IAB
Institute of Applied Biotechnologies

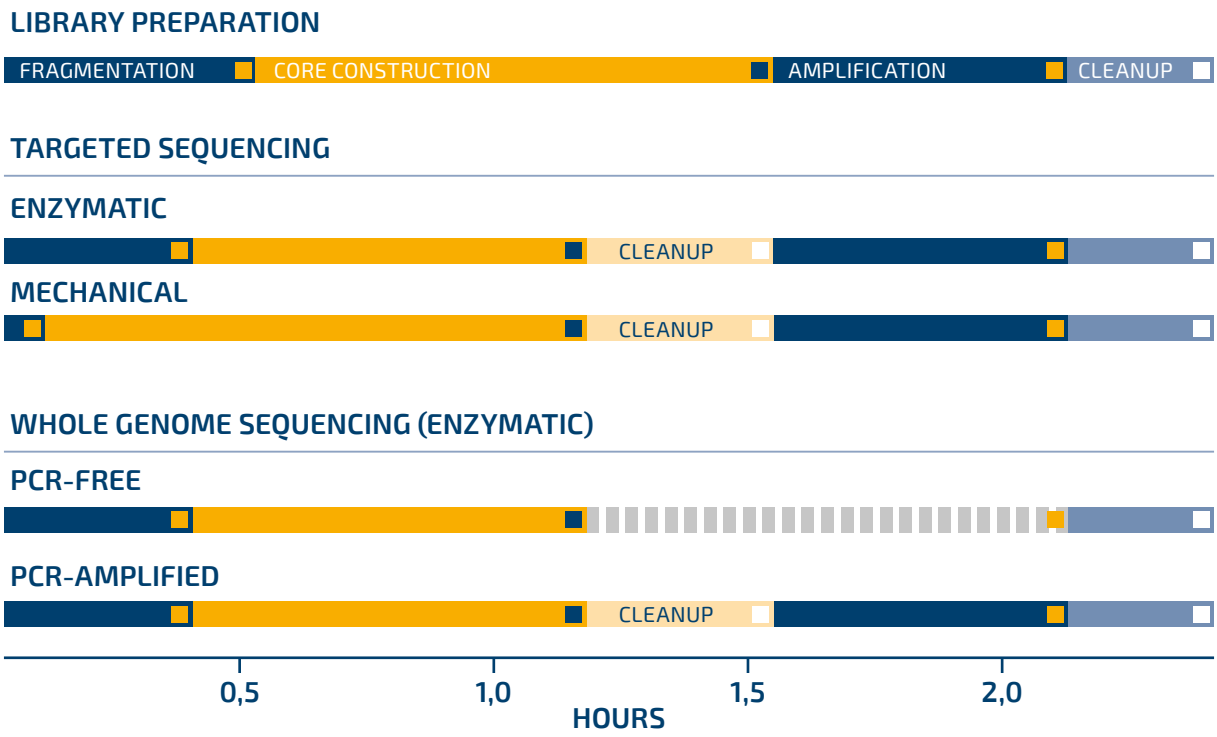
Twist Bioscience NGS portfolio

Twist NGS portfolio provides exceptional performance, greater flexibility, and maximized sequencing efficiency, coming hand in hand with significant cost reduction. Years of IAB´s hands-on experience assures that Twist solutions seamlessly integrate into your workflow. Open a new era of your experiments with the tools of the future.

NGS Library Preparation Kits

Twist Library Preparation Kits streamline the construction of high-quality DNA libraries for next-generation sequencing (NGS) applications. Two configurations accommodate either enzymatic or mechanical DNA fragmentation, and both are optimized to facilitate library preparation for whole genome sequencing and targeted enrichment. The kits combine library preparation steps into a single reaction for improved efficiency and consistent results. Flexible DNA sample input from 1 ng – 1 µg (enzymatic) can be converted into robust, amplified libraries in under 2.5 hours.

- Use **Enzymatic fragmentation** for automated, high-throughput gDNA
- Use **Mechanical fragmentation** for DNA input of varying types and quality
- Use with **Twist full-length CD adapters** for PCR-free library Preparation
- Use with the **Twist Universal Adapter (UDI) System** for maximum yield
- **PCR-free library preparation** is available for WGS



Whole Exome Sequencing

Twist Exome 2.0 covers 36.5 Mb of human protein coding & non-coding regions. The content of Exome 2.0 is thoughtfully curated, based on recent database releases (Gencode, Refseq, CCDS, Ensembl), includes coding targets for COSMIC pathogenic variants, ACMG73 genes, complete genes with >500 pubmed citations, and more.

