

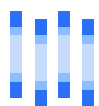
# How Automation Enables NGS In Your Lab



Having a lab robot run library preparation enables more scientists to use the latest sequencing methods

**Written by**  
Opentrons





## OVERCOMING SEQUENCING BOTTLENECKS

# Growing Interest In NGS Drives Prices Down

Across a range of metrics, the interest in sequencing keeps climbing, and the interest in sequencing is growing alongside the number of scientific applications. The graphics in Figure 1, for example, show dramatic increases in the percentage of grants from the U.S. National Institutes of Health that reference sequencing and the number of publications in PubMed that used next-generation sequencing (NGS). Plus, a recent market summary projects that the global market for NGS will grow from \$4.533 billion in 2018 to \$18.565 billion by 2026.<sup>1</sup>

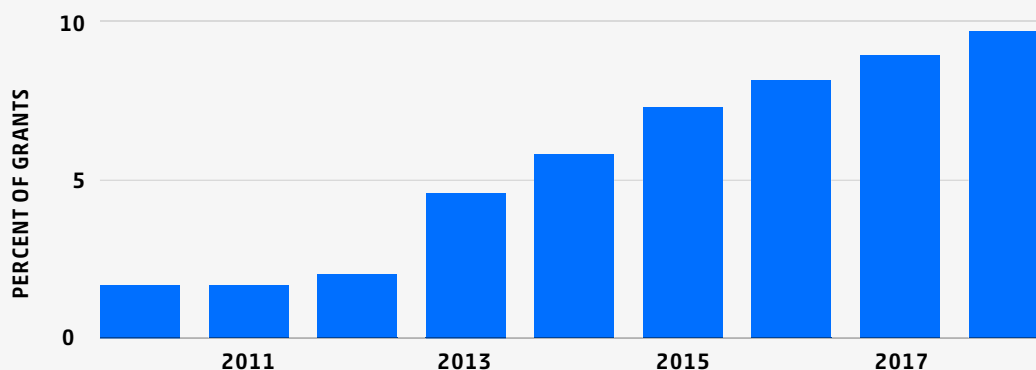
**"With the cost of sequencing dropping so low, the bottlenecks for labs looking to scale up their NGS projects are often no longer price—they are the processes upstream and downstream of the sequencing," says Dr. Christopher Mason.**

The interest in sequencing is growing alongside the number of scientific applications, including metagenomics, expressional analysis, diagnostic gene panels, DNA data storage and many more approaches.

According to the National Human Genome Research Institute (NHGRI), the cost of sequencing a million DNA bases dropped from almost \$5,300 in 2001 to \$0.1 in 2019.<sup>2</sup> "With the cost of sequencing dropping

FIGURE 1

### NIH Grants with Sequencing



## OVERCOMING SEQUENCING BOTTLENECKS: GROWING INTEREST IN NGS DRIVES PRICES DOWN

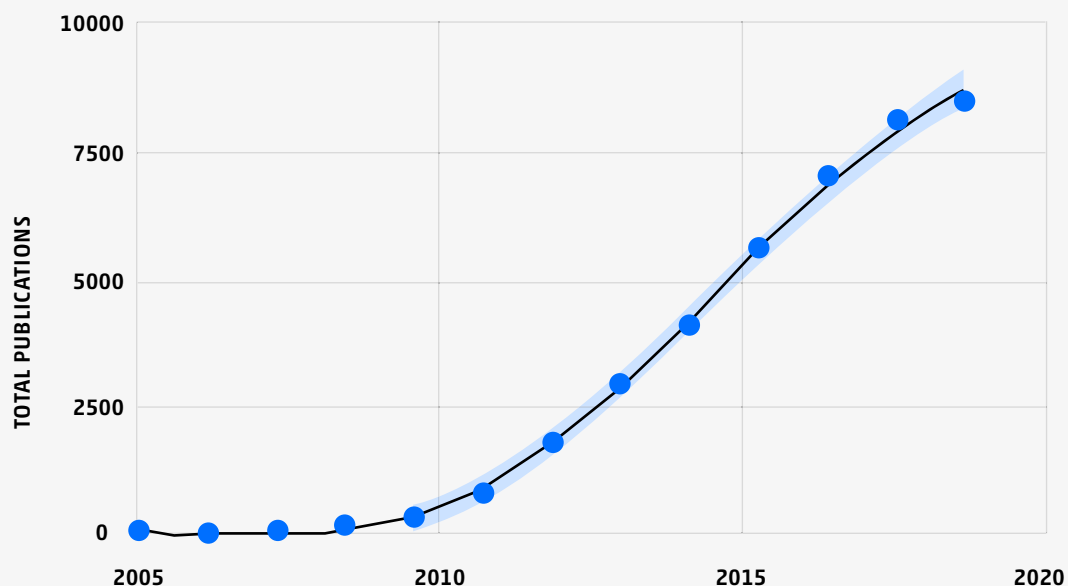
so low, the bottlenecks for labs looking to scale up their NGS projects are often no longer price—they are the processes upstream and downstream of the sequencing,” says Dr. Christopher Mason, a sequencing expert and associate professor of physiology and biophysics. “The sample prep remains a complex and laborious upstream process, and the data analysis is also still challenging for many labs after the sequencers have run.”

