software. You can efficiently perform multiple tasks alongside other functions without the need to transfer data between different programs.

With Molecule Profiler software, you can also easily navigate between the impurity and metabolite discovery functions and the highly customizable quantitative workflows of the Analytics module within SCIEX OS software.





Experience flexibility across molecule types

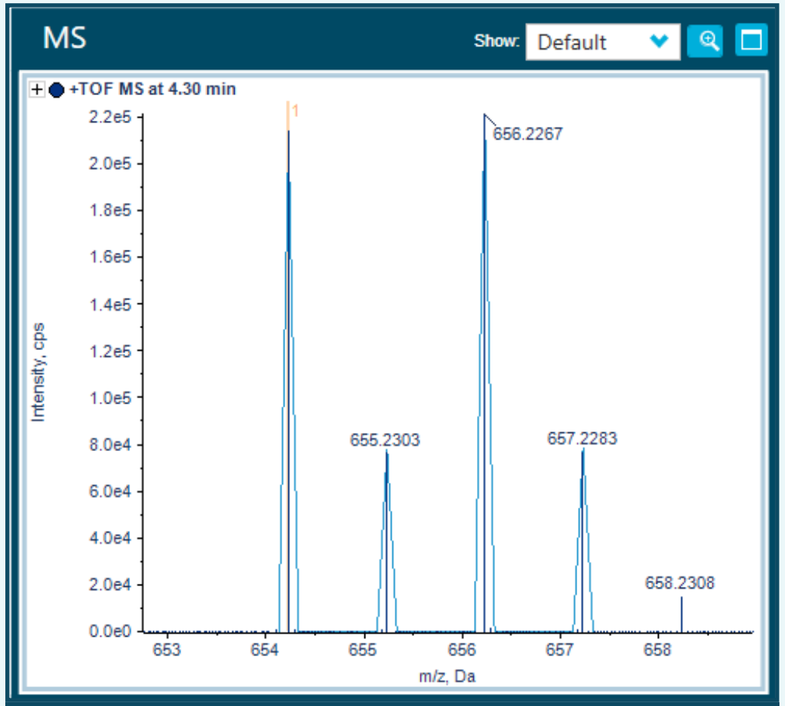
Why have a separate piece of software for every type of molecule you develop?

You can now use a single tool to provide insights about impurities and biotransformations across molecular classes, including lipids, therapeutic oligonucleotides, small molecule drugs, peptide therapeutics and even antibody-drug conjugates.

