

# Explore protein data at scale with Illumina Connected Multiomics

Powerful, intuitive, scalable multiomic analysis



Illumina Connected Multiomics enables researchers to explore protein data at scale and perform multimodal and multiomic analyses without the need for advanced bioinformatics expertise. With an easy-to-use graphical user interface, Connected Multiomics provides access to powerful statistical algorithms and publication-ready visualizations.



Unlock deeper  
biological insights



Intuitive and  
streamlined analysis



Scale studies  
with ease

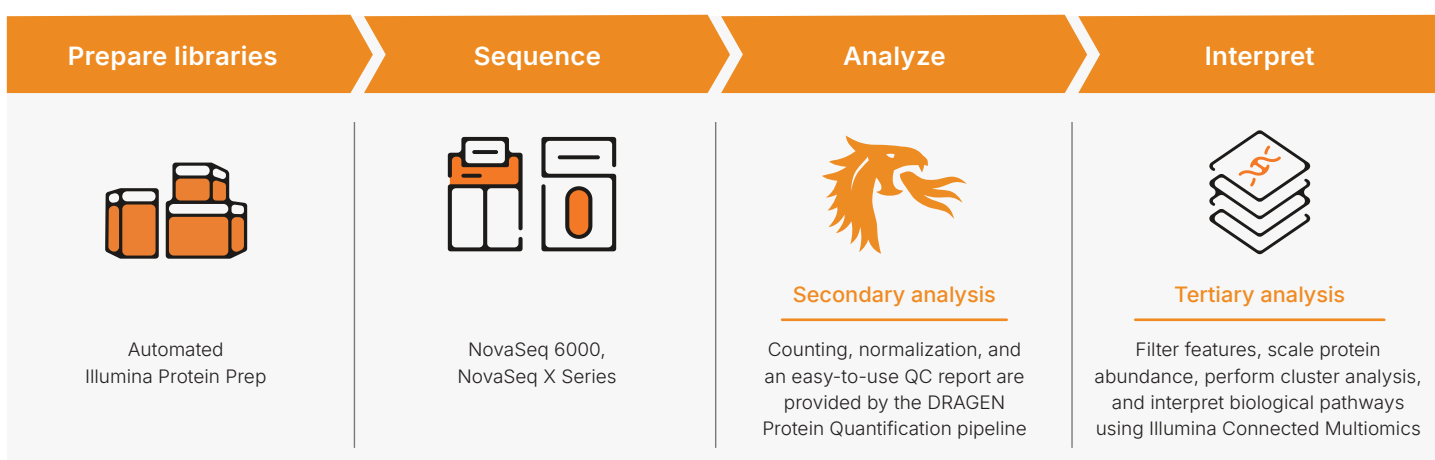
## Connected workflow

A single integrated workflow takes proteomic studies from sample preparation to data interpretation.

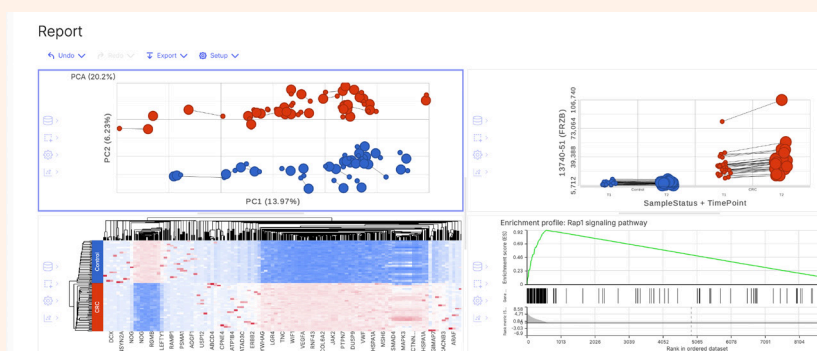
Start with an [Illumina protein prep kit](#) and your preferred [Illumina high-throughput sequencing system](#) for serum or plasma. Next, leverage the power of [Illumina DRAGEN](#) for secondary analysis. Continue with differential analysis in Illumina Connected Multiomics, and complete your analysis with pathway analysis using the integrated [Correlation Engine](#) knowledgebase.

## Advanced features include:

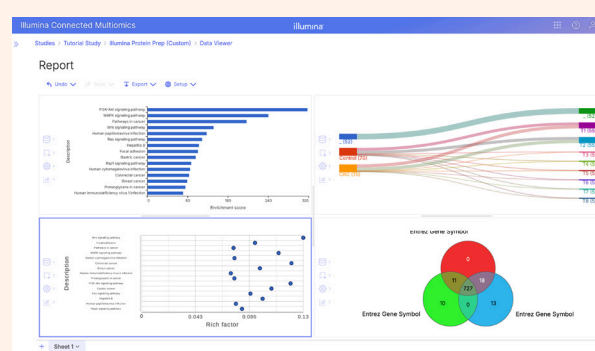
- ✓ Sample filtering
- ✓ Dimension reduction
- ✓ Cluster analysis
- ✓ Correlation and similarity analysis
- ✓ Differential protein expression identification
- ✓ Biological interpretation with pathway analysis



## Bring your proteomics studies to life with beautiful, interactive visualizations



PCA scatter plot displaying two sample groups; dot plot showing protein FRZB expression; heatmap of protein expression; Raspi showing the signaling pathway enrichment profile.



Barchart showing enriched pathways; Sankey plot with sample metadata information; scatterplot displaying enriched pathways; Venn diagram depicting overlap of three protein lists.

