

Plasma proteomics at population scale: the peer-reviewed evidence base for Aurora Series® columns

Comprehensive review of peer-reviewed publications establishes IonOpticks Aurora Series® columns as the chromatographic platform of choice for deep, reproducible, high-throughput plasma proteome analysis in applications spanning biomarker discovery through clinical validation.

40,000+

Plasma samples analysed across 353 days of continuous MS acquisition on Aurora® Rapid™ 8×150 (Albrecht et al., 2025). [4]

4,636

Protein identifications with P2 nanoparticle enrichment, ~8× more than neat plasma, on Aurora® Elite™ 15×75 (Völlmy et al., 2026). [7]

Astral to Stellar

Biomarker translation from plasma discovery to targeted clinical validation on the same Aurora® column chemistry (Wahle et al., 2025). [9]

Highlights from the peer-reviewed evidence

Eight peer-reviewed studies citing Aurora Series® columns have been reviewed.

01 SCALE AND LONGEVITY

40,000+ samples, 353 days

Population-scale plasma proteomics on Aurora® Rapid™ 8×150 - 11.5-min gradients at 100 SPD, ~1,300 protein IDs per injection, 16.0% median CV across 1,705 interspersed QC runs.

Albrecht et al., Mol Cell Proteomics 2025

02 DEPTH WITH ENRICHMENT

4,636 proteins ~8× more than neat plasma

P2 nanoparticle enrichment vs neat, benchmarked head-to-head across six workflows on an Aurora® Elite™ 15×75.

Völlmy et al., J Proteome Res 2026

03 DISCOVERY TO CLINIC

5,437 precursors
1,305 validated targets

Orbitrap Astral discovery to Stellar MS targeted assay on the same Aurora® Rapid™ chemistry - 85% of precursors at CV <20%, with assay development cut from months to under a week.

Wahle et al., Mol Cell Proteomics 2025

04 DEPTH OF COVERAGE

5,644 protein groups, 10.7% median CV

Aurora® Ultimate™ 25×75 with Proteograph XT on timsTOF Pro 2 - 4.2× neat plasma.

Soni, Clinical Proteomics 2024

05 DEEP IDENTIFICATIONS FROM NEAT PLASMA

1 µL of plasma, no depletion,
1,092 proteins

Aurora® Ultimate™ 25×75 on a timsTOF Pro 2 - 811 protein groups at 24 SPD from neat plasma, rising to 1,092 with EV-boost search. Deep plasma proteomics without enrichment.

Metatla et al., Clinical Proteomics 2024

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KEYWORDS

Plasma proteomics, serum, Aurora Series®, Aurora® Rapid™, Aurora® Elite™, Aurora® Ultimate™, IonOpticks, packed emitter column, nanoZero®, C18, 1.7 µm, biomarker discovery, population-scale cohorts, clinical translation, Orbitrap Astral, Orbitrap Exploris 480, Stellar MS, timsTOF Pro 2, timsTOF HT, timsTOF Ultra, Evosep One, Vanquish Neo, nanoElute 2, DIA, diaPASEF, PRM, PCA-N, nanoparticle enrichment, bead-based enrichment, neat plasma, immunodepletion, pre-analytical variability, reproducibility, coefficient of variation, retention-time stability, spray stability, column longevity, high-throughput, samples per day.

Why Aurora Series® columns work for plasma

The published evidence is converging on a consistent mechanical explanation for why Aurora® columns deliver on plasma cohort work where other architectures have struggled. Four design choices matter most.

01 Zero post-column dead volume

The Aurora® packed-emitter architecture integrates the packed column bed directly into the ESI emitter and features our unique nanoZero® fitting, eliminating the pre- and post-column dead volumes that are the largest source of peak broadening in nano- and capillary-flow LC-MS. For low-abundance plasma proteins such as cytokines, tissue-leakage markers, secreted signalling proteins, this difference determines whether a signal is detectable or not. The bead-based enrichment studies in Section 2 (Korff et al. [5], Völlmy et al. [7]) detect proteins across >4 orders of magnitude in plasma, including tissue-leakage markers at ng/mL concentrations that less-resolved workflows miss. Every paper cited in Section 2 relies on this capability.

02 Optimised stationary phase at 1,700 bar

Aurora Series® columns use 1.7 µm C18 stationary phase and are validated beyond 1,700 bar. On modern UHPLC systems (Vanquish Neo, nanoElute 2), this provides the pressure headroom to run higher flow rates or longer columns without sacrificing throughput. The cited studies demonstrate this range: from Korff et al.'s [5] 11.5-minute 100-SPD cohort workflow to Kasai et al.'s 30-minute deep gradients [6], both maintaining <20% median CVs on Aurora® columns.

03 Spray stability and run-to-run consistency

Plasma's dynamic range means small ionisation fluctuations translate directly into quantitative noise. Kasai et al. [6] reported ≥0.945 Pearson correlation across three independent operators running 12 replicates, with 85% of proteins quantified in every run. This demonstrates that Aurora® columns maintain spray stability across both time and users, and are essential tools for cohort studies where batch effects would otherwise require complex statistical correction.

04 Column longevity at cohort scale

Aurora Series® columns are robust enough to take on the most challenging samples, including plasma, maintaining chromatographic performance over thousands of injections. Albrecht et al. [4] analysed 40,000+ plasma samples continuously over 353 days using the PCA-N workflow, achieving consistent protein identification depths and quantitative precision throughout the acquisition period across 2 separate LC-MS platforms. For population-scale studies where column changes can introduce batch effects and instrument downtime, the longevity and consistency between Aurora® columns limits any batch effects.

05 Cross-platform method portability

The same Aurora® performance is available in XT (Thermo EASY-Spray / Nanospray Flex), CSI (Bruker CaptiveSpray), XS (SCIEX OptiFlow) and UNI (universal) formats. For clinical-proteomics groups operating mixed fleets across Orbitrap Astral, timsTOF, Stellar MS or ZenoTOF, this enables methods to be transferred across instruments without switching column type. The Mann Lab's Astral-to-Stellar workflow [9] is a direct example of this versatility.



The choice of analytical column is no longer a discrete, up-front consumable decision but a central and defining choice that can determine the success of large cohort studies.

01 The plasma proteomics challenge

Plasma is the workhorse biofluid of clinical proteomics research as it is accessible, minimally invasive to sample, and carries a protein signature that reflects the physiological and pathological state of virtually every tissue in the body and thus for biomarker discovery, patient stratification and translational medicine, it is the natural starting point. However, the dynamic range of analytes in plasma spans more than ten orders of magnitude in protein concentration, with a handful of abundant carrier proteins masking the tissue-leakage proteins, cytokines and circulating signals that carry the most biological and clinical interest. For these reasons, plasma remains one of the most analytically demanding samples a mass spectrometer will encounter.

The community has documented the scale of this challenge in its own assessments. The 2024 HUPO Human Plasma Proteome Project perspective catalogued 4,608 proteins across 113 datasets in the latest PeptideAtlas build, yet identified only 785 proteins with cross-platform confidence between affinity-based and mass spectrometry methods, exposing how platform-specific biases shape the detectable proteome [1]. In 2025, comprehensive head-to-head benchmarking of eight platforms using identical plasma samples reinforced this conclusion, revealing that although over 13,000 unique proteins were quantified in aggregate, only 36 were measurable across all platforms, and technical coefficients of variation ranged from 5.3% for the most precise affinity assay to 26.4% for discovery mass spectrometry [2]. An earlier HPPP review in 2019 had already established the foundational problem, showing that despite technological advances enabling detection of over 3,500 plasma proteins, the 500 most abundant were consistently reported in only 50% of mass spectrometry studies, a reproducibility gap attributed to methodological variability in sample handling, chromatographic configuration, and data acquisition rather than biological differences [3]. These reviews converge on a shared imperative for standardised, robust liquid chromatography to close the reproducibility gap, achieve the throughput required for clinical translation, and ensure that biomarker signals reflect biology rather than analytical drift.

This imperative has grown more acute as the addressable sample cohort size for proteomic analysis has expanded from tens of samples to tens of thousands, bringing plasma proteomics into the realm of true utility at clinical scale and powering discovery science at unprecedented breadth. In these applications, the choice of analytical column is no longer a discrete, up-front consumable decision but a central and defining choice that can determine the success of large cohort studies. A column that performs well for ten QC runs may not be the column that delivers across 40,000+ injections of clinical plasma over 353 days. This application note sets out the peer-reviewed evidence that IonOpticks Aurora Series® columns, in particular the Aurora® Rapid™ 8×150, Aurora® Rapid™ 8×75, Aurora® Elite™ 15×75 and Aurora® Ultimate™ 25×75 formats, meet this bar.



02

The peer-reviewed evidence base

Eight studies spanning population-scale cohort work, longitudinal disease profiling, sample-preparation workflow benchmarking, low-input workflows, and biomarker discovery-to-validation pipelines. Each cites IonOpticks Aurora Series® columns in its methods, and each has been published in a peer-reviewed journal. Citation numbers refer to the reference list in Section 5.

