Nanomics

Data Sheet

Automate SP3 Proteome Workflow via Proteonano™ Platform

Reliable, Reproducible, and Ready for Large-Scale Proteomics

Nanomics Biotech offers a powerful SP3-based sample preparation workflow built on the Proteonano™ platform. This solution combines the **Proteonano™ SP3 Proteome Extract Kit**—featuring advanced multi-affinity magnetic nanoprobes for efficient, reproducible protein capture—with the **Nanomation™ G1 Pro automated workstation**, enabling fully standardized sample preparation in 96-well plate. Validated across cells, tissues, and plant samples, this workflow ensures robust performance and scalability for proteomics and precision medicine research

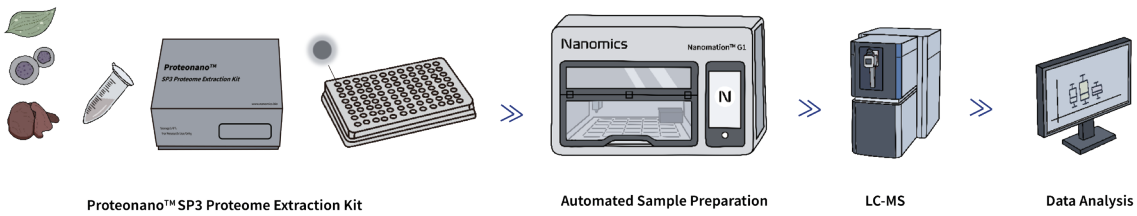

Figure 1: Proteonano™ ultraplex proteomics platform integrated with SP3 technology combined with LC-MS for proteomic analysis of biological sample

Experimental design

- Sample enrichment with Proteonano™ SP3 Proteome Extraction Kit
- Automated sample prep by Proteonano workflow (G1 Pro)
- Vanquish Neo (ES906), Astral 14 min DIA
- DIA-NN (V1.8.1), w/o normalization

Comparison Between the Proteonano™ Kit and Precipitation Method.

Wide proteome coverage

Using equal injection volumes, the Proteonano™ SP3 Proteome Extract Kit achieved protein identification numbers comparable to those from traditional organic reagent precipitation methods in HeLa samples.

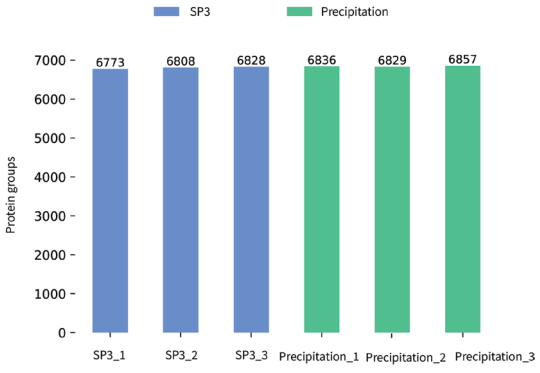

Figure 2: Proteomic analysis of HeLa cell samples processed using SP3 Kit (blue) and precipitation method (green).

Excellent accuracy and correlation

Protein identification results showed strong agreement between the SP3 and precipitation workflows, with all correlation coefficients exceeding 0.90.

Highly reproducible performance

The average correlation coefficient across replicates reached 0.96, confirming the method' s consistency and robustness in quantitative proteomics.

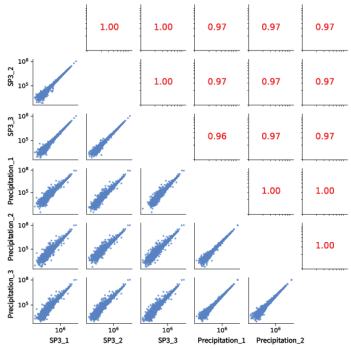

Figure3: Protein quantitative correlation between proteonano™ SP3 and precipitationmethod.

Comparison of Manual and Automated Sample Preparation Methods

Wide proteome coverage

Both manual SP3 and the Proteonano™ automated system identified over 6,700 proteins from mouse liver samples, showcasing the platform' s depth of proteome coverage.

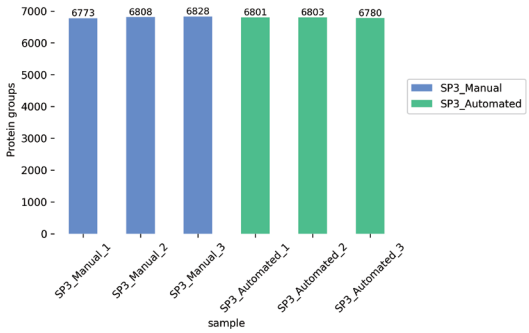

Figure 4: Proteomic analysis of mouse liver samples processed manually and with an automated system using the SP3 kit

Outstanding reproducibility

Coefficients of variation (CVs) were 6.764% (manual) and 6.544% (automated), indicating highly consistent results across workflows.

