Agilent MassHunter BioConfirm Software

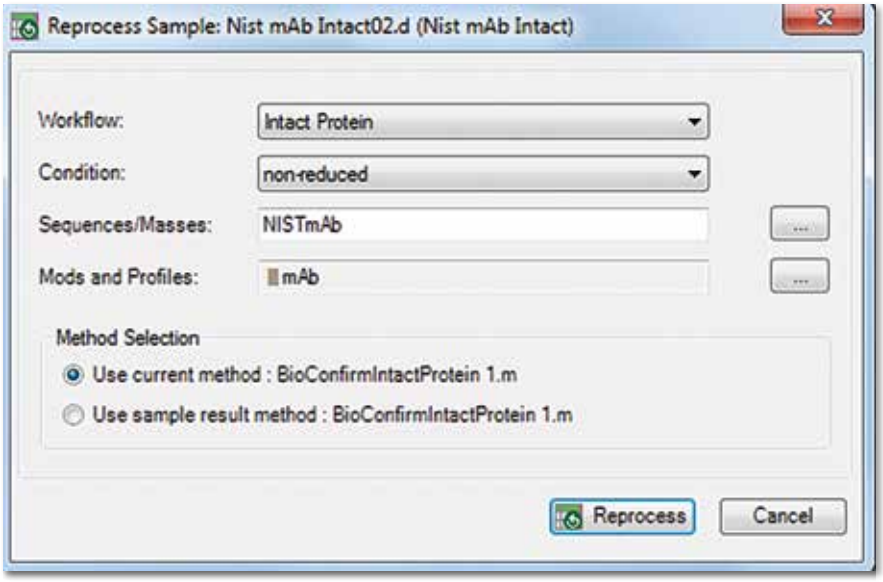
NEW FRONTIERS IN THE CHARACTERIZATION OF BIOMOLECULES

Agilent Technologies

NEW WORKFLOWS FOR INTACT PROTEINS AND PROTEIN DIGESTS

Biopharmaceutical discovery and development labs demand speed and accuracy for the analysis of new biological entities like monoclonal antibodies. Agilent's enhanced BioConfirm software ramps up lab productivity with a new user interface that satisfies the needs of both lab administrators and their biologist users. Analyses for intact proteins and protein digests can be set up quickly with few parameters; changes to methods can be restricted to authorized expert users.

Answer 4 questions about your sample:



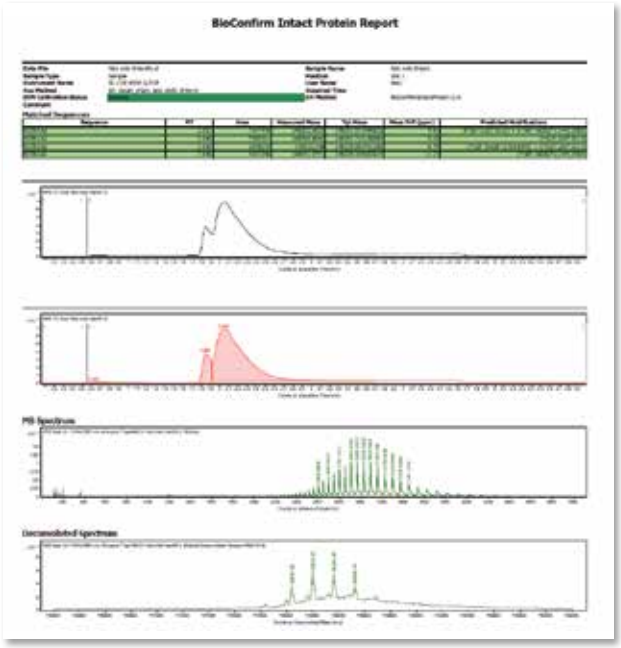
BioConfirm Software delivers:

- Workflow-based views of your data
- One-click focuses on the specific chromatograms and spectra
- Fast review of results

FAST REVIEW OF RESULTS MEANS PRODUCTIVITY

MassHunter BioConfirm allows you to set up a method and execute a workflow—for intact protein, protein digest, or a custom workflow. One click will run your analysis and present your results in a table with color-coded Confirmation Status.

