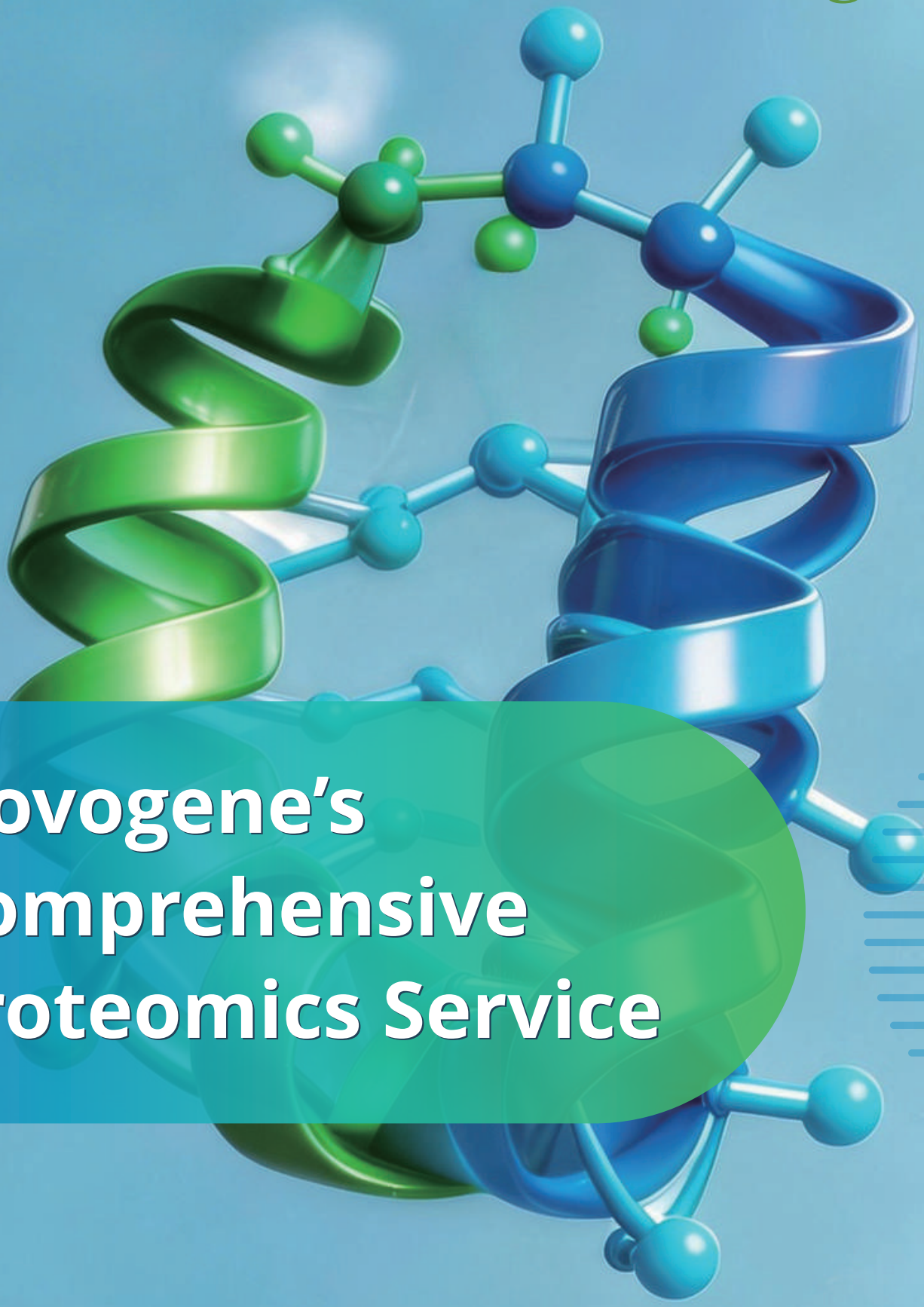
Novogene



Novogene's Comprehensive Proteomics Service

Table of Contents

The proteome has been defined as the protein complement expressed by an organism under specific spatiotemporal conditions. Meanwhile, it' s a dynamic map that is controlled by both environmental factors and physiological processes, which directly determining the phenotype of the organism. Proteomics provides deeper insight into dynamic regulatory layers encoded at the protein level, such as posttranslational modifications, subcellular localization, cell signaling, and protein–protein interactions, as well as a comprehensive understanding for biological processes. At Novogene, we offer Mass Spec-based proteomics (Quantitative proteomics, Phosphoproteomics) and Olink proteomics solutions to meet diverse research needs.

