# Article information:

Comprehensive Analysis of mRNA Methylation Reveals Enrichment in 3' UTRs and Near Stop Codons - PMC
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3383396/>

# Article summary:

1. A method for transcriptome-wide m6A localization has been developed, which combines m6A-specific methylated RNA immunoprecipitation with next-generation sequencing (MeRIP-Seq).

2. This method reveals that m6A is a common base modification of mRNA and is regulated in a tissue-specific manner.

3. m6A sites are enriched near stop codons and in 3' UTRs, and there is an association between m6A residues and microRNA binding sites within 3' UTRs.

# Article rating:

May be slightly imbalanced: The article presents the information in a generally reliable way, but there are minor points of consideration that could be explored further or claims that are not fully backed by appropriate evidence. Some perspectives may also be omitted, and you are encouraged to use the research topics section to explore the topic further.

# Article analysis:

The article “Comprehensive Analysis of mRNA Methylation Reveals Enrichment in 3' UTRs and Near Stop Codons” provides a comprehensive overview of the prevalence, regulation, and functional roles of m6A in the transcriptome. The authors present a method for transcriptome-wide m6A localization which combines m6A-specific methylated RNA immunoprecipitation with next-generation sequencing (MeRIP-Seq). This method reveals that m6A is a common base modification of mRNA and is regulated in a tissue-specific manner. Additionally, the authors find that m6A sites are enriched near stop codons and in 3' UTRs, as well as uncovering an association between m6A residues and microRNA binding sites within 3' UTRs.

The article appears to be reliable overall; it cites relevant research studies to support its claims, provides detailed descriptions of the methods used to conduct the study, and presents clear results from the analysis conducted. The authors also provide potential implications for their findings regarding epigenetic regulation of the mammalian transcriptome. However, there are some potential biases present in the article which should be noted. For example, while the authors discuss potential implications for their findings regarding epigenetic regulation of the mammalian transcriptome, they do not explore any counterarguments or alternative explanations for their results. Additionally, while they cite relevant research studies to support their claims throughout the article, they do not provide any evidence or data to back up these claims beyond citing other studies; this could potentially lead to one-sided reporting or unsupported claims if readers do not have access to these cited studies themselves.

In conclusion, while this article appears to be reliable overall due to its detailed descriptions of methods used and clear presentation of results from analysis conducted, there are some potential biases present which should be noted when considering its trustworthiness and reliability.

# Topics for further research:

* Epigenetic regulation of transcriptome
* mRNA methylation regulation
* m6A functional roles
* MicroRNA binding sites
* MeRIP-Seq method
* mRNA 3' UTRs enrichment

# Report location:

<https://www.fullpicture.app/item/cb1cc56e73282053c17fec3bde2716f4>