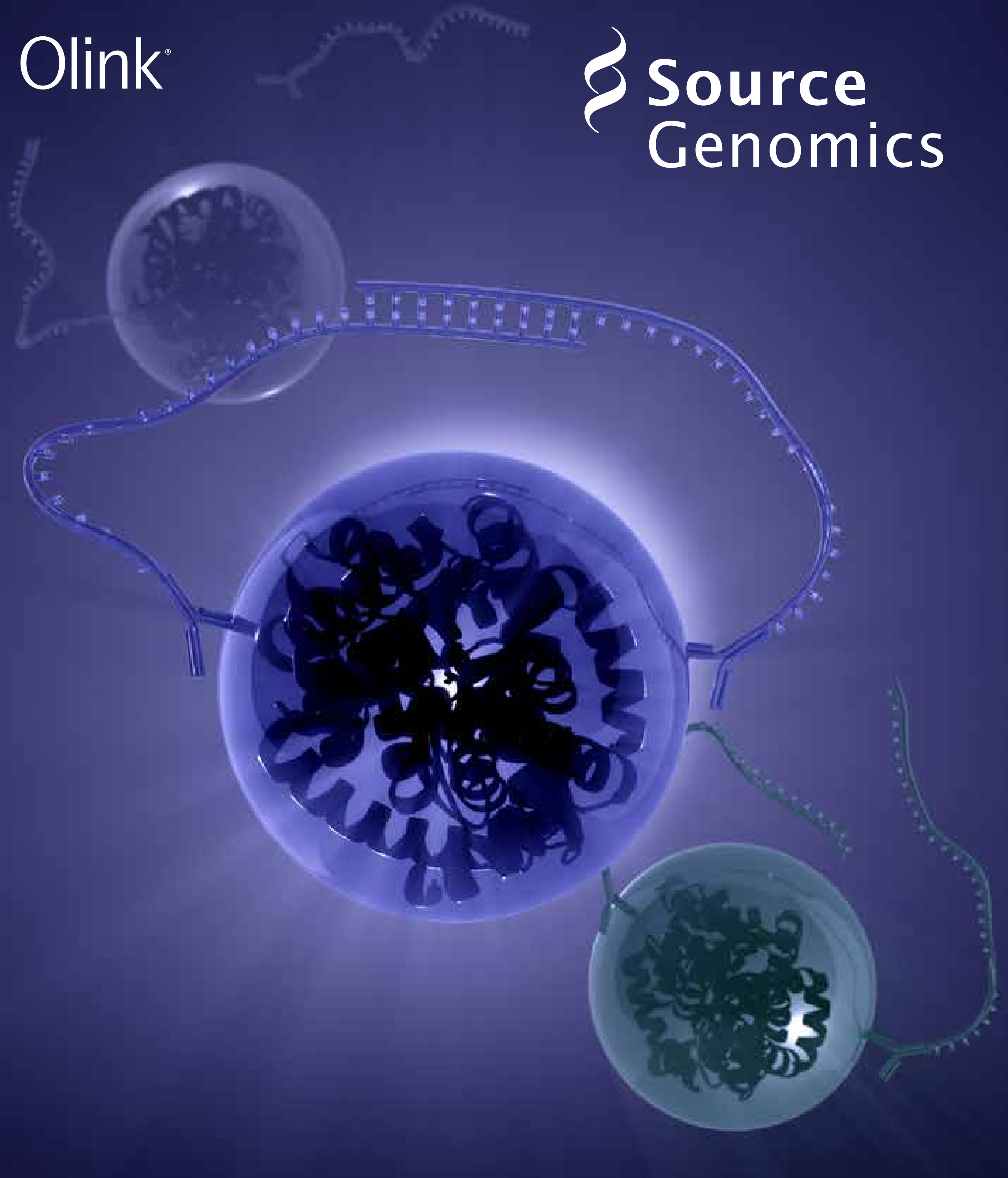
