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# The Omics Sciences

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Any field of research in the biological sciences that ends in -omics, such as transcriptomics, proteomics, metabolomics, or genomics, is referred to as omics. The study subjects in these domains, such as the transcriptome, metabolome, proteome, or genome, are

denoted by the suffix -ome. More precisely, genomics is the study of genome structure, function, evolution, and mapping with the goal of characterizing and quantifying genes, which, with the help of messenger molecules and enzymes, control the synthesis of proteins. A single cell, tissue, or organism's transcriptome is its collection of all messenger RNA molecules. In addition to the chemical IDs, it also contains the quantity or concentration of every RNA molecule

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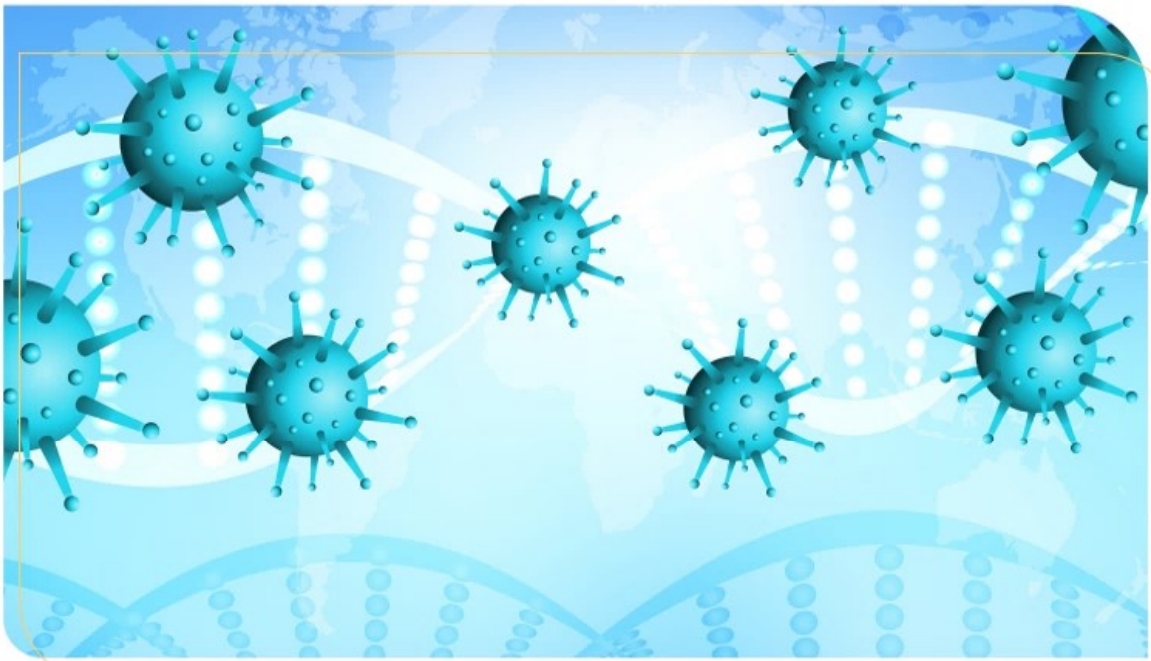

## Introduction

"OMICS," which is defined as examining and evaluating a substantial volume of data that represents the composition and functionality of a certain biological system at a particular level, has fundamentally changed how we examine biological systems. Put another way, "top down" methods, which are primarily related to the creation of "omics," combined with "bottom up" techniques provide a comprehensive instrument for effective biological system research. As a result, the idea of deconstructing complex disorders, such as cancers, has evolved from static, low-throughput delineation between cell malignant and healthy states to spatiotemporal, dynamic, global-unbiased deconvolution of complex systems involving multi-layer modifications at the genomic, transcriptomic, proteomic, and metabolic levels.

The aim of the omics sciences is to identifying, describing, and quantifying every biological molecule involved in the dynamics, structure, and function of a cell, tissue, or organism.

Technologies for omics investigation have advanced rapidly ever since DNA microarray, the first high-throughput tool, was established (Schena et al., 1995). In accordance with the fundamental concept, post translational modifications (PTMs), spatiotemporal proteome dynamics, alternative splicing, temporal transcriptome perturbations, and static genomic abnormalities have all been captured by omics technologies (Chakraborty et al., 2018). Beyond this, omics technologies have been extended to analyze different omics at the molecular interactions (i.e., different levels of interactome), disease associated hallmarks (i.e., metabolome and immunome), and epi-level (such as epigenome, epitranscriptome, and epiproteome that are defined as the collection of all modifications of the referred omics beyond information it covered in a single cell).