2.1

Population-scale plasma cohorts

2.2

Sample-preparation workflows and pre-analytical bias

2.3

Biomarker discovery-to-validation pipelines

2.4

Disease-specific plasma applications

2.1 Population-scale plasma cohorts

PAPER 01 · REFERENCE [4]

One year. 40,000+ injections. Exceptional longitudinal stability on the Aurora® Rapid™ column. This is the robustness customers running large cohorts need.

Democratising population-scale plasma proteomics: PCA-N + Aurora® Rapid™ 8×150 delivers deep coverage at extreme throughput

Albrecht, V., Müller-Reif, J. B., Brennstetter, V., & Mann, M. (2025). A Simplified Perchloric Acid Workflow With Neutralization (PCA-N) for Democratizing Deep Plasma Proteomics at Population Scale. *Molecular & Cellular Proteomics*, 24(11), 101071.

Study snapshot: PCA-N combined with Aurora® Rapid™ 8×150 in an Evosep One + Orbitrap Astral workflow enabled deep and precise proteomic analysis across 40,000+ plasma samples.

INSTRUMENTATION USED



Aurora® Rapid™ 8×150

8 cm × 150 µm ID, 1.7 µm C18



Evosep One

100 SPD, 11.5 min gradients



Orbitrap Astral

Thermo Scientific, DIA

Population-scale plasma proteomics holds transformative potential for biomarker discovery, yet existing workflows face critical tradeoffs between analytical depth, throughput, and cost that limit widespread adoption. Albrecht et al. address these constraints by introducing PCA-N, an optimised perchloric acid precipitation workflow with neutralisation that eliminates solid-phase extraction and enables direct enzymatic digestion. The streamlined protocol reduces sample requirements tenfold from 50 µL to just 5 µL of plasma while doubling proteomic depth compared to neat plasma analysis. By leveraging 384-well plate compatibility and strategic workflow scheduling, PCA-N achieves preparation of over 10,000 samples per day at reagent costs under one dollar per sample. Rigorous validation according to CLSI C64 guidelines demonstrated excellent reproducibility and biological resolution, with long-term stability confirmed across 1,705 quality control samples interspersed among 40,000+ measurements over 353 days. For LC-MS analysis, an IonOpticks Aurora® Rapid™ column (8 cm × 150 µm ID) was integrated with an Evosep One system and coupled to an Orbitrap Astral, enabling rapid 11.5-minute separations at 100 samples per day throughput. This democratised workflow establishes a new paradigm for extreme-scale clinical studies, making deep plasma proteomics technically and economically feasible for large cohort analyses previously considered impractical.

WHY THIS PAPER MATTERS

- **Real-world scale:** validated across 40,000 samples in 353 days, proving long-term robustness and throughput.
- **Cost-and-input efficiency:** deep proteome coverage from 5 μ L plasma at near-\$1 reagent cost per sample.
- **Automation-friendly:** compatible with 384-well parallelisation and Evosep One workflows used for high throughput.

WHAT IONOPTICKS PRODUCTS CONTRIBUTED

- **Rapid high-resolution separations:** 11.5-minute gradients at 100 samples/day on Aurora® Rapid™ 8×150 delivered ~1,300 protein identifications per injection, proving that throughput need not sacrifice depth.
- **Longitudinal quantitative stability:** sustained 16.0% median CV across 1,705 QC samples over 353 days with 82.6% of proteins maintaining stable quantification, enabling year-long cohort monitoring with minimal chromatographic degradation.
- **Seamless batch integration:** consistent peptide separation supporting effective ComBat correction, with post-correction data revealing no instrument- or batch-driven separation, confirming robustness for distributed multi-site studies.

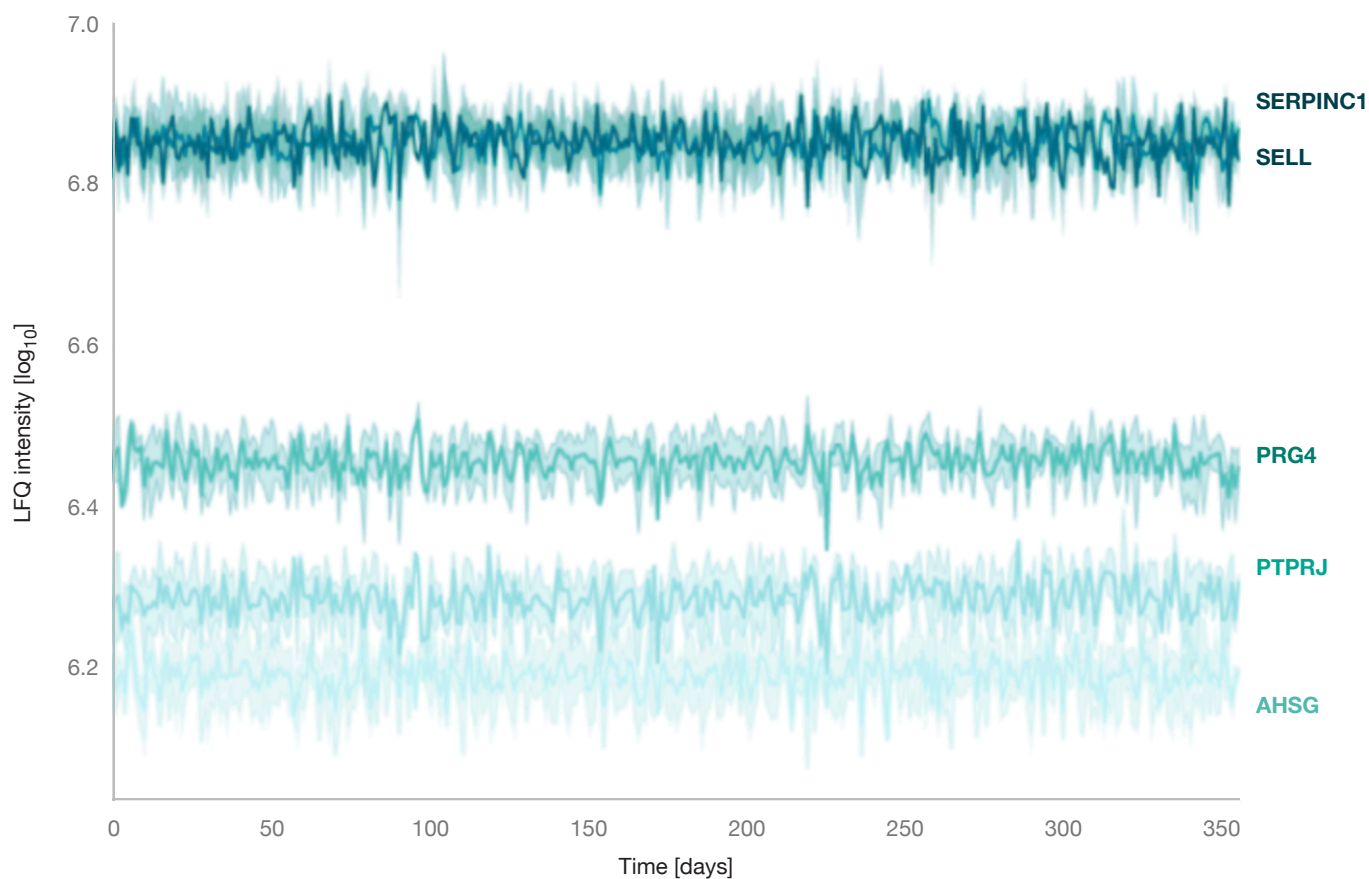


Figure 1. Longitudinal stability: PRG4, SERPINC1, LAMP1, BST1, HEG1 with CVs 4.9–8.8% over 353 days.

Adapted from Albrecht et al., *Molecular & Cellular Proteomics*, 2025; 24(11):101071, <https://doi.org/10.1016/j.mcpro.2025.101071> (CC BY 4.0).

Recoloured to the IonOpticks palette and re-labelled to house style; the plotted data are unaltered.

2.2 Sample-preparation workflows and pre-analytical bias

PAPER 02 · REFERENCE [5]

When benchmarking plasma workflows for contamination bias, the Aurora[®] Rapid[™] XT delivers the speed and stability needed to run hundreds of samples across multiple methods while maintaining the quantitative precision required for reliable pre-analytical assessment.

Pre-analytical bias benchmarking across five plasma proteomics workflows on IonOpticks Aurora[®] Rapid[™] columns: PCA-N delivers a contamination-resistant alternative with Aurora[®] Rapid[™] 8×150

Korff, K., Müller-Reif, J. B., Fichtl, D., Albrecht, V., Schebesta, A.-S., Itang, E. C. M., Winter, S. V., Holdt, L. M., Teupser, D., Mann, M., & Geyer, P. E. (2025). Pre-Analytical Drivers of Bias in Bead-Enriched Plasma Proteomics. *EMBO Molecular Medicine*, 17(11), 3174–3196.

Study snapshot: Systematic comparison of five plasma proteomics workflows with spike-ins of platelets, erythrocytes, PBMCs, and yeast showing that bead-based methods inflated protein IDs by thousands due to contamination, while PCA-N demonstrates selective resistance to erythrocyte contamination. Confirmed on the Evosep One with Orbitrap Astral and IonOpticks Aurora[®] Rapid[™] 8×150 column.

