

NGS enables proteomic discoveries at scale

Unlock unprecedented biological insights with the broadest coverage of the proteome and market-leading performance of Illumina Protein Prep

Genomics Epigenomics Transcriptomics **Proteomics**

Proteomics studies bridge the gap between genotype and phenotype, providing a real-time snapshot of cellular activity in health and disease states.

Proteomics research is poised for significant growth

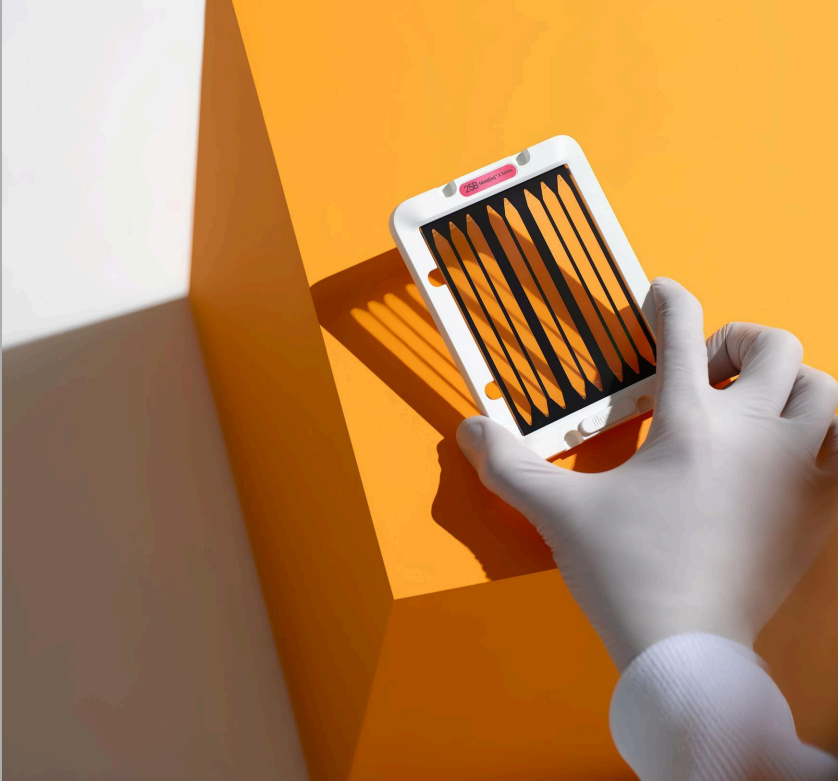
>17K
proteomics publications in 2024 alone¹

~55%
of researchers conducting genomic or transcriptomic studies also use proteomics²

The power of NGS-based proteomics

Combining ultrahigh-plex proteomics assays with the power and scalability of next-generation sequencing (NGS) enables simultaneous interrogation of thousands of proteins in a single sample, maximizing the discovery power of proteomic studies.

NGS makes it possible to integrate rich proteomic data with other layers of omic data, providing a multidimensional view of cellular function not visible when studying individual -omes in isolation.



Key applications of NGS-based proteomics research

<p>Biomarker discovery</p> <p>Large-scale proteomic studies can accelerate the discovery of biomarkers for early detection and monitoring of cancer and other diseases</p>	<p>Drug target identification</p> <p>Proteogenomic studies can identify robust links between gene variants and protein expression that can be used to guide drug discovery</p>	<p>Precision medicine</p> <p>Proteomic profiles can be analyzed to guide therapy selection and facilitate the development of next-generation liquid biopsies when combined with other omic data sets</p>	<p>Disease pathobiology</p> <p>Proteomic data can uncover molecular mechanisms of disease and improve risk assessment for complex diseases when integrated with polygenic scores</p>	<p>Population-level omics</p> <p>Proteomic data combined with other omic findings from large-scale studies can increase our understanding of causality and traits at the population level</p>
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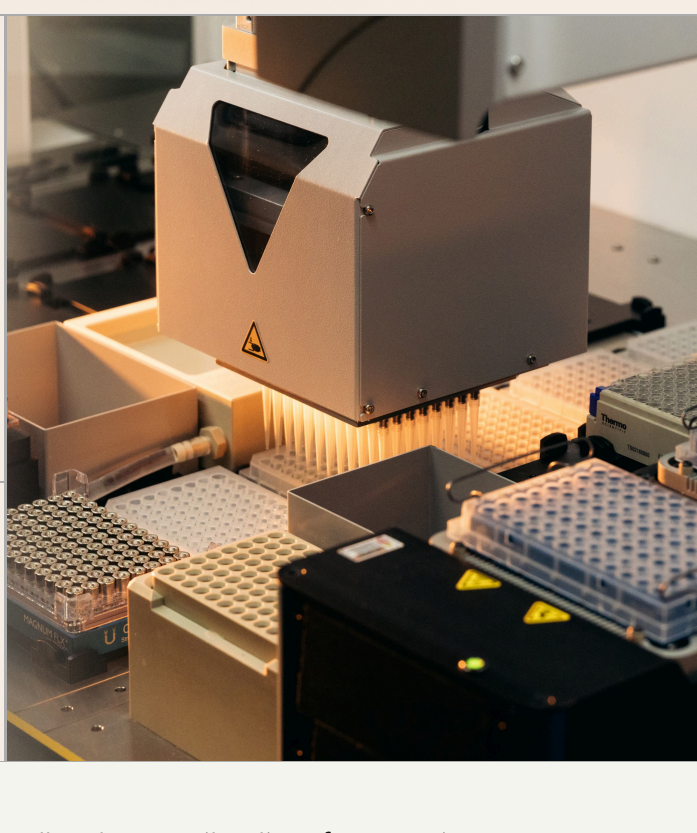
Establish a new standard in proteomics