Mass Spectrometry-based Proteomics

- Quantitative Proteomics
  - Deep DIA (60 SPD)
  - Rapid DIA (180 SPD)
  - Plasma & Serum Proteomics (60 SPD)
- Post-Translational Modifications Proteomics (PTM)
  - Deep Phosphoproteomics (60 SPD)

SPD: Sample per day

Mass Spectrometry Platforms: Thermo Orbitrap Astral

The Orbitrap Astral mass spectrometer integrates three advanced mass analyzers: a high-resolution quadrupole mass filter, an Orbitrap mass analyzer, and the innovative Astral mass analyzer. Together, these analyzers leverage their unique strengths to deliver exceptional performance, enabling accurate and precise quantitation with unparalleled data depth and throughput.

Astral Mass Analyzer: Key Characteristics			
Sensitivity	Single ion detection	Mass accuracy	RMS < 5 ppm
HRAM scan rate	Up to 200 Hz	Mass range	m/z 40 - 6,000
Interscan dynamic range	> 1,000 with single microscan	Scan mode	SIM, DDA, DIA, PRM
Resolution	80,000 at m/z 524		

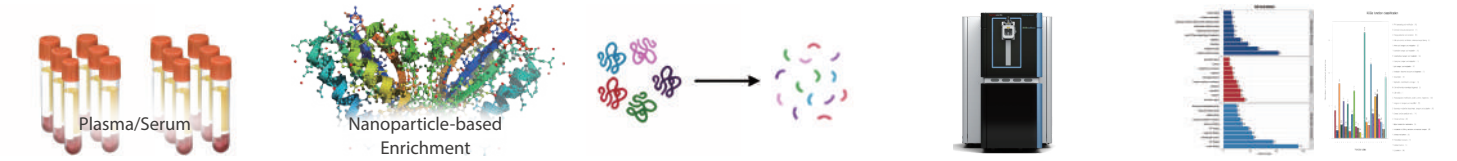
Quantitative Proteomics

Introduction

Quantitative proteomics aims to systematically determine the expression levels of proteins, and perform accurate quantitative comparisons. Quantitative proteomics is a branch of proteomics that involves the identification and quantification of proteins in a sample, often using techniques like mass spectrometry. It allows researchers to compare the abundance of proteins between different samples, such as cells in a healthy state versus cells under disease conditions.

Project Workflow

The workflow of Deep DIA, Rapid DIA Proteomics



The workflow of Plasma & Serum Proteomics

Data Analysis

Application

1. Discover biomarkers & drug targets: Conduct broad, untargeted screening of proteome profiles to identify differentially expressed proteins with potential.

2. Elucidate disease mechanisms: Compare protein abundances between diseased and healthy states to uncover the molecular drivers of pathogenesis.

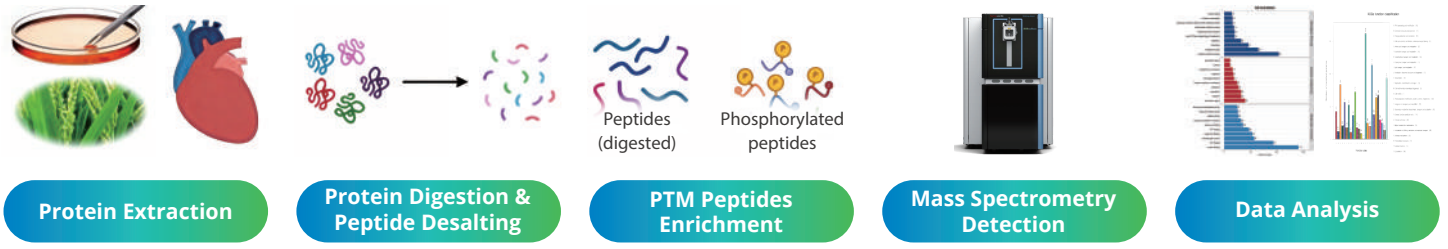
3. Map signaling pathways: Perform preliminary discovery-phase analysis to investigate dynamic changes in cellular signaling networks and pathway activities.

