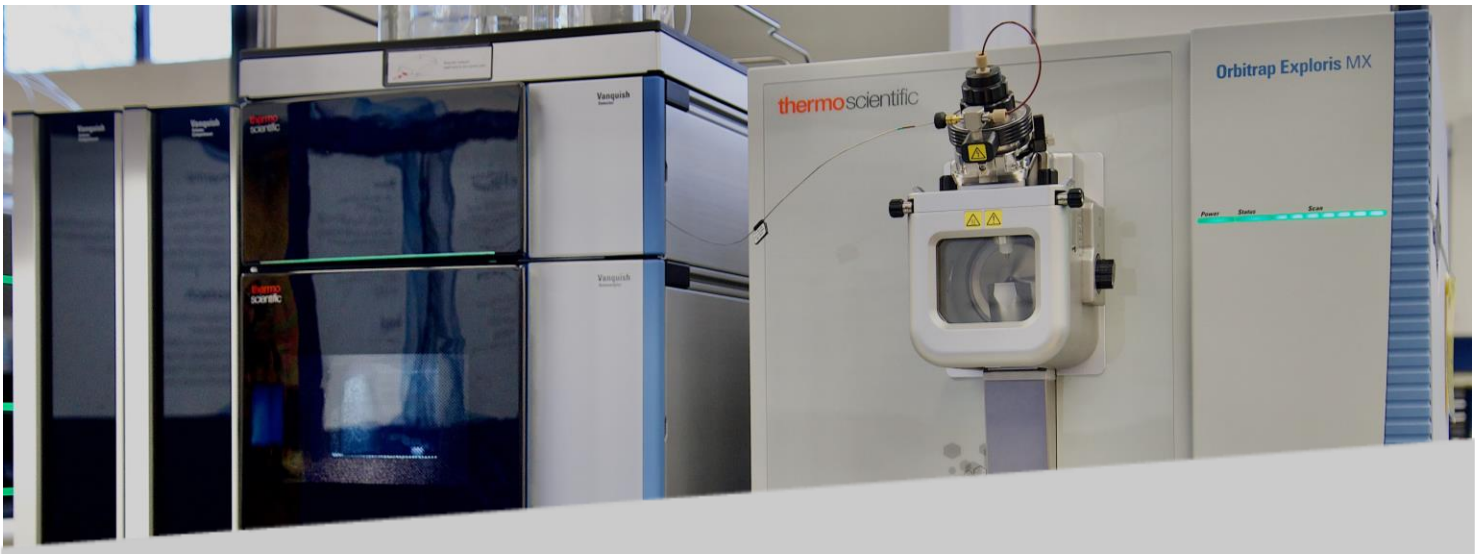
OLIGO HTCS MASS ANALYZER

TOTAL SOLUTION FOR OLIGO MS CHARACTERIZATION



The Oligo HTCS System is the first exclusive LCMS system to automate every aspect of oligonucleotide mass spectral analysis. The HTCS takes care of sample injection, desalting, MS detection, as well as data processing and reporting. With a sample throughput of ~2400 samples/day (~36 seconds per sample), there is not an LCMS system on the planet that can match it.

In addition, the HTCS allows you to characterize long (e.g., >120-mers) or labile oligos that are not amenable to MALDI-TOF. Our ProMass software ties it all together, allowing you to process and communicate your results effortlessly.

Oligo HTCS Orbitrap Exploris MX HRMS with Vanquish UHPLC
**including dual gradient pumps for maximum speed and flexibility!*

FEATURES AND BENEFITS

- ~2400 samples/day throughput
- < 3ppm mass accuracy with 180k resolution
- Analyzes oligos exceeding 120 bases
- Switches automatically from HT mass confirmation to detailed LCMS
- On-line desalting eliminates need for off-line sample processing and improves data quality
- One-click automated data processing with web-based results display
- Confirms target masses and identifies sequence failures and other impurities
- HTML, XML, and Excel results output

OLIGO HTCS SYSTEM INCLUDES

- Thermo Orbitrap Exploris MX
- Thermo Vanquish UHPLC Flex Autosampler
- ProMass HR Deconvolution Software
- Oligo HTCS Methods Package
- Full Installation, Training, 1-Year Warranty, and Application Support

novatia

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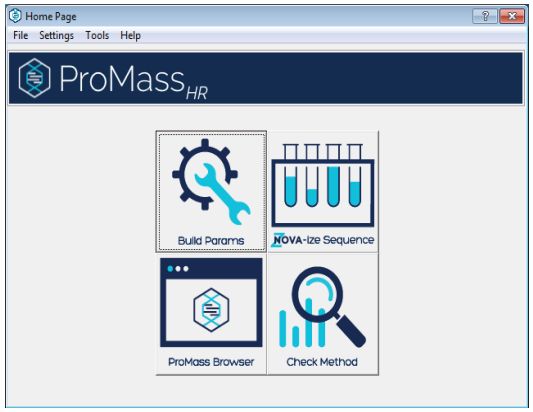
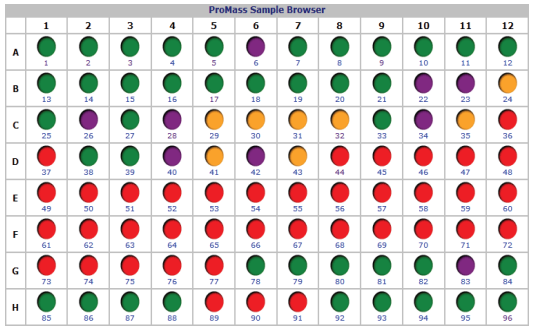


