# LAMPIRAN

**Lampiran 1**. File gridbox dalam format txt (grid.txt)

receptor = protein.pdbqt

ligand = ligand.pdbqt

center_x = -4.055

center_y = -12.232

center_z = -17.416

out = hasil.pdbqt

size_x = 10

size_y = 20

size_z = 16

**Lampiran 2.** File ion.mdp pada tahap netralisasi

```
; LINES STARTING WITH ';' ARE COMMENTS
title                    = Minimization      ; Title of run

; Parameters describing what to do, when to stop and what to save
integrator  = steep      ; Algorithm (steep = steepest descent minimization)
emtol     = 1000.0       ; Stop minimization when the maximum force < 10.0 kJ/mol
emstep  = 0.01       ; Energy step size
nsteps   = 50000          ; Maximum number of (minimization) steps to perform

; Parameters describing how to find the neighbors of each atom and how to calculate
the interactions
nstlist  = 1                ; Frequency to update the neighbor list and long range forces
cutoff-scheme   = Verlet
ns_type           = grid          ; Method to determine neighbor list (simple, grid)
rlist                = 1.0          ; Cut-off for making neighbor list (short range forces)
coulombtype      = cutoff       ; Treatment of long range electrostatic interactions
rcoulomb          = 1.0          ; long range electrostatic cut-off
rvdw                = 1.0          ; long range Van der Waals cut-off
pbc                  = xyz          ; Periodic Boundary Conditions
```

**Lampiran 3.** File em.mdp pada tahap minimisasi energi

```
; LINES STARTING WITH ';' ARE COMMENTS
title                    = Minimization       ; Title of run

; Parameters describing what to do, when to stop and what to save
integrator       = steep  ; Algorithm (steep = steepest descent minimization)
emtol   = 1000.0         ; Stop minimization when the maximum force < 10.0 kJ/mol
emstep               = 0.01      ; Energy step size
nsteps               = 50000 ; Maximum number of (minimization) steps to perform

; Parameters describing how to find the neighbors of each atom and how to calculate
the interactions
nstlist          = 1      ; Frequency to update the neighbor list and long range forces
cutoff-scheme   = Verlet
ns_type          = grid          ; Method to determine neighbor list (simple, grid)
rlist                = 1.2           ; Cut-off for making neighbor list (short range forces)
coulombtype      = PME       ; Treatment of long range electrostatic interactions
rcoulomb         = 1.2           ; long range electrostatic cut-off
vdwtype          = cutoff
vdw-modifier      = force-switch
rvdw-switch       = 1.0
rvdw             = 1.2                   ; long range Van der Waals cut-off
pbc              = xyz                   ; Periodic Boundary Conditions
DispCorr         = no
```

**Lampiran 4.** File NVT.mdp pada tahap ekuilibrasi 1

```
title                    = Protein-ligand complex NVT equilibration
define                   = -DPOSRES  ; position restrain the protein and ligand
; Run parameters
integrator               = md        ; leap-frog integrator
nsteps                   = 50000     ; 2 * 50000 = 100 ps
dt                       = 0.002     ; 2 fs

; Output control
nstenergy                = 500   ; save energies every 1.0 ps
nstlog                   = 500   ; update log file every 1.0 ps
nstxout-compressed       = 500   ; save coordinates every 1.0 ps
; Bond parameters
continuation             = no        ; first dynamics run
constraint_algorithm     = lincs     ; holonomic constraints
constraints              = h-bonds   ; bonds to H are constrained
lincs_iter               = 1         ; accuracy of LINCS
lincs_order              = 4         ; also related to accuracy
; Neighbor searching and vdW
cutoff-scheme            = Verlet
ns_type                  = grid      ; search neighboring grid cells
nstlist                  = 20        ; largely irrelevant with Verlet
rlist                    = 1.2
vdwtype                  = cutoff
vdw-modifier             = force-switch
rvdw-switch              = 1.0
rvdw                     = 1.2       ; short-range van der Waals cutoff (in nm)
; Electrostatics
coulombtype              = PME       ; Particle Mesh Ewald for long-range electrostatics
rcoulomb                 = 1.2       ; short-range electrostatic cutoff (in nm)
pme_order                = 4         ; cubic interpolation
fourierspacing           = 0.16      ; grid spacing for FFT
; Temperature coupling
tcoupl                   = V-rescale                     ; modified Berendsen thermostat
tc-grps      = Protein_UNK Water_and_ions    ; two coupling groups - more accurate
```

(Lanjutan)

```
tau_t                = 0.1   0.1              ; time constant, in ps
ref_t              = 310.15  310.15     ; reference temperature, one for each group, in K
; Pressure coupling
pcoupl               = no        ; no pressure coupling in NVT
; Periodic boundary conditions
pbc                  = xyz       ; 3-D PBC
; Dispersion correction is not used for proteins with the C36 additive FF
DispCorr             = no
; Velocity generation
gen_vel              = yes       ; assign velocities from Maxwell distribution
gen_temp             = 300       ; temperature for Maxwell distribution
gen_seed             = -1        ; generate a random seed
```

