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The power of multiomics

More to see
More to understand
More with multiomics

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Introduction

Advances in genomic technologies are giving researchers the tools to access more molecular data than ever before, enabling transcriptomics, epigenetics, proteomics, and beyond. To see the full picture of biology, scientists are increasingly turning towards a multiomic approach that integrates these various omic methods. This eBook provides examples from the scientific literature of how multiomics can provide unique discovery power for deeper biological insights and comprehensive answers to mechanisms of disease.

Why adopt multiomics

Biology is multilayered and complex. The central dogma reiterates the intertwined relationship between DNA, RNA, and protein. 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 provide a different perspective to power discovery across multiple levels of biology. This biological analysis approach combines genomic data with data from other modalities measuring gene expression, gene activation, and protein levels to enable a more comprehensive understanding of molecular changes contributing to normal development, cellular response, and disease. Using multiomics, researchers can better connect genotype to phenotype and fuel discovery of novel drug targets and biomarkers.

"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**."
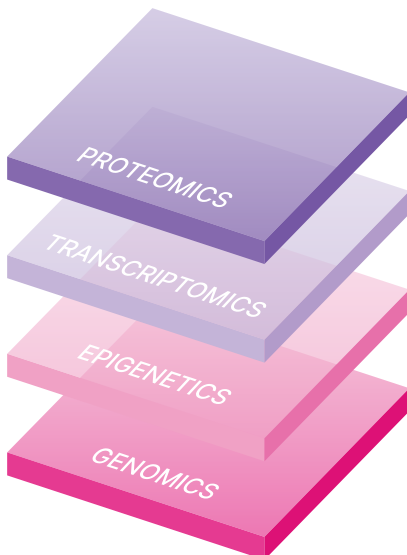
Danny Wells, PhD
Scientific Co-Founder and Senior Vice President of Strategic Research, Immunai

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.

"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 Computational Biology, Scripps Research

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 modality is a piece of the puzzle offering important insights into the details of biological and disease mechanisms. Additionally, high-resolution approaches like single-cell sequencing or spatial analysis offer another layer of fundamental detail to examine heterogeneity in complex cell populations.

Through the combined lens of multiomics, researchers can witness the complicated interplay between the molecules of life. Integrating these complementary metrics into multiomic data sets brings a more comprehensive picture of cellular phenotypes and helps pull more high-quality information from each sample.
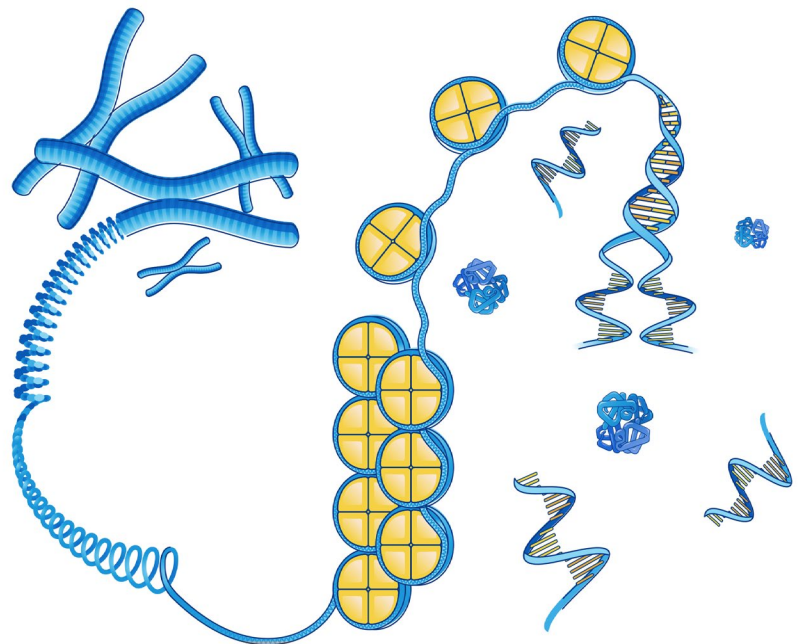
Bigger picture biology through multiomics—Multiomics goes beyond the genome to unlock deeper biological insights. Using every piece of molecular data available can accelerate biological discoveries and transform our understanding of human health.