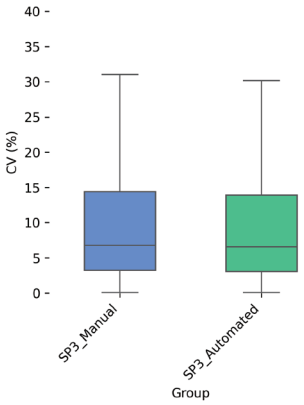

Figure 5: CV of protein groups detected in samples processed manually and with an automated system.

Strong correlation

Over 98% protein overlap between manual and automated methods confirms the Proteonano™ SP3 Kit delivers equivalent performance in both settings.

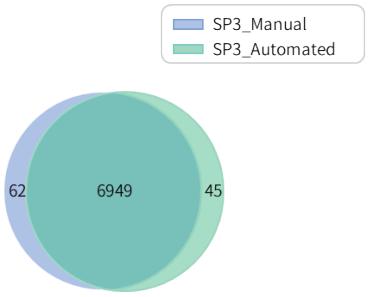

Figure 6: Overlap of protein groups identified from manual (blue) and automated (green) SP3-based sample preparation workflows.

Scalable and reliable

The Proteonano™ system supports high-throughput, standardized SP3 sample preparation—ideal for large-scale proteomics studies

Proteonano™ Platform'ss Performance in Different Biological Sample s

High protein yield across species

Using the Proteonano™ Ultraplex Proteomics Platform with the SP3 Proteome Extract Kit, 9,414 proteins were identified in frozen Arabidopsis thaliana and 9,916 in frozen tobacco samples.

Enhanced sensitivity over competing kits

Compared to other nanoparticle-based quantification kits, the SP3 workflow consistently detected 100–400 more proteins per sample.

Exceptional coverage in fresh plant tissues

In fresh samples, 11,934 proteins were detected in corn and 12,521 in soybean using the SP3-based workflow.

Outperforms traditional methods

Compared to the FASP method, the SP3 kit enabled identification of 800–1,000 additional proteins in soybean samples, demonstrating superior proteome coverage.

MS platform	Kit	Sample	Initial sample protein amount (μg)	Injection volume (ng)	Gradient (min)
Orbitrap Astral	Proteonano™ SP3 Proteome Extract Kit	Arabidopsis thaliana	100	300	8
		Corn			
		Tobacco			
		Soybean			
		rabbit intestinal organoids			
		Hela Cell	10		13

Table 2: Mass spectrometry experimental parameters of different biological sample

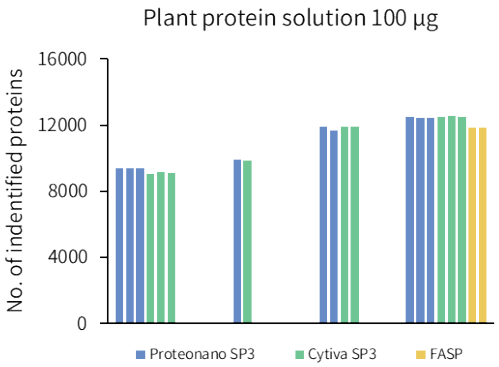

Figure7: Protein identification numbers detected in plant samples processed using the proteonano™ SP3 proteome extract kit(blue), cytiva SP3 kit(green), and FASP (yellow) methods.

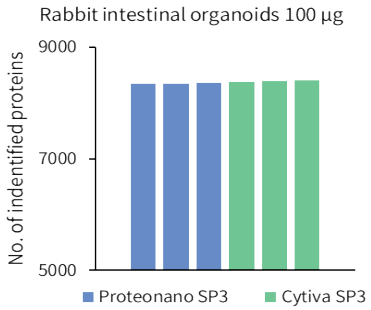

Figure 8: Number of protein identifications detected in rabbit intestinal organoids samples processed using the proteonano™ SP3 proteome Extract Kit (blue) and cytiva SP3 kit(green).

Highlight

Automated & Scalable
Fully automated 96-well SP3 workflow for high-throughput proteomics.

Accurate & Reproducible
Correlation coefficients >0.95; CVs ~6.5% across sample types.

Broad Sample Compatibility
Proven across cells, tissues, and plants with deep proteome coverage.

