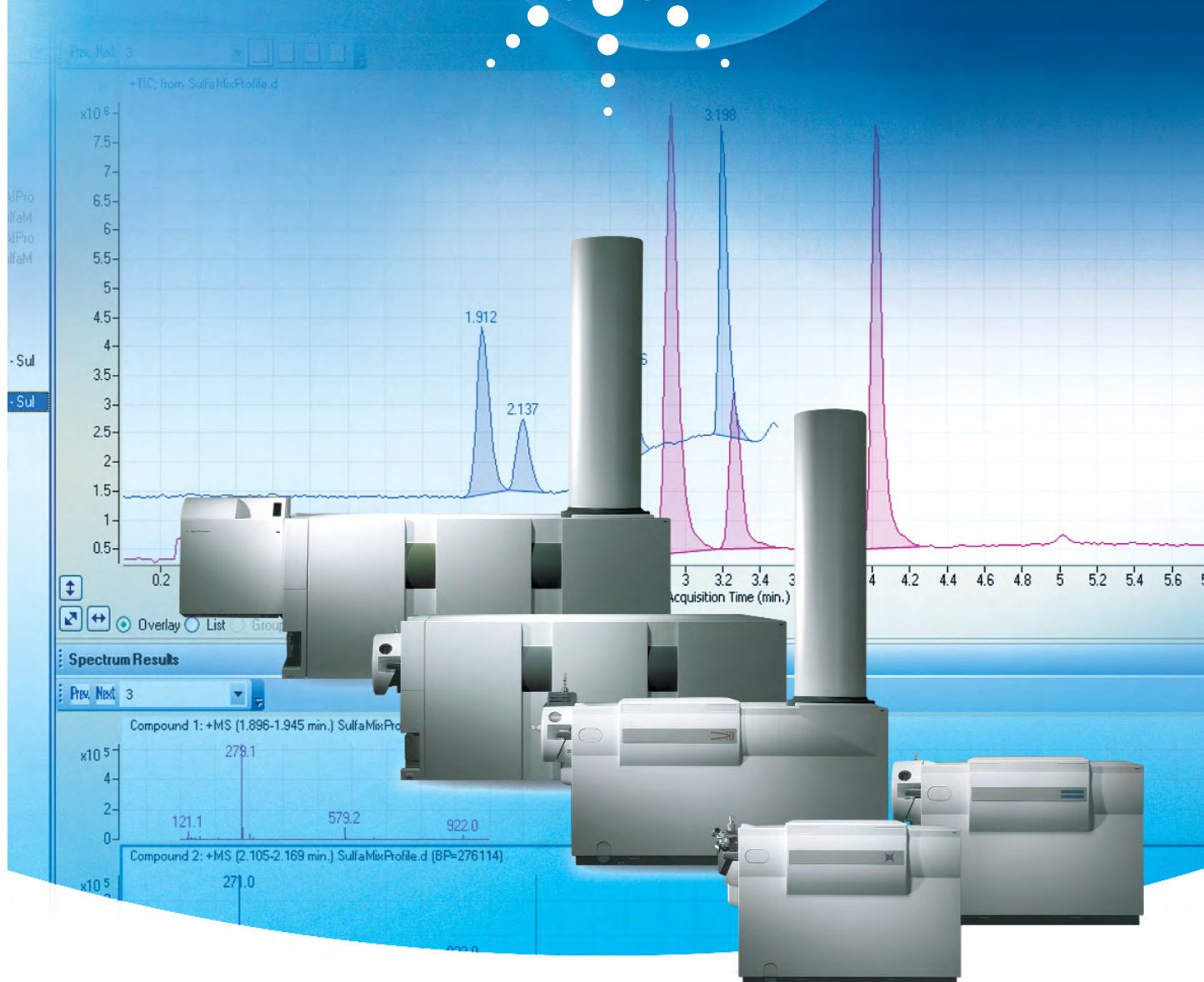


**Introducing the New  
Agilent MassHunter Workstation Software  
for 6000 Series LC/MS Systems**

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

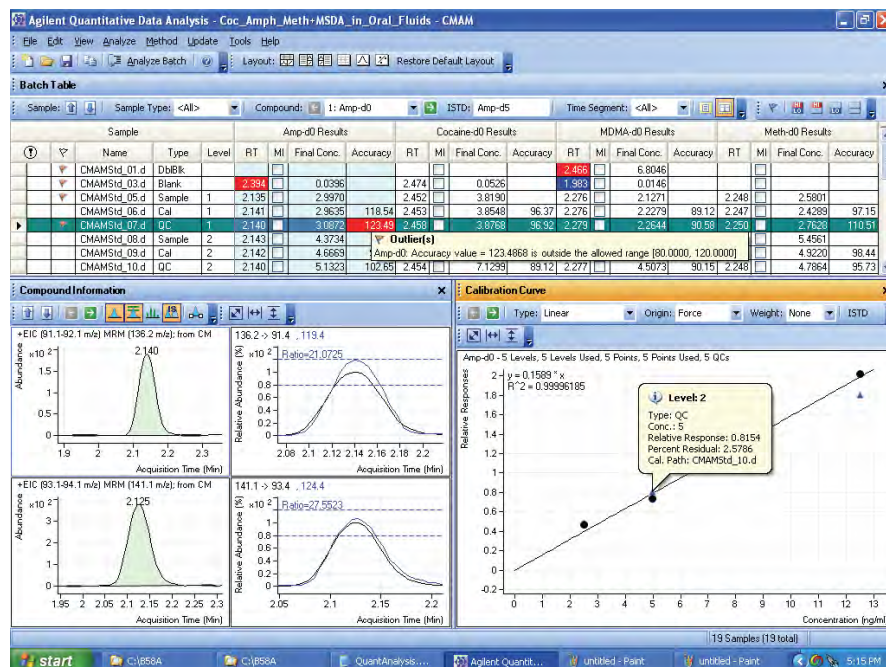
The MassHunter Workstation software makes instrument operation and method development as easy as possible. Fast, reliable automated tuning, a rarity in both triple quadrupoles and