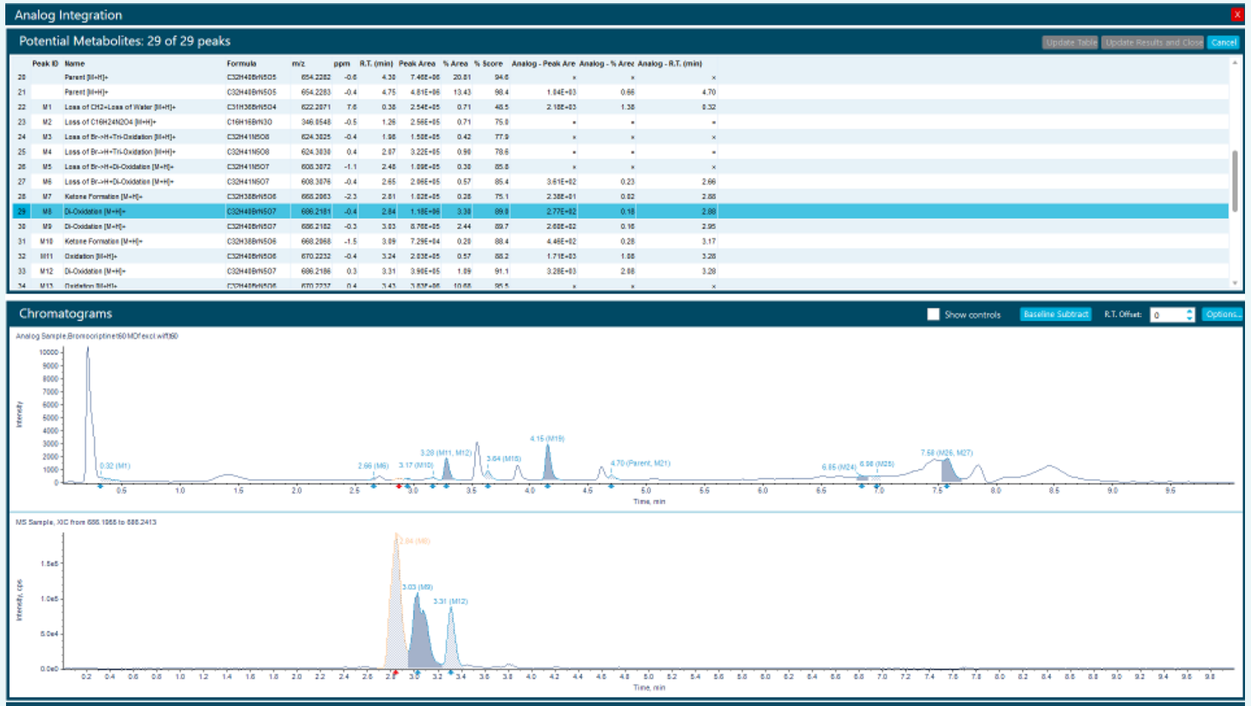
Increase confidence through MS/MS

Many impurities and biotransformations result in isoelemental species that an MS-only workflow cannot solve.

With the ability to incorporate UV, MS and MS/MS information, you can get clear and unambiguous results that give you complete confidence.



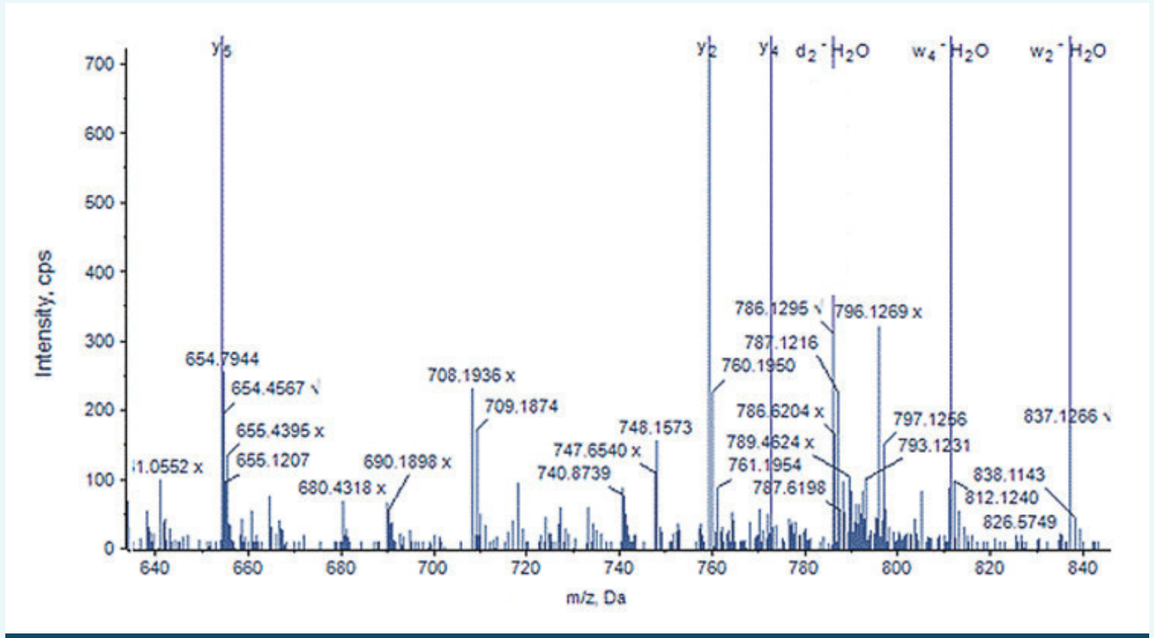
1. Use mass accuracy and isotope ratio matching for MS-level identification.