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 as well as new applications. The scientific community can generate more detailed data from their samples or interrogate their samples at multiple levels for greater insights.
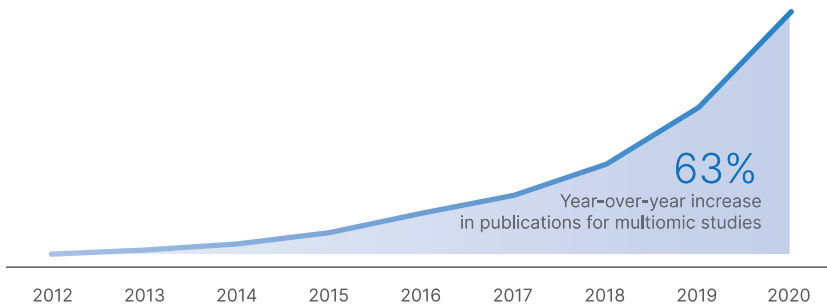
Trends in multiomics grant funding and publications

In part due to the decreasing cost of sequencing technologies and the speed at which they generate data, more labs are adopting multiomics. The rapid rise of multiomic approaches is evidenced by a growing presence in the current literature and an expanding 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

2012 2013 2014 2015 2016 2017 2018 2019 2020

Multiomics publications 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

2012 2013 2014 2015 2016 2017 2018 2019 2020
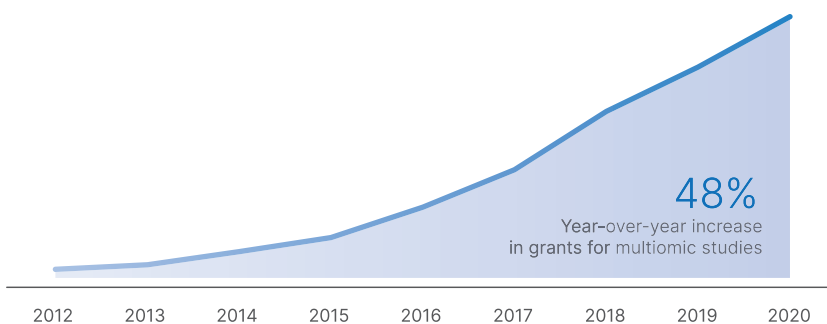
Grant funding growth for multiomics—Since 2012, there has been a 48% average year-over-year increase in the number of active or starting grants for multiomic studies.[1]

"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

How multiomics is fueling discovery

Scientists using multiomics are able to make discoveries they may have missed if using a single method alone. Here we highlight the most common multiomic combinations and share examples from recent literature to demonstrate how multiomics is providing novel insights into biological function and disease mechanisms.

Genomics + transcriptomics

Genome-wide association studies (GWAS) have successfully identified genetic variants associated with complex diseases. The genotype offers information on susceptibility to the disease; however, determining the specific genes and pathways affected by those variants is more difficult. Incorporating RNA sequencing (RNA-Seq) can help researchers annotate and prioritize variants uncovered in GWAS for functional analysis to understand mechanisms of disease. Gene expression analysis informs if and when the genes of interest are down- or upregulated in the disease samples. This multiomic approach to functional genomics can help power drug target identification and biomarker discovery.

74%
of genomic-focused researchers also use transcriptomics

Genomics-focused researchers

Transcriptomics-focused researchers
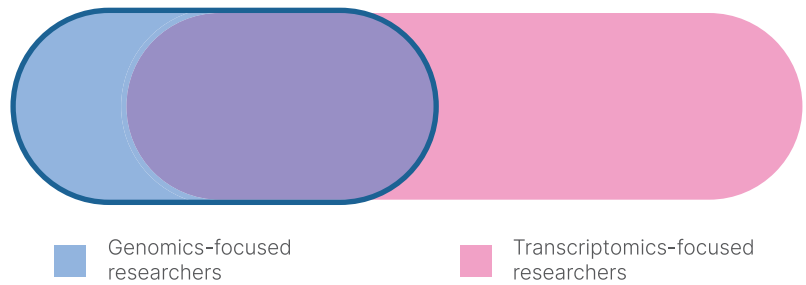
Basic science researchers combining genomics + transcriptomics—Of researchers focused on genomics methods (blue), 74% also use transcriptomics methods. Of researchers focused on transcriptomics methods (pink), 46% also use genomics methods.[2]

