SERVICE GUIDE

Olink®- Target

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Service Guide

Olink - Target

1.0 Overview

AGRF offers access to the Olink® Target workflows, using the Olink® Signature Q100 system, which enables streamlined proteomic analysis through a range of highly specialized panels designed for targeted biomarker studies.

The Olink® Signature Q100 is a compact and intuitive system designed for high-throughput proteomic studies, offering precise quantification of proteins through Olink's specialised biomarker panels. Unlike the HT protocol, which utilizes NGS technology, the Q100 employs qPCR technology, providing a streamlined and accessible solution for protein biomarker analysis.

Key Olink® Target workflows available Through AGRF

- **Target 96 Panels**

Focused on specific diseases or biological processes, these panels allow the relative quantification of 92 carefully selected proteins within 88 samples. Researchers can access a library of over 1100 human proteins across 14 distinct 96-plex panels.

- **Target 48 Panels**

Tailored for studies involving inflammatory diseases or processes, these panels analyze 43–45 proteins across 40 samples. Absolute quantification is provided alongside relative concentrations, ensuring robust and reliable data.

Advantages of the Olink® Platform at AGRF

The Olink® platform employs Proximity Extension Assay (PEA) technology combined with qPCR readouts, enabling unparalleled specificity and sensitivity for proteomic studies.

Olink is purpose built for plasma serum proteomics, but has shown published utilities in a number of alternative matrices, including;

- Human EDTA Plasma/Serum
- Mouse Plasma/Serum
- Conditioned Media
- Cell/Tissue Lysates
- Cerebrospinal Fluid (CSF)
- Urine
- Interstitial Fluid/Microdialysis
- Ocular Fluids
- Dried Blood Spots
- Exosomes
- Synovial Fluid

Please note that Olink antibodies are specific for human proteins. Therefore, if using matrices of non-human origin, proteome coverage will be variable.

The analysis metrics quoted by Olink are from samples processed from Human EDTA Plasma/Serum. Please contact AGRF if you are intending to use other types of matrices. Additional information on treatment and effects of using conditional media can be found here.

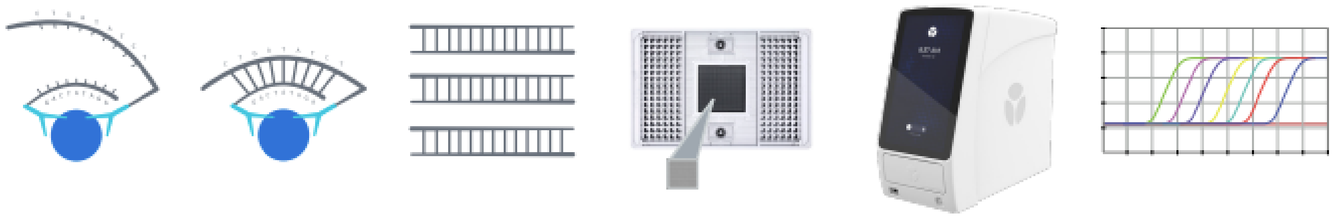
2.0 Workflow

The Olink® Signature Q100 utilizes a precise workflow to deliver reliable protein biomarker data.

Antibodies tagged with DNA bind to specific proteins, forming highly selective recognition pairs for accurate detection. DNA polymerase then extends these tags to create unique barcodes, which are amplified using PCR to ensure clarity and sensitivity, even for low-abundance proteins. The amplified DNA and reagents are loaded into a microfluidic biochip, prepared for high-throughput analysis. The Q100 system reads the biochip, translating the DNA quantities into protein concentrations reported in either pg/mL or Normalized Protein Expression (NPX) units.

Quality control is performed using the Olink NPX Signature software.

Figure 1 Olink® Signature Q100 Workflow



3.0 Technical Considerations

When utilizing the Olink® Target service, several technical considerations ensure optimal performance and data quality.

Sample integrity is critical; samples must be free from contaminants, such as hemolysis or lipids, that can interfere with the Proximity Extension Assay (PEA) technology.

