INNSPUB

International Journal of Biosciences | IJB |
ISSN: 2220-6655 (Print) 2222-5234 (Online)
http://www.innspub.net
Vol. 25, No. 3, p. 40-57, 2024

REVIEW PAPER OPEN ACCESS

Recent advancements in transcriptomics and its application in basic medical and clinical sciences

Shafee Ur Rehman*[1], Kudaibergen Osmonaliev[1], Dawood Khan[2], Lobzova Aleksandra[1], Atta Ur Rahman[3], Inamur Rehman[4]

[1]*Faculty of Medicine, Ala-Too International University, Bishkek, Kyrgyzstan*

[2]*Spinghar Institute of Higher Education, Jalalabad, Afghanistan*

[3]*Animal Resources Department, Ministry of Municipality State of Qatar*

[4]*Semey Medical University, Abai Street 103, Semey, Kazakhstan*

Key words: Transcriptome, RNA, Medical, Clinical, Diseases

http://dx.doi.org/10.12692/ijb/25.3.40-57 Article published on September 05, 2024

Abstract

Transcriptomics or transcriptome profiling emerged as one of the major powerful approaches in the science of medicine and clinical practices. Over the last decades, the application of transcriptome has been significantly applied in oncology, cardiology, gastro infection, and pathogenic diseases. Advancements in sequencing technologies like RNA sequencing, biomarkers, gene signature, expression profiling of genes, and their aberrant expression affect disorders. Further, the application of transcriptomics also includes the discoveries of molecular targeted therapies for numerous disorders. The contribution of transcriptomics in medicine and clinical sciences has revolutionized the understanding of the nature of the disease, biological and molecular pathways, and insight into personalized medicine and therapies for many disorders. This essay could explore the current state of transcriptome technology in medicine and clinical sciences. It could discuss the techniques, such as RNA sequencing, and their potential applications for understanding diseases and developing new treatments. Additionally, the essay could delve into the ethical considerations surrounding transcriptome technology and its use in research and clinical practice. Furthermore, advancement in transcriptomics application may allow standardization and cost reduction analysis which should make transcriptomics one of the significant contemporary in the field of medicine and clinical sciences.

* **Corresponding Author:** Shafee Ur Rehman ✉ shafeeur.rehman@alatoo.edu.kg

Introduction

The science of transcriptomics including the analysis of products and pathways involved in the cell, it include the expression of mRNA, Non-coding RNA (Sendinc and Shi, 2023). In other words it is the measurement of products like amino acid, nucleotides co-factors and fatty acid. In molecular sciences the transcriptomics and its development from last 15 years play critical role.

Although whole transcriptome including mRNA, and other non-coding RNA and the expression mechanism and analysis through bioinformatics approaches. Various bioinformatics tools are used to quantify and functional analysis of the different transcripts of the cells (LaRossa, 2013).

The central phenomenon of molecular biology is understanding the structure of proteins, the expression of genes and the pathways of gene expression. Modern biological techniques have helped the scientific community to understand gene expression and its function (Tian *et al.,* 2023). The main functional study of genes is to study the type of genetic codes in genes for amino acids that make phenotypes (Tian *et al.,* 2023). Transcriptomics dramatically revolutionized the study of gene expression. Transcriptome makes it easier to study the genome, RNA and gene expression (Wang *et al.,* 2023). Transcriptome is the term used for the RNA produced by a single cell or tissue (Miranda *et al.,* 2023). Recent developments in technology significantly unveiled the complexity of transcriptome. In the study of genome function, transcriptome is the primary product of the genome (Fig. 1).

The human genome sequencing was done a long time ago, but the research on the genome continues. Now, the researchers are trying to understand better the mechanisms of gene expression, that is, how? When? The gene is expressed in healthy individuals and patients. Recently, much effort was carried out to measure gene expression. The term transcriptome is used for the total RNA expressed. In clinical and medical sciences, transcriptomes play a key tool in understanding the mechanism of gene expression. The study of gene expression in pathogenesis, cancer, cardiovascular disorders and genetic disorders is the key to understanding the molecular mechanism at cellular, tissue and organ levels (Wheeler and Wang, 2023).

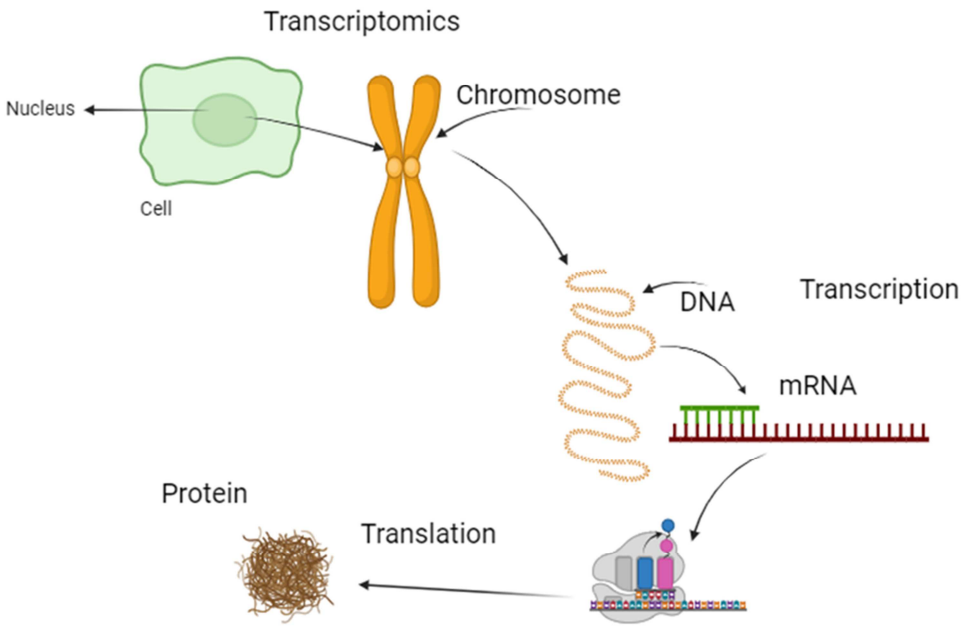

Fig. 1. Schematic view of gene expression in eukaryotic cells

The DNA or heredity materials are present in the nucleus; the coding region of DNA is known as genes with information for a protein molecule. The DNA molecule is transcribed into mRNA, and ribosomes translate the RNA into Protein. Development in genomic technologies provides possibilities to understand the variation that occurs in DNA/RNA over time or in response to a challenge. Genomic information is the fundamental tool to understand the blueprint of cell tissue and organs (Li *et al.,* 2023). Transcriptomics technology provides significant information about gene expression and phenotypes. Medicine and clinical studies around the globe mostly lack molecular information. However, recent advances in transcriptome have changed the terminology of clinical and medical practices performing analysis at the molecular level (Fan *et al.,* 2023). Transcriptomics in basic clinical and medical sciences provide the development of targeted medicine, clinical diagnosis and production and enhancement of precise medicine in multiple disorders (Long and Du, 2023). This review was designed to study the current application of Transcriptome technology in medicine and clinical sciences.

Profiling of transcriptome, transcriptomics

In the field of genetics, transcriptome term is used to understand the complete set of total RNA in a cell or tissue. In transcriptomics different types of RNA (mRNA, tRNA, rRNA, microRNA, non-coding RNA, etc.) are identified, and their function and expression pattern are investigated (Wang *et al.,* 2023). Moreover, transcriptomics focus on the expression and regulation of transcripts at different levels in cell or tissue. Various methods are used in transcriptomics. Some common methods are RNA sequencing and genechips, which involve measuring gene expression on microarray (Wang *et al.,* 2023). Genechip method mainly focuses on mRNA, which encodes a protein, genechips methods need to pre design means the content on the array is based on the preexisting knowledge about the exons, which can easily be detected in genome data (Zhao *et al.,* 2023).