Phosphoproteomics

Introduction

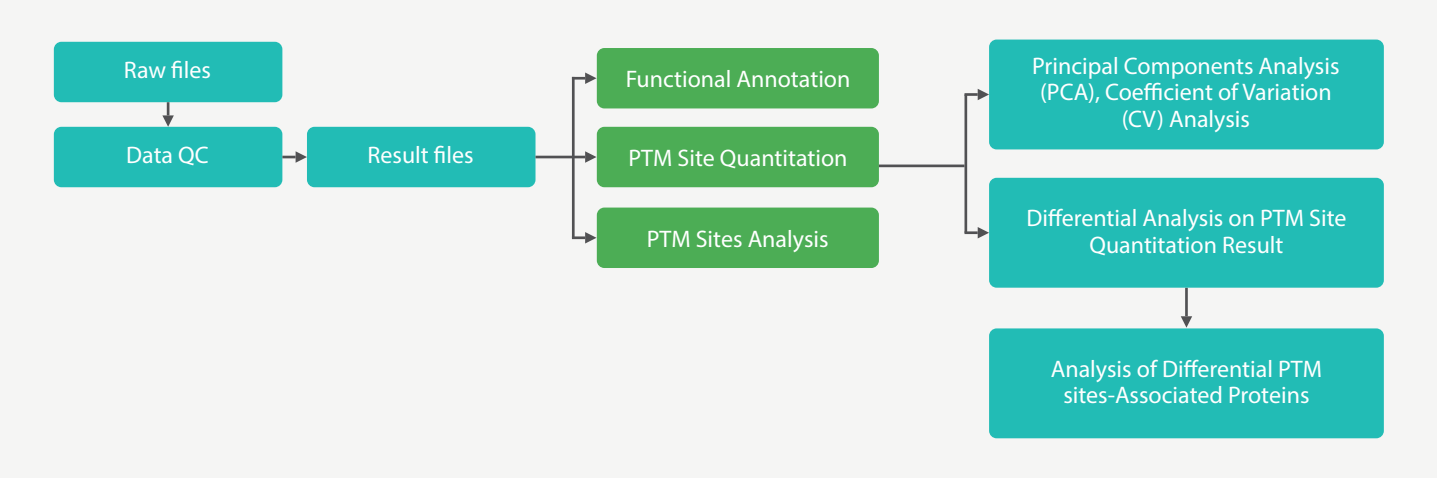
PTM proteomics systematically characterizes the types, sites, and dynamics of protein post-translational modifications across the proteome. PTMs constitute core mechanisms of fine-tuned cellular regulation by: Instantly modulating protein activity, localization, and interactions; Orchestrating critical processes: signal transduction, metabolic reprogramming, disease pathogenesis and others. Large-scale analysis of protein phosphorylation sites is a useful tool for defining signaling network regulation and dysregulation.

Protein phosphorylation is one of the most common and important PTMs. This reversible mechanism occurs through protein kinases and consists of the addition of a phosphate group (PO4) to the polar group R of various amino acids (eg. Serine/S, threonine/T, or tyrosine/Y).



The workflow of phosphoproteomics

Data Analysis



Application

1. Regulation of protein function: PTMs precisely control protein activity, stability, localization, and interactions. This allows cells to dynamically fine-tune protein behavior in response to stimuli, regulating essential processes from signal transduction and metabolism to gene expression.

2. Enzyme regulation: PTMs directly regulate enzyme activity. For instance, phosphorylation can activate or inhibit catalytic function, thereby controlling key cellular signaling and metabolic pathways.

3. Targeted protein degradation: PTMs tag proteins for destruction. Ubiquitination, for example, marks damaged or unnecessary proteins for proteasomal degradation, facilitating their removal from the cell.

Our Key Features and Advantages

1. High Reproducibility, Stability, and Reliability: Routine instrument maintenance and thorough sample quality control ensure the delivery of consistent and high-quality data.

2. Comprehensive Protein Identification: Provide extensive proteomic coverage.

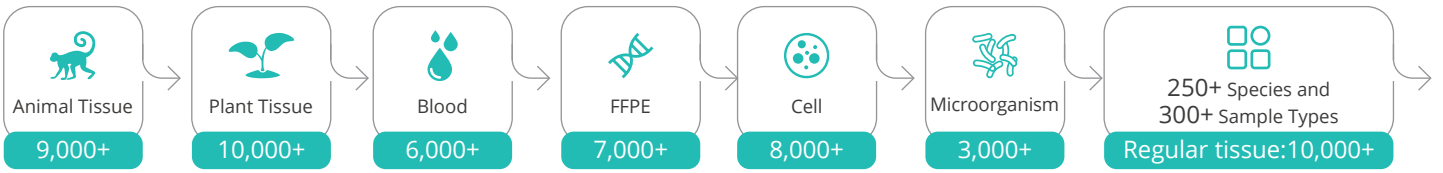
3. Expert Bioinformatics Analysis: Perform diverse functional analyses for in-depth exploration and interpretation of your proteomics data.

