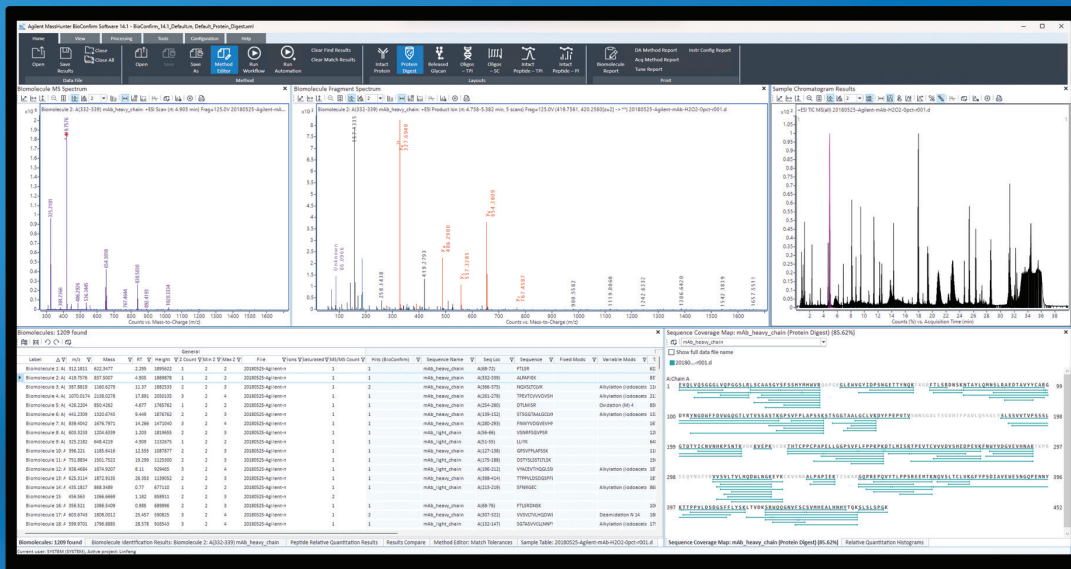


Take a Giant Step Forward in Biomolecule Characterization

Agilent MassHunter BioConfirm software





Confidently Analyze for Major Critical Quality Attributes (CQAs)

Understanding a biologic's critical quality attributes and the processes that affect them is essential to ensuring product quality, safety, and efficacy.

Agilent MassHunter BioConfirm software streamlines the characterization of complex biomolecules through intuitive workflows for therapeutic peptides, oligonucleotides, intact proteins, peptide mapping, and released glycan analysis

Agilent MassHunter BioConfirm
software, part of the complete
Agilent biopharma workflow