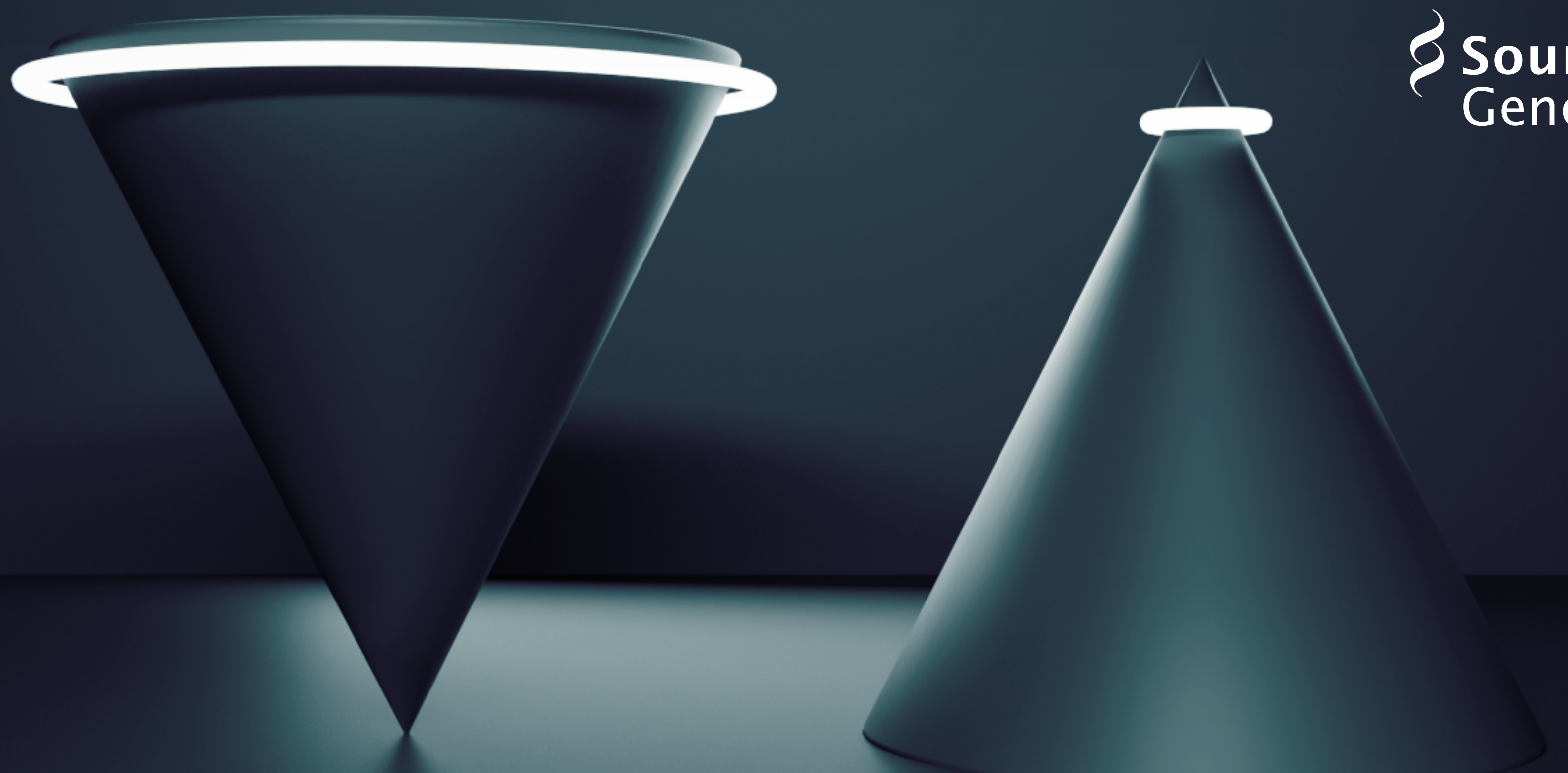
Olink®

