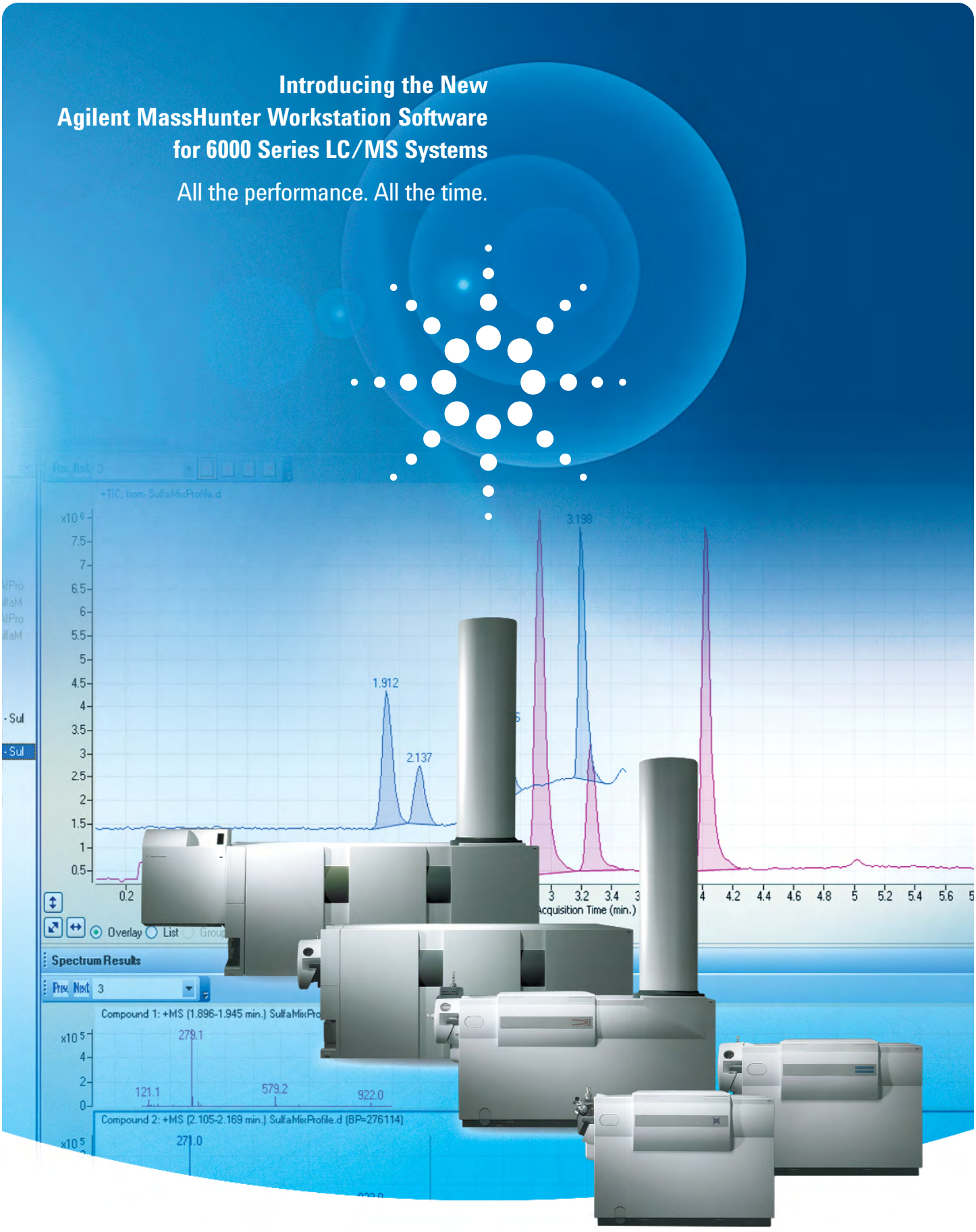
Introducing the New Agilent MassHunter Workstation Software for 6000 Series LC/MS Systems

All the performance. All the time.



Agilent Technologies

Control. Acquire. Analyze. Agilent MassHunter Workstation Software.

The all new Agilent MassHunter Workstation software provides intuitive, yet powerful, instrument control, data acquisition, and qualitative and quantitative data analysis for your Agilent 6410 Triple Quadrupole and 6510 Q-TOF LC/MS systems. It can be complemented by new application-specific MassHunter software packages that provide even more power and streamlined operation for specialized analytical tasks.