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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 tease apart details of the immune cell response during kidney transplant rejection.[3]

In solid organ transplant, it's 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. With a multiomic approach, WES determined genetic variation between donor and recipient. Then, by sequencing transcripts from individual immune cells from human kidney biopsies, researchers could match the single nucleotide variants in expressed genes to identify cell origin.[3]

Single-cell immune profiling was used to look at the transcriptomes of over 80,000 cells simultaneously, including over 5000 macrophages and 3600 lymphocytes. Recipient-origin macrophages and T-cells showed distinct proinflammatory gene expression patterns and donor-derived cells could persist for years after organ transplant. Understanding the mechanisms of organ transplant rejection could lead to more targeted immunosuppression drugs.[3]

"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

Genomics + epigenetics

The majority of human variation identified by GWAS is in the noncoding regions of the genome, including introns, promoters, or enhancers. Comprehensive epigenetic profiling can reveal patterns of gene regulation to help find the function of those variants. NGS-based epigenetic techniques include chromatin immunoprecipitation (ChIP-Seq), assay for transposase-accessible chromatin (ATAC-Seq), and chromosome conformation capture (Capture C, HiC). DNA methylation patterns are also conserved and can represent a new class of biomarkers. Multiomic approaches that combine methylation, or other epigenetic profiling, with genetic information can connect functional layers to decipher complex pathways and disease mechanisms.
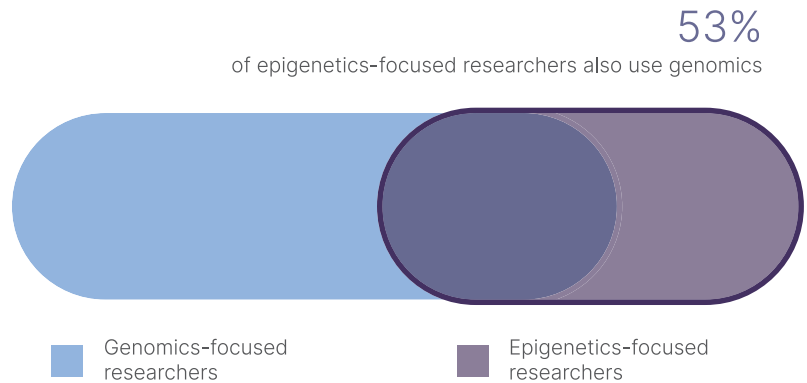
"A multiomic approach increases our understanding of biology by helping us **see things that would be hidden with one type of data**."

Pejman Mohammadi, PhD
Associate Professor of Computational Biology, Scripps Research

53%
of epigenetics-focused researchers also use genomics

Genomics-focused researchers

Epigenetics-focused researchers

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

MULTIOMICS RESEARCH EXAMPLE

GWAS + methylation arrays

Methylation risk score improves prediction of major depressive disorder

A study led by a team at the University of Edinburgh built upon GWAS and explored how epigenetic markers contribute to risk for major depressive disorder.[4]

Variation in DNA methylation is associated with lifestyle risk factors for depression, such as smoking and body mass index (BMI), thus methylation patterns can capture a "record" of these environmental influences. Using the Infinium™ MethylationEPIC Array from Illumina, researchers determined the genome-wide CpG methylation signatures of 9873 samples from Generation Scotland: the Scottish Family Health Study.[4]

Based on longitudinal phenotypic data, the calculated "methylation risk score" additively improved prediction of depression when combined with risk scores based on genetic variation. Methylation explained 1.75% of the variance seen in major depression and remained significant even after adjusting for lifestyle factors. This study demonstrates that using a risk score based on multiomic data sets can offer greater clinical power to predict and potentially prevent major depressive disorder.[4]

