M5c regulator

M5c (5-methylcytosine) regulators are proteins or enzymes involved in the control and regulation of DNA methylation at specific sites in the genome. DNA methylation is a crucial epigenetic modification in which a methyl group (CH3) is added to the cytosine base of DNA. This modification can have significant effects on gene expression and genome stability.

There are several types of M5c regulators, including:

DNA Methyltransferases: These enzymes are responsible for adding methyl groups to cytosine residues in DNA. The most well-known DNA methyltransferases are DNMT1, DNMT3A, and DNMT3B.

Demethylases: Demethylases, such as TET proteins (Ten-Eleven Translocation), are enzymes that can remove methyl groups from 5-methylcytosine, thereby reversing DNA methylation.

Methyl-CpG Binding Proteins: These proteins can bind to methylated CpG sites (regions of DNA where cytosine is followed by guanine) and play a role in gene regulation and chromatin structure. Examples include MeCP2 and MBD proteins.

Chromatin Modifiers: Various chromatin modifiers, such as histone methyltransferases and demethylases, can interact with M5c regulators to influence gene expression through a combination of DNA methylation and histone modifications.

RNA-Mediated Regulation: Non-coding RNAs, like microRNAs and long non-coding RNAs, can also influence DNA methylation patterns by interacting with M5c regulators.

The interplay between these regulators and DNA methylation is critical for controlling gene expression, maintaining genomic stability, and playing a role in various biological processes, including development, differentiation, and disease.

Research in the field of epigenetics continues to uncover new M5c regulators and their roles in gene regulation, and our understanding of these regulators is constantly evolving. It's essential to consult the latest scientific literature for the most up-to-date information on M5c regulators and their functions.

Numerous studies illustrated the importance of 5-methylcytosine (m5C) RNA modification to tumorigenesis. However, the prognostic value and immune correlation of m5C in glioma remain unclear. Xiao et al. obtained RNA expression and clinical information from The Cancer Genome Atlas (TCGA) and The Chinese Glioma Genome Atlas (CGGA) datasets to analyze. Nonnegative matrix factorization (NMF) was used to classify patients into two subgroups and compare these patients in survival and clinicopathological characteristics. CIBERSORT and single-sample gene-set algorithm (ssGSEA) methods were used to investigate the relationship between m5C and the immune environment. The Weighted correlation network analysis (WGCNA) and univariate Cox proportional hazard model (CoxPH) were used to construct a m5C-related signature. Most m5C RNA methylation regulators presented differential expression and prognostic values. There were obvious relationships between immune infiltration cells and m5C regulators, especially NSUN7. In the m5C-related module from WGCNA, we found SEPT3, CHI3L1, PLBD1, PHYHIPL, SAMD8, RAP1B, B3GNT5, RER1, PTPN7, SLC39A1, and MXI1 were prognostic factors for glioma, and they were used to construct the

signature. The great significance of m5C-related signature in predicting the survival of patients with glioma was confirmed in the validation sets and CGGA cohort [1)]

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Xiao Z, Li J, Liang C, Liu Y, Zhang Y, Zhang Y, Liu Q, Yan X. Identification of M5c regulator-medicated methylation modification patterns for prognosis and immune microenvironment in glioma. Aging (Albany NY). 2023 Nov 6;15. doi: 10.18632/aging.205179. Epub ahead of print. PMID: 37934565.