Transforming bottlenecks into breakthroughs.

Solutions for single-cell sequencing workflows

revvity

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- Address experimental bottlenecks
- Reduce batch effects
- Recover complete biology
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Get answers with single-cell sequencing

There are 40 trillion cells in the human body, each with its unique genetic blueprint that governs its behavior and contributes to the dynamic complexity of biological systems.

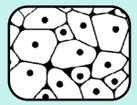
Conventional bulk sequencing methods have offered fundamental understandings into the typical genetic makeup of cell populations. However, they can lack the capacity to capture the rich heterogeneity within these populations, masking critical variations between individual cells.

Single-cell sequencing revolutionizes research by enabling investigation of the genomic, transcriptomic, epigenomic, and proteomic profiles of individual cells within diverse populations. This transformative method surpasses bulk analysis limitations, revealing hidden diversity, rare subpopulations, and dynamic cellular states overlooked by conventional methods.

Through genomic deciphering the complexities of disease pathology, single-cell sequencing can unravel the fundamental principles governing cellular identity, function, and regulation to ultimately create better predictive biomarkers and targets for therapeutic intervention.

Our ability to peer into the cellular universe with exceptional clarity is helping to pave the way for transformative discoveries and new insights.

Your pathway to discovery



Investigate sample heterogeneity

Examine different development states

Find rare cells

Investigate existing treatments

Identify new targets and biomarkers

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Solve experimental bottlenecks

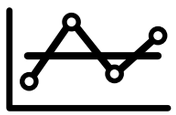
Over the last decade, advances in technology have rapidly boosted the adoption of single-cell sequencing experiments – by increasing the number of cells analyzed and reducing the cost and complexity.

Central to these advances, and the creation of single-cell sequencing data, is the ability to generate tens of thousands of single-cell partitions, each containing an identifying barcode for downstream analysis. Each of these technologies (including droplet, combinatorial indexing, and nanowell) has its own strengths and is chosen based on the specific requirements of the experiment.

To help you extract more value from your experiments, Revvity has created innovative platforms that address key challenges introduced both upstream and downstream of your partitioning and barcoding technology.

Select a challenge to see how Revvity helps to solve your bottlenecks:

Batch effects



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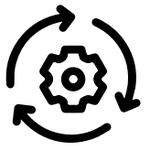
Cell recovery



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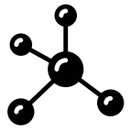
Data clarity



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Processing restrictions

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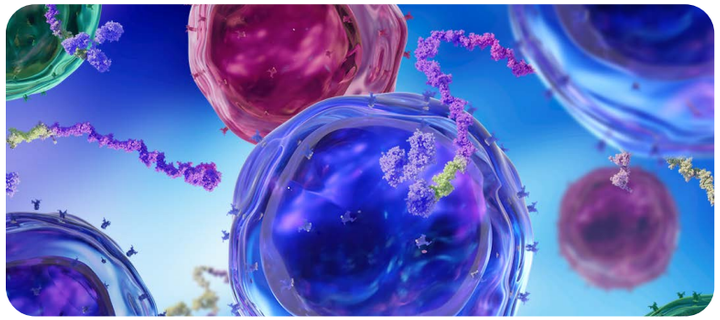
Reduce batch effects

Non-biological factors that introduce variation between datasets can complicate the biological interpretation during the integration and analysis of data between samples, posing challenges in addressing the research question effectively. Our technologies look to physically reduce technical variation to help preserve the biological heterogeneities.

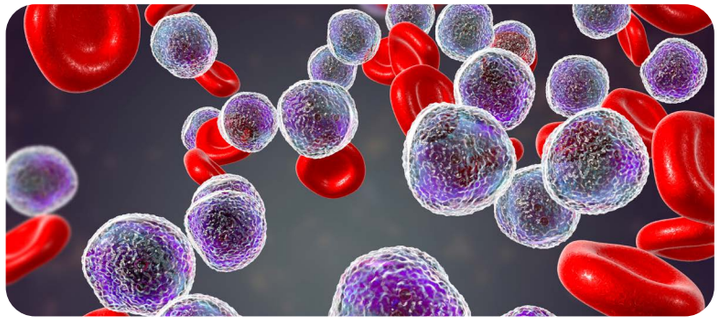


Pool samples

Multiplexing samples can minimize technical variability between samples by running them in a single experiment. It also provides the ability to load a significantly higher number of cells, a process known as super-loading, or pool smaller samples into a single channel of a single-cell encapsulation device. This allows for higher throughput and reduced cost per sample.

