ABSTRAK

Alzheimer merupakan penyakit neurodegeneratif yang ditandai dengan penurunan fungsi kognitif. Senyawa serpentin terbukti potensial sebagai penghambat enzim asetilkolinesterase (AChE) untuk penyakit Alzheimer. Penelitian ini bertujuan untuk mengidentifikasi interaksi dan stabilitas interaksi serpentin-AChE secara *in silico*. Parameter yang digunakan dalam penelitian ini adalah nilai *root mean square deviation* (RMSD) penambatan ulang, energi ikatan penambatan molekul serpentin, RMSD *backbone* AChE dan *LigandMovement* yang dianalisis pada 5 ns terakhir *production run*. Hasil penelitian menunjukkan bahwa nilai RMSD penambatan ulang huprine X dan penambatan molekul serpentin ≤ 2,000 Å. Interaksi aromatik dan hidrofobik pada kompleks huprine X-AChE teramati juga pada kompleks serpentin-AChE yang mengindikasikan bahwa serpentin memiliki mekanisme penghambatan yang sama dengan ligan *native* huprine X terhadap AChE. Hasil simulasi dinamika molekul juga menunjukkan bahwa pada analisis 5 ns terakhir *production run*, nilai ΔRMSD *backbone* dan *LigandMovement* ≤ 2,000 Å. Hasil ini mengindikasikan bahwa serpentin dapat menstabilkan konformasi AChE. Pada simulasi dinamika molekul yang telah dilakukan, serpentin dapat mempertahankan konformasi yang stabil pada sisi aktif AChE dan berinteraksi pada residu asam amino Phe330, Trp84, Tyr70, Tyr 121, dan Ile439.

Kata Kunci: Alzheimer, Asetilkolinesterase, Serpentin, Penambatan Molekul, Simulasi Dinamika Molekul

ABSTRACT

Alzheimer's is a neurodegenerative disease characterized by a decline in cognitive function. Serpentine compound has been proven to be a potential inhibitor of acetylcholinesterase (AChE) enzyme for Alzheimer's disease. This study aimed to identify the interaction and stability of the serpentine-AChE interaction in silico. The parameters used in this study were the root mean square deviation (RMSD) values of redocking, the binding energy of docked serpentine resulted from molecular docking, the RMSD of the AChE backbone, and the LigandMovement, which were analyzed in the last 5 ns of the production run. The results showed that the RMSD values of the redocking of huprine X and the molecular docking of the serpentine were ≤ 2.000 Å. The aromatic and hydrophobic interactions of huprine X-AChE were observed in serpentine-AChE, indicating that serpentine has the same inhibition mechanism as the native ligand huprine X against AChE. The molecular dynamics simulations results also showed that in the analysis of the last 5 ns of the production run, the ΔRMSD values of the AChE backbone and LigandMovement were ≤ 2.000 Å. These results indicated that serpentine could stabilize the conformation of AChE. In the molecular dynamics simulations carried out, serpentine could maintain a stable conformation at the active site of AChE and interacted with amino acid residues of Phe330, Trp84, Tyr70, Tyr121, and Ile439.

Keywords: Alzheimer's disease, Acetylcholinesterase, Serpentine, Molecular Docking, Molecular Dynamics Simulations