High Sensitivity
Detects more proteins than traditional precipitation and FASP methods

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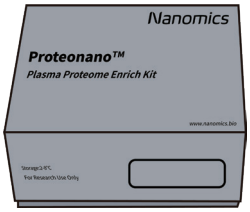
About Nanomics

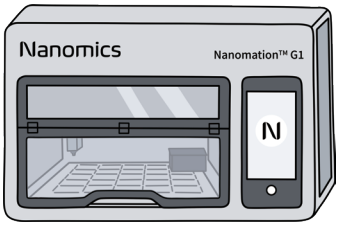
Nanomics biotech is committed to creating world's most integrative proteomic platform for early detection of cancer and other diseases. Following in the footsteps of genomics, proteomics will usher in a new era of precision medicine in liquid biopsy, companion diagnostics, and early screening. By assembling nanotech, automation, and artificial intelligence, our fully automated, high throughput platform will enable large-scale, rapid mining of the complete set of human plasma proteome and fundamentally transform the way we discover new biomarkers and drug targets.

Nanomics's mission is to create a world where no one would have to lose beloved ones early. Our Proteonano™ platform can detect 1500-5000 plasma proteins covering 2000 sig-naling pathways, supporting research institutes, pharmaceutical companies, and medical enterprises.

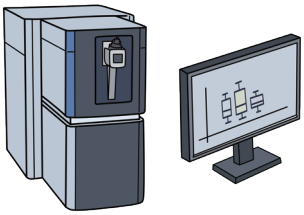
Proteomics Kits

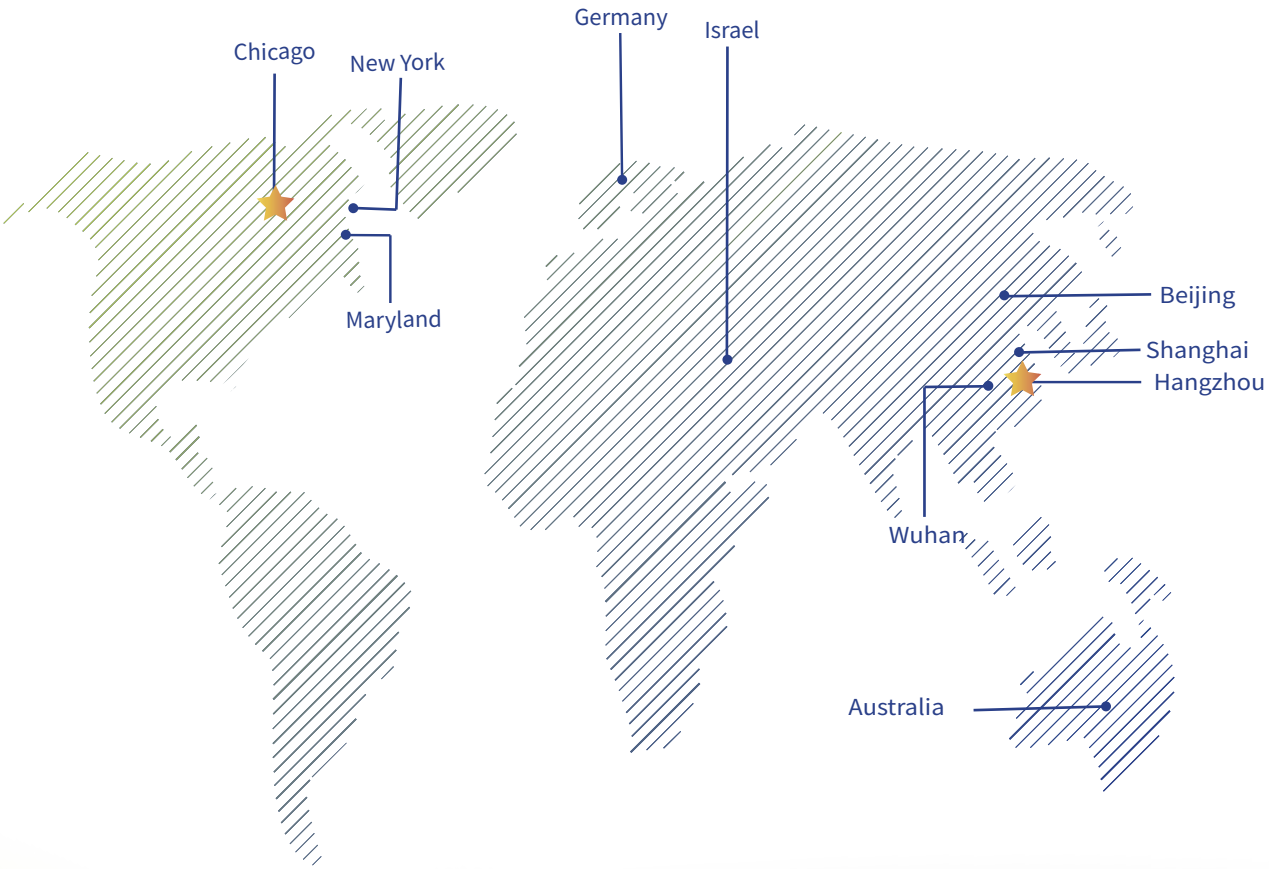


Robots



Service





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