**Lampiran 5.** File NPT.mdp pada tahap ekuilibrasi 2

```
title                    = Protein-ligand complex NPT equilibration
define                   = -DPOSRES  ; position restrain the protein and ligand
; Run parameters
integrator               = md        ; leap-frog integrator
nsteps                   = 50000     ; 2 * 50000 = 100 ps
dt                       = 0.002     ; 2 fs
; Output control
nstenergy                = 500       ; save energies every 1.0 ps
nstlog                   = 500       ; update log file every 1.0 ps
nstxout-compressed       = 500       ; save coordinates every 1.0 ps
; Bond parameters
continuation             = yes       ; continuing from NVT
constraint_algorithm     = lincs     ; holonomic constraints
constraints              = h-bonds   ; bonds to H are constrained
lincs_iter               = 1         ; accuracy of LINCS
lincs_order              = 4         ; also related to accuracy
; Neighbor searching and vdW
cutoff-scheme            = Verlet
ns_type                  = grid      ; search neighboring grid cells
nstlist                  = 20        ; largely irrelevant with Verlet
rlist                    = 1.2
vdwtype                  = cutoff
vdw-modifier             = force-switch
rvdw-switch              = 1.0
rvdw                     = 1.2       ; short-range van der Waals cutoff (in nm)
; Electrostatics
coulombtype              = PME       ; Particle Mesh Ewald for long-range electrostatics
rcoulomb                 = 1.2
pme_order                = 4         ; cubic interpolation
fourierspacing           = 0.16      ; grid spacing for FFT
; Temperature coupling
tcoupl                   = V-rescale                     ; modified Berendsen thermostat
tc-grps      = Protein_UNK Water_and_ions    ; two coupling groups - more accurate
tau_t                    = 0.1   0.1                     ; time constant, in ps
ref_t                    = 310.15   310.15  ; reference temperature, one for each group, in K
```

(Lanjutan)

```
; Pressure coupling
pcoupl          = C-rescale             ; pressure coupling is on for NPT

pcoupltype      = isotropic             ; uniform scaling of box vectors
tau_p           = 2.0                   ; time constant, in ps
ref_p           = 1.0                   ; reference pressure, in bar
compressibility = 4.5e-5                ; isothermal compressibility of water,
bar^-1
refcoord_scaling = com
; Periodic boundary conditions
pbc             = xyz       ; 3-D PBC
; Dispersion correction is not used for proteins with the C36 additive FF
DispCorr        = no
; Velocity generation
gen_vel         = no        ; velocity generation off after NVT
```

**Lampiran 6.** File md.mdp pada tahap produksi

```
title                    = Protein-ligand complex MD simulation
; Run parameters
integrator               = md       ; leap-frog integrator
nsteps                   = 25000000   ; 2 * 25000000 = 50000 ps (50 ns)
dt                       = 0.002    ; 2 fs
; Output control
nstenergy                = 5000     ; save energies every 10.0 ps
nstlog                   = 5000     ; update log file every 10.0 ps
nstxout-compressed       = 5000     ; save coordinates every 10.0 ps
; Bond parameters
continuation             = yes      ; continuing from NPT
constraint_algorithm     = lincs    ; holonomic constraints
constraints              = h-bonds   ; bonds to H are constrained
lincs_iter               = 1        ; accuracy of LINCS
lincs_order              = 4        ; also related to accuracy
; Neighbor searching and vdW
cutoff-scheme            = Verlet
ns_type                  = grid     ; search neighboring grid cells
nstlist                  = 20       ; largely irrelevant with Verlet
rlist                    = 1.2
vdwtype                  = cutoff
vdw-modifier             = force-switch
rvdw-switch              = 1.0
rvdw                     = 1.2      ; short-range van der Waals cutoff (in nm)
; Electrostatics
coulombtype              = PME      ; Particle Mesh Ewald for long-range electrostatics
rcoulomb                 = 1.2
pme_order                = 4        ; cubic interpolation
fourierspacing           = 0.16     ; grid spacing for FFT
; Temperature coupling
tcoupl                   = V-rescale                    ; modified Berendsen thermostat
tc-grps      = Protein_UNK Water_and_ions   ; two coupling groups - more accurate
tau_t                    = 0.1   0.1                    ; time constant, in ps
ref_t          = 310.15   310.15       ; reference temperature, one for each group, in K

; Pressure coupling
pcoupl                   = Parrinello-Rahman            ; pressure coupling is on for NPT
```