Automate sample preparation

AssayMAP Bravo



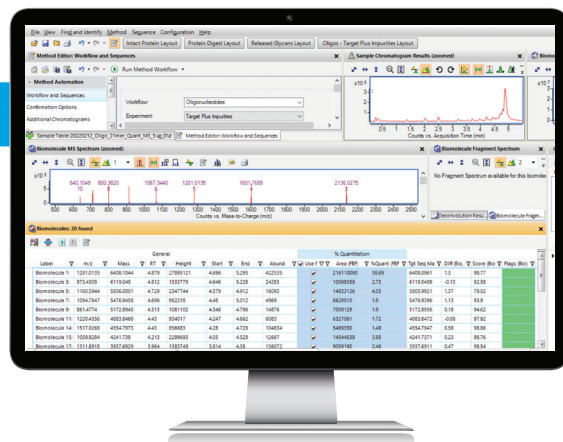
Separate

1290 Infinity II LC



Analyze and report

MassHunter BioConfirm software



Detect

6545XT AdvanceBio LC/Q-TOF



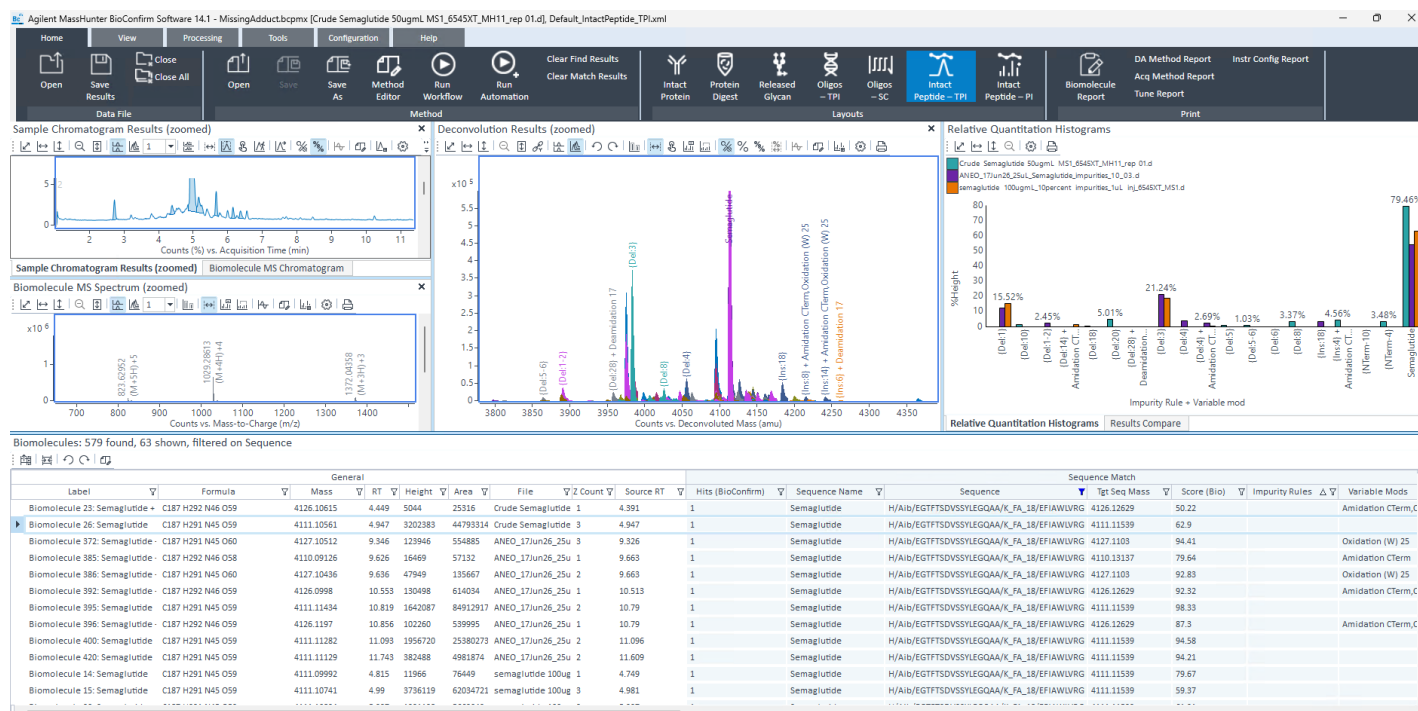
Intact Peptide Characterization

BioConfirm provides two workflows for intact peptide analysis that also support nonnatural amino acids and modified peptides:

Target Plus Impurities (TPI) workflow

Characterizing therapeutic peptides can be challenging, especially when identifying sequence variants, impurities, and modifications. The BioConfirm Target Plus Impurities (TPI) workflow helps scientists rapidly assess peptide identity, purity, and composition through automated analysis and integrated LC/MS quantitation. By simplifying data interpretation and reducing manual review, TPI enables faster development decisions, stronger quality oversight, and greater confidence in results