INSTRUMENTATION USED



Aurora[®] Rapid[™] XT 8×150

8 cm × 150 µm ID, 1.7 µm C18



Evosep One

100 SPD, 11.5 min gradients



Orbitrap Astral

Thermo Scientific, DIA

Bead-based enrichment has emerged as a promising strategy to overcome plasma's extreme dynamic range and access low-abundance proteins, yet its robustness against pre-analytical variation remains insufficiently characterised. Korff et al. address this critical gap by systematically evaluating five plasma proteomics workflows, including three bead-based methods, neat plasma, and perchloric acid precipitation with neutralisation (PCA-N), and use carefully designed spike-in experiments with defined cellular contaminants. They demonstrate that while bead-based approaches enhance detection of low-abundance proteins, they are highly susceptible to systematic bias from platelet and PBMC contamination, potentially inflating results by thousands of proteins and distorting the true circulating proteome. This vulnerability persisted even at low contamination levels, with non-magnetic beads maintaining over 4,500 protein identifications at moderate platelet concentrations where neat workflows identified only 2,100. Critically, the team establishes that centrifugation at 3,000 × g for 30 minutes can partially rescue compromised samples, and develops validated contamination indices and cell-specific marker panels for quality assessment across workflows. For LC-MS analysis, the team employed an Aurora[®] Rapid[™] XT UHPLC column (8 cm × 150 µm ID) on an Evosep One coupled to an Orbitrap Astral, enabling rapid 11.5-minute separations. These findings provide a quantitative framework for assessing workflow performance under variable sample quality, offering essential guidance for biomarker discovery and clinical proteomics applications.

WHY THIS PAPER MATTERS

- **Quantifies workflow-specific contamination risk:** bead-based methods identified up to 8,000 proteins at moderate contamination levels (~500,000 erythrocytes/ μL + 50,000 platelets/ μL + 500 PBMCs/ μL) versus ~3,000 with neat plasma.
- **Establishes practical quality control tools:** validated marker panels and contamination indices for platelets, erythrocytes, and PBMCs that work consistently across workflows.
- **Provides actionable pre-analytical guidance:** $3,000 \times g$ for 30 min centrifugation reduces platelet signal by >90% in bead workflows, with clear recommendations on tube types and anticoagulants.

WHAT IONOPTICKS PRODUCTS CONTRIBUTED

- **Supported the entire study:** all 640 samples were separated at 100 SPD (11.5 min gradients) on Evosep One coupled to Orbitrap Astral, delivering consistent performance across neat, PCA-N, and bead-based workflows.
- **Supported high-throughput benchmarking:** the column's robustness allowed direct comparison of contamination susceptibility and yeast spike-in recovery across 56 bead-buffer combinations without drift in quantitative precision.
- **Facilitated detection of low-abundance yeast proteins:** the 100 SPD method on the Aurora[®] Rapid[™] 8 $\times$ 150 maintained quantitative linearity down to 0.01% yeast spike-in in bead workflows, enabling precise measurement of dynamic range compression.
- **Enabled contamination index calculation:** consistent chromatographic performance supported quantitative measurement of 30 cell-specific marker proteins per cell type, allowing derivation of contamination indices for objective sample quality assessment across workflows.

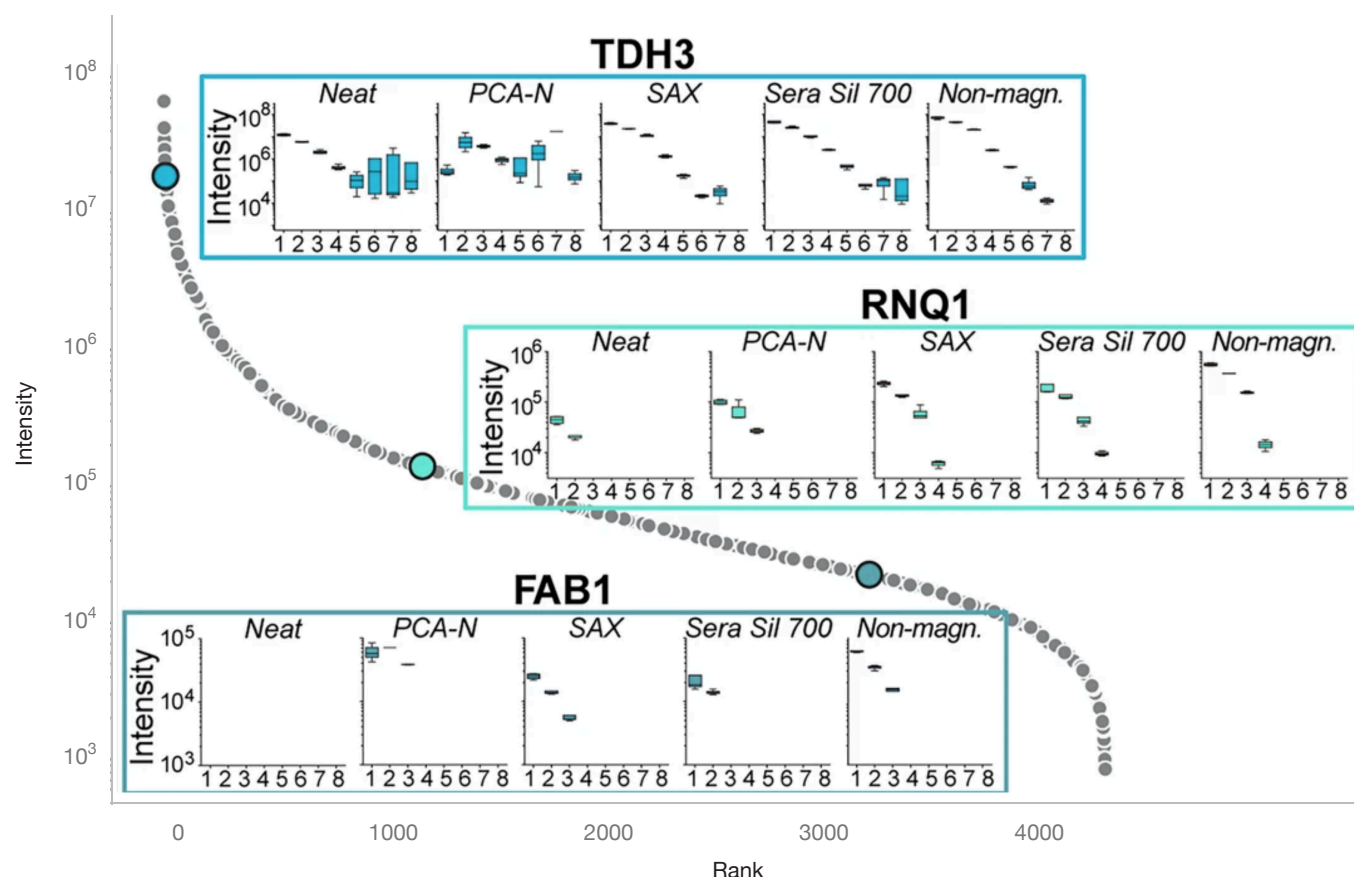


Figure 2. Aurora[®] Rapid[™] 8 $\times$ 150 column resolves low-abundance yeast peptides in bead-based analyses for 0.01% detection limit, a 100-fold sensitivity improvement over the neat workflow, enabling deep contaminant profiling and trace-level biomarker detection.

Adapted from Korff et al., EMBO Molecular Medicine, 2025; 17:3174–3196, <https://doi.org/10.1038/s44321-025-00309-0> (CC BY 4.0). Reproduced from the publication-resolution figure, recoloured to the IonOpticks palette with the main axes re-labelled to house style; the plotted data are unaltered.

Validating commercial plasma sources for multi-site studies? The Aurora[®] Ultimate[™] 25 cm on timsTOF HT delivers 5,000+ protein depth to reveal how collection protocols shape the proteome, so preanalytical variation becomes a variable you can see and account for.

SOP differences exposed: ENRICHplus enrichment reveals 2.8–6.2× deeper proteome coverage and detects pre-analytical variability invisible to conventional workflows

Kasai, T., Weiss, L., Wohlfahrt, J., Matamalas, J. T., Shlayan, G., Kirsch, Z. J., Aikawa, M., Aikawa, E., & Singh, S. A. (2026). Impact of Variations in Commercial Standard Operating Procedure on Plasma Proteome Recovery. *Journal of Proteome Research*, 25(4), 1941–1950.

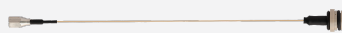
Study snapshot: Five commercial plasma sources were compared using both neat plasma and ENRICHplus bead-based enrichment workflows on Exploris 480 and timsTOF HT platforms, revealing that differences in blood-to-plasma SOPs (anticoagulant, centrifugation, apheresis) drive major proteome variation that is only detectable after enrichment. ENRICHplus achieved 2.8- to 6.2-fold higher protein yields in LC-MS analyses while exposing significant source-to-source variability attributable to blood-to-plasma SOP differences, including apheresis depletion, 4-hour hold times, and centrifugation protocols. These remained completely undetectable with conventional methods.

