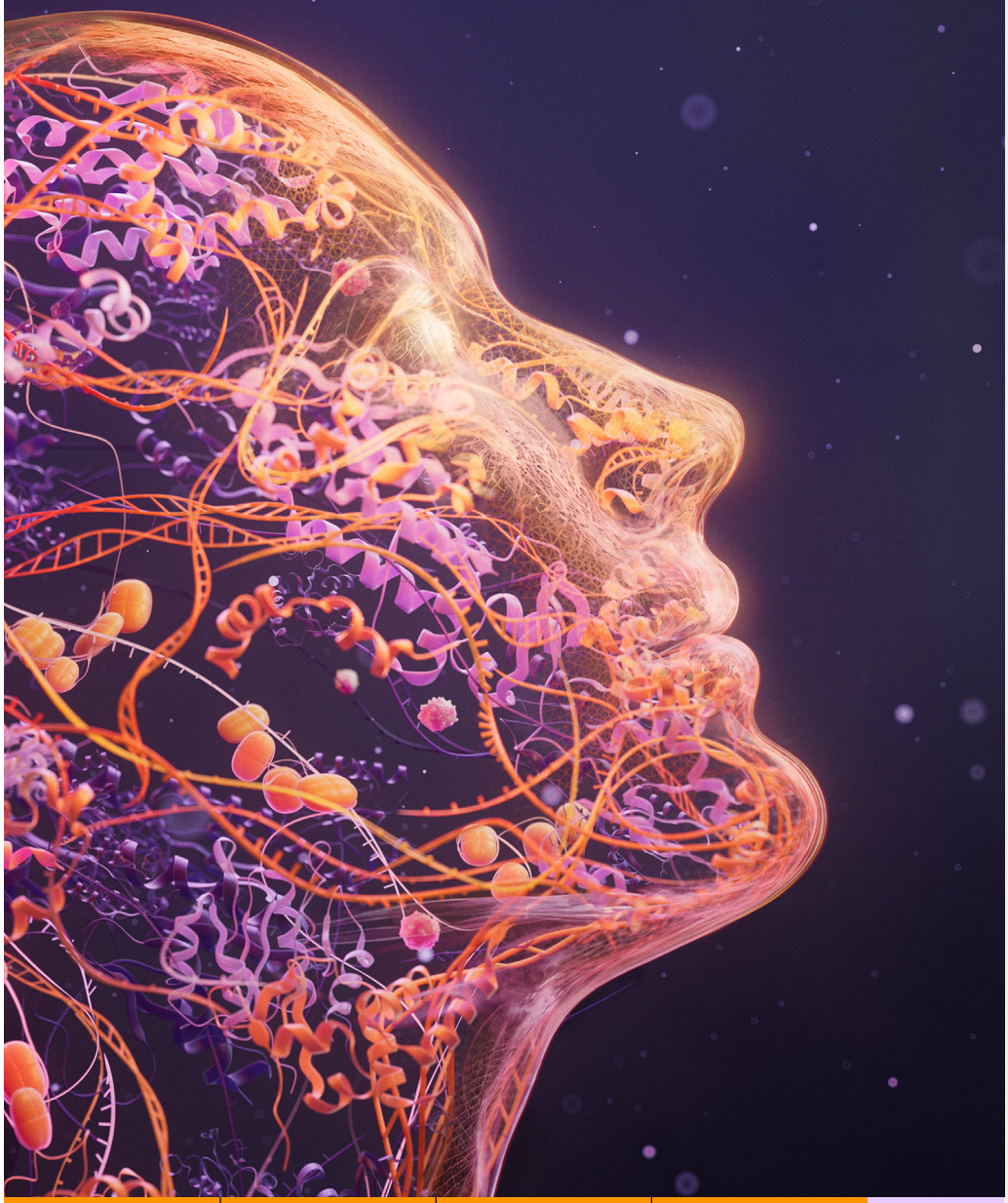
Connect the omes

Multiply your insights



illumina®

GENOMICS | EPIGENOMICS | TRANSCRIPTOMICS | PROTEOMICS

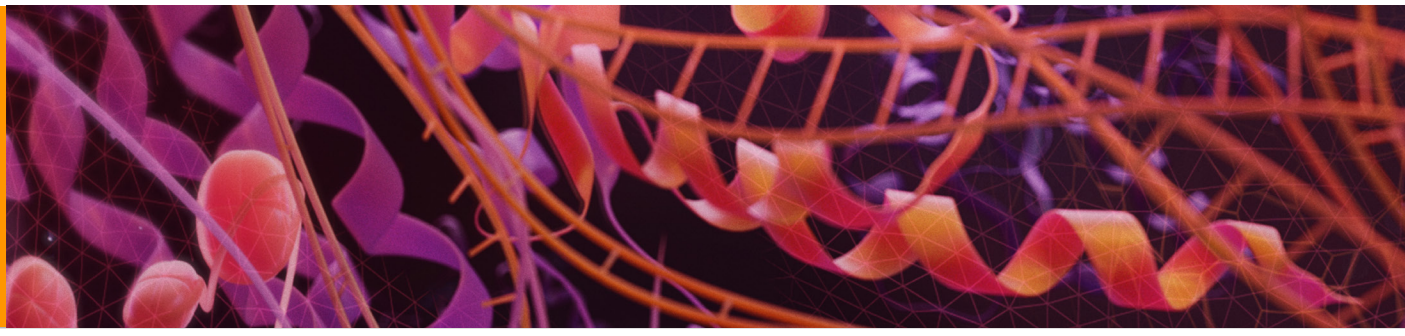
M-GL-00120 v3.0

Table of contents

Introduction

Advances in genomic technologies are enabling the generation and integration of transcriptomic, epigenomic, proteomic, and other molecular data sets at an unprecedented scale. To gain a more complete view of biology, scientists are increasingly turning to a multiomic approach that integrates multiple omic methods. This eBook introduces core concepts in multiomics and highlights examples from current research that illustrate how integrated molecular data can reveal deeper biological insights and more complete views of development, health, and disease.

> "Single omics can be useful for straightforward questions, but for some of the most complex problems in biology, you want to have as much information as possible. **That's where multiomics really shines.**"
>
> **Danny Wells, PhD**
> Co-founder and former Senior Vice President of Strategic Research, Immunai



Why adopt multiomics

Biology is multilayered and complex. Information flow from DNA to RNA to protein underscores how closely these molecules are interconnected. Genetic variation at the DNA level can impact RNA expression or protein function in diverse and unpredictable ways. Environmental factors can also alter regulatory pathways and cellular metabolism to affect biology and human health.

Multiomics provides a broader perspective to power discovery across multiple levels of biology. This approach combines genomic data with data from additional biological layers measuring gene expression, gene activation, and protein levels to enable a more integrated understanding of molecular changes contributing to normal development, cellular response, and disease. Using multiomics, researchers can better connect genotype to phenotype and advance the discovery of novel drug targets and biomarkers.

PROTEOMICS

Assesses protein expression and properties to understand cellular function and disease biology.