Epigenetics + transcriptomics

Epigenetics and transcriptomics offer complementary information to study the details of cellular differentiation and response. Combining epigenetic and RNA-Seq methods allows researchers to directly measure the ties between gene regulation and gene expression, instead of simply inferring those connections. Integrating epigenetics and RNA-Seq can help researchers identify candidate genes and understand the mechanisms controlling interesting phenotypes. This holistic, non-biased multiomics approach can uncover new regulatory elements for biomarkers and therapeutic targets.
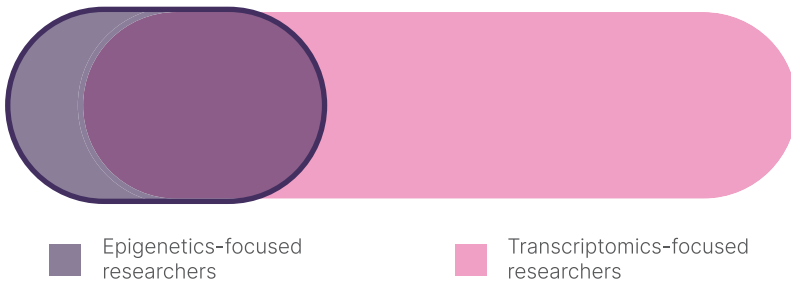
Unify single-cell gene expression and chromatin accessibility
Enable RNA-Seq and ATAC-Seq measurements from the same single cells in the same assay.

Read Technical Note

77%
of epigenetics-focused researchers also use transcriptomics

- Epigenetics-focused researchers
- Transcriptomics-focused researchers

Basic science researchers combining epigenetics + transcriptomics—Of researchers focused on epigenetics methods (purple), 77% also use transcriptomics methods. Of researchers focused on transcriptomics methods (pink), 34% also use epigenetics methods.[2]

MULTIOMICS RESEARCH EXAMPLE

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.[5]

Comparing healthy older and younger postmortem brain tissue with tissue from brains of Alzheimer's patients, this team performed total RNA-Seq and epigenetic sequencing assays, including ChIP-Seq and 5-hydroxymethylcytosine (5hmC) analysis.[5]

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.[5]

Transcriptomics + proteomics

RNA-Seq offers unparalleled discovery power to interrogate the transcriptome without prior knowledge. Incorporating protein detection with RNA-Seq can tie new discoveries back to known canonical markers and historical clinical outcomes.

Simultaneous bulk protein and gene expression profiling
BEN-Seq method uses Illumina NGS and oligo-conjugated antibodies for easy quantification of multiple protein targets.
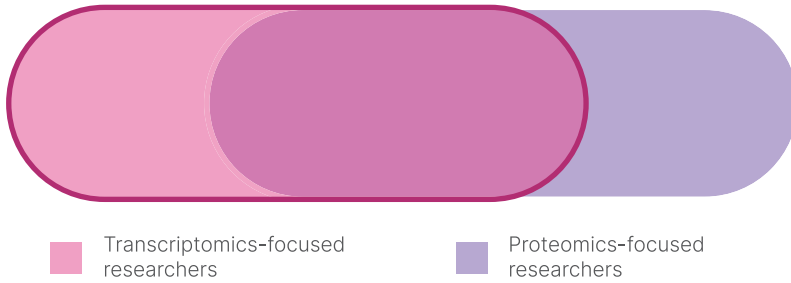
Read Application Note