(Lanjutan)

```
pcoupltype          = isotropic             ; uniform scaling of box vectors
tau_p               = 2.0                   ; time constant, in ps
ref_p               = 1.0                   ; reference pressure, in bar
compressibility     = 4.5e-5                ; isothermal compressibility of water,
bar^-1
; Periodic boundary conditions
pbc                 = xyz       ; 3-D PBC
; Dispersion correction is not used for proteins with the C36 additive FF
DispCorr            = no
; Velocity generation
gen_vel             = no        ; continuing from NPT equilibration
```

**Lampiran 7**. File Masukan MMPBSA.in

Sample input file for PB calculation building the Amber topologies
from structures. Please refer to the section "How gmx_MMPBSA works"
&general
startframe=1,
endframe=5001,
temperature=310.15
forcefields="oldff/leaprc.ff99SB,leaprc.gaff2"
/
&pb
istrng=0.15, fillratio=4.0
/

**Lampiran 8**. File Masukan MMGBSA.in

Sample input file for GB calculation

#This input file is meant to show only that gmx_MMPBSA works. Although, we tried to use the

input files as recommended in the

#Amber manual, some parameters have been changed to perform more expensive calculations

in a reasonable amount of time. Feel free to change the parameters

#according to what is better for your system.

&general

sys_name="Prot-Lig-ST",

startframe=1,

endframe=5001,

temperature=310.15

forcefields="oldff/leaprc.ff99SB,leaprc.gaff2"

