White paper

How Olink® technology complements mass spectrometry

Highlights

- The Olink proximity extension assay (PEA™) and liquid chromatography mass spectrometry (LC-MS) are complementary techniques for protein biomarker discovery and characterization
- Both technologies have their advantages: PEA has exceptional specificity and high sample throughput, while LC-MS can achieve higher protein coverage at the expense of sample throughput
- An expanded approach is justified to effectively achieve goals to increase proteome coverage, verify candidate biomarkers, and perform multiomic analyses

Introduction

As the functional regulators of phenotype, proteins are a primary focus of translational and clinical research. Technologies for protein expression profiling are generally classified as being targeted or untargeted. Targeted assays analyze a pre-selected set of proteins and generally rely on affinity-based reagents (e.g., antibodies) to bind specific proteins. Untargeted assays, on the other hand, measure proteins in a theoretically global manner without the use of affinity reagents.

Two commonly used proteomic technologies for targeted and untargeted analyses are PEA and "bottom-up" LC-MS, respectively. This white paper provides an overview of how these technologies work and compare to each other, and highlight the complementarity of these proteomic methods in protein profiling, biomarker discovery, and multiomics research.

How the technologies work

PEA technology

PEA combines the high specificity and affinity of antibodies with the exceptional sensitivity of PCR. Briefly, two antibodies that bind to the same target protein are conjugated with complementary DNA oligonucleotides ("oligos") (Figure 1). Each uniquely identified "barcoded" oligo has a sequence that is specific to the target protein (1). When the correct antibody pair binds to its target protein, the complementary oligos hybridize and form a double-stranded oligo that is amplified by PCR. The resulting amplicons, which are proportional to the protein concentration, are then quantified with quantitative PCR (qPCR) or next generation sequencing (NGS). Finally, the readout is proportional to the original concentration of the targeted protein.

Due to the PEA technology's high specificity and sensitivity, full validation data is publicly available for each analyte. In addition, as many as 352 samples can be analyzed at once (Table 1), accommodating up to two runs per day.

By using unique DNA-based barcodes with a qPCR or NGS readout, PEA facilitates a range of protein assay multiplexing levels that can be used throughout the biomarker pipeline (Table 1).

Table 1. Overview comparison of Olink® biomarker platforms

Olink platform	Data readout	Library size [1] (# proteins)	# Proteins measured at one time	# Samples measured at one time	# multiplex panels	Sample consumption per panel	Biomarker discovery & exploratory proteomics [2]	Biomarker validation [2]
Olink® Explore HT	NGS	5400+	5400+	344	1	2 µL	+++	+
Olink® Explore 3072/384	NGS	2900+	2900+	352	8	1 µL	+++	+
Olink® Target 96	qPCR	~ 1100	92	88	15	1 µL	++	++
Olink® Target 48	qPCR	89 (human) + 43 (mouse)	45	40	3	1 µL	+	++
Olink® Flex	qPCR	~ 200	5 - 30	40	Mix-&-match panel	1 µL	+	+++
Olink® Focus	qPCR	5000+	Up to 21	144 or 160	1 custom panel	1 µL		+++

[1] For the most up-to-date library size, visit *olink.com*, [2] Applicability: high (+++), moderate (++), low (+)

It also consumes a minute sample volume 1- 2 µL.

Depending on the Olink platform, data readout is also identified with the correct sample based on additional barcoding or the location of the sample on an integrated fluidic circuit. Protein biomarker panels with a qPCR readout are analyzed using the Olink® Signature Q100, which is a compact, benchtop system that enables a seamless integration from panel analysis to data output.

Liquid Chromatography – Mass Spectrometry (LC-MS)

Since the early 1990s, LC-MS has become a "gold standard" method in discovery proteomics due to its versatility, ability to detect thousands of proteins in one experiment, and rapid technological advancements. By far, "bottom-up" LC-MS, or shotgun proteomics, is the most popular MS method for analyzing proteins. In the first step, proteins are typically digested with trypsin and the resulting tryptic peptides are then separated on an LC column. The mass-to-charge ratios (m/z) of the peptides (MS1) and their peptide fragments (MS2) are then measured using a mass spectrometer (MS) instrument (Figure 2). Peptides are assigned to proteins via statistical comparisons of MS1 and MS2 spectral data against expected values, which are generated from an *in silico* enzymatic digestion of a protein database. The peptides are often further fragmented into product ions (MSn) to obtain higher specificity.