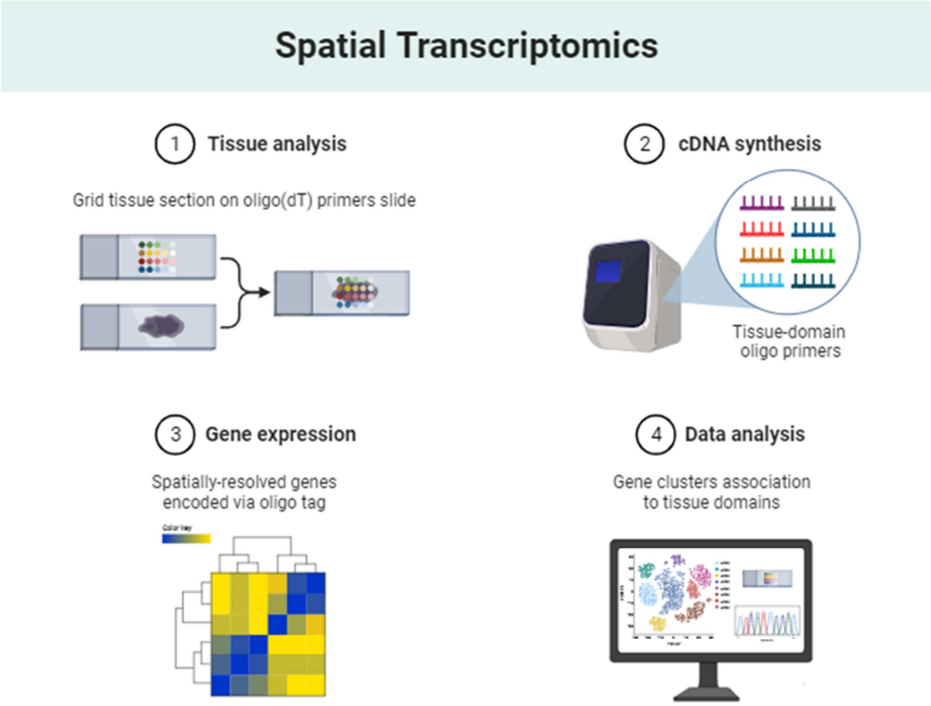

Fig. 2. Illustration of transcriptomic approaches and analysis of transcription

Genechips method provides us a snapshot of the transcriptional changes of mRNA, although the analysis of genechips method is limited. Some advanced arrays, like transcript based and tiling arrays, give us more comprehensive information about the transcriptional changes. However, the

arrays are limited to preexisting data and do not provide new information about the transcriptome and the sequence data (Fig. 2). Therefore, the informative data about the sequence is lost (Jang *et al.,* 2023). Although some genechip methods provide information about alternative gene expression, more specialized chips are needed to design, which give us information about sequences such as micro-RNA (Jang *et al.,* 2023). Most important sequences are lost in genechips method. Hence RNA sequencing is a significant tool to investigate the transcriptome in detail. Hence, RNA sequencing has become a significant method in Transcriptomics studies (Wang *et al.*, 2023; Zhang *et al.*, 2023).

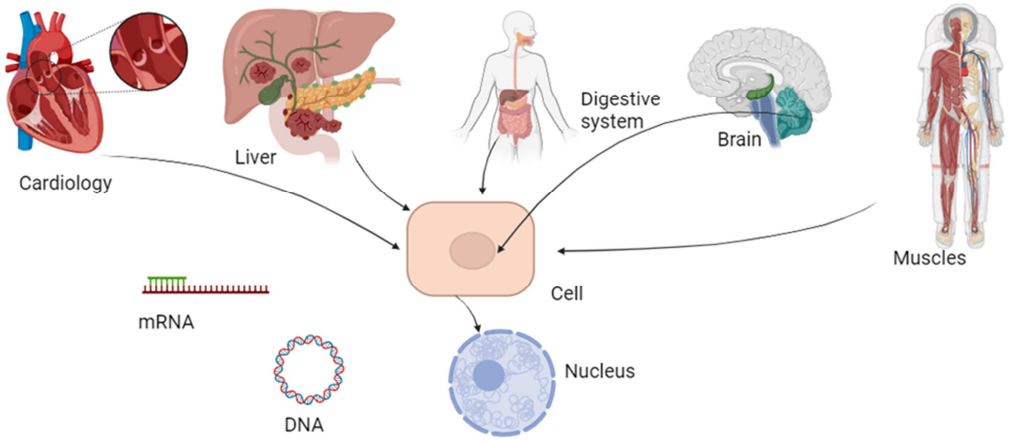

Fig. 3. Schematic view of different sources from where we can extract RNA, further the digram also shown the expression of genes in different parts of human bod

Sources of the transcriptome

Environmental changes enhance the cell's ability to express genes according to the stimulus threshold. The key medical transcriptomics factor is identifying the affected tissue or cell (Fig. 3). The easiest way to justify the tissue affected is on the assumption of knowing the targeted tissue. For this, we need to understand the timeline and the pathological changes in the tissue. Although the assumption may be wrong, it is difficult to identify the affected tissue in some disorders, and the symptoms may be late, like in the central nervous system. So, the tissue can be identified by postmortem examination of the brain rather than waiting for symptoms. It may take years (Shi *et al.*, 2023; Brokowska *et al.*, 2023).

Although the analysis of disease tissue is important during the pathogenesis of the disease, sample repetition during the disease provides a significant analysis of the disease. Urine and blood sampling are important during disease diagnosis. Urine, blood, skin, and the microbiome enable us to study the transcriptomics during the treatment and diagnosis of the disorder (Magro *et al.*, 2024; Mohr *et al.*, 2024).

In complicated cases, mostly for transcriptomics analysis, tissue is obtained from surgical procedures at hospitals; this option is mostly applied in oncology (Ludwig *et al.,* 2023). Most of the samples for transcriptomics analysis were obtained from skin and blood. Studies have shown skin and blood are more significant than other tissues, even in complicated disorders like Parkinson (Hibi *et al.,* 2023). Blood and skin show clear transcriptomics differences in case-control studies; this tissue could be useful for diagnosing and treating diseases. Urine can also be used for transcriptomics analysis, but the limitation is low-quality transcriptomics due to the low concentration of RNA. Therefore, other fluids, like blood, are good sources of transcriptomics (Moufarrej and Quake, 2023).

RNA extraction and transcriptomics analysis from blood samples

The blood type of connective tissue is easy to access for transcriptomics analysis. Using blood for transcriptomics, a few basic decisions are needed to follow, like whole blood or particular parts of blood are used for transcriptomics analysis. PBMC or peripheral blood mononuclear cells are popular methods to isolate cells from blood and to use them for RNA analysis. But, only white blood cells are extracted in PBMC, not other types of cells. Therefore, using PBMC does not fulfil the need for transcriptomics analysis (Baliña-Sánchez *et al.,* 2023). Moreover, studies showed that whole blood is significant for transcriptomics analysis (Bamberg, 2023). Whole RNA isolation from blood could give greater advantages than PBMC (Bamberg, 2023).

Transcriptomics analysis generates huge amounts of data, so the complexity needs a suitable protocol for significant advantages. Moreover, sampling, storing, and transportation of tissue also needed proper protocol due to variation can be introduced. RNA extraction from biopsy, blood and other tissue need suitable methods. Transcriptomics analysis in clinical sciences needs proper gaudiness and standardized protocol. Other factors like storing also affect the quality of RNA, and recent studies have shown that RNA analysis from frozen tissue is more significant than formalin fixed paraffin embedded method (Schmøkel *et al.,* 2023). RNA extraction from fluid biopsy samples needs more work and extra effort (Pais *et al.,* 2023). Hence, proper methods and guidelines studies are needed to obtain significant results from transcriptomics analysis.

Recent advances in transcriptomics in medical sciences

According to research, about 93% of the human genome is transcribed into RNA, of which 2% is protein-coding RNA (Bai *et al.,* 2023). These molecules have information called genetic codes for amino acids, essential protein components (Wang *et al.,* 2024). The remaining RNAs play various roles in synthesizing tRNA rRNA and controlling miRNA, snRNA and snoRNA (Shimizu *et al.,* 2023). The study of these non-coding RNA could be useful for the treatment and diagnosis of many disorders. We have reviewed some recent transcriptomics studies in medical and clinical sciences here.