TRANSCRIPTOMICS

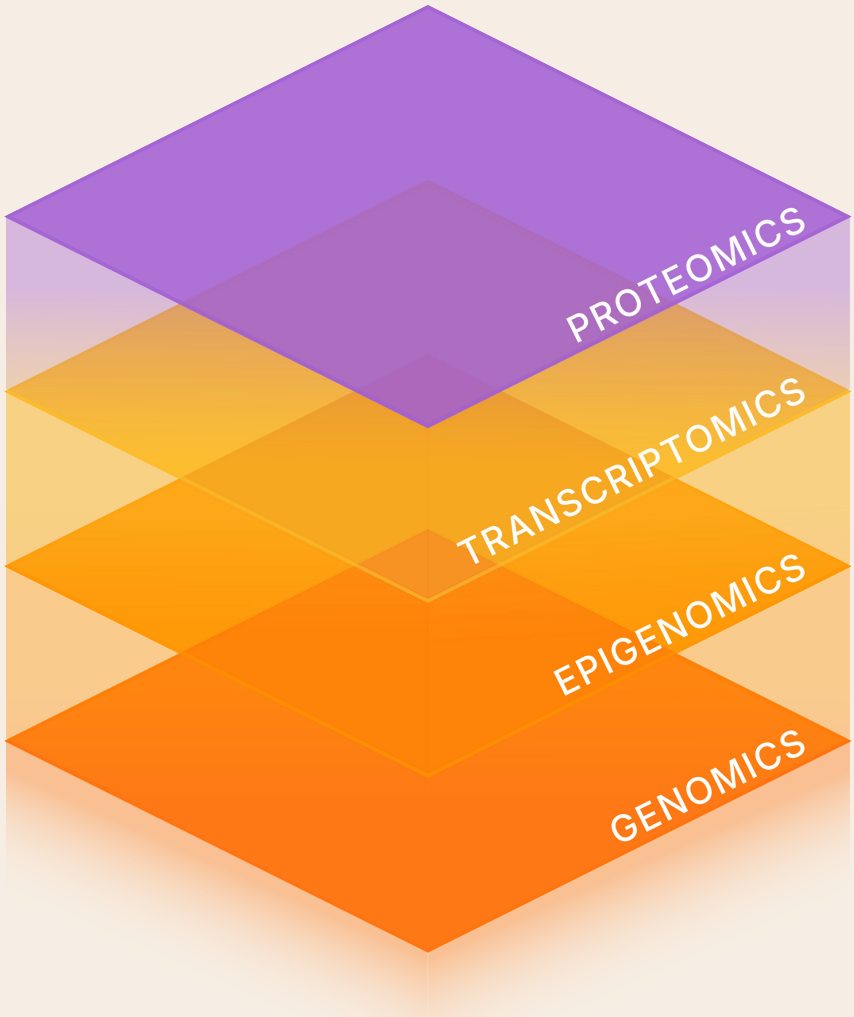
Measures RNA transcripts to assess gene expression and transcriptome composition.

EPIGENOMICS

Examines DNA methylation and chromatin modifications that regulate gene activity.

GENOMICS

Studies DNA sequence variation and genome structure using next-generation sequencing- and array-based methods.



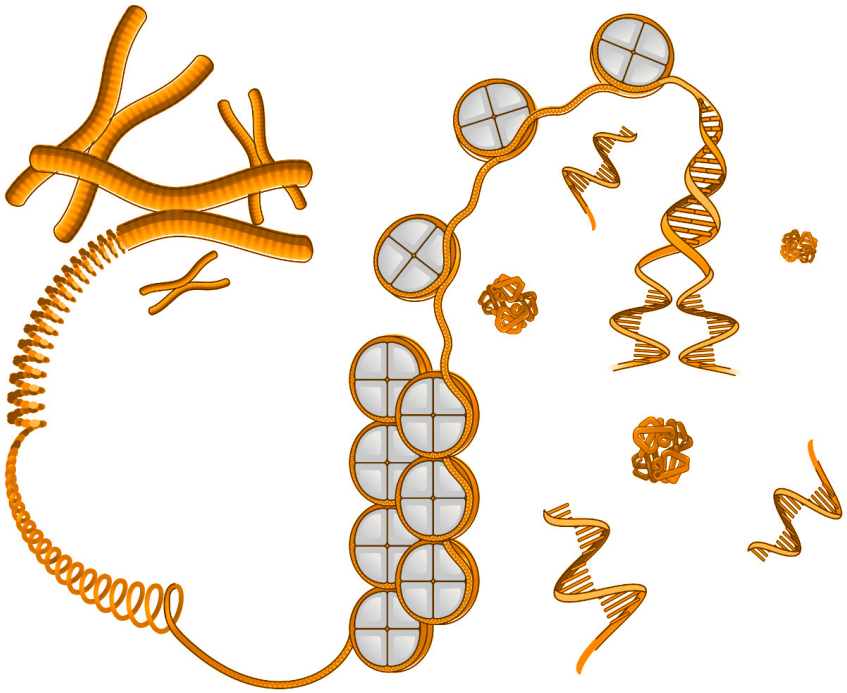
Multiple layers of information connect genotype to phenotype—Combining DNA, epigenetics, RNA, protein, or other molecular measurements into a full cellular readout provides researchers with novel scientific insights that cannot be found from single-omic methods alone.

Multiomics multiplies your discovery power

Massively parallel genomic technologies, like next-generation sequencing (NGS) and microarrays, have expanded the scope and scale of what researchers can study to include whole genomes, exomes, transcriptomes, epigenomes, and more. Each omic is a piece of the puzzle, offering important insights into the details of biological and disease mechanisms. Considered together, these modalities support a progressively more detailed understanding of biological and disease mechanisms. In addition, higher-resolution approaches enable finer distinctions within complex cell populations.

Through the combined lens of multiomics, researchers can examine the complicated interplay between the molecules of life. Integrating these complementary metrics into multiomic data sets brings a more cohesive view of cellular phenotypes and helps extract greater analytical value from each sample.

> "I think the thing that is cool about using multiomics is that it gives you **multiple views into the same problem.** It's like in reality—the world happens in multiomics."
>
> **Pejman Mohammadi, PhD**
> Associate Professor of Immunology, University of Washington



Bigger picture of biology through multiomics—Multiomics goes beyond the genome to unlock deeper biological insights. Integrating multiple molecular data types can accelerate biological discoveries and transform our understanding of human development, health, and disease.

Multiomics is more accessible than ever

The cost of sequencing has decreased tremendously over the past decade, enabling sequencing studies of greater scale and depth and supporting a broader range of applications. As a result, researchers can generate more detailed data from their samples or examine them across multiple molecular levels for deeper insight.

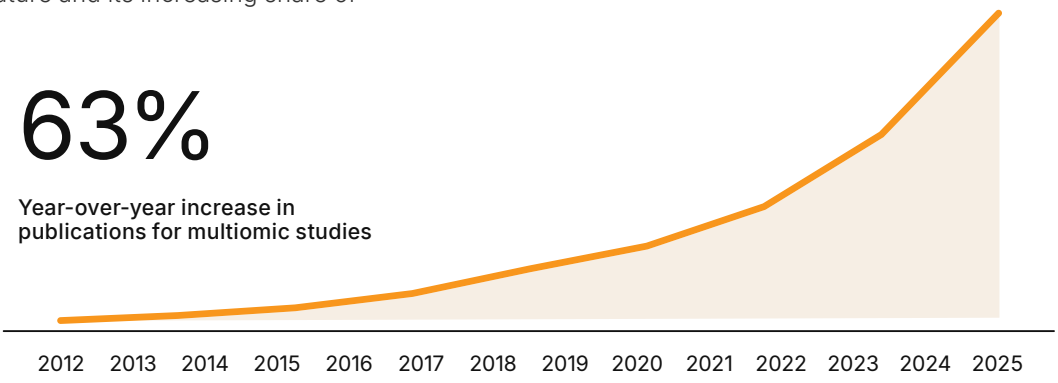
Trends in multiomics grant funding and publications

With the increasing affordability and speed of sequencing technologies, more labs are incorporating multiomic approaches into their research. The rapid rise of multiomics is evidenced in its growing presence in scientific literature and its increasing share of grant funding.