TotalSeq™ cell hashing reagents enable sample multiplexing, minimizing sample to sample variability by running them in a single experiment.

Read more about our TotalSeq reagents



Normalize sample loading

Samples analyzed for single-cell sequencing using Trypan blue yield inconsistent viability and concentration measurements. Dual fluorescent cell counting for single-cell sequencing provides a consistent method assessing viability and concentration.

Our Cellometer™ cell counters utilize AOPI viability staining solution to identify nucleated from non-nucleated cells.

Read more about our cell counting instruments

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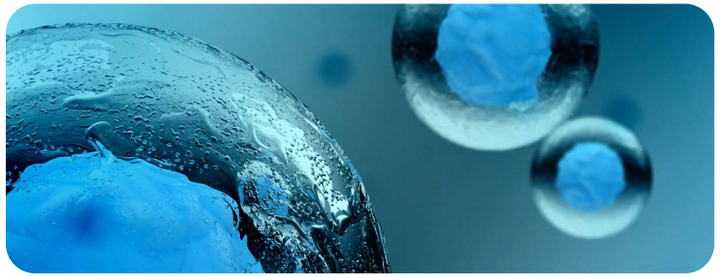
Recover complete biology

Often, critical cell types or populations are lost during cell preparation, making it difficult to decipher disease processes for therapeutic intervention. Our select technologies help limit fragile cell loss and unintended stress responses, providing you with the opportunities to capture vital information.



Sample dissociation

Obtaining single-cell suspensions from tissue samples can be challenging. Most methods are manual and crude, unamenable to scaling throughput, or rely on harsh chemicals, excessive mechanical force, or heat. This may not only induce unwanted stress responses in cells, but could cause more fragile cell types to lyse.

Our new dissociation protocols on the **Omni Bead Ruptor Elite** use gentle agitation coupled with optimized enzymatic disruption to capture the intended repertoire of cells.

Read more about the Omni Bead Ruptor Elite

Dead cell removal

To ensure reliable analysis of single-cell sequencing data, it is crucial to generate high-quality single-cell suspensions by effectively removing dead cells. Although there may be exceptions, typically you do not want to have a single-cell dataset contaminated with data generated from dying cells as they have poor RNA quality and can contribute to background noise of the assay, compromising the quality of the data.

MojoSort™ dead cell removal kits gently remove dead and dying cells through a negative selection process, which leaves your target cells unlabeled, untouched, and ready for downstream processing. These kits do not require high calcium or buffer exchange to remove dead cells, resulting in superior live cell yield for downstream analysis.

Read more about MojoSort

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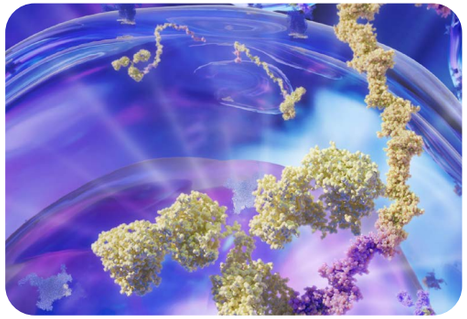
Improve data clarity

Understanding single-cell sequencing data is demanding and time-intensive. As a result, researchers are increasingly relying on our technologies to assist them in generating distinct cell clusters, reducing background noise, and facilitating easier digestion of expression data.