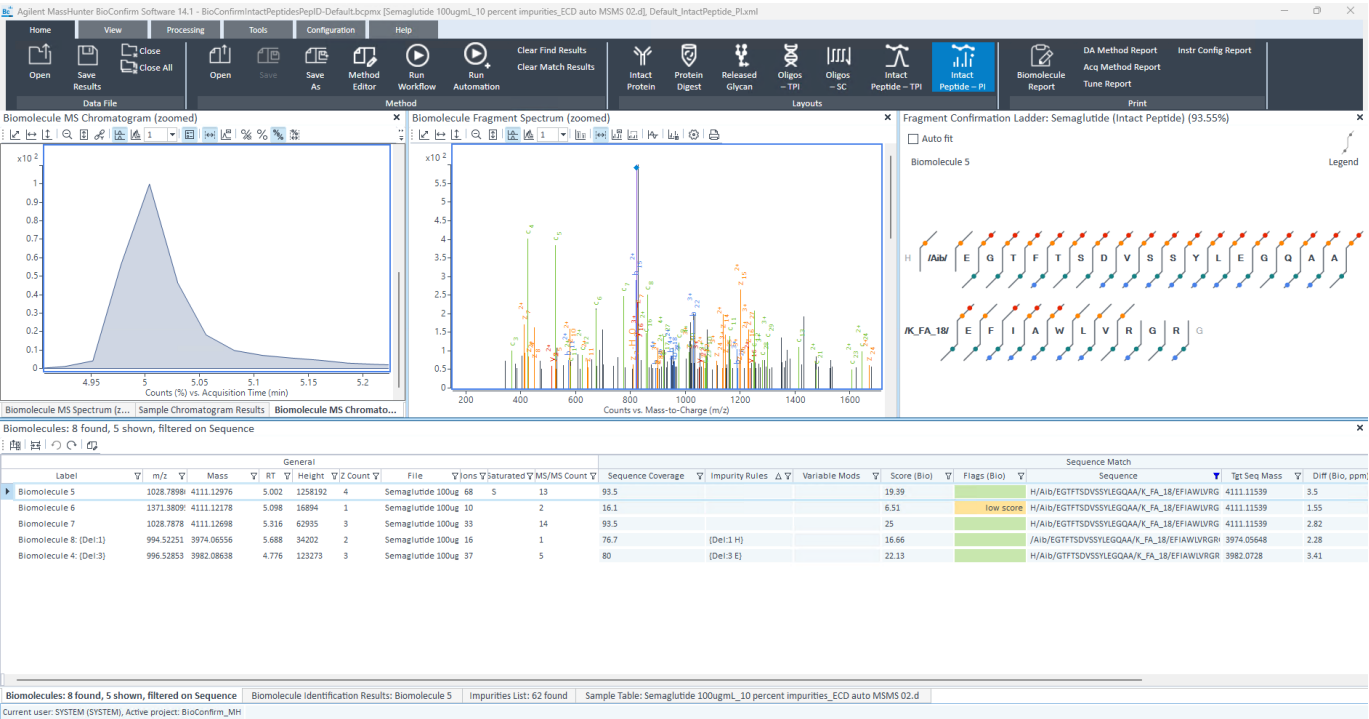
Simplify intact peptide characterization with the BioConfirm Target Plus Impurities (TPI) workflow. Designed for peptide therapeutics such as GLP-1 RAs, TPI automatically identifies sequence variants, truncations, insertions, deletions, and modification-related impurities while providing confident biomolecule identification and purity assessment. Integrated MS- and LC-based quantitation delivers deeper insight into sample composition, and intelligent controls reduce result complexity and improve processing efficiency. By turning complex peptide data into actionable results, TPI helps scientists accelerate development, strengthen quality monitoring, and make faster decisions with confidence.



