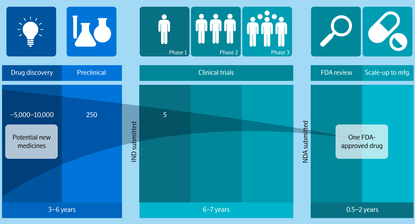
Olink

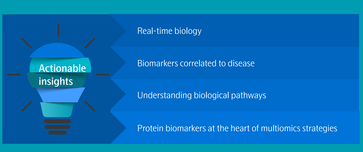
Link genomics with proteomics to accelerate the search for effective drug targets

Many therapeutic studies fail because they are not targeting the right proteins or not developed for the right patient. Using proteomics, researchers can determine early on whether a potential protein target will be worthwhile pursuing, saving pharma companies money while also ultimately helping patients and healthcare systems via opportunities for drug differentiation and label expansion.

Current situation



Studies show that drug development programs are twice as likely to succeed if they include genetic data — **adding proteomics will further strengthen your chances.**



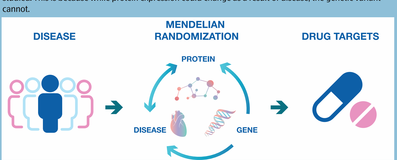
Read more

Proteogenomics with Mendelian Randomization to establish disease causality

Observational studies of protein levels cannot address the question of causality, as the change observed could either be driving the process under study, or merely reflect an outcome of that process.

This is particularly important for drug target identification, where causality is a prerequisite to take the protein into a drug discovery and development program.

Combining proteomics with genomics ("proteogenomics") can effectively address this problem by linking gene variants to protein expression levels. These types of statistically significant associations are called protein Quantative Trait Loci (pQTLs) and are particularly interesting if the genetic variant is located very close to the gene for the protein that is affected ("cis-PQTLs"). If both the genetic variant and protein expression level can be robustly associated with a phenotypic outcome using Mendelian Randomization (MR), this provides the best possible evidence that the protein is causally involved in the disease being studied. This is because while protein expression could change as a result of disease, the genetic variant cannot.



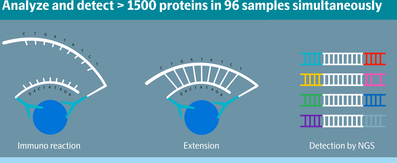
Olink proteomics solutions at the heart of your multiomics strategies

High throughput multiplex – data you can trust

The sensitive Proximity Extension Assay needs less than one drop of blood to measure the protein profile in a patient sample.

- Matched pairs of antibodies, carrying unique DNA-tags, bind to the respective proteins in the sample.
- When the matched DNA are brought into close proximity, they can hybridize.
- Only the correctly hybridized tags are extended to an amplicon with a unique sequence for each protein.
- Depending on the study, readout can be done with NGS or qPCR.
- Olink Explore using NGS enables readout of 1536 assays in 96 samples simultaneously.

Analyze and detect > 1500 proteins in 96 samples simultaneously



Explore 1536

Measure 1,536 proteins with minimal biological sample. Soon 3K and 4.5K proteins covering the low abundant dynamic plasma proteome.

Target 96

Choose from fifteen carefully designed panels built for specific area of disease or key biology process.

Focus

Custom-designed for your specific need Measure up to 21 proteins simultaneously with relative or abbsolute quantification and two validtion levels.

Explore 384

Remarkably small sample volume, 1 µL and outstanding throughput, 1,35 M measurements per week/system.

Read more

Target 48

Introducing our Inflammation 48-plex panel with absolute quantification.

Read more

Read more

Related content

Protein biomarkers at the heart of multiomics strategies

Visit our information page to learn more about the power of multiomics studies and how proteomics is set to take centre stage in the next era of biological research and the development of precision medicine.

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The genetics of the proteome

SCALLOP (Systematic and Combined AnaLysis of Olink Proteins) is an independent, collaborative consortium for the discovery and follow-up of genetic associations with proteins using the Olink platform.

Read more

A multiomics longitudinal wellness study

View a recorded Science webinar from Sept 2020 featuring Professor Mathias Uhlén (KTH Royal Institute of Technology, Stockholm), "When proteins get personal: A new concept for highly sensitive, multiplexed plasma."

View webinar

Driving next-generation medicine discovery with proteogenomics

View a recorded Science webinar from Feb 2021 featuring Dr. Anders Mälarstig (Pfizer & Karolinska Institute) and colleagues from the SCALLOP consortium.

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