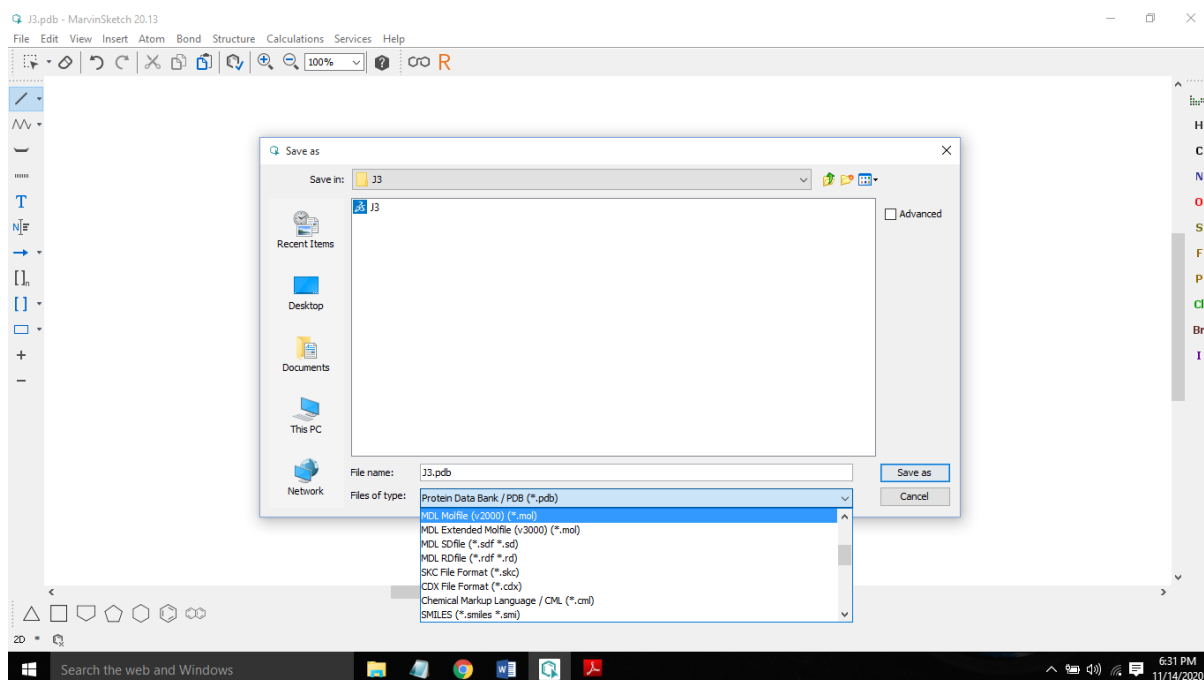
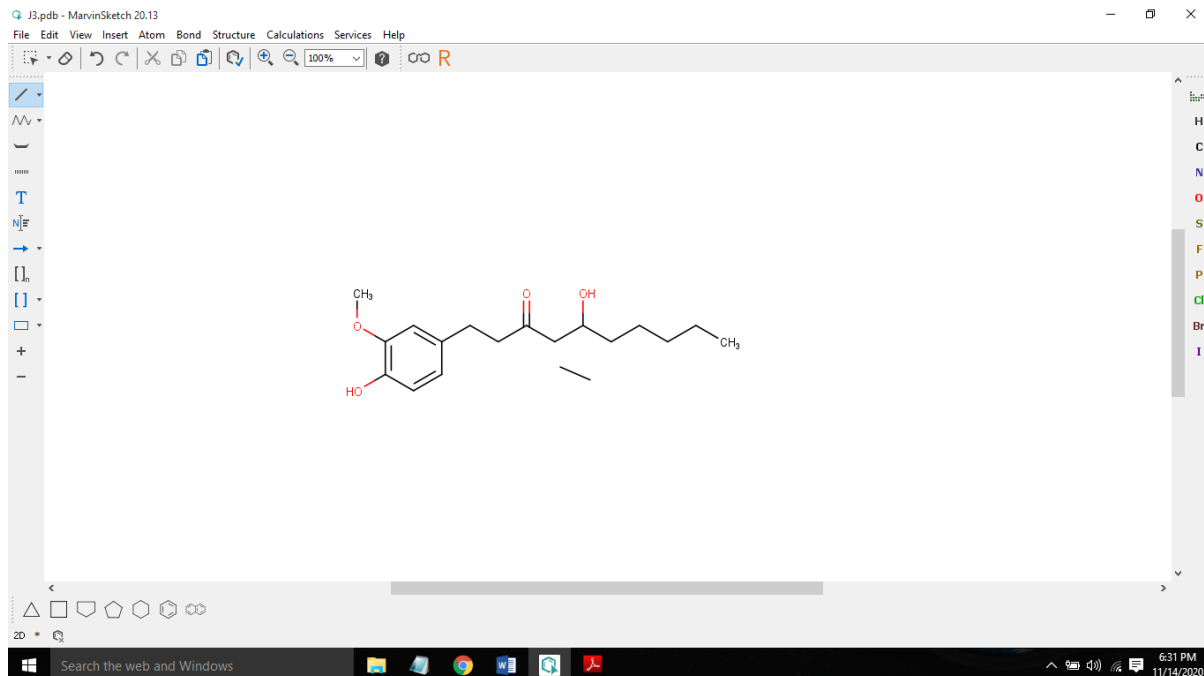
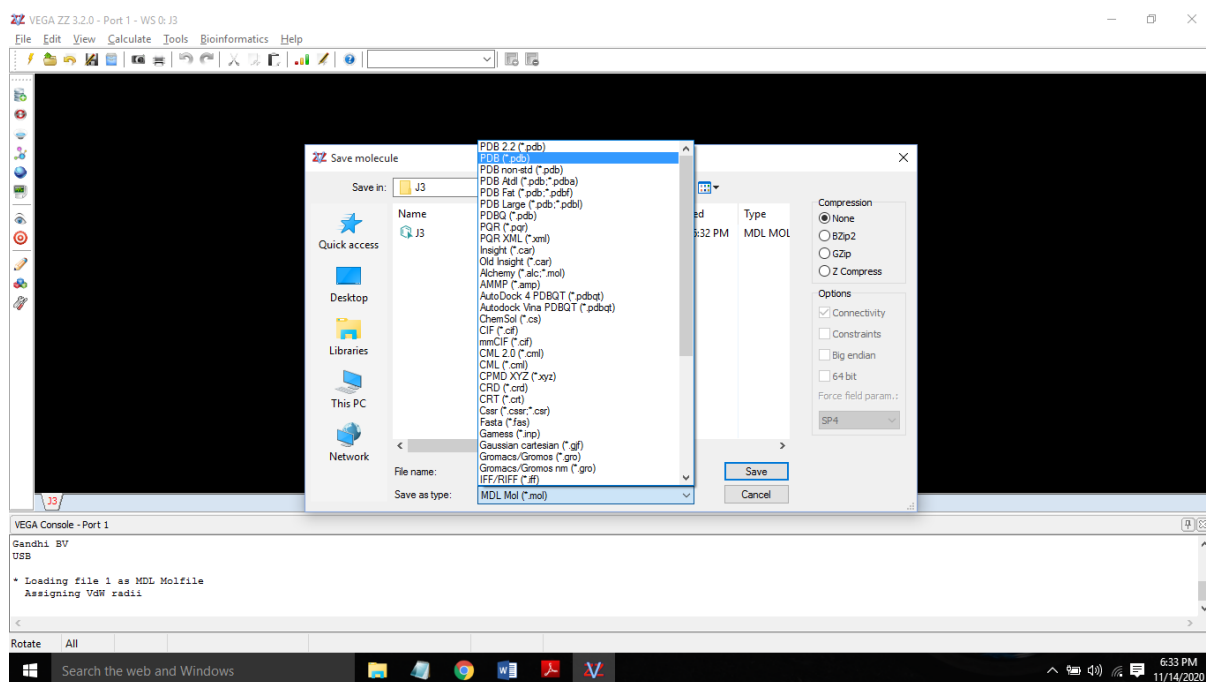
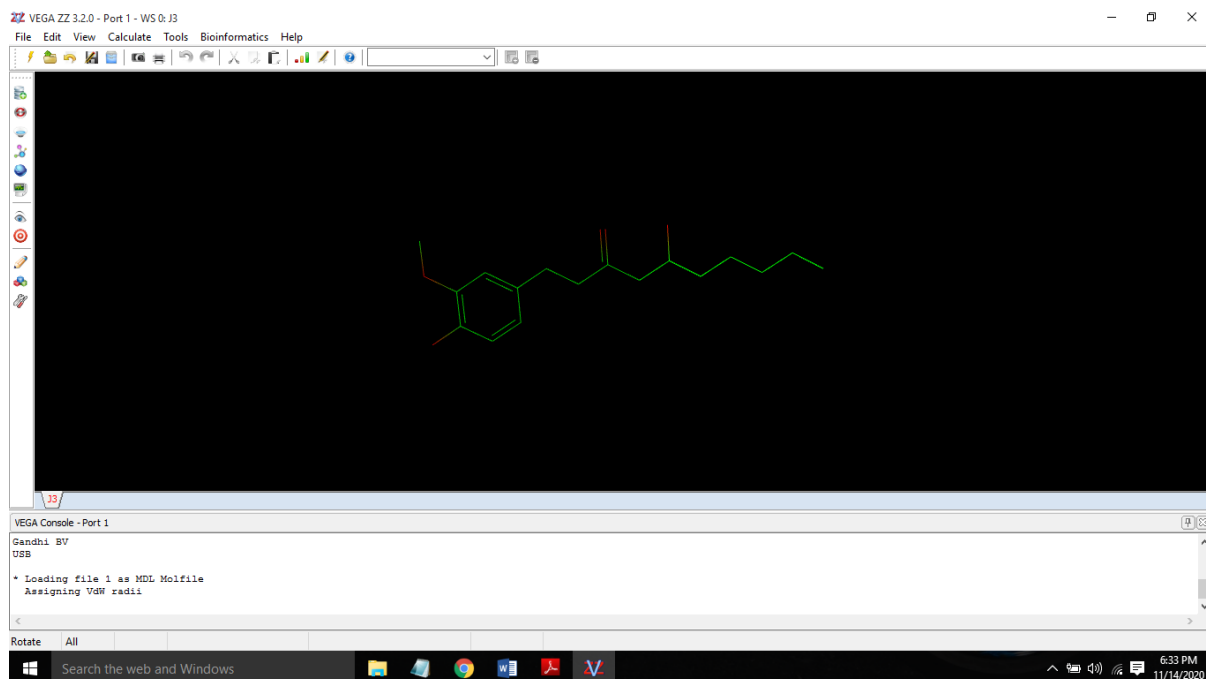