- Save money by reducing off-target and over-sequencing with **best-in-class on-target rate and coverage uniformity** of Twist Exome 2.0
- Easily **spike-in custom content** into the Exome 2.0 panel or pick from pre-designed spike-in options
- See **Comprehensive Exome** or **Alliance VCGS Exome** for additional options

Enzymatic Fragmentation 2.0 Kit

- Library Preparation
- Library Amp Mix

Mechanical Fragmentation Kit

- Library Preparation
- Library Amp Mix

Standard Hybridization v2

- Std Wash Buffers
- Hybridization Reagents

Fast Hybridization

- Fast Wash Buffers
- Hybridization Reagents

Exome 2.0

- Probes

Dry Down Beads

- DNA purification beads
- Streptavidin binding beads

Custom Panels

Twist Custom Panels can be designed and built to cover a wide range of panel sizes, target regions, and multiplexing requirements — all with exceptional and consistent performance. Whether you design your own panel from scratch or add targets to enhance the content of existing panels, you can use your **Twist Custom Panel with Twist's modular library preparation kits** or seamlessly integrate them into your existing workflow. It is always possible to add content or enhance existing content easily.

- **Effective design, accurate synthesis,** and **unparalleled quality**
- **Lightning-fast turnaround time** from your idea to the final panel
- **Easy ordering and quick support** of the panel design and use
- Pricing based on the number of probes and number of reactions

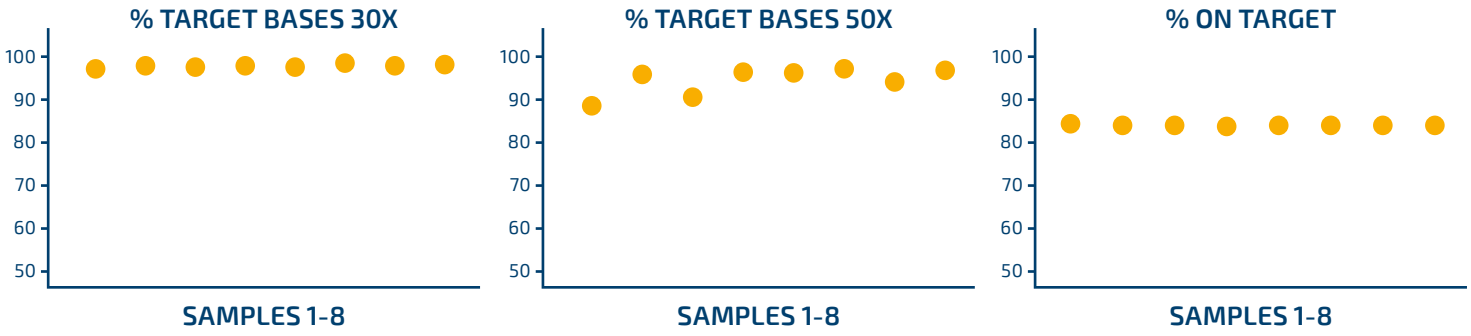
IVDR Workflow for Whole Exome Sequencing

Twist's Precision Dx Products present a whole exome sequencing library preparation and target enrichment workflow with IVDR certification. The suite includes **Twist Precision Prep and Enrichment Dx Kit** for library preparation and target enrichment, and the **Twist Precision Exome Dx Panel** with capture probes for exome enrichment. Additionally, you can order both these items together with **Twist Precision Exome Dx Kit**, which covers the whole library prep and exome enrichment workflow in one IVDR-compliant package.

- Precision of previous Twist solutions, but **compliant with EU IVDR 2017/746 regulation**
- Library preparation using **enzymatic fragmentation**
- The only **IVDR-compliant** panel on the market
- 98% of target bases covered ≥30x, enrichment probes covering 37.7 Mb targets in the human genome

Twist's Precision Dx Products Portfolio:

- Twist Precision Prep and Enrichment Dx Kit
- Twist Precision Exome Dx Panel
- Twist Precision Exome Dx Kit



The Twist Precision Exome Dx Panel shows high-quality performance, with an 85% on-target rate, indicating a strong enrichment for targted loci. Additionally, the panel design enables 50x and 30x sequencing coverage over 95% and 98% of targets, respectively.

The Twist Precision Exome Dx Kit is a complete, IVDR-compliant solution for WES library preparation and target enrichment.

cfDNA Library Preparation Kit

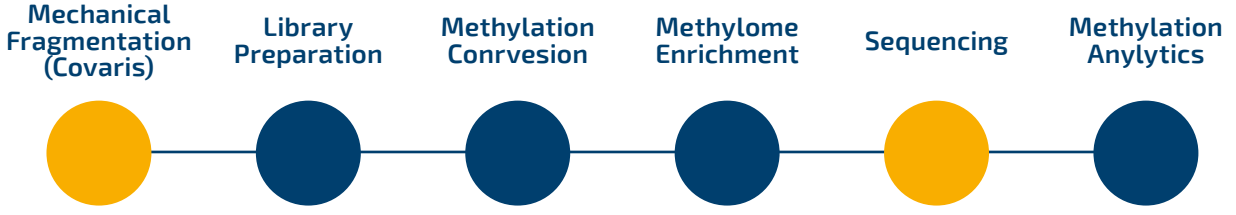
The Twist cfDNA Library Preparation Kit addresses challenges associated with library preparation from circulating cell-free DNA (cfDNA). Liquid biopsies have gained prominence in oncology research, particularly for investigating potential biomarkers within genetic material from tumors circulating in peripheral blood. This kit enables high conversion cfDNA library generation for next-generation sequencing (NGS) on Illumina systems, overcoming the technical challenges associated with low-input and degradation of cfDNA, as well as other samples that are hard to acquire and have limited DNA abundance (i.e. urine and CSF samples).

