Histone H3 as a redox switch in the nucleosome core particle: insights from molecular modeling

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Abstract

Cancer is caused by genetic mutations disrupting normal cell growth regulation. It is a major global health concern. With an alarming increase in new cases projected by 2050, researchers try to develop effective therapeutic strategies. Among the various treatments, epigenetic therapy holds promise. Epigenetic marks, chemical modifications on DNA and histone proteins, dynamically regulate gene expression and chromatin structure. Here, we study the impact of two oxidative histone H3 modifications, S-sulfenylation (SOH) and S-nitrosylation (SNO) on nucleosome dynamics. Employing molecular dynamics simulations and advanced structural analyses, we reveal distinct structural signatures for S-sulfenylation and S-nitrosylation in the nucleosome core particle, suggesting different roles in regulating chromatin dynamics. These findings offer insights for targeted therapeutic interventions in cancer treatment.

Keywords: Molecular Modeling, Molecular Dynamics (MD), post-translational modification, DNA compaction, anti-cancer