As an untargeted method, LC-MS can analyze hundreds to thousands of proteins simultaneously without the use of affinity reagents for protein profiling and biomarker discovery. However, high sample complexity and ion competition reduce the number of proteins that can be detected. This is particularly relevant for serum and plasma, which have concentrations of individual proteins spanning over 10 orders of magnitude and 99% of their protein content is comprised of only 22 proteins (2). Additional steps during sample processing can increase proteome coverage and sample multiplexing. For a more thorough review, please refer to articles in the "References" section (3, 4).

LC-MS can also target specific peptide sequences using similar approaches called multiple reaction monitoring (MRM) using a quadrupole-based mass spectrometer, which is routinely performed for biomarker validation and clinical assays. Here, the mass spectrometer isolates and analyzes parent and daughter ions based on their specific m/z. Often, peptides-of-interest of known quantities are isotopically labeled and mixed with the sample. The unlabeled sample peptides and labeled spike-in peptides co-elute from the LC column and then parent and fragment ions are quantified by MS. Up to 100 proteins are analyzed simultaneously with MRM (5). A similar approach that is also used to analyze specific peptides is parallel reaction monitoring (PRM). Bottom-up approaches are hereafter referred to as "LC-MS" and MRM as "LC-MRM-MS."

A comparison of PEA with LC-MS

The key differences between PEA and LC-MS are described below and summarized in Table 2.

Sample types

PEA measures intact proteins in their native state whereas LC-MS analyzes protein cleavage products (i.e., peptides) (Figures 1 and 3, Table 2). Both technologies can analyze a wide variety of sample types, such as plasma, cerebrospinal fluid, vitreous fluid, cell lysates, and tissue lysates. However, formalin-fixed paraffin-embedded tissues are incompatible with PEA and sub-optimal for LC-MS where fixation can modify amino acid residues that interfere with protein identification. LC-MS is also unsuited for samples that contain polymers and surfactants like polyethylene glycol (PEG) and sodium dodecyl sulfate (SDS). PEA, on the other hand, is compatible with < 2.5% v/v PEG, < 0.1% w/v ionic detergents (e.g., SDS), and < 1% v/v non-ionic detergents (e.g., Tween® 20, Triton™ X-100, NP-40).

Specificity

PEA has exceptional specificity because it requires a pair of cognate antibodies to bind to the target protein and the complementary oligonucleotides to hybridize to each other. The antibodies employed in current PEA platforms target "total" proteins, or proteins that may or may not have post-translational modifications (PTMs). Low abundance and small proteins are identified with equal confidence with PEA.

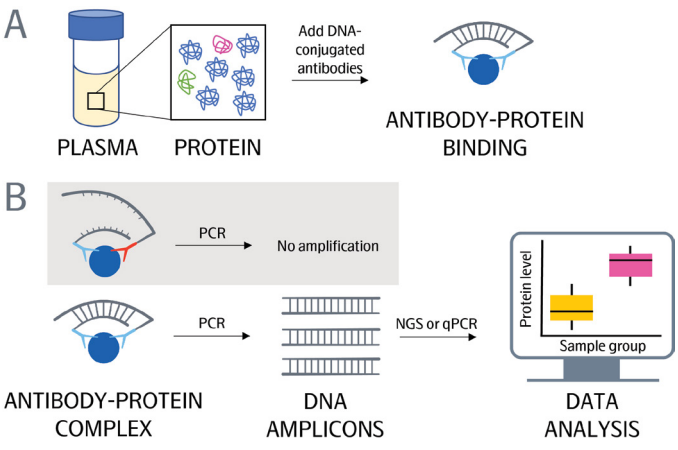

Figure 1. General workflow of PEA technology. (A) Plasma (or alternative) samples are aliquoted and mixed with paired antibodies labeled with complementary DNA oligonucleotides. (B) An antibody pair binds to its target protein: the oligonucleotides hybridize, are amplified, and then analyzed with NGS or qPCR. Data output is then converted to protein levels with software.