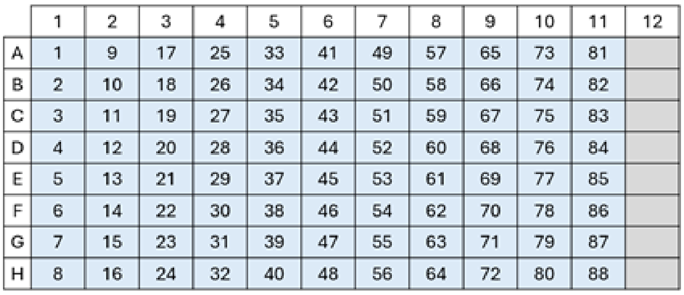
Proper selection of panels based on the research focus is essential, as different panels target specific disease areas or biological processes. Additionally, the PEA workflow includes built-in controls and quality checkpoints to ensure assay specificity and sensitivity, with all results subjected to stringent quality control using NPX normalization. Researchers should also consider the level of quantification needed, as results can be provided in either relative or absolute concentrations depending on the chosen panel.

The volume of sample required will vary depending on how many panels will be used. AGRF request no less than 50 ul per sample, supplied in a plate. If this is not possible, then please contact us to discuss.

- It is recommended when a study is to be run across multiple plates and multiple runs, then multi-plate normalisation methods must be considered. Reference sample normalisation must be applied if multiple plates are being run at different times for the same study. This involves selection a minimum of 20 samples to be included to all plates across a study, such that run to run, batch to batch and lot to lot variability may be controlled. Additional sample will be required for samples to be used for batch control.
- Clients are advised to randomise their samples and submit as sample plates. However, if this is not done then samples must be randomised across plates such that row or column effects are minimised. Please note that only 88 samples should be loaded into each plate as 8 wells are required for Olink controls. See figure 2.
- Biomarker discovery involves analyzing complex biological samples, such as serum, bodily fluids, or tissues, which present a wide dynamic range of protein concentrations. This inherent variability is characteristic of proteomics. All samples are processed alongside controls, and quality control (QC) data is carefully screened before final data delivery. As a result, not all biomarkers may be represented in your dataset.
- The impact of interference should be carefully considered when comparing samples collected in different blood collection tubes. To minimize variability, clients should, where possible, use samples from the same tube type.

Please follow the plate layout as shown in figure 2, keeping wells empty to for Olink controls.

Figure 2. Plate layout when submitting more than 88 samples.



	1	2	3	4	5	6	7	8	9	10	11	12
A	1	9	17	25	33	41	49	57	65	73	81	
B	2	10	18	26	34	42	50	58	66	74	82	
C	3	11	19	27	35	43	51	59	67	75	83	
D	4	12	20	28	36	44	52	60	68	76	84	
E	5	13	21	29	37	45	53	61	69	77	85	
F	6	14	22	30	38	46	54	62	70	78	86	
G	7	15	23	31	39	47	55	63	71	79	87	
H	8	16	24	32	40	48	56	64	72	80	88	

4.0 Submitting Samples

4.1 Online Submission

Temperature

- Storage temperature: -80 °C
- Shipping temperature: Dry ice shipping.

Long-term storage

- Samples that are 20-30 years old have been used successfully.

4.2 Packaging of Samples

- Frozen samples must be sent on dry ice.
- Sample tubes should be in a zip-lock bag or box to avoid direct contact with dry ice.

AGRF can organise dry ice shipment for your samples as part of your quoted services or you can use our free shipping between nodes once a week service. For information on this service go to Free Shipping.

Send/deliver samples to the addresses below:

In the client portal, select the service dropdown menu.

- Enter your species and submission format (tube).
- Complete and upload the template file.

Submit the form and print the submission receipt to be included with your sample package.

Physical address (courier)*

ATTN Proteomics AGRF Ltd.
VCCC Loading Dock 14 Flemington Road
North Melbourne, VIC 3051

*Note: our loading dock is open from 7am to 3.30pm weekdays.

5.0 Sample Returns/Discards

Samples are stored with AGRF for 1 month after you receive your data. If you wish for your samples to be returned, you must discuss this with your account manager during quoting or contact us after you receive your data. At the completion of your project, we can return samples by courier with dry ice (please ask your account manager for a quote).

If we are not notified within the specified time frame, samples will be automatically discarded.

6.0 Results and Data Outputs

Data output is workflow dependent but is provided as .CSV file containing normalised protein expression (NPX) values or pg/mL values

7.0 Quality Statement

AGRF Ltd. is a Certified Service Provider for Olink Explore HT and Explore 3072.