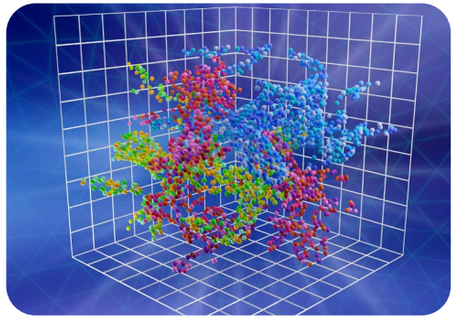


Cluster resolution

Cells that are transcriptomically similar are challenging to differentiate using only scRNA-seq data alone.

Our **TotalSeq reagents** detect protein expression along with RNA, allowing for less dropouts, allowing for less dropouts, and better cell identification and state characterization.

Read more about TotalSeq reagents

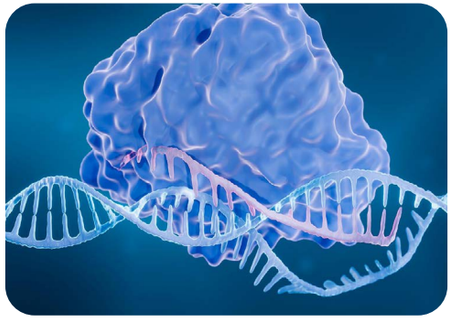


Simplify cluster analysis

Analyzing the depth of data in single-cell experiments requires specialized tools, annotation processes and, most importantly, experience.

Multiomics Analysis Software (MAS) allows you to simply define your cell populations of interest before sharing with data analysis teams - speeding up time to results.

Read more about MAS



Read enrichment

Up to 50% of the reads typically obtained during single-cell sequencing are uninformative.

The **NEXTFLEX™ Cas9-gRNA depletion enzyme kits** offer a unique Cas9-based solution to remove abundant and uninformative fragments before sequencing.

Read more about NEXTFLEX

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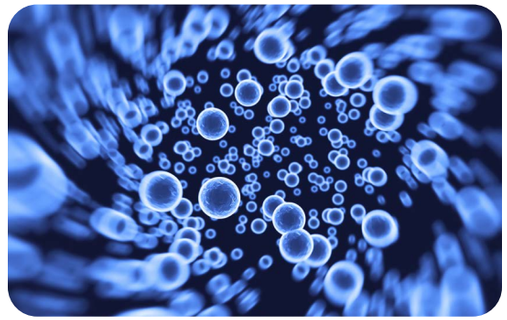
Remove sample processing restrictions

Depending on the sample type and sequencing method, processing time can range from 3 to 10 days, from initiation to completion. Our sample dissociation, cell counting, and nucleic acid QC technologies enable researchers to enhance sample throughput and processing speed, thereby accelerating the overall process.

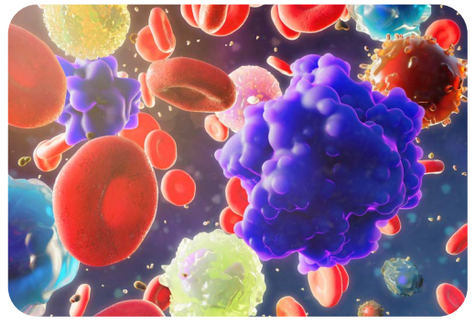


Sample dissociation

Manually creating single-cell suspensions is not only time consuming, but tends to introduce technical variation before meaningful data can be generated.

Our **Omni Bead Ruptor Elite** bead mill homogenizer provides a streamlined protocol for sample dissociation.

Read more about the Omni Bead Ruptor Elite

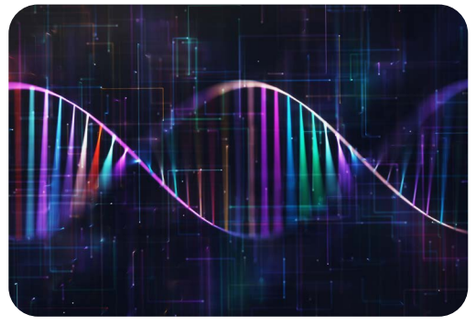


Cell counting

The tedious and time-consuming process of manually counting cells was greatly alleviated in recent years with the advent of automated cell-counting instruments.