Antibodies tagged with oligonucleotide barcodes enable analysis of cell surface proteins with results read by sequencing, which scales to a much higher number of 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 in context with tissue morphology.
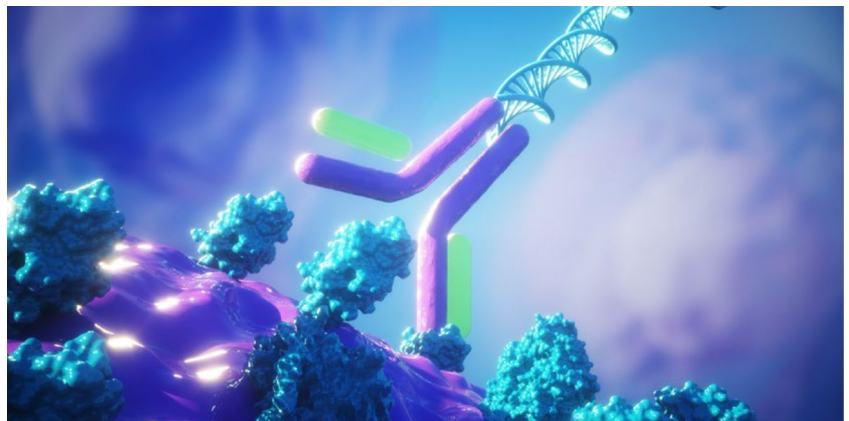
Protein detection with sequencing—DNA-tagged antibodies allow for detection of cell surface proteins with results read by sequencing. When cell surface markers are more robustly analyzed through multiomics, there are two chances to catch an important signal.

66%

of transcriptomics-focused researchers also use proteomics

Transcriptomics-focused
researchers

Proteomics-focused
researchers

Basic science researchers combining transcriptomics + proteomics—Of researchers focused on transcriptomics methods (pink), 66% also use proteomics methods. Of researchers focused on proteomics methods (lavender), 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
Scientific Co-Founder and Senior Vice President of Strategic Research, Immunai

MULTIOMICS RESEARCH EXAMPLE

Spatial RNA-Seq + spatial protein analysis

Uncovering spatial heterogeneity in SARS-CoV-2 lung infection

A research group at Massachusetts General Hospital used spatial multiomics to examine the relationship between SARS-CoV-2 lung infection and the severity of pulmonary disease.[6]

The team performed spatial molecular analysis of both RNA and protein in 24 lung specimens from autopsies of COVID-19 patients. Using a spatial profiling system, they looked at over 1800 RNA markers to identify cell regions with high or low viral load. The researchers also examined 79 protein markers to identify immune cell phenotypes in different lung regions.[6]

The combined data uncovered spatial relationships between virus location and immune cell abundance, suggesting two phases of infection. During early infection, high levels of virus triggered expression of interferon-related genes. A later phase showed surprisingly little viral replication in the lungs, but severe tissue damage. These details may help scientists learn how COVID-19 can be fatal.[6]

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"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 Computational Biology, Scripps Research

Genomics + proteomics

This multiomic approach directly connects genotype to phenotype for more informed research on disease and therapeutics development. Linking genetic variation to protein expression at the single-cell level can reveal the functional impact of somatic mutations on human cancers to better understand tumor evolution and disease progression.

63%
of genomics-focused researchers also use proteomics

| Genomics-focused researchers | Proteomics-focused researchers |
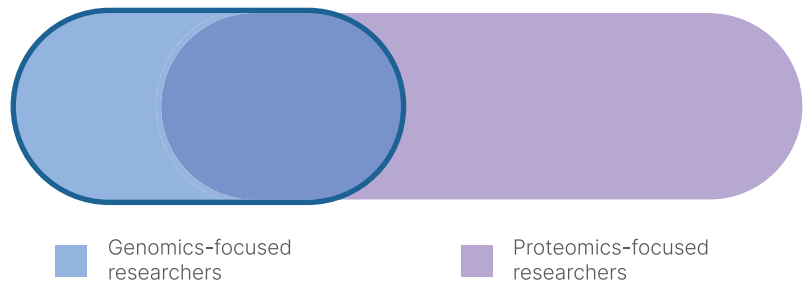
Basic science researchers combining genomics + proteomics—Of researchers focused on genomics methods (blue), 63% also use proteomics methods. Of researchers focused on proteomics methods (lavender), 38% also use genomics methods.[2]

MULTIOMICS RESEARCH EXAMPLE
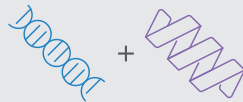
Single-cell targeted resequencing + single-cell cell surface protein analysis