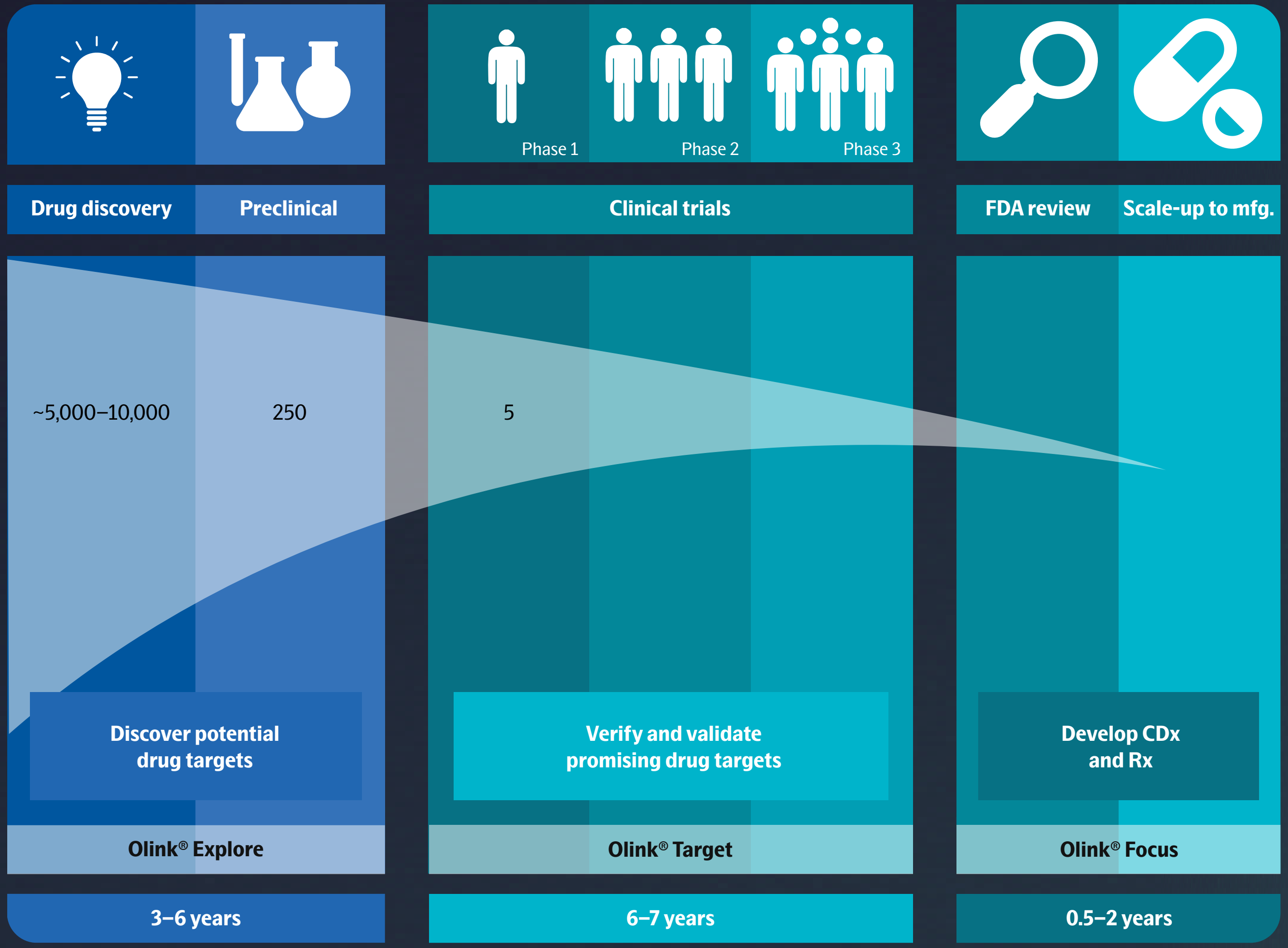
Source
Genomics



One proteomics platform.
Endless possibilities.

How efficient is your drug development process?





The drug discovery and development process faces many problems, including protracted time to market, high attrition rates, and inefficiency in identifying novel drug targets.

Methods thus far have used genomics and transcriptomics as proxies for proteins, which are the targets of most drugs on the market. DNA and RNA studies cannot, however, provide comprehensive information on drug efficacy and safety, and patient stratification in clinical trials. There is a clear and pressing need for improvement in delivering the right dose, to the right patient, at the right time.