Lampiran

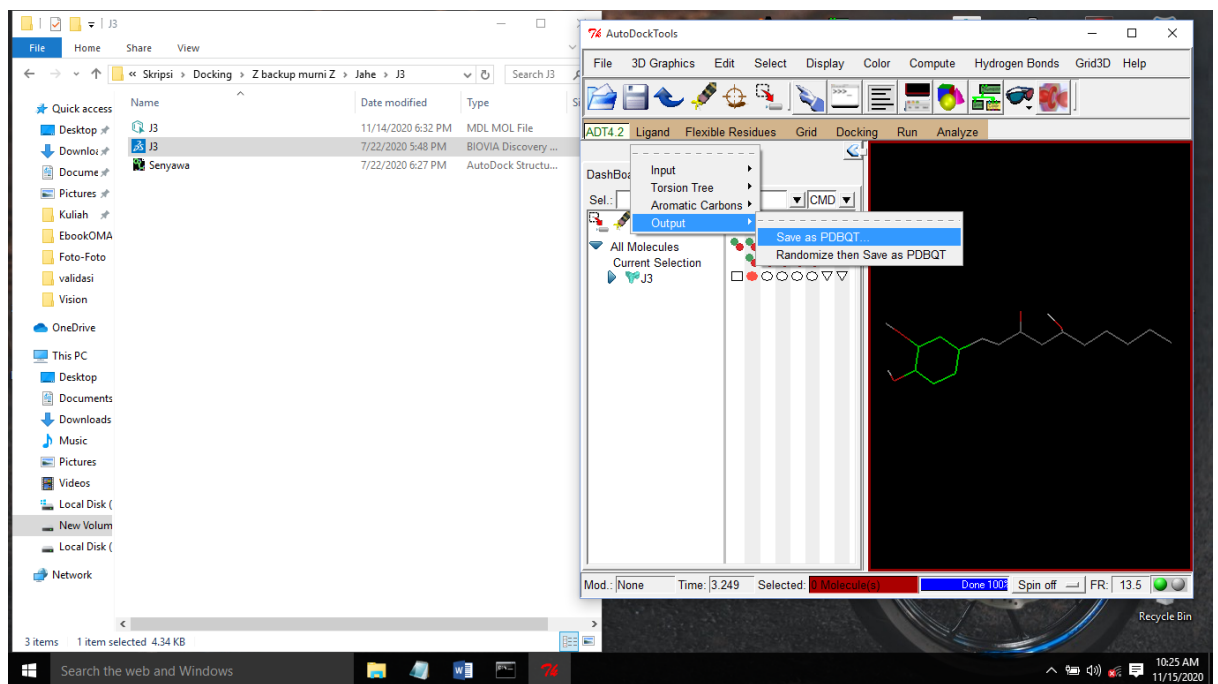
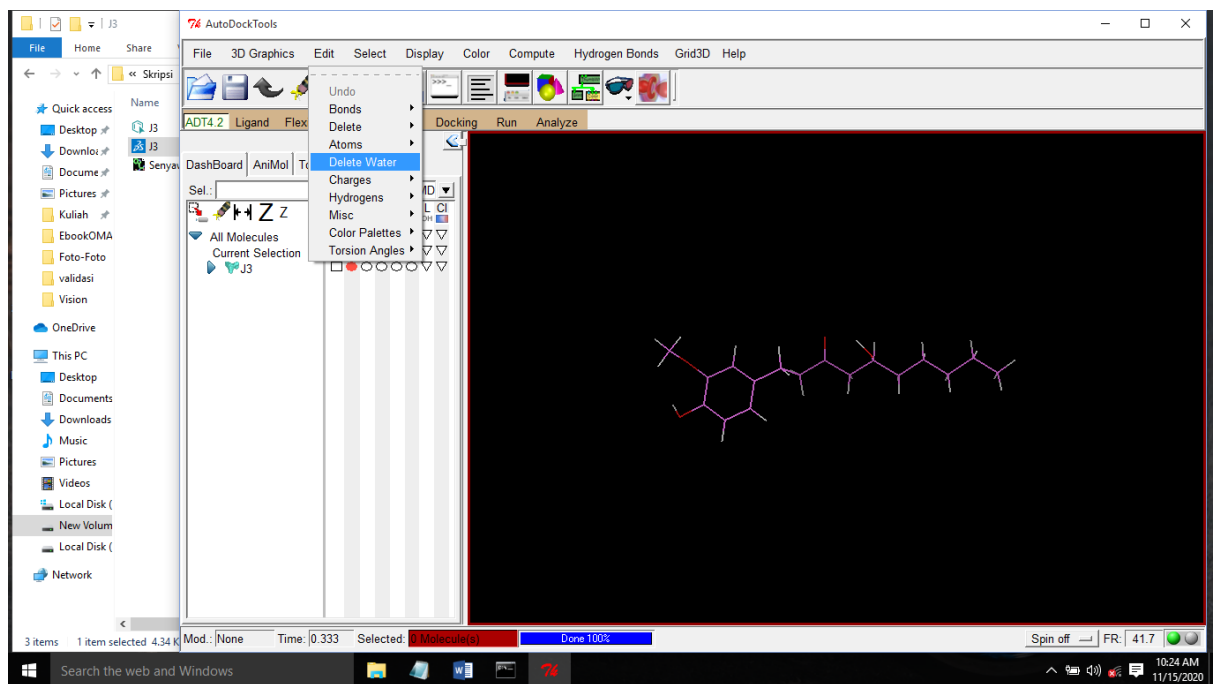
1. Menggambar 2 Dimensi Struktur



2. Konversi Struktur menjadi pdb



3. Preparasi Ligan uji



4. Mengetahui dan Memisahkan Ligan Asli

RCSB PDB - 6XA4: Crystal structure of Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) main protease (PDB ID: 6XA4) in complex with inhibitor UAW241.

Find proteins for **P0DT01** (Severe acute respiratory syndrome coronavirus 2) Explore **P0DT01** Go to UniProtKB: **P0DT01**

Protein Feature View Expand

Reference Sequence: 6XA4_1

PDB ENTITY SEQ 6XA4.1
UNIPROT ALIGN P0DT01
UNMODELED 6XA4.A
ARTIFACT

Find similar proteins by: Sequence | Structure

Entity ID: 2

Molecule	Chains	Sequence Length	Organism	Details	Image
Inhibitor UAW241	B	4	synthetic construct	Mutation(s): 0	

AutoDockTools

File 3D Graphics Edit Select Display Color Compute Hydrogen Bonds Grid3D Help

ADT4.2 Ligand Flexible Residues Grid Docking Run Analyze

Dashboard AnimMol Tools

Mod: None Time: 0.003 Selected: Chain(s) Done 100%

Spin off FR: 9.3

32 items 1 item selected 236 KB

File Explorer: validasi

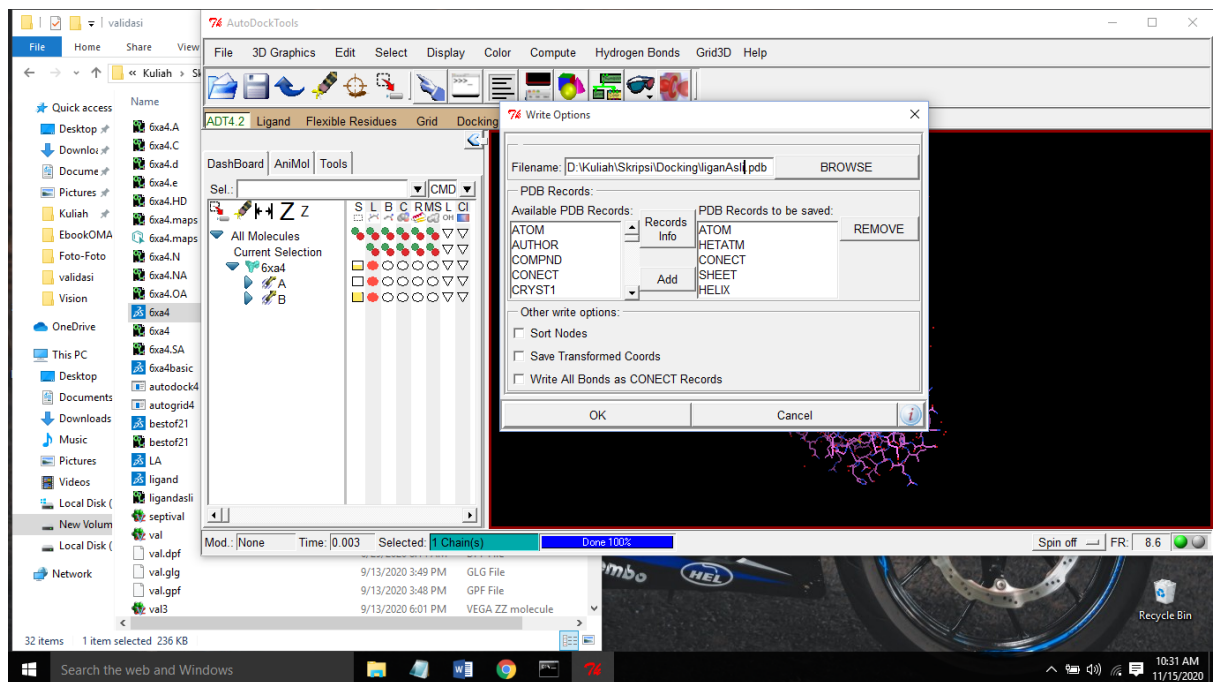
File Home Share View

Quick access: Desktop, Downloads, Documents, Music, Pictures, Videos, Local Disk (C:), Network