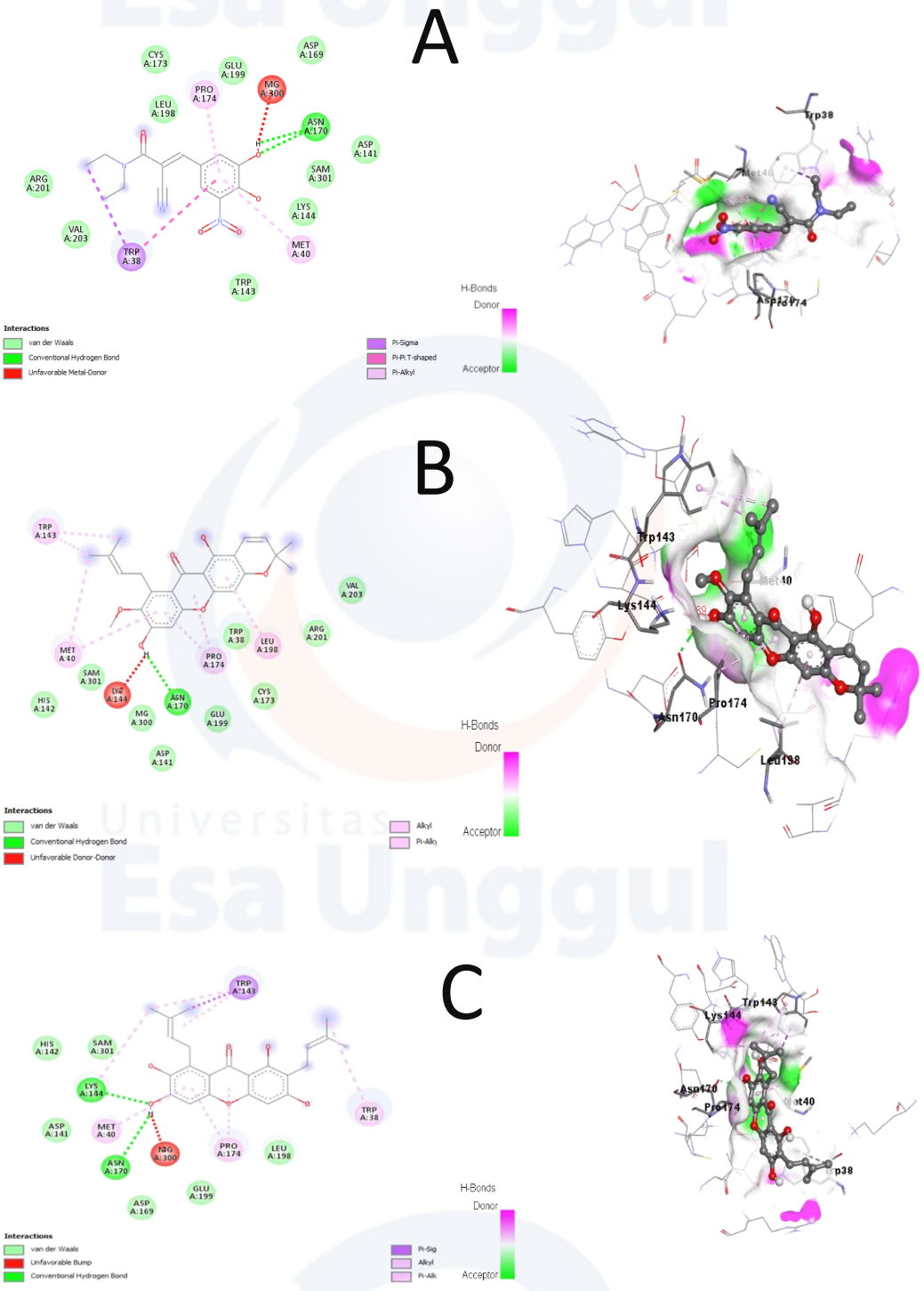
/

&gb

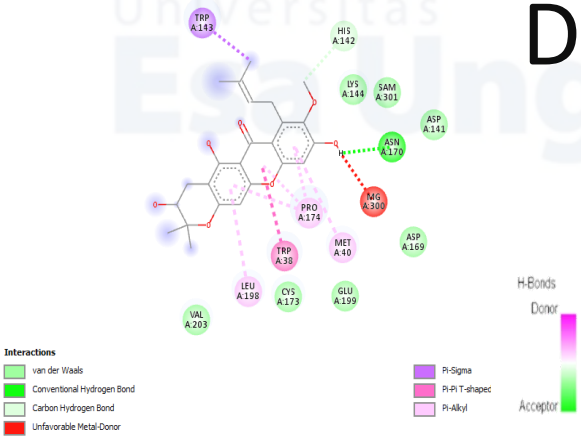
igb=5, saltcon=0.150,

/

**Lampiran 9**. Hasil visualisasi 2D dan 3D interaksi antara ligan dengan protein reseptor COMT



D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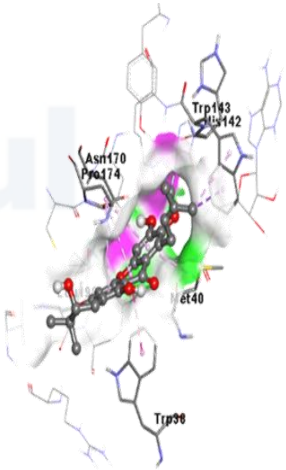
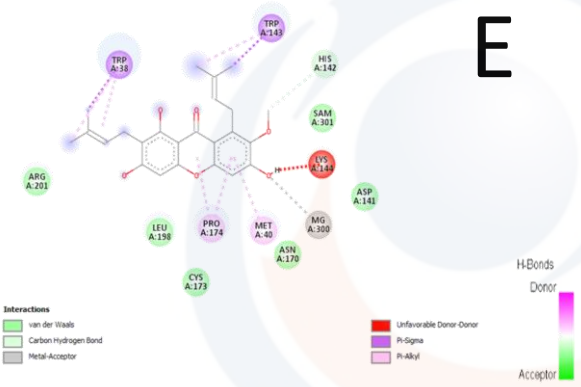
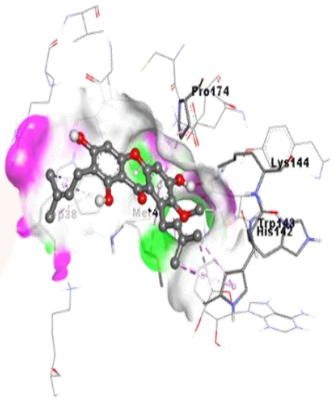
HIS A:142
LYS A:144
SAM A:301
ASP A:141
ASN A:170
MG A:300
PRO A:174
MET A:40
TRP A:38
ASP A:169
LEU A:198
CYS A:173
GLU A:199
VAL A:203
H-Bonds
Donor
Acceptor
Interactions
van der Waals
Conventional Hydrogen Bond
Carbon Hydrogen Bond
Unfavorable Metal-Donor
Pi-Sigma
Pi-Pi T-shaped
Pi-Alkyl

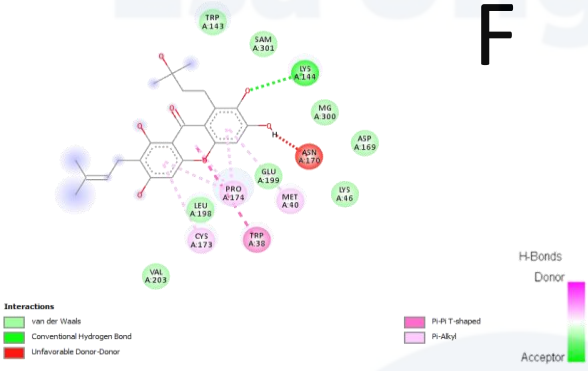

Trp143
His142
Asn170
Pro174
et40
Trp38

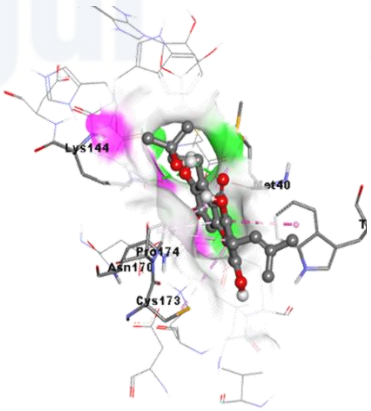
E


TRP A:143
TRP A:38
HIS A:142
SAM A:301
LYS A:144
ARG A:201
ASP A:141
LEU A:198
PRO A:174
MET A:40
MG A:300
ASN A:170
CYS A:173
H-Bonds
Donor
Acceptor
Interactions
van der Waals
Carbon Hydrogen Bond
Metal-Acceptor
Unfavorable Donor-Donor
Pi-Sigma
Pi-Alkyl