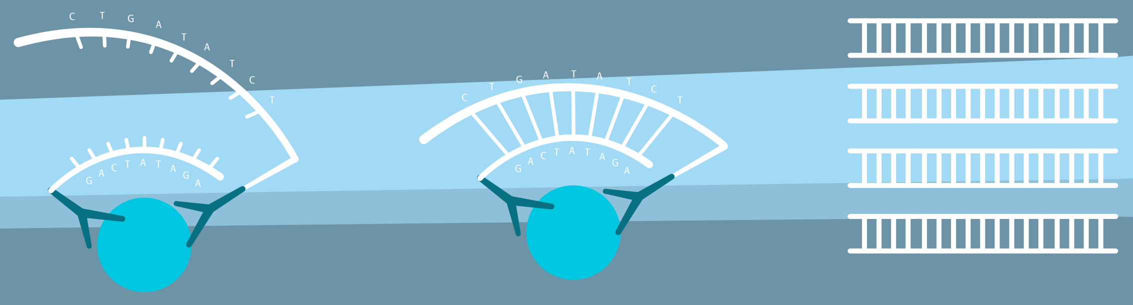
Proteomics offers several key benefits to improve drug discovery and development:

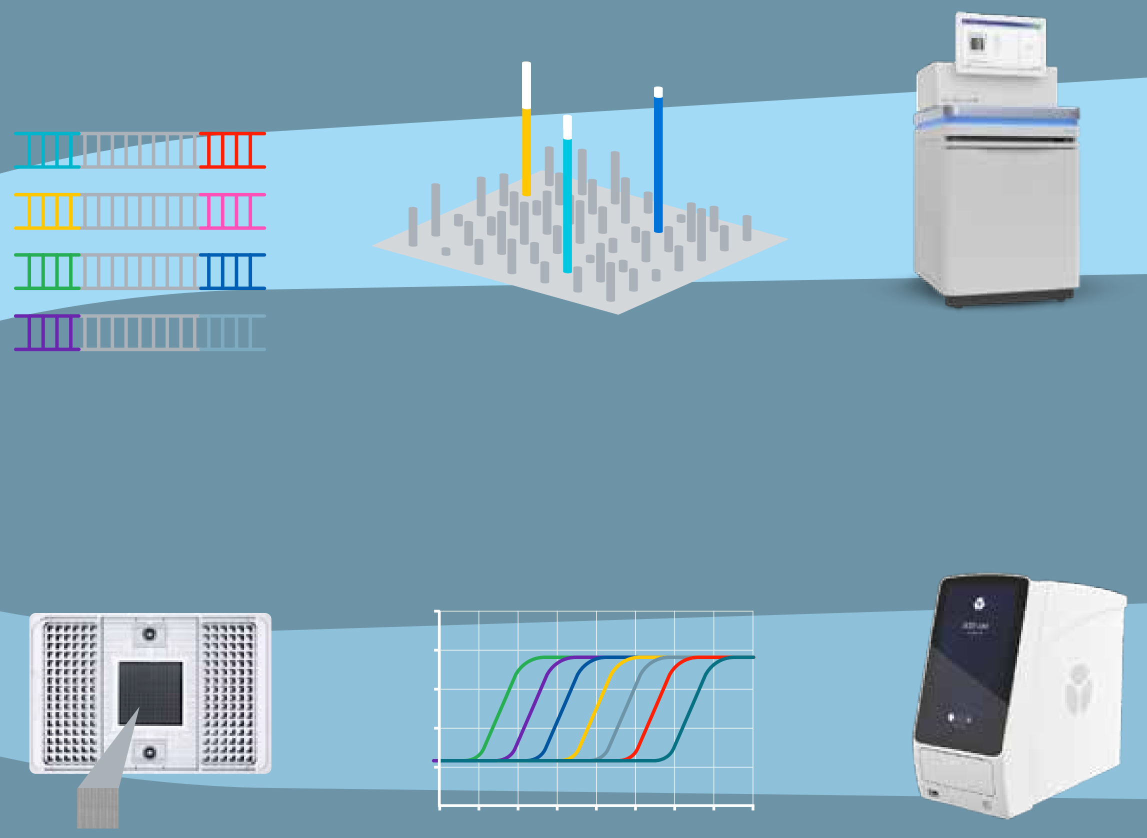
- Combined with genetic and phenotypic data, it offers a uniquely powerful approach to determine protein *causality* in disease, via protein Quantitative Trait Loci (pQTLs) – essential to identify new, robust drug targets.
- Provides the best possible picture of dynamic changes in the human body in response to drugs or disease progression to better understand mode of drug action and drug response.
- Identifies actionable biomarkers that support the entire drug development process through providing pathobiological insights, stratifying patients and acting as surrogate markers for drug efficacy and safety.