Cholesteatoma is a condition that mostly originates from tympanic membrane self-denial and is characterized by intractable local bone erosion, which leads to hearing loss and abscess brain formation. Recent studies have been conducted to investigate the single-cell transcriptomics analysis of the disorder. The study findings showed that expression of inhibin βA in large amounts causes the erosion of bone. The activin A, a homodimer of inhibin βA promotes osteoclast differentiation. The finding of this study suggested that activin A- producing fibroblast in the tissue of cholesteatoma resulted in bone destruction (Wang *et al.,* 2024).

Bulk and Single-cell RNA sequencing methods were performed in a recent study to investigate the craniofacial disorders arising during pregnancy. Tissue was obtained from 4-8 weeks post conception. Gene expression analysis was carried out to study the patterning of the craniofacial region. Other human tissue analyses revealed that 239 genes are significantly expressed during craniofacial development. The study identified 539 genes likely to contribute to craniofacial disorders, suggesting that high de novo mutation in these genes in orofacial clefting patients' needs more studies (Yankee *et al.,* 2023).

Kidney failure due to diabetics is one of the major cause of renal failure. Transcriptomics approach was used in recent research for the identification of gene expression analysis in human diabetic kidney disease. Tissue samples from diabetic kidney disease patients were taken and expression analysis were performed. The differentially expressed genes in diabetics kidney disease was 1831 in diabetic tubuli, 1700 in glomeruli and 330 were differentially expressed in both glomeruli and tubuli (Woroniecka *et al.,* 2011). Many glomerulus infection are caused due to injury in

Podocyte, glomerulus disease are also caused due to HIV, FSGS infection (Sakairi *et al.,* 2010). Transcriptomics approach was used to investigate the gene expression in Podocyte (Okamura *et al.,* 2013). The study revolved that ribosomal pathways was one of the enriched pathways that contribute to the expression of APOL1 variant induced podocyte injury (Yoshida *et al.,* 2023).

Diabetic's type I and II are the major cause of kidney failure (Thomas *et al.,* 2015). Due to available treatment and management of diabetics the disease record is reduced over the past 30 years, although the risk of renal failure is remain higher. Recent studies showed that diabetic kidney disease is common in families in different population worldwide this is due to genetics (Alicic et al., 2017; , Zhang *et al.,* 2023). Hence to deep understand the mechanism transcriptome application should be useful tool. A recent transcriptomics study on DKD, revolved the gene expression which are enriched with urogenital system development, platelet alpha granule, kidney development and glycosaminoglycan biding pathways (Zhang *et al.,* 2023).

Leishmaniasis is one of the significant tropical infections distribute worldwide, effecting human and other animal (Zhang *et al.,* 2023). There is no cure available although chemotherapy and other drugs are used, but in some patients resistant were observed to therapy. Currently a study was conducted to investigate the gene expression in host cell THP-1 after infection. The study showed that 58 differentially expressed genes were observed in THP-1 cell infected with leishmaniasis, the observed gene expression was similar to the other data published (Cheng *et al.,* 2023).

Liver fibrosis is one of the major caused of mortality worldwide. Many significant approaches were applied for the treatment and analysis of liver fibrosis (Addissouky *et al.,* 2024; Parola and Pinzani, 2024). Transcriptomics analysis of liver tissue samples were performed in a recent study. The transcriptomics data were compared with NASH data, the analysis shows the significant correlation between expression of protein and regulated genes. Moreover the data also shows significant changes in plasma (Zhao *et al.,* 2024).

Transcriptomics analysis from blood is significant approach for the detail study of phenotype and nature of disease in medical and clinical sciences. Recently transcriptomics analysis were performed of 3388 blood samples together with all other demographic factors. The results finds two major transcriptomics groups 1 and group 2. Group1 transcriptomics was common in men, elder and overweight individuals and the expression was associate with inflammation and heme metabolism enhancement. While type 2 transcriptome was found common in woman immune response, cellular function and ribosome and mitochondria (Schmidt *et al.,* 2020).

Transcriptomics in oncology

Mutation in some genes associated with cell division and cell growth causes cancer. Further epigenetic disorders also cause cancer (Stupp *et al.,* 2005; Hoogstrate *et al.,* 2023). Changes in DNA methylation lead to the spreading of helicobacter pylori, and inflammation leads to DNA methylation disorders. In cancer, DNA mutation and epigenetics are the major factors of neoplasia. Genetic changes are either inherited or due to environmental changes. In both cases, the changes lead to impairment in the function of genes, including proto oncogensis, DNA repair genes and Tumor suppressor genes (Kraboth and Kalman, 2020). Changes in these genes bring on cancer. Although each person has a unique genetic pattern, each person has a unique genetic variation related to cancer. Hence, cancer development in patients with unique characteristics. Therefore, for treatment and diagnosis, it is important to study the genetics of the patients (Fig. 4). Further, transcriptomics analysis of cancer could be a significant tool to study the mechanism and pathway of gene changes that lead to cancer. Some of the recent studies performed in cancer transcriptomics are as follows.

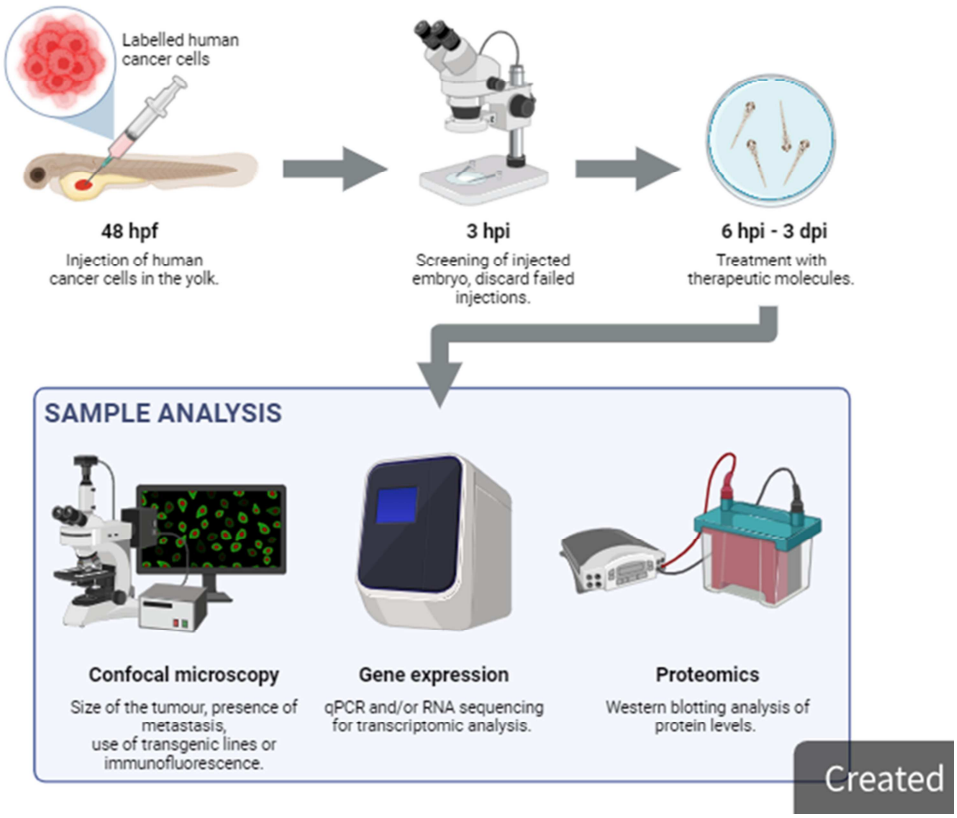

Fig. 4. Schematic view of cancer therapy, using RNA sequencing and Transcriptomics approaches

Studies in a patient with ovarian cancer found that over-expression of the P53 gene with missense mutation exhibits resistance to some chemotherapy procedures like platinum (Roy *et al.,* 2020; Draaisma *et al.,* 2020; Weller *et al.,* 2021). Another study suggested that over expression of collagen VI, XI alpha 1 and SUSD2 genes showed resistance to cisplatin chemotherapy (Wang et *al.,* 2017; Bai *et al.,* 2024). In breast cancer, studies have found that over expression of heat shock protein is resistant to drugs (Zhang and Bi, 2024). HER2, BARD1 and BARCA1 gene overexpression and genetic polymorphism in ABCC2 and CYP2D6 genes lead to resistance to tamoxifen drugs (Barthel *et al.,* 2019; Hoogstrate *et al.,* 2023). Patients with triple negative breast cancer have a heterogeneous tumour lacking progesterone receptor expression, human epidermal growth regulator factor and estrogen receptor. This type of cancer lacks therapy and is not sensitive to hormonal therapy or targeted therapy except chemotherapy. The researcher worldwide focuses on TNBC targeted therapy. Hence, transcriptomic analysis is used to identify possible therapeutic goals to improve the survival of patients (Mundi *et al.,* 2023; Glodzik *et al.,* 2023).