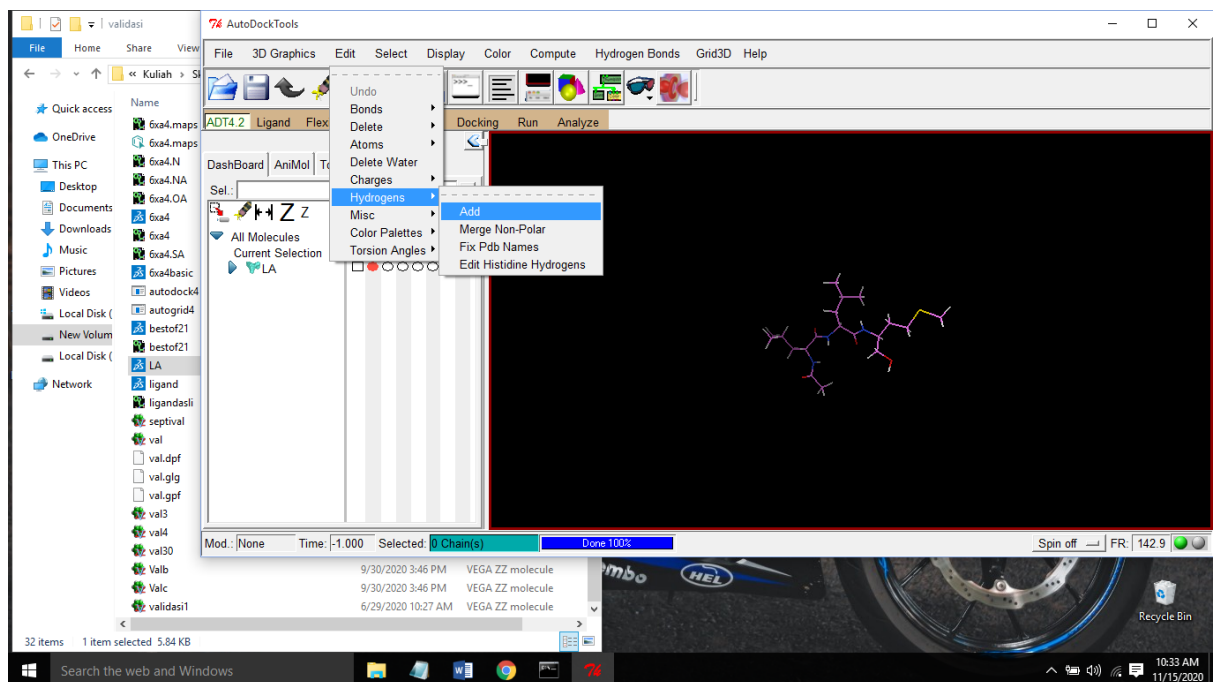
File Explorer contents:

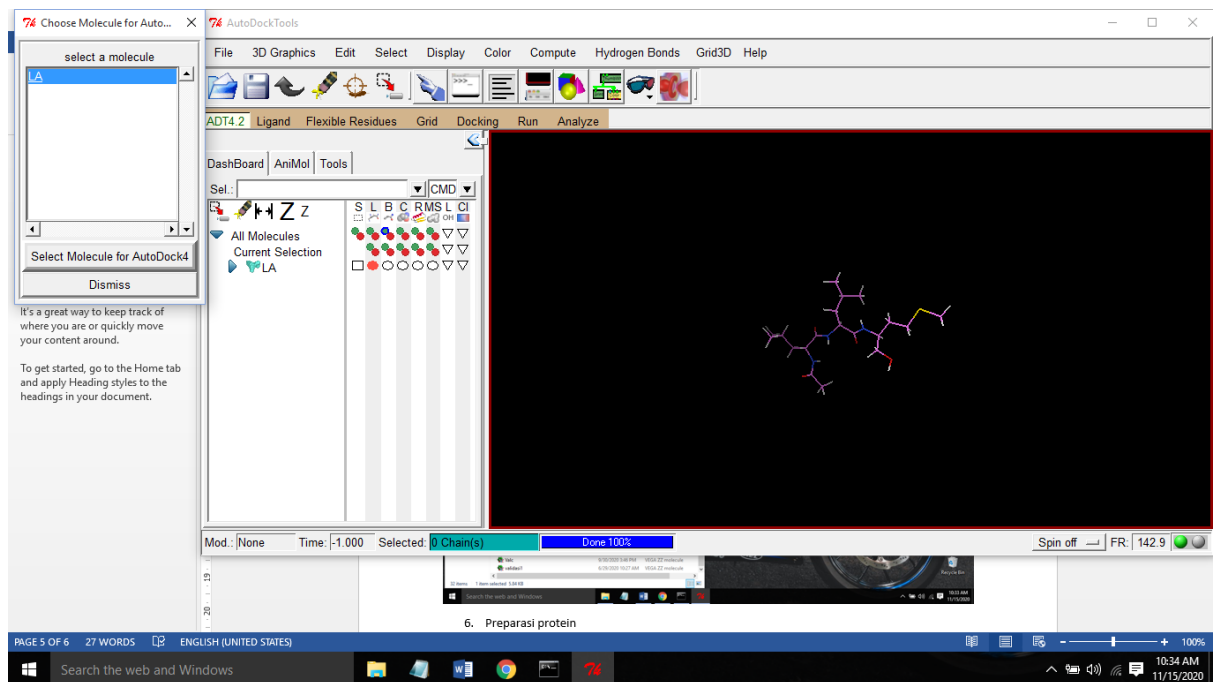
- 6xa4.A
- 6xa4.C
- 6xa4.d
- 6xa4.e
- 6xa4.HD
- 6xa4.maps
- 6xa4.maps
- 6xa4.N
- 6xa4.NA
- 6xa4.OA
- 6xa4
- 6xa4
- 6xa4.SA
- 6xa4basic
- autodock4
- autogrid4
- bestof21
- bestof21
- LA
- ligand
- ligandasli
- septival
- val
- val.dpf
- val.glg
- val.gpf
- val3

AutoDockTools interface showing a 3D molecular model of the protein-ligand complex. The protein is shown in a ribbon representation, and the ligand is shown as a stick model. The interface includes various toolbars and a file explorer on the left.