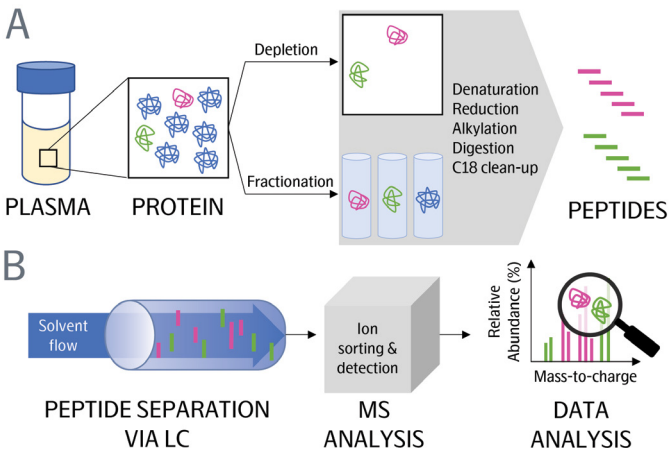

Figure 2. General workflow of bottom-up LC-MS. (A) Plasma samples are often depleted of the most abundant proteins or fractionated to decrease sample complexity. (B) Peptides are separated via LC, which is coupled to a mass spectrometer that measures the mass-to-charge of each peptide ion. The peptide mass spectra or fingerprints match a sequence database, and then the peptides are assigned to proteins from a protein database.

LC-MS requires software algorithms and statistical parameters, such as false discovery rate (FDR) cutoffs, to predict protein identification. In other words, a certain pre-defined percentage of false positives is built into the final data. Moreover, the confidence of accurate protein identification and quantification is decreased for lower abundant or smaller proteins that are often only identified with one or two peptides. Unlike PEA, LC-MS can distinguish between proteins with and without PTMs, which may be involved in cellular homeostasis, disease progression, and drug resistance.

Key distinctions between PEA & LC-MS

PEA technology combines antibodies and PCR to analyze protein concentrations, with high specificity, wide dynamic range, low sample-to-sample variability, and support for high throughput analysis.

LC-MS has many techniques available for both targeted and untargeted approaches, is widely used, and can identify thousands of proteins at the cost of lower sample throughput.

Sensitivity

PEA and LC-MS can both measure protein concentrations in the fg/mL range. While the PEA workflow is identical for all sample types, additional steps are required to analyze lower abundance proteins with LC-MS where high abundance peptides contribute to a phenomenon called "ion suppression" where the detection of lower abundance peptide ions is inhibited (6).

To address the negative impact of high abundance proteins on sensitivity, LC-MS analysis of plasma includes either depleting the 2 – 14 most abundant proteins or fractionating the sample using an additional LC separation step (Figure 2). Depletion and fractionation are not without their drawbacks (7). Depletion may result in concomitant removal of low and medium abundance proteins that bind to high abundance proteins. Fractionation decreases sample throughput since each fraction requires a separate LC-MS analysis.

Dynamic range

Olink Explore has a dynamic range spanning 10 orders of magnitude, which is particularly relevant for the analysis of plasma (2). The dynamic range of each Olink Target panel is, on average, 10^4. The dynamic range of LC-MS is not as straightforward since it depends on various factors, including sample processing. For example, the linear dynamic range of LC-MS for crude plasma is about 10^3. It can increase to 10^5 – 10^7 following additional processing steps, such as depletion or fractionation as described above (8, 9). With extensive multi-dimensional fractionation, a dynamic range of 11 orders of magnitude can be achieved (10).

Protein and sample throughput

PEA technology supports low- to high-plex analyses. For example, Olink Flex, Focus and Olink Target measure 5 – 92 proteins across 40 – 160 samples at one time with a qPCR readout (Table 1). Olink Explore 3072 measures nearly 3000 proteins in 352 samples in one next-generation sequencing (NGS) run, while Olink Explore HT measures over 5400 proteins in 344 samples in one next-generation sequencing (NGS) run. Importantly, multiplexing capability of PEA does not change based on sample type.