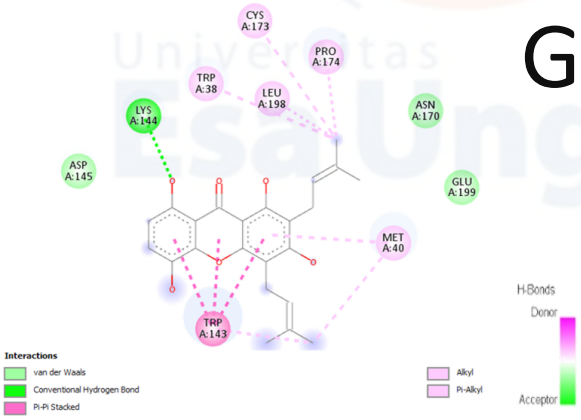

Pro174
Lys144
Trp143
His142

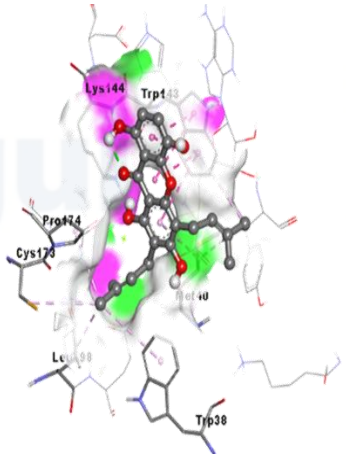
F


TRP A:143
SAM A:301
LYS A:144
MG A:300
ASP A:169
ASN A:170
GLU A:199
PRO A:174
MET A:40
LYS A:46
LEU A:198
CYS A:173
TRP A:38
VAL A:203
H-Bonds
Donor
Acceptor
Interactions
van der Waals
Conventional Hydrogen Bond
Unfavorable Donor-Donor
Pi-Pi T-shaped
Pi-Alkyl

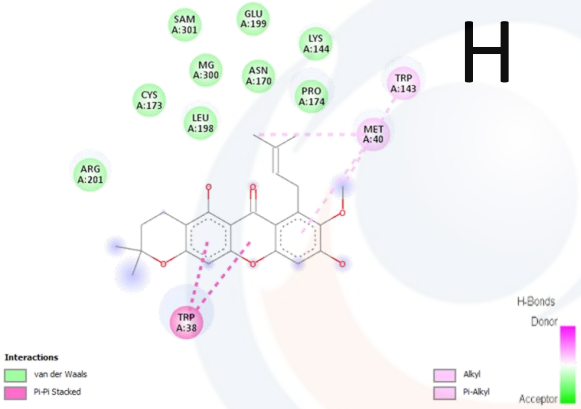

Lys144
et40
Pro174
Asn170
Cys173

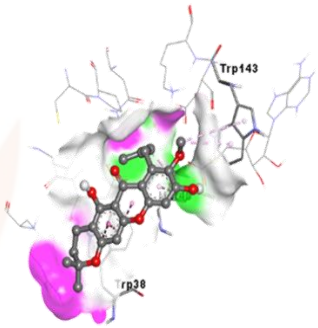
G


CYS A:173
PRO A:174
TRP A:38
LEU A:198
LYS A:144
ASN A:170
ASP A:145
GLU A:199
MET A:40
TRP A:143
Interactions
van der Waals
Conventional Hydrogen Bond
Pi-Pi Stacked
Alkyl
Pi-Alkyl
H-Bonds
Donor
Acceptor