Tracking clonal evolution in myeloid cancers

Scientists at Memorial Sloan Kettering Cancer Center and the University of California San Francisco applied single-cell multiomics to track clonal evolution in 146 samples from 123 patients with myeloid cancers. Oligo-conjugated antibodies enable high-throughput single-cell proteomics with sequencing. Using targeted sequencing panels, this group performed simultaneous single-cell mutational analysis and cell-surface protein quantification for more than 740,000 cells. This level of scale and detail coupling genotype with phenotype allowed the researchers to finely map the dynamics of cancer cell clonal complexity and its effect on disease progression.[7]

See how more scientists are using multiomics

Multiomics is revolutionizing research and pushing limits with novel scientific insights that make new discoveries possible. Explore additional examples from the literature demonstrating the power of multiomic approaches that combine two, three, or more modalities.

Genomics + transcriptomics

Opposing immune and genetic mechanisms shape oncogenic programs in synovial sarcoma
Jerby-Arnon L, Neftel C, Shore M, et al. *Nat Med.* 2021;27(2):289-300. doi:10.1038/s41591-020-01212-6
Genetic identification of cell types underlying brain complex traits yields insights into the etiology of Parkinson's disease
Bryois J, Skene NG, Hansen TF, et al. *Nat Genet.* 2020;52(5):482-493. doi:10.1038/s41588-020-0610-9
Genetic identification of brain cell types underlying schizophrenia
Skene NG, Bryois J, Bakken TE, et al. *Nat Genet.* 2018;50(6):825-833. doi:10.1038/s41588-018-0129-5

Genomics + epigenetics + transcriptomics

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

Epigenetics + transcriptomics

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
Single-cell multiomics sequencing reveals the functional regulatory landscape of early embryos
Wang Y, Yuan P, Yan Z, et al. *Nat Commun.* 2021;12(1):1247. doi:10.1038/s41467-021-21409-8
Epigenetic modulation of AREL1 and increased HLA expression in brains of multiple system atrophy patients
Rydbirk R, Folke J, Busato F, et al. *Acta Neuropathol Commun.* 2020;8: 29. doi: 10.1186/s40478-020-00908-7
Genome-scale Capture C promoter interactions implicate effector genes at GWAS loci for bone mineral density
Chesi A, Wagley Y, Johnson ME, et al. *Nat Commun.* 2019;10(1):1260. doi:10.1038/s41467-019-09302-x

Epigenetics + transcriptomics + proteomics

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

Transcriptomics + proteomics

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
Discovery of CD80 and CD86 as recent activation markers on regulatory T cells by protein-RNA single-cell analysis
Trzupek D, Dunstan M, Cutler AJ, et al. *Genome Med.* 2020;12(1):55. doi:10.1186/s13073-020-00756-z
Multiplexed detection of proteins, transcriptomes, clonotypes and CRISPR perturbations in single cells
Mimitou EP, Cheng A, Montalbano A, et al. *Nat Methods.* 2019;16(5):409-412. doi:10.1038/s41592-019-0392-0

Genomics + proteomics

Joint profiling of DNA and proteins in single cells to dissect genotype-phenotype associations in leukemia
Demaree B, Delley C, Vasudevan H, et al. *Nat Commun.* 2021;12(1):1583. doi:10.1038/s41467-021-21810
Integrating human brain proteomes with genome-wide association data implicates new proteins in Alzheimer's disease pathogenesis
Wingo AP, Liu Y, Gerasimov ES, et al. *Nat Genet.* 2021;53(2):143-146. doi:10.1038/s41588-020-00773-z

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"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

What's next for multiomics

The multiomic methods and research examples highlighted here represent a new holistic approach to understanding biology. As the cost of sequencing continues to decrease and the technology advances, multiomic assays will become more comprehensive and better integrated. Labs will be able to study more samples under different conditions to reveal dynamic properties of cells and systems. Sequencing will support proteomic studies with oligo-tagged antibodies for hundreds to thousands of markers. Single-cell multiomics will expand to a scale of millions of cells per experiment. More assays will incorporate multimodal measurements at higher resolution.