In order to build a thorough causal relationship between molecular signatures and phenotypic manifestations of a specific disease, multi-omics integration has gained popularity. Additionally, single cell sequencing provides extra resolving power that permits studies at the single cell level. We are now able to accurately and comprehensively identify the com-


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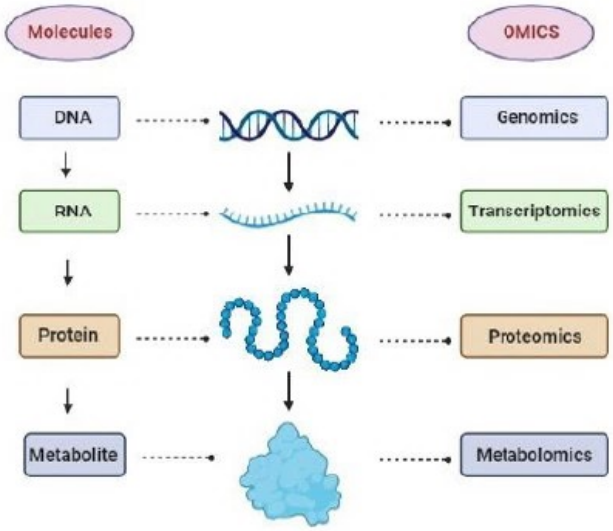
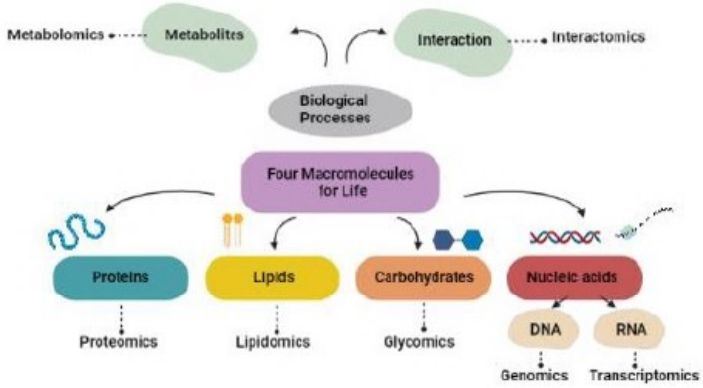
plex molecular mechanisms behind various phenotypic manifestations of disordered features thanks to the constantly expanding and quickly rising discipline of omics. Nonetheless, the development of fresh omics and related methodologies may continue to be propelled by the intricacy of cellular behavior and its decision-making mechanism.

Although, in theory, we are getting very near to the truth, our understanding of the complexity of the cell machinery is always changing because to the ever-expanding body of knowledge on cellular omics, which poses a hurdle to our objective of fully harnessing cell pathological state rewiring. Therefore, in order to predict what can be done in "omics" as a shortcut towards our aim, it is time to thoroughly analyze what has been done and is being done in omics-relevant studies.




## Branches and Types of Omics

The primary goal of the omics sciences is to identify, characterize, and measure the biomolecules and molecular mechanisms that underpin the structure and functionality of cells and tissues. The term "omics" refers to a loose category of scientific fields that include many biological disciplines with titles that finish in "omics," such proteomics, metabolomics, genomics, etc. Moreover, there is the term Ome, such as the genome, proteome, or metabolome, where the first scientists to extensively use the "-ome" suffix were bioinformaticians and molecular biologists (Cambridge, UK).

The sciences of omics include numerous branches. Proteomics, metabolomics, and genomics are a few well-established areas. Proteomics is the study of the full collection of proteins found in

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an organism's cells, known as the proteome, whereas genomics examines the structure and function of an organism's genome, or its whole set of genes. The study of metabolism, and more especially the roles and relationships between metabolites—products of metabolic breakdown—is known as metabolomics. Other areas of omics include lipidomics, which is concerned with lipids and the pathways involved in lipid signaling, and transcriptomics, which is the study of all the RNA found in an organism's cells. The area of interactomics, which combines biology and bioinformatics to study the interactions and interplay between proteins and other molecules as well as the relevance of those interactions, is a prime example of the interdisciplinary character of the omics sciences.

Any of a number of biological fields distinguished by the comprehensive examination of a particular biomolecule's complement or the entirety of a molecular process within an organism. The term "omics" in biology describes the total number of components in a cell.

> **The primary goal of the omics sciences is to identify, characterize, and measure the biomolecules and molecular mechanisms that underpin the structure and functionality of cells and tissues.**

## Varieties of Genetics

- Genomics: The study of genome structure, function, evolution, and mapping. Its goal is to characterize and quantify genes, which, with the help of messenger molecules and enzymes, control the synthesis of proteins.