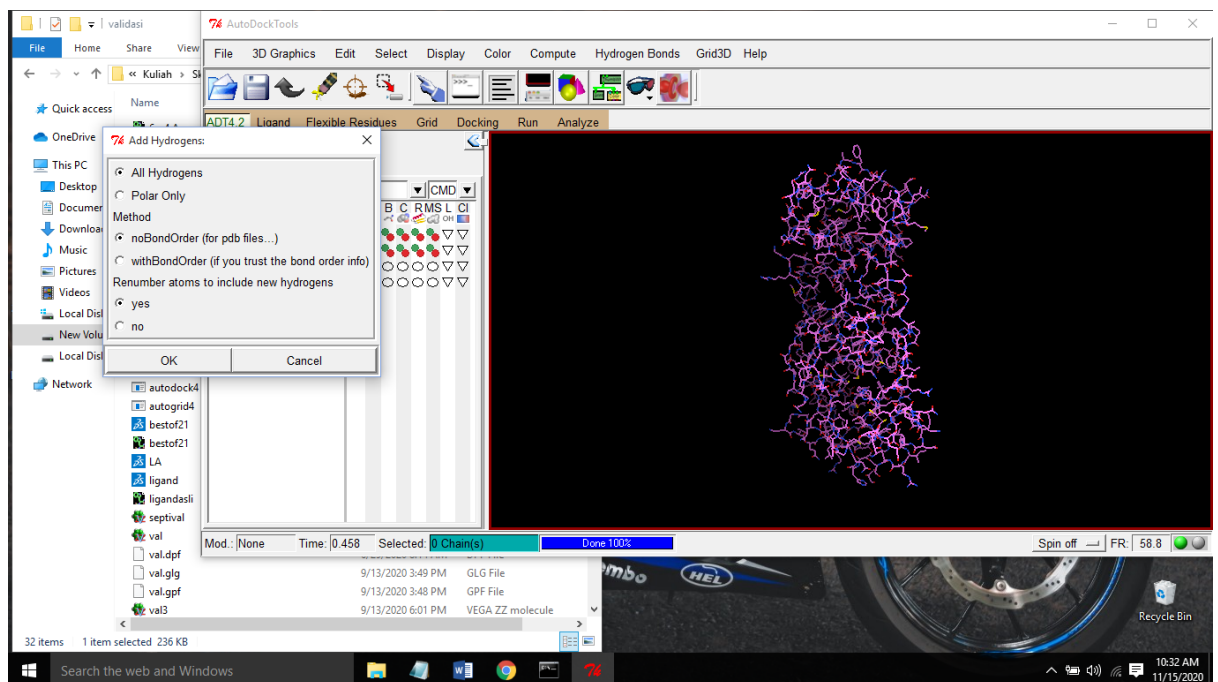


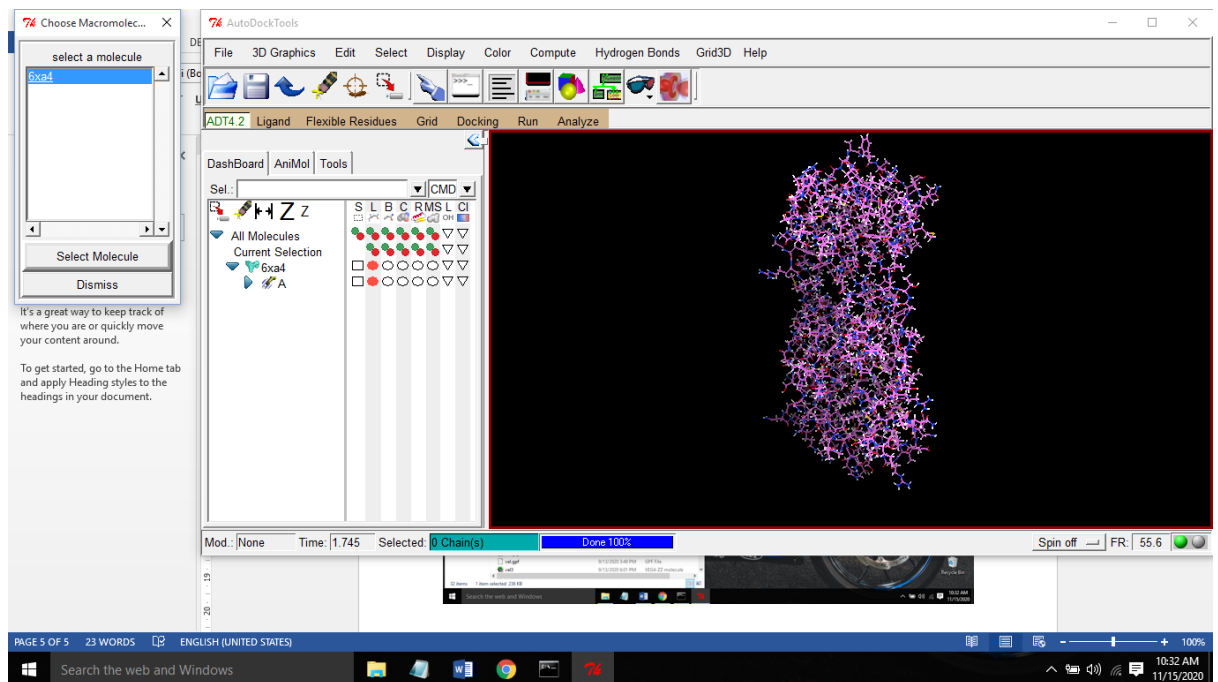
5. Preparasi ligan asli



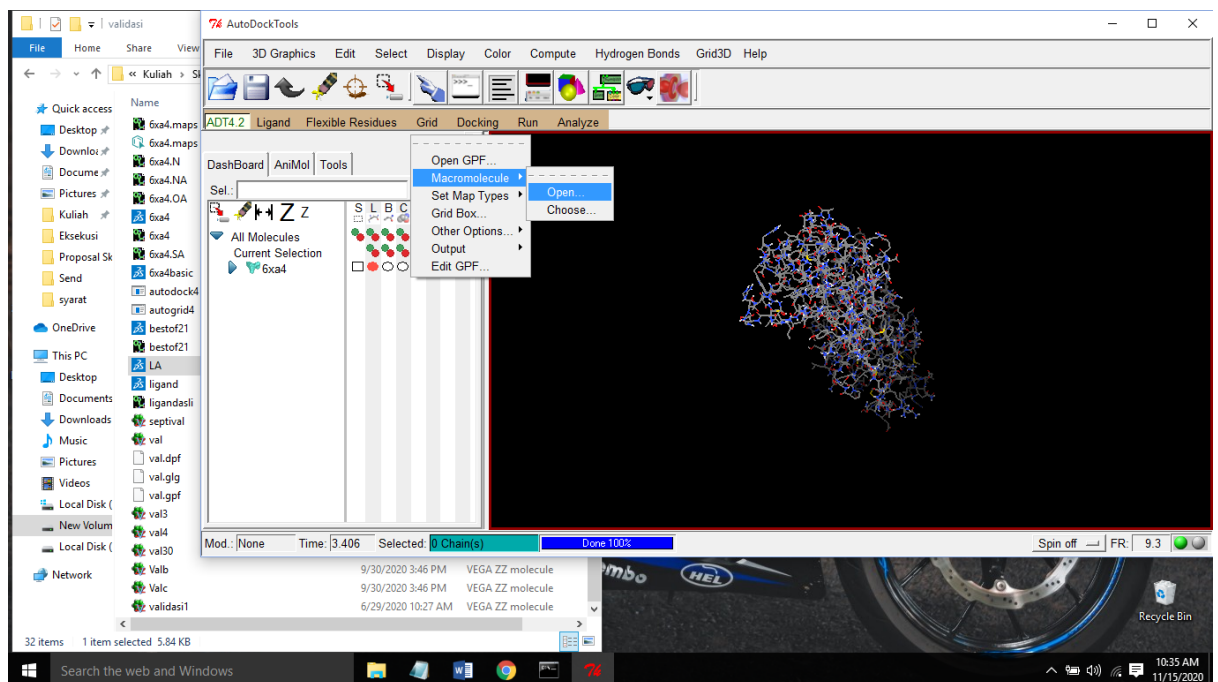


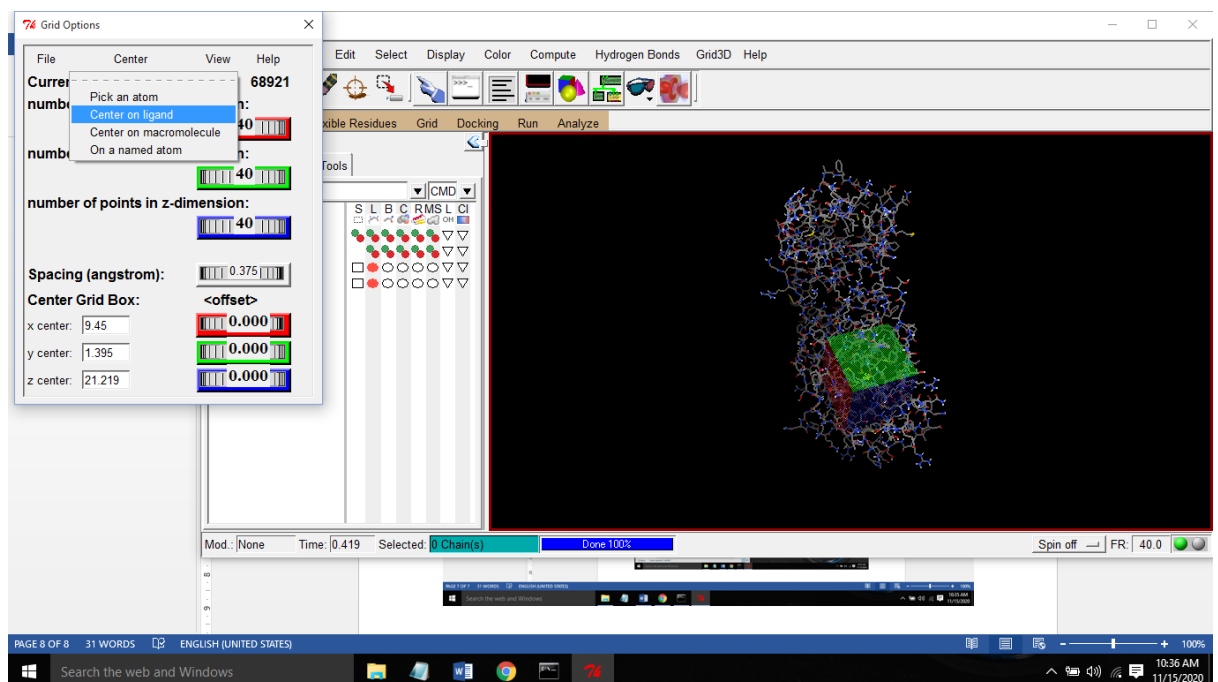
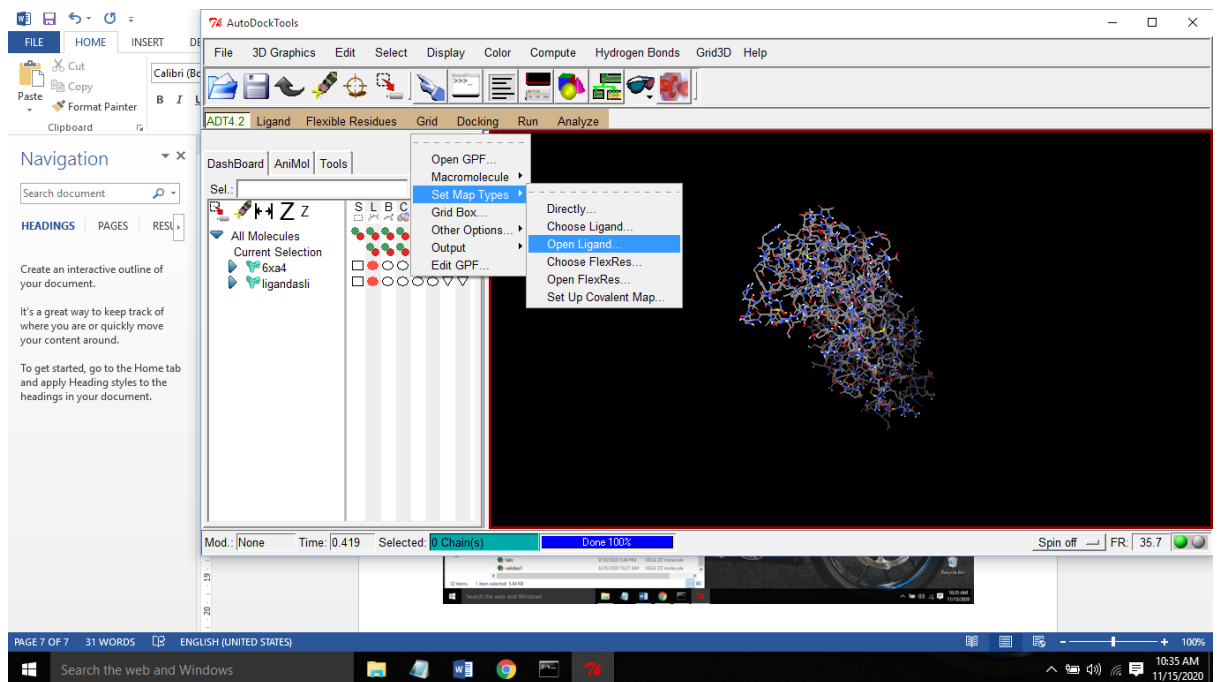
6. Preparasi protein

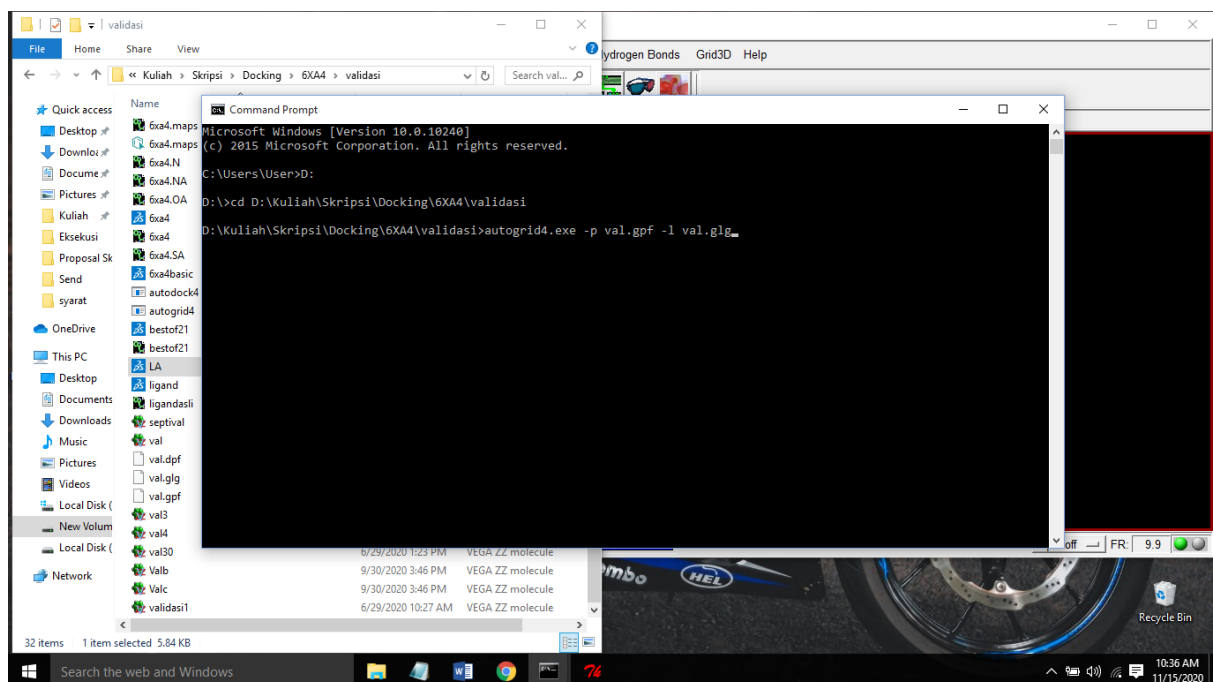
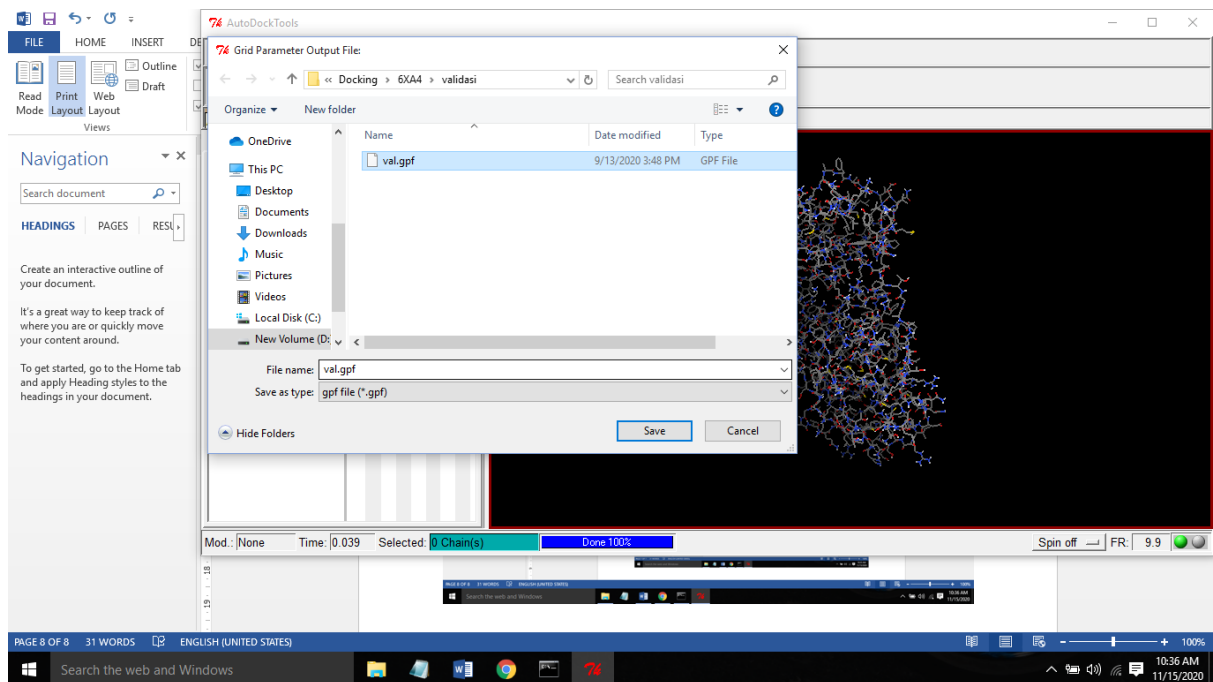