One of the biggest challenges for multiomic research is how to integrate different molecular data sets in a standardized way. Researchers need robust computational strategies to extract biologically meaningful insights from these vast amounts of data. Sophisticated bioinformatics tools like Seurat[8] enable normalization and integration of multimodal single-cell sequencing experiments. Machine learning methods will also help organize and filter complex multiomic data.

The comprehensive view provided by multiomics will illuminate new biomarkers and drug targets to advance precision medicine.

Increasing access to multiomic insights

How Illumina is powering multiomics

Illumina strives to accelerate impactful discoveries by delivering products that increase access to genomic data insights across the globe. Our scalable sequencing solutions enable data-rich methods like single-cell analysis and multiomic approaches. Illumina is continuing to invest in major technology innovations to provide integrative genomic capabilities and remove typical workflow and informatics bottlenecks.

Illumina powers multiomic analysis with a solution suite that offers industry-leading standards of data quality, flexibility, and scalability. The common readout across NGS approaches permits integration of multiple data types to help researchers maximize the genomic data potential for valuable research samples.

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Library prep and sequencing

Breakthrough innovations in library preparation for genome, exome, and transcriptome sequencing help researchers extract greater insights from multiomic approaches in less time. Illumina library prep workflows are easy to use, scalable for any size lab, and require few steps.

The NextSeq™ 1000 and NextSeq 2000 systems, NovaSeq™ 6000 system, and NovaSeq X series offer application flexibility to power multiomic approaches and make them more affordable. These sequencing systems allow for exceptional breadth of targets and scalability for sequencing at an accessible price point.

Bioinformatics

The Illumina software and informatics portfolio includes some of the fastest, most accurate, and advanced solutions for analysis, interpretation, and data aggregation.

The Illumina DRAGEN™ (Dynamic Read Analysis for GENomics) Bio-IT Platform provides accurate, ultra-rapid secondary genomic analysis of sequencing data.

BaseSpace™ Correlation Engine mines over 23,000 scientific studies to get data-driven answers for genes, experiments, drugs, and phenotypes. Researchers can analyze gene function across different species, and view pathways that play a role in disease development across multiple studies and data types.

Illumina Connected Analytics is a comprehensive cloud-based data management and analysis software platform empowering researchers to manage, analyze, and interpret large volumes of multiomics data in a secure, scalable, and flexible environment.

Learn more about single-cell techniques using Illumina sequencing platforms

Download the single-cell sequencing eBook

Explore Illumina bioinformatics solutions at illumina.com/products/by-type/informatics-products.html.

Arrays

Illumina microarrays offer high-quality data and exceptional genomic coverage to propel genomic studies of any size. Powered by widely adopted Infinium technology, Illumina microarrays provide the trusted data quality needed to accelerate research.

The Infinium MethylationEPIC Array quantitatively interrogates over 850,000 methylation sites for epigenome information to add to your multiomics study. Multiple samples, including formalin-fixed, paraffin-embedded (FFPE) tissue, can be analyzed in parallel to deliver high-throughput power while minimizing the cost per sample.

Arrays like the Infinium Global Diversity Array enable variant identification and can be combined with another omic technology like transcriptomics or epigenetics to help provide biological context to those variants.

Partnering to advance science further

Illumina offers integrated services and support to match the quality of our proven technology. When you choose Illumina products, it's the beginning of a relationship. Our technical support lines are staffed with experts, many with PhDs, and we have an extensive library of free online training resources.

Illumina is committed to supporting the breadth of applications across the DNA and RNA continuum. Illumina technology also makes possible emerging applications and multiomic approaches to sequencing, including proteomics and methylation analysis. Through partnerships with vendors such as BioLegend, 10x Genomics, Becton Dickinson, and Nanostring, we help provide multiomics product solutions to fit your research needs.

Learn how Illumina can help you further your research at illumina.com/science/technology/next-generation-sequencing/choose-ngs-company.html

Select multiomic methods

The following methods are building blocks for a multiomic experiment. Mix and match whole-exome sequencing with gene expression profiling or ATAC-Seq. Perform omic analysis with single-cell or spatial resolution. Or choose a multimodal approach like BEN-Seq or CITE-Seq with multiomic readouts built directly into the assay.

