

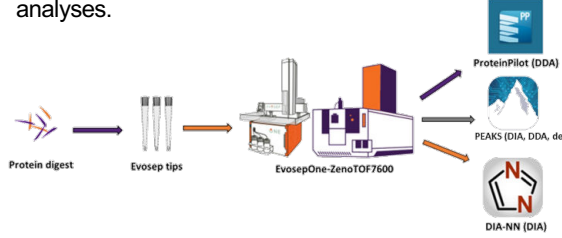


PROTEOMIC SERVICE PLATFORMS

<p>MASS SPECTROMETRY</p> <p>Targeted and untargeted mass spectrometry with a wide range of workflow options</p>	<p>MULTIPLEXED IMMUNOASSAYS</p> <p>Robust immunoassays that deliver unmatched coverage and reproducibility</p>	<p>PROTEOGENOMICS</p> <p>Deep unbiased proteogenomics through integration of proteomic and genomic services</p>	<p>MULTI-OMIC STUDIES</p> <p>Integrated NGS, cell biology, and pathology services with expert bioinformatic support</p>
<p>REPRODUCIBILITY</p>	<p>SCALABILITY</p>	<p>SPEED</p>	<p>CUSTOMIZATION</p>
			<p>DIVERSE</p>

Mass Spectrometry

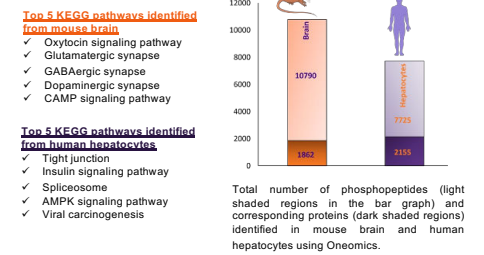
LC-MS/MS provides capabilities for a wide range of services including phenotypic screening, proteomic profiling, biomarker detection and validation, protein-protein interaction studies, expression of peptide variants, and PTM analyses.



a. The number of protein groups identified in HeLa and K562 using DIA. **b.** The number of protein groups identified in HeLa and K562 using DDA. **c.** The number of quantifiable proteins, those having a coefficient of variation across replicate intensities of < 20%, using the DIA method.

Method	HeLa	K562
DIA	~10,000	~10,000
DDA	~5,000	~5,000

Phosphoproteomics analysis boosts understanding of disease state, cell signaling, and cellular response to exogenous therapeutics. DLS offers services for untargeted, global phosphoproteomics analysis as well as targeted analysis.



- Biomarker discovery and validation
- Mechanism of action studies
- Phenotypic screening
- Post-translational modification
- Protein complex analysis

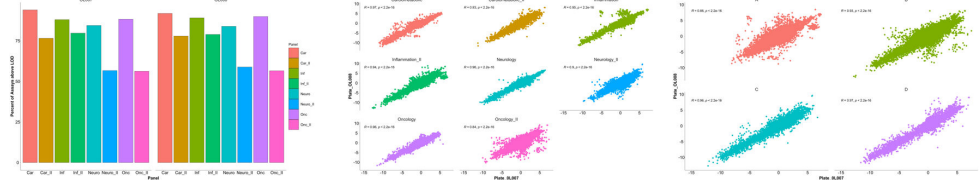
Immunoassays

Olink® Proximity Extension Assay

Explore 3072 is a high-throughput protein biomarker discovery platform. The highly multiplexed assay measures ~3000 proteins with highly specific, dual-antibody recognition. Using only microliters of sample, this high throughput assay can power large-scale proteomics studies with relative quantitation.



Target leverages the sensitivity of Explore for focused biomarker studies. These assays multiplex up to 92 protein targets with relative or absolute quantitation.



Olink Explore data acquired from two identical sample plates of 88 replicates of pooled plasma. **Left.** The percent of assays above the limit of detection (LOD) across all 88 samples. **Middle.** Reproducibility of assays across plates separated by panel. **Right.** Reproducibility of assays across plates separated by block. In general, block A measures proteins with lower plasma abundance while blocks B, C, and D measure proteins with increasing plasma abundance.

Luminex® xMAP INTELLIFLEX® Systems

Are targeted multiplexed panels for either protein or RNA.



ProcartaPlex assays are antibody-based magnetic-bead powered kits for absolute protein quantitation. Kits can be multiplexed to include up to 80 proteins.

QuantiGene Plex assays are hybridization-based assays utilizing branched DNA technology, which uses signal amplification for the measurement of RNA transcripts.

Kits can be customized and multiplexed for multi-omic analysis of common samples.

Custom Service Requests

DLS can provide custom solutions for your analytical needs. This can include characterization, target degradation, PTM analysis, and method development.

Using genomics and transcriptomics data to augment proteomics, DLS offers a custom protein identification pipelines. In these studies, deep proteomics data are searched against custom databases, allowing variant proteins and peptides to be uncovered.

PRESERVE PRECIOUS SAMPLES THROUGH INTEGRATED MULTI-OMIC WORKFLOWS

PROTEOMIC SERVICES

DISCOVERY BIOSPECIMEN SOLUTIONS



MOLECULAR PATHOLOGY SERVICES

IHC, mIF, ISH, Histology, Digital Pathology, Quantitative Gene Expression



GENOMIC SERVICES

RNA-Seq, WES, WGS, Targeted, HiFi Long-read, Single Cell Sequencing



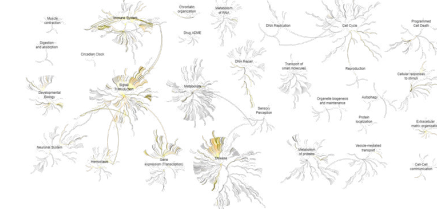
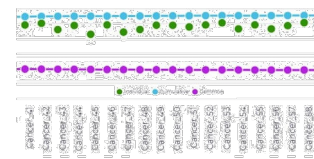
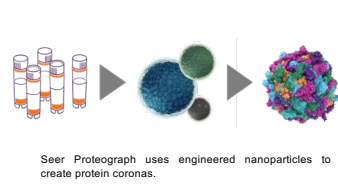
CELL BIOLOGY SERVICES

Flow Cytometry, FACS, Single Cell Analysis, Spatial Gene Expression, Immunomagnetic Cell Isolation, Cell Culture and Dissociation



Untargeted Plasma Proteomics

Seer Proteograph™ assays offer deep proteomic coverage from complex biological samples. The automated sample preparation utilizes engineered nanoparticles to reproducibly enrich lower abundance proteins by the formation of protein coronas. With focused validation on plasma proteomics, DLS has shown increased performance in complex biological samples.



Alternative Matrices: The engineered nanoparticles can provide selective and specific enrichment from a variety of complex biological samples, including serum, urine, cerebrospinal fluid, and dried blood spots. DLS has shown a 10X improvement in identified protein groups from DBS (206 neat to 1220 with Seer Proteograph™).

Protein groups detected from DBS digested neat (A) and enriched using the Seer Proteograph (B.) Data modeled against HPPP (2021-07 build): Human Plasma Proteome Project. Deustch et al. J Proteome (2021.) Panel (C) shows the overlap of proteins identified by the Proteograph and in neat DBS alone. This shows the power of the Proteograph to perform deep proteomics on alternative matrices.

