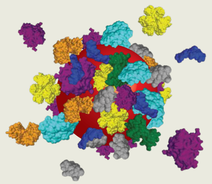

Nanoparticle-protein complex

Analytical validation of the multi-nanoparticle Proteograph™ platform for rapid and deep proteomic profiling

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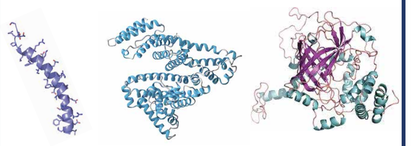
Proteomics is the gateway to understanding biology

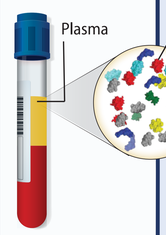
Proteomics



Large-scale, unbiased proteomics studies are essential to understanding the complexity of biology. Currently available technologies are unable to precisely and efficiently power deep unbiased analysis of the proteome.

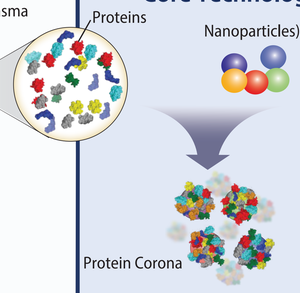
Proteograph: enabling efficient, deep, precise and unbiased proteomics for the first time

Our Proteograph product suite, powered by our proprietary nanoparticle technology, allows survey of the proteome across a broad range of sample types, including plasma, to enable novel discoveries and insights



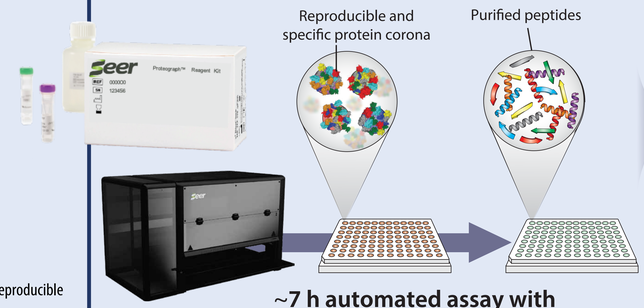
Broad range of samples

Core Technology

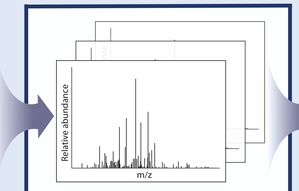


Nanoparticles form specific and reproducible protein coronas based on their physicochemical properties

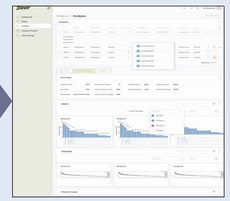
Seer's Proteograph Proteomics Suite: Assay, Instrument, Consumables and Analysis Tools



~7 h automated assay with 30 min setup time



Suitable for most LC-MS/MS instruments



Intuitive software for QC and data analysis

Research Applications

- Early disease detection
- Novel biomarker discovery
- Translational proteomics
- Drug target discovery

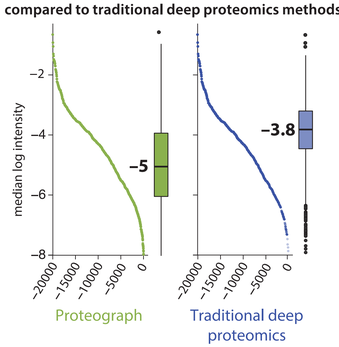
More information

For please visit seer.bio/publications or scan the QR code

Benchmark comparison vs traditional deep proteomics methods

Depth

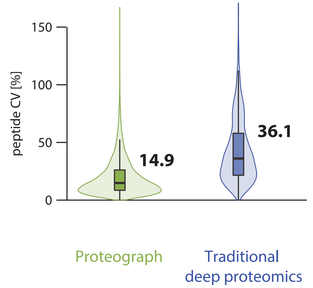
On average Proteograph, allows > 10x deeper interrogation of the dynamic range (median log intensity -5.3 vs -3.8) when compared to traditional deep proteomics methods.



Dynamic range of identified proteins matched with normalized protein intensities compared to deepest reported plasma proteome (Keshishian et al. 2015. Molecular and Cellular Proteomics, 14(9), 2375–2393).

Precision

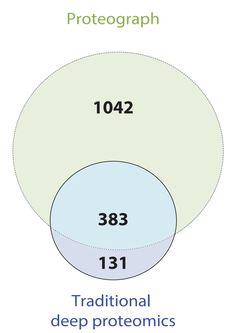
2.4x higher precision accross the 3 replicates is achieved with Proteograph vs. traditional deep proteomics methods.



Coefficient of variation (CV) of median normalized peptide intensities.

Coverage

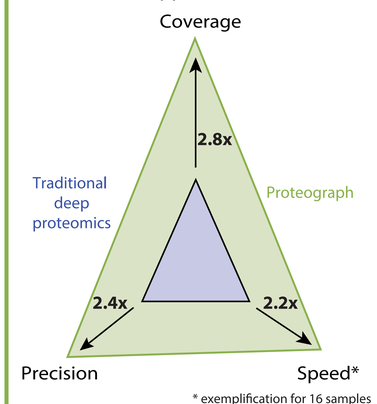
2.8x more protein groups (1427vs 514) were identified with Proteograph vs. traditional deep deep proteomics methods.



Number of protein IDs quantified in 3 out of 3 assay replicates.

Improvement

Concurrent improvement in coverage, precision and speed is achieved with Proteograph vs. traditional deep proteomics methods.

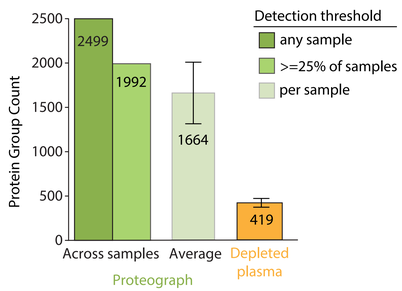


* exemplification for 16 samples

Exemplification

Rapid interrogation of ~2000 of proteins in 100's of samples in an NSCLC study

- 141 early (stage 1-3) lung cancer and control plasma samples
- ~4x improvement in protein IDs vs depleted plasma
- Total experiment time, 2.5-weeks



Proteograph was able to identify 2499 proteins across all 141 samples, and 1992 protein IDs were detected in at least 25% of all 141 subjects. 1664 proteins were found as average in Proteograph runs vs 419 in depleted plasma.

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Efficient and scalable profiling of an average of 1779 plasma proteins in 268 subjects with multi-nanoparticle (NP) Proteograph platform enables robust detection of early-stage non-small cell lung cancer (NSCLC) and classification vs. healthy and co-morbid subject.

A 5 NP optimized Proteograph panel compared to a traditional "deep" plasma proteomics: depletion (Agilent MARS-14 Column) and peptide fractionation (high-pH, 19 fractions concatenated into 9 injections). All were run on 30 min DIA (SWATH) method on a SCIEX 6600+ instrument.
Similar performance was obtained when compared to a CRO service for deep DDA proteomics on Thermo Scientific Orbitrap Fusion Lumos instrument (data not shown).