4. High Sample Throughput: Process up to 180 samples per day, making it ideal for large-scale cohort proteomic studies.

5. Library-free DIA: Enable DIA analysis without DDA reference library, making research easier

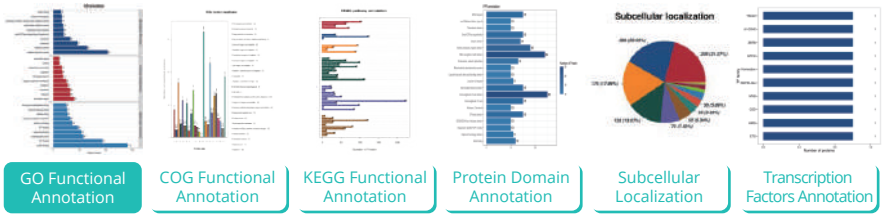
*Results may vary depending on sample quality and type.

Comprehensive Project Experience in Proteomics

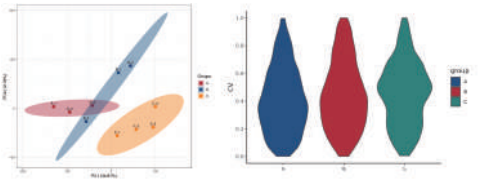


Number of Identifications

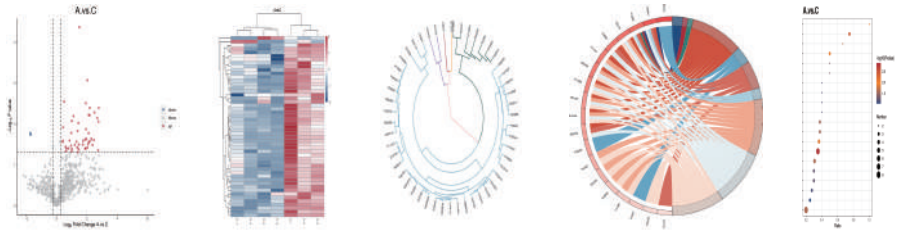
Demo Analysis Results



Protein Functional Annotation

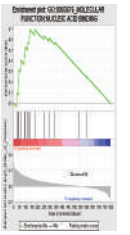


Protein Quantitative Analysis

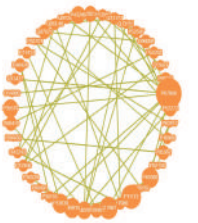


Differential Protein Expression Analysis

Functional Enrichment Analysis



GSEA Analysis



PPI Analysis

Publications Powered by Novogene

No.	Title	Service	Application	IF	DOI
1	Jute Nanocrystalline Cellulose Relieves Polystyrene Nanoplastic-Induced Acute Injuries by Modulating Gut Microbiota Gilliamella apicola	Quantitative Proteomics (Deep DIA)	Environmental toxicology	16	doi:10.1021/acsnano.5c04210
2	Targeting TTK Inhibits Tumorigenesis of T-Cell Lymphoma Through Dephosphorylating p38α and Activating AMPK/mTOR Pathway	Phosphoproteomics	Oncology, Molecular	14	doi:10.1002/advs.202413990
3	P21-Activated Kinase 2 as a Novel Target for Ventricular Tachyarrhythmias Associated with Cardiac Adrenergic Stress and Hypertrophy	Quantitative Proteomics (Deep DIA) & Phosphoproteomics	Ardiac arrhythmia, mitochondrial oxidative stress	14.1	doi: 10.1002/advs.202411987
4	Study on the degradation efficiency and mechanism of polystyrene microplastics by five kinds of edible fungi	Quantitative Proteomics & Transcriptomic	Biodegradation	12.2	doi: 10.1016/j.jhazmat.2025.138165
5	Multi-omic integration reveals subtype-specific predictors of neoadjuvant treatment response in breast cancer	Whole exome sequencing & Whole genome bisulfite sequencing & mRNA-Seq & Quantitative Proteomics	Oncology, Precision medicine	12.5	doi: 10.1126/sciadv.