INSTRUMENTATION USED



Aurora[®] Ultimate[™] 25x75

C18, 25 cm × 75 µm ID, 30 min gradient



Aurora[®] Ultimate[™] 25x75

C18, 25 cm × 75 µm ID, 30 min gradient



timsTOF HT

Bruker, 250 nL/min



Orbitrap Exploris 480

Thermo Scientific

Commercial plasma samples serve as essential controls for biomarker studies, yet the assumption that standard operating procedures are comparable across vendors remains largely untested. Kasai et al. address this critical knowledge gap by systematically evaluating how variations in commercial plasma preparation impact proteome recovery and composition. Pooled plasma from five U.S. commercial sources was analysed using ENRICHplus bead-based enrichment alongside conventional neat plasma preparation. Striking differences emerged between sources. Plasma derived from vendors with prolonged whole blood holding exhibited significant platelet activation signatures, while apheresis-collected plasma showed depleted apolipoproteins yet 2.1- to 2.3-fold higher overall protein IDs with ENRICHplus enrichment, attributed to filter-based depletion of high-abundance proteins during apheresis, versus immediate centrifugation protocols. These preanalytical variations created distinct proteomic profiles that could confound biomarker discovery, with protein IDs ranging from fewer than 750 to 1,500 on the same instrument platform. For LC-MS/MS analysis on timsTOF HT, the team employed an IonOpticks Aurora[®] Ultimate[™] C18 column (25 cm × 75 µm ID) over a 30-minute gradient, enabling sensitive detection of these SOP-driven proteomic differences. The study establishes that nanoparticle-based enrichment workflows reveal hidden preanalytical variability invisible to conventional neat plasma analysis, providing essential guidance for selecting appropriate commercial controls and interpreting data across multi-site studies.

WHY THIS PAPER MATTERS

- **SOP variability quantified:** commercial plasma sources showed greater than 2-fold differences in protein identifications (720–1,062 vs. 1,500–2,558 proteins) driven by pre-analytical variables including apheresis filtration, blood hold times, and immediate centrifugation protocols. These differences will confound biomarker studies if uncontrolled.
- **ENRICHplus biological sensitivity:** bead-based enrichment detected 29% of the proteome (511 of 1,792 proteins) consistently across all five sources while revealing source-specific biological signatures: 87 platelet proteins enriched in delayed-centrifugation samples and 54 apolipoproteins depleted in apheresis samples. These changes were invisible to neat plasma workflows.
- **Clinical translation relevance:** demonstrated that nanoparticle-based enrichment can reveal hidden pre-analytical variability invisible to conventional neat plasma analysis, providing essential guidance for selecting appropriate commercial controls and interpreting multi-site plasma proteomics data.

WHAT IONOPTICKS PRODUCTS CONTRIBUTED

- **Absolute depth for SOP signature detection:** Aurora® Ultimate™ 25 cm delivered 5,434 protein identifications on timsTOF HT, exceeding the depth achieved on standard columns and enabling high-confidence detection of apolipoprotein depletion and platelet protein enrichment patterns across commercial plasma sources.
- **Operator-independent reproducibility:** 30-minute gradients at 250 nL/min supported reliable label-free quantification with negligible technical variability (Kendall's $W = 0.0385$, 85% protein overlap between three independent researchers, Pearson correlation value ≥ 0.945), ensuring observed source differences reflected true biological variation.
- **Cross-platform validation:** Aurora® Ultimate™ 25 cm on timsTOF HT independently confirmed SOP-driven proteomic patterns with 98% protein overlap to Exploris 480 data, validating that observed differences reflected true pre-analytical variation rather than chromatographic platform effects.

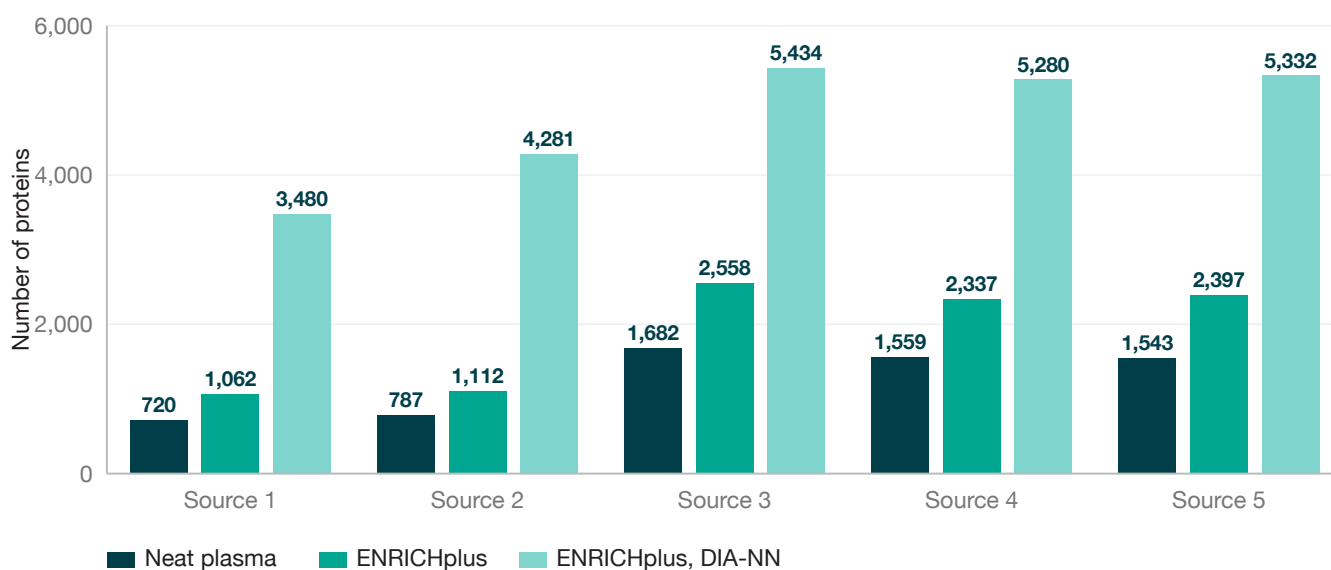


Figure 3. Aurora® Ultimate™ 25 cm on timsTOF HT, combined with ENRICHplus sample preparation, delivers 3,480–5,434 protein identifications via DIA-NN (right bars), providing the depth required to reveal SOP-dependent variation including apolipoprotein depletion and platelet protein enrichment patterns.

Redrawn from the published values in Kasai et al., *Journal of Proteome Research*, 2026; 25(4):1941–1950.

DOI: <https://doi.org/10.1021/acs.jproteome.5c01012>.

When benchmarking plasma proteomics methods for depth, reproducibility, and preanalytical robustness, IonOpticks Aurora Series® columns deliver the chromatographic performance needed to reveal the true strengths and biases of each workflow.

4,636 proteins at 17.8% CV: P2 nanoparticle enrichment outperforms five competing workflows but reveals acute centrifugation sensitivity, while the secreted proteome remains stable across conditions

Völlmy, F., Kaushik, P., Eckert, S., Paschen, C., Tavalaei, S., Fidelin, J., Weiser, S., & Bantscheff, M. (2026). Comparison of Common Plasma Proteomics Workflows Reveals Distinct Preanalytical Biases by Sample Preparation and Nanoparticle Enrichment. *Journal of Proteome Research*, 25(6), 3178–3187.

Study snapshot: Six plasma proteomics methodologies (Neat plasma, Top14 depletion, ENRICH-iST, Mag-Net, P2, and Proteograph XT) were directly compared using DIA on an Orbitrap Astral, demonstrating that bead-based enrichment methods achieve superior depth (up to 4,600 proteins) but are highly susceptible to preanalytical cellular contamination, while secreted protein abundances remain robust across workflows.

INSTRUMENTATION USED



Aurora® Elite™ 15x75

15 cm × 75 µm ID, 26 min active gradient



Vanquish Neo UHPLC
Thermo Scientific



Orbitrap Astral
150 × 4 Th DIA-MS

Human blood plasma offers unparalleled diagnostic potential, yet its extraordinary dynamic range, which spans up to 10^{12} , has historically constrained mass spectrometry discovery to a few hundred proteins. Völlmy et al. address this limitation by conducting the first rigorous head-to-head comparison of six contemporary plasma proteomics workflows: Neat plasma, Top14 immunodepletion, ENRICH-iST, Mag-Net, P2, and Proteograph XT. The technology-focused benchmarking reveals that nanoparticle-based enrichment methods achieve substantially greater depth, with P2 identifying 4,636 unique protein groups and Proteograph XT quantifying 4,402, compared to merely 584 for Neat plasma. However, it was demonstrated that this expanded coverage derives primarily from cellular contaminants including platelets, erythrocytes, and cellular debris rather than extracellular vesicle enrichment alone. Critically, secreted plasma proteins remain quantitatively stable even under stringent ultracentrifugation, suggesting the soluble plasma proteome can be reliably measured when appropriate preanalytical controls are applied. For peptide separation, the team employed an Aurora® Elite™ column (15 cm × 75 µm ID) on a Vanquish Neo UHPLC system coupled to an Orbitrap Astral. These findings provide an evidence-based framework for selecting plasma proteomics workflows, with direct implications for biomarker discovery and clinical study design.

