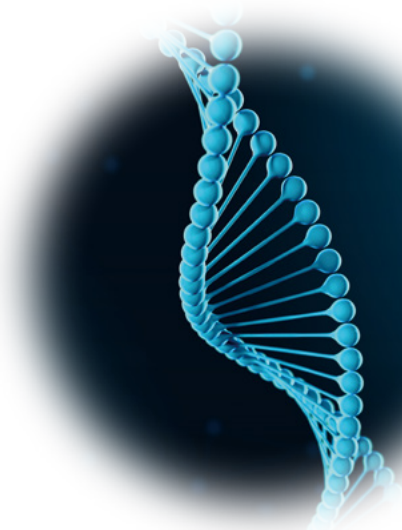


Software for Oligonucleotide Characterization

LabSolutions Insight Biologics

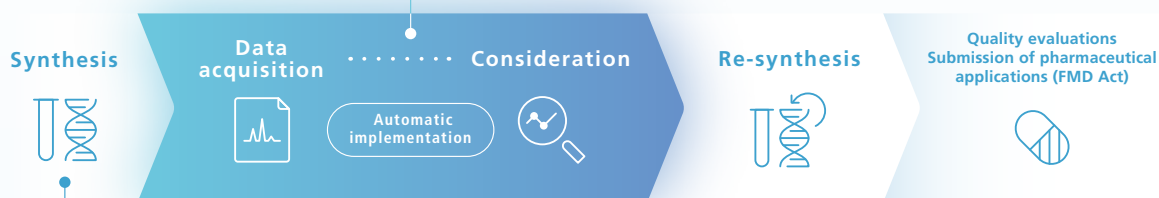
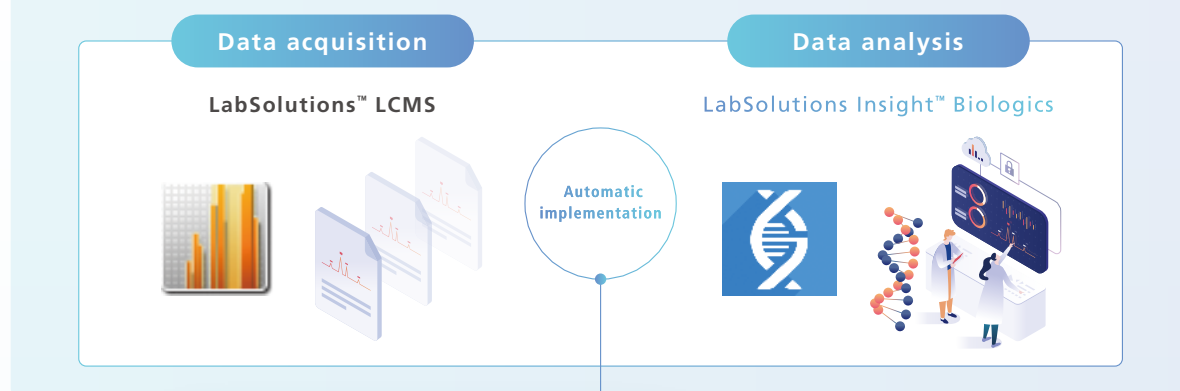


LabSolutions Insight™ Biologics

A Dedicated Workspace for Oligonucleotide Characterization

LabSolutions Insight Biologics is a dedicated software platform for oligonucleotide characterization using the LCMS-9030 or LCMS-9050 quadrupole time-of-flight type (Q-TOF) mass spectrometer. Main product and impurity identification includes several core editors for sequence, nucleotides, linkers, ribose and base modifications. Together with processing and integration for target modifications, Insight Biologics is a comprehensive workspace for data review, processing, and reporting.

Complete workflow from data acquisition to analysis and reporting



Analysis of Synthetic Samples



Insight Biologics provides an easy method to input sequence information, configure target modifications, and set data analysis parameters. Using sequence information, Biologics comprehensively identifies chain length differences, nucleotide gaps, modifications, conversions, adducts, and other impurities. Q-TOF Data Dependent Acquisition (DDA) records MS and MS/MS spectra. MS spectra are used to identify the molecular weights of impurities, and corresponding MS/MS fragment spectra are used to confirm sequences. Visual displays of sequence coverage enhance the confidence of identifications. Seamless processing and reporting with audit trail support make Insight Biologics a comprehensive solution for oligonucleotide characterization.

UX A Superior User Experience

UX 1

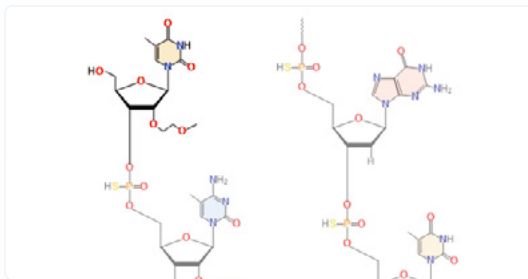
Depiction of the Structural Formula

In the window for setting the oligonucleotide sequences, the structural formula of the sequence that was entered is displayed in real time, enabling quick and easy verification of the information. Also, the nucleobases used in the sequence, as well as the backbone linker, ribose, and base modifications, can be added and edited.