> "My advice is to dive right in. **Multiomic workflows have become quite standard and just about anybody can do this type of work.** The field is moving so quickly, if you wait for a time when it seems like it's mature, it will already have moved on to the next great thing."
>
> **Ben Humphreys, MD, PhD**
> Chief of the Division of Nephrology, Washington University in St. Louis

63%

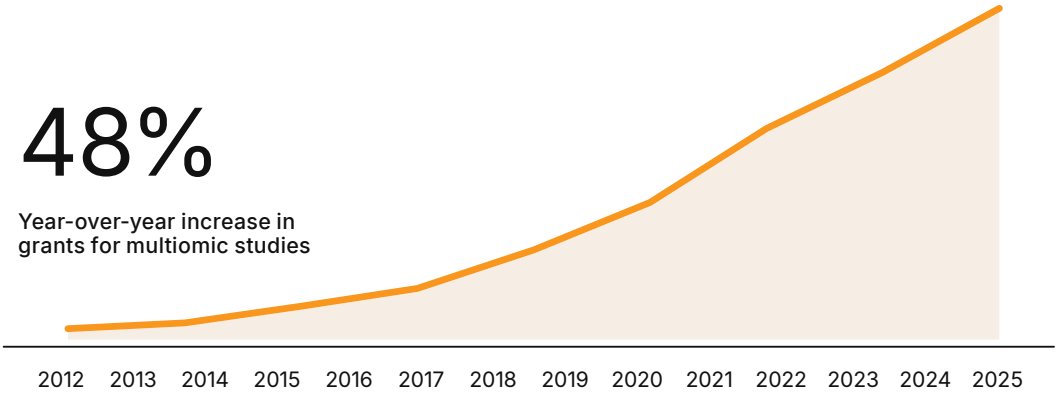
Year-over-year increase in publications for multiomic studies



Multiomics publications are on the rise—Since 2012, there has been a 63% average year-over-year increase in the number of publications featuring multiomic data.[1]

48%

Year-over-year increase in grants for multiomic studies



Grant funding growth for multiomics—Since 2012, there has been a 48% average year-over-year increase in the number of active or starting grants for multiomic studies.[1]

How multiomics is fueling discovery

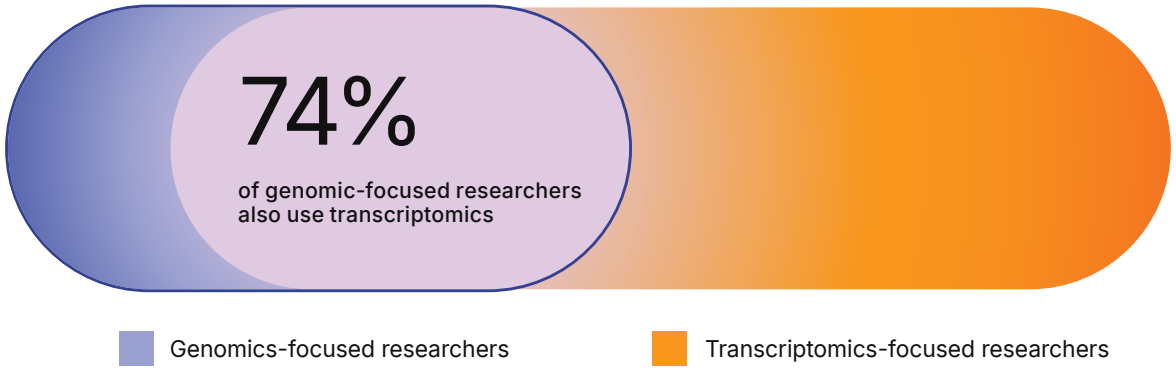
Scientists are increasingly finding that the most profound biological insights are hidden within the gaps of single-omic data sets. If you are currently focused on a single layer—such as whole genome or transcriptome—you already hold a critical piece of the puzzle. However, adding even one omic dimension can fundamentally transform your perspective. This transition from a single analytic perspective to a multilayered analysis enables you to move beyond measuring biological potential to observing functional reality. By integrating targeted molecular layers aligned to your research question, you can bridge the gap between genotype and phenotype and define disease-associated mechanisms.

Here, we explore common multiomic combinations, using real-world examples to illustrate how multiomics provides the clarity needed to resolve complex biological questions.

> "We most definitely have **found things we would have missed** had we not used a multiomic approach."
>
> **Minoli Perera, PharmD, PhD**
> Associate Professor,
> Northwestern University Feinberg School of Medicine

Functional genomics: genomics + transcriptomics

Genome-wide association studies (GWAS) have successfully identified genetic variants associated with complex diseases. The genotype offers information on disease susceptibility; however, determining the specific genes and pathways affected by those variants is more challenging. Incorporating RNA sequencing (RNA-Seq) can help annotate and prioritize variants identified in GWAS for functional analysis. Gene expression profiling indicates whether genes of interest are up- or down-regulated in research samples. This integrated approach strengthens functional genomic studies and supports drug target identification and biomarker discovery.



Basic science researchers combining genomics + transcriptomics—Among researchers focused on genomics methods (blue), 74% also use transcriptomics methods. Among those focused on transcriptomics methods (pumpkin), 46% also use genomics methods.[2]

MULTIOMICS RESEARCH EXAMPLE

Methods: WES + single-cell RNA-Seq

Dissecting the origins of immune cells involved in organ transplant rejection

Researchers at Washington University School of Medicine combined bulk whole-exome sequencing (WES) and single-cell RNA-Seq to clarify the immune cell response during kidney transplant rejection.[3]

In solid organ transplant, it is not known whether donor-derived immune cells decline with time after surgery or persist and play a role in rejection. Previous techniques to distinguish immune cells originating from donor or recipient were limited to sex-mismatched transplants and relied on identifying the Y chromosome. Using a multiomic approach, WES was used to characterize genetic differences between donor and recipient. Then, by sequencing transcripts from individual immune cells collected from human kidney biopsies, the researchers matched single-nucleotide variants in expressed genes to determine cell origin.

Single-cell immune profiling was used to examine the transcriptomes of more than 80,000 cells simultaneously, including over 5000 macrophages and 3600 lymphocytes. Macrophages and T cells of recipient origin exhibited distinct proinflammatory gene expression patterns, and do-nor-derived immune cells were found to persist for years after organ transplant. Understanding the mechanisms underlying transplant rejection could support the development of more targeted immunosuppression therapies.

> "We hope that our single-cell **multiomic studies will ultimately impact patients** by identifying therapeutic pathways that are targetable by drugs. This will lead to discovery programs and clinical trials to create drugs that will **improve the lives of patients around the world.**"
>
> **Ben Humphreys, MD, PhD**
> Chief of the Division of Nephrology, Washington University in St. Louis

Epigenomic regulation: genomics + epigenomics

Most variation identified by GWAS occurs in noncoding regions such as promoters, enhancers, and introns. Epigenetic profiling provides important context for interpreting these loci by capturing chromatin accessibility, transcription factor binding, and methylation patterns. Epigenomic assays that use NGS include assay for transposase-accessible chromatin using sequencing (ATAC-Seq) and chromatin immunoprecipitation sequencing (ChIP-Seq) to capture chromatin state, as well as chromosome conformation methods such as Capture-C and Hi-C, which map three-dimensional genomic interactions.

In addition, array-based methylation profiling offers high-throughput, single-base resolution measurement of cytosine methylation in population-scale studies. These data can be paired with genomic or transcriptomic measurements to investigate regulatory mechanisms, classify disease subtypes, or support biomarker discovery.

Integrating genetic and epigenetic information within a multiomic framework helps link noncoding variants to functional outcomes, improving the interpretation of regulatory pathways and disease-associated loci.

> "A multiomic approach increases our understanding of biology by helping us **see things that would be hidden with one type of data.**"
>
> **Pejman Mohammadi, PhD**
> Associate Professor of Immunology, University of Washington

Basic science researchers combining genomics + epigenetics—Among researchers focused on epigenetics methods (blue), 53% also use genomics methods. Among researchers focused on genomics methods (pumpkin), 38% also use epigenetics methods.[2]

5-base chemistry for combined genetic and epigenetic analysis

Emerging 5-base methods enable simultaneous detection of genomic variants and DNA methylation within a single assay. These approaches use enzymatic or chemical strategies to distinguish 5-methylcytosine (5mC) from unmodified cytosine while maintaining four-base sequence complexity to support accurate alignment and variant detection. By capturing both genetic and epigenetic information from the same DNA molecules, 5-base chemistry can provide an integrated view of regulatory mechanisms and reveal functional relationships that may be difficult to detect when these molecular layers are analyzed separately.