Large research consortiums, like COLLIBRI, CORAL, SCALLOP, and UKB-PPP (UK Biobank Pharma Proteomics Project), have utilized the high throughput, multiplexing capability of PEA. The UKB-PPP, for example, used Olink Explore to profile 1472 unique proteins in plasma from 54,306 participants (11). To analyze these many samples with Olink Explore HT, it would take 26 weeks using one NGS system (i.e., Illumina NovaSeq 6000 with two S4 flow cells per run).

LC-MS typically measures < 300 or 300 – 500 proteins simultaneously in naïve or depleted plasma, respectively, with a total analysis time of 1 – 2 hours per sample (2, 4, 8, 12). With extensive depletion, fractionation, or LC gradient length that will decrease sample throughput, around 5000 plasma proteins can be identified per sample with LC-MS (9, 13). The Orbitrap Astral, an advanced mass spectrometer released in 2023, measures over 600 or 1000 proteins per sample of naïve plasma with a daily throughput of 180 or 24 samples, respectively (16). Thus, there is a tradeoff between protein coverage and sample throughput. A large-scale project with over 54,000 participants like the UKB-PPP, for example, would theoretically take over six years to analyze depleted plasma one at a time using a 1-hour LC gradient and a single mass spectrometer!

LC-MS analyses of other sample types, such as cell and tissue lysates, usually result in the detection of 2500 - 7500 proteins (14-17). However, higher protein multiplexing can be achieved with different, and often more complex, instrumentation set-up and analyses (18). For example, nearly 10,000 proteins were detected in cell and tissue lysates following sample fractionation and extending the total analysis time to 16 hours per sample (19).

Sample multiplexing is also possible with LC-MS to increase throughput. Here, peptides from different samples are labeled with unique stable isotopes (SILAC approach) or isobaric tags (e.g., TMT™ reagents) (3). This enables peptides with the same amino acid sequence but different m/z ratios to be differentiated from each other during MS analysis. Up to 18 samples are routinely analyzed at one time using commercially available kits, although as many as 27 samples have been analyzed simultaneously using isobaric tags (20). Unfortunately, quantification accuracy with LC-MS can be severely affected by sample multiplexing (21). A dedicated MS3 fragmentation event is thus employed to improve the accuracy, but this results in decreased sensitivity. This has led to limited adoption of multiplexed analysis with complex samples like plasma.

Precision

To measure the technical reproducibility, the same sample is analyzed multiple times. The coefficient of variation (CV) of PEA within the same plate (intra-CV) and across different plates (inter-CV) is <10% and <20%, respectively. The inter-assay CV of LC-MS, on the other hand, is 20 – 50% for complex proteomic samples (5, 12, 22, 23). In general, the CV of LC-MS increases as protein abundance decreases (24).

Number of replicates

Olink platforms include numerous internal and external controls, thus enabling samples to be analyzed without replicates. In contrast, a minimum of three technical replicates are routinely analyzed with LC-MS because sampling of complex mixtures results in low repeatability (i.e., identification of the same peptides). For example, one study showed that the same yeast sample analyzed three to six times with the same instrument set-up had a median repeatability of only 45% (25).

Table 2. Key differences between PEA and LC-MS in protein profiling, including workflow and data types affected by plasma and serum analyses