- Cognitive genomics: The study of how genetic profiles can alter cognitive functions.

- Comparative genomics: Analyzing the connections between genome structure and function among various biological species or strains.

- Functional genomics: Explains the relationships and roles of genes and proteins (typically uses transcriptomics). Function-based genomics aims to provide answers on the role of DNA in genes, RNA transcripts, and protein products.

- Personal genomics: A subfield of genomics concerned with individual genome sequencing and analysis.

 ISSN 3397-2974 (Print) - ISSN 3400-2974 (online)

- Metagenomics: The study of metagenomes, or genetic material extracted straight from environmental specimens.

- Neurogenomics: The study of how genes affect the growth and operation of the neurological system.

- Pangenomics: The study of all the genes or genomes present in a specific species.

- Transcriptomics: A single cell, tissue, or organism's transcriptome is its collection of all messenger RNA molecules. In addition to the chemical IDs, it also contains the quantity or concentration of every RNA molecule.

- Proteomics: The total amount of proteins in a cell, tissue, or organism is referred to as its proteome. The study of these proteins' biochemical characteristics, functional roles, and the ways in which their amounts, changes, and structures alter during development and in response to both internal and external stimuli is known as proteomics.

- Metabolomics: is the scientific field that examines all chemical reactions involving metabolites is called. Metabolome, more precisely, is the study of all small-molecule metabolite profiles and the chemical fingerprints that particular biological processes leave behind while they are active.

- Epigenomics: is the study of all epigenetic alterations on a cell's genetic material, or the epigenome. The genome can be instructed what to do by a wide range of chemical molecules known as the epigenome.

- Pharmacogenomics and nutrigenomics: Personalized responses to drugs and nutrients are studied in the fields of pharmacogenomics and nutritional genomics.

- "Numerous other "Omics" include: lipidomics, glycogenomics, pharmacogenomics, toxicogenomics, connectomics, and foodomics".

## Developments and Patterns in Omics Technology

Throughout human history, there has been a swift increase in technology like mass spectrometry and high-throughput sequencing, which have given rise to the notion of "omics" and improved methods for methodically examining cellular systems. However, the increasing diversity of chemicals and regulatory mechanisms that are being found keeps changing our knowledge of the functioning of cells. This makes cell omics appear to be infinitely expanding, much like the universe, and makes our objective of fully harnessing the biological system all but unachievable. In order to forecast what can be

 ISSN 3397-2974 (Print) - ISSN 3400-2974 (online)

done towards the translation of omics information to disease control with the least amount of cell disturbance, it is necessary to assess what has been done and is being done. We outline the hierarchies of these omics, together with their epiomics and interactomics, and examine technology created for interrogation, with an emphasis on the "four big omics," or genomes, transcriptomics, proteomics, and metabolomics.

## Technology-Based Omics

The fundamental experimental methods available to us in our exploration of the omics of a particular biological system are mass spectrometry (MS) and sequencing. Proteome, metabolome, and interactomes that do not involve DNA/RNA can be examined using MS-based techniques, whereas sequencing-based procedures are viable for studies on the

genome, transcriptome, their epitomes, and interactomes including DNA/RNA.

## a. The Genomics

By sequencing the target genome, genomic techniques are used to study inter-individual differences at the germline and somatic levels. The ability to sequence the entire genome or exome with enough depth to characterize the mutational landscape of a given sample has been made possible by advancements in DNA microarray technology (Thomas et al., 2020), first generation Sanger sequencing (Moniruzzaman et al., 2020), second generation massively parallel sequencing, also known as the next generation sequencing (NGS) (Chen et al., 2021), and ultimately third generation long reads sequencing (TGS) (Ou et al., 2020). When thousands of probes were affixed to a surface and samples were labelled with fluorescent dyes for identification following hybridization, (Schena et al., 1995) first developed the DNA microarray method (Kinaret et al., 2020). DNA microarrays are classified into two types: 1-channel and 2-channel arrays. The common commercial arrays are Affymetrix GeneChip (Graham et al., 2011), which is for 1 channel, and Agilent (Painter et al., 2013), which is for 2 channels. After hybridising both samples, labelled with two types of fluorescent dyes like Cy®5 and Cy®3, on the array, the gene expression of the treated sample

