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Illumina Stranded mRNA Prep | A clear view of the coding transcriptome https://www.illumina.com/products/by-type/sequencing-kits/library-p...

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A rapid, cost-effective workflow for accurate, unbiased detection of the protein-coding transcriptome with precise measurement of strand information.

Illumina Stranded mRNA Prep, Ligation

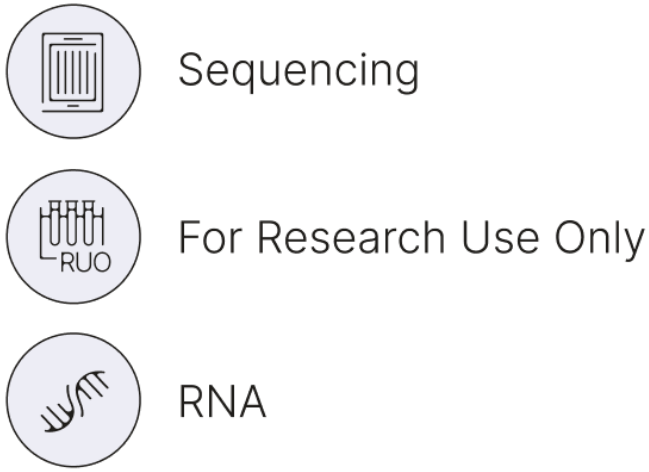
Data sheet | PDF < 1 MB | 5 versions

6.5 hr
Assay time

< 3 hr
Hands-on time

25-1000 n...
Input quantity

See full details in the specifications table



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comprehensive analysis across the coding transcriptome for discovery of features such as novel isoforms, gene fusions, and allele-specific expression.

Key features

Precise measurement of strand orientation—Enables detection of antisense transcription, enhances transcript annotation, and increases alignment efficiency

Exceptional performance—Provides excellent polyA capture efficiency and coverage uniformity, minimizing required sequencing depth for accurate, unbiased detection of the coding transcriptome.

Learn more about the technology

High-quality data from low-input samples—Achieves highly sensitive results from as little as 25 ng of high-quality RNA*

Fast library preparation workflow—Prepares libraries ~40% faster than TruSeq Stranded mRNA; shorter incubation times and reduced sample cleanup steps result in a total assay time of 6.5 hr

*Not compatible with FFPE samples

Specifications

Assay time	6.5 hr
Automation capability	Liquid handling robot(s)
Automation details	**Explore available automation methods**
Content specifications	Captures the coding transcriptome with strand information
Description	A simple, cost-effective solution for analysis of the coding transcriptome with precise strand information
Instruments	**NextSeq 550 System**, **NextSeq 2000 System**, **NextSeq 1000 System**, **NovaSeq X System**, **NextSeq 500 System**, **NovaSeq 6000 System**, **NovaSeq X Plus System**
Mechanism of action	PolyA capture, ligation-based addition of adapters and indexes
Method	**mRNA sequencing**
Multiplexing	Up to 384 Unique Dual Indexes (UDIs)
Nucleic acid type	RNA
Specialized sample types	Not FFPE-compatible, Low-input samples
Species category	Mammalian, Bovine, Mouse, Human, Rat
Species details	Works with high-quality RNA from any species with polyA tails
Strand specificity	Stranded
System compatibility details	Library prep is designed to be compatible with all Illumina sequencing systems, and is extensively validated on the NextSeq 500/550 and NovaSeq 6000 Systems.
Technology	Sequencing
Variant class	Single nucleotide polymorphisms (SNPs), Gene fusions, Novel transcripts, Transcript variants

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FAQs

What is stranded mRNA-Seq?

How long does Illumina Stranded mRNA library prep take?

How do you prepare mRNA for sequencing with Illumina Stranded mRNA Prep?

Frequently purchased

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For Research Use Only

Not for use in diagnostic procedures (except as specifically noted).

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INNOVATIVE TECHNOLOGIES

At Illumina, our goal is to apply innovative technologies to the analysis of genetic variation and function, making studies possible that were not even imaginable just a few years ago. It is mission critical for us to deliver innovative, flexible, and scalable solutions to meet the needs of our customers. As a global company that places high value on collaborative interactions, rapid delivery of solutions, and providing the highest level of quality, we strive to meet this challenge. Illumina innovative sequencing and array technologies are fueling groundbreaking advancements in life science research, translational and consumer genomics, and molecular diagnostics.

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