WHY THIS PAPER MATTERS

- **Unprecedented workflow depth comparison:** direct benchmarking reveals P2 achieves ~8× more proteins than neat plasma (4,636 vs. 584) and 5.4× more than Top14 depletion (4,636 vs. 866) at recommended volumes, with Proteograph XT delivering comparable performance (4,402 proteins), providing definitive guidance for platform selection based on sample availability and study goals.
- **Pre-analytical bias quantified:** all nanoparticle methods show dramatic centrifugation sensitivity, with P2 and Proteograph XT identifications shown to correlate inversely with centrifugation stringency, while secreted proteins (median log₂FC -0.05 to +0.37) remain stable versus cellular proteins (median log₂FC -1.02 to -2.74) that are depleted, demonstrating that standard 2000 × g plasma contains substantial cellular/vesicular contributions that inflate protein counts but can be removed by stringent centrifugation without affecting secreted biomarker quantification.
- **Reproducibility-performance trade-off mapped:** P2 and Proteograph XT achieve median CVs of 17.8–18.4% versus 20.6–23.6% for Mag-Net and ENRICH-iST and 33.4% for Top14 depletion, showing that nanoparticle enrichment delivers both superior depth and precision, while depletion methods exhibit higher variability despite lower coverage.

WHAT IONOPTICKS PRODUCTS CONTRIBUTED

- **Standardised chromatographic foundation:** all six workflows were analysed using the Aurora® Elite™ 15 cm × 75 µm ID column on Vanquish Neo UHPLC coupled to an Orbitrap Astral, ensuring that observed differences reflected sample preparation variables rather than chromatographic variability, which is critical for fair cross-platform comparison.
- **High-throughput depth delivery:** 26-minute active gradients (30-minute total runtime) on Aurora® Elite™ enabled over 5,300-protein identification capacity for enriched samples, enabling systematic characterisation of the impacts of differential centrifugation during pre-analytical processing.
- **DIA quantification reliability:** consistent Aurora® Elite™ performance supported 150 × 4 Th DIA-MS with library-free Spectronaut processing, enabling reliable label-free quantification of proteins across centrifugation conditions and workflows.

When selecting plasma proteomic workflows across species and biofluids, the IonOpticks Aurora® Ultimate™ and Elite columns provide the matched discovery-to-throughput chromatographic platform needed to benchmark preparation strategies with confidence.

No one-size-fits-all in plasma proteomics: eight workflows benchmarked across human plasma, human serum, and rat plasma reveal >90% of detected proteins are significantly altered by workflow choice

Emery-Corbin, S. J., Steele, J. R., Multari, D. H., Tanuwidjaya, E., Hanchapola, I., Sivaraman, K. K., Lee, H.-C., Blundell, S. A., Ali, I., O'Brien, T. J., Faridi, P., & Schittenhelm, R. B. (2026). 'If the Shoe Fits?' – Benchmarking Plasma Proteomic Sample-Preparation Workflows Across Human and Rat Biofluids. *Molecular & Cellular Proteomics*. Article in press.

Study snapshot: Eight sample-preparation workflows (neat STrap/SP3, PerCa depletion, MagNet HILIC/SAX, Enrich-iST, ProteoNano) were benchmarked across human plasma, human serum, and rat plasma on an Orbitrap Astral using two plasma-optimised DIA methods, identifying 2,726 human and 3,767 rat proteins across all workflows and methods combined, and demonstrating that workflow choice profoundly reshapes the detectable proteome, with >90% of proteins significantly altered between workflows.

INSTRUMENTATION USED



Aurora® Ultimate™ 25×75

Discovery method, 65 min gradients



Aurora® Elite™ 15×75

Throughput method, 30 min gradients



Orbitrap Astral

Two plasma-optimised DIA methods

Plasma proteomics has seen rapid methodological innovation, yet systematic evaluations that consider both biological variables (biofluid type, species) and technical parameters (MS methods) remain limited. Emery-Corbin et al. address this gap by benchmarking eight sample-preparation workflows spanning neat approaches, depletion, and corona-enrichment strategies across human plasma, human serum, and rat plasma. All samples were analysed on an Orbitrap Astral using two plasma-optimised DIA methods: a discovery-maximised method employing an IonOpticks Aurora® Ultimate™ 25 cm column with 65-minute gradients, and a throughput-maximised method using an Aurora® Elite™ 15 cm column with 30-minute gradients. The study identified 2,726 human and 3,767 rat proteins across all workflows and methods, including approximately 1,000 from neat plasma alone. Increasing throughput incurred a 20–30% reduction in depth depending on workflow and species, while EV-enrichment methods (MagNet) produced the deepest proteomes but with distinct compositions relative to neat, depleted, and secreted-protein-enriched samples. Several workflows performed significantly better in rat plasma, supporting improved sensitivity for preclinical analyses, and statistical analysis revealed that >90% of detected proteins were significantly altered between workflows, underscoring how strongly workflow choice shapes the downstream proteome.

WHY THIS PAPER MATTERS

- **Context-dependent workflow selection established:** through benchmarking of eight preparation workflows across three biofluids and two species, this study demonstrates that no universal plasma preparation strategy can be prescribed, and that workflow choice should be guided by the organs, immune targets, or inflammatory signals most relevant to the study.
- **Deepest coverage from corona enrichment:** particle-based corona enrichment delivered the highest protein yields, with MagNet workflows identifying approximately 1,700 proteins in human biofluids and 3,000 in rat plasma via the Discovery method, confirming that bead-based enrichment exposes low-abundance sub-proteomes that neat and depletion workflows cannot reach.
- **Depth-throughput trade-off quantified:** the matched comparison of discovery and throughput DIA methods on the same samples provides direct evidence that shorter gradients and lower loads incur a 20–30% depth reduction, with enrichment workflows more affected than neat preparations, giving researchers concrete guidance for method selection.

WHAT IONOPTICKS PRODUCTS CONTRIBUTED

- **Matched discovery-throughput platform:** the Aurora® Ultimate™ 25×75 column enabled 65-minute gradient separations delivering maximum proteome depth, while the Aurora® Elite™ 15×75 column supported 30-minute throughput gradients at half the sample load, allowing direct head-to-head comparison of these two Aurora® formats on identical plasma samples. Aurora® Elite™ 15×75 retained 70–80% of Aurora® Ultimate™ 25×75 depth at half the gradient time and load.
- **Analytical consistency enabling workflow-driven variance:** principal component analysis showed that proteomic variation was driven predominantly by sample-preparation workflow rather than by chromatographic or analytical variability, confirming that the Aurora® column platform delivered sufficient consistency to isolate true workflow-specific signals.
- **Best-in-class neat plasma depth:** the Aurora® Ultimate™ 25 cm column delivered >1,000 protein identifications from neat human plasma on the Discovery method, exceeding results reported in recent Astral-based benchmarking studies, and demonstrating superior resolving power for the most analytically demanding plasma workflow.

2.3 Biomarker discovery-to-validation pipelines

PAPER 06 · REFERENCE [9]

When moving from discovery to absolute quantification with ^{15}N -labeled proteins, Aurora[®] Rapid[™] columns on Evosep deliver the speed, stability, and retention time precision required to turn thousands of Orbitrap Astral candidates into a validated clinical assay in days, not months.

From discovery to clinic in days: Stellar MS refines 5,437 Astral-identified precursors to 1,305 high-quality targeted assays with 85% achieving CV < 20%

Wahle, M., Remes, P. M., Albrecht, V., Lorenz, M. B., Mueller-Reif, J., Steigerwald, S., Heymann, T., Niu, L., Lössl, P., Horning, S., Jacob, C. C., & Mann, M. (2025). A Novel Hybrid High-Speed Mass Spectrometer Allows Rapid Translation From Biomarker Candidates to Targeted Clinical Tests Using ^{15}N -Labeled Proteins. *Molecular & Cellular Proteomics*, 24(9), 101050.

Study snapshot: Rapid translation of plasma proteomics discoveries into clinical-grade targeted assays using the novel Stellar MS, transferring 5,437 precursors from Orbitrap Astral DIA discovery (median CV < 15%) to a refined Stellar MS assay of 1,305 high-quality targets with >60% meeting stringent quality criteria (dotp $\geq$ 0.8) and achieving median CV ~17.4%. Absolute quantification of 7 liver disease biomarkers via ^{15}N -labeled protein standards delivered pg/mL-level LOQs while delivering quantitation up to hundreds of micrograms per mL, using the IonOpticks Aurora[®] Rapid[™] 8 cm column as the primary chromatographic platform with the 5 cm column supporting high-throughput ^{15}N -labeled protein characterisation.

