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Omni**Scape**™

MS Software

A New Era of Confidence in Top-Down Sequence Analysis

Transform unknown protein spectra
into confirmed proteoform sequences

Innovation with Integrity

Proteoform Characterization - Powerful yet Challenging

Despite offering a more complete view of proteins (proteoforms), top-down methods lag behind bottom-up analysis. Congested MSn spectra contain overlapping peaks, multiply charged ions, and a broad range of intensities, hindering routine data interpretation. Furthermore, comprehensive characterization often requires data from multiple ionization and activation methods, and the ability to align results of the various data sets.

Analysis of recombinant proteins:

Protein biologics have a critical place in the Pharma pipeline. As their complexity increases, better tools are required to resolve their heterogeneity. Top-down analysis can reveal the identity and the position of distributed modifications that are difficult to access by other means.

Proteoform classes recognized at the intact level are much harder to identify and quantify by bottom-up analyses.
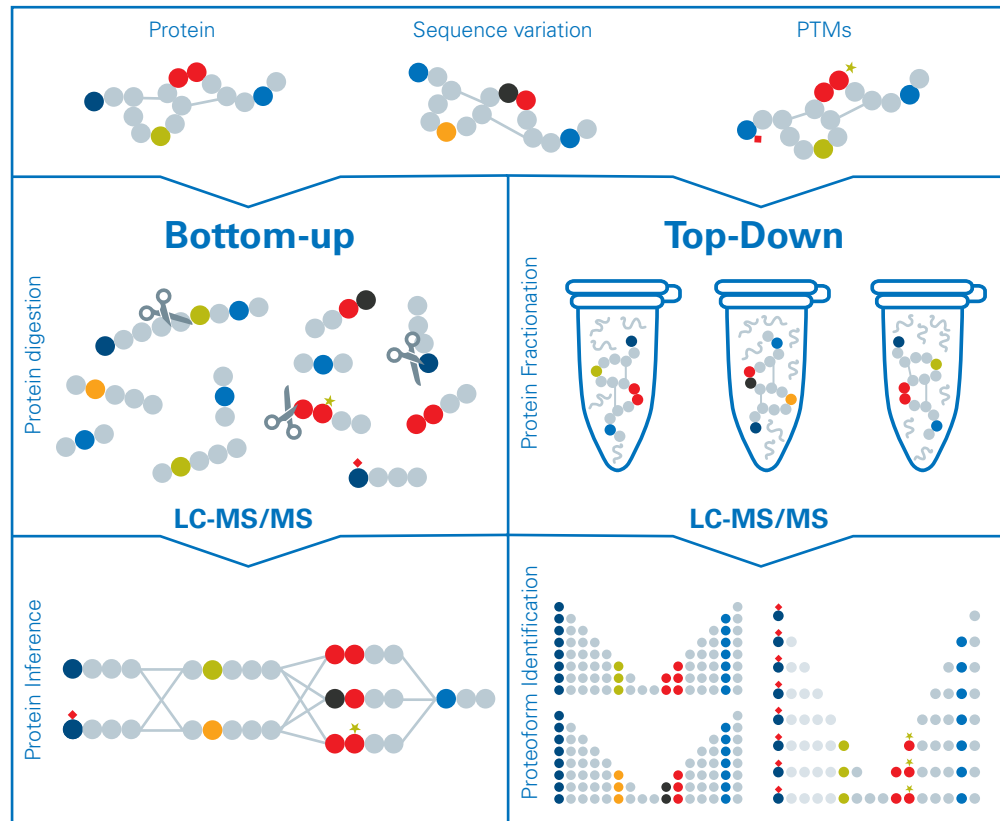
Dr. Boris Krichel