Our **Cellometer™ and Cellaca™ cell counting platforms** take it to another level, by providing a flexible workflow from slide-based counting to automated plate-based systems.

Read more about cell counting platforms



Nucleic acid QC

Traditionally, sizing and quantitation of nucleic acids is conducted on agarose gels which is both slow and requires a lot of manual handling.

Now you can simplify traditional gel separations, while improving the repeatability of your data in a fraction of the time using the **LabChip™ GX Touch™ nucleic acid analyzer.**

Read more about the LabChip

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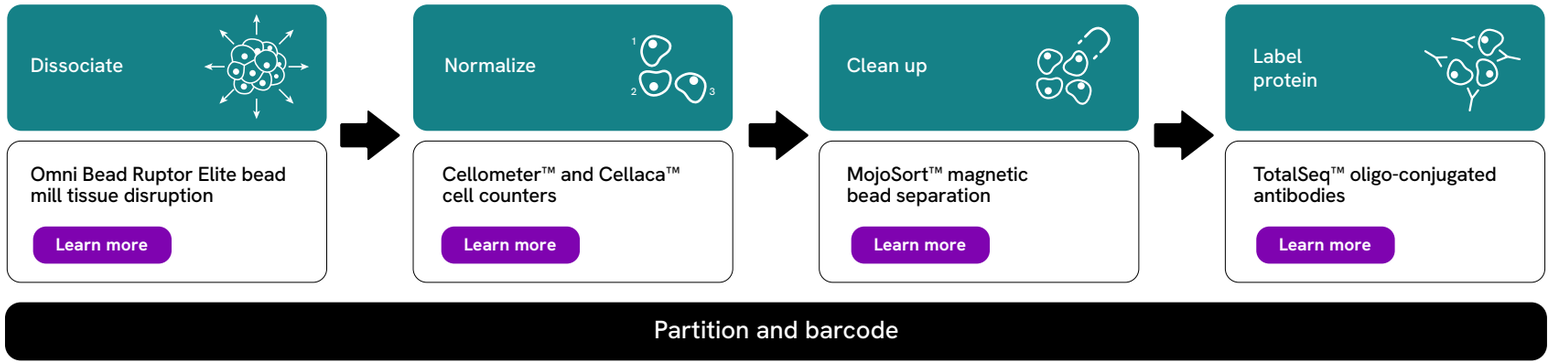
Supporting single-cell sequencing technologies

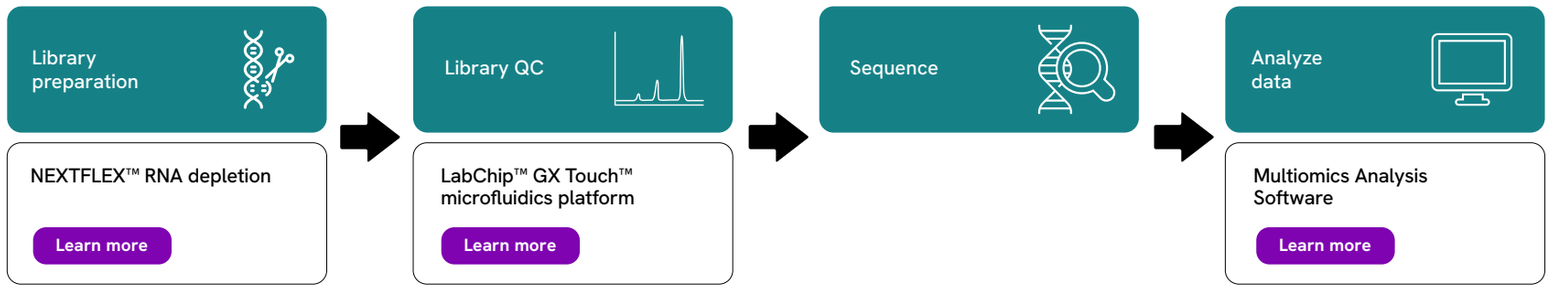
Untangling the complexity of deeply heterogeneous samples at high resolution requires robust approaches to all aspects of the workflow. By addressing technical barriers across the entire single-cell sequencing process, capturing biological variations becomes easier allowing you to create your discoveries faster.