Learn more about 5-base combined genetic and methylation analysis:

An introduction to the Illumina 5-base solution

MULTIOMICS RESEARCH EXAMPLE

Methods: whole-genome sequencing + 5-base methylation detection

Using multiomic analysis to explore genetic and epigenetic variation in rare diseases

A collaborative research team based at Western University and London Health Sciences Centre is using Illumina 5-base solution to detect genetic variants and methylation patterns within a single assay to investigate rare diseases.[4] In a cohort of previously unsolved rare disease cases, 5-base data reproduced known disorder-specific methylation signatures with high sensitivity and identified disease-associated variants not detected by standard genome sequencing.

Integrating methylation signatures with genomic findings helped to prioritize variant analysis, support interpretation of variants of uncertain significance, and reveal cases consistent with newly defined gene-episignature relationships.

These findings highlight how multiomic analysis can provide complementary genomic and epigenomic context for investigating rare disease mechanisms.

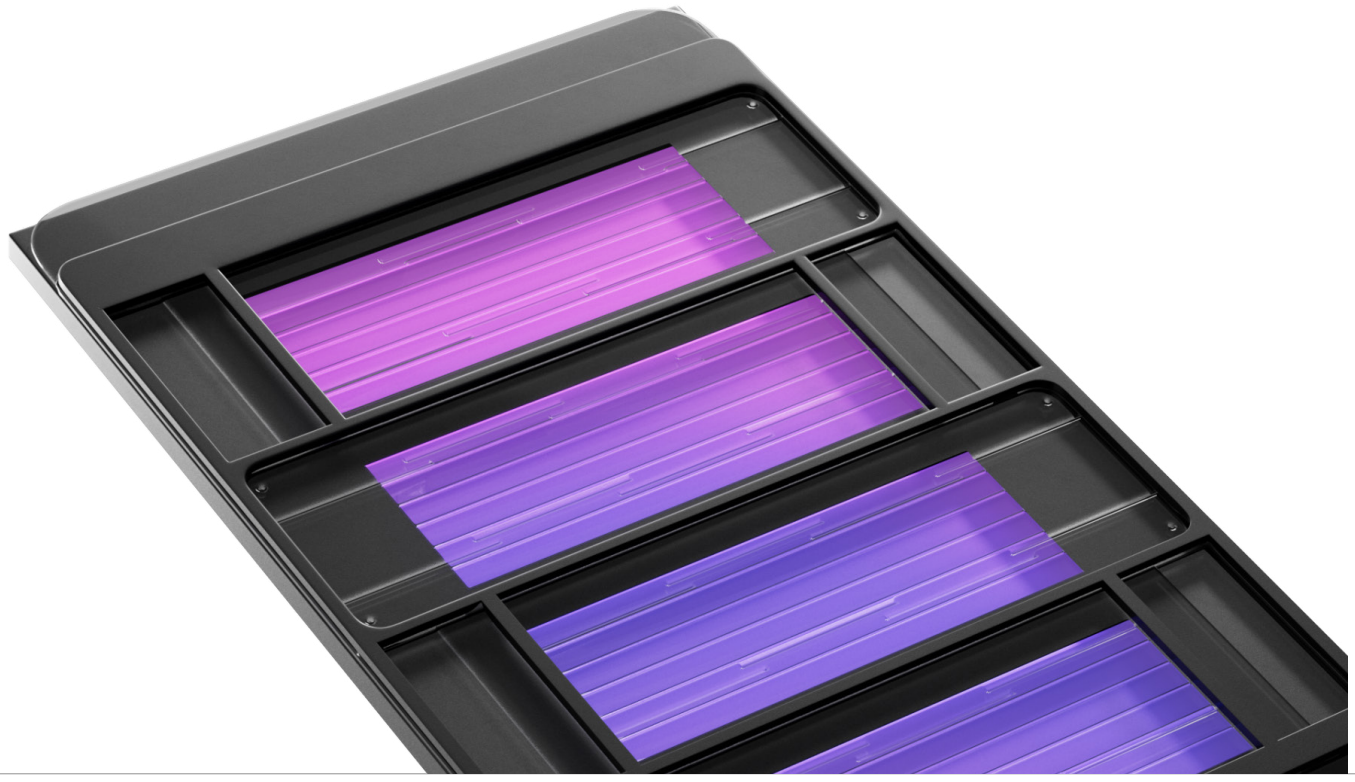
MULTIOMICS RESEARCH EXAMPLE

Methods: GWAS + methylation arrays

Multiomic approaches enhance disease risk prediction in a diverse biobank cohort

Researchers at UCLA developed methylation risk scores (MRS), an epigenetic analog to polygenic risk scores (PRS), using DNA methylation array data from a large, diverse biobank cohort with matched genetic and electronic health record (EHR) data.[5] In this study, MRS outperformed PRS in imputing a wide range of clinical outcomes, including medication use, laboratory values, and diagnosis codes. For example, MRS improved imputation accuracy for 139 outcomes, compared to only 22 for PRS, and led to substantial median increases in predictive accuracy for medications, labs, and diagnoses.

Importantly, the study demonstrated that adding MRS to state-of-the-art EHR imputation methods further increased the accuracy of clinical data imputation, with a median R^2 increase of 47.6% for laboratory tests. The authors concluded that integrating genetic and epigenetic information provides a more comprehensive and dynamic view of disease risk and patient status than genetic data alone, highlighting the value of multiomics in precision medicine and clinical decision making.



Gene regulatory mechanism: epigenomics + transcriptomics

Epigenetics and transcriptomics offer complementary views of cellular differentiation and response. Combining epigenetic and RNA-Seq methods allows researchers to measure directly the relationship between gene regulation and gene expression, rather than inferring it. Integrating epigenetics and RNA-Seq can help researchers identify candidate genes and clarify the mechanisms underlying key phenotypes. This unbiased multiomics approach can reveal regulatory elements to inform biomarker identification and therapeutic research.

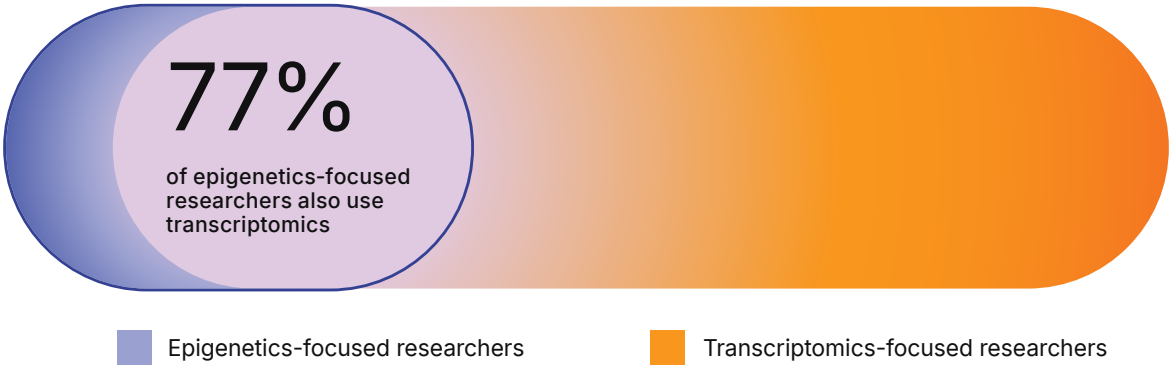
Unify single-cell gene expression and chromatin accessibility

Enable RNA-Seq and ATAC-Seq measurements from the same single cells in the same assay.

