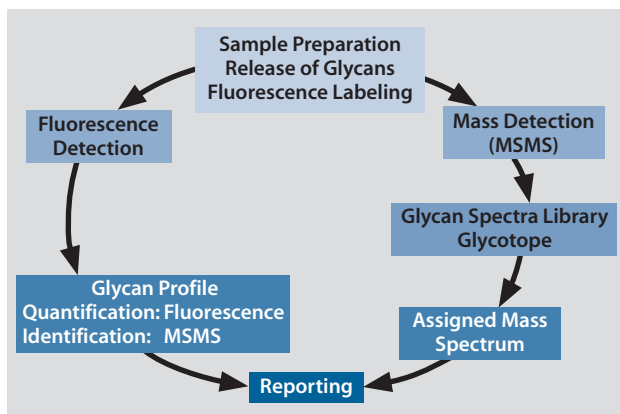


Characterization of proteins | Quality control for development | Product release assays

N- and O-glycoprofiling service

- Innovative combination and automation of analytical methods for high-throughput analysis of complex glycans
- Unambiguous identification of isobaric glycan structures employing CID-MS/MS
- Precise quantification based on sensitive fluorescence detection
- Calculation of biologically relevant glycan parameters like fucosylation, galactosylation, sialylation etc.
- Comparison to reference standards
- Analysis of complex glycan patterns of >100 individual structures
- Experienced under GxP environment

Workflow automated glycoprofiling

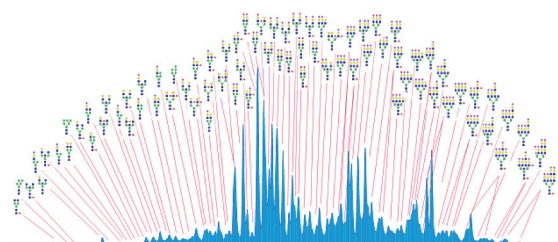


Site-specific glycoprofiling

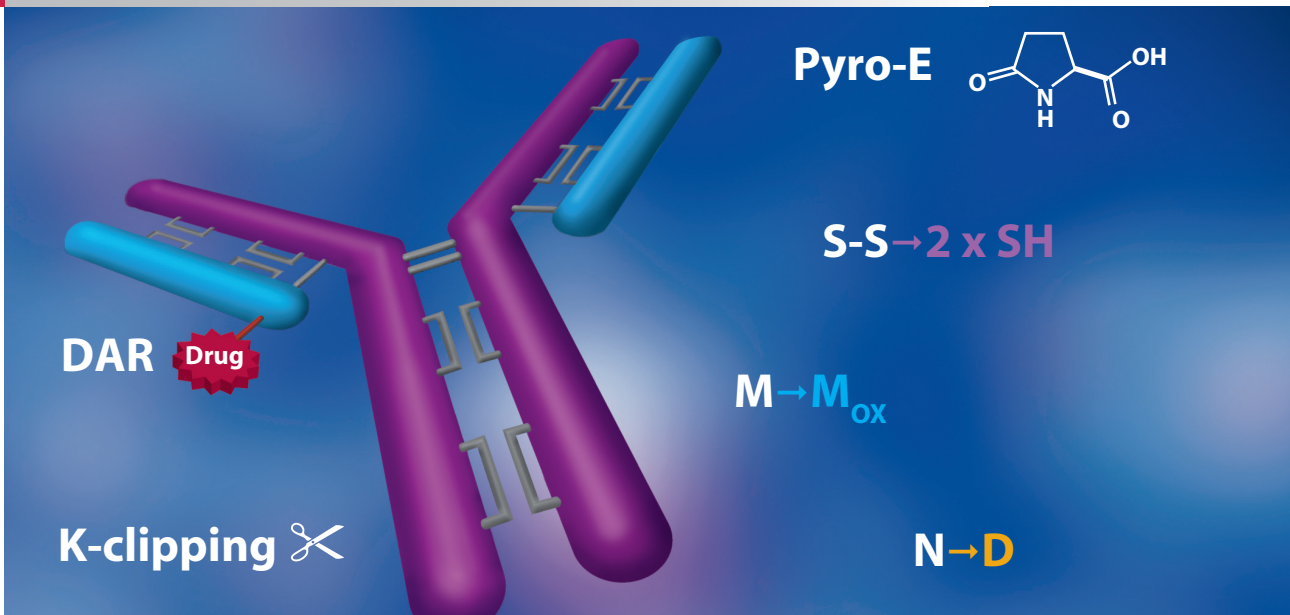
- Innovative combination of peptide and glycan profiling for **precise site-specific identification and quantification**
- Fractionation of glycopeptides comprising the same glycosylation site
- Glycosylation of human and rodent cells
- Quantitative profiling of glycans released from one glycosylation site

Accessories for glycoprofiling

- Glycoprotein standards for glycoprofiling
- GlycoLib – the glycan library
- MSMS spectra library comprising approx. 300 mAb glycans and 750 glycans from other proteins
- Characteristic fragments for identification of glycopeptides
- Intensity patterns of glycan fragments for identification of glycan structures



Glycotope – your competent partner for analysis of standard and complex glycosylation patterns



Identification and quantification of PTM's by high-resolution UPLC-ESI-QTOF mass spectrometry

Integrity of the protein by peptide analysis:

- Peptide mapping
- Sequence verification
- Truncation
- Disulfide bridges

Overall and site-specific analysis of PTM's

- Oxidation
- Deamidation
- Lysine clipping
- Pyroglutamate

Analysis of special PTM's

- Amidation, glycation, sulfation, phosphorylation, isomerisation, N-terminal acetylation, acylation, hydroxylation, racemisation etc.

Verification of glycosylation sites

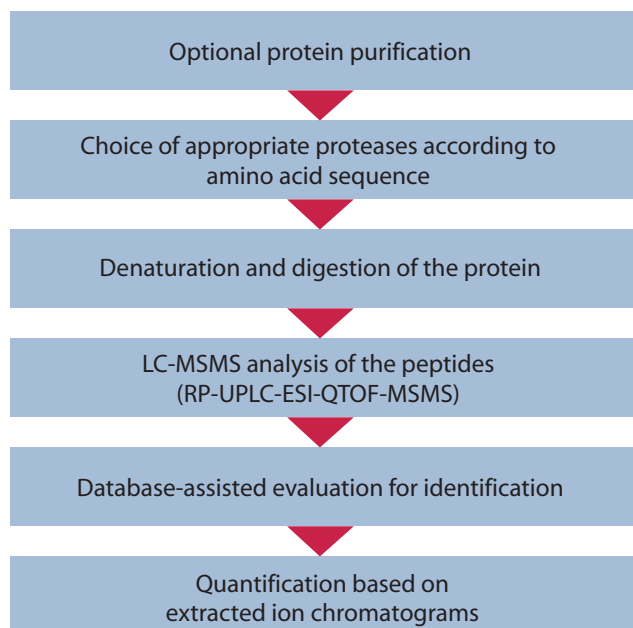
- Identification and characterization of glycopeptides

Intact protein and middle-up analysis

- Molecular mass
- Integrity of the amino acid sequence and glycosylation
- Fragments
- Truncation

Occupancy of glycosylation sites

- Quantification of the amount of glycans attached to a glycosylation site or to the complete protein



For more information please contact us

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