 ISSN 3397-2974 (Print) - ISSN 3400-2974 (online)

relative to the control is quantified by the ratio of the 2-channel intensities of each spot (Smyth and Altman, 2013). The fluorescence-labeled sample cDNAs are hybridised in a 1-channel array using oligonucleotide probes that are synthesised on the slide surface. The total intensity of the hybridization signal is then measured (Liu et al., 2010). Illumina BeadArray creates barcoded probes on the surface of microbeads as an adaptation of the 1-channel array (National Center for Biotechnology Information, 2022). Given the availability of several well-established experimental platforms and analytical tools, DNA microarray technology is rather mature (Slonim and Yanai, 2009). However, because DNA microarray technologies rely on probes made in accordance with known nucleotide sequences, their primary limitation is their inability to detect transcripts created from scratch. Additionally, the high frequency of cross-hybridization events in highly repetitive genomes makes DNA microarray an unfeasible platform for analysing genomes with high levels of repetition, since it can result in erroneous signal intensity estimation (Draghici et al., 2006).

## b. The Microbiomics

In microbiomics, all of the microorganisms in a given environment—referred to as the microbiome—are analyzed to determine the possible role that these microorganisms may play in diseases. This is done by gathering, characterizing, and quantifying the molecules responsible for the structure, function, and dynamics of a microbial community through the integration of multiple omics information, such as genomics, transcriptomics, proteomics, and metabolomics (Marchesi and Ravel, 2015 and Kumar, 2021). Trillions of bacteria live inside the human body and interact with their host to form the human microbiome, which was discovered in 2008 through the human microbiome project (Hawkins and O'Doherty, 2011). Strong links have been found between human diseases and microbiomes, according to data from rodent models of microbiome research (Chen et al., 2010). Microbiomes can offer special insights into human diseases, as they have been shown to be remarkably adept at examining and modifying the communities that coexist with humans (Grice and Segre, 2012).

 ISSN 3397-2974 (Print) - ISSN 3400-2974 (online)

## C. The Transcriptomics

Transcriptome, in contrast to genome, is dynamic and made up of various players. It is impacted by changes brought about by the stage of cell development, internal and/or external stimuli, and the measurement time of the signals. Although the term "transcriptome" generally refers to mRNA transcripts, it can also be used to refer to other transcript types, such as circular RNAs (circRNA), long non-coding RNAs (lncRNAs), and microRNAs. The goal of transcriptomics methods is to identify and measure RNA molecules that are being transcribed from a specific genome at a certain moment (Wang et al., 2009).

## d. The Epigenomics

One important regulatory mechanism on gene transcription is explained by epigenomics, which describes changes in the regulation of gene activity that function without changing genetic sequences (Piunti and Shilatifard, 2016). It includes the identification of DNA/RNA modifications such DNA/RNA methylation and higher-level chromatin structure, which together make up the DNA-DNA interactome (Wang and Chang, 2018).

## e. The Epitranscriptomics

While RNA modification focuses on altered nucleotides in mRNA, epitranscriptomics aims to clarify

the role of RNA structure and changes in controlling gene expression (Anreiter et al., 2021).

There are three types of sequencing-based approaches for mapping RNA structures: chemical-based in vivo methods, enzyme-based in vitro methods, and sequencing-based in vitro methods (Nguyen et al., 2018). The following are examples of enzyme-based in vitro techniques: protein interaction profile sequencing (PIP-seq) (Kramer and Gregory, 2019), fragmentation sequencing (FragSeq) (Uzilov and Underwood, 2016), parallel analysis of RNA structures with temperature elevation (PARTE) (Wan et al., 2012), and parallel analysis of RNA structure (PARS) (Kertesz et al., 2010). With the use of epitranscriptomic sequencing tools, we have been able to better comprehend biological systems, including a prototype baculovirus (Torma et al., 2022), by profiling the landscape of epitranscriptomic RNA changes (Pichot et al., 2021).

 ISSN 3397-2974 (Print) - ISSN 3400-2974 (online)

## f. The DNA-RNA Interactomics

Numerous tools have been developed to study the DNA-RNA interactome in light of the prevalence of interactions between DNA and RNA at transcription start sites (Li et al., 2017 and Sridhar et al., 2017), the diversity of chromatin-RNA interaction modes (Engreitz et al., 2013, Colak et al., 2014 and Miao et al., 2018), and the strong association between RNA-chromatin attachment and histone modification events like H3K27ac and H3K4me3 (Sridhar et al., 2017). These methods fall into two categories: mapping all chromatin-interaction RNAs along with their genomic interacting areas, and mapping the genome-wide locations of a particular RNA.