Key differences	PEA	LC-MS [1]
Sample type	Intact proteins	Digested proteins
Sample incompatibility	Formalin-fixed samples	Samples containing certain polymers and surfactants (e.g., PEG, SDS)
Sample preparation	Sample dilution for some Olink panels	Digestion, reduction, alkylation, & C18 clean-up [2]
Sample processing time for 96 samples	0 – 15 min	≥ 6 hours
Analysis time per 96-well plate	~1 day (Olink Target) to 2.5 days (Explore 3072)	4 - 8 days using a 1-hr LC gradient
Detection of low abundance proteins in plasma	No additional sample processing required	Depletion of highly abundant proteins or sample fractionation required
Detection of PTMs	No	Yes
Requires affinity reagents	Yes, paired antibodies	No, but included in some workflows
Specificity	High, due to a vigorous validation process and dual recognition method	High for high abundant or large proteins. Lower specificity for lower abundant or small proteins. A percentage of false positives built into the final data.
Sensitivity (or lower limit of detection, LLOD)	fg/mL	fg/mL
Dynamic range (orders of magnitude)	Regardless of sample type, 10^{10} with Olink Explore; ~10^{8} across Olink Target library; and ~10^{4} within each Olink Target panel, on average	~10^{3} with crude plasma, ~10^{5} – 10^{7} following plasma depletion or fractionation; and ~10^{11} possible with extensive multi-dimensional fractionation
Protein multiplexing or throughput	+5400	100s – 10,000 depending on the upstream workflow and sample type
Sample multiplexing or throughput	40 – 352	2 – 18 using commercially-available kits
Precision	< 10% intra-assay CV < 20% inter-assay CV	N/A intra-assay CV 20 – 50% inter-assay CV
Number of replicates	1	At least 3 recommended
Sample consumption (plasma)	1 - 2 µL	15 – 200 µL plasma
Sample consumption (other sample types)	1 µL per panel at 0.5 – 1.0 µg/µL (0.5 – 1.0 µg)	A minimum of 5 µL at 0.1 µg/µL (> 0.5 µg)
Relative quantification	All Olink platforms	All mass spectrometers
Absolute quantification	Ready-to-use kits (Olink Target 48, Olink Flex, Olink Focus)	Quadrupole-based mass spectrometers. User may need to test and optimize assay parameters.
Data analysis	Minimal training via easy-to-use software	Extensive training

[1] Common workflows, [2] Additional steps, such as depletion or fractionation, may be required

Sample consumption

PEA requires minimal sample volume for profiling proteins in plasma. For example, only 1 µL of plasma is consumed per Olink Target panel, which can measure up to 92 proteins simultaneously. Only 2 µL of plasma are consumed to measure over 5400 proteins with Olink Explore HT (26, 27).

With sample matrices other than plasma, Olink and LC-MS consume similar sample volumes. For instance, each Olink panel uses 1 - 2 µL with a starting protein concentration of 0.5 – 1.0 µg/µL (i.e., 0.5 – 1.0 µg total) whereas LC-MS can use a minimum of 5 µL at a starting protein concentration of 0.1 µg/µL (i.e., > 0.5 µg total).

Quantification

While relative quantification calculates the fold differences in protein levels across samples, absolute quantification calculates the protein concentration in standard units (e.g., pg/mL). Relative and absolute quantification are possible with PEA (Table 1). For MS studies, LC-MS can be used for relative quantification and LC-MRM-MS for absolute quantification.

Absolute quantification is available with certain Olink panels. The kits are ready-to-use and do not require constructing a standard curve; the reference standards have been optimized. Furthermore, Olink® Analyze software quickly converts signal readout to relative or standard units, depending on the platform.

Performing absolute quantification with LC-MRM-MS can be challenging due in part to incomplete digestion and technical variability in sample handling. Stable isotope-labeled peptides (required to perform reliable absolute quantification) are expensive and sometimes difficult to synthesize. In addition, the burden of quantification validation typically falls on the shoulders of the user who must identify, test, and optimize analysis parameters for the peptide(s) of interest.

Publications demonstrating the complementarity of PEA and LC-MS

The publications featured here successfully utilized both PEA and LC-MS to increase the proteome coverage, validate results, or perform multiomic analyses (Table 3). The authors of these studies concluded that PEA and LC-MS are "potentially complementary to each other," the protein measurements "highly correlated" across both technologies, and there were "benefits of merging the unbiased detection of shotgun MS and the sensitivity of PEA" (28-30).

Increase proteome coverage

In a crude plasma study by Petrera et al. where PEA and two forms of LC-MS were compared directly to each other, 672 (60.9%) of the 1104 identified proteins were detected only with PEA using eight Olink Target 96 panels while over 300 were identified by the two forms of LC-MS: data dependent acquisition (DDA) and data independent acquisition (DIA) (14). Only 35 proteins were measured by all three technologies (Olink, DDA-MS, DIA-MS) (31). PEA data thus represent a 155% increase in proteome coverage compared to using LC-MS techniques alone.