Read technical note

Accessible, scalable single-cell RNA sequencing with PIPseq chemistry

Read here



Basic science researchers combining epigenetics + transcriptomics—Among researchers focused on epigenetics methods (blue), 77% also use transcriptomics methods. Among researchers focused on transcriptomics methods (pumpkin), 34% also use epigenetics methods.[2]

MULTIOMICS RESEARCH EXAMPLE

Methods: ChIP-Seq + total RNA-Seq

Epigenetic landscape associated with Alzheimer's disease

A research team from the University of Pennsylvania led a multiomics study to examine epigenetic dysregulation in early Alzheimer's disease. Even though protein aggregation is a hallmark of Alzheimer's disease, therapies that target those proteins have not been effective.[6]

The team performed total RNA-Seq and epigenetic sequencing assays, including ChIP-Seq and 5-hydroxymethylcytosine (5hmC) analysis, on postmortem brain tissue from healthy younger and older individuals and patients with Alzheimer's disease.

Results showed that a reconfiguration of the epigenomic landscape occurs with Alzheimer's disease. Certain transcription- and chromatin-related genes are upregulated, which then disable protective pathways of healthy aging and initiate epigenetic changes that drive disease. The discovery of these regulatory feedback loops suggests potential epigenetic strategies for early intervention against Alzheimer's disease.

Phenotypic validation: transcriptomics + proteomics

RNA-Seq offers extensive discovery power to interrogate the transcriptome without prior knowledge. Incorporating protein detection with RNA-Seq can link transcript-level findings to established protein markers and known biological functions.

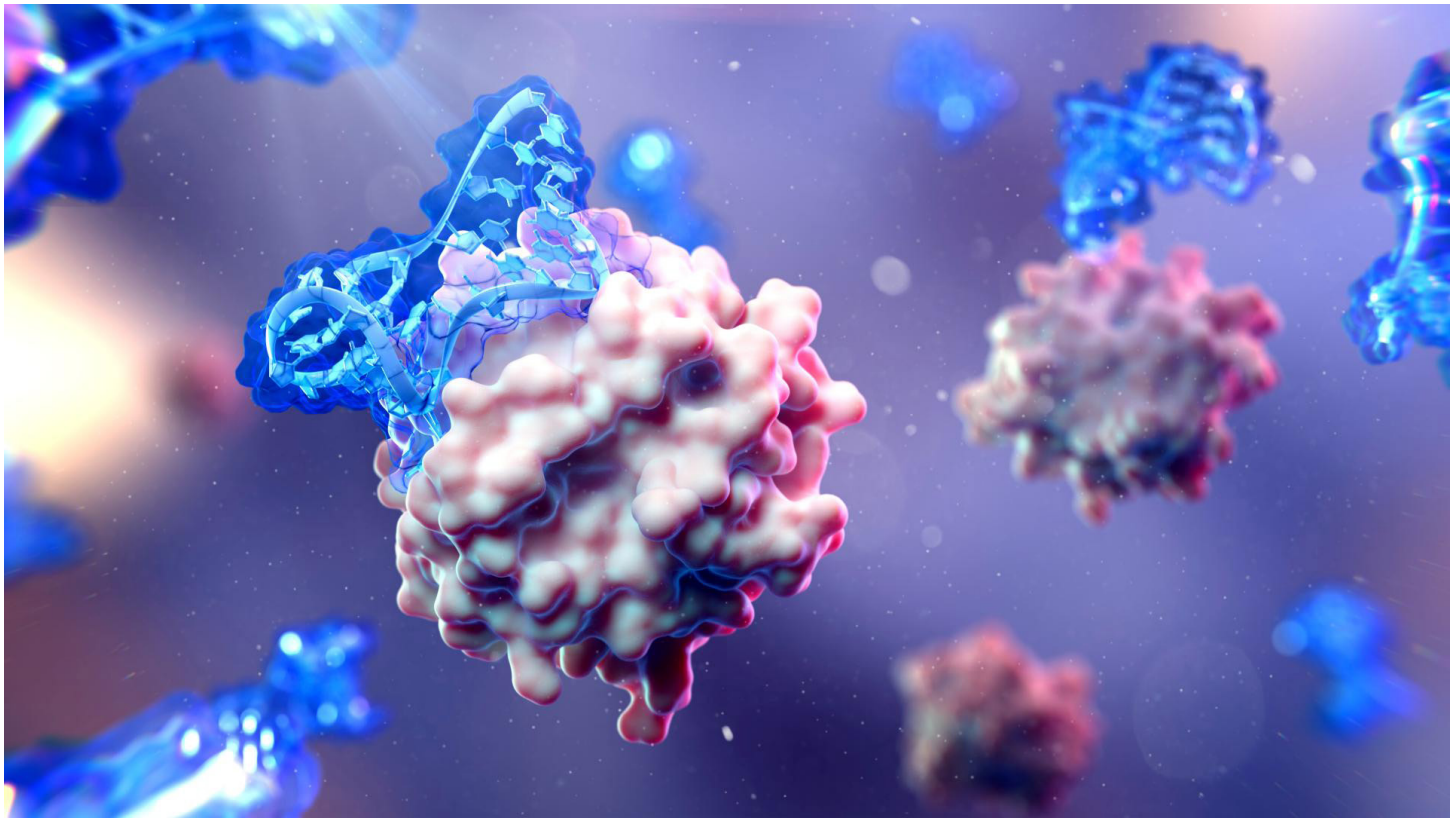
Antibodies tagged with oligonucleotide barcodes enable analysis of cell surface proteins with results read by sequencing, allowing evaluation of many more parameters than flow cytometry or mass cytometry. Methods like CITE-Seq (cellular indexing of transcriptomes and epitopes by sequencing) combine single-cell RNA-Seq with cell surface protein analysis. BEN-Seq (bulk epitope and nucleic acid sequencing) is performed at the bulk level. Spatial transcriptomics interrogates RNA and proteins within the architectural context of intact tissue.

Simultaneous bulk protein and gene expression profiling

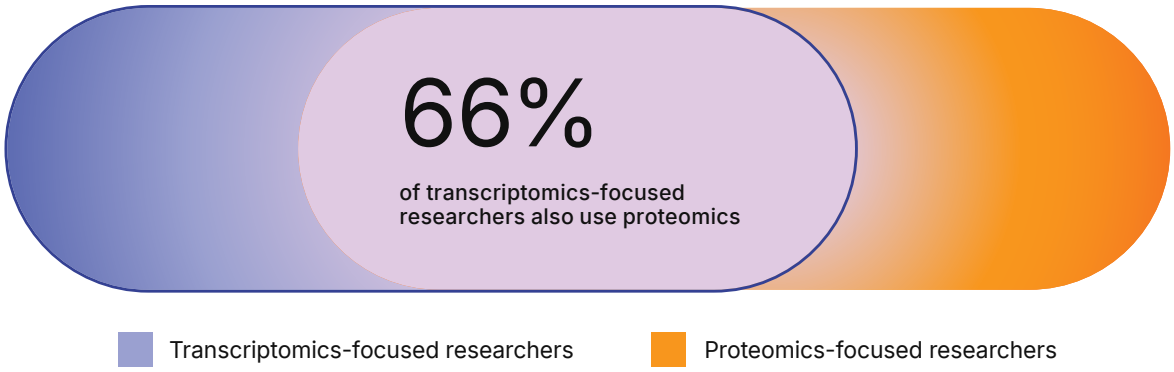
BEN-Seq method uses Illumina NGS and oligo-conjugated antibodies for easy quantification of multiple protein targets.

See how BEN-Seq is used in a real-world application:

Read application note



Protein detection with sequencing can also be achieved using aptamer-based affinity methods—Synthetic DNA–labeled aptamers bind protein epitopes based on their three-dimensional structure, enabling highly specific and multiplexed protein quantification by sequencing. When combined with transcriptomic data, these measurements support integrated interpretation across RNA and protein layers, enabling more robust characterization of biological processes.