In oncology tumor heterogeneity is one of the major obstacle, and significant challenge for drugs discovery and development. Tumor identification its landscape and nature is the key factors provide useful tools for drug and treatment of cancer. In a recent research works a transcriptomics approach are applied for drug discovery profiling of four tissue sample and eighty thousand and twenty four different spot in different tissue (Fan *et al.,* 2020; Cao *et al.,* 2024). In cancer resistant to program cell death is one of hallmark. In drug discovery the PCD pathways and the molecule which crosstalk's between PCD Pathways impeding the development of targeted drug therapy (Bansal, 2023). PANoptosis is recently identified signaling pathways in PCD pathways. In a recent study gene expression and transcriptomics application were used to identify the gene expression in PANoptosis (Xiong, 2023). The result revolved high PANoptosis gene expression was found which

determined low grade glioma (LGG) and carcinoma of kidney renal cell (Wang *et al.,* 2024). The expression of ZBP1, CASP3, CASP4, ADAR, and CASP8and GSDMD showed negative effect on prognosis of LGL across multiple survival Models while CASP3, CASP4 and TNFRSF10 have negative effect on kidney renal carcinoma. However the expression of PANoptosis in skin was beneficial for cutaneous melanoma. The study further suggest biomarkers from PANoptosis which could be used as targeted for cancer therapy (Ocansey *et al.,* 2024).

Kidney allograft dysfunction is caused due to interstitial fibrosis and tubular atrophy which is the major cause of kidney allograft loss (Peng *et al.,* 2024). Currently transcriptomics approached was applied in a study on kidney allograft loss and healthy patients total of 23, 980 nuclei from kidney transplant patients and 17, 913 nucleoli from healthy people were isolated and transcriptomics analysis were performed. The results suggested that MT1 in injured tubular cell activate fibroblast and myofibroblast markers activate ECM which enhance inflammatory cells and lead to fibrosis. The study further identified molecular markers which could be used to prevent fibrogenic in kidney transplant patients (Imle *et al.,* 2024). Transcriptomics investigation was performed in patients with kidney cancer was performed recently, the study suggest that transcriptomics approaches identified risk factors and prediction of controlling kidney cancer (Si *et al.,* 2024).

One of the aggressive form of brain tumor is Glioblastoma in adults, the patients survival is for less than 15 months (Sabouri *et al.,* 2024). Treatment like chemotherapy and radiotherapy and surgical methods are mostly used (Sadowski *et al.,* 2024). There is no standard methods to care of disease progression although tumor are invariably recur (Melosky *et al.,* 2024). However, the treatment lead to enhance the survival, but the treatment and therapeutic approach are limited but need more studies. Currently genetics studies have been conducted to study the molecular mechanisms and treatment Glioblastoma (Świątek *et al.,* 2024). From the study of Glioblastoma tumor during treatment could be useful for the identification resistance related factors to therapy (Virtuoso *et al.,* 2024). To understand the nature of Glioblastoma recently transcriptomics approach was used. RN sequencing Glioblastoma was performed. The results of the study shows that genes are not significantly altered. Although increase in gene expression in extra cellular matrix was examined. The decrease in tumor purity decreased over time and co increase in genes associated with oligodendrocyte and neuron and independently tumor macrophages. The result further revolved that Glioblastoma involved mainly the reorganization of microenvironment rather than molecular pathways in tumor cells (Boccacino *et al.*, 2024).

Transcriptomics in cardiology

Cardiovascular disorders are one of the leading causes of death worldwide. The use of transcriptomics can be significant in comprehending genetic mechanisms and finding treatments for heart-related conditions (Fig. 5). According to the literature, the transcriptome is a complex mechanism that includes total RNAs. Noncoding RNAs have not received much attention despite some research being conducted. Research shows that these RNA are key regulators in development, homeostasis, pathology and cardiology (Acharya *et al.,* 2024).

Recently, a transcriptomics study has been conducted on COVID-19 patients and cardiovascular infection. Biopsy tissue of the heart was collected, and transcriptomics approaches were used. The results revealed that COVID-19 was not detected in tissue, although host transcriptomics showed genes associated with DNA damage and repair, heat shock and M1 like macrophage were upregulated. Further, the results showed pH1N1 upregulation of interferon-stimulated genes.

Next-generation sequencing facilitates the identification of omic biomarkers for cardiovascular diseases (CVDs). RNA sequencing (RNA-seq) detects

differentially expressed genes by comparing gene expression profiles of CVD samples with those of control samples. B, Chromatin immunoprecipitation sequencing (ChIP-seq) identifies transcription factor activity by detecting peaks formed by mapping DNA sequence reads that bind to transcription factor proteins. Transcription factor activity correlates with gene expression. C, Exome sequencing detects genetic variants such as single nucleotide polymorphisms that may correlate with CVD phenotypes. D, Methyl-CpG-binding domain sequencing (MBD-seq) is similar to ChIP-seq, but identifies regions of DNA methylation, which can affect gene expression (Wu *et al.,* 2014).

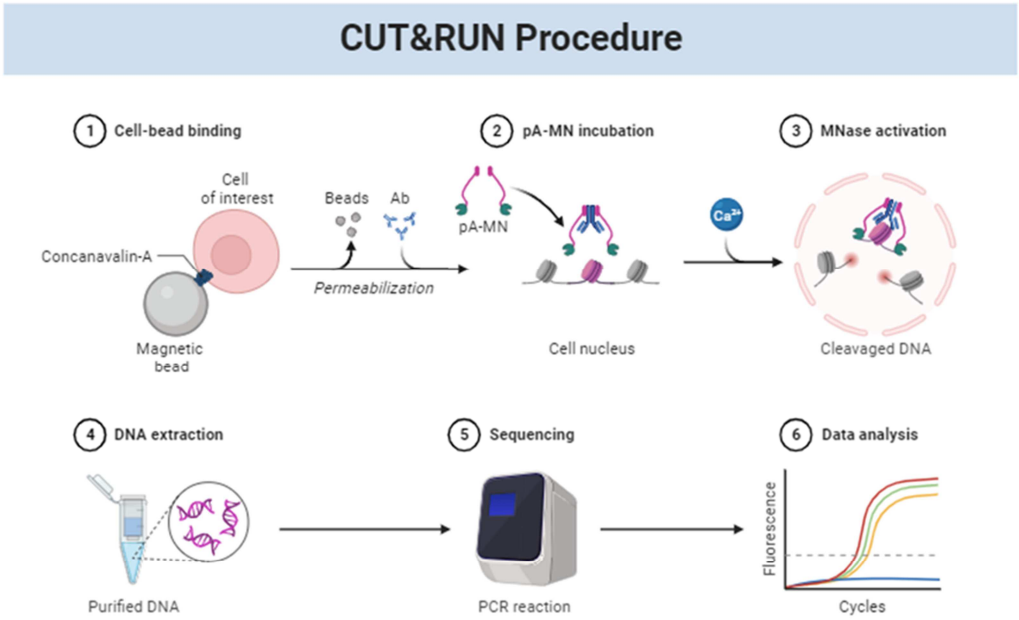

Fig. 5. Illustartion of transcriptomic analysis, RNA extraction, cDNA library, Sequencing and analysis

Transcriptomics analysis of left ventricle tissue of 64 samples was analyzed. Genes were significantly expressed associated with heart failure (Drakos *et al.,* 2023). Transcriptomics analysis of heart patients were performed in a study and were compared with healthy donors (Sweet *et al.,* 2018). The study identified the expression of DCM and RCM for protein coding regions and long non-coding RNAs. 5 genes encoding different members of the mediator complex were found differentially expressed. Furthermore, the study found significant results about genes that are never associated with heart failure and 27 non-coding RNAs significantly altered in heart failure patients (Sweet *et al.*, 2018). In the tissue of the Right ventricle, a transcriptomics profile was carried out in a recent study. They also use Real-Time PCR analysis.