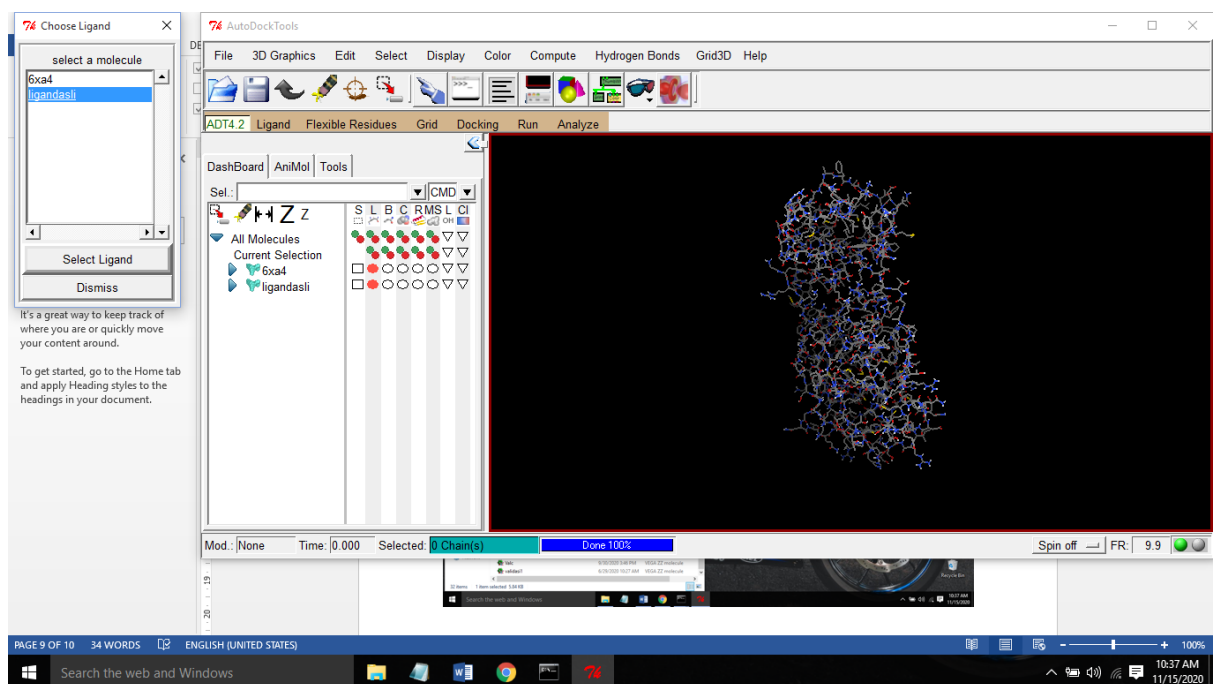
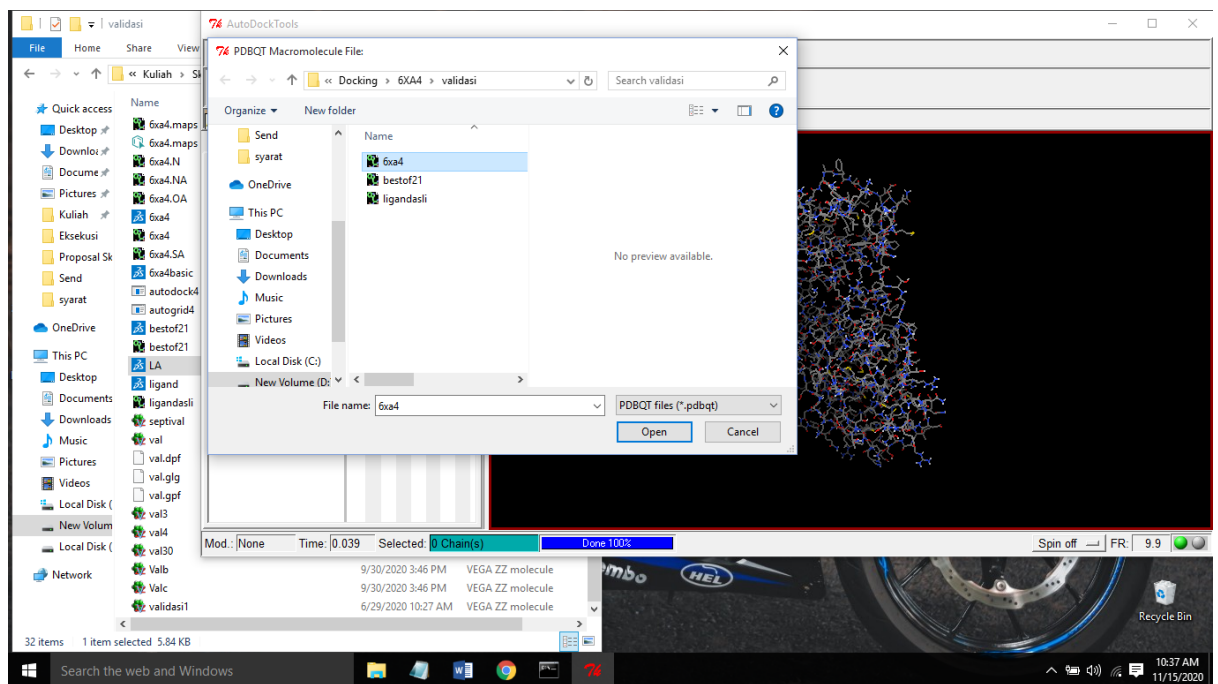
7. Preparasi grid validasi

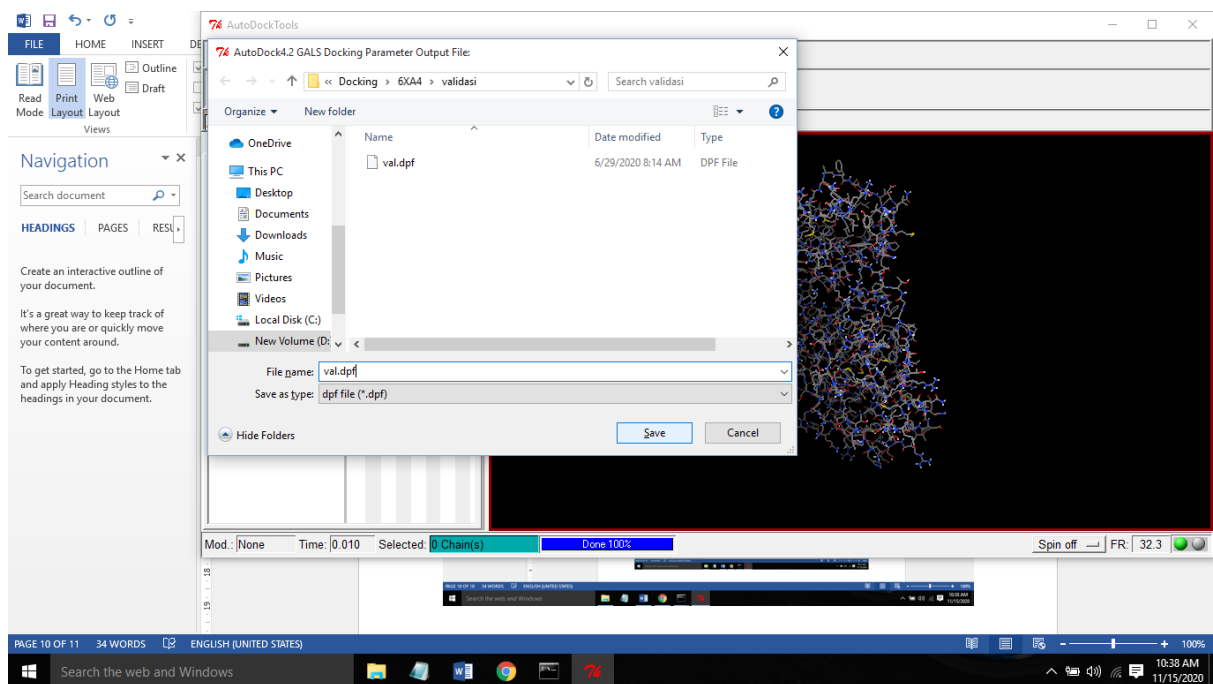
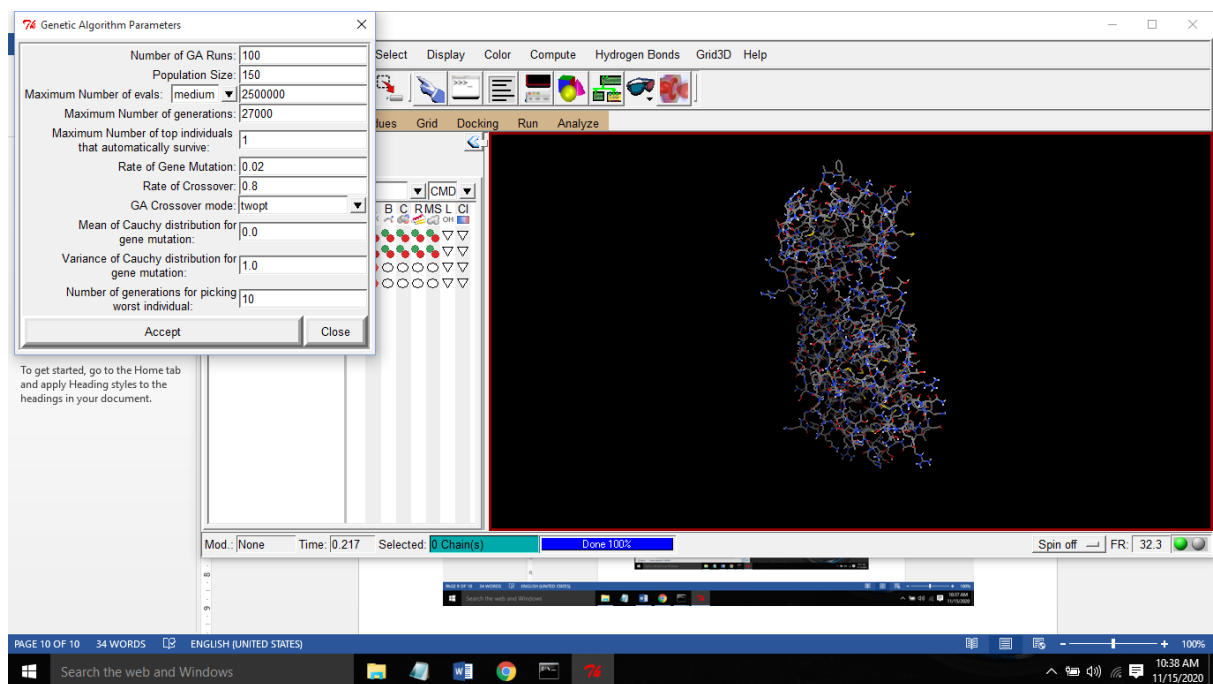