Peptide Identification (MS/MS) workflow

Gain deeper confidence in peptide characterization with the BioConfirm Peptide Identification (MS/MS) workflow. [AA1.1] Using advanced MS/MS sequencing, the workflow identifies both target peptides and detected impurities, enabling comprehensive characterization in a single analysis. Automated fragment matching, sequence coverage calculations, and visual fragment ladders help scientists rapidly confirm peptide identity, localize modifications, and assess product quality with greater confidence. By combining impurity identification with sequence-level verification, the workflow delivers actionable insights that support peptide development, quality control, and regulatory readiness.[KU2.1]

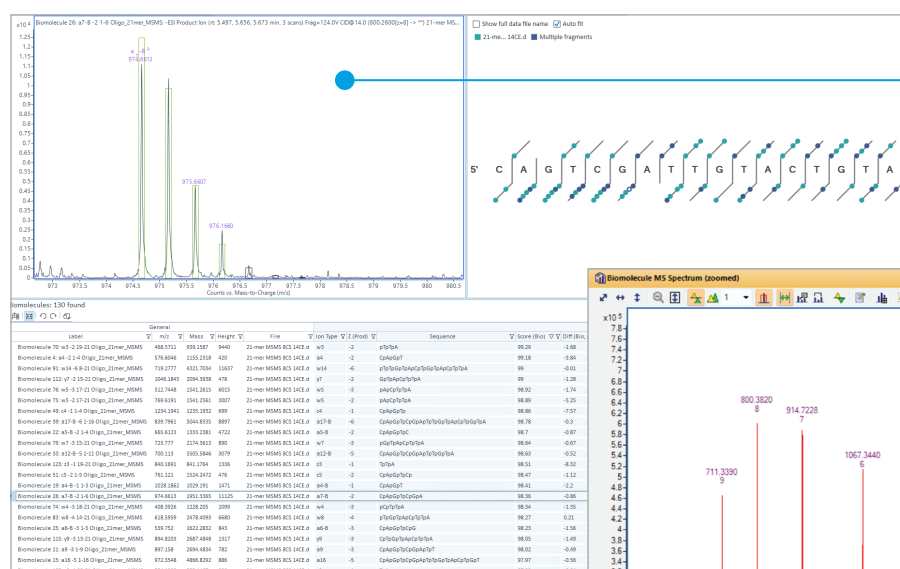
Characterizing therapeutic peptides requires confidence in both sequence identity and impurity assessment. The BioConfirm Peptide Identification (MS/MS) workflow helps scientists rapidly confirm peptide sequences, localize modifications, and identify impurities in a single analysis. Automated data interpretation, sequence coverage analysis, and visual fragment mapping simplify complex results, enabling faster decisions and greater confidence in product quality



Oligonucleotide Characterization: Elevate Your Expectations for Speed and Accuracy

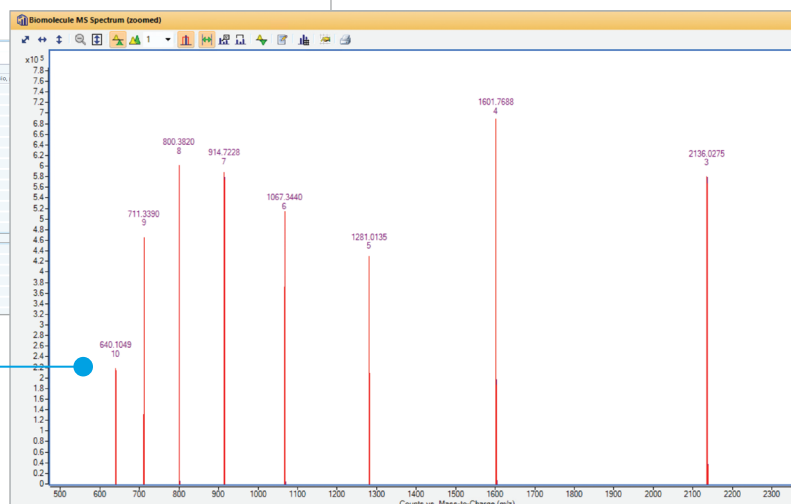


BioConfirm software enables you to rapidly set up two workflows, Target Plus Impurities, and sequence confirmation for oligonucleotide confirmation.



MS spectra

MS spectra show the oligonucleotide biomolecule annotated at each charge state.