Upstream sample preparation



Partition and barcode

Downstream fragment analysis



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Omni Bead Ruptor Elite bead mill sample dissociation

The Omni Bead Ruptor Elite bead mill homogenizer is a versatile tabletop unit, engineered with a unique carriage motion that helps with thorough sample dissociation. Coupled with optimized dissociation tubes, samples are uniformly disaggregated into viable single-cell suspensions for downstream applications.

- Whole tissue samples or subsections of tissue samples are simply placed inside optimized tissue dissociation tubes for disaggregation steps.
- Technically-validated tissue protocols accommodate dissociation of up to 12 samples simultaneously. More protocols are being developed continually.

Increase throughput and gain confidence in obtaining meaningful results by optimizing your single-cell isolation protocols with our sample disaggregation technology to replace your manual preparation methods.

Single-cell workflow

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MojoSort magnetic selection

Because of its exceptional efficiency and versatility, FACS is regarded as the gold standard technique for enriching or isolating your desired cell population. Nevertheless, the high-pressure conditions of FACS sorting may subject cells to mechanical stress, which could impact cellular viability and gene expression profiles.

The bead-based dead cell removal kit effectively removes dead cells to enrich human or mouse samples with high cell viability without using a specialized buffer containing high calcium concentrations. It utilizes a complex formed between Apo-Monomer and Streptavidin nanobeads, which bind to phosphatidylserine residues exposed on the surface of apoptotic and dead cells with high affinity.

Well-defined cell populations can be enriched or isolated using both negative and positive selection. If using positive selection, the cells of interest are bound by antibody-conjugated magnetic nanobeads which are separated under an external magnetic field.

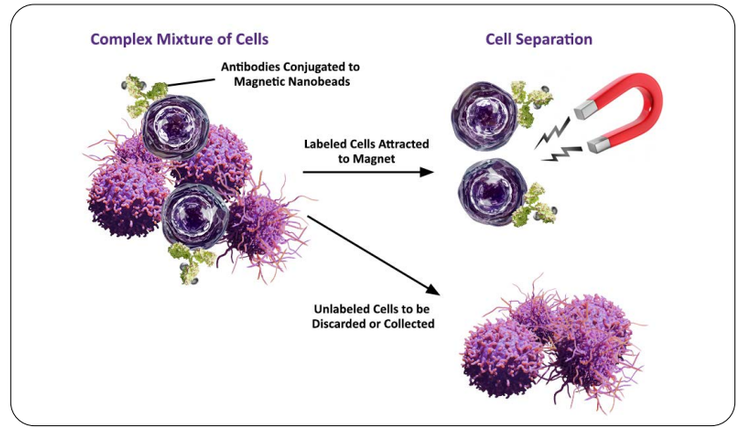
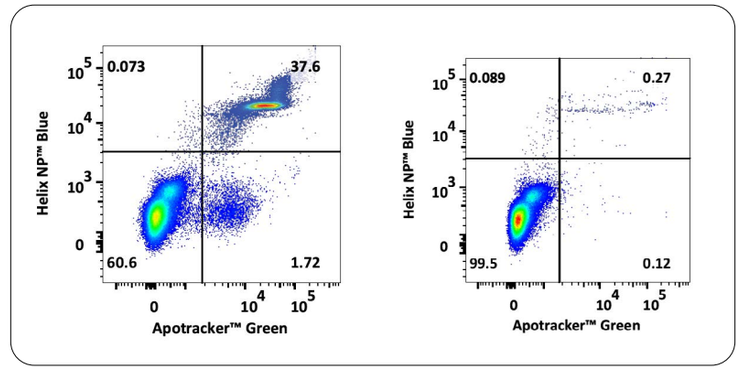


Illustration of negative selection process which leaves target cell population untouched.



Single-cell suspension of human PBMCs before and after dead cell separation.