- **High conversion** rate reliably detects rare variants (≤0.1% VAF)
- Produces high coverage libraries **compatible with single-UMI** or duplex-UMI workflows
- Reliable and robust performance with a **sample input range of 1–20 ng**

Targeted Methylation Sequencing

The **Twist Targeted Methylation System** introduces a complete solution that produces highly complex and uniform sequencing reads for methylation analysis. The end-to-end protocol achieves this by combining an innovative, enzymatic conversion process, optimized target enrichment workflow, and highly developed panel design process. Twist Bioscience partnered with New England Biolabs to offer **NEBNext® EMseq (enzymatic methyl-sequencing)** library prep as part of the Twist Targeted Methylation System. A simple workflow modification enables secondary panels (or spike-ins) to be added to the methylome, useful when investigating new applications or areas of epigenetic research.

- The **Twist Human Methylome** contains 3.98M CpG sites through the 123 Mb of genomic content, targeting the most current, annotated, and relevant CpG methylation regions in the genome
- The panel provides much **broader coverage versus average microarray**. Compared to competitor, additional 105,288,339 bases of subsequent shores, shelves, and open sea CpG's and base pairs are covered.



Twist RNA Solutions

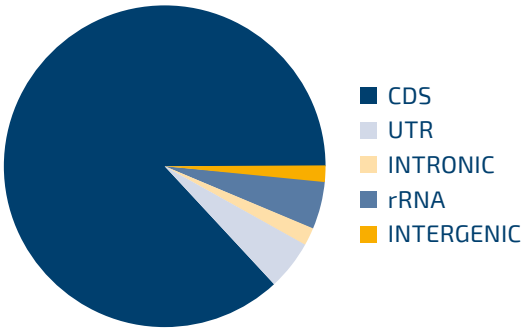
Besides the **Twist Whole Transcriptome RNAseq**, Twist also offers transcriptome target enrichment with the **Twist RNA Exome**. Together with the **Twist RNA Library Prep** and **Twist Target Enrichment**, it provides a reliable method of generating transcriptome sequencing data from RNA extracted from a variety of sources including FFPE. RNA Exome increases the signal while requiring fewer sequencing reads. This enables the detection of low expressing targets that are critical for an accurate picture of the transcriptional state of the cell.

TWIST TARGETED SEQUENCING WORKFLOW

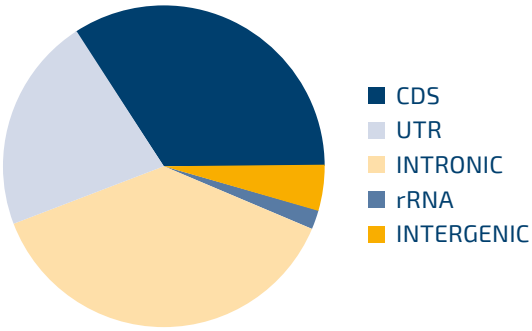
TWIST WHOLE TRANSCRIPTOME SEQUENCING WORKFLOW

- **Exon-aware probe designs** for protein coding regions, fusions and isoforms
- **Targets 35.8Mb bases, 19,708 genes and 63,215 isoforms**
- Fewer reads per sample for higher throughput

TWIST RNA EXOME



TWIST WHOLE TRANSCRIPTOME



Synthetic Reference Material

The **Twist cfDNA Pan-Cancer Reference Standard v2** is a comprehensive tool created to assist researchers in both the development and quality monitoring of clinically relevant variants for developing NGS-based assays. Additionally, researchers can utilize these reference standards to define two essential analytical parameters: the Limit of Detection (LoD) and the Limit of Blank (LoB) for their assays. Composed of wild-type (WT) background cell-free DNA (cfDNA) from a cell-line and synthetic oligos carrying mutant alleles, this reference material offers the precision and sensitivity needed for researching liquid biopsy assay development.

- **456 unique naturally occurring cancer variants, 132 literature-curated, clinically relevant variants**
- Covers **84 different genes** involved in cancer
- Meticulously designed to assist in determining the analytical Limit of Detection (LoD) and the Limit of Blank (LoB)

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At the Forefront of Digital Genomics

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