CHEMPARTNER
DEDICATED TO LIFESCIENCE

BIOLOGICS ANALYTICAL

ChemPartner offers a full-range of biologics analytical capabilities supporting the discovery and development of preclinical antibodies and therapeutic proteins. We are equipped with the most knowledgeable scientists, advanced facilities, physicochemical property characterization, and Biacore/Octet based biomolecular interaction analysis.

CAPABILITIES

	PARAMETER	METHOD
PRIMARY SEQUENCE	Composition	Amino Acid Analysis (AAA)
	Sequence Confirmation	Peptide Mapping, LC-MS/MS
	Glycosylation Analysis	LC-MS/MS
	Disulfide Bond Shuffling	LC-MS/MS
	Charge Analysis	cIEF, IEX
	Degradation	SEC, RPC, SDS-PAGE, cIEF, IEX,
SECONDARY STRUCTURE	CD, FTIR	
TERTIARY STRUCTURE	Intrinsic Fluorescence	
	2nd Derivative UV	
AGGREGATION	Aggregates	SEC-MALLS, SDS-PAGE, AUC
	Size	Dynamic Light Scattering, AUC
THERMAL STABILITY	Capillary DSC	
	High Throughput Light Scattering	
ACTIVITY	Biacore, ELISA, Cell-based Assays (FACS, MSD)	

EQUIPMENT

- GE Biacore 8K
- Thermo Exactive Plus EMR
  - Equipped with TriVersa NanoMate
- SCIEX TripleTOF® 5600

PROTEIN CHARACTERIZATION BIOPHYSICS ANALYSIS

CHARGE VARIANCE ANALYSIS

- Capillary isoelectric focusing (cIEF)
- Ion-exchange chromatography (SCX, WCX, SAX, WAX)

THERMAL STABILITY

- Capillary differential scanning calorimetry (DSC)
- Static light scattering (SLS)

PROTEIN STRUCTURAL ANALYSIS

- 2nd-derivative UV spectroscopy (A2DUV)
- Intrinsic fluorescence
- Circular dichroism (CD)

PROTEIN CHARACTERIZATION LC-MS BASED ANALYSIS

PROTEIN CHEMISTRY

- Amino acid composition analysis (AAA)

PROTEIN CONCENTRATION

- Extinction coefficient: Spectrophotometry (A280)

IMPURITY/GEL BAND ANALYSIS

- Host-cell protein analysis: Western Blot, Cap-LC or nano-LC MS/MS analysis

CONFIRMATION OF PRIMARY SEQUENCE

- Peptide mapping
  - HPLC mapping
  - LC-MS/MS mapping (sequence coverage)
  - Intact protein mass analysis - RPLC-MS, SEC-MS, Native-MS (Cysteinyl-linked ADC)

DEGRADATION

- C/N terminus analysis: HPLC mapping, LC-MS

POST-TRANSLATION MODIFICATION ANALYSIS (PTM)

- Deamidation, oxidation, phosphorylation, glycosylation

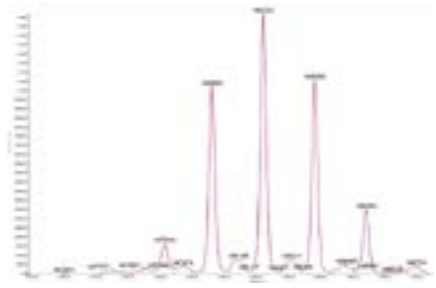
GLYCOSYLATION

- Glycosylation site ID, Site occupancy
- MW measurement of glycoforms
- Glycoform profiling
- Quantitative analysis of N-glycans (2AB labeling: HILIC and MS)

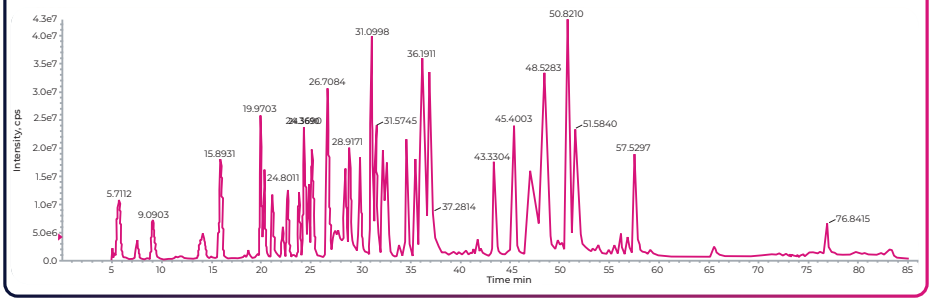
DISULFIDE BONDS MAPPING AGGREGATES AND PARTICLES

- SEC-UV, SEC-MALLS

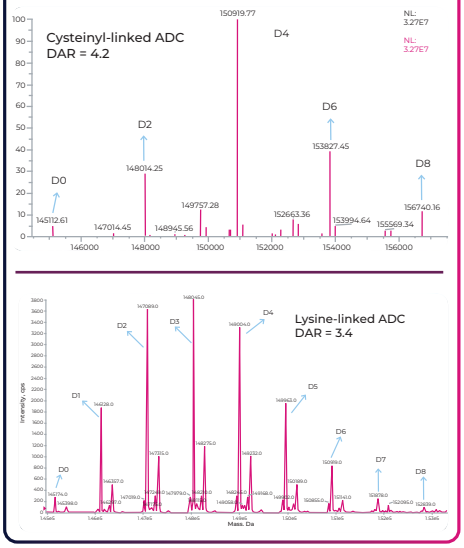
INTACT MS ANALYSIS



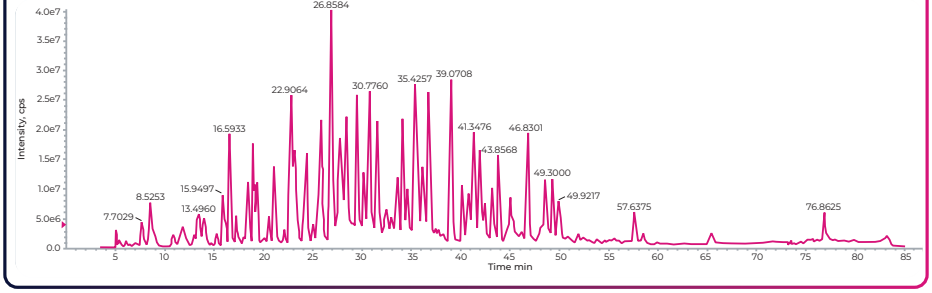
PEPTIDE MAPPING BY LC-MS/MS (TRYPSIN DIGESTION)



Antibody Drug Conjugate Tested for DAR



PEPTIDE MAPPING BY LC-MS/MS (CHYMOTRYPSIN DIGESTION)



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