

Multi-Omics Strategies to

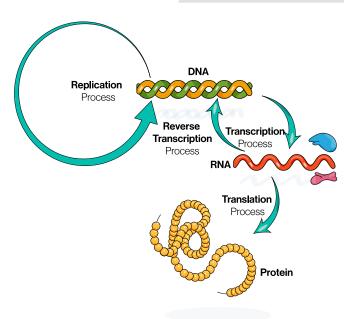
Decode Molecular

Mechanisms at Every Level



Multi-omics, an integrative approach combining genomics, transcriptomics, epigenomics, proteomics, and metabolomics, decodes the complex web of biological systems to provide unprecedented insights into molecular interactions and systemic behaviors. Overcoming the limitations of singleomics studies, it correlates data across various molecular layers, facilitating the discovery of novel biomarkers and mechanistic pathways.

Understanding these nuances in today's research landscape is crucial. This guide not only defines and outlines the core principles and technologies of multi-omics but also explores its applications in fundamental research, agriculture, and environmental sciences. Furthermore, it highlights the technological platforms and analytical methods essential for multi-omics integration, offering a comprehensive overview of the associated benefits and challenges.



As a trailblazer in genomics services, CD Genomics combines advanced sequencing platforms with expert bioinformatics to deliver high-quality multi-omics data analysis, ensuring precision and reliability for your research.

## What is Multi-omics Analysis?

#### **Definition and Core Concepts**

#### **Q** Definition:

Multi-omics analysis is an integrative research approach that combines data from genomics, transcriptomics, epigenomics, proteomics, and metabolomics to explore the molecular composition and interactions within living systems from a holistic perspective.

#### **#** Highlights:

Compared to single-omics approaches, multi-omics synchronously analyzes multiple layers from DNA, RNA, proteins, to metabolites. This allows researchers to gain a comprehensive understanding of the dynamic relationships and regulatory mechanisms among molecules.

#### **o** Objectives:

The aim of multi-omics is to identify key molecular features and uncover genes, regulatory factors, and metabolic pathways that play central roles in complex biological states, thereby advancing the understanding of how biological systems operate.





## **Technical Principles**

Multi-omics analysis involves four major stages:

**Q** Data Acquisition:

Systematic collection of genomic, transcriptomic, epigenomic, proteomic, and metabolomic datasets using high-throughput technologies.

Data Preprocessing:

Quality control, normalization, and noise reduction to ensure data integrity across omic layers.

Application of methods such as Multi-Omics Factor Analysis (MOFA), correlation analyses, and network construction to uncover interrelationships.

📊 Data Analysis and Interpretation:

Advanced bioinformatics and statistical techniques are employed to extract meaningful biological insights, including pathway enrichment and predictive modeling.

## Advantages of Multi-omics

## **Comprehensive Profiling**

Enables simultaneous investigation across multiple molecular layers for a multidimensional understanding of biological systems.

High Sensitivity and Resolution

Detects low-abundance genes, proteins, and metabolites with superior accuracy.

Integrated Insights

Enhances biological discovery through advanced data integration and deep computational analysis.

Greater Reproducibility

Improves research reliability through cross-layer validation and reduced data noise.







## Why is Multi-omics the Future of Biological Analysis?



## Comprehensiveness

Multi-omics analysis surpasses the constraints inherent in single-omics approaches by providing a more integrative biological perspective. By synthesizing data from multiple omic layers, it facilitates a multidimensional understanding essential for elucidating complex biological systems.



### **Precision:**

The integration of diverse datasets in multi-omics analysis allows for the highly precise identification of biomarkers and potential drug targets. Such precision is paramount for the advancement of personalized medicine and the optimization of therapeutic interventions...



#### Innovation:

Multi-omics is spearheading innovation within the realm of biomedical research. The development and deployment of methodologies such as single-cell multi-omics and spatial multi-omics are transforming our methodologies for probing cellular and molecular intricacies...



#### Interdisciplinary Collaboration:

Multi-omics analysis stimulates interdisciplinary collaboration, bridging the fields of biology, data science, and medicine. This confluence fosters scientific advancement by uniting diverse expertise to tackle complex biological questions, thereby extending the frontiers of research.

## Applications of Multi-omics Analysis



Multi-omics analysis, by integrating molecular data from different levels, offers an unprecedented comprehensive perspective for biological research. It not only uncovers intricate biological processes and disease mechanisms but also shows vast potential across various fields. Below are the principal application scenarios and their significance.





## Disease Research

- Identify Biomarkers: Discover driver genes, mutations, and metabolic changes to characterize disease mechanisms.
- Reveal Mechanisms: Map disease-related pathways and regulatory networks.
- **Monitor Progression:** Track molecular and cellular changes over time to understand biological shifts during different stages of a condition.