Easier method set-up and instrument control

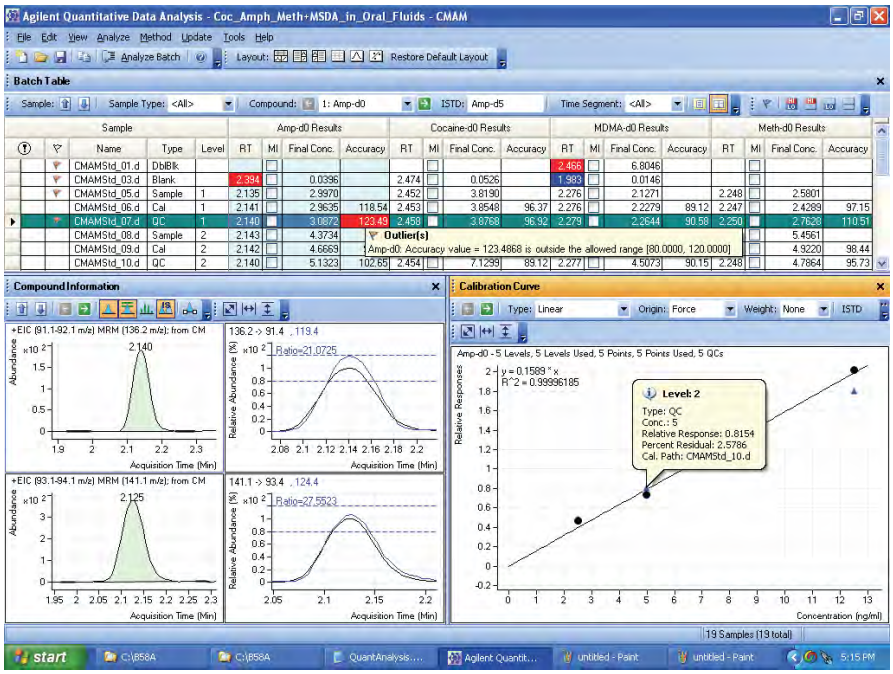
The MassHunter Workstation software makes instrument operation and method development as easy as possible. Fast, reliable automated tuning, a rarity in both triple quadrupoles and Q-TOFs, maximizes instrument performance without complicated manual adjustments. Creation of long worklists can be simplified by importing information from a CSV file. And you can adjust the real-time data monitoring to suit your needs and interests.

Better qualitative analysis

The MassHunter Workstation software's qualitative analysis tools allow you to immediately focus on the important aspects of data when reviewing chromatographic and mass spectral results. Advanced algorithms help you find all compounds, or "molecular features", in a chromatographic run, not just the peaks.

More powerful quantitative analysis

Application-centric quantitation in the MassHunter Workstation software ensures that you spend less time analyzing your data. It includes helpful features such as a curve-fit assistant, dynamically linked results, outlier flagging, batch-at-a-glance data review, and customizable views.



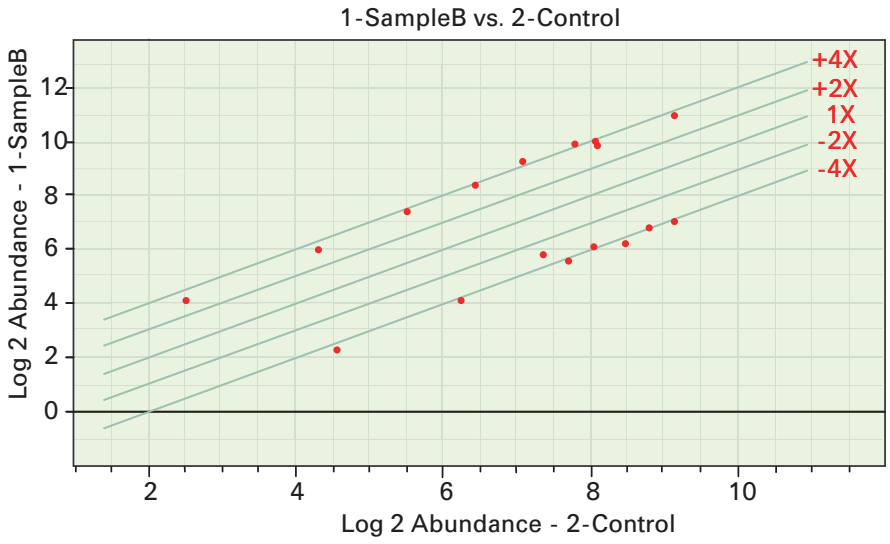
The MassHunter Workstation quantitative analysis software allows batch-at-a-glance data review, and includes effort-saving features like parameterless integration and a curve-fit assistant.