Bioinformatics and gene enrichment analysis were also carried out. The result of the study showed that a total of 169 long non coding RNA were differentially expressed. Among them, 101 were upregulated, and 68 were downregulated. 898 mRNA were expressed among them, 623 were upregulated, and 275 were found downregulated in the RV failure. Further, the results were confirmed through qrtPCR. The expression of long non-coding RNAs in RV myocardium of PAH rate with acute RV failure showed significant insight into the role of lncRNAs to heart failure in PAH model Cao *et al.*, (2024). Transcriptomics analysis of heart failure was performed in a recent study. The result suggested that 19 genes (AEBP1, CA3, HBA2, HBB, HSPA2, MYH6, SERPINA3, SOD3, THBS4, UCHL1) were differentially expressed in Disig and 15 genes were differentially expressed on IsSig (AEBP1, APOA1,

BGN, CA3, CFH, COL14A1, HBA2, HBB, HSPA2, LTBP2, LUM, MFAP4, SOD3, THBS4, UCHL1). According to biological mechanisms, these genes were expressed in stress, extracellular matrix, and beta growth factors in heart muscles (Portokallidou *et al.,* 2024).

A transcriptomics analysis of 93 patients with heart problem were investigated in a recent research. The study was conducted to analyzed signal pathways operative in normal and failure heart patients. The analysis suggested that total 1341 transcripts and 288 phosphopeptides were identified, which are differentially expressed in heart tissue with patient having heart failure. Further 29 transcripts and 93 phosphopeptides were significantly identified in heart patients that are distinguished responder after LVAD unloading. Further analysis highlighted that these two pathways play key regulator in cell cycle regulation and extracellular matrix (Drakos *et al.,* 2023).

Transcriptomics application in infectious diseases

A study analysed recent raw transcriptomics data obtained through next-generation sequencing. The transcriptomics data were obtained from 105 blood samples from patients having uncomplicated bacterial infections. The data analysis showed that gene expression occurs in patients responding to bacterial infection (Herwanto *et al.,* 2021). Recently, a study investigated the genes in metabolic pathways associated with sepsis and Mets. The data was downloaded from GEO database. Differential expression analysis showed that 122 genes were upregulated and 90 genes were downregulated in sepsis and Mets. This study identified seven Hub genes that work as co diagnostic markers for sepsis and Mets. The results of this study also revealed that diagnostic genes play a key role in immune cell metabolic pathways (Tao *et al.,* 2023). In another study, transcriptomics analysis of 72 septic-shock genes was carried out. Further, the study investigated that upregulated genes were enriched in neutrophil activation and T cell activation in septic shocks (Zhao *et al.,* 2023). In another study, the transcriptomics analysis in septic patients identified 21 septic-associated iron metabolic genes, which may play a vital role in the diagnosis and therapeutic biomarkers of sepsis. The findings of this study could be useful for future diagnosis and treatment of sepsis. The complement component C5a-C5aR1 axis is an important driver in more severe inflammation. The transcriptomics analysis from blood samples revolved around the expression of long non-coding RNAs and coding RNAs against the microorganism. In a recent study Alu-elements, which are important elements in cell inflammations, make fat trajectories which lead to severe disease. The bulk RNA method was approached, and the analysis revolved around immune genes containing 48 Alu- insertion. The results also showed that 1 of the 48 candidates was located in complement receptor gene C5aR1, which is a target for RNA therapeutics (Li *et al.,* 2023).

Many diseases, including cancer, AIDS, and neurodegenerative disorders, are difficult to treat in their early stages (Singh *et al.,* 2024). Not all patients respond the same to cancer chemotherapy despite the availability of medicines. Some patients exhibit tolerance to certain treatments. Some treatments showed significant results, although sometimes, in some patients, the response of treatment failed. Further, these responses are due to genetics, environment and life style differences among the patients (Anand *et al.,* 2023).

Some diseases like diabetes and cystic fibrosis are caused by multiple factors, e.g., mutations (Putman *et al.,* 2023). Therefore, the treatment needs different mechanisms to provide and obtain successful results. Scientists and researchers around the globe are trying to identify approaches for valuable and achievable results. This approach included the nature of the disease and the response of patients. Genetic advancements, particularly identifying SNPS, gene sequencing and human genome sequence, have led to dramatic medical revolutions to access the disease (Khodadadian *et al.,* 2020). These advancements in genetics led to the development of a new field of medicine called precision medicine (Fig. 6).

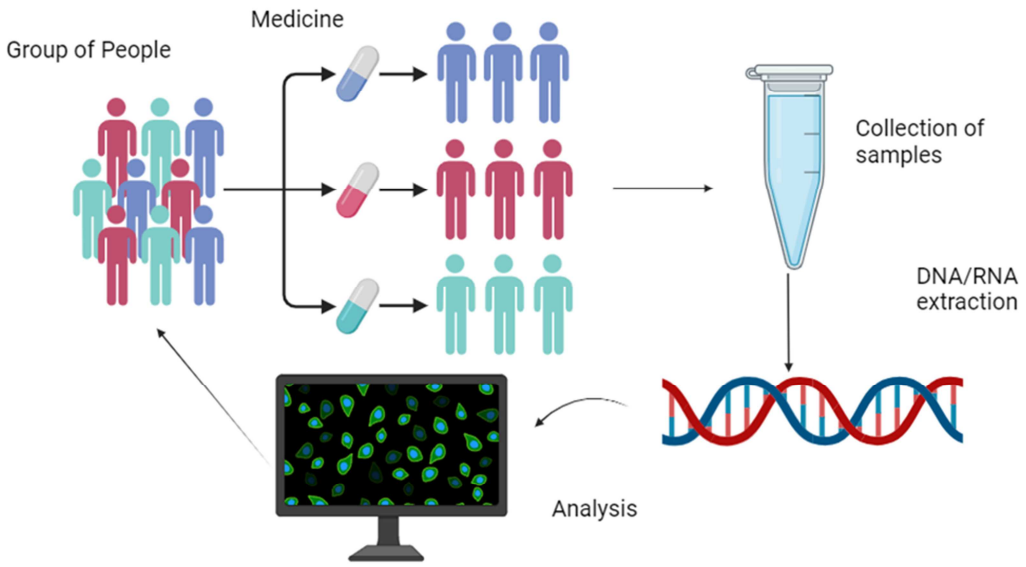

Fig. 6. Illustration of personalized medicine. Transcriptomics application are used for the development of precision medicine

This field designs personalized medicine that is not based on traditional procedures. These new methods try to minimize the cost and side effects. This method's common features are personalized genotyping, clinical records and lifestyle. In short, these techniques are used to understand the diseases in detail and design drugs and therapeutics. An example of this procedure is the development of ivacaftor and lumacafter for cystic fibrosis (Khodadadian *et al.,* 2020). Another example is BiDil, which was certified in 2005 for heart failure, but only in African-Americans (Callier *et al.,* 2022).

Alternative gene splicing is the function of a gene in which two or more rearrangements can occur in one mRNA in a cell. Hence, many proteins are formed by one mRNA without any change in the gene. Examples of alternative gene splicing, like nuclear pre RNA from the fibronectin gene, are converted into 20 mRNAs and encode 20 different types of protein (Kretova *et al.,* 2023). Thus 20 mRNA and 20 proteins are formed without altering the gene sequence. Alternative splicing mostly affects 95% of exonic genes (Marasco *et al.,* 2023). The error occurrence at this level may cause several disorders, such as in β+thalassaemia, in which β-globin protein level and anaemia (Marasco *et al.,* 2023). Moreover, any disturbance in this pathway can lead to disorder.

The gene variation and the effect of alternative gene splicing are not easily detectable in the genome. Hence, transscriptomics analyses are performed to investigate the expression of genes in a particular tissue or cell and organs. The science of genomics revolves around information stored in DNA, while transcriptomics investigates the expression of RNA. Transcriptomics technology plays a vital role in gene expression analysis in a cell or tissue during disease or environmental factors. Transcriptomics, the study of a cell's entire set of RNA, is crucial in understanding the mechanism of a disease or environmental factors, including non-coding RNAs. Transcriptomics also involves post transcriptional analysis, which provides useful information about variation not provided in genomics. Hence, transcriptomics information helps to remove the gap between transcriptomics and genomics. The knowledge of transcriptomics is an excellent approach for developing personalized medicine and more reliable treatment. Transcriptomics include a variety of methods like single gene, small set of genes, or whole transcripts.