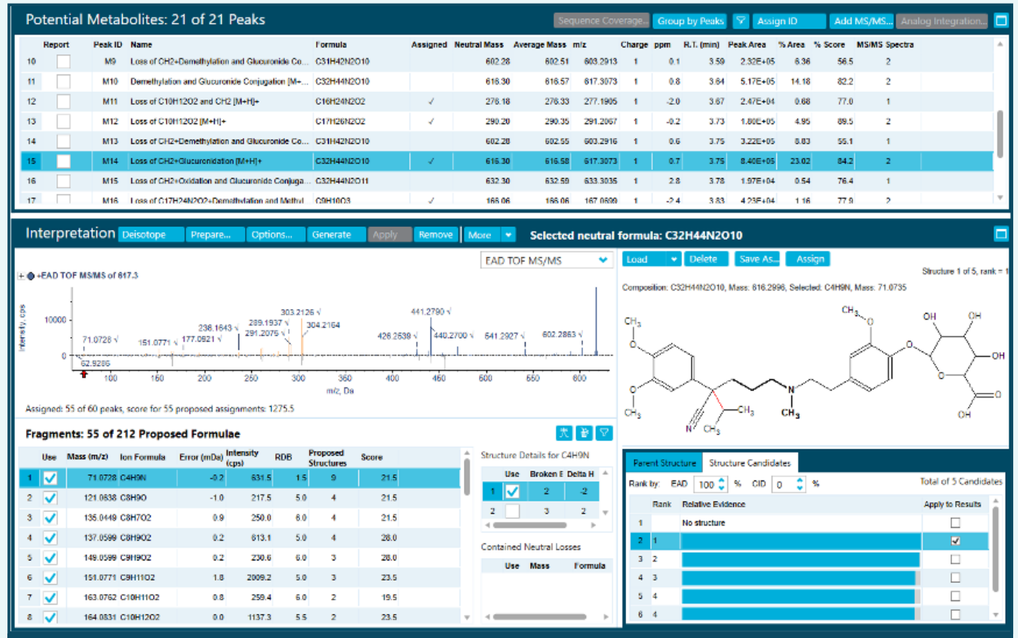
2. Incorporate UV, MS and MS/MS data to interrogate your data for impurities and metabolites.

Increase confidence through MS/MS

Analyze MS/MS spectra efficiently with customizable search criteria and gain detailed insights into fragment ion spectra.



