ABSTRAK

Diabetes melitus tipe 2 disebabkan oleh hilangnya sekresi insulin sel beta yang adekuat secara progresif sering dengan latar belakang resistensi insulin. Salah satu obat oral untuk pengobatan diabetes melitus tipe 2 yaitu inhibitor Dipeptidil Peptidase-IV (DPP-IV). Senyawa alam yang dapat dimanfaatkan sebagai obat diabetes yaitu senyawa flavonoid, salah satunya *quercetin*. Mekanisme *quercetin* sebagai inhibitor DPP-IV dapat diamati melalui simulasi dinamika molekul. Penelitian ini bertujuan untuk mengetahui stabilitas kompleks Dipeptidil Peptidase IV (DPP-IV) dan *quercetin* dalam simulasi dinamika molekul 50 ns. Jenis penelitian ini merupakan penelitian teoretis deskriptif eksploratif dengan parameter nilai *Root Mean Square Deviation* (RMSD) ≤ 2 Å, *Root Mean Square Fluctuation* (RMSF) < 0,5 Å, dan *Molecular Mechanic/Poisson-Boltzmann Surface Area* (MM/PBSA) < 0 kJ/mol. Hasil penelitian ini menunjukkan bahwa terbentuk kompleks Dipeptidil Peptidase IV (DPP-IV) dan *quercetin* yang stabil dengan nilai ΔRMSD atom-atom *backbone* dan *ligand move* berturut-turut sebesar 0,478 Å dan 1,487 Å pada 5 ns terakhir dalam *production run*. Kemudian nilai RMSF yang diperoleh pada sisi katalitik yaitu residu Ser630, Asn710 dan His740 berturut-turut sebesar 0,86 Å, 1,09 Å, dan 0,62 Å, serta nilai MM/PBSA atau nilai rata-rata *binding free energy* (ΔG) sebesar 32,932 kJ/mol.

Kata kunci: Dipeptidil Peptidase-IV (DPP-IV), *quercetin*, dinamika molekul, RMSD, RMSF, MM/PBSA

ABSTRACT

Type 2 diabetes mellitus is caused by a progressive loss of adequate beta-cell insulin secretion, often against a background of insulin resistance. One of the oral drugs for the treatment of type 2 diabetes mellitus is the Dipeptidyl Peptidase-IV (DPP-IV) inhibitor. Natural compounds that can be used as diabetes drugs are flavonoid compounds, one of which is quercetin. The mechanism of quercetin as a DPP-IV inhibitor can be observed through molecular dynamics simulations. This research aims to determine the stability of the Dipeptidyl Peptidase IV (DPP-IV) complex and quercetin in 50 ns molecular dynamics simulation. This is a descriptive explorative theoretical research with parameter values of Root Mean Square Deviation (RMSD) ≤ 2 Å, Root Mean Square Fluctuation (RMSF) < 0.5 Å, and Molecular Mechanic/Poisson-Boltzmann Surface Area (MM/PBSA) < 0 kJ/mol. The results of this research indicate that a stable Dipeptidyl Peptidase IV (DPP-IV) and quercetin complex was formed with ΔRMSD values of the backbone atoms and ligand move of 0.478 Å and 1.487 Å in the last 5 ns of the production run, respectively. Furthermore, the RMSF values obtained on the catalytic side, namely Ser630, Asn710 and His740 residues were 0.86 Å, 1.09 Å and 0.62 Å respectively, as well as the MM/PBSA value or the average value of binding free energy (ΔG) of 32.932 kJ/mol.

Keywords: Dipeptidyl Peptidase-IV (DPP-IV), quercetin, molecular dynamics, RMSD, RMSF, MM/PBSA