

**KAJIAN INTERAKSI SENYAWA ANTIPSIKOTIK  
ARIPIPRAZOL DENGAN RESEPTOR DOPAMIN D3 MENGUNAKAN  
METODE SIMULASI DINAMIKA MOLEKULAR**

Puji Budi Asih  
09/284128/PA/12843

**INTISARI**

Kajian interaksi senyawa aripiprazol dengan reseptor protein dopamin D3 menggunakan simulasi dinamika molekular telah dilakukan. Tujuan dari penelitian ini untuk mengetahui kelarutan ligan (aripiprazol dan ETQ) dalam air, dan interaksi kompleks dopamin D3-aripiprazol. Penelitian diawali dengan proses *docking* ligan aripiprazol berdasarkan *binding site* hasil *docking* ligan ETQ (*eticopride*) pada reseptor. Berdasarkan konformasi terbaik hasil *docking* ligan dilakukan simulasi dinamika molekular *free energy perturbation* (FEP) untuk memprediksi energi solvasi ligan dan simulasi dinamik dopamin D3-aripiprazol pada kondisi NPT (*number, pressure, temperature*) tetap.

Hasil penelitian menunjukkan energi solvasi aripiprazol ( $-233,82 \pm 0,89$  kJ/mol) dalam pelarut air lebih rendah dibanding ligan ETQ ( $-181,98 \pm 3,19$  kJ/mol) dalam air. Hal ini menunjukkan bahwa kelarutan aripiprazol dalam air lebih besar dibanding dengan ETQ. Dalam kondisi NPT 500-600 ps terekam maksimal terjadi 6 ikatan hidrogen ETQ dengan pelarut, dan 7 ikatan hidrogen aripiprazol pelarut. Hasil *docking* aripiprazol memiliki ikatan hidrogen berjumlah 3 dengan residu asam amino yaitu asam aspartat (Asp79 O•••H-N5), tirosin (Tyr5 H•••O=C30), treonin (Thr392 H•••O=C30). Hasil simulasi dinamik dopamin D3-aripiprazol dapat membentuk 5 ikatan hidrogen dengan berinteraksi dengan residu asam amino : asam aspartat (Asp79 O•••H-N5), tirosin (Tyr5 H•••O=C30 dan Tyr5 O•••H-N7), treonin (Thr392 H•••O=C30) dan sistein (Cys83 H•••N6).

Kata kunci : aripiprazol, reseptor D3 dopamin, simulasi dinamika molekular

***STUDY ON INTERACTION OF ANTIPSYCHOTIC COMPOUND  
ARIPIPAZOLE WITH D3 DOPAMINE RECEPTOR USING MOLECULAR  
DYNAMICS SIMULATION METHOD***

Puji Budi Asih  
09/284128/PA/12843

**ABSTRACT**

Study on interaction between aripiprazole with D3 Dopamin receptor using molecular dynamics simulation had been performed. The purpose of this study are to know solubility of ligands (aripiprazole and ETQ) in water, and interaction of D3 dopamine-aripiprazole complex. Firstly, docking of aripiprazole to d3 dopamine receptor was performed based on ETQ's binding site. The best conformation of ligand docking used to perform molecular dynamics simulation-free energy perturbation to predict solvation energy of ligands and dynamics simulation of D3 dopamine-aripiprazole complex in constant NPT (number, pressure, temperature).

The result showed that solvation energy of aripiprazole ( $-233,82 \pm 0,89$ ) was lower than ETQ ( $-181,98 \pm 3,19$  kJ/mol) in water. It showed that solubility of aripiprazole was higher than ETQ in water. In 500-600 ps of simulation recorded that ETQ maximum could make 6 hydrogen bonds with water and aripiprazole maximum could make 7 hydrogen bonds with water. Docking's result showed that aripiprazole could make 3 hydrogen bonds with 3 amino acid residues : aspartad acid (Asp79 O•••H-N5), tyrosine (Tyr5 H•••O=C30) and threonine (Thr392 H•••O=C30). Dynamics simulation's result showed that aripiprazole could make 5 hydrogen bonds with amino acid residues : aspartad acid (Asp79 O•••H-N5), tyrosine(Tyr5 H•••O=C30 and Tyr5 O•••H-N7), threonine (Thr392 H•••O=C30) dan cysteine (Cys83 H•••N6).

Keyword : aripiprazole, D3 dopamine receptor, molecular dynamics simulation