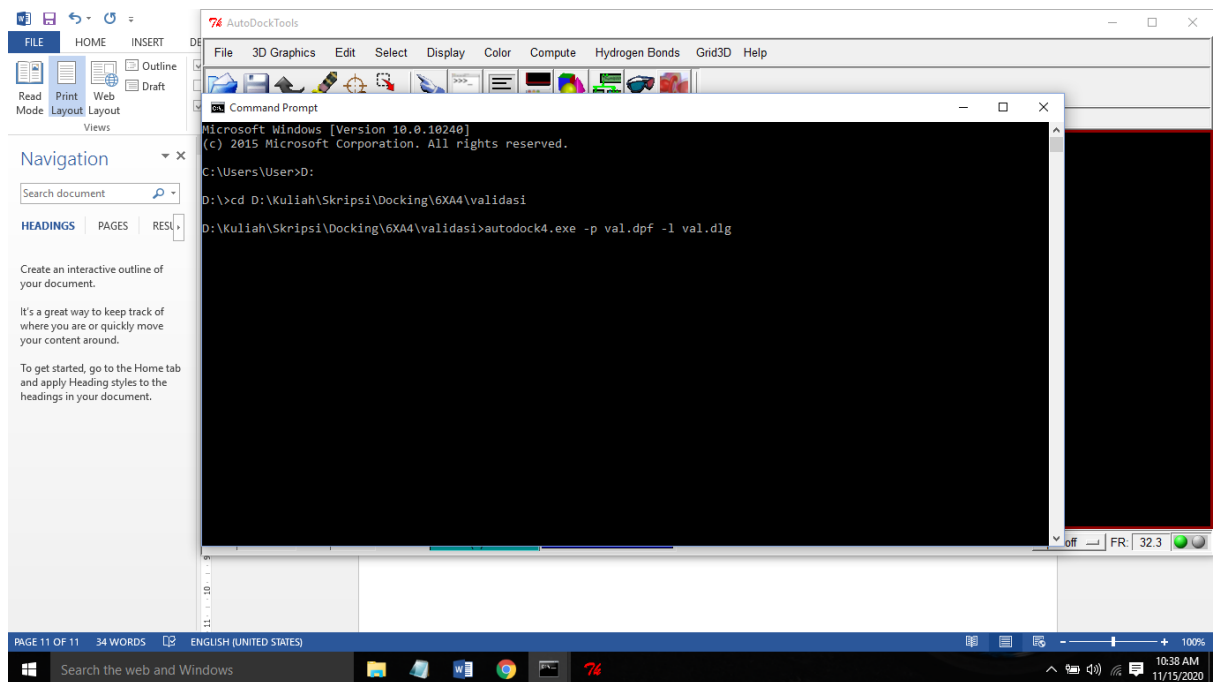




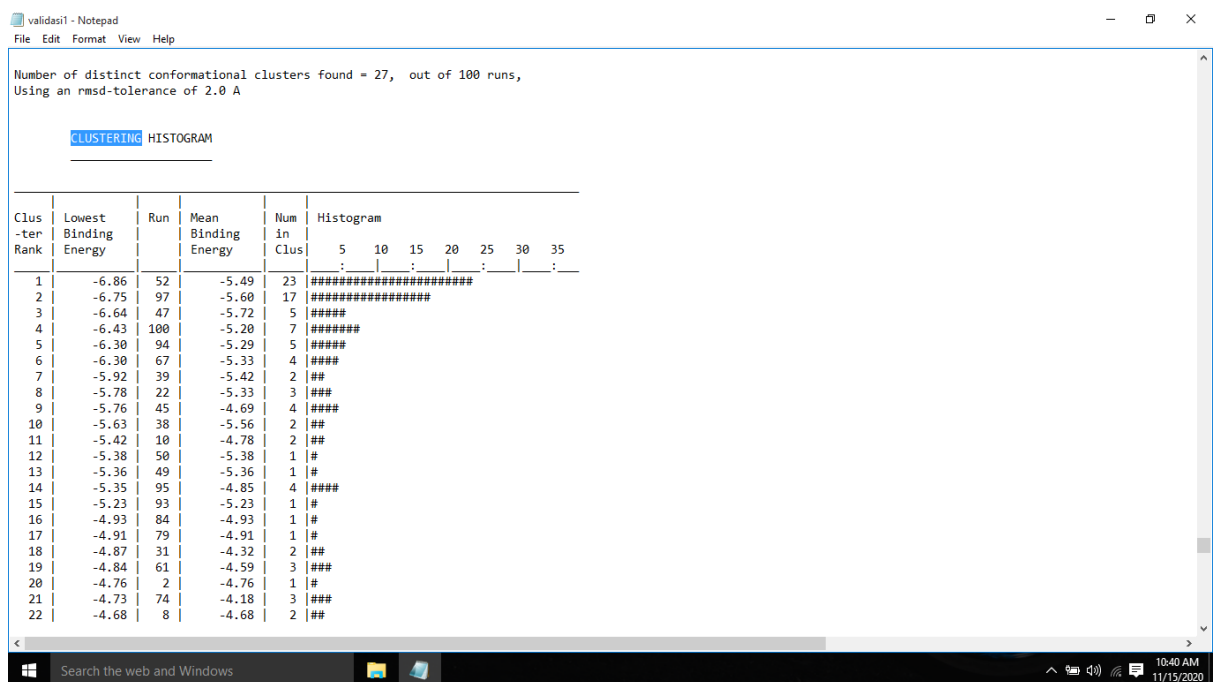
8. Validasi docking

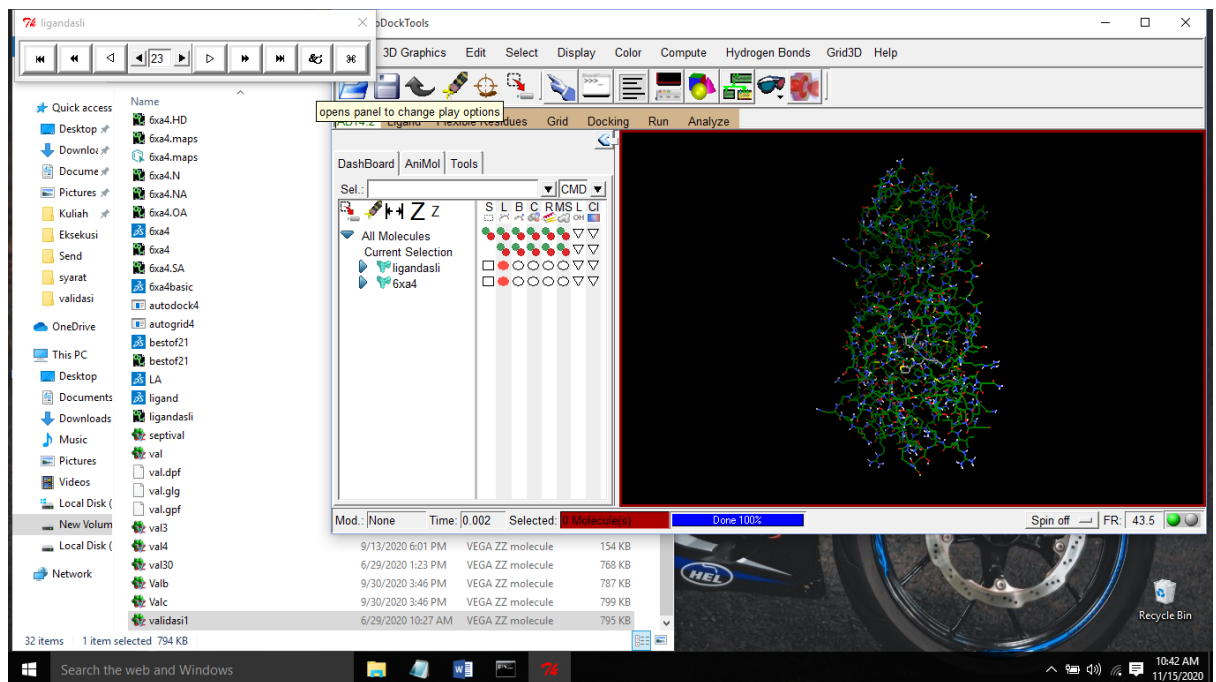




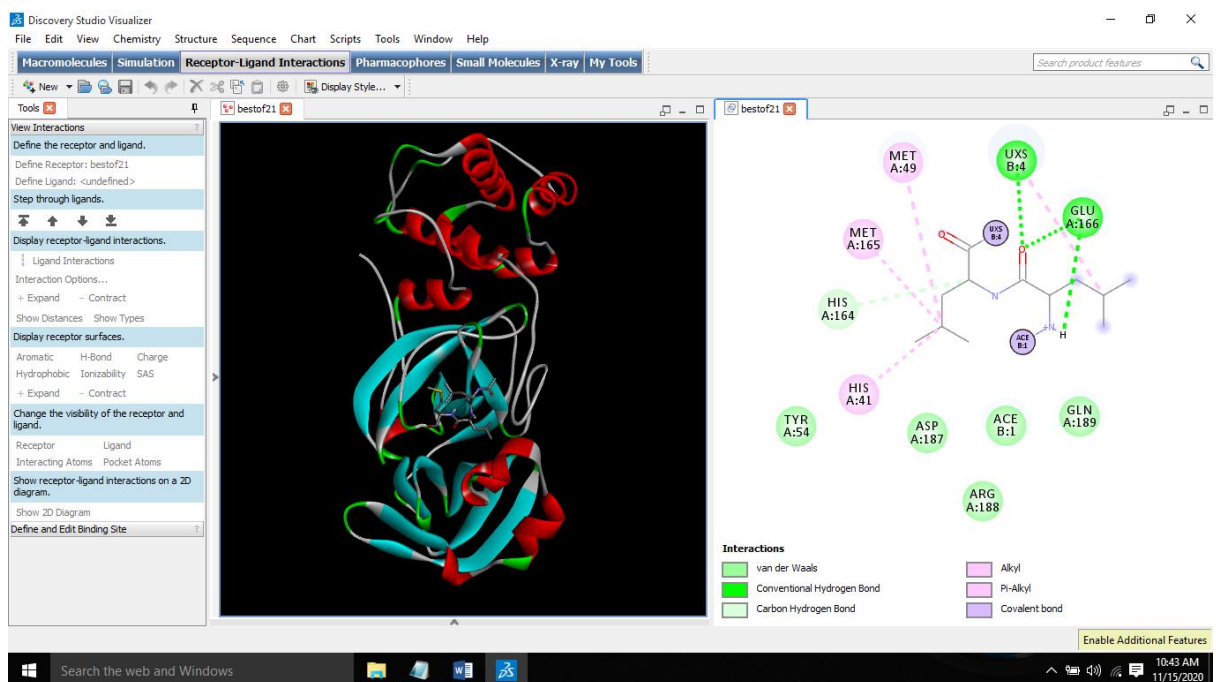


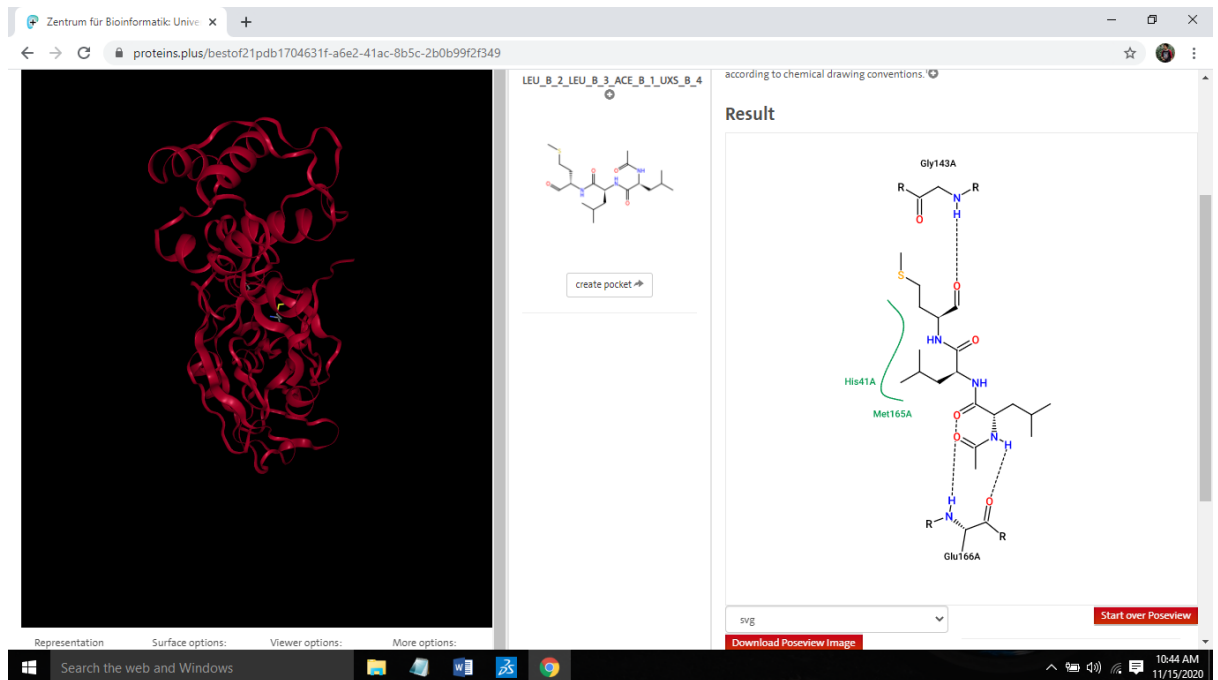
9. Pemilihan energi ikatan terbaik



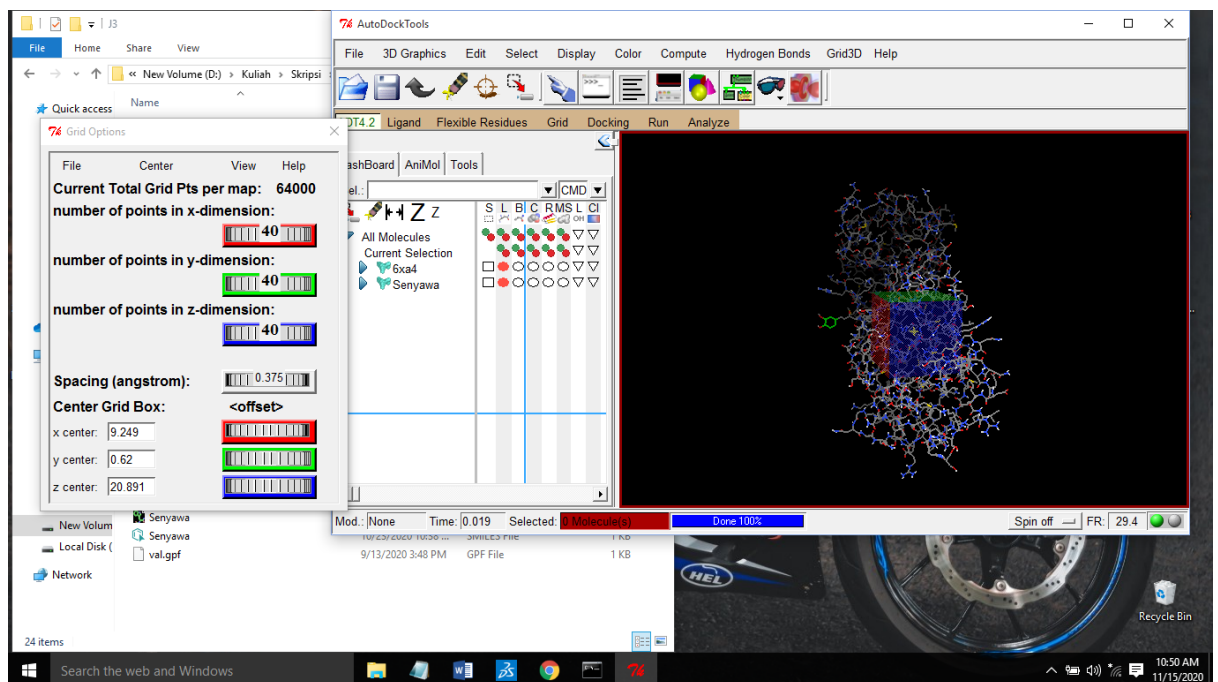


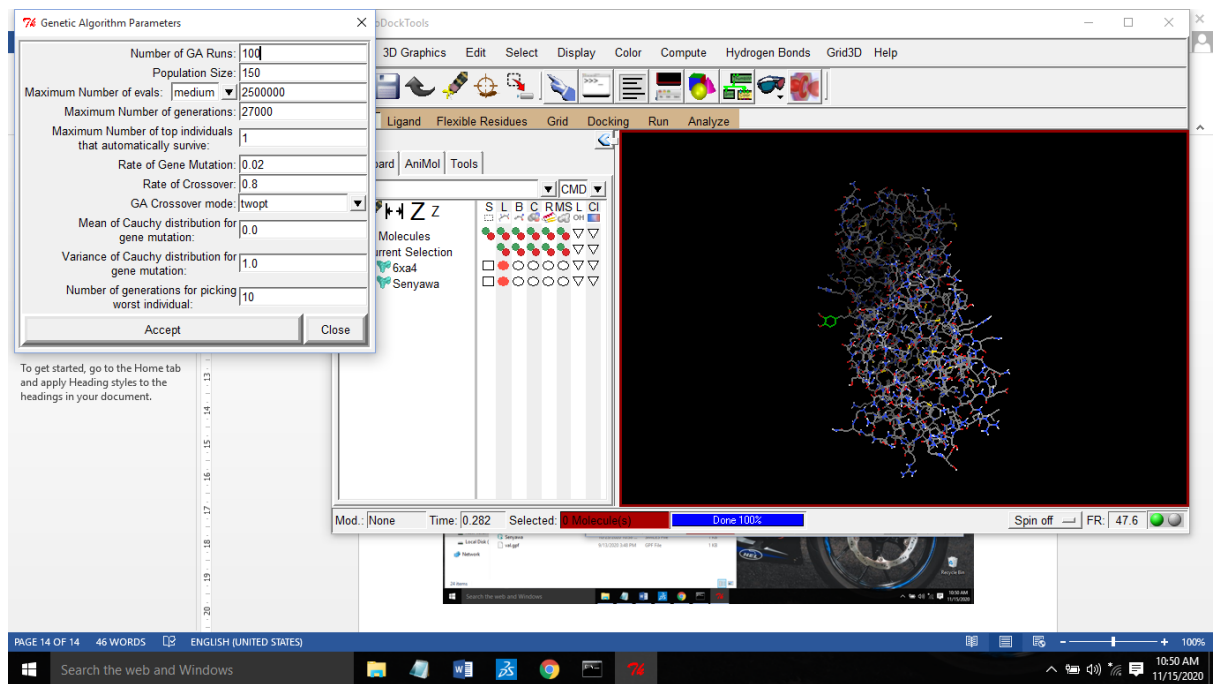
10. Visualisasi



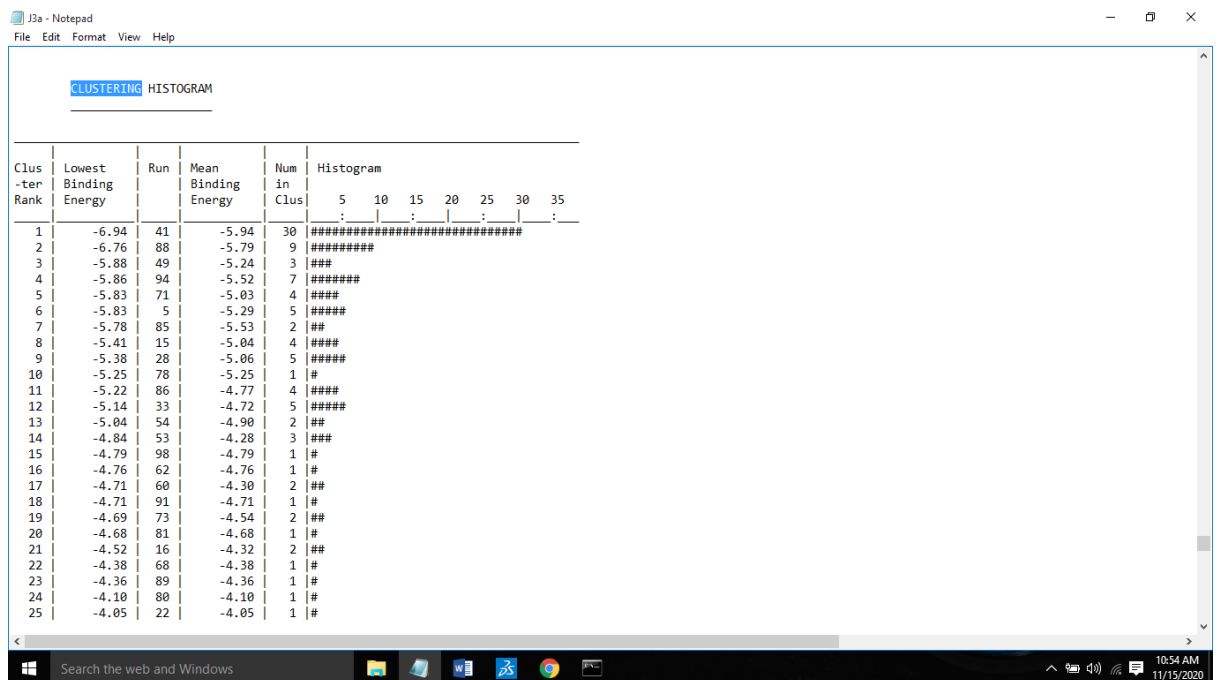


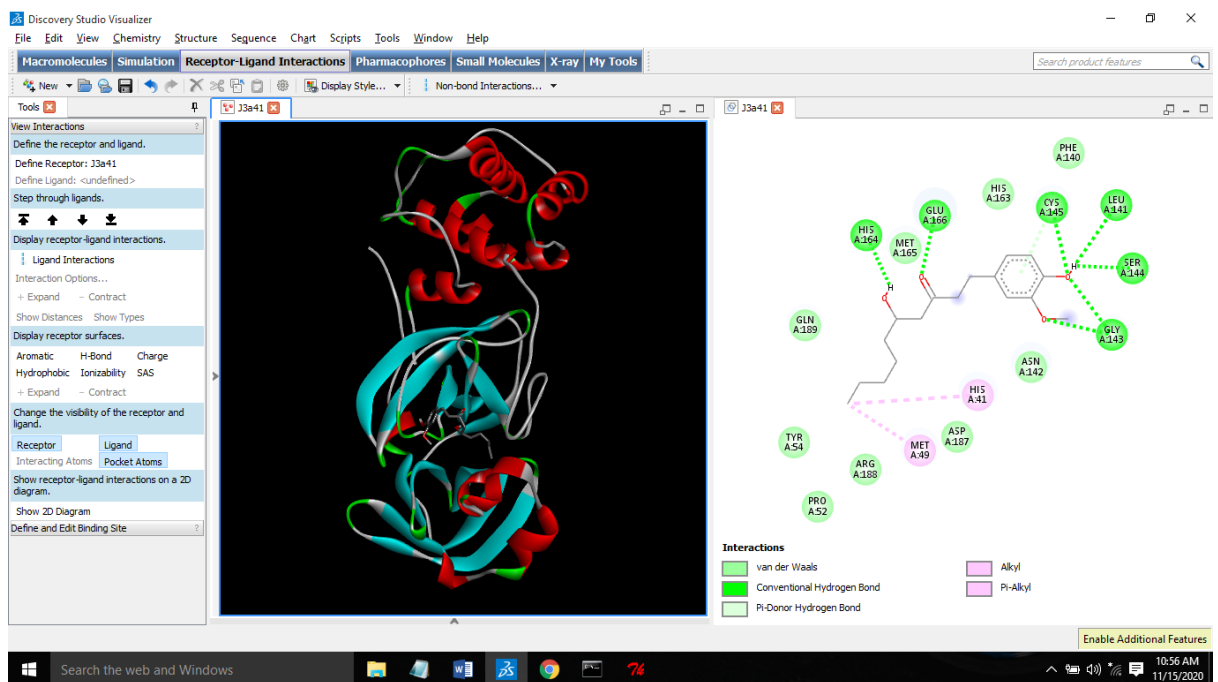
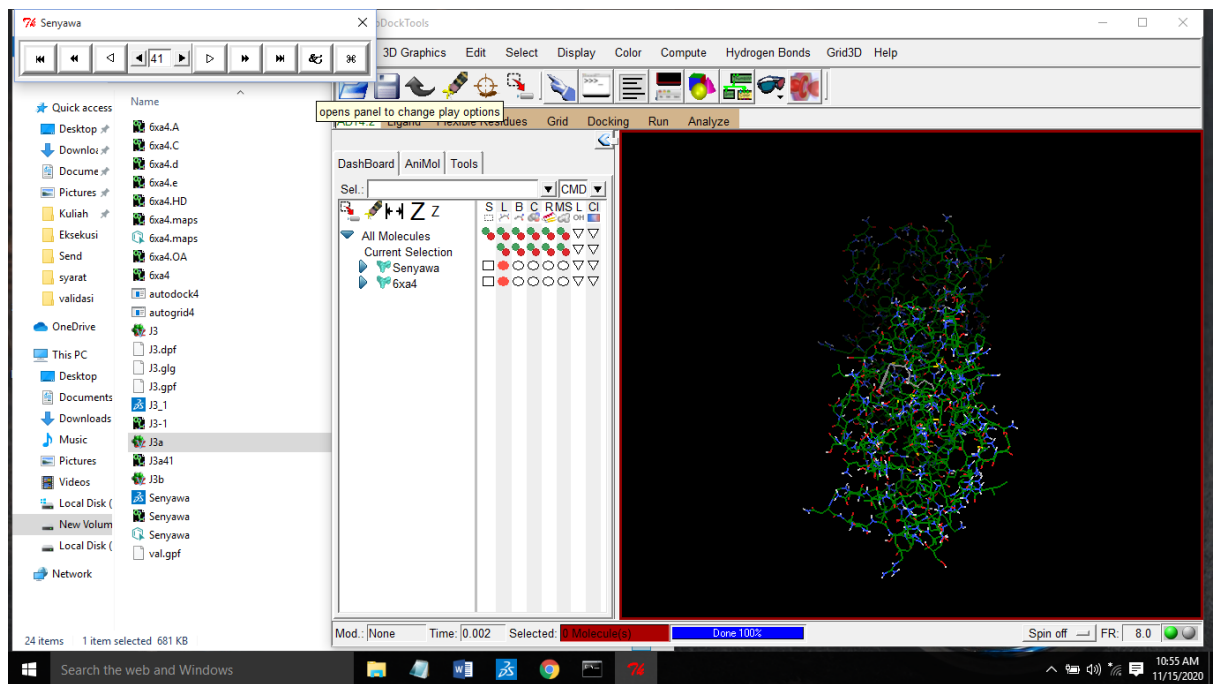
11. Docking dengan ligan uji





12. Visualisasi hasil docking





The screenshot shows a Windows desktop with three open windows:

- Senyawa - Notepad**: A Notepad window containing a chemical structure (SMILES) for a complex molecule, likely a cannabinoid derivative, with various substituents in parentheses.
- Untitled - Notepad**: A Notepad window displaying a table of data, possibly a list of chemical structures or their properties, with columns for numerical values and chemical identifiers.