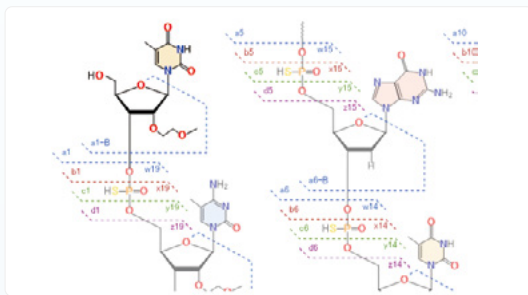
Input oligonucleotide sequences

#	Name	Base	Base Modification	Linker	Ribose	Formula	Mono-isotopic
1	Cd	Cytosine	None	----	Decoy	C ₉ H ₁₁ N ₃ O ₂	193.08513
2	sTd	Thymine	None	Phosphorothioate	Decoy	C ₁₀ H ₁₃ N ₂ O ₆ P S	320.02319
3	sGd	Guanine	None	Phosphorothioate	Decoy	C ₁₀ H ₁₂ N ₅ O ₅ P S	345.02968
4	sCd	Cytosine	None	Phosphorothioate	Decoy	C ₉ H ₁₂ N ₃ O ₅ P S	305.02353
5	sTd	Thymine	None	Phosphorothioate	Decoy	C ₁₀ H ₁₃ N ₂ O ₆ P S	320.02319
6	sAd	Adenine	None	Phosphorothioate	Decoy	C ₁₀ H ₁₂ N ₅ O ₄ P S	329.03476
7	sGd	Guanine	None	Phosphorothioate	Decoy	C ₁₀ H ₁₂ N ₅ O ₅ P S	345.02968

The structural formula of sequences is shown in real time

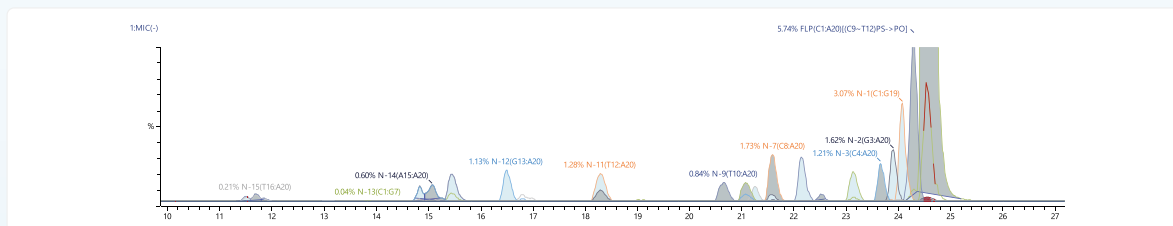


Base modifications can be added and edited



UX 3

Component Chromatogram Display

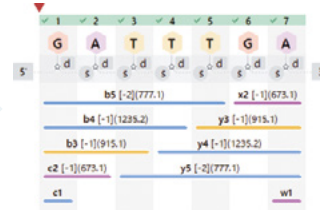


UX 2

Display of Fragment Coverage

The software includes a coverage display which indicates fragment spectral assignments. The coverage display switches to match the items to be checked. Reports can also be output.

Checking ion intensity and coverage

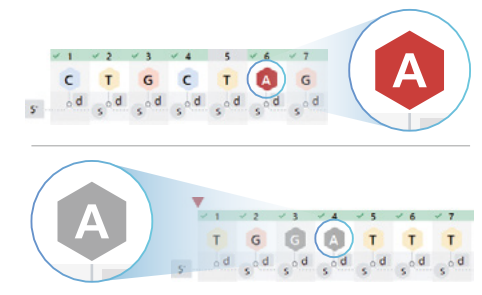


Switchable coverage display

Checking the fragment sequence



Modification positions are also clearly identified



The impurity peaks are displayed as a component chromatogram. The UV and MS chromatograms can be checked simultaneously.

List of Basic Functions

Applications:

Comprehensive identification and quantitative determination of oligonucleotide impurity sequences

- | | |
|---|---|
| <ul style="list-style-type: none"> • Can easily create and import the principal component sequences of oligonucleotides | <ul style="list-style-type: none"> • Three types of reports are available (full, summary, and method) |
| <ul style="list-style-type: none"> • Display of structural formulas for the principal component sequences | <ul style="list-style-type: none"> • Data analysis can be implemented together with a batch analysis using LabSolutions LCMS |
| <ul style="list-style-type: none"> • Selection of target modifications (impurities) and editing of target lists | <ul style="list-style-type: none"> • Audit trail compatibility |
| <ul style="list-style-type: none"> • Display of component chromatogram | <ul style="list-style-type: none"> • Can analyze oligonucleotides 140 bases long |
| <ul style="list-style-type: none"> • Simultaneous display of MS1 spectrum and polyvalent ion data analysis spectrum | <ul style="list-style-type: none"> • Available in Japanese, English, and Chinese |
| <ul style="list-style-type: none"> • The method for calculating the impurity ratio can be selected to suit the objective | |

System Requirements

Operating System

OS	Windows® 10/11
Software	LabSolutions LCMS 5.120 or later

Compatible models

LC	Nexera series such as Nexera XS inert
LC-MS	LCMS-9030, LCMS-9050

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