For many scientists, the growing interest in sequencing with the plummeting price per base, sample preparation creates a new bottleneck in NGS.

Whereas historically NGS has been too expensive for any but the richest labs to do on a large scale, the decreasing cost of sequencing on a per-sample basis opens this technology to small- and medium-size labs. But that's not enough to democratize NGS. Even with the price per sample going down, scientists still need a fast and affordable way to prepare NGS samples. Until now, preparing libraries to get your samples sequenced required 6 or more hours of a skilled biologist's time, or an expensive robot. But an affordable NGS automation solution is now available, alleviating the sample-prep bottleneck to NGS for the majority of labs in the world.

FIGURE 2

### Next Generation Sequencing



## OVERCOMING SEQUENCING BOTTLENECKS: GROWING INTEREST IN NGS DRIVES PRICES DOWN

FIGURE 3

### Next Generation Sequencing Applications

INPUT DNA  
SAMPLE

DNA FRAGMENTATION  
60 MINUTES

ADAPTER LIGATION  
40 MINUTES

LIGATION  
PURIFICATION/CLEAN-UP  
40 MINUTES

PCR AMPLIFICATION  
90 MINUTES

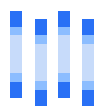
OUTPUT CONSTRUCTED  
DNA LIBRARIES

PCR  
PURIFICATION/  
CLEAN-UP  
40 MINUTES

With all of the steps and expense of traditional sample preparation for NGS, automation delivers a range of benefits, from consistency and accuracy to scalability and walk-away time. The starting nucleic acid sample gets broken into fragments and adapters get connected to both ends of the fragments. Some

commercial solutions vary this procedure somewhat, such as fragmenting and adding adapters in one step. No matter how it gets done with previous technology, it's expensive—costing up to and sometimes beyond \$170 per sample.

Instead of investing in an expensive robot and the ongoing high costs of preparing samples, scientists can make a more economical choice—one that uses an economical robot and far less expensive cost per sample in NGS library preparation.



## COST SAVINGS

# Savings In Time, Training—and Money

There are both semi- and fully automated library preparation solutions depending on a lab's needs. In the best-case scenario, a scientist loads the nucleic-acid sample and a device delivers a library that's ready to go to a sequencer.

Today's options give scientists a simpler choice. In the past, scientists selected between manually pipetting samples or high-cost automation. Now, scientists can still opt for high-cost automation or pick a low-cost alternative that provides almost all of the same capabilities.

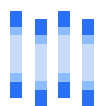
As shown on the previous page in Figure 3, scientists can save a lot of time by automating a full library prep. In order to start preparing a library by hand, a lab can easily spend tens of thousands of dollars to train new technicians over the cost of days between paying for training, purchasing reagents, and taking time away from experiments in the lab. Plus, preparing an NGS library by hand takes lots of time. In three days, an experienced technician probably prepares eight libraries. On the other hand—actually, with mostly no hands—an automated NGS preparation kit cranks out up to 24 libraries in just one day. That means that in one 5-day week of work, a technician could prepare

about 13 libraries with the manual method—or 120 with low-cost automation. So even in just one week, the increase in output really makes a difference. And all along, a lab prepares more samples for NGS and gains more time to do other things—from planning new experiments and analyzing older ones to, well, whatever task provides the most return for the lab and its personnel.

Beyond saving time and money, automating NGS sample prep produces better results. “Assuming automation works well,” says Mason, “it can eliminate or reduce the batch effects, which are a tragically common part of NGS pipelines that my lab has published extensively on.”<sup>3</sup>

This automation also makes results more reproducible. As Mason and his colleagues wrote: “Automation and robotics have improved the throughput for most laboratories, but they have also raised questions about the impact on reproducibility. The common advantage of robotic approaches to library preparation is the consistency of yield and library size from the automation and usually an increase in speed or throughput.”<sup>4</sup>