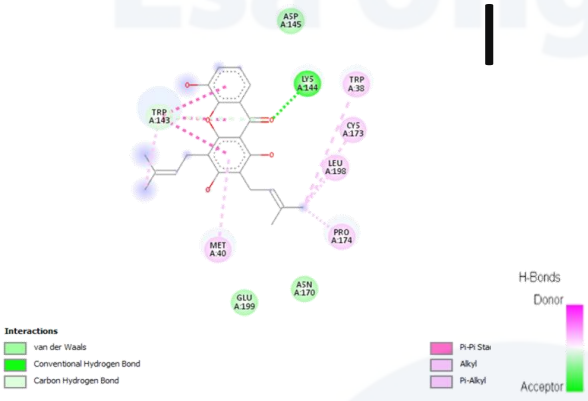

Lys144
Trp143
Pro174
Cys173
Trp38

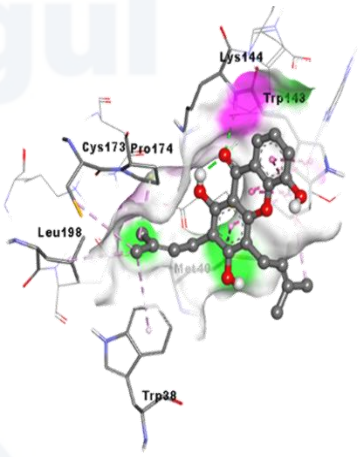
H


SAM A:301
GLU A:199
LYS A:144
MG A:300
ASN A:170
TRP A:143
CYS A:173
PRO A:174
LEU A:198
MET A:40
ARG A:201
TRP A:38
Interactions
van der Waals
Pi-Pi Stacked
Alkyl
Pi-Alkyl
H-Bonds
Donor
Acceptor

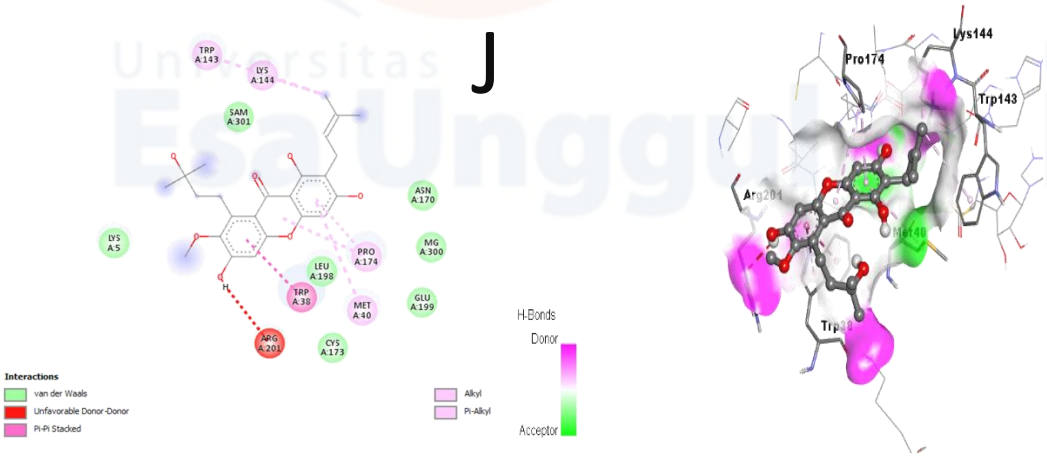

Trp143
rp38

I


ASP A:145
LYS A:144
TRP A:38
TRP A:143
CYS A:173
LEU A:198
PRO A:174
MET A:40
ASN A:170
GLU A:199
Interactions
van der Waals
Conventional Hydrogen Bond
Carbon Hydrogen Bond
Pi-Pi Sta
Alkyl
Pi-Alkyl
H-Bonds
Donor
Acceptor


Lys144
Trp143
Cys173
Pro174
Leu198
Trp38

J




(A) Entacapone, (B) Garciniafuran (C) ɣ-mangostin, (D) Mangostanol (E) α-mangostin, (F) Garcinone C, (G) Gartanin, (H) 3-Isomangostin, (I) 8-Deoxygartanin, (J) Garcinone D

**Lampiran 10.** File Notepad hasil penambatan molekuler (Energi afinitas)

```
Scoring function : vina
Rigid receptor: protein.pdbqt
Ligand: garciniafuran.pdbqt
Grid center: X -4.055 Y -12.232 Z -17.416
Grid size  : X 10 Y 20 Z 16
Grid space : 0.375
Exhaustiveness: 8
CPU: 0
Verbosity: 1

Computing Vina grid ... done.
Performing docking (random seed: -379132837) ...
0%   10   20   30   40   50   60   70   80   90   100%
|----|----|----|----|----|----|----|----|----|----|
**************************************************

mode |   affinity | dist from best mode
     | (kcal/mol) | rmsd l.b.| rmsd u.b.
-----+------------+----------+----------
   1       -8.032          0          0
   2       -7.449      2.387      8.076
   3       -7.315       2.09      3.789
   4       -7.274      2.872      8.161
   5       -6.996      2.503      8.505
   6       -6.416      1.996      7.912
   7       -6.062      1.833      2.127
   8       -5.337      3.374      8.409
   9       -4.017      2.162      4.138
```

**Garciniafuran**

```
Scoring function : vina
Rigid receptor: protein.pdbqt
Ligand: Gammamangostin.pdbqt
Grid center: X -4.055 Y -12.232 Z -17.416
Grid size  : X 10 Y 20 Z 16
Grid space : 0.375
Exhaustiveness: 8
CPU: 0
Verbosity: 1

Computing Vina grid ... done.
Performing docking (random seed: -1489154644) ...
0%   10   20   30   40   50   60   70   80   90   100%
|----|----|----|----|----|----|----|----|----|----|
**************************************************

mode |   affinity | dist from best mode
     | (kcal/mol) | rmsd l.b.| rmsd u.b.
-----+------------+----------+----------
   1       -7.057          0          0
   2       -6.785      1.559      2.255
   3       -6.246      2.469      8.565
   4       -5.652      2.699      8.619
   5       -5.596      1.459      7.647
   6       -5.574      2.086      7.022
   7       -5.462      2.431      8.167
   8         -5.4      2.423      8.121
   9       -5.238      2.628      4.386
```