Olink Proteomics

Olink™ Reveal Certified Service Provider

Over 1,000 proteins for broad coverage of the proteome and deep profiling of inflammation processes for disease research.

Olink™ Reveal

Introduction

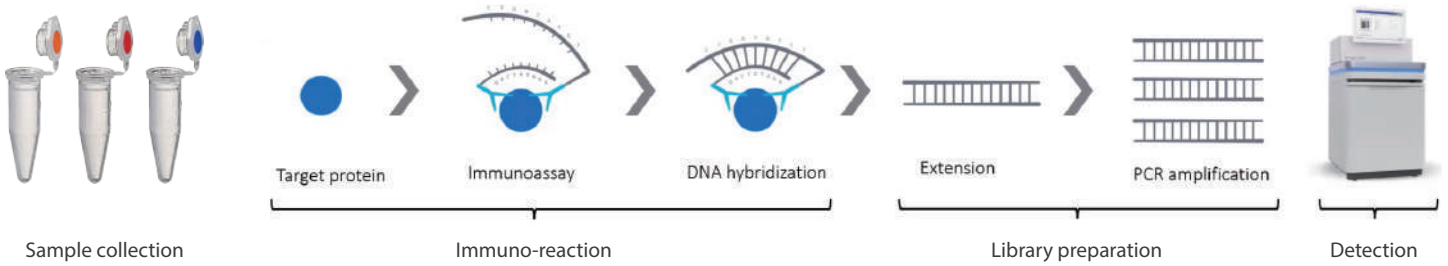
Olink Proteomics is a **high-throughput proteomics solution** for protein biomarker discovery in human body fluids, such as plasma, serum, cerebrospinal fluid, and urine, with exceptional efficiency. Olink Proteomics employs **Proximity Extension Assay (PEA™) technology** to target thousands of proteins, which are subsequently quantified via Next-Generation Sequencing (NGS). This unique combination delivers:

High Sensitivity: Detects as low as fg/ml

High Precision: Dual-antibody PEA technology to ensure precise target recognition

High Throughput: Screen ~1,000 proteins with a deep Inflammation profiling and immune mechanisms

Project Workflow



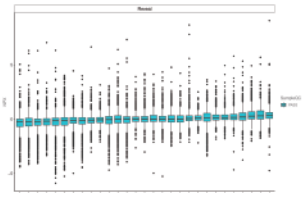
Application

1. Proteomic profiling: Screen disease-specific biomarkers; identify protein signatures for precision medicine or treatment response.

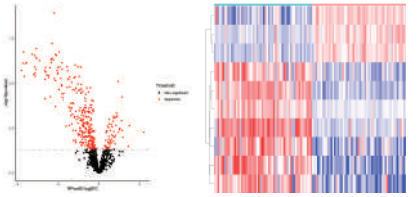
2. Disease classification: Develop diagnostic and prognostic model by integrating proteomics with genomic and clinical data.

3. Drug development: Identify drug targets and therapeutic biomarkers, gain insights into drug efficacy and mechanism-of-action.

