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In Silico Evaluation of Anti-Cancer Ligands Targeting LGR4 Receptor

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Abstract

Leucine-rich repeat-containing G protein-coupled receptor 4 (LGR4/GPR48) has recently emerged as a critical player in various malignancies, including breast cancer, participating in tumor progression, invasion, and metastasis [1,2]. LGR4 inhibitors are currently being explored for a variety of medical applications, with cancer therapy being the most promising application. The extracellular domain of LGR4 (LGR4-ECD) has shown potential as a new therapeutic for cancer [3]. In this study, a molecular docking-based screening approach was used to identify the natural compounds with anti-breast cancer activities. The 3D structure of LGR4 protein (PDB ID: 4QXE) was retrieved from PDB, RCSB. Several natural compounds including Myricetin, Quercetin, Apigenin, Luteolin and Baicalein were chosen to be investigated as LGR4 binders. Ligands were acquired in their 3D conformer forms from the PubChem database (https://pubchem.ncbi.nlm.nih.gov/). The structures of both the protein and ligands were subsequently prepared for molecular docking using Molegro Virtual Docker (MVD). From protein-ligand interaction analysis and binding energies determined following docking, we found that the Baicalein had the highest binding affinity to the target protein (MolDock Score of −118.95). These findings may provide important information for developing anti-breast cancer therapeutics targeting LGR4.

Key words: LGR4, Breast cancer, docking simulations, 3D structure

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