**ɣ-mangostin**

```
Scoring function : vina
Rigid receptor: protein.pdbqt
Ligand: Mangostanol.pdbqt
Grid center: X -4.055 Y -12.232 Z -17.416
Grid size  : X 10 Y 20 Z 16
Grid space : 0.375
Exhaustiveness: 8
CPU: 0
Verbosity: 1

Computing Vina grid ... done.
Performing docking (random seed: 533353877) ...
0%   10   20   30   40   50   60   70   80   90   100%
|----|----|----|----|----|----|----|----|----|----|
**************************************************

mode |   affinity | dist from best mode
     | (kcal/mol) | rmsd l.b.| rmsd u.b.
-----+------------+----------+----------
   1       -7.051          0          0
   2        -6.58      3.227      8.079
   3       -6.531      3.826        8.3
   4       -6.494      2.201      8.379
   5       -6.217      3.348      7.835
   6       -4.628      2.478        8.2
   7       -4.611      2.685      7.941
   8       -4.386      1.821      2.223
   9       -4.275      2.672      8.295
```

**Mangostanol**

```
Scoring function : vina
Rigid receptor: protein.pdbqt
Ligand: Entacapone.pdbqt
Grid center: X -4.055 Y -12.232 Z -17.416
Grid size  : X 10 Y 20 Z 16
Grid space : 0.375
Exhaustiveness: 8
CPU: 0
Verbosity: 1

Computing Vina grid ... done.
Performing docking (random seed: -261749962) ...
0%   10   20   30   40   50   60   70   80   90   100%
|----|----|----|----|----|----|----|----|----|----|
**************************************************

mode |   affinity | dist from best mode
     | (kcal/mol) | rmsd l.b.| rmsd u.b.
-----+------------+----------+----------
   1       -6.915          0          0
   2       -6.749      1.276      6.777
   3       -6.359        3.5      5.928
   4       -6.265      1.147      6.945
   5       -6.232      3.667      6.113
   6        -5.79      4.097      6.826
   7       -5.534      4.718      7.383
   8       -5.452      5.326      8.939
   9       -5.351      3.181      4.563
```

**Entacapone (Standard)**

```
Scoring function : vina
Rigid receptor: protein.pdbqt
Ligand: Alphamangostin.pdbqt
Grid center: X -4.055 Y -12.232 Z -17.416
Grid size  : X 10 Y 20 Z 16
Grid space : 0.375
Exhaustiveness: 8
CPU: 0
Verbosity: 1

Computing Vina grid ... done.
Performing docking (random seed: 1186651612) ...
0%   10   20   30   40   50   60   70   80   90   100%
|----|----|----|----|----|----|----|----|----|----|
**************************************************

mode |   affinity | dist from best mode
     | (kcal/mol) | rmsd l.b.| rmsd u.b.
-----+------------+----------+----------
   1       -6.729          0          0
   2       -6.516      2.272      8.646
   3       -6.486      1.604      2.149
   4       -6.103      2.354      7.236
   5       -5.999      2.261      8.085
   6       -5.889      2.375       3.38
   7       -5.851      1.449       2.27
   8       -5.787      1.706      7.642
   9       -1.246      2.707      8.072
```

**α-mangostin**

```
Scoring function : vina
Rigid receptor: protein.pdbqt
Ligand: GarcinoneC.pdbqt
Grid center: X -4.055 Y -12.232 Z -17.416
Grid size  : X 10 Y 20 Z 16
Grid space : 0.375
Exhaustiveness: 8
CPU: 0
Verbosity: 1

Computing Vina grid ... done.
Performing docking (random seed: -361373806) ...
0%   10   20   30   40   50   60   70   80   90   100%
|----|----|----|----|----|----|----|----|----|----|
**************************************************

mode |   affinity | dist from best mode
     | (kcal/mol) | rmsd l.b.| rmsd u.b.
-----+------------+----------+----------
   1       -6.699          0          0
   2       -5.743      4.504      5.885
   3        -5.37      1.546      1.934
   4       -5.115      3.413      4.596
   5       -5.077      4.311      8.435
   6       -5.018      5.527      6.448
   7        -4.76      3.754      8.105
   8       -4.674      4.468      8.449
   9       -4.433      2.599      4.637
```