## g. The RNA-RNA Interactomics

Because of the RNA kingdom's diversity, adaptability, and complexity in terms of RNA kinds and molecular functions, RNA-RNA interactomics is a distinct omics layer that has garnered a lot of interest. By examining the RNA-RNA interactome, we have been able to build the higher-order transcriptome structure of living cells, which has facilitated the identification of lncRNA structures and functions (Lu et al., 2016). We have also been able to define the fundamentals of RNA interactions with other RNAs in ribosome biogenesis and gene regulation (Aw et al., 2016), as well as uncover new interactions between snoRNAs and mRNAs (Sharma et al., 2016).

## h. The Interactomics of DNA-Proteins

Protein-DNA interactions are essential for converting genetic information into functions. Electrophoretic mobility shift assays, DNase footprinting, ChIP, and systematic evolution of ligands by exponential enrichment (SELEX) are among the techniques used to characterise these interactions. Nevertheless, their applicability is limited if the DNA is not damaged.

## i. The Protein-Protein Interactomics

The most common and thoroughly researched molecular interactions in cells are protein-protein interactions (PPIs). Yeast two hybrid (Y2H) screening is the first high-throughput technique used for PPI detection. It operates by dividing two functional domains of a single TF that triggers signals when brought close together (Fields and Song, 1989). Y2H screening is time-consuming and is unable to detect many protein complexes in a single run (Lathouwers et al., 2018). This new technology has been used to screen candidate antibodies that are able to compete with the spike receptor-binding domain (RBD) of SARS-CoV-2 for human angiotensin-converting enzyme 2 (ACE2), as it can characterize the competitive binding of proteins for specific epitopes in addition to direct PPIs (Hunt et al., 2021).


ISSN 3397-2974 (Print) - ISSN 3400-2974 (online)

## j. The Protein- Metabolite Interactomics

In the normal state, protein-metabolite interactions are crucial for preserving cell homeostasis and coordinating the body's reactions to stress or disturbances from the outside or inside. The interactions between proteins and metabolites are common in cells, which are thought to number in the millions (Bennett et al., 2009, Milo, 2013 and Veenstra, 2021). Novel enzyme-substrate relationships and instances of metabolite-induced protein complex remodeling have been discovered through the analysis of the protein-metabolite interactome (Piazza et al., 2018). Additionally, a variety of proteins involved in lipid pathways have been pharmacologically characterized in mammalian cells, including the identification of a selective ligand for NUCB1, a substance that disrupts the hydrolytic and oxidative metabolism of endocannabinoids in cells (Niphakis et al., 2015).

## Data management and technology

Software and databases that enable sophisticated integrated analyses, along with a variety of high-throughput (automated) biochemical experiments, are essential technologies in the field of omics sciences. For instance, next-generation sequencing and tests made to find genetic variants are crucial to the identification and characterization of genes in the field of genomics. In the field of transcriptomics, microarray analysis and RNA sequencing are equally important, and methods such as liquid chromatography, mass spectrometry, and microarray are em-


ISSN 3397-2974 (Print) - ISSN 3400-2974 (online)

ployed in the identification and characterization of proteins. Large volumes of data are produced by these high-throughput experiments, which can be utilized for modelling and other types of analysis, but they also pose storage issues. To store and make publicly available the data from omics studies, several databases have been built. The ProteomeXchange Consortium, the Human Metabolome Database, the Proteomics Identifications Database, the International Cancer Genome Consortium, and the Cancer Genome Atlas are a few examples.

## Challenges

In medicine, the effects of omics are most noticeable. For example, the sequencing of the human genome has accelerated the field of personalized medicine, where patients' needs are taken into account when making decisions regarding illness prevention, diagnosis, and treatment. This is done by using data from genetic and genomic research. Specifically, genetic information has been crucial in the creation of illness prediction models and in guiding treatment choices, including those for cancer. New disease biomarkers found through metabolomics have revealed similar connections between omics and personalized therapy. One instance is the study of disruptions in metabolic pathways that impact the amounts of chemicals like fatty acids and bile acids; this, has produced biomarkers that may

help in the early detection of hepatocellular carcinoma. However, there are still a lot of issues in the omics sciences, particularly with regard to data administration, data complexity, and integrating data from omics studies with data from other sources, like clinical data collected during standard doctor visits. Some obstacles, including assay development and refinement, are more fundamental in nature. Agents intended to bind to certain proteins, for example, frequently have low sensitivity and specificity in large-scale proteomic analysis, which lowers their affinity for the target proteins and leads to less-than-ideal protein capture (Alaterre et al., 2021, Jiang et al., 2021, Liu et al., 2021 and Qu et al., 2021).


