

RNA sequencing analysis) is a powerful technique used to study the **transcriptome**—the complete set of **RNA transcripts** produced by the **genome** under specific conditions. Here's a concise definition:

RNA-seq Analysis

RNA-seq analysis refers to the bioinformatic and statistical processing of RNA sequencing data to quantify, compare, and interpret gene expression levels across samples.

It involves:

Sequencing RNA transcripts (usually after converting to cDNA)

Mapping the reads to a reference genome or transcriptome

Quantifying expression levels of genes or transcripts

Detecting differentially expressed genes (DEGs) between conditions

Exploring alternative splicing, fusion transcripts, non-coding RNAs, and allele-specific expression

This method allows researchers to:

Identify genes involved in disease

Compare expression between cell types or treatments

Discover novel transcripts

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Tags: **transcriptomics**, **gene expression**, **NGS**, **bioinformatics**, **differential expression**

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RNA-seq is widely used in cancer biology, developmental studies, and personalized medicine

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