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LAMPIRAN

Lampiran 1. Protokol Penelitian dan Protokol Post Docking

Preparasi Ligand

```
Menggambar struktur metronidazol di aplikasi marvinSketch  
simpan dalam bentuk file Metronidazol.mol2  
Buka discovery studio 3.5 dan buka metronidazol.mol2  
select ligand kemudian chemistry add hidrogen  
save as Metronidazol_01.pdb  
buka file di autodocktools  
ligand > input> open > all files > Metronidazol_01.pdb  
ligand > output> save as pdbqt > Metronidazol_01.pdbqt
```

Preparasi Protein 7dc8

```
Download protein reseptor IL-6 di RCSB (dalam bentuk polimer)  
Download 7dc8 dalam bentuk pdb format https://www.rcsb.org/structure/7dc8  
Buka file di aplikasi discovery studio  
kemudian view hierachy  
Hapus bagian B,C,D, air, hetatm, ligand co kristal  
simpan file dalam bentuk 7dc8.pdb
```

Menentukan Titik koordinat binding pocket dengan PLANTS 1.2 dan SPORES

```
cd programs  
wget http://www.tcd.uni-  
konstanz.de/plants_download/download/PLANTS1.2_64bit  
wget http://www.tcd.uni-konstanz.de/plants_download/download/SPORES_64bit  
chmod u+x PLANTS1.2_64bit SPORES_64bit  
cd ..  
mkdir Docking1  
cd Docking1  
wget https://files.rcsb.org/download/7dc8.pdb  
~/programs/SPORES_64bit --mode splitpdb 7dc8.pdb  
~/programs/PLANTS1.2_64bit --mode bind ligand_ATP301_0.mol2 5  
protein.mol2  
cp ligand_ATP301_0.mol2 ligand.mol2  
conda activate adt  
~/miniconda3/envs/adt/bin/prepare_receptor4.py -r protein.mol2  
~/miniconda3/envs/adt/bin/prepare_ligand4.py -l ligand.mol2  
conda deactivate  
cd
```

Penambatan Molekul menggunakan autodocktools

```
Buat folder bernama metronidazole_01  
Pindahkan file 7dc8.pdb Metronidazol_01.pdbqt Metronidazol_01.pdb dalam  
folder ini  
pada linux panggil aplikasi autodocktools /autodocktools  
pada aplikasi autodocktools  
file > read molecule > 7dc8.pdb  
edit > charge > kollman > oke  
Grid > macromolecule > choose > select 7dc8 > oke > 7dc8.pdbqt  
Grid > set map type > open ligand > Metronidazol_01.pdbqt  
Grid > grid box > x = 9.986; y = 23.091; z = 20.634  
Grid > output > save gpf > Metronidazol_01.gpf  
Docking > macromolecule > set rigid filename > 7dc8.pdbqt  
Docking > ligand > choose > Metronidazol_01 > select > accept  
Docking > search parameters > genetic algoritm > set GA 1000  
Docking > docking parameter > accept
```

```
Docking > output > lamarcian > Metronidazol_01.dpf > save
Pada linux buka terminal
ketik cd ~/Metronidazol_01
ls
autogrid4 -p Metronidazol_01.gpf -l Metronidazol_01.glg&
tail -f Metronidazol_01.glg

cd ~/Metronidazol_01
autodock4 -p Metronidazol_01.dpf -l Metronidazol_01.dlg&
tail -f Metronidazol_01.dlg

Buka file Metronidazol_01.dlg pada wordpad
Ctrl + F, lalu ketik "histogram"
Posisi ikatan ligan-protein paling stabil jika:
Energy paling kecil.
Jumlah anggota cluster paling banyak
Pilih cluster dengan anggota terbanyak. Perhatikan angka run-nya
Buka autodocktools.
Analyze lalu docking kemudian open.
Select file dlgs lalu open
Analyze lalu conformation kemudian play
Masukan angka 368 dan 216 lalu klik &
Pilih write current simpan 7dc8_02 docking pose 216.pdbqt 7dc8_02 docking
pose 368.pdbqt
Buka discovery studio 3,5 client
Buka file docking pose 216.pdbqt dan 7dc8_02 docking pose 368.pdbqt
buka file protein 7dc8.pdb
copy struktur 7dc8_02 docking pose 216 dan docking pose 368.pdbqt ke file
protein 7dc8
Klik scripts lalu ligan kemudian interaction show ligan binding site atom
Simpan hasil visualisasi
```