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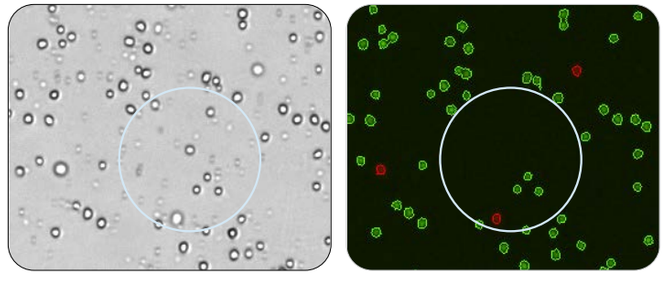
Cell counting

Before single-cell sequencing begins, Revvity's comprehensive portfolio of automated cell counters, image cytometry systems, cell counting reagents, and consumables offer fast and effective methods to identify cell populations from complex and messy samples for downstream quality control.

Our Cellaca and Cellometer cell counters:

- Discriminate non-nucleated cells
- Work with low sample volumes
- Reduce throughput bottlenecks

Revvity cell counting platforms are complemented by our comprehensive range of consumables, reagents, cell viability assay kits, microplates, slides, and counting beads.



Dual fluorescent staining counts only nucleated cells.

The Cellometer Ascend's single-use counting slides, with either 3 or 8 counting chambers, bring throughput flexibility to the benchtop.

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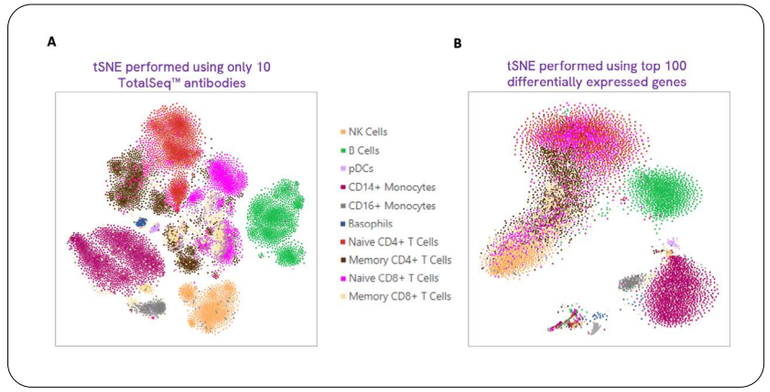
TotalSeq oligo-conjugated antibodies

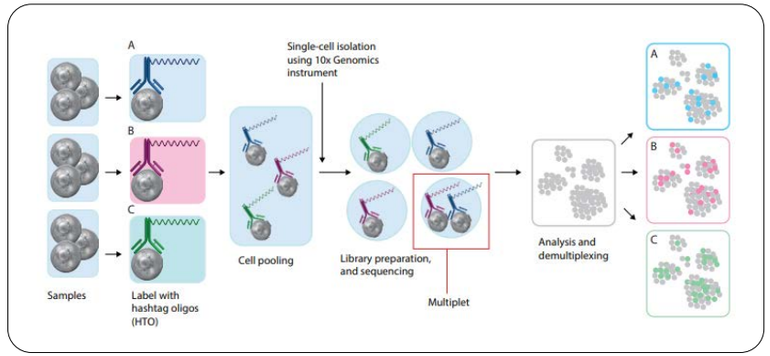
TotalSeq oligo-conjugated antibodies enable measurement of proteins at a single-cell level in applications that integrate simultaneous nucleic acid and protein detection, such as CITE-Seq or REAP-Seq, as well as those workflows available from 10x Genomics.

Barcoded antibodies can provide higher parameter phenotypic characterization when compared to CyTOF and other traditional cell analysis tools, by adding many more antibodies to characterize cellular proteins, and also convert single-cell RNA sequencing (scRNA-seq) into a true multiomic approach. This takes single-cell biology to unprecedented new levels by allowing:

- Combined insights, to increase sample clustering, reduce dropouts, and increase dimensionality (A)
- Pool samples, to reduce batch effects, for increased throughput by super-loading or pooling smaller sample sizes, often resulting in reduced experimental cost (B)



tSNE plots showing how the incorporation of results from TotalSeq antibody binding dramatically enhanced the resolution of the populations.