- Web Browser**: A web browser window displaying the CBDD Group website. The page includes a navigation bar with links like "Tools", "Resource", "Help", and "Contact". The main content area shows a "Select output file format:" dropdown menu set to "MDL MOL format(SDF)". Below this, there is a section titled "OpenBabel111520120120" containing a large table of data, likely a list of chemical structures or their properties, with columns for numerical values and chemical identifiers.

ADMET Prediction-Webserver-All Introduction-ChemDes-Molecules

admet.scbdd.com/calcpred/index/

Home Webserver Search Documentation Help Contact CADD GROUP

Click to select & calculate

- Physicochemical Property
 - LogS (Solubility) ☒
 - LogD (Distribution Coefficient D at PH=7.4)
 - LogP (Distribution Coefficient P)
- Absorption
 - LogPapp (Caco-2 Permeability)
 - Pgp-inhibitor
 - Pgp-substrate
 - HIA (Human Intestinal Absorption)
 - F (20% Bioavailability)
 - F (30% Bioavailability)
- Distribution
 - PPB (Plasma Protein Binding)
 - BBB (Blood-Brain Barrier)
 - VD (Volume Distribution)
- Metabolism
 - CYP450 1A2 inhibitor
 - CYP450 1A2-substrate

By Inputting SMILES

SMILES : [Example: Omeprazole](#)

By Uploading Files (*.sdf) [Format converter](#)

Choose : [Example: 20 compounds](#)

By Drawing Molecule from Editor Below

Model Performance

NOTE: Here display the details information of selected model.

Model Performance	
Endpoint	LogS
Method	RandomForest
Descriptor number	40
mtry	10
R ²	0.980
Q ²	0.860
R ² _T	0.979
RMSE _F	0.095
RMSE _{CV}	0.698
RMSE _T	0.712
Descriptor names	MATSm2, TIAC, GMTIV, ICI, narq, MATSm1, nsulph, Tpc, slogPVSA7, bcutp1, AWeight, Tnc, MRVSA9, bcutp3, IC0, AW, Hy, bcutv10, MRVSA6, PC6, bcutm1, bcutm8, slogPVSA1, IDET, Chl10, TPFA, Weight, Rnc, naccr, bcutp5, Chiv4, bcutm2, Chiv1,

Search the web and Windows

11:02 AM 11/15/2020