

# Protein Expression Analysis for Drug and Biologics Development

Protein expression analysis is crucial in drug and biologics development, offering vital insights into the behavior and efficacy of therapeutic candidates. By quantifying and characterizing protein levels, researchers assess drug potency, pharmacokinetics, and safety early in development. These insights guide decisions from discovery to clinical trials, ensuring the advancement of promising candidates and accelerating the development of innovative therapies that address medical challenges and improve patient care.

## Our Expertise

At Avance Biosciences, we excel in protein expression analysis using ELISA, MSD, and Jess (Western Blot). Our ELISA proficiency ensures accurate protein quantification, while MSD technology provides sensitive, multiplexed detection. With the Jess system, we offer automated, high-throughput Western blot analysis for precise and reproducible results. These advanced techniques allow us to deliver reliable, high-quality data to support your research and development needs.

## Methods Offered:

Platforms	Advantages	Applications
ELISA (Enzyme-linked Immunosorbent Assay)	High specificity, reproducibility, and suitability for high-throughput screening	Assessing protein levels in cell lysates, tissue extracts, and biological fluids for biomarker discovery, pharmacokinetic studies, and drug efficacy evaluations
MSD (Meso Scale Discovery)	High sensitivity, minimal sample volume requirements, and enhanced multiplexing capabilities	Multiplex analysis of biomarkers and cytokines in complex biological matrices, enhancing the understanding of drug effects on signaling pathways
Jess (Western Blot)	Qualitative and semi-quantitative analysis, capability to detect low-abundance proteins	Protein expression profiling, validation of target proteins, and assessment of protein modifications in cell and tissue lysates
LC/MS/MS	High specificity, sensitivity, and ability to analyze complex protein mixtures	Protein identification, characterization, and quantification for comprehensive proteomic analysis