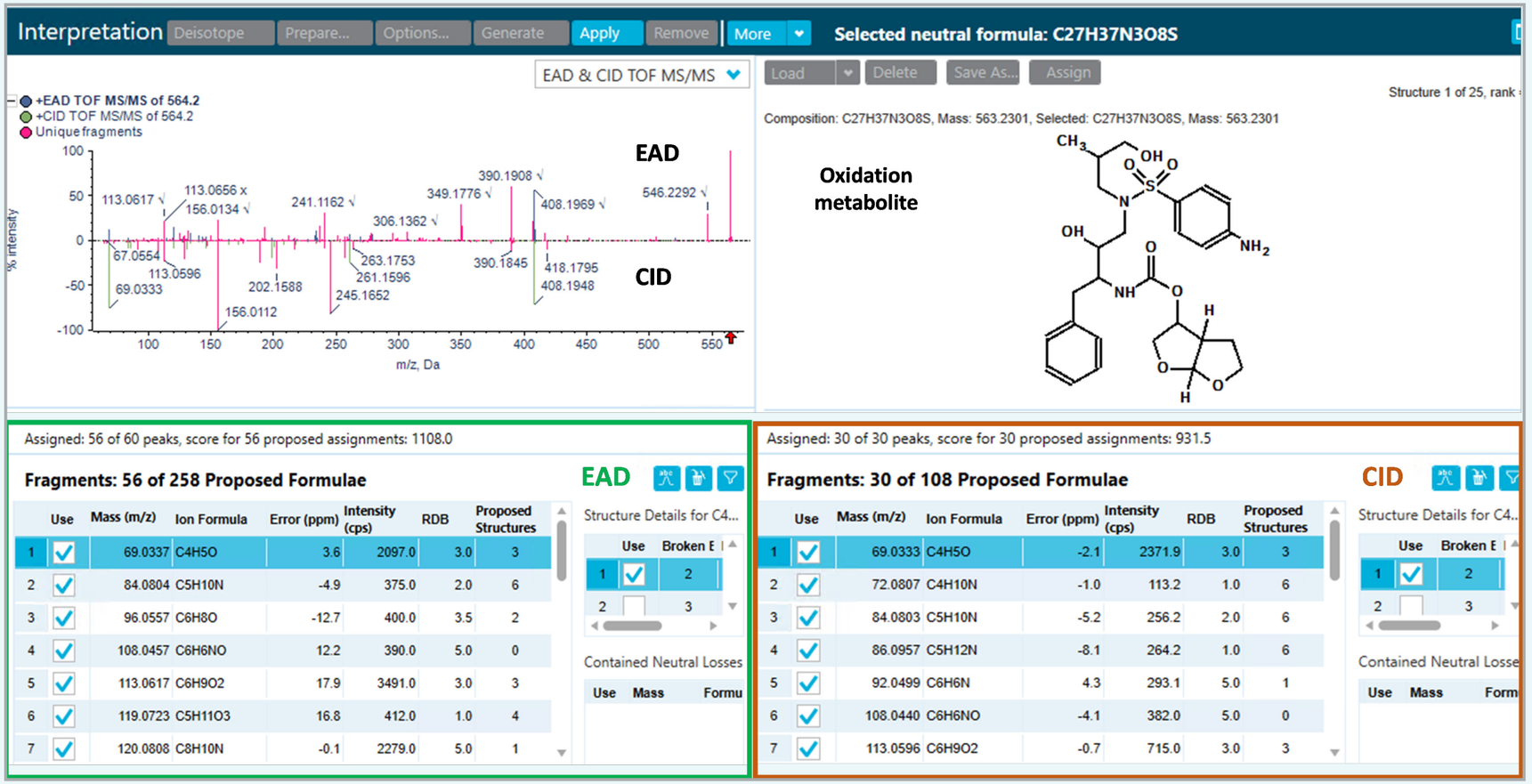
3. Easily customize your search criteria to match MS/MS spectra against in-silico generated impurities or metabolite fragments.



4. Switch between the results view and the interpretation view to get highly detailed information on your fragment ion spectra.

Small molecule metabolite identification with speed and ease

Automate your metabolite identification with confident metabolite structure assignments using both collision-induced dissociation (CID) and electron activated dissociation (EAD) data, saving time and money in your laboratory.



Get answers faster

Larger and more complex molecules such as lipids, oligonucleotides and peptides can produce very complex MS/MS data.

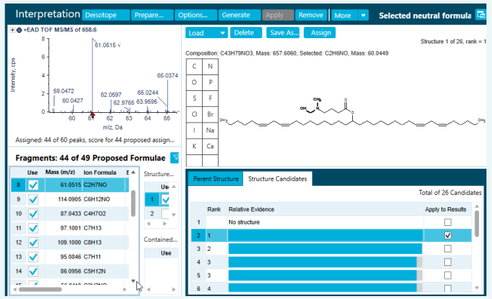
The powerful MS/MS engine in Molecule Profiler software can reduce the time it takes to get answers from days to hours.

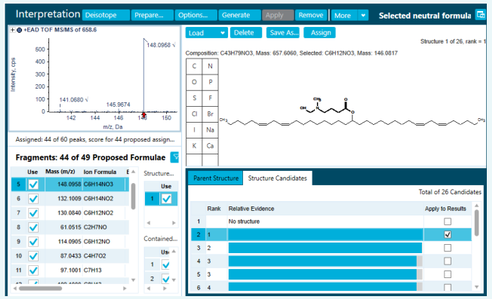
Easily build processing queues with the ability to choose multiple processing methods and controls. Each result analysis can be completed in just a few minutes.