Q-TOFs, maximizes instrument performance without complicated manual adjustments. Creation of long worklists can be simplified 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.



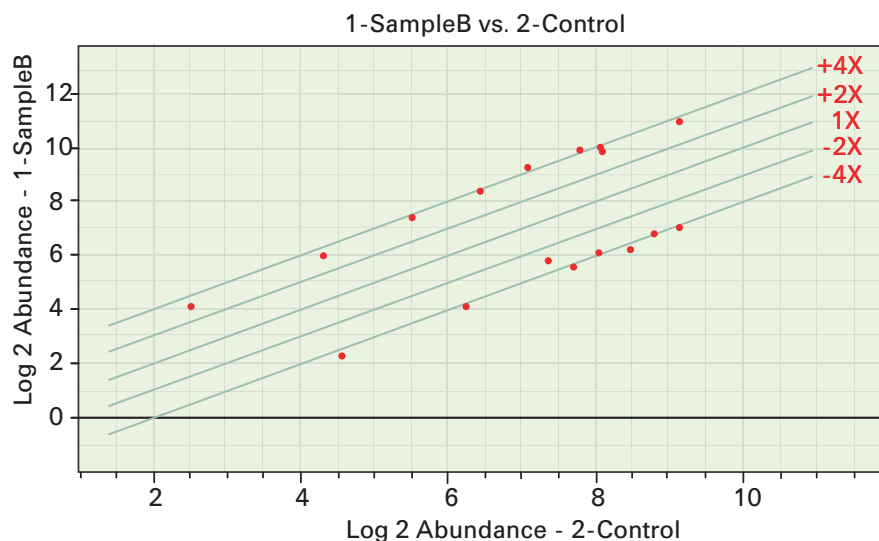
The MassHunter Workstation quantitative analysis software allows batch-at-a-glance data review, and includes effort-saving features like parameterless integration and a curve-fit assistant.