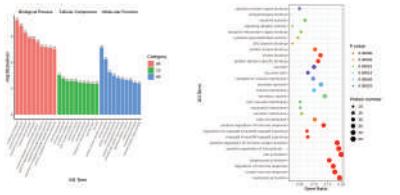
Data Analysis



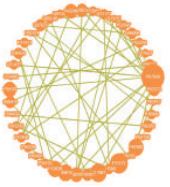
Data QC



Differential Expression Analysis



Functional Enrichment Analysis



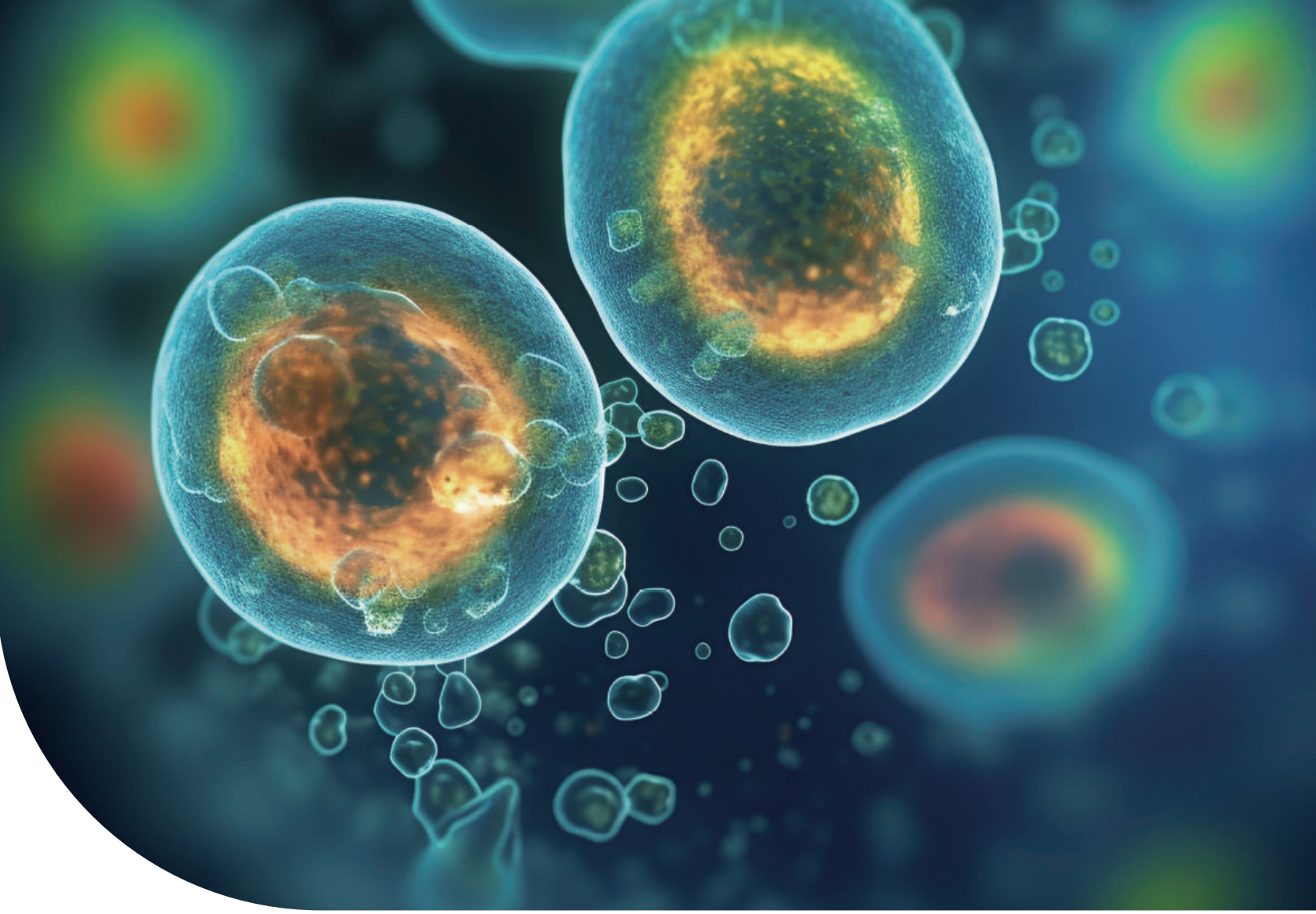
PPI Analysis

Our Key Features and Advantages

1. Olink Certified Service Provider: Global CSP for Olink™ Explore HT and Olink Reveal
2. Comprehensive Analysis: Bioinformatic expertise supporting multi-omic and customized analysis
3. Outstanding Project Management: Dedicated team supporting projects of any scale

Publications Powered by Novogene

No.	Title	Service	Application	IF	DOI
1	Plasma proteome adaptations during feminizing gender-affirming hormone therapy	Olink proteomics	Pathophysiology	48.5	https://-doi.org/10.1038/s41591-025-04023-9



Novogene is committed to be

Your Trusted Multi-omics Partner

- Trusted International Corporation
- Trusted Comprehensive Experience
- Trusted Expertise & Technology
- Trusted Service & Standardized Procedures
- Trusted Delivery Quality & Efficiency

Follow us on LinkedIn

Novogene Corporation Inc.

9730 SW Nimbus Ave., Beaverton OR 97008

916-252-0068 inquiry@novogeneusa.com www.novogene.com

Copyright© 2011 Novogene Corporation.
All Rights Reserved. Information and specifications are subject to change at any time without notice.