INSTRUMENTATION USED



Aurora[®] Rapid[™] 8x150

Primary platform, 60 SPD, 21 min



Aurora[®] Rapid[™] 5x75

^{15}N standard characterisation



Evosep One

60 SPD



Orbitrap Astral

DIA discovery



Stellar MS

Targeted PRM / MS3

Translating proteomics discoveries into clinical diagnostics remains a major bottleneck, with months typically required to develop targeted assays from discovery data. Wahle et al. address this challenge by introducing and validating the Stellar MS, a novel hybrid mass spectrometer that combines triple quadrupole robustness with advanced linear ion trap capabilities to enable rapid, sensitive parallel reaction monitoring. This study demonstrates transfer of peptide panels from Orbitrap Astral discovery data, where 5,437 precursors were identified with median CVs below 15%, to refined Stellar MS targeted assays comprising 1,305 high-quality precursors with median CVs of ~17.4% and 85% of precursors achieving CV < 20%. The platform supports both PRM and MS3 acquisition modes, with MS3 further improving sensitivity for longer peptides. Critically, the authors establish a streamlined workflow using ^{15}N -labeled protein standards and IonOpticks Aurora[®] Rapid[™] 8 cm $\times$ 150 μm ID columns for chromatographic separation, enabling absolute quantification of liver disease biomarkers ranging from picograms to hundreds of micrograms per millilitre in a single run. The study demonstrates that thousands of Orbitrap Astral-identified plasma peptides can be targeted on Stellar MS with assay development reduced to just a few days. This technology bridges the gap between research discovery and clinical implementation, offering a path to replace numerous single-protein biomarker assays with comprehensive, multiplexed clinical tests.

WHY THIS PAPER MATTERS

- **Rapid assay development:** reduced biomarker-to-clinic timeline from months to days, with Stellar MS enabling direct transfer of discovery data to targeted PRM/MS3 assays with adaptive real-time retention time alignment, eliminating traditional method development bottlenecks.
- **Platform bridging:** demonstrates a complete workflow from discovery to absolute quantification in just a few days, with 5,437 precursors from Orbitrap Astral discovery (median CV < 15%) filtered to 1,305 high-quality targets on Stellar MS (median CV ~17.4%, 85% of precursors with CV < 20%), demonstrating robust cross-platform translation while maintaining quantitative precision.
- **Achieves clinically relevant sensitivity for absolute quantification:** ^{15}N -labeled full-length protein standards enabled absolute quantification of 7 clinically relevant biomarkers (SERPINC1, QSOX1, TTR, ALDOB, ITIH4, ATRN, SELENOP) with >99% isotope incorporation efficiency and LOQs down to the low attomole range (1.02×10^{-5} pmol for QSOX1), covering a dynamic range spanning from pg/mL to $\mu\text{g/mL}$ in single runs.

WHAT IONOPTICKS PRODUCTS CONTRIBUTED

- **Unified chromatographic platform:** Aurora® Rapid™ 8 cm $\times$ 150 μm ID column on Evosep running at 60 SPD enabled consistent 21-minute separations for both Orbitrap Astral discovery (DIA) and Stellar MS targeted validation (PRM/MS3), ensuring seamless transfer of retention times between platforms via adaptive RT realignment.
- **High-precision ^{15}N -labeled protein quantification:** the Aurora® Rapid™ 8 $\times$ 150 column provided stable chromatography for absolute quantification of liver disease biomarkers using ^{15}N -labeled full-length protein standards, delivering median CV of 5.2% (96% of precursors <20% CV) for light/heavy peptide ratio measurements across a 25 ng to single-digit-pg dilution series.
- **High-throughput clinical compatibility:** the 150 μm ID format supported direct loading of 500 ng plasma digest onto Evtotips without offline fractionation, enabling 60 samples/day throughput while maintaining sufficient peak capacity (21 min gradients) for the 1,305-target refined assay, critical for translating the workflow to clinical lab settings.

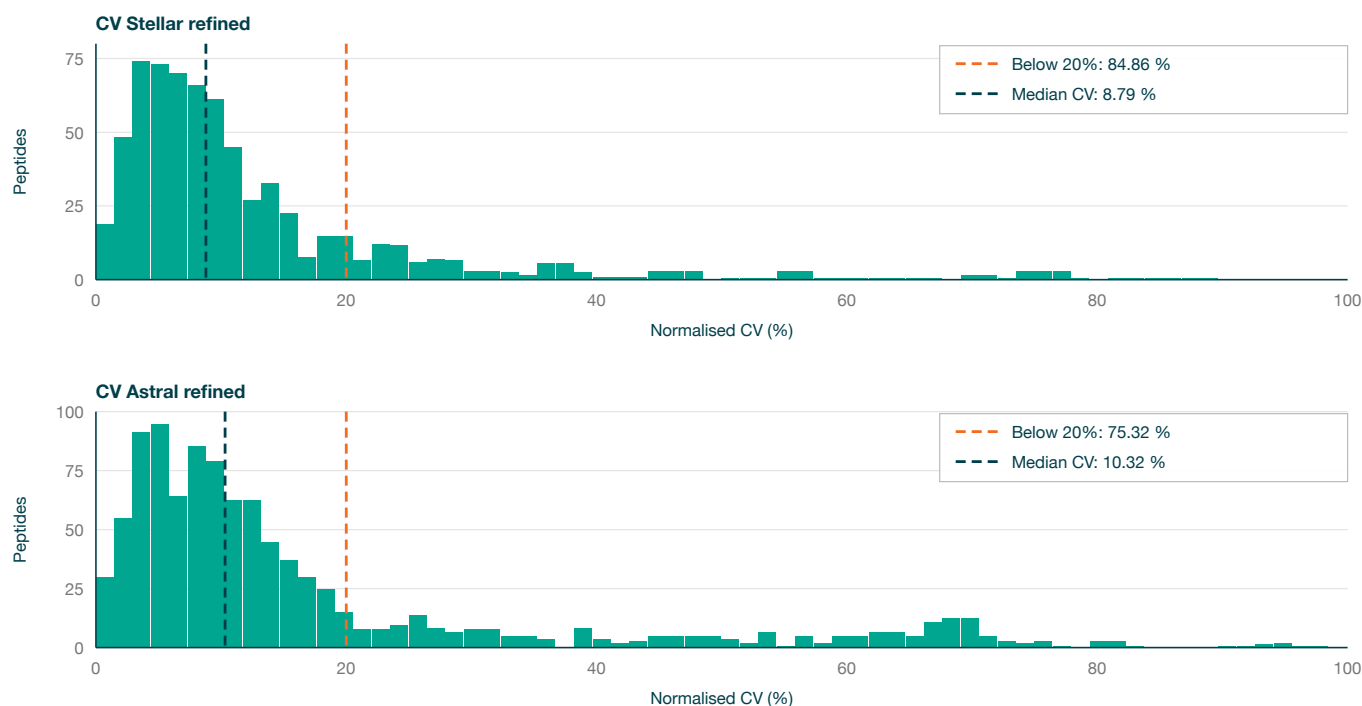


Figure 4. Aurora® Rapid™ 8 cm column enables 85% of precursors with CV < 20% on Stellar MS, and 75% on Astral MS, delivering clinical-grade reproducibility for discovery-to-validation workflows.

Redrawn from Wahle et al., *Molecular and Cellular Proteomics*, 2025; 24(9):101050, <https://doi.org/10.1016/j.mcpro.2025.101050> (CC BY 4.0). Bin heights digitised from the published figure across 68 bins per panel; the below-20% and median values are as published.

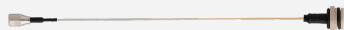
When running large plasma cohort studies for early disease biomarkers, the IonOpticks Aurora® Ultimate™ 25 cm column on timsTOF Pro 2 paired with the automated Proteograph XT workflow delivers the depth, reproducibility, and automation needed to finally make low-abundance secretome proteins routine targets.

4.2× depth, 2.3× better precision: Proteograph XT nanoparticle enrichment outperforms bead-based and neat workflows for secretome biomarker discovery, validated on IonOpticks Aurora® Ultimate™

Soni, R. K. (2024). Frontiers in Plasma Proteome Profiling Platforms: Innovations and Applications. *Clinical Proteomics*, 21(1), 43.

Study snapshot: Systematic benchmarking of three plasma proteomics workflows (Neat Plasma, ENRICH-iST bead-based enrichment, and Proteograph XT nanoparticle enrichment) reveals that Proteograph XT identified 4.2-fold more protein groups than Neat Plasma and 2.4-fold more than ENRICH-iST while achieving 2.3× better reproducibility (median CV 10.7% vs. 24.6% for Neat Plasma and 21.0% for ENRICH-iST). Proteograph XT also demonstrated 6.3-fold dynamic range expansion and 39% secretome database coverage with enrichment of cytokines, interleukins, and immune signalling pathways critical for early disease detection, all using the IonOpticks Aurora® Ultimate™ 25 cm column.

INSTRUMENTATION USED



Aurora® Ultimate™ CSI 25x75

Integrated CaptiveSpray emitter, 300 nL/min



timsTOF Pro 2

Bruker, dia-PASEF, 65 min gradients

Blood-based biomarker discovery is transforming clinical diagnostics and precision medicine, yet realising this potential requires navigating an increasingly diverse landscape of high-throughput proteomics technologies with distinct capabilities and limitations. Soni et al. advance this goal by systematically comparing three sample preparation strategies: manual Neat Plasma, bead-based ENRICH-iST enrichment, and fully automated Proteograph XT nanoparticle enrichment, to identify optimal configurations for sensitive, reproducible biomarker discovery. This work reveals that Proteograph XT dramatically outperforms alternatives, delivering 4.2-fold more protein groups and 6.7-fold more peptides than Neat Plasma, with superior reproducibility at just 10.7% median CV. This performance was enabled by an IonOpticks Aurora® Ultimate™ CSI column (25 cm × 75 µm ID) with integrated CaptiveSpray emitter, interfaced with a timsTOF Pro 2 operating in dia-PASEF mode. The column, run at 300 nL/min over 65-minute gradients, provided the chromatographic resolution necessary to identify low-abundance tissue leakage markers, cytokines, and interleukins that evade conventional approaches. The automated workflow's exceptional coverage of secretome proteins establishes a robust foundation for large-cohort clinical studies driving precision medicine and early disease detection.