ISSN 3397-2974 (Print) - ISSN 3400-2974 (online)

# Conclusion

Systems biology is a broad and in-depth quantitative study of how every interaction among all the parts of a biological system functions. These analyses are conducted by researchers from several disciplines (biology, computer science, engineering, bioinformatics, physics, immunology, and neuroscience), who can also build the necessary technologies and computational tools. Automated DNA sequencers offer genome sequencing and polymorphism detection; transcript analysis is done by microarrays; proteomic and metabolomics profiling is made possible by MS. These high throughput techniques yield a vast amount of biological data on the functional and/or structural changes within the cell, including genetic sequences, cell populations, and protein samples. These enormous amounts of data are analyzed using a computational approach that combines bioinformatics and computational biology. Through the use of these approaches, all genome information offers insight into the functioning of cells within biological systems. By examining the connections between many components, systems biology and omics technologies jointly offer a global understanding of the mechanisms and provide useful flow information on biological systems. Even with a thorough grasp of each component alone, a total comprehension of the entire system cannot be predicted by its constituent parts. A holistic approach to systems biology and omics technology provides thorough and useful information that helps overcome obstacles in a variety of contexts,

## Recommendations

Technologies related to omics and omics offer a number of benefits and drawbacks. Therefore, it is preferable to do more than one or two omics jointly in order to solve the problems originating from distinct omics. The key is to choose a way that can overcome the drawbacks of a different approach. Moreover, care should be taken in the integration and interpretation of data.


ISSN 3397-2974 (Print) - ISSN 3400-2974 (online)

# References


1. Alaterre E, Vikova V, Kassambara A, Bruyer A, Robert N, Requirand G, et al. RNA-sequencing-based transcriptomic score with prognostic and theranostic values in multiple myeloma. J Pers Med. (2021) 11:988. doi: 10.3390/jpm11100988

2. Anreiter I, Mir Q, Simpson JT, Janga SC, Soller M. New twists in detecting mRNA modification dynamics. Trends Biotechnol. (2021) 39:72–89. doi: 10.1016/j.tibtech.2020.06.002

3. Aw JG, Shen Y, Wilm A, Sun M, Lim XN, Boon KL, et al. In vivo mapping of eukaryotic rna interactomes reveals principles of higher-order organization and regulation. Mol Cell. (2016) 62:603–17. doi: 10.1016/j.molcel.2016.04.028

4. Bennett BD, Kimball EH, Gao M, Osterhout R, Van Dien SJ, Rabinowitz JD. Absolute metabolite concentrations and implied enzyme active site occupancy in Escherichia coli. Nat Chem Biol. (2009) 5:593–9. doi: 10.1038/nchembio.186

5. Chakraborty S, Hosen MI, Ahmed M, Shekhar HU. Onco-multi-OMICS approach: a new frontier in cancer research. Biomed Res Int. (2018) 2018:9836256. doi: 10.1155/2018/983625

6. Chen T, Yu WH, Izard J, Baranova OV, Lakshmanan A, Dewhirst FE. The Human Oral Microbiome Database: a web accessible resource for investigating oral microbe taxo-

nomic and genomic information. Database. (2010) 2010: baq013. doi: 10.1093/database/baq013

7. Chen X, Dong Y, Huang Y, Fan J, Yang M, Zhang J. Whole-genome resequencing using next-generation and Nanopore sequencing for molecular characterization of T-DNA integration in transgenic poplar 741. BMC Genomics. (2021) 22:329. doi: 10.1186/s12864-021-07625-y

8. Colak D, Zaninovic N, Cohen MS, Rosenwaks Z, Yang WY, Gerhardt J, et al. Promoter-bound trinucleotide repeat mRNA drives epigenetic silencing in fragile X syndrome. Science. (2014) 343:1002–5. doi: 10.1126/science.1245831

9. Draghici S, Khatri P, Eklund AC, Szallasi Z. Reliability and reproducibility issues in DNA microarray measurements. Trends Genet. (2006) 22:101–9. doi: 10.1016/j.tig.2005.12.005

10. Engreitz JM, Pandya-Jones A, McDonel P, Shishkin A, Sirokman K, Surka C, et al. The Xist lncRNA exploits three-dimensional genome architecture to spread across the X chromosome. Science. (2013) 341:1237973. doi: 10.1126/science.1237973

11. Fields S, Song O. A novel genetic system to detect protein-protein interactions. Nature. (1989) 340:245–6. doi: 10.1038/340245a0

12. Graham NS, May ST, Daniel ZC, Emmerson ZF, Brameld JM, Parr T. Use of the Affymetrix Human GeneChip array and genomic DNA hybridisation probe selection to study ovine transcriptomes. Animal. (2011) 5:861–6. doi: 10.1017/S1751731110002533

