Abstrak

ANALISIS POTENSI SENYAWA AKTIF ANTIKANKER SEBAGAI INHIBITOR *HER-2* SECARA *IN SILICO*

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Latar Belakang : Kanker payudara merupakan kanker yang terjadi akibat overekspresi HER-2. Hal tersebut dapat diatasi menggunakan terapi tertarget berupa inhibitor HER-2 seperti Transtuzumab. Namun reaktivasi reseptor, penurunan persinyalan, dan mutasi menimbulkan resistensi pada Transtuzumab. Penelitian ini bertujuan untuk mengetahui potensi inhibisi 11 senyawa antikanker sebagai terapi adjuvan inhibitor HER-2.

Metodologi : Penelitian eksperimental dilakukan secara *in silico* melalui penambatan molekul antara 11 senyawa dengan HER-2 dan uji aturan Lipinski. Analisis data dilakukan dengan membandingkan nilai energi ikatan dengan Erlotinib sebagai kontrol positif dan sifat fisikokimia dengan parameter uji lipinski.

Hasil Penelitian : Nilai energi ikatan yang diperoleh dari 11 senyawa tersebut yaitu alashanoid B (-6,5), alfa mangostin (-9,0), andrografolid (-7,9), sinamaldehida (-7,5), kurkumin (-9,4), EPMC (-7,1), galangin (-9,0), gamma mangostin (-9,2), pinocembrin (-9,3), pinostrobin (-9,5), dan xanthorizol (-8,8) dengan kontrol erlotinib (-9,0) dan ligan natif (-11,3) dengan jenis ikatan yang umum terjadi yaitu interaksi hidrofobik. Hasil uji Lipinski menunjukkan 10 senyawa selain alfa mangostin telah memenuhi aturan Lipinski.

Kesimpulan : Senyawa pinostrobin, kurkumin, dan pinocembrin menunjukkan potensi tertinggi sebagai terapi adjuvan inhibitor HER-2..

Kata Kunci : Inhibitor HER-2, *molecular docking*, Lipinski

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Abstract

IN SILICO ANALYSIS OF POTENTIAL ANTI-CANCER ACTIVE COMPOUNDS AS HER-2 INHIBITOR

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Background : Breast cancer is a type of cancers due to overexpression of HER-2. This can be overcome using targeted therapy by targeting against the kinase domain of HER-2 inhibitors such as Transtuzumab. Transtuzumab facing challenges such as receptor reactivation, decrease signaling, or mutations that causing resistance. This study aims to determine the inhibition potential of 11 anticancer compounds as adjuvant therapy for HER-2 inhibitors.

Method : Study in silico through molecular docking between 11 compounds with HER-2 followed by the Lipinski rule test. Data analysis was performed by comparing the affinity energy values with Erlotinib as a positive control and physicochemical properties with Lipinski parameters.

Results : Binding affinity energy value from these anticancer compounds are alashanoid B (-6.5), alpha mangostin (-9.0), andrographolide (-7.9), cinnamaldehyde (-7.5) , curcumin (-9.4), EPMC (-7.1), galangin (-9.0), gamma mangostin (-9.2), pinocembrin (-9.3), pinostrobin (-9.5), and xanthorizol (-8.8) with control of erlotinib (-9.0) and native ligand (-11.3) while the most common type of bond is hydrophobic interaction. The Lipinski's data showed 10 compounds have met Lipinski's rules except for alpha mangostin.

Conclusion : Pinostrobin, curcumin, and pinocembrin showed the highest potential as adjuvant therapy for HER-2 inhibitors.

Keywords : HER-2 inhibitor, molecular docking, Lipinski

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