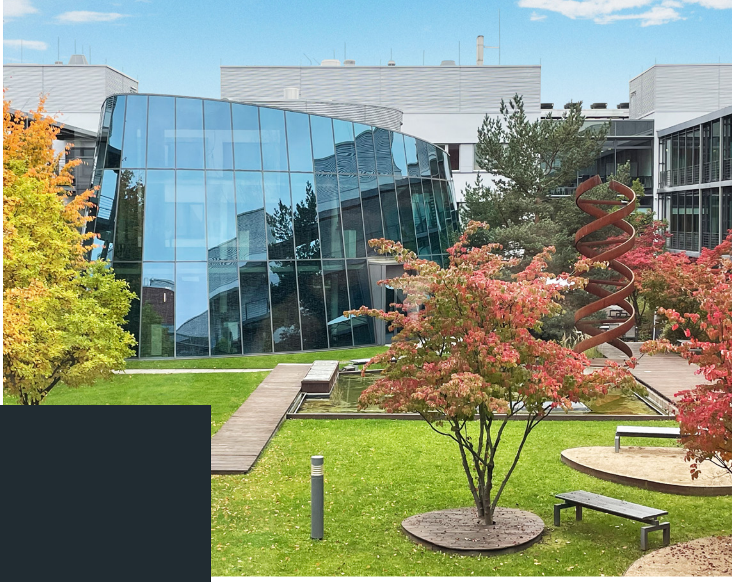

Excellence in Genomics, Transcriptomics, Epigenetics and Bioinformatics

TrueQuant RNA-Seq Protocol

optimized for
- FFPE samples
- Liquid biopsies
- Plasma samples and EV'S
- Degraded RNA / Low RIN-value

RNA & small RNA Analyses

Genomics

Epigenomics

Microgenomics

Bioinformatics

GenXPro is a biotechnology company based in Germany specializing in specific 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.

www.genxpro.de

Smart NGS Solutions and Bioinformatics for Research and Health

GenXPro
Molecular Data for
Research & Health

Kits

We develop and sell RNA sequencing kits for NGS laboratories worldwide. These are based on our TrueQuant (TQ) method, which later became known as "Molecular Barcoding" or "Unique Molecular Identifiers" (UMI).

We offer NGS kits such as the TQ MACE-Seq kit, the TQ small RNA-Seq kit and the TQ pan-RNA-Seq kit for the simultaneous analysis of small RNAs and mRNAs from one sample. What all kits have in common is their high sensitivity, with the lowest sample input of just 10 pg and the advantage that even highly degraded RNA such as FFPE-derived samples or from liquid biopsies can be successfully analyzed.

Services

Our customers can also order full service by entrusting us with their native sample material or already isolated RNA or DNA. A broad variety of methodologies are available including bioinformatics analyses such as ATAQ-Seq, TQ MACE-Seq (3'mRNA-Seq), TQ small RNA-Seq, TQ pan-RNA-Seq, Amplicon-Sequencing, Aptamer-Sequencing, CAGE-Seq, tRNA-Seq, WES, Methyl-Seq, Ribo-Seq, Degradome-Seq / PARE and many more.

Bioinformatics

Our bioinformatics department reached a major milestone in 2024 with the release of our GXP BioInfonomics Suite with an unprecedented quality and comprehensiveness.

After mapping, annotation and quantification of the raw-reads, our highly standardized bioinformatics pipelines generate a comprehensive series of downstream analyses, quality / bias assessments, mutations, fusions, copy numbers, mutation-signatures, actionable clinical information for DNA, and Gene Set Enrichment Analyses (GSEA), Overrepresentation Analyses to decipher pathways, potential drug-interventions, numerous signature-scores etc. for RNA-data.

Simply upload your NGS Illumina raw-data or fastqc data to our webserver, start the required analyses and receive your results a few minutes to hours later.