Conclusion

The sequence of the human genome is a milestone in the field of genetics, The human genome revolves around all the significant information about phenotypes and

genotypes of humans. The sequencing industry is rapidly advancing, which facilitates understanding the nature and mechanisms of diseases such as infection, inflammation, and organ failure. Technologies like transcriptomics revolutionized the field of medicine and clinical sciences. Many genes that play significant roles in disease development were identified and expressed in response to pathogenic interaction in tissue or cells. Hence, the current study was carried out to analyze transcriptomics' application and current status in medicine and clinical sciences. Further research is necessary as the conclusions drawn from these publications do not currently meet the criteria.

Furthermore, modifications are needed in obtaining and selecting tissue or cells. Our analysis found that mostly single cell RNA transcriptomics was used more than other approaches. Most of the work done in oncology, infection mostly bacterial infection and a little bit on cardiology. Hence, we recommended more work on liver fibrosis, diabetics, acute organ failure and, most importantly, heart failure at younger age. We recommended a comprehensive study on younger heart failure, as we have studied in literature that the heart failure occurs mostly in older individuals. The question is, why does it occur in younger ages, like 21 to 30? So, detailed transcriptomics studies like whole transcriptomics could be significant for future treatment and control of this disease. Additionally, patients' bodies can react negatively to the operation when receiving treatment, medicines, or having organs transplanted. Thorough analysis is necessary for detecting diseases and developing effective treatments, which can be informed by studying genetics and molecular-level host-pathogen reactions. To achieve significant results and desired goals, transcriptomics data and genomic information about the diseases must be obtained, and to store and analyzed this data, we need more powerful systems and software. In Pakistan, most of the medical faculty are far from research, and medical doctors have very limited knowledge about genetics and research. To overcome this issue, we must establish research and expertise in medicine and clinical science to achieve our goals.

Aknowlegments

The Author is thankful to Ala-Too International University for financial Support.

References

Acharya P, Parkins S, Tranter M. 2024. RNA binding proteins as mediators of pathological cardiac remodeling. Frontiers in Cell and Developmental Biology **12**, 1368097.

Addissouky TA, Ali MM, Sayed IE, Wang Y. 2024. Emerging advanced approaches for diagnosis and inhibition of liver fibrogenesis. The Egyptian Journal of Internal Medicine **36**(1), 19.

Alicic RZ, Rooney MT, Tuttle KR. 2017. Diabetic kidney disease: challenges, progress, and possibilities. Clinical Journal of the American Society of Nephrology **12**(12), 2032-2045.

Anand U, Dey A, Chandel AK, Sanyal R, Mishra A, Pandey DK, De Falco V, Upadhyay A, Kandimalla R, Chaudhary A, Dhanjal JK. 2023. Cancer chemotherapy and beyond: current status, drug candidates, associated risks and progress in targeted therapeutics. Genes & Diseases **10**(4), 1367-1401.

Bai H, Xian N, Zhao F, Zhou Y, Qin S. 2024. The dual role of SUSD2 in cancer development. European Journal of Pharmacology **977**, 176754.

Bai YM, Yang F, Luo P, Xie LL, Chen JH, Guan YD, Zhou HC, Xu TF, Hao HW, Chen B, Zhao JH. 2023. Single-cell transcriptomic dissection of the cellular and molecular events underlying the triclosan-induced liver fibrosis in mice. Military Medical Research **10**(1), 1-22.

Baliña-Sánchez C, Aguilera Y, Adán N, Sierra-Párraga JM, Olmedo-Moreno L, Panadero-Morón C, Cabello-Laureano R, Márquez-Vega C, Martín-Montalvo A, Capilla-González V. 2023. Generation of mesenchymal stromal cells from urine-derived iPSCs of pediatric brain tumor patients. Frontiers in Immunology **14**, 1022676.

Bamberg M. 2023. RNA-based identification of forensically relevant body fluids/tissues–novel strategies and methods for casework implementation. (Doctoral dissertation, Universität Ulm).

Bansal MP. 2023. Cancer Metastasis, ROS/Redox Signaling, and PCD Resistance/Redox Metabolism. In Redox Regulation and Therapeutic Approaches in Cancer. Singapore: Springer Nature Singapore **173-206**.

Barthel FP, Johnson KC, Varn FS, Moskalik AD, Tanner G, Kocakavuk E, Anderson KJ, Abiola O, Aldape K, Alfaro KD, Alpar D. 2019. Longitudinal molecular trajectories of diffuse glioma in adults. Nature **576**, 112–120.

Boccacino JM, dos Santos Peixoto R, Fernandes CF, Cangiano G, Sola PR, Coelho BP, Prado MB, Melo-Escobar MI, de Sousa BP, Ayyadhury S, Bader GD. 2024. Integrated transcriptomics uncovers an enhanced association between the prion protein gene expression and vesicle dynamics signatures in glioblastomas. BMC Cancer **24**(1), 199.

Brokowska J, Gaffke L, Pierzynowska K, Cyske Z, Węgrzyn G. 2024. Cell cycle disturbances in mucopolysaccharidoses: Transcriptomic and experimental studies on cellular models. Experimental Biology and Medicine **247**, 1639–1649.

Callier SL, Payne Jr PW, Akinniyi D, McPartland K, Richardson TL, Rothstein MA, Royal CD. 2022. Cardiologists' perspectives on BiDil and the use of race in drug prescribing. Journal of Racial and Ethnic Health Disparities **9**(6), 2146-2156.

Cao J, Li C, Cui Z, Deng S, Lei T, Liu W, Yang H, Chen P. 2024. Spatial Transcriptomics: A Powerful Tool in Disease Understanding and Drug Discovery. Theranostics **14**(7), 2946.

Cheng XY, Zhang YS, Cao ZF. 2023. Applications and advances of spatial transcriptomics in oncology research. Zhonghua bing li xue za zhi Chinese Journal of Pathology **52**(6), 643-646.

Draaisma K, Chatzipli A, Taphoorn M, Kerkhof M, Weyerbrock A, Sanson M, Hoeben A, Lukacova S, Lombardi G, Leenstra S, Hanse M. 2020. Molecular evolution of IDH wild-type glioblastomas treated with standard of care affects survival and design of precision medicine trials: a report from the EORTC 1542 study. Journal of Clinical Oncology **38**, 81–99.

Drakos SG, Badolia R, Makaju A, Kyriakopoulos CP, Wever-Pinzon O, Tracy CM, Bakhtina A, Bia R, Parnell T, Taleb I, Ramadurai DK. 2023. Distinct transcriptomic and proteomic profile specifies patients who have heart failure with potential of myocardial recovery on mechanical unloading and circulatory support. Circulation **147**(5), 409-424.

Fan J, Slowikowski K, Zhang F. 2020. Single-cell transcriptomics in cancer: computational challenges and opportunities. Experimental & Molecular Medicine **52**, 1452–1465.

Fan Y, Andrusivová Ž, Wu Y, Chai C, Larsson L, He M, Luo L, Lundeberg J, Wang B. 2023. Expansion spatial transcriptomics. Nature Methods **20**(8), 1179-82.

Glodzik D, Selenica P, Rogge RA, Silverman IM, Mandelker D, Harris S, Zhao J, Zinda M, Veloso A, Malani N, Riaz N. 2023. Detection of biallelic loss of DNA repair genes in formalin-fixed, paraffin-embedded tumor samples using a novel tumor-only sequencing panel. The Journal of Molecular Diagnostics **25**(5), 295-310.

Herwanto V, Tang B, Wang Y, Shojaei M, Nalos M, Shetty A, Lai K, McLean AS, Schughart K. 2021. Blood transcriptome analysis of patients with uncomplicated bacterial infection and sepsis. BMC Research Notes **14**, 1-3.