**Garcinone C**

(Lanjutan)

```
Scoring function : vina
Rigid receptor: protein.pdbqt
Ligand: Gartanin.pdbqt
Grid center: X -4.055 Y -12.232 Z -17.416
Grid size  : X 10 Y 20 Z 16
Grid space : 0.375
Exhaustiveness: 8
CPU: 0
Verbosity: 1

Computing Vina grid ... done.
Performing docking (random seed: -1008741948) ...
0%   10   20   30   40   50   60   70   80   90   100%
|----|----|----|----|----|----|----|----|----|----|
**************************************************
```

| mode | affinity (kcal/mol) | dist from best mode rmsd l.b. | rmsd u.b. |
|---|---|---|---|
| 1 | -6.671 | 0 | 0 |
| 2 | -6.259 | 1.625 | 4.828 |
| 3 | -6.18 | 5.403 | 9.306 |
| 4 | -5.926 | 3.902 | 6.458 |
| 5 | -5.738 | 4.969 | 8.892 |
| 6 | -5.52 | 4.033 | 7.372 |
| 7 | -5.402 | 4.46 | 8.085 |
| 8 | -5.356 | 3.844 | 6.837 |
| 9 | 12.28 | 3.646 | 6.505 |

**Gartanin**

```
Scoring function : vina
Rigid receptor: protein.pdbqt
Ligand: 3_isomangostin.pdbqt
Grid center: X -4.055 Y -12.232 Z -17.416
Grid size  : X 10 Y 20 Z 16
Grid space : 0.375
Exhaustiveness: 8
CPU: 0
Verbosity: 1

Computing Vina grid ... done.
Performing docking (random seed: 2084557400) ...
0%   10   20   30   40   50   60   70   80   90   100%
|----|----|----|----|----|----|----|----|----|----|
**************************************************
```

| mode | affinity (kcal/mol) | dist from best mode rmsd l.b. | rmsd u.b. |
|---|---|---|---|
| 1 | -6.596 | 0 | 0 |
| 2 | -6.523 | 2.585 | 8.385 |
| 3 | -6.469 | 3.069 | 4.938 |
| 4 | -5.864 | 2.348 | 7.654 |
| 5 | -5.814 | 1.806 | 8.083 |
| 6 | -5.265 | 2.528 | 8.088 |
| 7 | -5.099 | 2.333 | 8.192 |
| 8 | -4.596 | 2.993 | 3.949 |
| 9 | -4.468 | 2.972 | 8.332 |

**3-Isomangostin**

```
Scoring function : vina
Rigid receptor: protein.pdbqt
Ligand: 8_deoxygartanin.pdbqt
Grid center: X -4.055 Y -12.232 Z -17.416
Grid size  : X 10 Y 20 Z 16
Grid space : 0.375
Exhaustiveness: 8
CPU: 0
Verbosity: 1

Computing Vina grid ... done.
Performing docking (random seed: 1445452280) ...
0%   10   20   30   40   50   60   70   80   90   100%
|----|----|----|----|----|----|----|----|----|----|
**************************************************
```

| mode | affinity (kcal/mol) | dist from best mode rmsd l.b. | rmsd u.b. |
|---|---|---|---|
| 1 | -6.53 | 0 | 0 |
| 2 | -6.169 | 1.77 | 4.847 |
| 3 | -6.15 | 5.279 | 9.211 |
| 4 | -5.999 | 3.922 | 8.149 |
| 5 | -5.579 | 3.591 | 8.294 |
| 6 | -5.568 | 4.379 | 7.721 |
| 7 | -5.513 | 4.863 | 10.01 |
| 8 | -5.502 | 4.114 | 9.444 |
| 9 | -5.477 | 3.773 | 5.86 |

**8-Deoxygartanin**

```
Scoring function : vina
Rigid receptor: protein.pdbqt
Ligand: GarcinoneD.pdbqt
Grid center: X -4.055 Y -12.232 Z -17.416
Grid size  : X 10 Y 20 Z 16
Grid space : 0.375
Exhaustiveness: 8
CPU: 0
Verbosity: 1

Computing Vina grid ... done.
Performing docking (random seed: 1098971865) ...
0%   10   20   30   40   50   60   70   80   90   100%
|----|----|----|----|----|----|----|----|----|----|
**************************************************
```

| mode | affinity (kcal/mol) | dist from best mode rmsd l.b. | rmsd u.b. |
|---|---|---|---|
| 1 | -6.185 | 0 | 0 |
| 2 | -5.871 | 2.132 | 7.505 |
| 3 | -5.397 | 2.636 | 7.226 |
| 4 | -5.114 | 1.857 | 2.598 |
| 5 | -5.097 | 1.82 | 7.772 |
| 6 | -5.079 | 3.282 | 7.542 |
| 7 | -4.765 | 2.272 | 4.568 |
| 8 | -4.348 | 2.641 | 7.994 |
| 9 | -4.096 | 2.219 | 4.717 |

**Garcinone D**