**RNA Methylation Modification (m6A/m1A) and Human Cancers**

RNA modification system has been identified recent and has been demonstrated play important roles in human cancer, immune diseases as well as mental diseases including N6-methyladenosine (m6A), N1-methyladenosine (m1A) variations in these disease systems. In the past decades, the general functions and roles of m6A modification have been well described, including m6A machines and systems, the role of m6A on splicing, RNA exporting, RNA stability, protein translate and specific abnormal in individual cancers. However, the pan-cancer and cancer specific m6A variation or characteristics are still unknown.

Recent technological advancements like MeRIP-Seq/m6A-seq have allowed considerable progress in understanding the role played by m6A/m1A RNA modification mechanisms in pathogenesis of human cancers. Since epigenetic changes are not detectable at the DNA sequence level, epigenome mapping, which explores genome-wide chromatin modification patterns, may help in discovering disease-causing genes and in developing novel diagnostic and treatment strategies. For example, it has been shown that distinct patterns of DNA and RNA methylation are associated with specific cancer types, showed interesting prognostic potentials, and can help in suggesting the most favorable treatment. Genome-wide RNA methylation studies have also allowed for the identification of m6A/m1A changes in disease-causing genes in the most widely studied cancers such as liver cancer, lung cancer. However, he genome-wide RNA profiles for majority of cancer are still unknown.

Hence, in this Research Topic, we would like to focus on mRNA modification in human cancers. We welcome the submission of Mini-reviews, Reviews and Original Research articles related to genetic variation, epigenetic regulation to m6A/m1A genes as well as m6A/m1A genes and the role of m6A/m1A modification variation in human cancers. The topics that this Research Topic will cover include, but are not limited to, the followings:

1, Genome-wide m6A/m1A landscape research for different human cells or tissues and compared the profile difference between different cancers. Identify interesting m6A/m1A sites which are involved in gene expression regulation, mRNA stability and protein translation efficiency. For such research, we require solid technique should be applied such as [MeRIP-Seq/m6A-seq and we welcome all novel m6A/m1A detection biotech assay and computational analysis pipeline to accelerate m6A related research. We require all the NGS data must be deposited to public database such as GEO and SRA.](https://www.illumina.com/science/sequencing-method-explorer/kits-and-arrays/merip-seq-m6a-seq.html)

2, Association between Genetic variants in mRNA modification (writer, eraser, and reader genes) and human cancers, especially rare variants or somatic mutations or rare copy number variations occurred in mRNA modification gene regions. We welcome the pheWAS study based on large population cohort such as UK-biobank, eMERGE to identify interesting genetics association between m6A/m1A systems with complex human diseases with a large phenotypes.

3, Genetic and epigenetic regulations of mRNA modification proteins (writer, eraser, readers) including identify eQTLs, TFBS and DNA methylation, histone modification and miRNAs as well as the corresponding interaction on how to transcriptional regulate mRNA modification gene expression.

4, Pathway analysis to show how m6A modification are involved in different disease pathways, especially cancer related pathway, such as ferroptosis, immune tolerance pathway and epithelial–mesenchymal transition pathway.

**Keywords**: RNA methylation (m6A/m1A), Post-transcriptional regulation, Human cancers, Epigenetics

**Important Note**: All contributions to this Research Topic must be within the scope of the section and journal to which they are submitted, as defined in their mission statements. Frontiers reserves the right to guide an out-of-scope manuscript to a more suitable section or journal at any stage of peer review.

Dr. Shicheng Guo,

Department of Medical Genetics, School of Medicine and Public Health, University of Wisconsin-Madison, Madison, WI, USA

Center for Precision Medicine Research, Marshfield Clinic Research Institute, Marshfield, WI, United States, 54449

Dr. Xiangqian Zheng

Department of Thyroid and Neck Tumor, Tianjin Medical University Cancer Institute and Hospital, National Clinical Research Center for Cancer

Key Laboratory of Cancer Prevention and Therapy, Tianjin’s Clinical Research Center for Cancer, Tianjin 300060, People’s Republic of China