IDENTIFICATION OF CYANINE 7 DOCKING SITE ON PROTEIN ETANERCEPT SUBUNITS USING AUTODOCK4 SCRIPT

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Tumor necrosis factor (TNF) is a small protein from the group of cytokines, important signaling molecule in various inflammatory conditions including atherosclerosis, rheumatoid arthritis, and cancer. In particular, it could be secreted by adipose tissue to promote low-grade inflammation in other tissues leading to metabolic syndrome, insulin resistance, and type II diabetes [1]. The most common medication suppressing TNF effect is etanercept (ETN). It is a fusion protein composed of two extracellular domains of TNFR2 and the Fc region of IgG1.

Cyanine dyes are widely used in bioimaging research due to its low toxicity, ability to accumulate in tissues in enough amounts to be useful for fluorescence-based techniques to visualize blood vessels and tumors [2].

It is still under the question if cyanine dye injection could prevent ETN suppressing TNF activity. ETN effect is based on ability to bind TNF molecules thus preventing them from interaction with transmembrane TNF receptors.

In this work, we researched the possibility of cy7 cyanine dye molecule docking to the TNF-specific TNFR2 subunit binding site using AutoDock4 – a molecular docking experiment script [3]. Before running AutoDock4 we used Lamarckian Genetic Algorithm to select possible protein binding sites to cy7 with minimal binding energy including electrostatic, hydrogen bonding, Van der Waals, desolvation energy.

We found that the most energy efficient regions for cy7 docking to ETN are located on IgGl-Fc subunit of ETN far from TNF binding site, so there is a little chance that cy7 could prevent TNF and TNF2 subunit of ETN interaction.

References:

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