Multiplexing workflow using TotalSeq hashtags.

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LabChip GX Touch nucleic acid analyzer

DNA and RNA quantitation and sizing can be accomplished in seconds using modern chip-based microfluidic technology. Less than 150 nL of sample is used for sizing and concentration analysis, generating high-resolution, repeatable data.

The system offers:

- LabChip microfluidic technology to modernize gel electrophoresis
- Fully automated genomic sample analysis in real time, with sample process in as fast as 30 seconds
- A digitized data format for convenient analysis, review, share, and archive
- Quantitative metric of RNA and DNA sample integrity to ensure only the best samples go downstream
- Native high-throughput capability to support up to 384 samples in a single run

For sequencing labs that handle rare and valuable samples, PCR-free libraries, or quantifying individual fragments for genotyping, the LabChip GX Touch nucleic acid analyzer offers simplicity, and affordability, as well as high throughput to ease the burden of an ever-increasing workload.

Flexible display allows to instantly see your results in e-gram, virtual gel or table formats.

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Multiomics Analysis Software

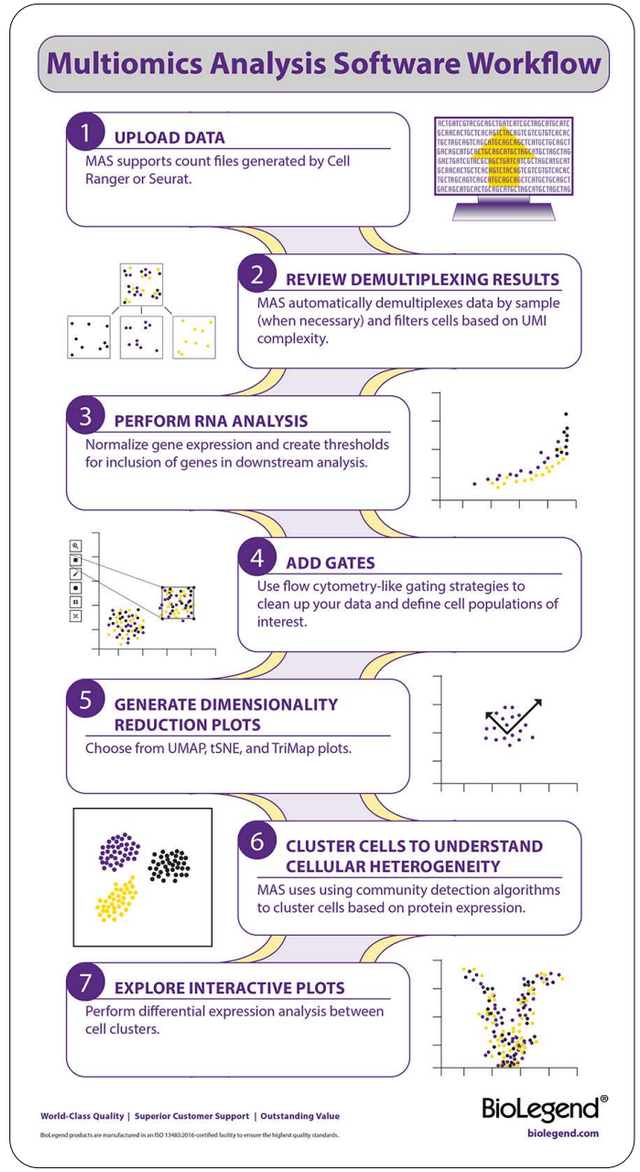
Interrogating single-cell proteogenomic data demands specialized analysis tools and expertise, which can be inaccessible to many researchers.

To simplify single-cell data analysis, we provide the Multiomics Analysis Software (MAS). This cloud-based program is freely available and enables users to efficiently explore CITE-Seq data and generate high-quality images for publication, even without extensive bioinformatics skills.

