Comparing the Effects of NSD2 and Its Cancerous Mutation on Nucleosomes to Identify Potential Routes for Inhibition

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Lysine methyltransferases (KMTs) are an essential group of enzymes that regulate gene expression. In an attempt to track rising cancer cases, scientists discovered a detrimental mutation of a KMT called NSD2. It differs from the regular enzyme by one amino acid, causing it to malfunction. Because of its unpredictable nature, scientists have yet to find a cure. In this study, the effects of NSD2 and its cancerous mutation on nucleosomes under natural conditions were investigated to explore potential routes for inhibition. The activity, binding affinity, and melting points of both enzymes were tested using a western blot, MST, and PCR machine, respectively. The results of the western blot suggest that the mutation is more active, as more demethylation detecting antibodies bound to the sample. Additionally, the PCR machine showed that the mutation has a lower melting point, indicating that it is less stable. This is believed to affect enzyme activity and lead to the abnormal expression of genes. Upon testing factors that affect its activity, it was found that their binding affinities overlap, suggesting that it does not contribute to the enhanced activity of the mutation. These findings set the foundation for further studies to evaluate the biochemical properties of NSD2, which may have potential applications for drug development and other epigenetic studies.