WHY THIS PAPER MATTERS

- **Superior biomarker discovery depth:** Proteograph XT quantified 5,644 protein groups versus 1,323 for Neat Plasma and 2,305 for ENRICH-iST, a 4.2× and 2.4× improvement, respectively, enabling detection of low-abundance secreted proteins (cytokines, interleukins, interferons) that remain invisible to conventional workflows.
- **Unmatched reproducibility:** fully automated nanoparticle enrichment delivered median CV 10.7% versus 24.6% (Neat Plasma) and 21.0% (ENRICH-iST), critical for large cohort studies where technical variation can obscure biological signals.
- **Shows functional biomarker relevance:** the quantified proteins cover 39% of the secretome database with significant enrichment of complement/coagulation cascades, cytokine-cytokine receptor interactions, PI3K-AKT signalling, and TNF- α pathways, key secretome components actively secreted from cells and tumours that serve as prime candidates for early detection of cancer, CVD, and neurological diseases.

WHAT IONOPTICKS PRODUCTS CONTRIBUTED

- **Deep proteome separation:** the Aurora® Ultimate™ 25 cm × 75 μ m ID column provided the peak capacity and resolution required to separate the expanded dynamic range of proteins enriched by Proteograph XT nanoparticles, which is critical for resolving low-abundance cytokines and tissue leakage markers from high-abundance carriers.
- **Integrated CaptiveSpray sensitivity:** the Aurora® Ultimate™ CSI column's integrated CaptiveSpray emitter delivered stable ionisation across 65-minute gradients at 300 nL/min, providing the sensitivity required to detect low-abundance secreted proteins spanning 4.6 orders of magnitude in dynamic range, foundational to achieving the 39% secretome database coverage in the Proteograph XT workflow.
- **Ion mobility compatibility:** the Aurora® Ultimate™ column paired seamlessly with timsTOF Pro 2 diaPASEF acquisition, supporting the deep proteome coverage required to quantify 66,987 peptides in the Proteograph XT workflow.

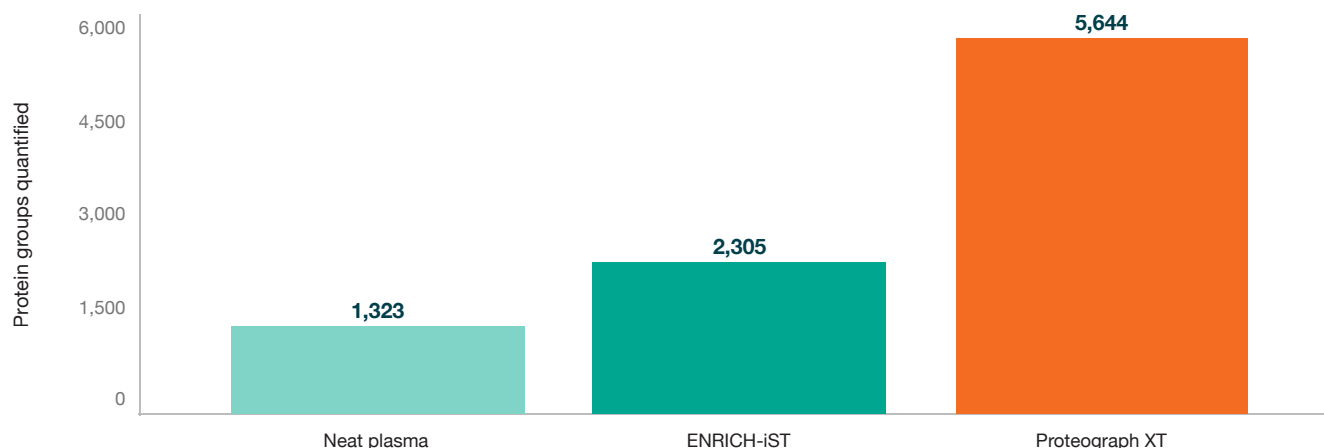


Figure 5. Aurora® Ultimate™ 25 cm column delivers the chromatographic resolution to separate Proteograph XT-enriched samples, enabling detection of 5,644 proteins - 4.2× neat plasma and 2.4× bead-based enrichment. Peptide identifications follow the same order: 66,987 with Proteograph XT, 6.7× neat plasma and 4.0× ENRICH-iST.

Redrawn from Soni, Clinical Proteomics, 2024; 21:43, <https://doi.org/10.1186/s12014-024-09497-2> (CC BY 4.0). Protein-group values as published; the peptide panel of the original figure is reported here as counts rather than redrawn.

2.4 Disease-specific plasma applications

PAPER 08 · REFERENCE [11]

When you need deep, reproducible neat plasma proteomics without depletion or expensive enrichment kits, the Aurora[®] Ultimate[™] 25 cm column on the nanoElute, paired with optimised diaPASEF and EV-boost, delivers exceptional coverage and throughput for large-scale clinical cohort studies.

'Getting the best out of the worst': EV-boost search adds 38% protein IDs to reach 1,092 from neat plasma at 24 SPD for scalable clinical studies

Metatla, I., Roger, K., Chhuon, C., Ceccacci, S., Chapelle, M., Schmit, P.-O., Demichev, V., & Guerrero, I. C. (2024). Neat Plasma Proteomics: Getting the Best Out of the Worst. *Clinical Proteomics*, 21(1), 22.

Study snapshot: Optimised neat plasma proteomics for disease biomarker discovery: broad dia-PASEF acquisition increased protein identifications by 21–24% versus narrow window acquisitions, 30-minute gradients on 25 cm columns delivered 811 proteins (24 SPD) versus 479 proteins (12 min), and EV-boost search leveraging extracellular vesicle files as a reference boosted protein IDs by 38% (794 to 1,092). This enabled IonOpticks Aurora[®] Ultimate[™] to deliver scalable, cost-effective analysis of a 33-sample clinical cohort without depletion or enrichment.

INSTRUMENTATION USED



Neat plasma proteomics remains the most accessible approach for clinical biomarker discovery, yet the extreme dynamic range of plasma (spanning 12 orders of magnitude) severely limits protein detection and reproducibility across studies. Metatla et al. address this challenge by systematically optimising diaPASEF acquisition parameters and chromatographic conditions to maximise coverage without costly depletion or enrichment steps, establishing a practical workflow for large-scale clinical applications. Expanding ion mobility and mass ranges to capture smaller, more hydrophilic peptides was shown to increase protein identifications by 21–24% compared to standard settings. Critically, this study also showcases a comparison of LC configurations using an IonOpticks Aurora[®] Ultimate[™] (25 cm × 75 µm ID) column on nanoElute LC coupled to timsTOF Pro 2, showing that 30-minute gradients achieve superior depth with over 800 protein groups quantified at 24 samples-per-day throughput, substantially exceeding shorter 12-minute gradients (479 proteins). For intermediate throughput applications, an Aurora[®] Elite[™] (15 cm × 75 µm ID) column using the Whisper 40 SPD method provided a balanced alternative with excellent reproducibility. The study further introduces an innovative 'EV-boost' strategy, leveraging extracellular vesicle fractions from just five donors to increase neat plasma protein identifications by 38% (from 794 to 1,092) through match-between-runs. Through systematic comparisons of gradient length, benchmarking of Evosep and nanoElute LC architecture, and sample-prep strategies on Aurora[®] column chemistry, this article establishes a practical, cost-effective framework for deep plasma proteomics applicable to large cohort studies.

WHY THIS PAPER MATTERS

- **Democratising deep plasma proteomics:** identified 1,092 protein groups from neat plasma using EV-boost search, approaching depths achieved by enrichment-based methods but with 1 μ L sample volume, no depletion, and an automatable workflow, making large cohort studies feasible for resource-limited labs.
- **diaPASEF parameter optimisation:** broad ion mobility range (0.67–1.29 Vs $\cdot$ cm²) and extended m/z range (400–1027 Da) captured hydrophilic, low-molecular-weight peptides excluded by standard methods, yielding 21–24% more proteins and 37–45% more peptides with direct impact on biomarker detection sensitivity.
- **EV-boost bioinformatics innovation:** using EV-derived peptide libraries for MBR exploits the biological reality that 90% of neat plasma proteins are also present in EV fractions, effectively 'borrowing' depth from EV analysis to boost neat plasma identifications without additional sample preparation.

