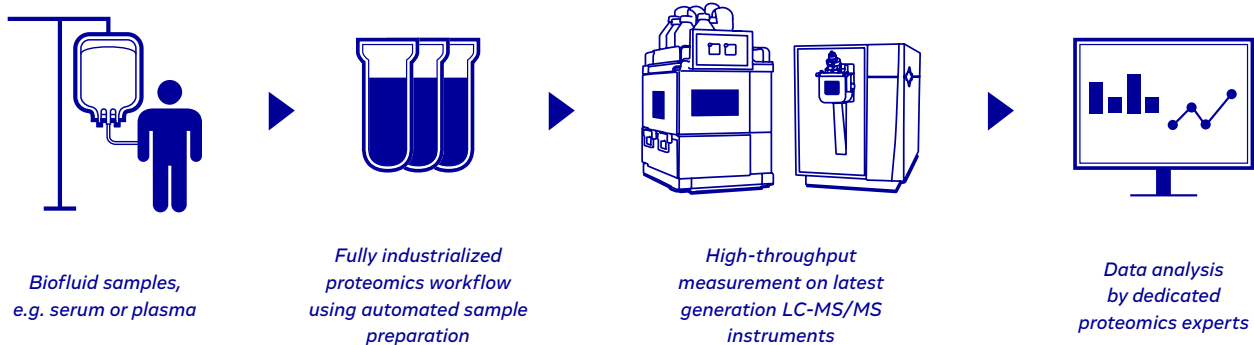


Clinical Proteomics: A Focus on Bodyfluids

Evotec is one of the largest providers of services in the field of mass-spectrometry-based proteomics in Europe with more than 20 years experience and more than 50 MS machines hosted across our sites.

- ▶ **ScreenPep™**: A high-throughput and deep coverage proteomics platform, adapted for fully automated plasma and serum proteomics, yielding up to 1,000 protein identifications from just 1–5 µl input material
- ▶ Evotec is the only Center of Excellence in Europe offering nanoparticle based **Proteograph™** technology: Allowing identification of up to 5,000 proteins from human biofluids (e.g. serum, plasma, cerebrospinal fluid (CSF), secretome)
- ▶ Integrated solutions for translational biomarker development, from discovery using unbiased proteomics to validation using targeted mass spectrometry or affinity based methods and application in clinical trials under GCP
- ▶ Access to our PanOmics platforms increasing the probability of success by combining proteomics data with transcriptomics and metabolomics data
- ▶ Proteomics analysis of extracellular vesicles enriched from bodyfluids using our in-house **extracellular vesicle** platform

High Throughput Clinical Proteomics Workflow





Custom services tailored to your needs

- ▶ Optimization of study design for proteomics experiments
- ▶ Model and input versatility, adjusting sample preparation workflows to meet specific client requirements

- ▶ High-end MS expertise using latest generation of timsTOF and Orbitrap type instruments

High-throughput neat workflows	Depletion of top abundant proteins	Extracellular vesicle (EV) enrichment	Proteograph™ Product Suite
Minimum amount of input material required: 1–5 µl (e.g. plasma, serum, CSF); applicable to all species	10–30 µl plasma/serum sample required, multiple methods available depending on required throughput and species; restricted to murine & human samples	100 µl plasma/serum required, for CSF 600 µl-2 ml for best results; applicable to all species	100–250 µl input material required for optimal results, highly standardized workflow for biofluids (plasma, serum, CSF, urine, secretome); applicable to all species
<ul style="list-style-type: none"> ▶ Single sample: ~800 protein IDs ▶ Patient cohort for plasma/serum: up to 1,500 proteins ▶ CSF: ~2,500 proteins ▶ High-throughput workflow in 96-well format 	<ul style="list-style-type: none"> ▶ Single plasma/serum sample: 1,200–1,500 protein IDs ▶ Larger plasma/serum study: up to 2,000 protein IDs ▶ Depletion of specific proteins (e.g. albumin) via spin-filter or MARS columns 	<ul style="list-style-type: none"> ▶ Serum/plasma: 1500–1800 protein IDs ▶ CSF (600 µl): 2400–2800 protein IDs ▶ High-throughput SEC enrichment (but also other methods like ultra-centrifugation, ultra-filtration, precipitation available) ▶ QC: nanoFCM, TEM 	<ul style="list-style-type: none"> ▶ Plasma cohort: 4-fold increase of identification with up to 5,000 protein IDs ▶ Single sample: 2,500 protein IDs ▶ Continuous development to optimize and extend nanoparticle based proteomics workflow in collaboration with Seer^{INC}

How does Evotec support MultiOmics data analysis and biomarker discovery?

- ▶ Dedicated team of bioinformaticians developing our in-house proteomics pipeline
- ▶ State-of-the-art software tools for protein identification and quantification in direct exchange with developers
- ▶ MultiOmics data integration on Evotec's PanHunter platform

Why choose mass spectrometry based proteomics over affinity based techniques?

- ▶ Unbased measurement of all proteins and detection of protein isoforms and post-translational modifications
- ▶ Not limited to standard species, can be used for animal models and animal health studies e.g. on cat, dog, horse
- ▶ Limited or no impact of post-translation modifications and 3D confirmation on quantification of proteins