Basic science researchers combining transcriptomics + proteomics—Among researchers focused on transcriptomics methods (blue), 66% also use proteomics methods. Among researchers focused on proteomics methods (pumpkin), 64% also use transcriptomics methods.[2]

> "**We chose a multiomic approach because the complexity of the immune system demands it.** There are some populations of immune cells that can only be read out in a particular type of omic technology."
>
> **Danny Wells, PhD**
> Co-founder and former Senior Vice President of Strategic Research, Immunai

MULTIOMICS RESEARCH EXAMPLE

Methods: spatial RNA-Seq + spatial protein analysis

Uncovering spatial heterogeneity in SARS-CoV-2 lung infection

Researchers at Massachusetts General Hospital used spatial multiomics to examine the relationship between SARS-CoV-2 lung infection and the severity of pulmonary disease.[7]

Spatial molecular analysis of both RNA and protein was conducted on 24 lung specimens collected during autopsies of individuals who had COVID-19. Using a spatial profiling system, researchers analyzed more than 1800 RNA markers to identify cell regions with high or low viral load and assessed 79 protein markers to characterize immune cell phenotypes across the lung.

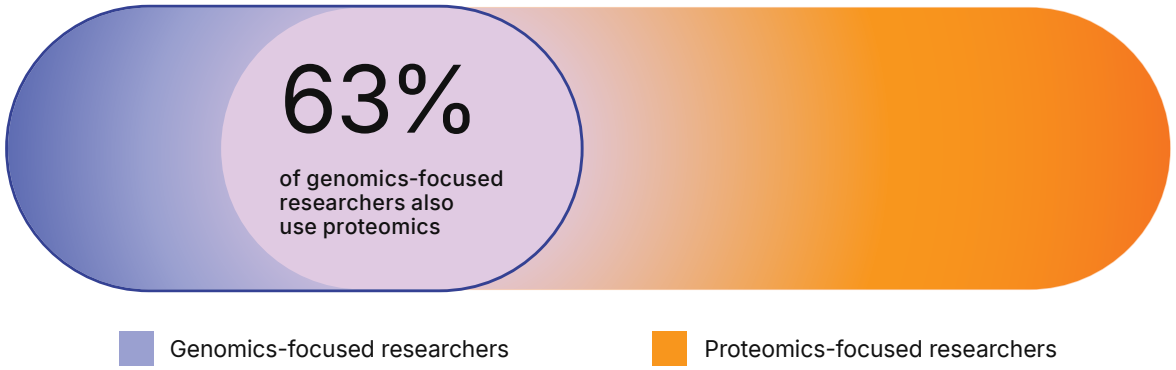
The combined data revealed spatial relationships between virus location and immune cell abundance, suggesting two phases of infection. Early infection was marked by high viral load and increased expression of interferon-related genes, while later infection showed minimal viral replication but severe tissue damage. These insights may help identify the biological processes that contribute to the most severe forms of COVID-19.

Proteogenomic mapping: genomics + proteomics

Multiomic approaches that connect genotype to phenotype can deepen insight into disease biology and therapeutic development. Linking genetic variation to protein expression at the single-cell level can reveal the functional impact of somatic mutations on human cancers and advance understanding of tumor evolution and disease progression.

"In the future, I'm looking forward to modeling large-scale data sets that come from the transcriptome, the proteome, and even the metabolome. This will help us **understand how different types of biomolecules are connected to each other** in a mechanistic way."

Pejman Mohammadi, PhD
Associate Professor of Immunology,
University of Washington



Basic science researchers combining genomics + proteomics—Among researchers focused on genomics methods (blue), 63% also use proteomics methods. Among researchers focused on proteomics methods (pumpkin), 38% also use genomics methods.[2]

MULTIOMICS RESEARCH EXAMPLE

Methods: WGS + high-plex proteomics

Expanding rare disease discovery via proteogenomic mapping

While WGS has transformed the landscape of rare disease research, the molecular diagnostic yield, defined as the proportion of sequenced individuals who receive a confirmed genetic diagnosis, has been reported at approximately 25% in large-scale clinical sequencing programs.[8] To address the remaining unsolved cases and investigate sources of missing heritability, Genomics England conducted a large-scale proteogenomic evaluation of participants within the 100,000 Genomes Project.[9]

As part of a broader multiomic initiative, researchers analyzed a cohort of 1530 participants with rare disease. The study used Illumina Protein Prep to profile 6056 proteins per serum sample, demonstrating a high-sensitivity workflow with strong concordance to established proteomic data sets. Integration of proteomic data resulted in a 7.5% increase in disease classification within previously undiagnosed participants. The identification of distinct, differentially abundant proteins across disease categories highlights proteogenomic mapping as a powerful tool for advancing biomarker discovery and elucidating the functional biology underlying rare genetic disorders.

See how scientists are using multiomics

Multiomics is a rapidly advancing frontier, with integrated analysis now at the heart of modern biological research. The studies highlighted here serve as a brief window into the diverse and expanding ways scientists are using these technologies to redefine our view of development, health, and disease.

Genomics + transcriptomics

Whole genome and transcriptome integrated analyses guide clinical care of pediatric poor prognosis cancers

Deyell RJ, Shen Y, Titmuss E, et al. *Nat Commun.* 2024;15(1):4165. doi: 10.1038/s41467-024-48363-5

Integrative pan-cancer genomic and transcriptomic analyses of refractory metastatic cancer

Pradat Y, Viot J, Yurchenko AA, et al. *Cancer Discov.* 2023;13(5):1116-1143. doi:10.1158/2159-8290.CD-22-0966

Opposing immune and genetic mechanisms shape oncogenic programs in synovial sarcoma

Jerby-Arnon L, Neftel C, Shore ME, et al. *Nat Med.* 2021;27(2):289-300. doi:10.1038/s41591-020-01212-6

Genomics + epigenomics + transcriptomics

Multi-omics analyses reveal biological and clinical insights in recurrent stage I non-small cell lung cancer

Wang C, Li J, Chen J, et al. *Nat Commun.* 2025;16(1):1477. doi:10.1038/s41467-024-55068-2

Epigenome-wide association study identifies cardiac gene patterning and a novel class of biomarkers for heart failure

Meder B, Haas J, Sedaghat-Hamedani F, et al. *Circulation.* 2017;136(16):1528-1544. doi:10.1161/CIRCULATIONAHA.117.027355

Genomics + epigenomics

Multimodal cell-free DNA whole-genome TAPS is sensitive and reveals specific cancer signals

Vavoulis, DV, Cutts, A, Thota, N et al. *Nat Commun.* 2025;16:430. doi.org/10.1038/s41467-024-55428-y

Multimodal analysis of cfDNA methylomes for early detecting esophageal squamous cell carcinoma and precancerous lesions

Liu, J, Dai, L, Wang, Q. et al. *Nat Commun.* 2024;15:3700. doi.org/10.1038/s41467-024-47886-1

Epigenomics + transcriptomics

Single-cell transcriptomics and epigenomics unravel the role of monocytes in neuroblastoma bone marrow metastasis

Fetahu IS, Esser-Skala W, Dnyansagar R, et al. *Nat Commun.* 2023;14(1):3620. doi:10.1038/s41467-023-39210-0

Single cell transcriptional and chromatin accessibility profiling redefine cellular heterogeneity in the adult human kidney

Muto Y, Wilson PC, Ledru N, et al. *Nat Commun.* 2021;12(1):2190. doi:10.1038/s41467-021-22368-w

Epigenomics + transcriptomics + proteomics

- **A histone-centric multi-omics study shows that increased H3K4 methylation sustains triple-negative breast cancer phenotypes**

  Noberini R, Robusti G, Vai A, et al. *Nat Commun*. 2025;16:8716. doi:10.1038/s41467-025-63745-z

