Terminologies

Transcriptome: 转录组： 由DNA转录出来的东西的统称

Interactome：互作组，研究各种RNA， 蛋白质之间的相互作用

Histone：组蛋白，染色质的构成结构

Epitranscriptomics, or RNA epigenetics, refers to the presence of chemical modifications on RNAs post-transcriptionally. Epi：表观，在这里就只在转录之后发生的一些变化

snoRNA：核仁小RNA（small nucleolar RNA），分布于真核生物细胞核仁的小分子非编码RNA，主要参与rRNA的加工；反义snoRNA指导rRNA核糖甲基化。

MicroRNA (miRNA) : 是一类由内源基因编码的长度约为22 个核苷酸的非编码单链RNA分子，它们在动植物中参与转录后基因表达调控。miRNA可以通过破坏靶mRNA的稳定性、抑制靶mRNA的翻译来对靶mRNA发挥调控作用

RNA-modifying proteins (RMPs)：催化RNA modification的蛋白质

SNV (Single Nucleotide Variant): 单核苷酸变异

SNP: Single Nucleotide Polymorphism, 单核苷酸多态性

flanking sequence: 侧翼序列:存在于编码区第一个外显子和最末一个外显子的外侧的一段不被翻译的核苷酸序列

RBP: RNA-binding proteins

RMP: RNA-modifying proteins

RNP：核糖核蛋白（Ribonucleoprotein, RNP）

Nucleic acid structure (<https://en.wikipedia.org/wiki/Nucleic_acid_structure>)

* Primary structure: sequence of nt
* Secondary structure:  set of interactions between bases, i.e., which parts of strands are bound to each other.

For RNA: 4 basic elements: Helices Bulges Loops Junctions

* Tertiary structure: locations of the atoms in three-dimensional space, taking into consideration geometrical and [steric](https://en.wikipedia.org/wiki/Steric) constraints

CLIP related technologies

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## CLIP

1. What is CLIP: Crosslinking and Immunoprecipitation

ultraviolet crosslinking followed by immunoprecipitation (CLIP).

Can map the RNA interactome, yielding transcriptome-wide protein–RNA atlases that have contributed to key mechanistic insights into gene expression and gene-regulatory networks (map protein RNA interactions)

1. How to work

Crosslinking: Cells or tissues are treated with ultraviolet (UV) light to induce covalent crosslinks between RNA and associated proteins. (covalent crosslinks: stable chemical bonds formed between molecules, typically between proteins and nucleic acids (like RNA or DNA), that result in a permanent linkage.)

Immunoprecipitation: After crosslinking, the RNA–protein complexes are extracted, and specific RBPs are isolated using antibodies that target those proteins. This step enriches the sample for the proteins of interest. (by choosing the wanted protein, can get the wanted RNA)

Library Preparation and Sequencing: The RNA fragments are ligated to adapters, converted into complementary DNA (cDNA), and then subjected to high-throughput sequencing. This allows researchers to determine the sequences of the RNA that were bound by the proteins.

Misc technologies:

1. icSHAPE (in vivo Click Selective 2'-Hydroxyl Acylation and Profiling Experiment) is a technology used to determine RNA secondary structures in vivo. It allows researchers to profile the structural dynamics of RNA across the entire transcriptome in living cells. The method involves modifying RNA with a chemical that selectively labels the 2'-hydroxyl groups of nucleotides, which can then be detected and analyzed to infer the structural conformation of the RNA. This information is crucial for understanding RNA-protein interactions, as the structure of RNA can significantly influence how it interacts with RNA-binding proteins (RBPs) and its overall functionality in cellular processes
2. RNA Bind-N-Seq (RBNS) is an **in vitro high-throughput method** used to identify the binding preferences of RNA-binding proteins (RBPs).