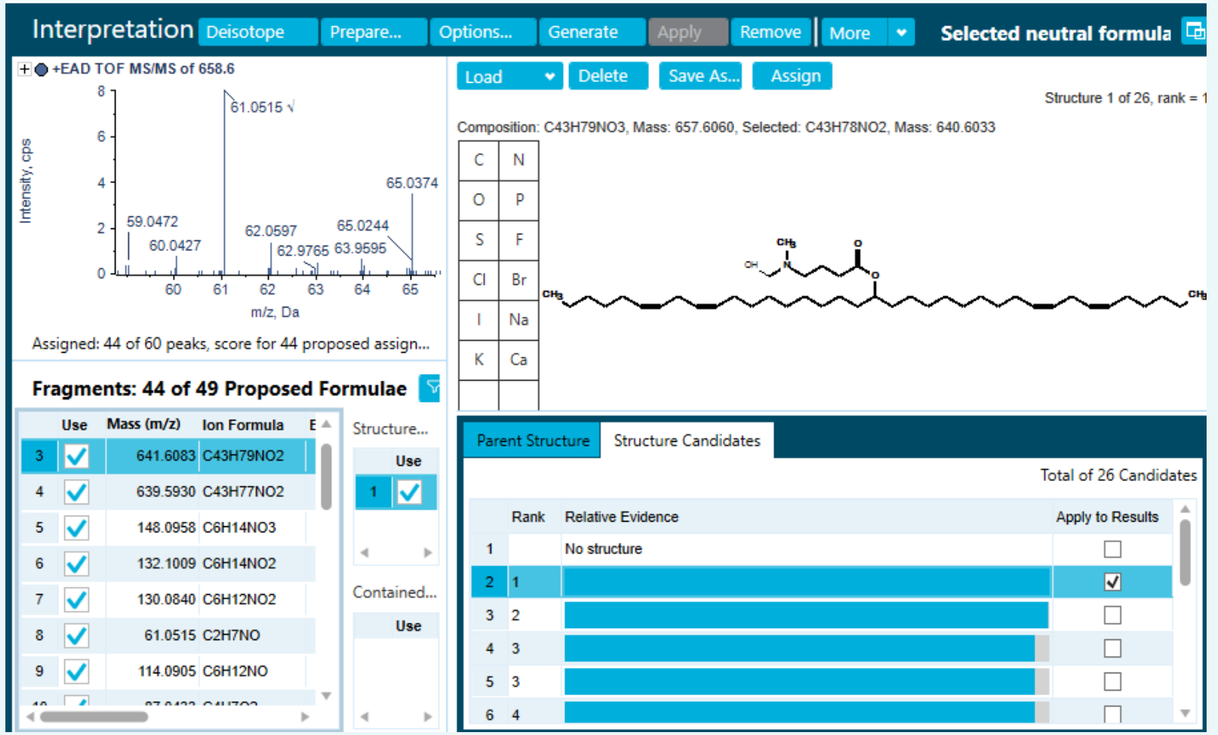
Explore structural depth with confidence in lipids

Lipid raw materials and lipid nanoparticles (LNPs) must be fully characterized to differentiate impurities, such as oxidation from ionizable lipids, which can affect product safety and efficacy.

With the ability to automatically process EAD and CID data, you can streamline workflows to get reliable answers faster and ensure the quality of the nucleic acid, including mRNA, in LNPs.