- **A roadmap to the molecular human linking multiomics with population traits and diabetes subtypes**

  Halama A, Zaghlool S, Thareja G, et al. *Nat Commun*. 2024;15(1):7111. doi: 10.1038/s41467-024-51134-x

- **Simultaneous trimodal single-cell measurement of transcripts, epitopes, and chromatin accessibility using TEA-seq**

  Swanson E, Lord C, Reading J, et al. *Elife*. 2021;10:e63632. doi:10.7554/eLife.63632

Genomics + proteomics

- **Mendelian randomization identifies proteins involved in neurodegenerative diseases**

  Belbasis L, Morris S, van Duijn C, et al. *Brain*. 2025;148(7):2412-2428. doi:10.1093/brain/awaf018

- **Joint profiling of DNA and proteins in single cells to dissect genotype-phenotype associations in leukemia**

  Demaree B, Delley CL, Vasudevan HN, et al. *Nat Commun*. 2021;12(1):1583. doi:10.1038/s41467-021-21810

Transcriptomics + proteomics

- **Multi-omic profiling reveals age-related immune dynamics in healthy adults**

  Gong Q, Sharma M, Glass MC, et al. *Nature*. 2025;648:696–706. doi.org/10.1038/s41586-025-09686-5

- **Multi-omics resolves a sharp disease-state shift between mild and moderate COVID-19**

  Su Y, Chen D, Yuan D, et al. *Cell*. 2020;183(6):1479-1495.e20. doi:10.1016/j.cell.2020.10.037

Genomics + transcriptomics + proteomics

- **Integrative multi-omics approaches identify molecular pathways and improve Alzheimer's disease risk prediction**

  Venkatesh R, Cardone KM, Bradford Y, et al. *Alzheimer's & Dementia*. 2025;21(11):e70886. doi:10.1002/alz.70886

Spatial trancsriptomics + spatial proteomics

- **Spatial signatures for predicting immunotherapy outcomes using multi-omics in non-small cell lung cancer**

  Aung TN, Monkman J, Warrell J, et al. *Nat Genet*. 2025;57(10):2482-2493. doi:10.1038/s41588-025-02351-7

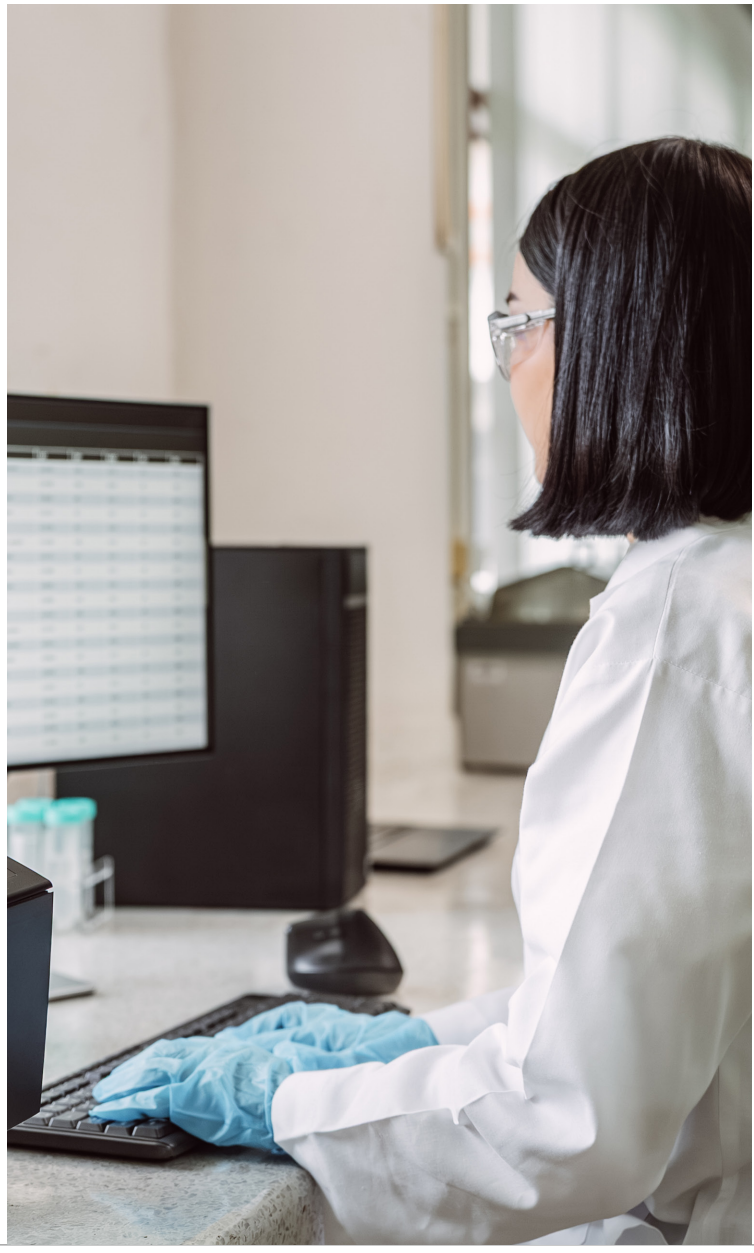
What's next for multiomics

The multiomic approaches discussed in this eBook reflect a broader shift toward integrated methods for biological research. As sequencing costs continue to decrease and chemistries and workflows improve, multiomic assays are becoming more comprehensive and easier to incorporate into diverse study designs.

These advances will enable laboratories to analyze larger sample sets under varied conditions and capture the dynamic properties of cells and tissues with greater precision. Sequencing will increasingly support proteomic measurements for panels spanning hundreds to thousands of targets. Single-cell multiomics is expected to scale to experiments profiling millions of cells, and multimodal assays will continue to offer higher resolution across genomic, epigenetic, transcriptomic, and proteomic layers.

One of the greatest challenges for multiomic research is how to integrate different molecular data sets in a standardized way. Robust computational methods are required to unify diverse data types and uncover interpretable biological patterns. Addressing these challenges requires tools and platforms that make multiomic analysis more accessible, scalable, and integrated across laboratories of all sizes.

> "The opportunities to understand the biology of different cell types by combining multimodal data sets are extremely exciting. **This allows us to uncover a much deeper level of biology.**"
>
> **Ben Humphreys, MD, PhD**
> Chief of the Division of Nephrology, Washington University in St. Louis



Increasing access to multiomic insights

How Illumina is powering multiomics

Illumina strives to accelerate impactful discoveries by delivering technologies that expand access to genomic insights worldwide. Our scalable sequencing solutions support high-resolution approaches such as single-cell analysis and spatial transcriptomics, generating detailed molecular profiles that capture cellular states and spatial context. These capabilities provide a foundation for integrated multiomic analysis.

Building on advances in chemistry, library preparation, and analysis workflows, Illumina continues to develop integrated capabilities that minimize workflow and informatics bottlenecks. A sequencing readout common across assays enables researchers to integrate genomic, epigenomic, transcriptomic, single-cell, and spatial data types, helping them make the most of limited or valuable samples.

Library preparation

Innovations in library preparation are redefining what can be learned from a single sequencing readout. The Illumina multiomics portfolio comprises an expanding range of solutions designed to streamline workflows and maximize the biological information obtained from limited samples (Table 1), whether processing occurs in house or through core facilities and service providers. Researchers can interrogate the genome, epigenome, transcriptome, and proteome using solutions optimized to support both accessibility and translational relevance.

To support flexibility in experimental design, Illumina platforms are compatible with a broad ecosystem of partners offering specialized, interoperable solutions. This compatibility allows researchers to select methodologies aligned to specific research objectives while maintaining a standardized sequencing readout for consistent analysis. A summary of supported methodologies across the Illumina ecosystem is available in the Multiomics Methods Technical Resource.

