

Reveal the Full Spectrum of Genomics

From WGS to Transcriptomes



The CoolIMPS 600 is a high-efficiency, mid-throughput sequencer powered by our signature CoolIMPS™ and DNBSEQ technologies. Delivering **Q40 accuracy** and up to **2.4 Tb** of data per run, its optimized performance and flexible sequencing options allow scientists to explore everything from WGS to full-length transcriptomes on a single instrument—without sacrificing cost-effectiveness.



Flexible

Independent flowcell based operation and WGS scale output



Accurate

Enhance breakthroughs with Q40 accuracy and novel read lengths



Versatile

Comprehensive genomics with novel WGS and full transcriptomics

Enabling Comprehensive Genomic Analysis

Human Whole Genome Sequencing (WGS) is an application that can provide novel insights over alternative methods, but often must be done in larger labs. The CoolIMPS 600 seeks to enable labs of all sizes to engage in WGS, full length transcriptomics, alongside other applications with meaningful batch sizes at an accessible price per sample without sacrificing the quality that is required.

CoolIMPS™ Technology



Higher Signal Intensity



Longer Read Length



Higher Accuracy

CoolIMPS™ technology utilizes nucleotides with natural bases and extension blocks, combined with labeled antibodies that are both base-specific and block-dependent.

In the traditional method, scarring—one of the main limiting factors for long-read lengths—can occur, but this issue is eliminated with the CoolIMPS approach.

In the CoolIMPS method, each nucleotide (dNTP) is linked to 2-4 fluorescent dyes via antibodies, resulting in higher signal intensity and much better imaging. This contributes to exceptional sequencing accuracy and reliable long-read performance.

Traditional Methods

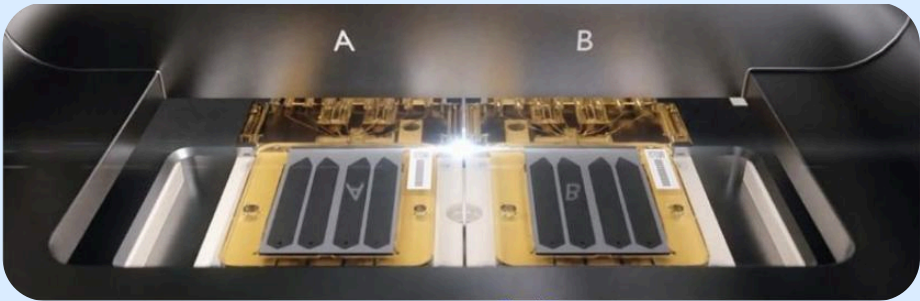


CoolIMPS



Unrivaled Flexibility

CoolMPS 600 offers independent dual flow cell operation, allowing researchers to run two flow cells independently, at any time, with various sequencing options.



Performance Parameters

# of Flow Cells	Reads ^a	Read Length	Data Output ^b	Run Time ^c	Q40
2	2.4B	SE600	1.2 Tb	<50 hr	>80%
		PE150	600 Gb	27 hr	>90%

a. Reads per FC. The maximum number of effective reads is based on the sequencing of an internal standard library. Actual output may vary with sample types and library preparation methods.
b. The listed data output is per flow cell, meaning the total output per run doubles when utilizing both flow cells.
c. Run time is based on the dual flow cell module, including sample loading, sequencing, and FASTQ generation.

To learn more, visit completegenomics.com/CoolMPS-600
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