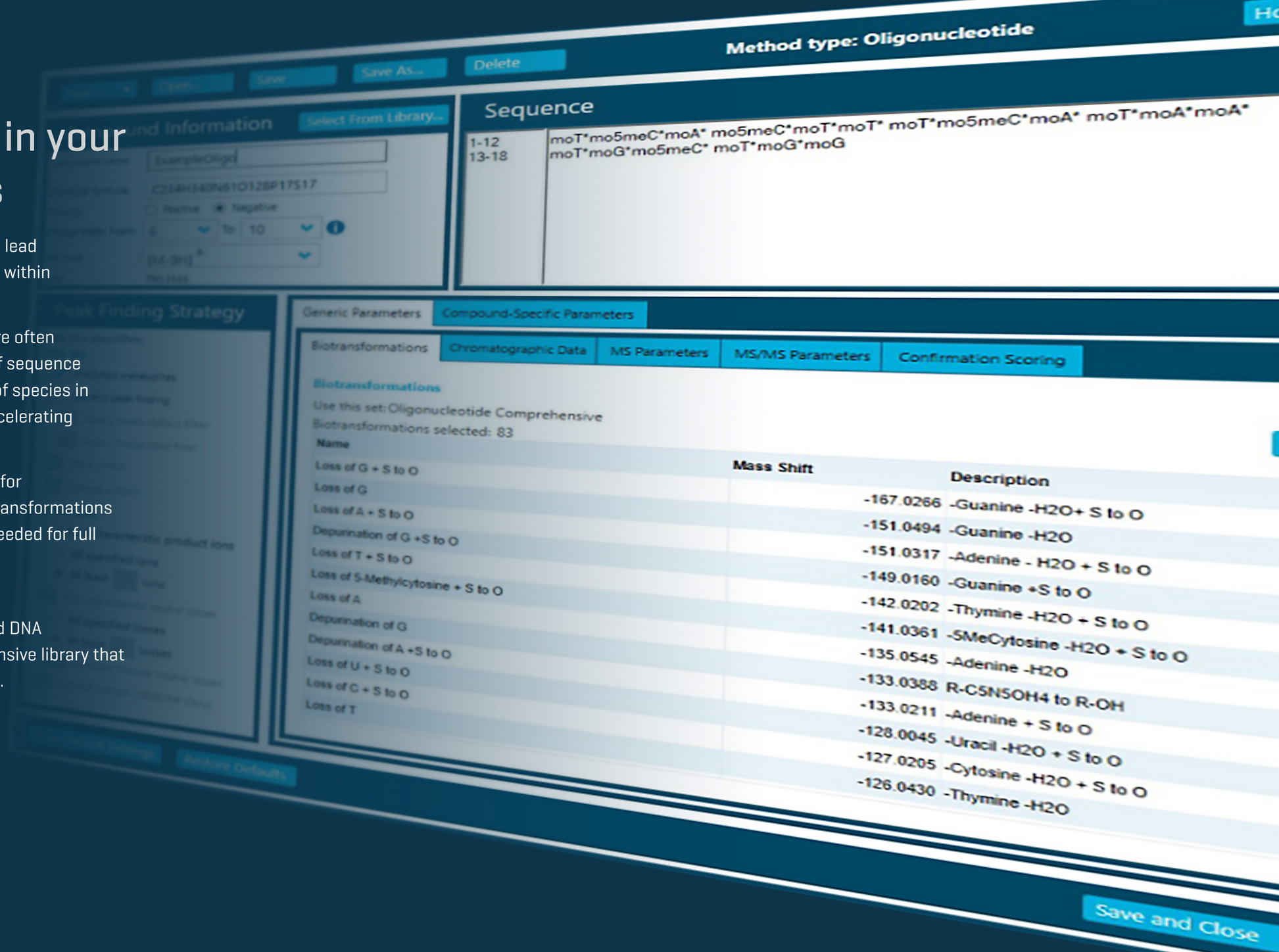
Gain confidence in your oligonucleotides

Side reactions during synthesis can lead to enormous numbers of impurities within oligonucleotide products.

Furthermore, biotransformations are often complex given the high variability of sequence modifications. Quick identification of species in a product or sample is crucial to accelerating development.

Choose from off-the-shelf libraries for oligonucleotide impurities and biotransformations to get a head start and amend as needed for full flexibility.

SCIEX has partnered with Integrated DNA Technologies to create a comprehensive library that helps ensure your sequence is right.



Molecule Profiler software is compatible with SCIEX accurate mass spectrometers

ZenoTOF 7600 system

This accurate mass spectrometer provides comprehensive data with innovations that have never been seen in an accurate mass system. The introduction of electron activated dissociation (EAD) fragmentation and the Zeno trap pave the way for precise and accurate MS and MS/MS data.

X500B and X500R QTOF systems

With simple workflows, robust hardware, sensitivity and precision, theX500B and X500R QTOF systems are the first LC-MS/MS systems designed for both characterization and quantitation.

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SCIEX Now

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- SCIEX Now Learning Hub success programs provide LC-MS and capillary electrophoresis (CE) training customized to meet your exact needs
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- Starting with a clear understanding of your desired learning outcomes, we aim to help you improve lab productivity and consistency by designing and delivering a program that is focused on knowledge advancement and retention

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Headquarters
500 Old Connecticut Path
Framingham, MA 01701 USA
Phone 508-383-7700
sciex.com

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