Chemical Data Dictionary Editor

Proteins Oligonucleotides

Building Blocks

Linkers

Modifications

Search

Code	Name	Formula	Building Block Type
/BaseA/	Adenine	C5H5N5	Fragment
/BaseC/	Cytosine	C4H5N3O	Fragment
/BaseG/	Guanine	C5H5N5O	Fragment
/BaseT/	Thymine	C5H7N2O2	Fragment
/BaseU/	Uracil	C4H4N2O2	Fragment
/H/	H	H	Fragment
/H2O/	H2O	H2O	Fragment
/MOEtA/	2-Methoxyethoxy A	C13H19N5O5	Nucleoside
/MOEtC/	2-Methoxyethoxy C	C13H21N3O6	Nucleoside
/MOEtG/	2-Methoxyethoxy G	C13H19N5O6	Nucleoside
/MOEtT/	2-Methoxyethoxy T	C13H20N2O7	Nucleoside
/OH/	OH	OH	Fragment
A	Deoxyadenosine	C10H13N5O3	Nucleoside
C	Deoxycytidine	C9H13N3O4	Nucleoside
dA	Deoxyadenosine	C10H13N5O3	Nucleoside
dc	Deoxycytidine	C9H13N3O4	Nucleoside

New building block code

Code: /BaseA/

Name: Adenine

Molecular formula: C5H5N5

Base formula:

The code represents

Chemical Data Dictionary

The Chemical Data Dictionary has been enhanced to enable defining oligonucleotide building blocks, linkers, and modifications the way you want them.

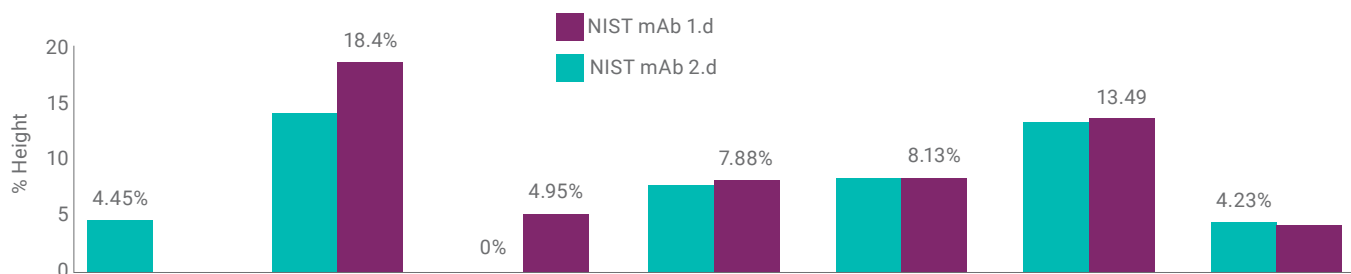
Intact Protein Analysis: Confirm PTMs with Certainty



BioConfirm rapidly deconvolutes your intact protein mass spectrometry data to determine molecular weights and confirm post-translational modifications (PTMs). PTMs like glycoforms can be labeled on the mass spectrum and inspected by their relative quantitative amounts using tables or histogram plots. Also, cysteine disulfide bonds can be either individually specified in the protein sequence or listed in total, speeding up your setup time.

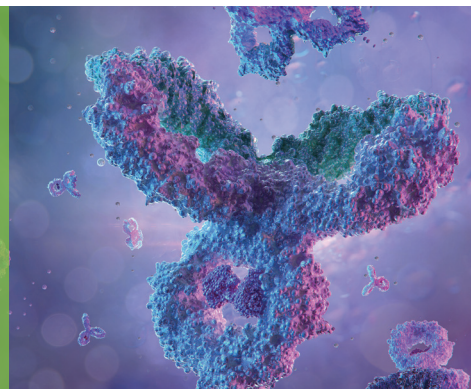
Intact protein analysis in MassHunter BioConfirm also works well with the low-vacuum environment of the Agilent 6545XT AdvanceBio LC/Q-TOF mass spectrometer. It allows more proteins to get through for greater sensitivity.

Predicted modifications



Relative quantitative results of glycoforms are displayed as histogram plots, allowing you to monitor a process.