However, until now proteomics methods were relatively low throughput and neither robust nor sensitive enough to measure the low abundant human plasma proteome, which best reflects our real-time biology as it responds to disease and pharmacological interventions.

The Olink® proteomics platform is a game changer in that it can measure the broad dynamic range of the plasma proteome, can be scaled to be used in all steps of the drug development process from large-scale biomarker discovery to a more targeted approach, and provides high quality, replicable proteomics data to help you develop better, more effective pharmaceuticals.

Unrivaled data quality at any scale: The Proximity Extension Assay (PEA)



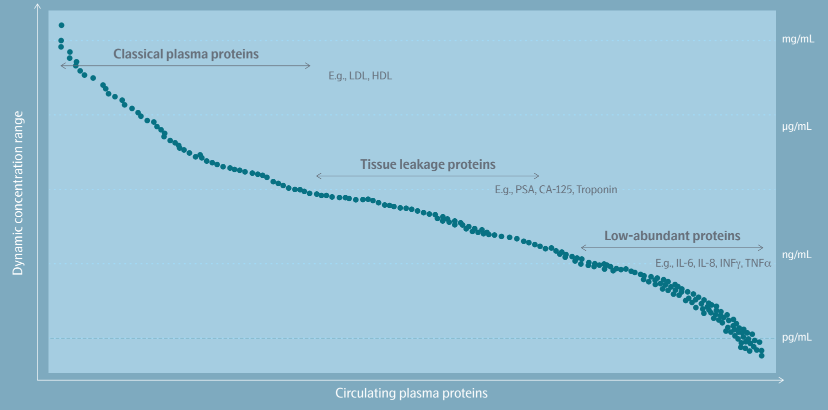


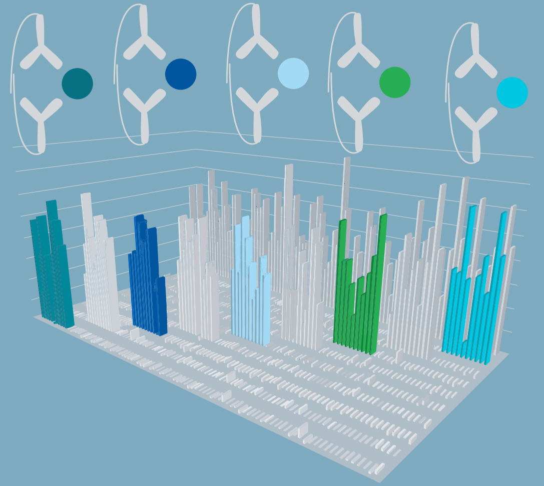
PEA technology combines the best of antibody and DNA-based methodologies to provide unique, enabling tools for protein biomarker discovery and development.

PEA consists of three core-steps; Immune reaction, generation of barcodes and amplification, followed by readout using either qPCR or NGS. The strength of our platform is that we have taken the best from two worlds: the high affinity of antibody-ligand binding assays, and a DNA-based readout, which gives a very high signal amplification and throughput, allowing for protein profiling of thousands of samples per week and minimal sample consumption (e.g. measure ~3000 proteins using less than 6 µL plasma or serum). Moreover, the dual-recognition assay format, requiring the binding of two matched antibodies linked to complementary oligo DNA sequences, offers exceptional specificity even at very high multiplexing levels.

Extensive quality controls are built into each assay, allowing full visibility and control over its technical performance, as well as the samples themselves. Internal controls are spiked into our assays to monitor every step of the process, while external controls are run on each plate to monitor variation between plates. This avoids having to re-run samples and helps ensure the generation of reliable data.

Covering the broad range of the plasma proteome





Our comprehensive validation

All of our assays are rigorously quality controlled and our validation data is made freely available on our website.