Customizable reports

Presenting critical information from your MS experiments allows you to make important scientific or business decisions. With the flexibility to fully customize reports, the MassHunter Workstation software also offers Microsoft® Excel capability for custom calculations and reporting while providing access to all system parameters through XML data interchange format.

Discover differentially expressed features with MassHunter Profiling software

For challenging expression profiling and biomarker discovery applications, the MassHunter Workstation software first simplifies a complex data set of accurate mass MS results with intelligent feature identification algorithms. Once relevant molecular features are identified, the MassHunter Profiling software employs a variety of statistical methods and visualization tools to allow the identification of meaningful differences between sample groups (e.g., healthy versus diseased). In addition, the profiling software calculates ratios of abundances of differentially expressed features, and allows flexible selection of the comparison criteria and inspection of any selected feature.



Log2-Log2 abundance plot from MassHunter Profiling software makes it easy to identify features that are differentially expressed (up and down) between samples.

Use Spectrum Mill software for protein identification and quantitation

Spectrum Mill for MassHunter Workstation quickly identifies proteins and peptides via fast database searches, and provides automatic and manual match validation. The Spectrum Mill software also offers *de novo* spectral interpretation for peptides not found in any database. Proteins of interest can be quantified by comparing relative abundances of all component peptides observed for a given protein, revealing twofold or higher changes in relative abundance without the need for labeling. When preferred, Spectrum Mill software supports stable- isotope-based and other labeling strategies.

