

Transcriptome sequencing

The set of genes which are transcribed in any one condition is called as transcriptome and sequencing those genetic codes transcribed into RNA and proteins and other genes related to them resulting from a throughput sequencing analysis for understanding and sequencing high transcripts of specific tissues. It gives all transcriptional products and structures of genes with good expressional level of individual transcripts during development. It employs 3' tailing and ligation of R1 Stubby Adapter to the first strand of cDNA. This does not need 2nd strand cDNA synthesis, degradation, or template switching methods. The RNA transcribed from the genes are further reverse transcribed and the active sites are studied from them. Along with mRNA the non sequencing RNAs and their respective proteins are also studied for their regulatory mechanisms. Also their unknown and rare transcripts identifying variable cleavage sites and cSNP (coding sequence single nucleotide polymorphism) for the holistic transcription. This technology is widely used in drug development, clinical research medicinal research.

Issued by:

NTHRYS OPC PVT LTD

Ph: +91 - 8977624748

Web: www.nthrYS.com

Email: smo@nthrYS.com

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