13. Grice EA, Segre JA. The human microbiome: our second genome. Annu Rev Genomics Hum Genet. (2012) 13:151–70.doi:10.1146/annurev-genom-090711-163814

14. Hawkins AK, O'Doherty KC. "Who owns your poop?": insights regarding the intersection of human microbiome research and the ELSI aspects of biobanking and related studies. BMC Med Genom. (2011) 4:72. doi: 10.1186/1755-8794-4-72

15. Hunt AC, Vögeli B, Kightlinger WK, Yoesep DJ, Krüger A, Jewett MC, et al. High-throughput, automated, cell-free expression and screening platform for antibody discovery. bioRxiv. (2021) 31:392–403. doi: 10.1101/2021.11.04.467378

16. Jiang L, Wang N, Cheng S, Liu Y, Chen S, Wang Y, et al. RNA-sequencing identifies novel transcriptomic signatures in intestinal failure-associated liver disease. J Pediatr Surg. (2021) 2021: S0022-346800846-0. doi: 10.1016/j.jpedsurg.2021.12.015

17. Kertesz M, Wan Y, Mazor E, Rinn JL, Nutter RC, Chang

HY, et al. Genome-wide measurement of RNA secondary structure in yeast. Nature. (2010) 467:103–7. doi: 10.1038/nature09322

18. Kinaret PAS, Serra A, Federico A, Kohonen P, Nymark P, Liampa I, et al. Transcriptomics in toxicogenomics, part i: experimental design, technologies, publicly available data, and regulatory aspects. Nanomaterials. (2020) 10:750. doi: 10.3390/nano10040750

19. Kramer MC, Gregory BD. Using protein interaction profile sequencing (PIP-seq) to identify RNA secondary structure and RNA-protein interaction sites of long noncoding RNAs in plants. Methods Mol Biol. (2019) 1933:343–61. doi: 10.1007/978-1-4939-9045-0_21

20. Kumar PS. Microbiomics: were we all wrong before? Periodontology. (2021) 85:8–11. doi: 10.1111/prd.12373

21. Lathouwers T, Wagemans J, Lavigne R. Identification of protein-protein interactions using pool-array-based yeast two-hybrid screening. Methods Mol Biol. (2018) 1794:29–48. doi: 10.1007/978-1-4939-7871-7_3

22. Li X, Zhou B, Chen L, Gou LT, Li H, Fu XD. GRID-seq reveals the global RNA-chromatin interactome. Nat Biotechnol. (2017) 35:940–50. doi: 10.1038/nbt.3968

23. Liu H, Bebu I, Li X. Microarray probes and probe sets. Front Biosci. (2010)2:325–38.doi:10.2741/e93
24. Liu Y, Wu Y, Liu B, Zhang Y, San D, Chen Y, et al. Biomarkers

and immune repertoire metrics identified by peripheral blood transcriptomic sequencing reveal the pathogenesis of COVID-19. Front Immunol. (2021) 12:677025. doi: 10.3389/fimmu.2021.677025

25. Lu Z, Zhang QC, Lee B, Flynn RA, Smith MA, Robinson JT, et al. RNA duplex map in living cells reveals higher-order transcriptome structure. Cell. (2016) 165:1267–79. doi: 10.1016/j.cell.2016.04.028

26. Marchesi JR, Ravel J. The vocabulary of microbiome research: a proposal. Microbiome. (2015) 3:31. doi: 10.1186/s40168-015-0094-5

27. Miao Y, Ajami NE, Huang TS, Lin FM, Lou CH, Wang YT, et al. Enhancer-associated long non-coding RNA LEENE regulates endothelial nitric oxide synthase and endothelial function. Nat Commun. (2018) 9:292. doi: 10.1038/s41467-017-02113-y

28. Milo R. What is the total number of protein molecules per cell volume? A call to rethink some published values. Bioessays. (2013) 35:1050–5. doi: 10.1002/bies.201300066

29. Moniruzzaman M, Hossain MU, Islam MN, Rahman MH, Ahmed I, Rahman TA, et al. Coding-complete genome sequence of SARS-CoV-2 isolate from Bangladesh by Sanger Sequencing. Microbiol Resour Announc. (2020) 9:e00626–e0. doi: 10.1128/MRA.00626-20

30. National Center for Biotechnology Information. Bead Ar-

rays. Available online at: https://www.ncbi.nlm.nih.gov/probe/docs/techbeadarray (accessed 31 March, 2022).