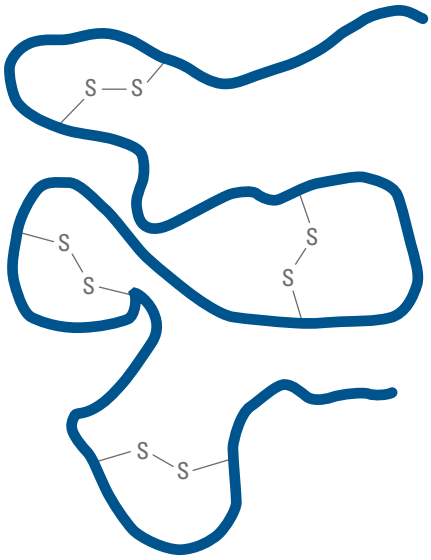
Results	Workflow				
Confirmation Status	Workflow	Condition	Sequence / Mass	Modification	Enzyme
Confirmed	Intact Protein	reduced	NISTmAb	III mAb	
Confirmed	Intact Protein	non-reduced	NISTmAb	III mAb	
Not confirmed	Protein Digest	non-reduced	NISTmAb	III mAb	Trypsin

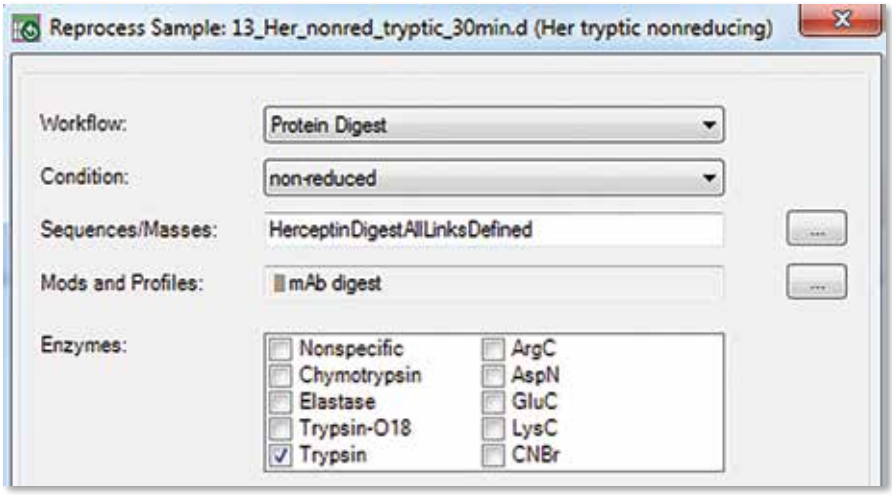


Reports can be automatically generated containing information that speaks the biologist's language. You don't have to be mass spec trained to get fast and accurate results from BioConfirm!

NEW WORKFLOWS FOR DISULFIDE BOND MAPPING AND SCRAMBLING

Cysteine disulfide bonds assist in maintaining the structure of proteins. However, incorrect disulfide linkages can generate protein misfolding. Sources of incorrect linkages may occur during production in the host cell or sample preparation. During the development of new biopharmaceuticals it is important to identify the location of disulfide bonds and confirm that they are correct.