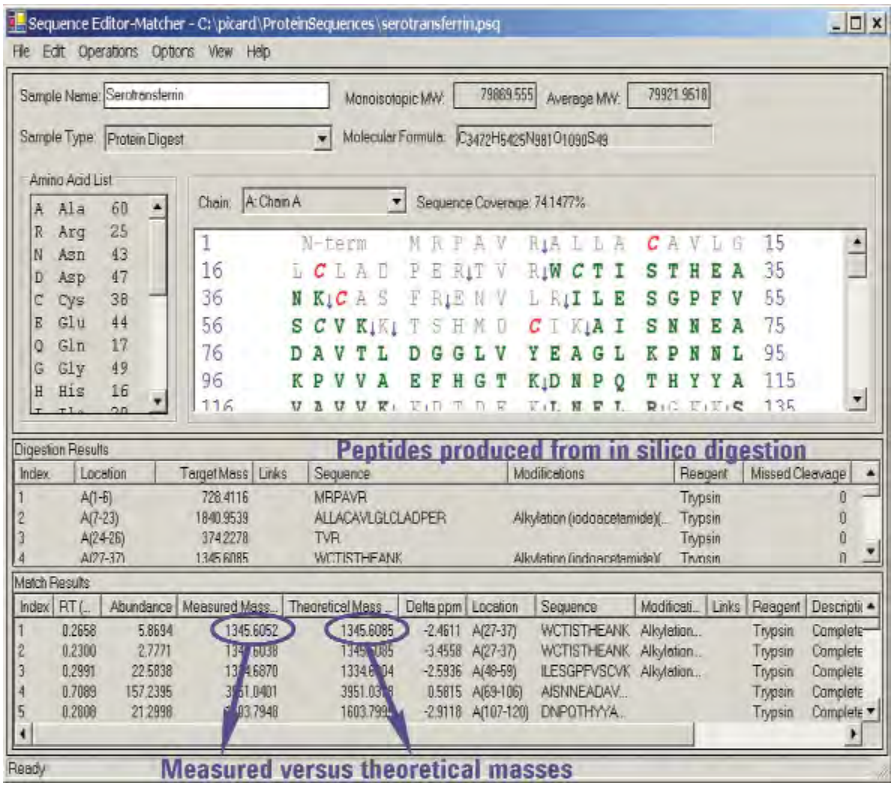
E_51_Br38 # spectra intensity	E_59_Br26 # spectra intensity	E_63_Br35 # spectra intensity	E_67_Br42 # spectra intensity	E_70_Br43 # spectra intensity	N_52_Br29 # spectra intensity	N_54_Br28 # spectra intensity	N_58_Br34 # spectra intensity	N_65_Br36 # spectra intensity	N_66_Br39 # spectra intensity	Protein Name
58 4.92e+008	23 2.69e+008	99 8.42e+008	20 1.69e+008	39 4.87e+008	11 1.81e+008	20 3.25e+008	0 0.00e+000	2 3.83e+007	1 3.40e+007	CALGRANULIN A (MIGRATION INHIBIT
0 0.00e+000	42 6.39e+008	23 2.48e+008	136 1.31e+009	25 4.38e+008	21 1.80e+008	0 0.00e+000	0 0.00e+000	4 4.19e+007	12 7.89e+007	C-REACTIVE PROTEIN PRECURSOR
8 6.26e+008	9 3.16e+008	31 7.34e+008	4 1.09e+008	6 6.34e+008	0 0.00e+000	0 0.00e+000	0 0.00e+000	1 4.01e+007	0 0.00e+000	RHO GDP-DISSOCIATION INHIBITOR 2
44 5.22e+008	35 1.17e+009	48 3.76e+008	18 1.06e+009	6 4.18e+008	6 1.96e+008	18 2.43e+008	4 7.43e+008	11 7.22e+007	6 2.03e+008	PROFILIN I
9 2.25e+008	104 6.83e+008	45 3.25e+008	22 5.05e+008	0 0.00e+000	2 3.72e+007	24 1.43e+008	110 1.83e+008	0 0.00e+000	37 3.76e+008	HEMOGLOBIN ALPHA CHAIN
24 7.04e+008	18 5.22e+008	14 5.01e+008	22 1.11e+009	12 1.08e+008	75 9.28e+008	10 2.72e+008	23 3.81e+009	129 3.19e+008	34 1.47e+009	IMMUNOGLOBULIN J CHAIN
3 7.96e+008	0 0.00e+000	3 4.50e+008	0 0.00e+000	4 7.64e+008	21 8.45e+008	13 2.63e+008	9 1.48e+008	58 5.02e+008	4 1.22e+009	APOLIPOPROTEIN D PRECURSOR
5 1.74e+008	4 4.37e+008	6 2.54e+008	9 1.54e+009	9 1.51e+008	12 8.55e+008	5 1.66e+007	6 6.44e+008	5 5.58e+007	0 0.00e+000	inter-alpha-trypsin inhibitor family heavy
3 5.80e+007	4 8.31e+008	14 3.73e+008	3 4.56e+008	0 0.00e+000	0 0.00e+000	1 2.76e+007	0 0.00e+000	1 6.04e+007	1 4.81e+008	14-3-3 PROTEIN BETA/ALPHA (PROTEIN
0 0.00e+000	12 1.16e+008	10 1.38e+008	14 2.50e+008	6 1.09e+008	0 0.00e+000	0 0.00e+000	0 0.00e+000	0 0.00e+000	0 0.00e+000	Ig G1 H Nie
0 0.00e+000	10 4.64e+008	21 4.46e+008	0 0.00e+000	0 0.00e+000	0 0.00e+000	0 0.00e+000	0 0.00e+000	0 0.00e+000	0 0.00e+000	OSTEOPONTIN PRECURSOR (BONE SI
3 5.42e+008	4 1.03e+009	18 5.30e+008	0 0.00e+000	3 7.20e+008	0 0.00e+000	0 0.00e+000	0 0.00e+000	0 0.00e+000	0 0.00e+000	TRIOSEPHOSPHATE ISOMERASE (TIM)

Spectrum Mill for MassHunter Workstation can accurately determine not only protein identities, but relative abundances of a given protein in multiple samples. Color coding makes relative abundances apparent at a glance.

Positively confirm peptide and protein identities with MassHunter Bioconfirmation software

Agilent MassHunter Bioconfirmation software is ideally suited for recombinant protein expression and process development, known-protein characterization, or synthetic peptide confirmation. Our bioconfirmination software will help you confirm identities and identify variants before you start expensive testing.

The biocomfirmation software program employs sophisticated algorithmic tools for truly automated, unattended or interactive confirmation and characterization of recombinant proteins or synthetic peptides. The result is accurate determination of the mass and abundance of each peptide.



When analysis of recombinant proteins indicates that the wrong protein was produced, the interactive Sequence Editor/Matcher in the Bioconfirmation software helps locate the site of the modification.

For more information

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