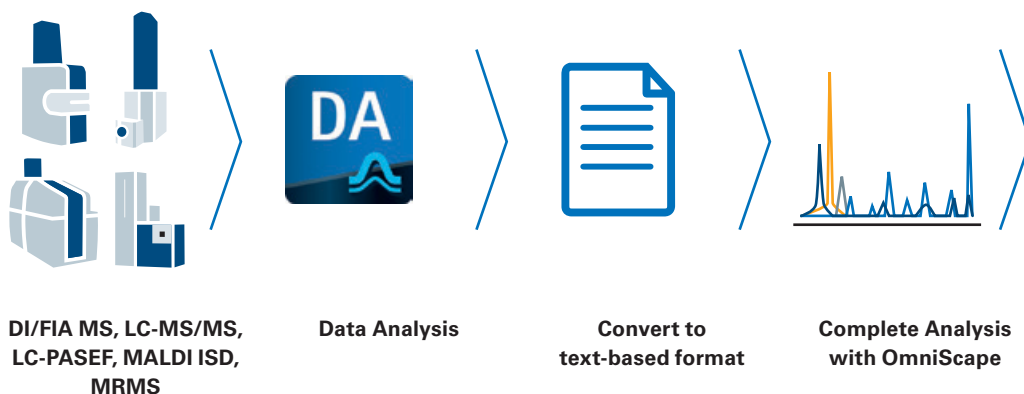Postdoctoral Fellow, University of Wisconsin–Madison, Ying Ge Lab

"I am excited about the de novo sequencing function, which will help us to discover and annotate proteins in untargeted Top-Down Proteomics runs. The most impressive function of OmniScape is the automatic suggestion of matching proteoforms based on multiple variable modifications."

OmniScape – Revolutionizing Top-Down Protein Identification

OmniScape uses the advanced OmniWave™ algorithm to tackle the challenge of analyzing complex top-down mass spectrometry data. This innovative software empowers researchers with the ability to:

- **Accurately identify proteins:** OmniScape's interactive validation tools give users confidence in the results while minimizing tedious tasks.
- **Localize modifications:** The software effectively locates post-translational modifications (PTMs) on proteins, providing deeper insights into their function.
- **Identify unknowns (de novo):** The OmniWave algorithm allows researchers to detect peaks and format sequence tags ready for homology-based searches even without prior information.
- **Simplify data interpretation:** By supporting a wide range of fragmentation modes and easily combining results, OmniScape streamlines the analysis workflow.
- **Flexible data import:** Spectra reader for both ESI and MALDI data as well as a wide range of MS instruments.

Multiple types of MSn data from ESI and/or MALDI can be used for peak list generation and sequence annotation.

| DI/FIA MS, LC-MS/MS, LC-PASEF, MALDI ISD, MRMS | Data Analysis | Convert to text-based format | Complete Analysis with OmniScape |

Key Tools for Top-Down Protein Sequence Analysis

1 De novo Protein Sequencing

2 Homology Search-Based Protein ID

3 N- and C-terminal Status Determination

4 Proteoform Assessment

Maximize Confidence With Multi-Method Analysis

Various top-down analytical strategies, such as collision-induced dissociation (CID), electron capture dissociation (ECD), and MALDI-time-of-flight ion mobility separation with in-source decay (MALDI-TIMS-ISD) spectra, yield different fragments of a protein. Combining these methods provides a more complete picture of the protein's structure and modifications, leading to more confident annotations and identification.

OmniScape seamlessly integrates this multi-method approach. Researchers submit spectra from various sources to OmniScape and utilize either the homology search or sequence confirmation workflows to obtain a highly detailed sequence coverage map for their target analyte.

» Dr. Christian Isak Jørgensen

Senior Science Manager, Novonesis, Denmark

"The OmniScape solution addresses a real need for us in the biotech industry producing recombinant proteins"

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OmniScape™

Benefit	Feature
Works with unknowns	De novo annotation and homology searches simplify the identification of unknowns
High confidence verification	Novel OmniWave deisotoping algorithm delivers unmatched performance to analyze congested MSn spectra
Flexible interface	Easy parameter optimization and flexible input format facilitate the use of multiple data sources

Online information
www.bruker.com/omniscape