WHAT IONOPTICKS PRODUCTS CONTRIBUTED

- **Aurora® Ultimate™ 25 cm for deep separation:** the Aurora® Ultimate™ 25 cm $\times$ 75 μ m ID column enabled 30-minute active gradients delivering 811 ± 78 protein groups (24 SPD), 70% more identifications than 12-minute gradients, by resolving hydrophilic peptides that co-elute in shorter runs.
- **Aurora® Elite™ 15 cm for higher throughput:** for Evosep One workflows, the Aurora® Elite™ 15 cm column enables 40 SPD throughput (Whisper method) with ~500 protein groups, trading ~40% depth for 67% higher sample throughput compared to the Ultimate 25 cm.
- **Low-volume optimisation:** the 75 μ m ID column format is ideally suited to the 1 μ L plasma samples processed by S-Trap digestion, enabling high-sensitivity analysis of minimal clinical material without requiring larger volumes or cartridge-based enrichment.
- **Retention time stability for MBR:** consistent chromatographic performance across 33-sample cohorts enabled reliable Match-Between-Runs, with 94% increase in protein IDs when searching all files together versus single-file analysis, critical for EV-boost search implementation.

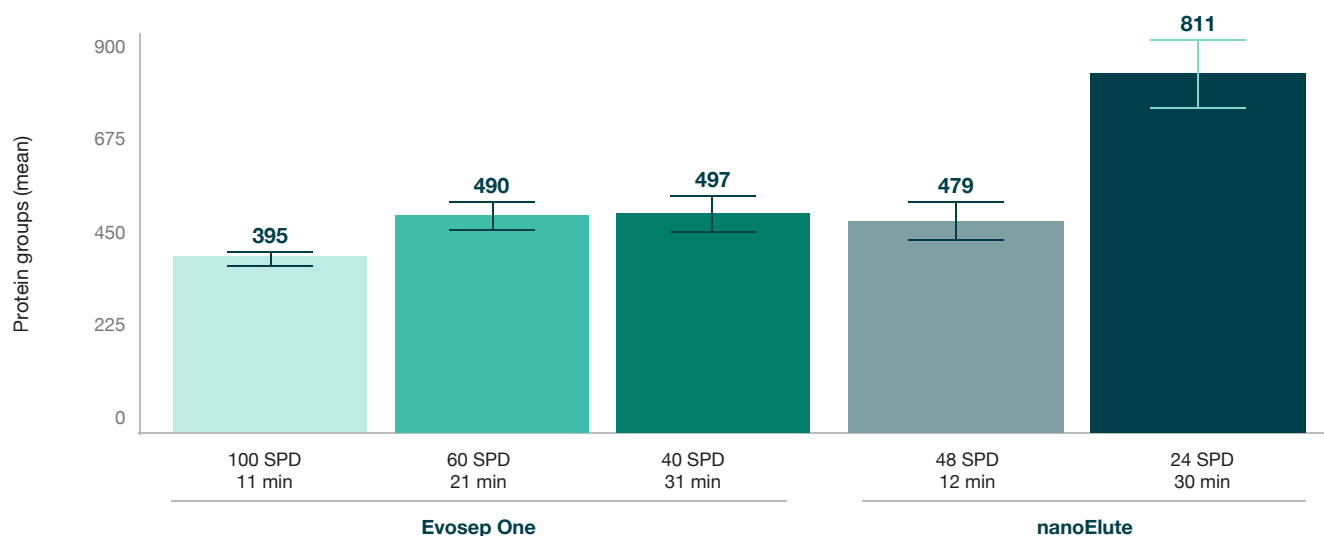


Figure 6. 30-minute gradients on Aurora® Ultimate™ 25 cm deliver 70% more proteins than 12-minute runs by resolving hydrophilic peptides. The 24 SPD condition quantified 811 ± 78 protein groups.

Redrawn from Metatla et al., Clinical Proteomics, 2024; 21:22, <https://doi.org/10.1186/s12014-024-09477-6> (CC BY 4.0). Error bars show $\pm$ SD, digitised from the published figure; the 24 SPD value is as published.

PLATFORMS REPRESENTED ACROSS THIS EVIDENCE BASE



Orbitrap Astral



Orbitrap Exploris 480



Stellar MS



timsTOF HT



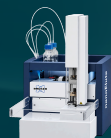
timsTOF Pro



timsTOF Pro 2



timsTOF Ultra



nanoElute



Evosep One



Vanquish Neo UHPLC

IONOPTICKS PRODUCTS FEATURED IN THIS NOTE



Aurora® Rapid™ 5x150

5 cm × 150 µm ID packed emitter for multi-laboratory screening and cohort validation at 80–150+ SPD.



Aurora® Rapid™ 8x150

8 cm × 150 µm ID. The column behind the largest published plasma proteomics workflow to date - 40,000+ injections over 353 days. Refs [4, 5, 9]



Aurora® Rapid™ 8x75

8 cm × 75 µm ID for low-input plasma below 200 ng, serum microsamples, capillary blood and enriched sub-proteomes.



Aurora® Elite™ 15x75

15 cm × 75 µm ID. Balanced depth and throughput for biomarker triage at 40–60 SPD. Refs [7, 8, 11]



Aurora® Ultimate™ 25x75

25 cm × 75 µm ID for deep-discovery separations, depletion and fractionation workflows, and method development at 20–40 SPD. Refs [6, 8, 10, 11]



NanoShield® C18 trap

5 cm × 100 µm trap column delivering in-line sample clean-up ahead of the analytical column, at near-direct-injection performance.



HeatSync™

Temperature-control ecosystem holding column temperature steady, so retention times hold across long cohort acquisitions.



nanoZero® fittings

The zero-dead-volume fitting at the heart of the packed-emitter architecture, plus source adapters and installation toolkits.

DECISION GUIDE

03 Choosing the right Aurora[®] column for your plasma workflow

The Aurora Series[®] includes several formats optimised for different plasma workflows. The table below summarises the main options; bracketed numbers are the references in Section 5 that used each format.

AURORA [®] COLUMN	FORMAT	TYPICAL PLASMA WORKFLOW	THROUGHPUT
Aurora[®] Rapid[™] 5×150	5 cm × 150 µm ID, 1.7 µm	Multi-laboratory plasma screening; high-throughput cohort validation; population-scale studies requiring robustness across sites.	80–150+ SPD
Aurora[®] Rapid[™] 8×150	8 cm × 150 µm ID, 1.7 µm	High-throughput plasma cohorts; bead-enriched and PCA-N workflows at population scale. [4, 5, 9]	50–100+ SPD
Aurora[®] Rapid[™] 8×75	8 cm × 75 µm ID, 1.7 µm	Low-input plasma (<200 ng), serum microsamples, capillary blood, enriched sub-proteomes.	60–120 SPD
Aurora[®] Elite[™] 15×75	15 cm × 75 µm ID, 1.7 µm	Balanced coverage/throughput plasma discovery; deep plasma for biomarker triage. [7, 8, 11]	40–60 SPD
Aurora[®] Ultimate[™] 25×75	25 cm × 75 µm ID, 1.7 µm	Deep-discovery plasma proteomics; depletion/fractionation workflows; method development. [6, 8, 10, 11]	20–40 SPD

Practical guidance. Groups operating at the boundary between biomarker discovery and biomarker validation should consider standardising on a single Aurora[®] chemistry across discovery (e.g. Aurora[®] Elite[™] 15×75 or Aurora[®] Ultimate[™] 25×75) and high-throughput screening (Aurora[®] Rapid[™] 8×150). This mirrors the Mann Lab's published Astral to Stellar translation workflow [\[9\]](#) and minimises chromatographic drift between study phases.

04

Summary

Plasma proteomics at the scale required for modern clinical and translational research demands a column that is simultaneously deep, reproducible, robust and fast. The peer-reviewed evidence consistently shows that Aurora Series® delivers on all four dimensions.

For laboratories building high-throughput plasma workflows on Orbitrap Astral, timsTOF, ZenoTOF or targeted MS platforms, Aurora® Rapid™ 8×150 is the column used in the largest published plasma proteomics workflows to date, with 40,000+ injections demonstrated across a single clinical workflow. For deeper-discovery or lower-input studies, Aurora® Elite™ and Aurora® Ultimate™ columns extend the same chromatographic architecture to 15 cm and 25 cm bed lengths on the same 1.7 µm chemistry, preserving method portability across discovery and validation phases.

IonOpticks works directly with plasma proteomics groups worldwide at academic medical centres, pharmaceutical discovery labs, CROs and clinical diagnostics programmes to configure the right column, cassette, heating and source interface for each laboratory's instrument ecosystem.

Contact your IonOpticks representative to discuss method development, cohort design, or evaluation samples for your plasma proteomics workflow.

05 References and notices

All references are peer-reviewed publications, peer-reviewed preprints or externally reviewed application/technical notes that explicitly cite IonOpticks Aurora Series® columns in their methods sections, or that establish foundational context for the plasma proteomics workflows described.

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Figures 1 and 2 are reproduced from those sources and recoloured to the IonOpticks palette, with their axis labelling reset in house type; no data values or plotted geometry have been altered. Figures 3 to 6 have been redrawn to a common house style from the values published in, or digitised from, the cited figures.

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For more information, contact
sales@ionopticks.com or visit
www.ionopticks.com

We work directly with plasma proteomics groups at academic medical centres, pharmaceutical discovery labs, CROs and clinical diagnostics programmes to configure the right column, cassette, heating and source interface for each laboratory's instrument ecosystem.

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