

BIOLOGICS

ANALYTICAL SERVICES

SERVICES OVERVIEW

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.

	Parameter	Method
Primary Sequence	Composition	Amino Acid Analysis (AAA),
	Sequenc 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)	



GE Biacore8K



Thermo Exactive Plus EMR - Equipped with TriVersa NanoMate



SCIEX TripleTOF® 5600

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 (Cysteinyllinked ADC)

DEGRADATION

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

POST-TRANSLATION MODIFICATION ANALYSIS (PTM)

- Deamidation, oxidation, phosphorylation, glycosylation

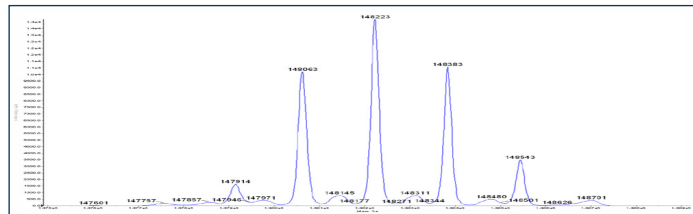
GLYCOSYLATION

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

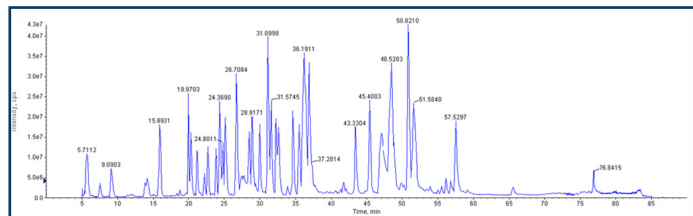
DISULFIDE BONDS MAPPING AGGREGATES & PARTICLES

- SEC-UV, SEC-MALLS

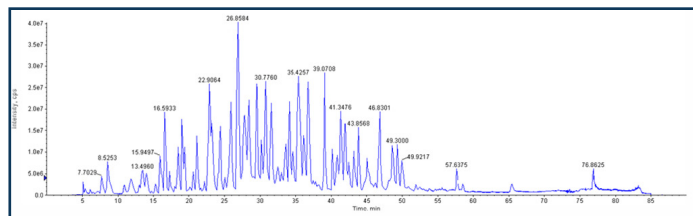
INTACT MS ANALYSIS



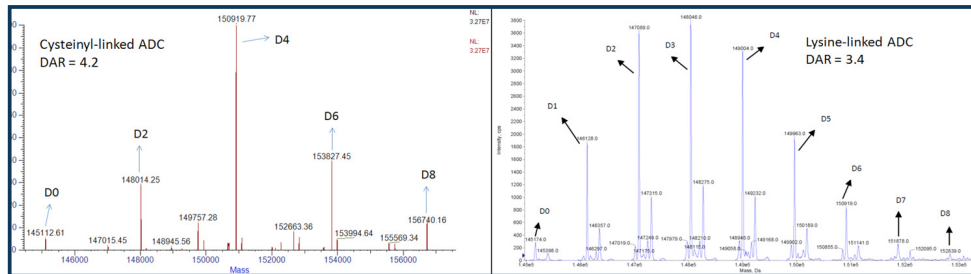
PEPTIDE MAPPING BY LC-MS/MS (TRYP SIN DIGESTION)



PEPTIDE MAPPING BY LC-MS/MS (CHY MOTRYP SIN DIGESTION)



ANTIBODY DRUG CONJUGATE TESTED FOR DAR



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)