- Sensitivity – similar to ELISA or better and we determine LOD, LLOQ and ULOQ.
- Precision (average intra %CV <10% and inter %CV <20%) applying across our product range, from high-multiplex assays to midplex ones.
- Specificity – no readout of cross-reactivity thanks to dual-recognition of two antibodies and DNA-barcoding that is unique to each protein. In the very rare cases where an assay measures two related proteins, Olink is completely transparent about this and provides the necessary information to customers.
- Dynamic range spanning more than 10 logs, which makes it ideal for the study of the plasma proteome.
- Fully validated for plasma and serum samples, but may also be used for other sample matrices.

Source Genomics

The high quality of our data ensures actionable insights

Our protein assay library covers every major biological pathway and function within the low abundant plasma proteome. Using less than a drop of blood, our platform generates millions of data points to help you gain actionable insights, fast.

Translate those data points into an understanding of real-time biology, disease, or development of effective drug targets by using our statistical service offering.

Sample data

Internal and external controls throughout our platform workflow ensures that your data is of the highest quality.

Data quality control

You receive your results via our Olink® MyData cloud solution and can easily contact us should you need our help. With Olink® NPX Data Analysis software, your data is run through a series of quality control checks.

Data normalization

Conversion of raw NGS/qPCR data into our proprietary Normalized Protein eXpression (NPX) format involves data normalization, which is handled by our Olink NPX Data Analysis software.

Data visualization

Olink MyData and our Olink® Statistical Analysis app allows you to explore your data using their inbuilt data visualization tools.