The aim of a study by Babacic et al. was to discover predictive biomarkers of treatment response in metastatic cutaneous melanoma (31). To perform LC-MS analysis, plasma was depleted of its 14 most abundant proteins prior to digestion and then peptides were labeled and separated into 72 fractions. Crude plasma was analyzed with one Olink Target 96 panel that detects 92 proteins. Of the total 118 differentially expressed proteins identified, 36 were identified only by PEA. Moreover, both technologies displayed the same increase in expression levels for two proteins (PD-1, CSF1) following treatment. By using PEA, the proteome coverage increased by 44%.

Previous studies have suggested a relationship between the umbilical cord (UCB) blood plasma proteome and the number of hematopoietic stem and progenitor cells (HSPCs). The objective of a study by Nilsson et al. was to investigate whether the UCB proteome could help identify blood units with high levels of HSPCs that could be used for transplantation to treat blood disorders (28). Sixty fractions per UCB sample were generated for LC-MS analysis while 460 proteins were measured across five Olink Target 96 panels (Table 3). Ninety-seven proteins were detected by both technologies, and 320 proteins were detected only by Olink Target 96.

By using PEA with LC-MS, the number of detected proteins in the study by Nilsson et al. increased 43% compared to using LC-MS alone. Nearly one-third (41/137) the differentially-expressed proteins in UCB with low or high HSPC counts were measured by PEA alone. Three differentially-expressed proteins were measured in both data sets with similar fold changes. Notably, 15 of the 96 differentially-expressed proteins identified by LC-MS were flagged as potential contaminants (e.g., keratin from skin during sample handling); no proteins analyzed with PEA were identified as potential artifacts. Analyses with additional Olink Target panels for this study as well as the study by Babacic et al. would have undoubtedly increased the proteome coverage further.

Validate Findings

Bhardwaj et al. used LC-MRM-MS and PEA to identify protein biomarkers in plasma of colorectal cancer (CRC) in patient samples using a multi-step approach (29). Using a discovery cohort, 270 unique proteins were first targeted by LC-MRM-MS and then measured using three Olink Target 96 panels (Table 3); 11 of the biomarker candidates identified by LC-MRM-MS were confirmed with PEA. The 11 proteins, along with a candidate biomarker only detected with PEA (AREG), were analyzed with PEA using an independent cohort in a true CRC patient screening setting (n = 259). Modeling identified a 5-marker signature of CRC, including AREG, with areas under the curve (AUCs) of 0.76 – 0.86 in the validation cohort. The authors considered its diagnostic performance "reasonably better for early detection of CRC than the first FDA-approved blood-based test for CRC screening."

Table 3. Summarized results of featured studies that have employed both PEA and LC-MS

Reference	Experimental goal	Sample type(s)	Olink Target 96 panels	Result of using PEA with LC-MS
(14)	To test and compare the performance of LC-MS with PEA	Crude plasma	8 panels: Cardiometabolic, Cardiovascular II, Cardiovascular III, Oncology II, Oncology III, Development, Immune response, Neurology	155% increase in proteome coverage
(33)	To discover predictive biomarkers of treatment response in cancer	Crude plasma (PEA), depleted and fractionated plasma (LC-MS)	1 panel: Immuno-oncology	44% increase in proteome coverage
(30)	To identify blood units with high levels of stem cells to treat blood disorders	Umbilical cord blood: crude plasma (PEA), depleted and fractionated plasma (LC-MS)	5 panels: Cardiometabolic, Cardiovascular II, Cardiovascular III, Development, Metabolism	43% increase in proteome coverage. 41 of the 137 differentially-expressed proteins identified only by PEA.
(34)	To identify biomarkers of chronic kidney disease in patients with myocardial infarction	Crude plasma (PEA, LC-MRM-MS)	1 panel: Cardiovascular I	106% increase in proteome coverage. 6 proteins of the 6-biomarker signature measured only by PEA.
(35)	To identify mediators that activate monocytic myeloid-derived suppressor cells	Cell culture supernatant (PEA), Cell lysate (LC-MS)	2 panels: Immune response, Inflammation	16 secreted biomarker candidates identified
(31)	To identify protein biomarkers of colorectal cancer	Crude plasma	2 panels: Oncology II, Immune response, Cardiovascular III	Validation of 11 biomarker candidates detected by LC-MS. 1 biomarker candidate only detected by PEA validated in second cohort.
(36)	To analyze drug-protein interactions using a combination of CETSA and PEA	Cell lysate	Custom panel	High throughput readout of CETSA results with small sample volumes. Concordant data for 27/29 proteins measured with LC-MS.
(37 - 44)	To identify proteomic and metabolomic biomarkers of disease and enviromental exposure	Crude plasma (PEA), Crude plasma or urine (LC-MS)	Various panels	Profiling of proteins involved in specific biological processes in plasma