Key features include:

- A simple user interface for exploring CITE-Seq data
- Accessible to all users irrespective of bioinformatics background
- Accessible through your web browser, no server access required
- Uses flow cytometry-like gating based on TotalSeq antibody staining
- Creates UMAP, tSNE, or TriMAP dimensionality reduction plots
- Easily share any workspace with collaborators or BioLegend technical services
- Exportable in **.h5ad format* for use in other single-cell analysis programs

Single-cell workflow



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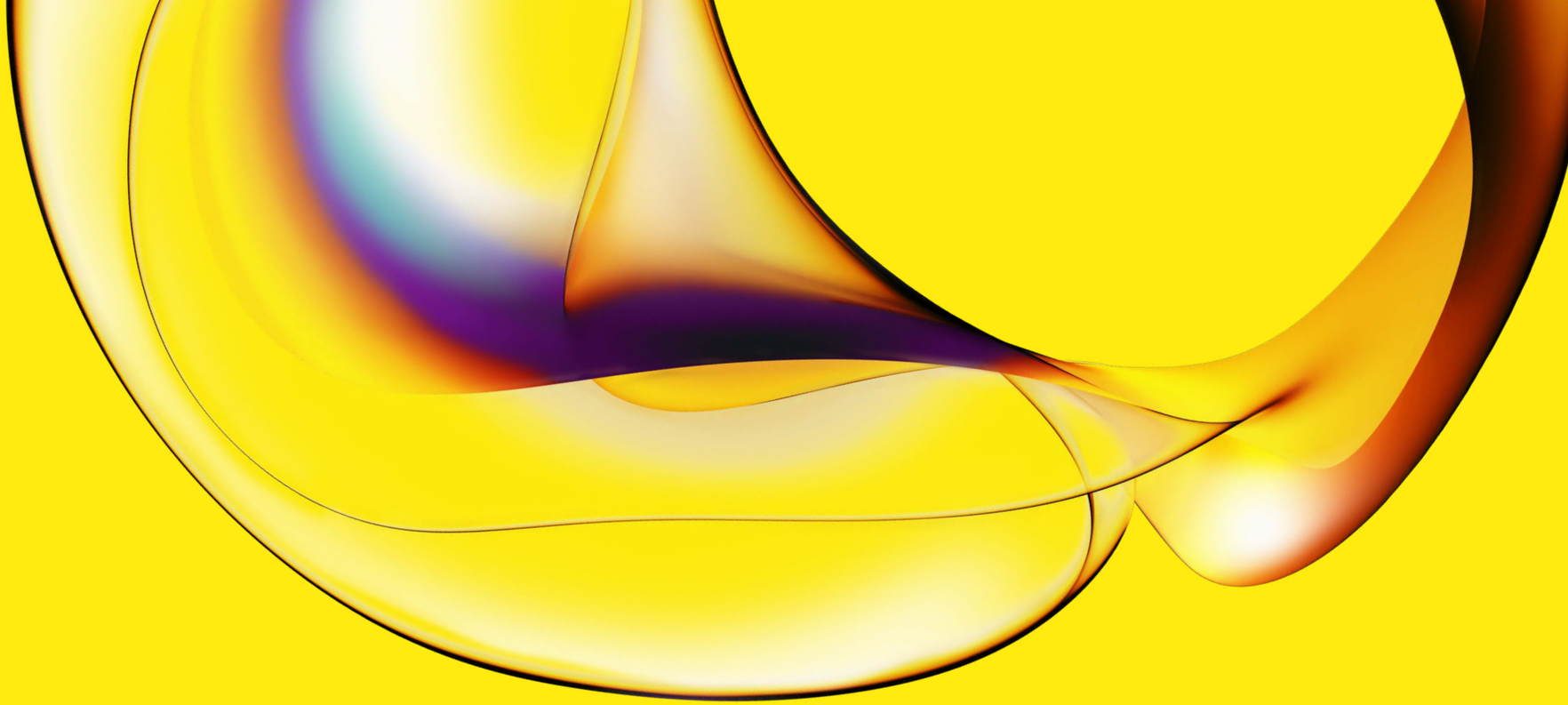

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