Table 1: Illumina library preparation solutions

If you want to study...	And your research objectives include...	Illumina offers a solution
The genome	Genome-wide discovery of genetic variants (SNVs, indels)[a]	Illumina DNA Prep product line Illumina Cell-Free DNA Prep
	Deep, targeted profiling of coding regions	Illumina DNA Prep with Exome 2.5 Enrichment Illumina FFPE DNA Prep with Exome 2.5 Enrichment
	Detection of complex genomic variation, including structural variants and haplotype phasing	Illumina TruPath™ Genome
	High-throughput genotyping for large-scale variant screening	Infinium™ genotyping arrays[b]
The epigenome	Genome-wide DNA methylation profiling to study epigenetic regulation	Infinium methylation arrays[b]
The genome + epigenome	Simultaneous detection of genetic variants and DNA methylation states in a single assay	Illumina 5-Base DNA Prep Illumina 5-Base DNA Prep with Enrichment
The transcriptome	Discovery and quantification of protein-coding transcripts	Illumina Stranded mRNA Prep
	Comprehensive profiling of coding and noncoding RNA	Illumina Stranded Total RNA Prep with Ribo-Zero™ Plus
	Quantitative gene expression profiling across defined transcript targets	Illumina RNA Prep with Enrichment
	Profiling of small regulatory RNA species, including microRNAs	Illumina miRNA Prep
	Single cell–level gene expression analysis to resolve cellular heterogeneity and rare cell populations	Illumina Single Cell 3' RNA Prep
	Spatially resolved gene expression analysis within intact tissue architecture	Illumina spatial technology (coming soon)
The proteome	High-multiplex protein quantification for biomarker discovery and validation	Illumina Protein Prep

a. SNVs, single nucleotide variants; indels, insertions-deletions.
b. Arrays run on the iScan or NextSeq 550 Systems.

Sequencing

Illumina sequencing systems form the backbone of an integrated multiomics ecosystem, delivering trusted data quality across a range of applications and research scales. The broader Illumina multiomics portfolio, including library preparation and informatics solutions, supports end-to-end data generation and interpretation. Table 2 provides an overview of supported applications accross Illumina systems to help you select the system best aligned to your needs, whether sequencing is performed in house or through the Illumina global network of service laboratories.

Arrays

Illumina microarrays offer scalable, cost-effective options for high-volume interrogation of specific genomic and epigenetic targets (Table 2).

The iScan™ System works with Infinium arrays to deliver reliable data quality with exceptional ecomomic efficiency. Arrays provide a practical option for adding layers of biological data in studies where sample throughput and cost per sample are key considerations.

Table 2: Applications supported by Illumina sequencing systems

	Sequencing			Microarray
				
Application	**MiSeq™ i100 Series**	**NextSeq™ 1000 and NextSeq 2000 Systems**	**NovaSeq™ 6000 System NovaSeq X Series**	**iScan System**
Genomics	✓	✓	✓	✓
Epigenomics		✓	✓	✓
Microbiome analysis	✓	✓	✓	
Bulk transcriptomics	✓	✓	✓	
Single-cell transcriptomics	✓	✓	✓	
Spatial transcriptomics		✓	✓	
Proteomics			✓	

Illumina provides a diverse portfolio of BeadChips designed to support various multiomic research objectives:

Epigenetic profiling: the Infinium Methylation Screening Array, MethylationEPIC array, Mouse Methylation BeadChip, Bovine Methylation Array, and Methyl Custom BeadChip generate precise, high-resolution methylation data across human and nonhuman samples. These arrays allow researchers to integrate an epigenetic layer into studies, extending standard genomic analyses into multiomic frameworks to capture a more complete picture of gene regulation.

Genomic foundations: the Infinium Global Diversity Array and the Infinium Global Clinical Research Array enable robust genome-wide variant detection and large-scale genotyping. These tools provide an efficient method for detecting genetic variants that can be paired with transcriptomic or epigenetic data to help elucidate complex regulatory mechanisms.

Bioinformatics

The Illumina software and informatics portfolio supports analysis, interpretation, and data aggregation across a range of applications.

The Illumina DRAGEN™ (Dynamic Read Analysis for GENomics) Platform provides fast, accurate secondary analysis for genomics, epigenomics, transcriptomics, and proteomics (at bulk and single-cell resolutions).

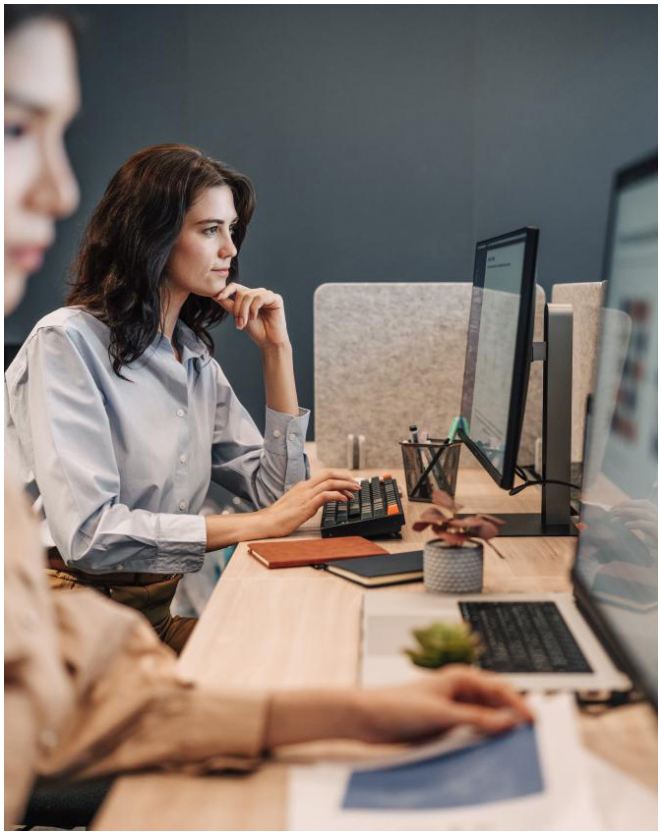
Illumina Connected Analytics is a comprehensive cloud-based platform designed to support management, analysis, and interpretation of large volumes of multiomic data in a secure, scalable, and flexible environment.

Illumina Connected Multiomics is a cloud-based analysis platform that enables researchers to explore and interpret single-omic and multiomic data sets at scale using intuitive visualizations and statistical tools. Streamlined integration with the Illumina ecosystem, from DRAGEN secondary analysis to biological interpretation with Correlation Engine and data management in Illumina Connected Analytics, supports an end-to-end workflow that simplifies multiomic analysis and enables deeper biological insights.

Correlation Engine mines more than 27,000 scientific studies to deliver data-driven insights for genes, experiments, drugs, and phenotypes. Researchers can examine gene function across species and identify pathways involved in disease development across multiple studies and data types.

Explore Illumina bioinformatics solutions at Informatics products

Learn how Illumina can help you further your multiomics research at Multiomics methods



Partnering to accelerate discovery

Illumina offers integrated services and support to complement the quality of our technologies. When you choose Illumina products, it marks the start of an ongoing partnership. Our technical support teams consist of highly trained specialists with deep knowledge of library preparation methods, sequencing platforms, and data analysis workflows, and we offer an extensive library of free online training resources to help researchers get the most from their workflows.

Illumina is committed to supporting the wide range of DNA and RNA sequencing applications. Our technologies are designed to enable emerging applications and multiomic approaches, including proteomic and methylation analyses. By collaborating with assay, reagent, and analysis tool developers, we work to ensure that researchers have access to complementary multiomics solutions that meet their experimental needs and help them achieve their scientific goals.

Summary

Multiomics is a rapidly emerging approach that is reshaping life science research through advanced sequencing and array technologies. By integrating multiple molecular data types within a single study, researchers can access a more complete view of biological systems and processes. These tools open the door to broad applications across fields, helping scientists uncover new mechanisms, refine disease understanding, and accelerate the pace of discovery.

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