Hibi M, Katada S, Kawakami A, Bito K, Ohtsuka M, Sugitani K, Muliandi A, Yamanaka N, Hasumura T, Ando Y, Fushimi T. 2023. Assessment of Multidimensional Health Care Parameters Among Adults in Japan for Developing a Virtual Human Generative Model: Protocol for a Cross-sectional Study. JMIR Research Protocols **12**(1), e47024.

Hoogstrate Y, Draaisma K, Ghisai SA, van Hijfte L, Barin N, de Heer I, Coppieters W, van den Bosch TP, Bolleboom A, Gao Z, Vincent AJ. 2023. Transcriptome analysis reveals tumor microenvironment changes in glioblastoma. Cancer Cell **41**(4), 678-92.

Imle R, Blosel D, Kommoss F, Zhao E, Autry R, Blume C, Lupar D, Schmitt L, Winter C, Wagner L, Placke S. 2024. Somatic gene delivery for flexible in vivo modeling of high-risk sarcoma. bioRxiv 2024, 2024-01.

Jang MJ, Coughlin GM, Jackson CR, Chen X, Chuapoco MR, Vendemiatti JL, Wang AZ, Gradinaru V. 2023. Spatial transcriptomics for profiling the tropism of viral vectors in tissues. Nature Biotechnology **41**(9), 1272-86.

Khodadadian A, Darzi S, Haghi-Daredeh S, Sadat Eshaghi F, Babakhanzadeh E, Mirabutalebi SH, Nazari M. 2020. Genomics and transcriptomics: the powerful technologies in precision medicine. International Journal of General Medicine **17**, 627-40.

Kraboth Z, Kalman B. 2020. Longitudinal characteristics of glioblastoma in genome-wide studies. Pathology and Oncology Research **26**, 2035–2047.

Kretova M, Selicky T, Cipakova I, Cipak L. 2023. Regulation of pre-mRNA splicing: indispensable role of post-translational modifications of splicing factors. Life **13**(3), 604.

LaRossa RA. 2013. Transcriptome, Editor(s): Stanley Maloy, Kelly Hughes, Brenner's Encyclopedia of Genetics (Second Edition). Academic Press, 101-103.

Li H, Wang X, Yang Q, Cheng L, Zeng HL. 2023. Identification of iron metabolism-related genes as diagnostic signatures in sepsis by blood transcriptomic analysis. Open Life Sciences **18**(1), 20220549.

Li H, Zhou J, Li Z, Chen S, Liao X, Zhang B, Zhang R, Wang Y, Sun S, Gao X. 2023. A comprehensive benchmarking with practical guidelines for cellular deconvolution of spatial transcriptomics. Nature Communication **14**(1), 1548.

Long X, Yuan X, Du J. 2023. Single-cell and spatial transcriptomics: Advances in heart development and disease applications. Computational and Structural Biotechnology Journal **21**, 2717-31.

Ludwig K, Wu Z, Bardai G, Mason P, Ward LM, Moffatt P, Rauch F. 2023. RNA sequencing of urine-derived cells for the characterization and diagnosis of osteogenesis imperfecta. Journal of Bone and Mineral Research **38**(8), 1125-34.

Magro D, Venezia M, Balistreri CR. 2024. The omics technologies and liquid biopsies: advantages, limitations, applications. Medicine in Omics **21**, 100039.

Marasco LE, Kornblihtt AR. 2023. The physiology of alternative splicing. Nature Reviews Molecular Cell Biology **24**(4), 242-54.

Melosky B, Vincent MD, McGuire AL, Brade AM, Chu Q, Cheema P, Martins I, Spicer JD, Snow S, Juergens RA. 2024. Modern era systemic therapies: expanding concepts of cure in early and locally advanced non-small cell lung cancer. International Journal of Cancer **155**(6), 963-78.

Miranda AM, Janbandhu V, Maatz H, Kanemaru K, Cranley J, Teichmann SA, Hübner N, Schneider MD, Harvey RP, Noseda M. 2023. Single-cell transcriptomics for the assessment of cardiac disease. Nature Reviews Cardiology **20**(5), 289-308.

Mohr AE, Ortega-Santos CP, Whisner CM, Klein-Seetharaman J, Jasbi P. 2024. Navigating challenges and opportunities in multi-omics integration for personalized healthcare. Biomedicines **12**(7), 1496.

Moufarrej MN, Quake SR. 2023. An inexpensive semi-automated sample processing pipeline for cell-free RNA extraction. Nature Protocols **18**(9), 2772-93.

Mundi PS, Dela Cruz FS, Ortiz MV, Grunn A, Diolaiti D, Alvarez MJ, Kung AL, Califano A. 2023. Evaluation of a transcriptomics-based precision oncology platform for patient-therapy alignment in treatment resistant malignancies. Cancer Research **83**(7_Supplement), 849.

Ocansey DK, Qian F, Cai P, Ocansey S, Amoah S, Qian Y, Mao F. 2024. Current evidence and therapeutic implication of PANoptosis in cancer. Theranostics **14**(2), 640.

Okamura K, Dummer P, Kopp J, Qiu L, Levi M, Faubel S, Blaine J. 2013. Endocytosis of albumin by podocytes elicits an inflammatory response and induces apoptotic cell death. PloS One **8**(1), e54817.

Pais RJ, Lopes F, Parreira I, Silva M, Silva M, Moutinho MG. 2023. Predicting cancer prognostics from tumour transcriptomics using an auto machine learning approach. In Medical Sciences Forum **22**(1), 6.

Parola M, Pinzani M. 2024. Invited review: liver fibrosis in NAFLD/NASH: from pathophysiology towards diagnostic and therapeutic strategies. Molecular Aspects of Medicine **95**, 101231.

Peng L, Wang C, Yu S, Li Q, Wu G, Lai W, Min J, Chen G. 2024. Dysregulated lipid metabolism is associated with kidney allograft fibrosis. Lipids in Health and Disease **23**(1), 37.

Portokallidou K, Dovrolis N, Ragia G, Atzemian N, Kolios G, Manolopoulos VG. 2023. Multi-omics integration to identify the genetic expression and protein signature of dilated and ischemic cardiomyopathy. Frontiers in Cardiovascular Medicine **10**, 1115623.

Putman MS, Norris AW, Hull RL, Rickels MR, Sussel L, Blackman SM, Chan CL, Ode KL, Daley T, Stecenko AA, Moran A. 2023. Cystic fibrosis–related diabetes workshop: research priorities spanning disease pathophysiology, diagnosis, and outcomes. Diabetes Care **46**(6), 1112-23.

Sabouri M, Dogonchi AF, Shafiei M, Tehrani DS. 2024. Survival rate of patient with glioblastoma: a population-based study. Egyptian Journal of Neurosurgery **39**(1), 1-9.

Sadowski K, Jażdżewska A, Kozłowski J, Zacny A, Lorenc T, Olejarz W. 2024. Revolutionizing glioblastoma treatment: a comprehensive overview of modern therapeutic approaches. International Journal of Molecular Sciences **25**(11), 5774.

Sakairi T, Abe Y, Kajiyama H, Bartlett LD, Howard LV, Jat PS, Kopp JB. 2010. Conditionally immortalized human podocyte cell lines established from urine. American Journal of Physiology-Renal Physiology **298**(3), F557-67.

Sakthikumar S, Roy A, Haseeb L, Pettersson ME, Sundström E, Marinescu VD, Lindblad-Toh K, Forsberg-Nilsson K. 2020. Whole-genome sequencing of glioblastoma reveals enrichment of non-coding constraint mutations in known and novel genes. Genome Biology **21**, 1-22.

Schmidt M, Hopp L, Arakelyan A, Kirsten H, Engel C, Wirkner K, Krohn K, Burkhardt R, Thiery J, Loeffler M, Loeffler-Wirth H. 2020. The human blood transcriptome in a large population cohort and its relation to aging and health. Frontiers in Big Data **3**, 548873.

Schmøkel SS, Nordentoft I, Lindskrog SV, Lamy P, Knudsen M, Jensen JB, Dyrskjøt L. 2023. Improved protocol for single-nucleus RNA-sequencing of frozen human bladder tumor biopsies. Nucleus **14**(1), 2186686.

Sendinc E, Shi Y. 2023. RNA m6A methylation across the transcriptome. Molecular Cell **83**(3), 428-41.

