

عنوان مقاله:

Bioinformatics approach for potential inhibitory of pyrogallol in ovarian cancer by CdcY&A targeting

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خلاصه مقاله:

Introduction: Pyrogallol, one of the natural polyphenols, was known to have anti-inflammatory andantitumor effects in some cancers. However, the underlying antitumor mechanisms of pyrogallol, still remainunclear so far. Cell division cycle ۲۵ A (Cdc۲۵A), is one of the most vital cell cycle regulators, and positivelycontrols the functions of CDKs that lead to cell cycle progression. Overexpression of CdcY&A promotestumorigenesis, and is observed in ovarian cancer. Therefore, the present study aimed to determine thepotential therapeutic effect of pyrogallol for CdcraA inhibition.Methods: Pyrogallol structure was drawn in the HyperChem software. CdcY&A protein structure was retrieved from the RCSB PDB database. For molecular docking and preparation of ligand and target protein, Autodock F.Y was used. CdcY&A protein structure docking studies were performed with this software. Nonpolar hydrogen atoms were assembled and fixed in ligand. Result: According to the molecular docking studies, pyrogallol showed high binding energies with CdcγδAprotein, with maximum values of -٣.ΥΥ kJ/mol. pyrogallol mostly interacts with H, R, K, S,G, I amino acids. Conclusion: This evaluation concludes that pyrogallol may be used as an anticancer drug for ovarian canceras it can suppress Cdcraa proteins and may stop the cell proliferation in cancers. Pyrogallol is recommendas an effective, safe, and commercial drug to inhibit tumor progression in patients with ovarian cancer

کلمات کلیدی:

Key words: Pyrogallol; CdcY&A; ovarian cancer; in silico

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