	Method	What you can do	Learn more
Bulk genomics	Whole-genome sequencing	Obtain a high-resolution, base-by-base view of the entire genome to capture both large and small variants that might be missed with targeted approaches	illumina.com/techniques/sequencing/dna-sequencing/whole-genome-sequencing.html
	Whole-exome sequencing	Focus sequencing on the protein-coding regions of the genome, which include ~85% of known disease-related variants	illumina.com/techniques/sequencing/dna-sequencing/targeted-resequencing/exome-sequencing.html
	Genotyping arrays	Survey millions of markers in cohorts or populations to identify disease associations across the whole genome	illumina.com/techniques/popular-applications/genotyping.html
Bulk epigenetics	Methylation arrays	Identify methylation sites across the genome at single-nucleotide resolution with extensive coverage of CpG islands, genes, and enhancers for epigenome-wide association studies	illumina.com/techniques/microarrays/methylation-arrays.html
	ChIP-Seq	Identify DNA binding sites for transcription factors and other proteins	illumina.com/techniques/sequencing/dna-sequencing/chip-seq.html
	ATAC-Seq	Profile accessible chromatin using a hyperactive Tn5 transposase that inserts sequencing adapters into open regions of the genome	illumina.com/techniques/popular-applications/epigenetics/atac-seq-chromatin-accessibility.html
Single-cell epigenetics + transcriptomics	Single-cell ATAC-Seq + mRNA-seq	Measure both gene expression and chromatin accessibility at the single-cell level to reveal gene regulatory networks and provide insights into cell heterogeneity	illumina.com/content/dam/illumina/gcs/assembled-assets/marketing-literature/10x-multiomics-tech-note-m-amr-00006/10x-multiomics-tech-note-m-amr-00006.pdf
Bulk transcriptomics	Whole-transcriptome sequencing (Total RNA-Seq)	Capture both coding and noncoding RNA transcripts to help idenitfy biomarkers and better understand phenotypes of interest	illumina.com/techniques/sequencing/rna-sequencing/total-rna-seq.html
	mRNA-Seq	Reveal alternative transcripts, gene fusions, and allele-specific expression patterns with a clear, comprehensive view of the coding transcriptome	illumina.com/techniques/sequencing/rna-sequencing/mrna-seq.html illumina.com/techniques/sequencing/rna-sequencing/rna-exome-capture-sequencing.html

	Method	What you can do	Learn more
Bulk combined transcriptomics + proteomics	BEN-Seq	Simultaneously profile cell surface proteins and gene expression to understand the relationship between cell markers and RNA	illumina.com/content/dam/illumina/gcs/assembled-assets/marketing-literature/biolegend-ben-seq-app-note-m-gl-00024/biolegend-ben-seq-app-note-m-gl-00024.pdf
Single-cell transcriptomics + proteomics	CITE-Seq	Use mRNA-Seq and oligo-tagged antibodies to evaluate both gene expression and protein levels simultaneously on a single-cell level	pages.10xgenomics.com/rs/446-PBO-704/images/10x_LIT089_Product-Sheet_Multiomic-Profiling_Letter_digital.pdf
Spatial transcriptomics + proteomics	Spatial RNA-Seq and protein analysis	Use spatial profiling to access RNA and protein expression in different tissue sections for pathway analysis and biomarker discovery	nanostring.com/products/geomx-digital-spatial-profiler/applications/
Single-cell genomics + proteomics	Proteogenomics	Link genomic variation to protein expression to reveal cell identities and inform disease research and therapeutics development	biolegend.com/Files/Images/BioLegend/totalseq/MissionBio_BioLegend_TotalSeq-D_App_Note.pdf

Summary

Multiomics is a rapidly emerging, transformative approach to life science research powered by cutting-edge sequencing and array technology. Integrating multiple omics research methods and data sets into your experiments brings a more holistic view to understanding biology. Multiomic tools enable limitless applications that are helping researchers discover novel scientific insights.

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