Illumina Protein Prep combines an innovative aptamer-based proteomics assay with NGS readout and integrated data analysis, delivering a high-throughput, highly scalable solution to maximize proteomics discovery power.

9.5K Human protein targets

200+ Biological pathways

1 Panel



Illumina Protein Prep uses SOMAmer® Reagents, which are 10× smaller than antibodies, for protein-capture enabling ultrahigh multiplexing in a single reaction without cross-reactivity.

Broadest coverage of the human proteome

Illumina Protein Prep detects more proteins across every major biological process than any other NGS-based proteomics assay on the market.³

<p><input checked="" type="radio"/> Illumina Protein Prep</p> <p><input type="radio"/> Leading antibody-based discovery assay</p>	<p>Immune system (total proteins 2096)</p> <p>1487</p> <p>872</p>	<p>Signal transduction (total proteins 2547)</p> <p>1593</p> <p>865</p>
	<p>Disease (total proteins 1832)</p> <p>1128</p> <p>545</p>	<p>Metabolism (total proteins 2157)</p> <p>1327</p> <p>582</p>

Numbers in the bars denote the number of proteins detected in each biological process by each assay.

Largest orthogonally validated panel

> 4000
more protein targets than the leading antibody-based discovery assay⁴

72%
of SOMAmer Reagents have at least one additional form of orthogonal validation³

Market-leading performance

> 10-log
dynamic range with femtomolar sensitivity³

~5.5%*
median coefficient of variation (CV) for the most precise NGS-based assay on the market³

*Using samples from healthy donors.

Fastest, streamlined workflow

2.5 days from sample to answer

4 hr hands-on time

1 platform for proteomics assay and library preparation automation



<p>Step 1: Automation*</p> <p>Proteomics assay</p>	<p>Step 2: Automation*</p> <p>Library preparation</p>	<p>Step 3</p> <p>Sequencing</p>	<p>Step 4</p> <p>Analysis</p>
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*Proteomics assay and library preparation are both automated on the Illumina Protein Prep Automation System, a custom Tecan Fluent 780.

Intuitive analysis

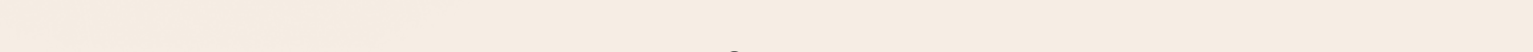
Generating insights from vast amounts of proteomic data and integrating these findings with other omic data sets can pose a significant bottleneck for labs. The Illumina Protein Prep solution includes data analysis software, enabling simplified analysis and visualization with Illumina Connected Multiomics and the DRAGEN™ Protein Quantification pipeline, available locally or on the cloud.

Explore every -ome, all on the NovaSeq™ X System

Illumina high-throughput sequencing systems are optimized for multiomic applications, providing deep sequencing needed for data-intensive studies and intuitive analysis to integrate insights.

Unlock unprecedented multiomic discovery power with

3.6 million
protein readouts per 384-sample run on the NovaSeq X 25B flow cell



Launch the next era of proteomics with Illumina

Access unmatched sensitivity and throughput for proteomics discovery at scale with the Illumina Protein Prep solution. With our end-to-end workflow and best-in-class performance, you can amplify your discovery power and answer your most complex biological questions.

Discover more at illumina.com/proteinprep

