

Streamlined & automated sample processing for in-depth proteomic analyses

Garwin Pichler

Ph.D., Co-founder and CEO PreOmics, Planegg/Martinsried, Germany

Proteomics workflows are becoming increasingly important for applications such as biomarker discovery and detections.

Proteomics workflows have been traditionally limited by LC-MS measurement time and sample preparation throughput. While advances in LC-MS instrument technologies and workflows have now significantly increased the number of samples that can be processed on a weekly basis, the bottleneck has shifted to efficient, robust, and reliable high-throughput sample preparation.

PreOmics' improved sample technology enables robust and reproducible sample preparation, resulting in reliable biological outcomes. The iST sample processing technology provides significant time savings, can be fully automated and combined with our new BeatBox technology for very efficient tissue homogenization.