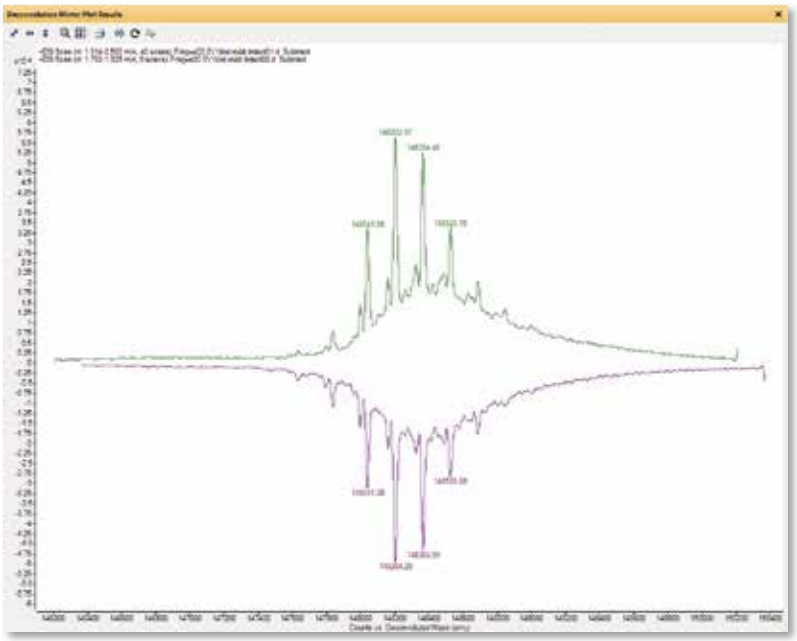


Scrambling occurs when the bonds break and then reattach in new, non-native positions. The enhanced BioConfirm software now has workflows for both disulfide bond mapping of defined linkages and scrambled linkages. Simply choose a protein digest workflow with a condition (reduced or non-reduced) and analyze the data file:

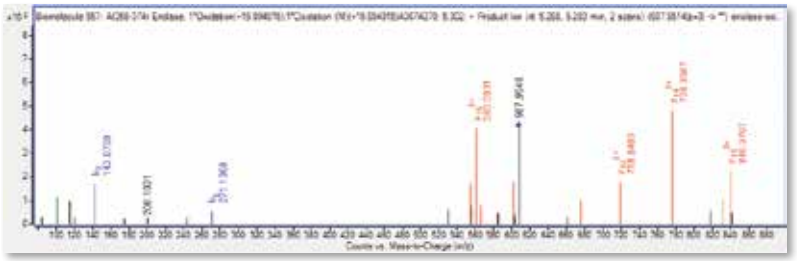
The Biomolecules table provides a Quality score to assess the confidence of the results:

VISUALIZE YOUR RESULTS

MassHunter BioConfirm features several visualizations to assist in the interpretation of your data:



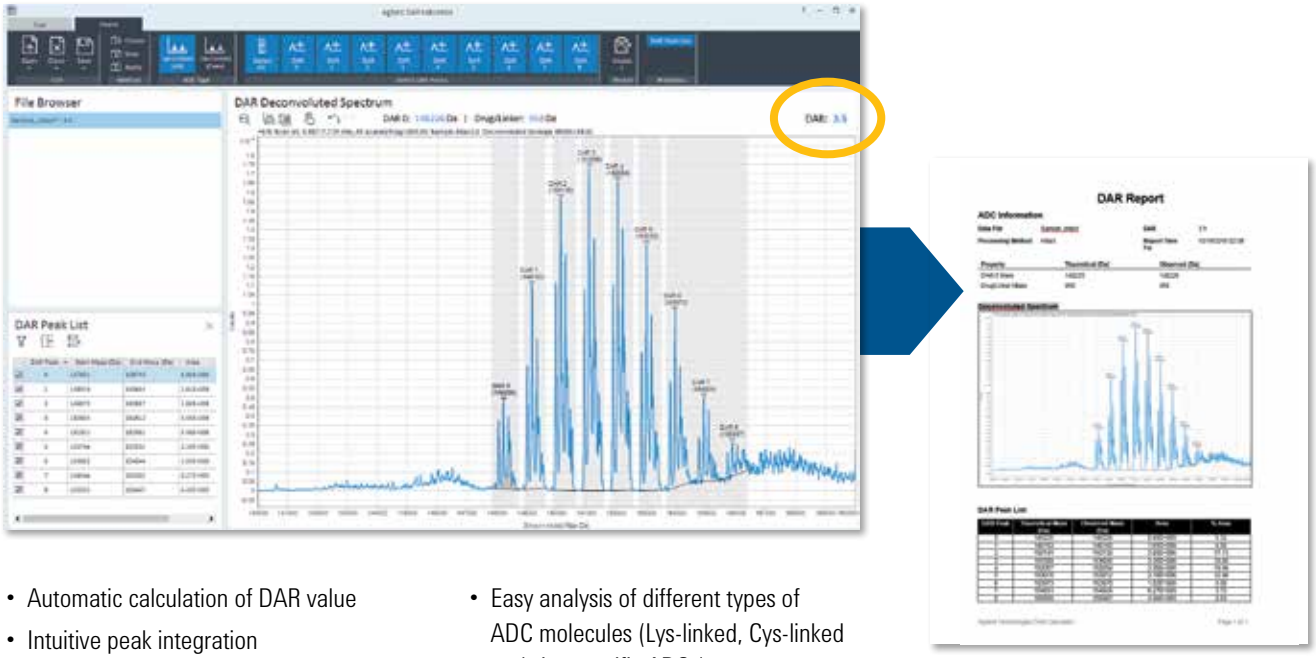
Mirror Plot (for the comparison of biosimilars or lot-to-lot variation)



