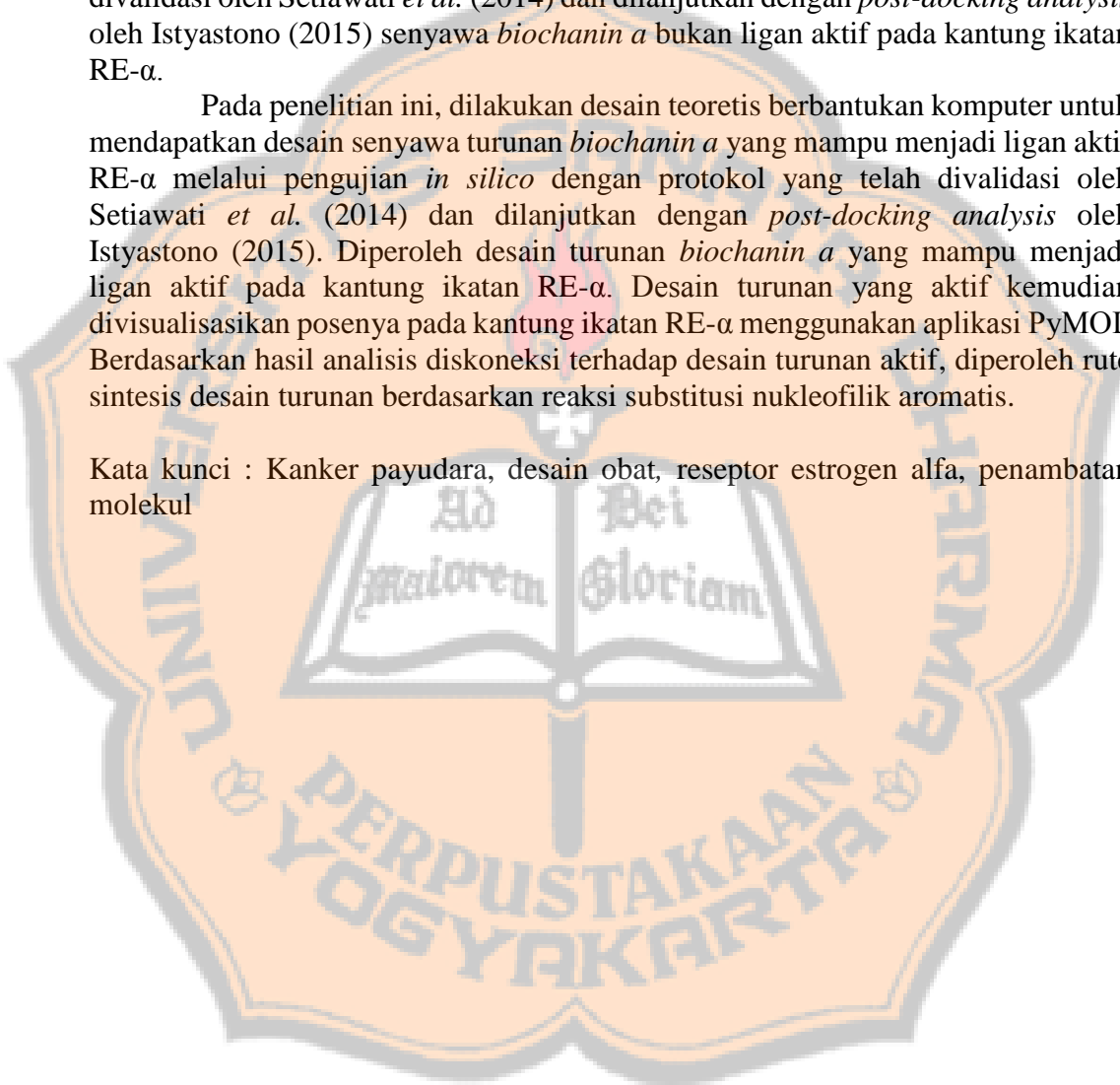


ABSTRAK

Kanker payudara adalah kanker dengan jumlah kasus 1,7 juta di seluruh dunia. Salah satu penyebab terjadinya kanker payudara adalah ekspresi berlebih reseptor estrogen alfa (RE- α) oleh hormon estrogen. Senyawa *biochanin a* merupakan senyawa fitokimia golongan isoflavon yang diketahui memiliki aktivitas anti-kanker, namun secara uji *in silico* dengan protokol yang telah divalidasi oleh Setiawati *et al.* (2014) dan dilanjutkan dengan *post-docking analysis* oleh Istyastono (2015) senyawa *biochanin a* bukan ligan aktif pada kantung ikatan RE- α .

Pada penelitian ini, dilakukan desain teoretis berbantuan komputer untuk mendapatkan desain senyawa turunan *biochanin a* yang mampu menjadi ligan aktif RE- α melalui pengujian *in silico* dengan protokol yang telah divalidasi oleh Setiawati *et al.* (2014) dan dilanjutkan dengan *post-docking analysis* oleh Istyastono (2015). Diperoleh desain turunan *biochanin a* yang mampu menjadi ligan aktif pada kantung ikatan RE- α . Desain turunan yang aktif kemudian divisualisasikan posenya pada kantung ikatan RE- α menggunakan aplikasi PyMOL. Berdasarkan hasil analisis diskoneksi terhadap desain turunan aktif, diperoleh rute sintesis desain turunan berdasarkan reaksi substitusi nukleofilik aromatis.

Kata kunci : Kanker payudara, desain obat, reseptor estrogen alfa, penambatan molekul



ABSTRACT

Breast cancer is type of cancer with 1.7 million cases around the world. One of the causes of breast cancer is the over-expression of estrogen receptor alpha (ER- α) by the estrogen hormone. Biochanin a is a phytochemical compound of isoflavone which is known to have anti-cancer activity, but according to *in silico* experiment with the protocol that had been validated by Setiawati et al. (2014) and continued with post-docking analysis by Istyastono (2015) that biochanin a compound is not an active ligand on ER- α binding pocket.

In this study, theoretical computer-aided design was conducted to obtain the design of derived compounds of biochanin a which was able to be an active ligand on ER- α binding pocket through *in silico* testing with the protocol that had been validated by Setiawati et al. (2014) and continued with post-docking analysis by Istyastono (2015). The design of derived compound of biochanin a which was able to be an active ligand on ER- α binding pocket had been obtained. Then, the pose of the design of the active derivative was visualized on ER- α binding pocket using PyMOL application. Based on the result of the analysis of the disconnection towards the active derivative design obtained the synthesis route of derivative design based on aromatic nucleophilic substitution reaction.

Keywords : Breast cancer, drug design, estrogen receptor alpha, molecular docking