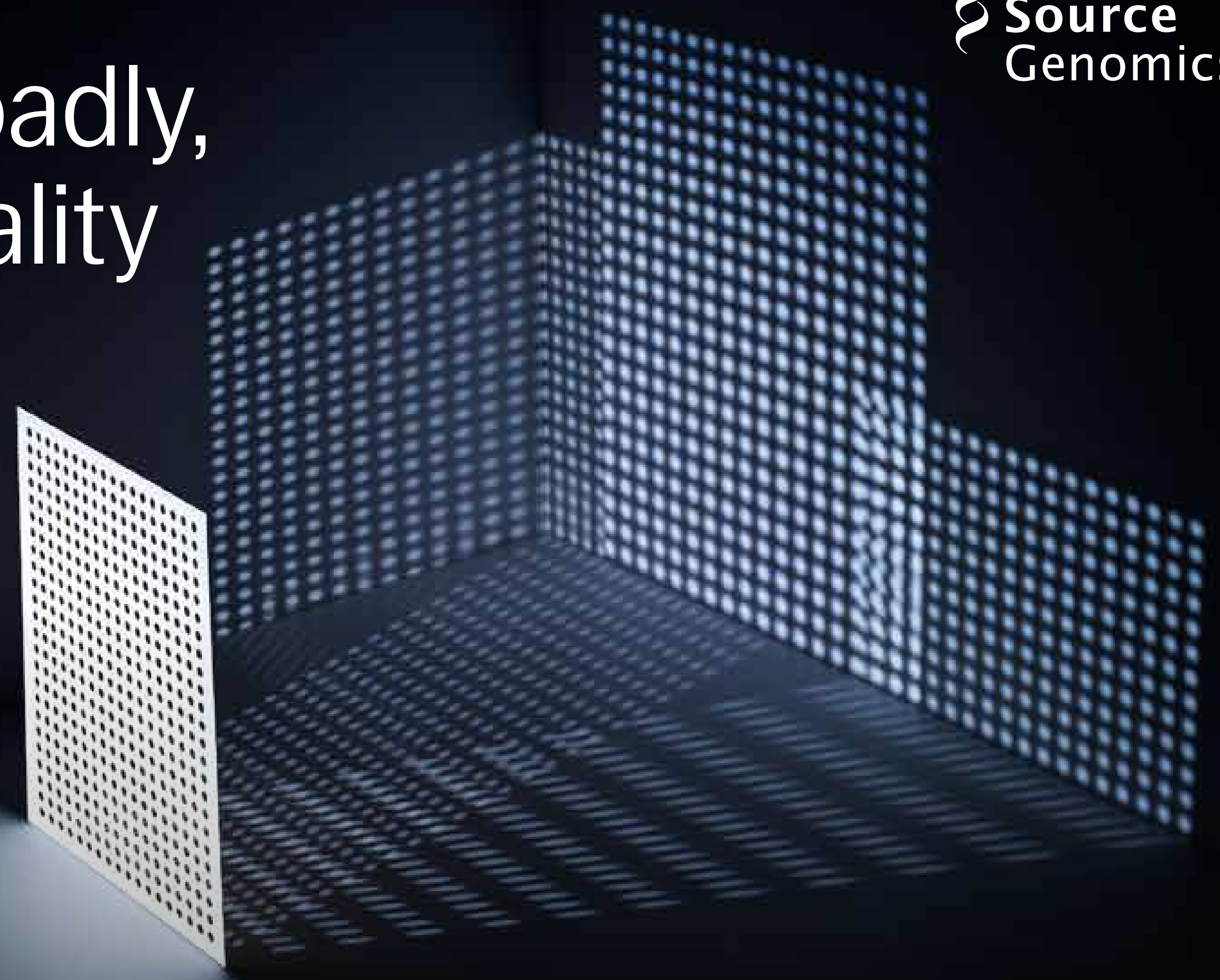
Statistical analysis

Perform basic data visualizations and statistical analyses using our Olink® Statistical Analysis app, or for those with R programming skills, the OlinkAnalyze, an R package that is available on GitHub. For more complex analyses, the experts in our Data Science team can help.

From data to actionable insights and knowledge-based decision making

The result of all this world-class technology and expert support? Actionable proteomics data that leads to faster drug development, more effective and safer clinical trials, and ultimately advances our healthcare systems.

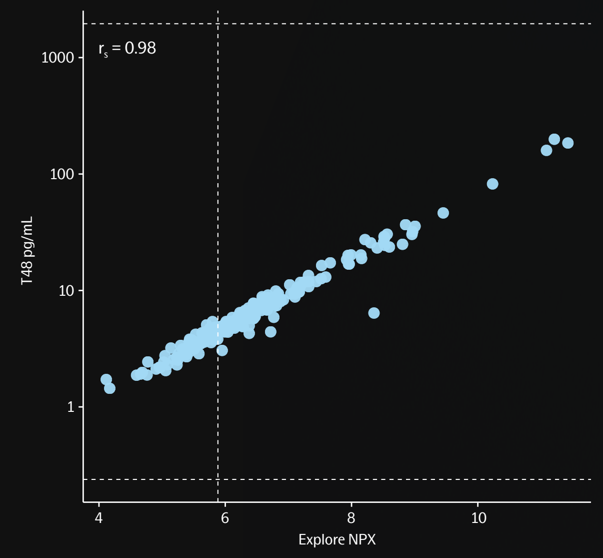
Discover novel drug targets — broadly, rapidly, and with unparalleled quality



Protein biomarker discovery with Olink Explore can provide vital new insights across the drug discovery and development process, from the identification of novel therapeutic targets, selection and development of the best drug candidates, better understanding of drug action mechanism, through to patient stratification and selection of surrogate markers for clinical trials.

The carefully designed Olink Explore library provides extensive coverage of proteins representing the dynamic plasma proteome. With the help of knowledgeable scientists including key opinion leaders in different fields, we have selected proteins that are likely to contribute the most to key research questions. Olink Explore includes thousands of proteins that can be classified into one or more of the following categories:

- Secreted proteins
- Organ specific blood biomarkers
- Inflammatory markers
- Approved and ongoing drug target proteins
- Exploratory proteins



A study investigating immune checkpoint blockade (ICB) treatment of metastatic melanoma patients performed proteomics analysis using both Olink Explore and Olink® Target 48. Comparison of the two datasets show very strong correlation for the biomarkers measured on both the Explore 1536 (NPX levels) and Target 48 (pg/mL) platforms. This shows that the readout technology used (NGS or qPCR) does not influence the end results.

The Olink Explore platform comprises eight 384-plex panels. These panels are organized into four disease areas:

- Olink® Explore 384 Cardiometabolic
- Olink® Explore 384 Inflammation
- Olink® Explore 384 Neurology
- Olink® Explore 384 Oncology

The Olink Explore platform is both flexible and scalable; customers may run the entire library or focus on one or more of the 384-plex panels. How you choose to have your samples analyzed is also flexible: they may be run at one of our Analysis Service labs in Uppsala or Boston, or at one of our many certified external service provider partners. Alternatively, Olink Explore kits can also be purchased directly for running in labs with the correct equipment set-up and training.