MS/MS spectra can be used to determine the location of post-translational modifications (PTMs) and disulfide bonds in the protein. Product ion spectra are labeled with b (blue) and y ions (red).

ONE CLICK ADC DAR CALCULATION

The drug-to-antibody ratio (DAR) is a critical quality attribute of antibody drug conjugates (ADCs) that must be carefully monitored during the development process. MassHunter DAR Calculator has been created to rapidly calculate DAR values for both intact and reduced ADCs with minimal user input.



- Automatic calculation of DAR value
- Intuitive peak integration
- Built-in support for intact and reduced ADCs

- Easy analysis of different types of ADC molecules (Lys-linked, Cys-linked and site-specific ADCs)
- Flexible control to define peaks of interest

- Dedicated ADC DAR report in PDF and MS Word

ACCESS TO LC/MS FOR EVERYONE

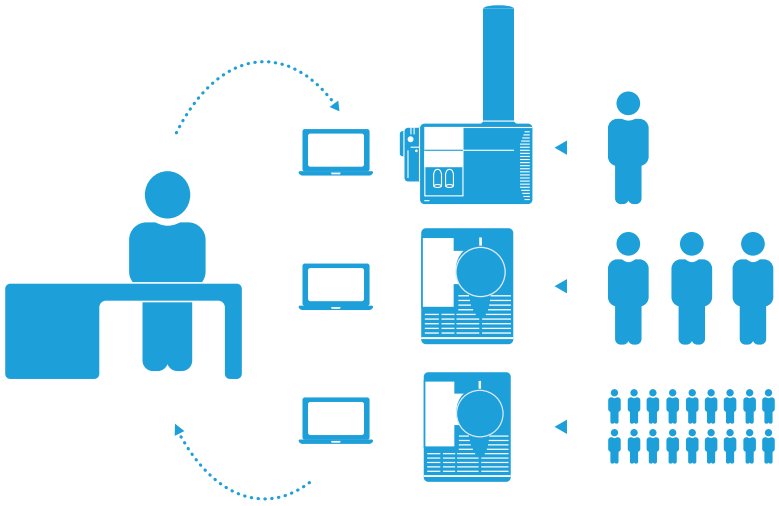
The MassHunter Walkup environment provides sample submitters with hands-on access to expert LC/MS capabilities—without requiring them to be LC/MS experts.

- Control sample preparation, treatment, and storage
- Access a broad range of applications:
  - Sample quality
  - Compound verification
  - Clone selection
  - Formulation optimization
  - Covalent inhibitor studies
- Accept protein sequences and drug-linker mass by the end user at the time of sample submission
- Get consistent data analysis and spectral deconvolution (e.g., pseudo first-order rate constants), for greater confidence during comparative studies

Overcome Common Open Access LC/MS Implementation Challenges for Biomolecules

Take full advantage of high resolution TOF and Q-TOF measurement with the integration of MassHunter Walkup and MassHunter BioConfirm offering biologists an open-access type environment previously only available for small molecule analysis.

- Eliminate risk
- Increase efficiency
- Automate interpretation and delivery of results



Easy open access facility administration in a multi-user, multi-instrument environment.

Learn more
www.agilent.com/chem/bioconfirm

Buy online
www.agilent.com/chem/store

Find a local Agilent customer center
in your country
www.agilent.com/chem/contactus

USA and Canada
1-800-227-9770
agilent_inquiries@agilent.com

Europe
info_agilent@agilent.com

Asia Pacific
inquiry_lsca@agilent.com

Printed in the USA March 31, 2017
5991-7722EN