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## Proteins that bind methylated DNA and human cancer: reading the wrong words

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DNA methylation and the machinery involved in epigenetic regulation are key elements in the maintenance of cellular homeostasis. Epigenetic mechanisms are involved in embryonic development and the establishment of tissue-specific expression, X-chromosome inactivation and imprinting patterns, and maintenance of chromosome stability. The balance between all the enzymes and factors involved in DNA methylation and its interpretation by different groups of nuclear factors is crucial for normal cell behaviour. In cancer and other diseases, misregulation of epigenetic marks is a common feature, also including DNA methylation and histone post-translational modifications. In this scenario, it is worth mentioning a family of proteins characterized by the presence of a methyl-CpG-binding domain (MBDs) that are involved in interpreting the information encoded by DNA methylation and the recruitment of the enzymes responsible for establishing a silenced state of the chromatin. The generation of novel aberrantly hypermethylated regions during cancer development and progression makes MBD proteins interesting targets for their biological and clinical implications.