Peptide Mapping: Be Sure of Your Sequences



The MassHunter BioConfirm peptide mapping algorithm uses MS/MS data to narrow the list of possible peptides—saving you manual inspection time. Results are displayed in a Sequence Coverage Map that allows you to review multiple samples (such as different digest enzymes) at the same time. Histogram plots let you compare multiple PTMs or conditions. In addition, fast disulfide bond mapping can be used to untangle the scrambling of disulfide bonds in a monoclonal antibody.



Sequence Coverage Map

The Sequence Coverage Map makes reviewing multiple samples easy and clearly denotes MS/MS and MS-only evidence of the sequence.

Peptide Relative Quantitation Results

Sequence Name ▾ Location ▾ Variable Mods ▾ %Quant (Vol) ▾ Volume ▾ %Quant (Height) ▴ ▾ Height ▾ F									
mAb_light_chain M4 [A] Oxidation (M) 11.11 4739 2018									
Sequence ▾	Seq Loc ▾	Fixed Mods ▾	Variable Mods ▾	RT ▾	Use for %Quant ▾	Height ▾	Volume ▾		
DIQMTQSPSSLSASV	A(1-24)		Alkylation (iodoacetam	19.404	☐	549267			
DIQMTQSPSSLSASV	A(1-18)			17.029	☒	37931			
DIQMTQSPSSLSASV	A(1-24)		Oxidation (M) 4, Alkylat	16.472	☐	41166			
DIQMTQSPSSLSASV	A(1-24)		Deamidation Q 6, Alkyl	19.544	☐	4041			
DIQMTQSPSSLSASV	A(1-18)		Oxidation (M) 4	12.9	☒	4739			
DIQMTQSPSSLSASV	A(1-24)		Deamidation Q 6, Alkyl	19.827	☐	2190			
DIQMTQSPSSLSA	A(1-13)			19.091	☐	1675			
DIQMTQSPSSLSASV	A(1-24)		Deamidation Q 6, Alkyl	20.154	☐	1971			
DIQMTQSPSSLSASV	A(1-24)		Deamidation Q 3, Alkyl	20.367	☐	1329			

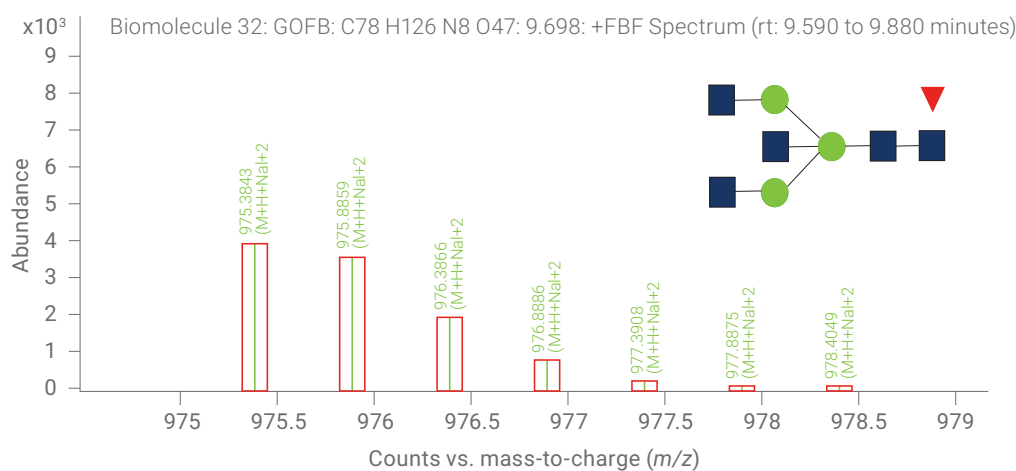
Relative quant results

Perform relative quantitation of modified and unmodified peptides.