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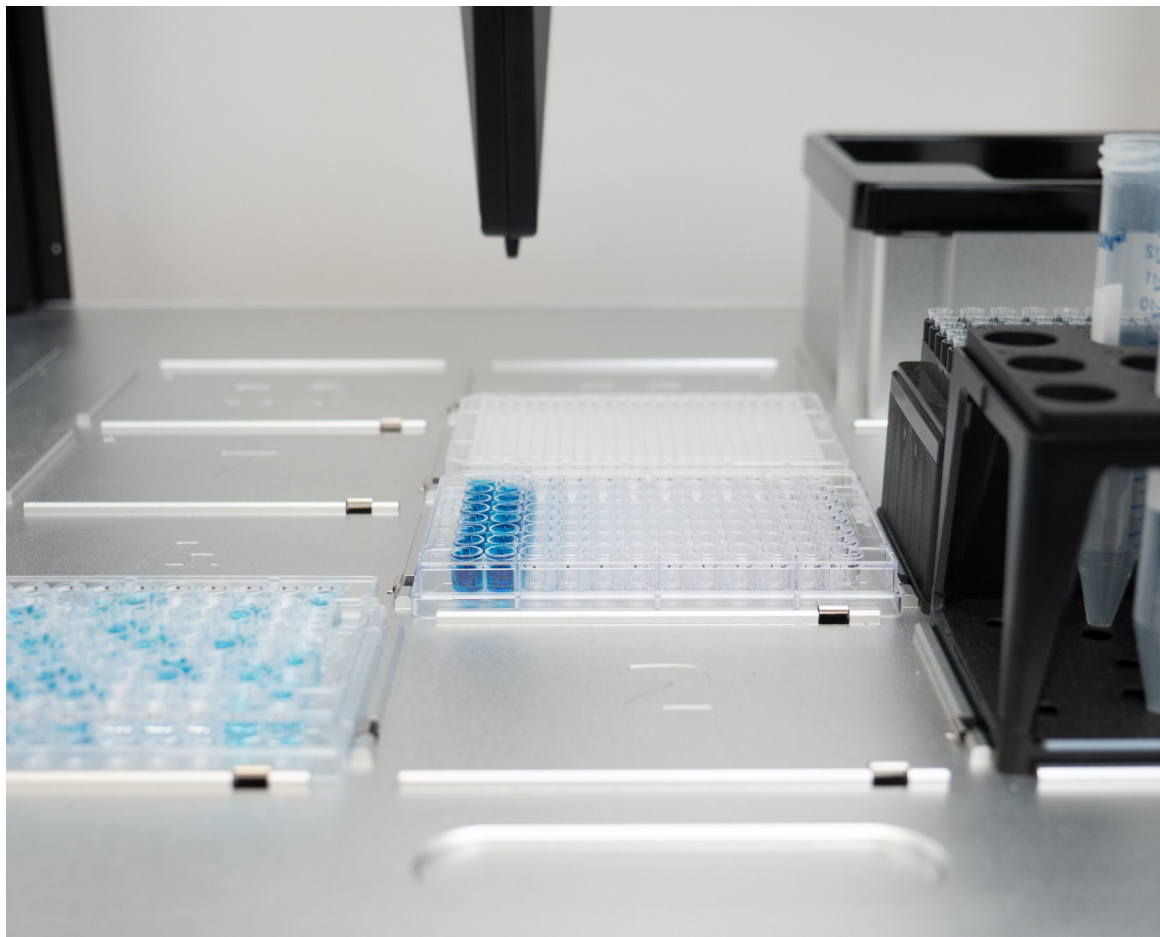
## OVERALL BENEFITS

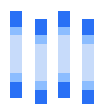
# Plug and Play NGS Library Prep

To get the most from an automated approach to preparing an NGS library, the kit needs to be optimized for the robot. With those features, the hardware-kit combination makes it easy for a lab to prepare an NGS library and makes it faster. For example, instead of developing and optimizing a protocol, a lab can just put a kit to work right away.

This fundamental technological change lets researchers move from deciding between manual pipetting or very expensive automation to an easier choice: low-cost automation that's easy to set up. In fact, this field just jumped to a plug-and-play automation option. With an easy-to-use combination of hardware, reagents and software, scientists benefit from a dramatic speed up in throughput, plus improved accuracy and consistency in building an NGS library.

By building in plug-and-play automation, a once-complex process transforms into something easy to do. Now, almost anyone can not only use NGS, but also benefit from it and expand how and where it will be used. With advanced, but accessible, automation for preparing NGS libraries, the recent growth in applying NGS probably represents only the tip of tomorrow's sequencing.





## APPENDIX

# Resources

1. [Pandey, S., Sumant, O. 2019. Next generation sequencing \(NGS\) market outlook – 2026. Allied Market Research.](#)
2. [Genome.Gov DNA Sequencing Costs Fact Sheet](#)
3. Li, S., Łabaj, P.P., Zumbo, P., et al. 2014. Detecting and correcting systematic variation in large-scale RNA sequencing data. [Nature Biotechnology](#). 32(9): 888–895.
4. Mason, C.E., Afshinnkoo, E., Tighe, S., et al. International standards for genomes, transcriptomes, and metagenomes. 2017. [Journal of Biomolecular Technology](#) 28(1):8–18.