31. Nguyen TC, Zaleta-Rivera K, Huang X, Dai X, Zhong S RNA. Action through Interactions. Trends Genet. (2018) 34:867–82. doi: 10.1016/j.tig.2018.08.001

32. Niphakis MJ, Lum KM, Cognetta AB 3rd, Correia BE, Ichu TA, Olucha J, et al. A global map of lipid-binding proteins and their ligandability in cells. Cell. (2015) 161:1668–80. doi: 10.1016/j.cell.2015.05.045

33. Ou YJ, Ren QQ, Fang ST, Wu JG, Jiang YX, Chen YR, et al. Complete genome insights into Lactococcus petauri CF11 isolated from a healthy human gut using second- and third-generation sequencing. Front Genet. (2020) 11:119. doi: 10.3389/fgene.2020.00119

34. Painter HJ, Altenhofen LM, Kafsack BF, Llinas M. Whole-genome analysis of Plasmodium spp. Utilizing a new agilent technologies DNA microarray platform. Methods Mol Biol. (2013) 923:213–9. doi: 10.1007/978-1-62703-026-7_14

35. Piazza I, Kochanowski K, Cappelletti V, Fuhrer T, Noor E, Sauer U, et al. A map of protein-metabolite interactions reveals principles of chemical communication. Cell. (2018) 172:358–72 e23. doi: 10.1016/j.cell.2017.12.006

36. Pichot F, Marchand V, Helm M, Motorin Y. Non-redun-

dant tRNA reference sequences for deep sequencing analysis of tRNA abundance and epitranscriptomic RNA modifications. Genes. (2021) 12:81. doi: 10.3390/genes12010081

37. Piunti A, Shilatifard A. Epigenetic balance of gene expression by Polycomb and COMPASS families. Science. (2016) 352:aad9780. doi: 10.1126/science.aad9780

38. Qu R, He K, Fan T, Yang Y, Mai L, Lian Z, et al. Single-cell transcriptomic sequencing analyses of cell heterogeneity during osteogenesis of human adipose-derived mesenchymal stem cells. Stem Cells. (2021) 39:1478–88. doi: 10.1002/stem.3442

39. Schena M, Shalon D, Davis RW, Brown PO. Quantitative monitoring of gene expression patterns with a complementary DNA microarray. Science. (1995) 270:467–70. doi: 10.1126/science.270.5235.467

40. Sharma E, Sterne-Weiler T, O'Hanlon D, Blencowe BJ. Global mapping of human RNA-RNA interactions. Mol Cell. (2016) 62:618–26. doi: 10.1016/j.molcel.2016.04.030

41. Slonim DK, Yanai I. Getting started in gene expression microarray analysis. PLoS Comput Biol. (2009) 5:e1000543. doi:10.1371/journal.pcbi.1000543

42. Smyth GK, Altman NS. Separate-channel analysis of

two-channel microarrays: recovering inter-spot information. BMC Bioinformatics. (2013) 14:165. doi: 10.1186/1471-2105-14-165

43. Sridhar B, Rivas-Astroza M, Nguyen TC, Chen W, Yan Z, Cao X, et al. Systematic mapping of RNA-chromatin interactions in vivo. Curr Biol. (2017) 27:610–2. doi: 10.1016/j.cub.2017.01.068

44. Thomas R, Pontius JU, Borst LB, Breen M. Development of a genome-wide oligonucleotide microarray platform for detection of DNA copy number aberrations in feline cancers. Vet Sci. (2020) 7:88. doi: 10.3390/vetsci7030088

45. Torma G, Tombacz D, Moldovan N, Fulop A, Prazsak I, Csabai Z, et al. Dual isoform sequencing reveals complex transcriptomic and epitranscriptomic landscapes of a prototype baculovirus. Sci Rep. (2022) 12:1291. doi: 10.1038/s41598-022-05457-8

46. Uzilov AV, Underwood JG. High-throughput nuclease probing of RNA structures using FragSeq. Methods Mol Biol. (2016) 1490:105–34. doi: 10.1007/978-1-4939-6433-8_8

47. Veenstra TD. Omics in systems biology: current progress

and future outlook. Proteomics. (2021) 21:e2000235. doi: 10.1002/pmic.202000235

48. Wan Y, Qu K, Ouyang Z, Kertesz M, Li J, Tibshirani R, et al. Genome-wide measurement of RNA folding energies. Mol Cell. (2012) 48:169–81. doi: 10.1016/j.molcel.2012.08.008

49. Wang KC, Chang HY. Epigenomics: technologies and applications. Circ Res. (2018) 122:1191–9. doi: 10.1161/CIRCRESAHA.118.310998

50. Wang Z, Gerstein M, Snyder M. RNA-Seq: a revolutionary tool for transcriptomics. Nat Rev Genet. (2009) 10:57–63. doi: 10.1038/nrg2484

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