Drug binding is often assessed using a combination of cellular thermal shift assay (CETSA) and LC-MS. After incubating with the drug, the modulated protein will have an altered melting temperature and mass spectra since the bound drug will block regions of the protein from enzymatic digestion. In the study by Al-Amin et al., PEA was chosen as the primary readout rather than LC-MS because of its ability to perform "parallel quantification of large sets of specific proteins in small sample aliquots" (34).

Cell lysate was incubated with kinase inhibitors, fractionated, and then each fraction was subjected to different temperatures (37 - 64 °C). The investigators analyzed sixty-seven unique protein drug targets with Olink Target 96, where signal would only be generated if the drug-bound proteins retained their three-dimensional structure upon heating. They also analyzed twenty-nine of these proteins with LC-MS. Twenty-seven proteins (93.1%) analyzed with LC-MS were concordant (23/29; $R^2 > 0.90$) or moderately concordant (4/29; $0.80 < R^2 < 0.89$) with PEA data. Overall, the authors demonstrated that using PEA as the readout for CETSA enables high throughput, reliable analyses using low sample volumes.

Multiomics research

Numerous studies have used LC-MS to measure metabolites and PEA to measure proteins (Table 3)(35-42). In the studies referenced here, PEA measured proteins exclusively in plasma, which is likely due to its relative ease of sample preparation and ability to detect low and medium abundance proteins without the need for depletion or fractionation. One author also stated that PEA was selected because of its "well established methods pertaining to proteomic analyses on small volume samples" (38).

Olink Explore and LC-MS employ multi-functional instruments that can enable multiple "omics" analyses. For example, LC-MS can be used to measure proteins, PTMs, lipids, and metabolites, and the NGS system used for data readout of Olink Explore can also analyze many kinds of genetic, mRNA, and epigenetic variation.

Conclusions

PEA and LC-MS are complementary methods that are used together to increase proteome coverage, verify candidate biomarkers, and perform multiomic analyses. Indeed, authors of a study that used both technologies for protein profiling concluded, "The limitations of MS-based approaches are sort of strengths of PEA, and vice versa, which supports the complementarity between the two analytical technologies" (30).

With PEA, intact proteins in their native state are measured using a highly specific and targeted approach. Antibodies must therefore be generated to measure specific proteins. The sample workflow and dynamic range are identical regardless of biological matrix, which is particularly relevant for complex samples like plasma. In addition, the sample throughput is high.

With LC-MS, proteins with and without PTMs can be differentiated from each other in an untargeted, hypothesis-free manner. While LC-MS can achieve higher proteome coverage than PEA, this is often at the expense of sample throughput. Finally, the sample matrix and complexity can negatively impact the number of detected proteins.

Learn more about Olink technology

Olink Explore HT: olink.com/products/olink-explore-ht

Olink Explore 3072: olink.com/products-services/explore/

Olink Target 96: olink.com/products-services/target/#relative

Olink Target 48: olink.com/products/olink-target-48

Olink Flex: olink.com/products-services/flex/

Olink Focus: olink.com/products-services/custom-panels/

Validation data information for Olink Explore and Olink Target panels: olink.com/resources-support/document-download-center/

Olink Signature Q100: olink.com/products-services/signature/

Contact us

For further information about Olink platforms, email us at info@olink.com.

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1328, v1.5, 2024-10-01