### 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.

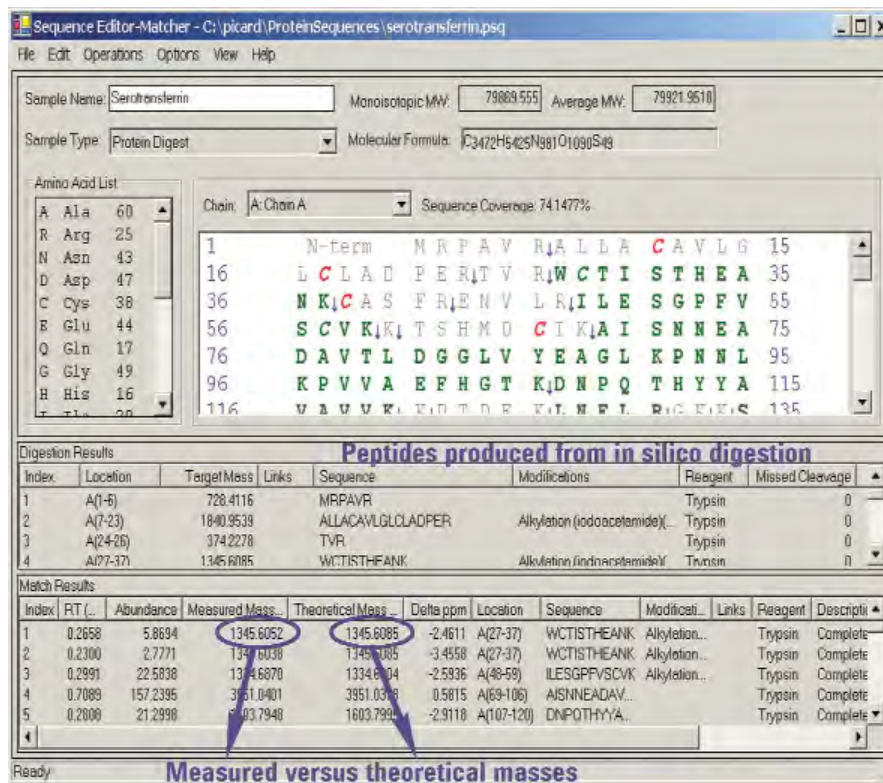
E_51_Br38 # spectra intensity	E_59_Br26 # spectra intensity	E_63_Br35 # spectra intensity	E_67_Br42 # spectra intensity	E_70_Br43 # spectra intensity	N_52_Br29 # spectra intensity	N_54_Br28 # spectra intensity	N_58_Br34 # spectra intensity	N_65_Br36 # spectra intensity	N_66_Br33 # spectra intensity	Protein Name
56 4.92e+003	28 2.69e+003	96 3.42e+003	20 1.89e+003	38 4.37e+003	11 1.81e+003	20 9.25e+002	0 0.00e+000	2 3.88e+007	1 3.40e+007	CALGRANULIN A(MIGRATION INHIBIT
0 0.00e+000	42 6.39e+003	23 2.45e+003	198 1.31e+003	25 4.39e+003	21 1.80e+003	0 0.00e+000	0 0.00e+000	4 4.19e+007	12 7.89e+007	C-REACTIVE PROTEIN PRECURSOR
8 1.21e+003	3 1.11e+003	31 3.36e+003	4 1.09e+003	6 6.34e+003	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+003	35 1.17e+003	40 3.76e+003	10 1.06e+003	6 4.16e+003	6 1.96e+003	19 2.43e+003	4 7.47e+002	11 7.22e+007	6 2.03e+003	PROFILIN I
9 2.25e+003	104 6.88e+003	45 3.25e+003	22 3.05e+003	0 0.00e+000	2 3.72e+007	24 1.43e+003	110 1.33e+003	0 0.00e+000	57 3.70e+003	HEMOGLOBIN ALPHA CHAIN
24 7.04e+003	15 3.22e+003	14 3.01e+003	28 1.11e+003	12 1.03e+003	75 2.28e+003	10 7.72e+002	73 3.31e+003	123 3.19e+003	54 1.47e+003	IMMUNOGLOBULIN J CHAIN
3 7.36e+003	0 0.00e+000	3 4.50e+003	0 0.00e+000	4 7.64e+003	21 6.45e+003	13 2.69e+003	9 1.49e+003	56 3.02e+003	4 1.22e+003	APOLIPOPROTEIN D PRECURSOR
5 1.74e+003	4 4.37e+003	6 2.54e+003	9 1.34e+003	3 1.51e+003	12 8.35e+003	5 1.66e+007	6 6.44e+003	5 5.58e+007	0 0.00e+000	Inter-alpha-trypsin inhibitor family heavy
3 5.80e+007	4 6.31e+003	14 3.73e+003	3 4.56e+003	0 0.00e+000	0 0.00e+000	1 2.76e+007	0 0.00e+000	1 6.04e+007	1 4.31e+003	14-3-3 PROTEIN BETA/ALPHA(PROTEI
0 0.00e+000	12 1.16e+003	10 1.39e+003	14 2.50e+003	5 1.03e+003	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+003	21 4.86e+003	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	OSTEOPOINTIN PRECURSOR (BONE SI
3 5.32e+003	4 1.03e+003	13 3.30e+003	0 0.00e+000	3 7.20e+003	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 bioconfirmation software will help you confirm identities and identify variants before you start expensive testing.

The bioconfirmation 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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