Why Source Genomics?

Elevating research capabilities in drug and biomarker discovery

Source Genomics is your trusted laboratory service partner for rapid and high-quality proteomics.

- Multi-omics service offering
- Highly qualified laboratory experts
- Market-leading turnaround times
- UK-based sample processing
- Local proximity to leading biotech and pharma organisations

Source Genomics

Contact us today: **enquiries@sourcebioscience.com**

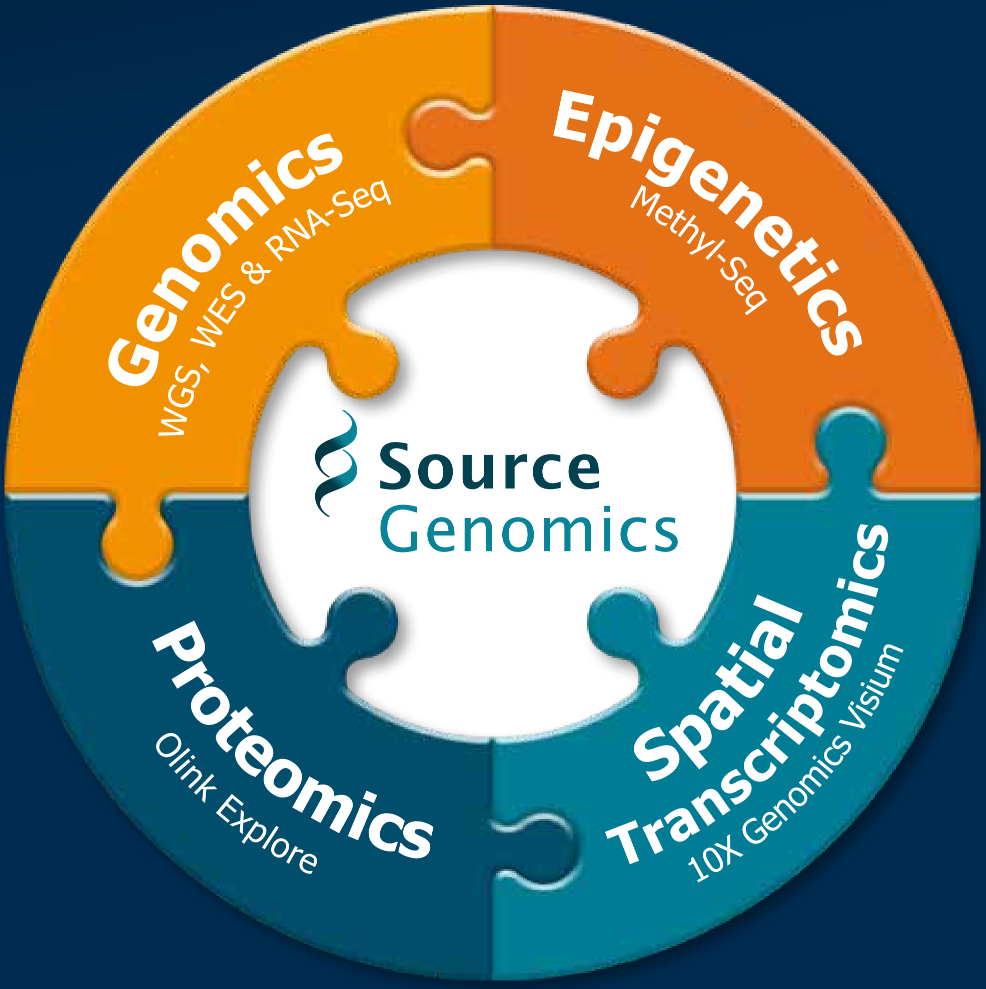
Endeavour House, Vision Park, Cambridge, CB24 9ZR

sourcebioscience.com

Notes

Unlock the benefits of end-to-end multiomics services

Source Genomics offers a multiomic approach for large-scale research projects, uncovering complex biological systems, disease mechanisms and therapeutic interventions.



Source Genomics

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