#### Agriculture & Environmental Science

- **Crop Improvement**: Breed resilient, high-yield varieties using genomics and metabolomics.
- Microbiome Research: Optimize soil health and crop growth by studying microbial communities.
- Environmental Monitoring: Assess pollutant impacts on ecosystems.



## **Microbial and Host-Microbe Interaction Studies**

- Functional Profiling: Link microbial genes and metabolites to ecological roles and metabolic functions.
- **Community Dynamics:** Analyze shifts in microbial populations under different environmental or biological conditions.
- Cross-species Communication: Study signaling molecules and pathways involved in host-microbe interactions.





## **Transcriptomics-Based Multi-Omics Integration Strategies**

Combination	Transcriptomics + Metabolomics
Description	Investigates biological queries from both causative and resultant dimensions, validating findings across data sets to identify key genes, metabolites, and pathways, offering insights into the complexity and integrity of biological development.
Combination	Transcriptomics + Proteomics
Description	Provides a holistic view of gene expression from RNA and protein levels, capturing the entire process and regulation steps, revealing novel findings overlooked by single-omics approaches.
Combination	Transcriptomics + Proteomics + Metabolomics
Description	Explores biological questions from multiple facets, cross-validating data to unearth more informative insights, deeply analyzing the intricacies of biological processes and elucidating underlying molecular mechanisms.

How CD Genomics Supports Transcriptomics-Based Multi-Omics Research

**Research Directions:** Growth and Development, Biomarkers, Immune Response, Disease Mechanisms, Genetic Breeding, Stress Resistance

Sequencing: RNA-Seq, Bacterial RNA Sequencing, Total RNA Sequencing, Targeted RNA Sequencing, LncRNA

Sequencing ...

**Bioinformatics Analysis:** <u>Transcriptomics Data Analysis</u>





## **Amplicon Sequencing-Based Multi-Omics Integration Strategies**

Combination	Amplicon Sequencing+ Metabolomics
Description	Merges two omics approaches to better understand how microbial communities influence host metabolic states through various interactions, providing insights into disease mechanisms and host-microbial interactions.
Combination	Metagenomics + Metabolomics
Description	Similar integration provides a comprehensive understanding of microbial community impacts on host metabolism, advancing insights into disease progression and ecological interactions.

How CD Genomics Supports Amplicon Sequencing-Based Multi-Omics Research

Research Directions: Functional Research/Drug Target Identification, Mechanism Studies, Biomarker Screening

Sequencing: 16S/18S/ITS Amplicon Sequencing, Absolute Quantitative 16s/18s/ITS Amplicon Sequencing, Microbial Identification, Microbial Whole Genome Sequencing, Metagenomic Shotgun Sequencing, Viral Metagenomic Sequencing, Metatranscriptomic Sequencing

Bioinformatics Analysis: Genomics Data Analysis, Long-Read Sequencing Data Analysis





## **Epigenomics-Based Multi-Omics Integration Strategies**

Combination	Epigenomics + Transcriptomics
Description	Correlates changes in epigenetic marks (e.g., DNA methylation, histone modification) with gene expression changes, uncovering regulatory mechanisms.
Combination	Epigenomics + Genomics + Transcriptomics

## How CD Genomics Supports Epigenomics-Based Multi-Omics Research

**Research Directions:** Gene Regulation, Developmental Biology, Disease Epigenetics, Variant Interpretation, Developmental Disorders

Sequencing: WGBS, RRBS, ChIP-Seq, EM-Seq, Epitranscriptomic Sequencing, RNA-Seq, WGS...

Bioinformatics Analysis: Epigenomics Data Analysis, Genomics Data Analysis, Transcriptomics Data Analysis

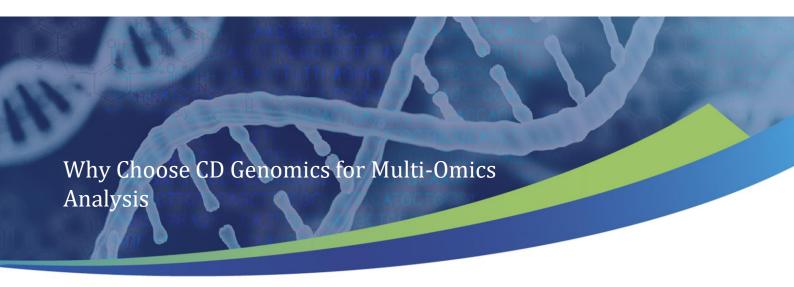
CD Genomics, specializing in genomics services, offers a wide range of high-throughput sequencing services, including genome, transcriptome, and metagenome sequencing, aiming to deliver comprehensive genomic solutions to the pharmaceutical, biotech sectors, and the academic community.