Released Glycan Profiling: Improve Sensitivity



Glycans are a challenging PTM to characterize given the diversity in their composition and the need for chemical tagging to ensure analytical sensitivity. BioConfirm released glycans workflow makes setup easy and accommodates many commercial and custom tags. You can also take advantage of a curated glycan database, which can easily be extended with custom glycans using MassHunter software tools. Learn more about N-glycan analysis at www.agilent.com/chem/glycan-sampleprep



The released glycans results include spectra annotated with the glycan structure and theoretical isotope distribution. The Agilent Find-by-Formula algorithm takes advantage of the glycan tendency to ionize with multiple adducts, resulting in finding species, such as M+H+Na, and giving greater specificity.

Reports done easily—your way

The PDF report builder makes it simple to create reports in your preferred layout. Templates for all workflows are provided and can be modified to highlight the information that is important to you.



Create PDF reports quickly

Add your company logo

Place tables, chromatograms, and spectra exactly where you want them

Compliance-ready features keep you in control

With advanced security capabilities and built-in technical controls, the BioConfirm Networked Workstation minimizes security risks while helping to preserve data integrity.

MANAGEMENT

Create Role

Edit Role

Delete Role

Roles

Administration <<

My Settings

Local Configuration

System Configuration

Security Policy

Users

Groups

Roles

System Activity Log

Licenses

Instrument Controllers

Diagnostics

Content Management

Administrative Reports

Roles - Control Panel

Name	Description
Everything	All privileges
System Administrator	Manage users and security settings
Instrument Administrator	Manage instruments and locations
Project Administrator	Manage projects and project groups
Instrument User	View and run instruments
Archivist	Archive and Dearchive
Content Management PDF Template Manager	View, Create, Update
Content Management Reader	View and Read content
Content Management Approver	View, Read, Add, Modify
Content Management Contributor	View, Read, Add, and Modify
Lab Manager	Lab Manager Role for MassHunter
Scientist	Scientist Role for MassHunter
Analyst	Analyst Role for MassHunter
Operator	Operator Role for MassHunter
Reviewer	Reviewer Role for MassHunter

Analyst

Analyst Role for MassHunter Workstation

View project or project group	Shared Services
Edit content of project	Shared Services
Access content using web client	
Annotate	MassHunter BioConfirm
Assign charge state	MassHunter BioConfirm
Assign time range(s)	MassHunter BioConfirm
Audit trail copy to Clipboard	MassHunter BioConfirm
Calculate signal-to-noise	MassHunter BioConfirm
Clear match results	MassHunter BioConfirm
Copy to Clipboard	MassHunter BioConfirm
Create biomolecule	MassHunter BioConfirm

Control Panel

The Control Panel allows you to set up roles and permissions to comply with regulatory guidance, such as 21 CFR Part 11 and Annex 11.

Audit trails

Audit trails make reviewing easy by highlighting entries that require review. Tamper detection is automatically included using checksums.