ProMass Deconvolution software completely automates oligonucleotide data processing and reporting.



ProMass sample plate view

OFFERING MORE THAN JUST SPEED

It's true, the Oligo HTCS instrument is the highest throughput LCMS system available for oligonucleotide analysis. The Oligo HTCS Vanquish MX application offers accurate mass accuracy (<3ppm), 180k resolution, and the ability to analyze oligos of virtually any length without compromise. The MX operates in peptide or protein mode. Protein mode utilizes ion accumulation in the multipole to allow the pressure in the storage multipole to be changed to optimize for different applications. Protein mode is enabled from the BioPharma option that has an extended range as well, up to m/z 8000!

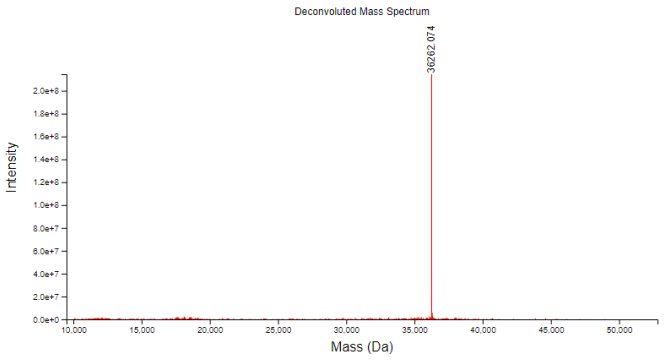
When you need more information than just a molecular weight, the HTCS is ready. Since the HTCS is an LCMS system, it has the flexibility to be operated in either high-throughput or detailed analysis modes. Finally, Novatia has the experience and application knowledge to ensure your success. Since we developed the HTCS system for use in our own contract analysis business, we have a detailed understanding of how the system works and how best to apply the system in your environment.

APPLICATION AREAS AND CAPABILITIES

- Oligonucleotide manufacturing QC
- DNA, RNA, therapeutics, diagnostics
- Detailed LCMS profiling for the identification of impurities, degradants, and metabolites
- Purity determination via LCMS and/or LCUV detection
- HRMS analysis of oligonucleotides with labile chemistries
- HRMS analysis of very long oligonucleotides

[<<]
Data File: D:\Novatia_Install\mass_accuracy2\std120.raw
Acquisition Date: 4/13/2023
Comments: 2.5 uM x 5 uL
Sample Name: 120 mer
Position: 19
Inj Vol: 5
Instrument Method: C:\Xcalibur\methods\oligo_htcs_needle_wash_HR
Processing Method: C:\Xcalibur\methods\oligo_htcs
ProMass Parameters: C:\Program Files\ProMassXcali\ZNova\deiso.PARAMS
Study: Mass Accuracy Specs
Client: ThermoFisher
Nucleotide:
CCA TCC ACT ACA ACT ACA TGT GTA ACA GTT CCT CCA TAT GTT CCT CCT CC
ATC CAC TAC TTG CCA TCC ACT ACA ACT ACA TGT GTA ACA GTT CCT CCA TA
TGT TCC CCA TCC ACT ACA AC
Average Mass (Da): 36279.2992
Monoisotopic Mass (Da): 36262.0122

ProMass



Oligo HTCS analysis of a 120-mer MW: 36262.0122 Da

Target Mass Summary

RT (min)	Target Mass (Da)	Observed Mass (Da)	Mass Error	Intensity	% Abundance (in Spectrum)	%Purity (Estimate)	Identity	Result Code
0.341	36262.0122	36262.074	0.0618 Da (1.7 ppm)	2.14E+008	73.40	95.45	Target Mass	

Chromatogram Summary

RT (min)	Base Peak Mass (Da)	Intensity	Spectral Quality	Base Peak Identity	LC/MS Peak Area	LC/MS Area Percent
0.341	36262.074	2.14E+008	ok	Target Mass: 36262.0122	4.48E+009	100.00

The Oligo HTCS detailed LCMS report confirms the presence of target masses, lists 5' sequence failures and provides a chromatogram summary listing the masses under each chromatographic peak. Chromatogram peak areas and area percentages are also reported. Since the results can be viewed from any web browser, results are easily shared among colleagues and clients.

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