Shi X, Yu Z, Ren P, Dong X, Ding X, Song J, Zhang J, Li T, Wang C. 2023. HUSCH: an integrated single-cell transcriptome atlas for human tissue gene expression visualization and analyses. Nucleic Acids Research **51**(D1), 1029-37.

Shimizu K, Kikuta J, Ohta Y, Uchida Y, Miyamoto Y, Morimoto A, Yari S, Sato T, Kamakura T, Oshima K, Imai R. 2023. Single-cell transcriptomics of human cholesteatoma identifies an activin A-producing osteoclastogenic fibroblast subset inducing bone destruction. Nature Communications **14**(1), 4417.

Si S, Liu H, Xu L, Zhan S. 2024. Identification of novel therapeutic targets for chronic kidney disease and kidney function by integrating multi-omics proteome with transcriptome. Genome Medicine **16**(1), 84.

Singh K, Sethi P, Datta S, Chaudhary JS, Kumar S, Jain D, Gupta JK, Kumar S, Guru A, Panda SP. 2024. Advances in gene therapy approaches targeting neuro-inflammation in neurodegenerative diseases. Ageing Research Reviews **8**, 102321.

Stupp R, Mason WP, Van Den Bent MJ, Weller M, Fisher B, Taphoorn MJ, Belanger K, Brandes AA, Marosi C, Bogdahn U, Curschmann J. 2005. Radiotherapy plus concomitant and adjuvant temozolomide for glioblastoma. New England Journal of Medicine **352**(10), 987-96.

Sweet ME, Cocciolo A, Slavov D, Jones KL, Sweet JR, Graw SL, Reece TB, Ambardekar AV, Bristow MR, Mestroni L, Taylor MR. 2018. Transcriptome analysis of human heart failure reveals dysregulated cell adhesion in dilated cardiomyopathy and activated immune pathways in ischemic heart failure. BMC Genomics **19**, 1-4.

Świątek W, Kłodziński O, Ciesielski M, Adamkiewicz Z, Podolak M, Mozdziak PE, Kranc W. 2024. Glioblastoma: A molecular insight into current discoveries and treatment directions. Medical Journal of Cell Biology **12**(1), 1-20.

Tao L, Zhu Y, Liu J. 2023. Identification of new co-diagnostic genes for sepsis and metabolic syndrome using single-cell data analysis and machine learning algorithms. Frontiers in Genetics **14**, 1129476.

Thomas MC, Brownlee M, Susztak K, Sharma K, Jandeleit-Dahm KA, Zoungas S, Rossing P, Groop PH, Cooper ME. 2015. Diabetic kidney disease. Nature Reviews Disease Primers **1**(1), 1-20.

Tian L, Chen F, Macosko EZ. 2023. The expanding vistas of spatial transcriptomics. Nature Biotechnology **41**(6), 773-82.

Virtuoso A, D'Amico G, Scalia F, De Luca C, Papa M, Maugeri G, D'Agata V, Caruso Bavisotto C, D'Amico AG. 2024. The interplay between glioblastoma cells and tumor microenvironment: New perspectives for early diagnosis and targeted cancer therapy. Brain Sciences **14**(4), 331.

Wang C, Li L, Wang F, Li X, Sun J, Li X, Lei T, Huang Q, Zhang G, Wang H, Li D. 2023. Single-cell transcriptomics dissects epithelial heterogeneity in HPV+ cervical adenocarcinoma. Journal of Medical Virology **95**(2), e28480.

Wang Q, Hu B, Hu X, Kim H, Squatrito M, Scarpace L, DeCarvalho AC, Lyu S, Li P, Li Y, Barthel F. 2017. Tumor evolution of glioma-intrinsic gene expression subtypes associates with immunological changes in the microenvironment. Cancer Cell **32**(1), 42-56.

Wang R, Peng G, Tam PP, Jing N. 2023. Integration of computational analysis and spatial transcriptomics in single-cell studies. Genomics, Proteomics & Bioinformatics **21**(1), 13-23.

Wang S, Song A, Xie J, Wang YY, Wang WD, Zhang MJ, Wu ZZ, Yang QC, Li H, Zhang J, Sun ZJ. 2024. Fn-OMV potentiates ZBP1-mediated PANoptosis triggered by oncolytic HSV-1 to fuel antitumor immunity. Nature Communications **15**(1), 3669.

Wang T, Wang L, Zhang L, Long Y, Zhang Y, Hou Z. 2023. Single-cell RNA sequencing in orthopedic research. Bone Research **11**(1), 10.

Wang X, Wu P, Fu Y, Yang R, Li C, Chen Y, He A, Chen X, Ma D, Ma J, Zhang T. 2024. The circular RNA expression profile of human auricle cartilage and the role of circCOL1A2 in isolated microtia. Cellular Signalling **115**, 111017.

Weller M, van den Bent M, Preusser M, Le Rhun E, Tonn JC, Minniti G, Bendszus M, Balana C, Chinot O, Dirven L, French P. 2021. EANO guidelines on the diagnosis and treatment of diffuse gliomas of adulthood. Nature Reviews Clinical Oncology **18**(3), 170-86.

Wheeler DA, Wang L. 2013. From human genome to cancer genome: The first decade. Genome Research **23**, 1054-1062.

Woroniecka KI, Park AS, Mohtat D, Thomas DB, Pullman JM, Susztak K. 2011. Transcriptome analysis of human diabetic kidney disease. Diabetes **60**(9), 2354-69.

Wu PY, Chandramohan R, Phan JH, Mahle WT, Gaynor JW, Maher KO, Wang MD. 2014. Cardiovascular transcriptomics and epigenomics using next-generation sequencing: challenges, progress, and opportunities. Circulation: Cardiovascular Genetics **7**(5), 701-10.

Xiong Y. 2023. The emerging role of PANoptosis in cancer treatment. Biomedicine & Pharmacotherapy **168**, 115696.

Yankee TN, Oh S, Winchester EW, Wilderman A, Robinson K, Gordon T, Rosenfeld JA, VanOudenhove J, Scott DA, Leslie EJ, Cotney J. 2023. Integrative analysis of transcriptome dynamics during human craniofacial development identifies candidate disease genes. Nature Communications **14**(1), 4623.

Yoshida T, Latt KZ, Rosenberg AZ, Shrivastav S, Heymann J, Halushka MK, Winkler CA, Kopp JB. 2023. Transcriptomic analysis of human podocytes in vitro: effects of differentiation and APOL1 genotype. Kidney International Reports **8**(1), 164-78.

Zhang M, Bi X. 2024. Heat shock proteins and breast cancer. International Journal of Molecular Sciences **25**(2), 876.

Zhang X, Chao P, Zhang L, Xu L, Cui X, Wang S, Wusiman M, Jiang H, Lu C. 2023. Single-cell RNA and transcriptome sequencing profiles identify immune-associated key genes in the development of diabetic kidney disease. Frontiers in Immunology **14**, 1030198.

Zhang Y, Zhu G, Tong Q, Ni J, Fang X, Chen X, Wang Z. 2023. Effects of organic and inorganic nitrogen sources on the transcriptome of gellan gum biosynthesis by *Sphingomonas paucimobilis*. Journal of Applied Microbiology **134**(4), lxad081.

Zhao S, Zhu K, Li X, Zhong X, Zhao Y, Le Z, Liu Z, Xiao Y, Lai D, Jiao N, Shu Q. 2024. Co-expression and interaction network analysis reveals dysregulated neutrophil and T-cell activation as the core mechanism associated with septic shock. Frontiers in Genetics **14**, 1132361.

Zhao Y, Wang T, Liu Z, Ke Y, Li R, Chen H, You Y, Wu G, Cao S, Du Z, Bai F. 2023. Single-cell transcriptomics of immune cells in lymph nodes reveals their composition and alterations in functional dynamics during the early stages of bubonic plague. Science China Life Sciences **66**(1), 110-26.

Zhao Y, Yakufu M, Ma C, Wang B, Yang J, Hu J. 2023. Transcriptomics reveal a molecular signature in the progression of nonalcoholic steatohepatitis and identifies PAI-1 and MMP-9 as biomarkers in in vivo and in vitro studies. Molecular Medicine Reports **29**(1), 15.