With state-of-the-art sequencing platforms, such as Illumina and PacBio, and a high-standard laboratory environment equipped with robust data storage and computational capabilities, CD Genomics is well-equipped to meet the demands of multi-omics analysis. Their experienced team, focused on genomics and bioinformatics, is dedicated to providing high-quality multi-omics data analysis services to enhance research and pharmaceutical developments.

If you are interested in exploring relevant case studies from our clients, please feel free to click and read our poster for more detailed examples.









## **Advanced Technological Support**

Armed with state-of-the-art sequencing platforms such as Illumina and PacBio, and operated in highstandard laboratory environments, we ensure the delivery of high-quality multi-omics data analysis services.



## **Comprehensive Solutions**

We offer an extensive range of high-throughput sequencing services including genomics, transcriptomics, and metagenomics, effectively meeting the diverse needs of the pharmaceutical, biotechnology, and academic sectors.



# **Robust Data Integration**

Leading the industry in integrating and analyzing diverse omics data, including genomics, transcriptomics, proteomics, and metabolomics, we help you achieve multi-level biological insights.



### **Expert Team Advantage**

Our bioinformatics team possesses rich expertise in genomics, enabling them to provide precise and valuable insights for your projects, supporting research and pharmaceutical development.



## Customized Analysis Services

Employing the latest statistical methods, pathway analyses, and machine learning techniques, we offer bespoke multi-omics data integration services tailored to your specific research objectives.



## Collaboration and Support

We promote interdisciplinary collaboration by leveraging expertise in biology, data science, and medicine, helping you tackle complex biological challenges and fostering innovation and progress in the field.





# Published Results at a Glance



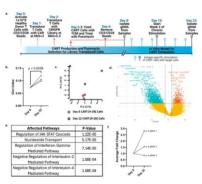
The following highlights represent selected publications from our clients who have leveraged CD Genomics' multi-omics services to advance their research.

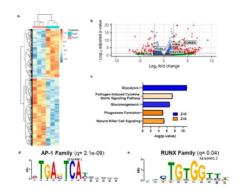
#### 1. IL-4 drives exhaustion of CD8+ CART cells

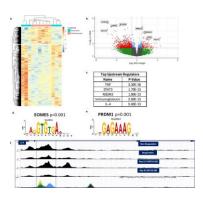
Nature Communications | 12 Sep 2024 | DOI: https://doi.org/10.1038/s41467-024-51978-3

Services: CRISPR Screen Sequencing, RNA-sequencing, ATAC-sequencing

Result Highlights



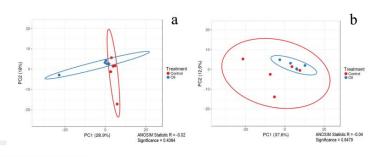


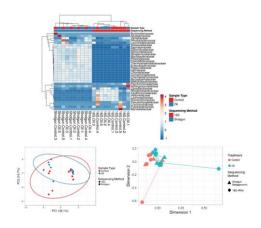


#### 2. Limited impact of weathered residues from the Deepwater Horizon oil spill on the gut-microbiome and foraging behavior of sheepshead minnows (Cyprinodon variegatus)

Journal of Toxicology and Environmental Health | 13 Oct 2023 | DOI: https://doi.org/10.1080/15287394.2023.2265413 Services: Metagenomic Shotgun Sequencing;16S/18S/ITS Amplicon Sequencing

### Result Highlights







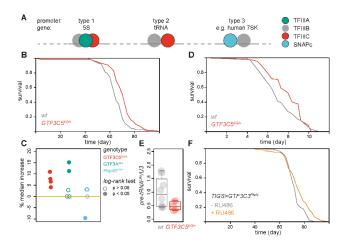


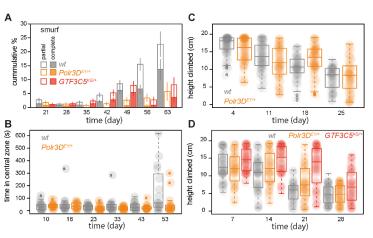
## 3. Disruption of tRNA biogenesis enhances proteostatic resilience, improves later-life health, and promotes longevity

Plos Biology | 22 October 2024 | DOI: https://doi.org/10.1371/journal.pbio.3002853

Services: Ribo-seq; RNA-seq

**Result Highlights** 





## 4. KMT2A associates with PHF5A-PHF14-HMG20A-RAI1 subcomplex in pancreatic cancer stem cells and epigenetically regulates their characteristics

Nature Communications | 14 September 2023 | DOI: https://doi.org/10.1038/s41467-023-41297-4

Services: ChIP-seq; RNA-seq

**Result Highlights** 