From 10/14/2025 To 10/15/2025

Find

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Name	Date	Description	Category	Reason	Host Name	Software Name	SW Version	Reviewer	Review Date	Review Comment	File Version
admin (admin)	2025-10-15-11:50:23+05:30	Completed Worklist sample run.	Acquisition	Sample Run	V-MHW11-02	Agilent MassHunter Workstation Acquisition (TOF/Q-TOF) 12.3.2	12.3.2.0				2025-1015-0619-
admin (admin)	2025-10-15-11:50:23+05:30	Completed Data Analysis for data file.	Acquisition	Sample Run	V-MHW11-02	Agilent MassHunter Workstation Acquisition (TOF/Q-TOF) 12.3.2	12.3.2.0				2025-1015-0619-
admin (admin)	2025-10-15-11:50:23+05:30	Running Data Analysis for data file.	Acquisition	Sample Run	V-MHW11-02	Agilent MassHunter Workstation Acquisition (TOF/Q-TOF) 12.3.2	12.3.2.0				2025-1015-0619-
admin (admin)	2025-10-15-11:50:23+05:30	Sample inserted with sample name '0001' and data file 'Synch1-WorklistData-0001-0001.d'	Acquisition	Sample DA Run	V-MHW11-02	Agilent MassHunter Workstation Acquisition (TOF/Q-TOF) 12.3.2	12.3.2.0				2025-1015-0619-
admin (admin)	2025-10-15-11:50:23+05:30	Completed Intelligent Reflex check for data file.	Acquisition	Sample DA Run	V-MHW11-02	Agilent MassHunter Workstation Acquisition (TOF/Q-TOF) 12.3.2	12.3.2.0				2025-1015-0619-
admin (admin)	2025-10-15-11:50:22+05:30	MS-Q-TOF returned fail for 'Iterative MS/MS' workflow check for data file.	Acquisition	Sample DA Run	V-MHW11-02	Agilent MassHunter Workstation Acquisition (TOF/Q-TOF) 12.3.2	12.3.2.0				2025-1015-0619-
admin (admin)	2025-10-15-11:50:22+05:30	Started Intelligent Reflex check for data file.	Acquisition	Sample DA Run	V-MHW11-02	Agilent MassHunter Workstation Acquisition (TOF/Q-TOF) 12.3.2	12.3.2.0				2025-1015-0619-
admin (admin)	2025-10-15-11:50:22+05:30	Completed acquisition for data file.	Acquisition	Sample Run	V-MHW11-02	Agilent MassHunter Workstation Acquisition (TOF/Q-TOF) 12.3.2	12.3.2.0				2025-1015-0619-
admin (admin)	2025-10-15-11:49:02+05:30	Override Parameters : MS/MS : MS/MS is overridden.	Acquisition	Sample Run	V-MHW11-02	Agilent MassHunter Workstation Acquisition (TOF/Q-TOF) 12.3.2	12.3.2.0				2025-1015-0619-
admin (admin)	2025-10-15-11:49:02+05:30	Datafile Information Datafile name : Synch1-WorklistData-0001.d (Version: NA) Datafile path : C:\Projects\Project-Q1\data Submitter : admin (admin)									
admin (admin)	2025-10-15-11:49:02+05:30	Sample name : Instrument name : V-MHW11-02 Method : C:\Projects\Project-Q1\Methods\IterativeMSMS.m (Version: NA) DA method : <Not specified>	Acquisition	Sample Run	V-MHW11-02	Agilent MassHunter Workstation Acquisition (TOF/Q-TOF) 12.3.2	12.3.2.0				2025-1015-0619-
admin (admin)	2025-10-15-11:49:02+05:30	Started acquisition for data file.	Acquisition	Sample Run	V-MHW11-02	Agilent MassHunter Workstation Acquisition (TOF/Q-TOF) 12.3.2	12.3.2.0				2025-1015-0619-
admin (admin)	2025-10-15-11:49:02+05:30	Started Worklist sample run.	Acquisition	Sample Run	V-MHW11-02	Agilent MassHunter Workstation Acquisition (TOF/Q-TOF) 12.3.2	12.3.2.0				2025-1015-0619-

Review



Which version of BioConfirm software should I choose?

MassHunter BioConfirm software is part of the Agilent biopharma workflow, spanning from sample preparation to separation and detection through data analysis and reporting. This chart will help you find the version of BioConfirm biopharmaceutical software for LC/Q-TOF that is best for your lab.

	Workstation	Networked Workstation
Software and license	•	•
Oligonucleotide workflow	•	•
Intact protein workflow	•	•
Protein digest workflow	•	•
Released glycans workflow	•	•
Access control	○	•
Audit trails	○	•
Recommended for GxP labs		•
Server-based content management		•
Single point access to data from multiple sources		•

○ = Optional feature

Supporting your success

CrossLab is an Agilent capability that integrates services and consumables to support workflow success, improve productivity, and enhance operational efficiency. Through CrossLab, Agilent strives to provide insight in every interaction to help you optimize the return you get on your instrument investment and achieve your business goals. Agilent CrossLab supports Agilent instruments and select non-Agilent instruments as well. We also provide consultative support for workflow enablement, lab analytics, regulatory compliance, inventory management, and asset management, including relocation services.

Learn more about CrossLab at www.agilent.com/crosslab



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