GenXPro GmbH

ABOUT

GenXPro is a biotechnology company based in Frankfurt, Germany specializing in highly sensitive Next Generation Sequencing (NGS) applications and bioinformatics.

Founded in 2005 by a team of experienced scientists, GenXPro has established itself as a reliable partner in the field of genomics, transcriptomics and epigenomics with customers around the world. The company provides cutting-edge and sensitive tools and services to academic and industrial customers seeking solutions to nucleic acid-related research questions and applications.

With a focus on precision, sensitivity and efficiency, GenXPro provides reliable methods for the analysis of RNA, DNA, and epigenetic modifications, helping to advance research in molecular biology, medical diagnostics / biomarkers, agriculture, and biotechnology.

Our powerful bioinformatics tools help customers to interpret the complexity of biological systems by connecting the multi-omics layers with up-to-date databases. By using a multitude of bioinformatics-tools in highly standardized pipelines as well as machine learning and language models, deep insights are generated, saving weeks of time for interpretation.

INDUSTRY TALK

Björn Rotter

Integrative Transcriptomics and Drug Response Prediction in Cancer: Advantages of panRNA-Seq, FFPE-Compatible NGS, and a case study: Patient-derived organoid models in colorectal cancer

Emerging technologies such as panRNA-Seq and FFPE-compatible library prep solutions have expanded the analytical potential of clinical samples, particularly for patient-derived organoid (PDO) models. In the context of the EU Horizon 2020 project REVERT (taRgeted thErapy for adVanced colorEctal canceR paTients), we applied these cutting-edge platforms developed by GenXPro to analyze transcriptomic signatures from PDOs derived from colorectal cancer patients.

Using GenXPro's TQ pan-RNA-Seq, which simultaneously captures coding and non-coding RNAs, we generated high-quality expression data from minute RNA amounts, including degraded FFPE samples. This data was cross-referenced with public RNA-Seq datasets from clinical cohorts to assess clinically relevant biomarkers and subtype classifications. Expression profiles were evaluated using Consensus Molecular Subtypes (CMS) scoring, and subsequently utilized in in silico drug sensitivity prediction pipelines.

Finally, all findings were integrated into a comprehensive decision-support report - the ClinXPro Report - offering actionable insights for precision therapy based on subtype-specific vulnerabilities and predicted drug responses.

Our study underscores the power of multi-modal transcriptomics, bioinformatics pipelines, and patient-derived organoid systems to guide personalized treatment strategies in colorectal cancer.