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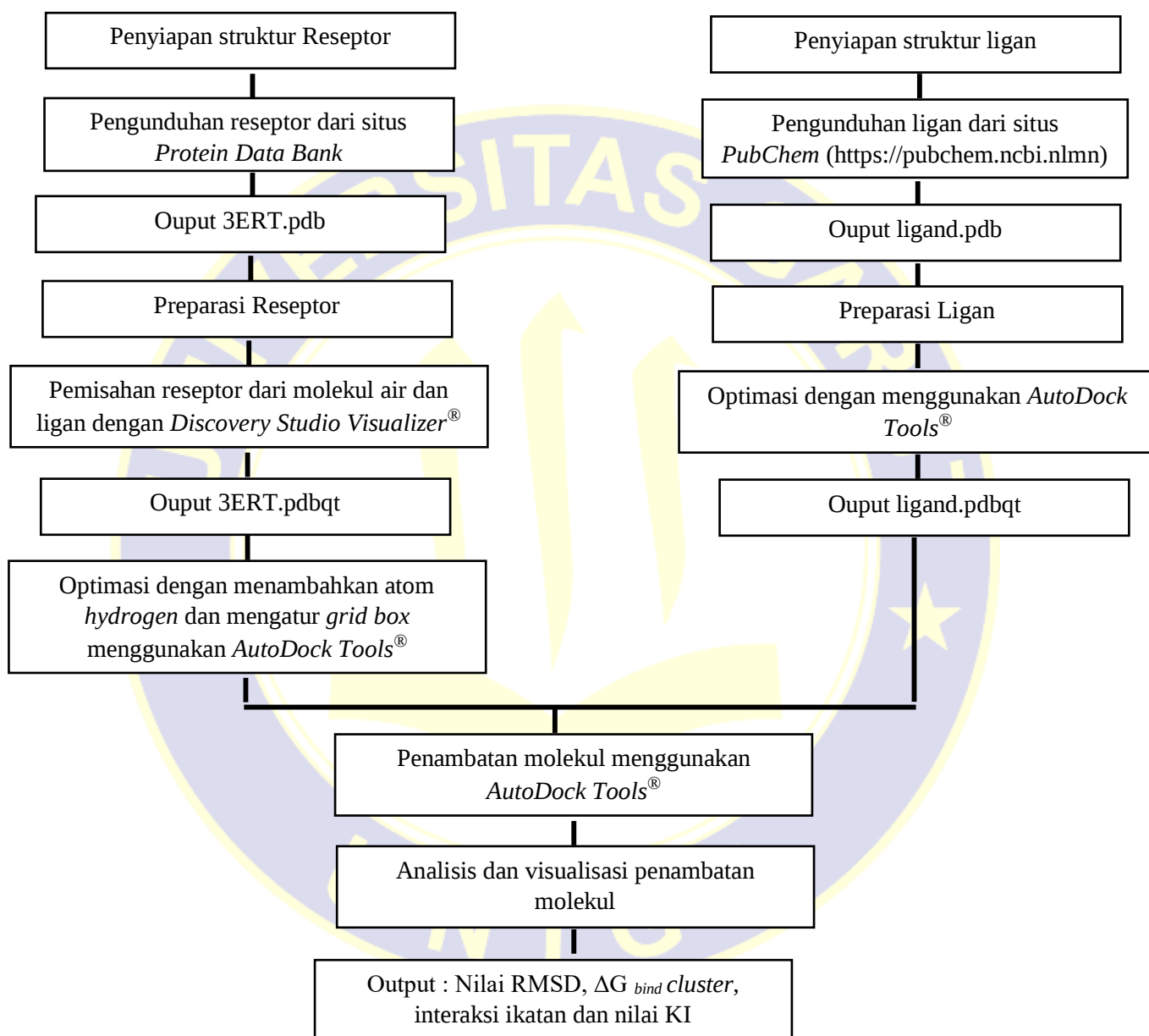
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LAMPIRAN 1

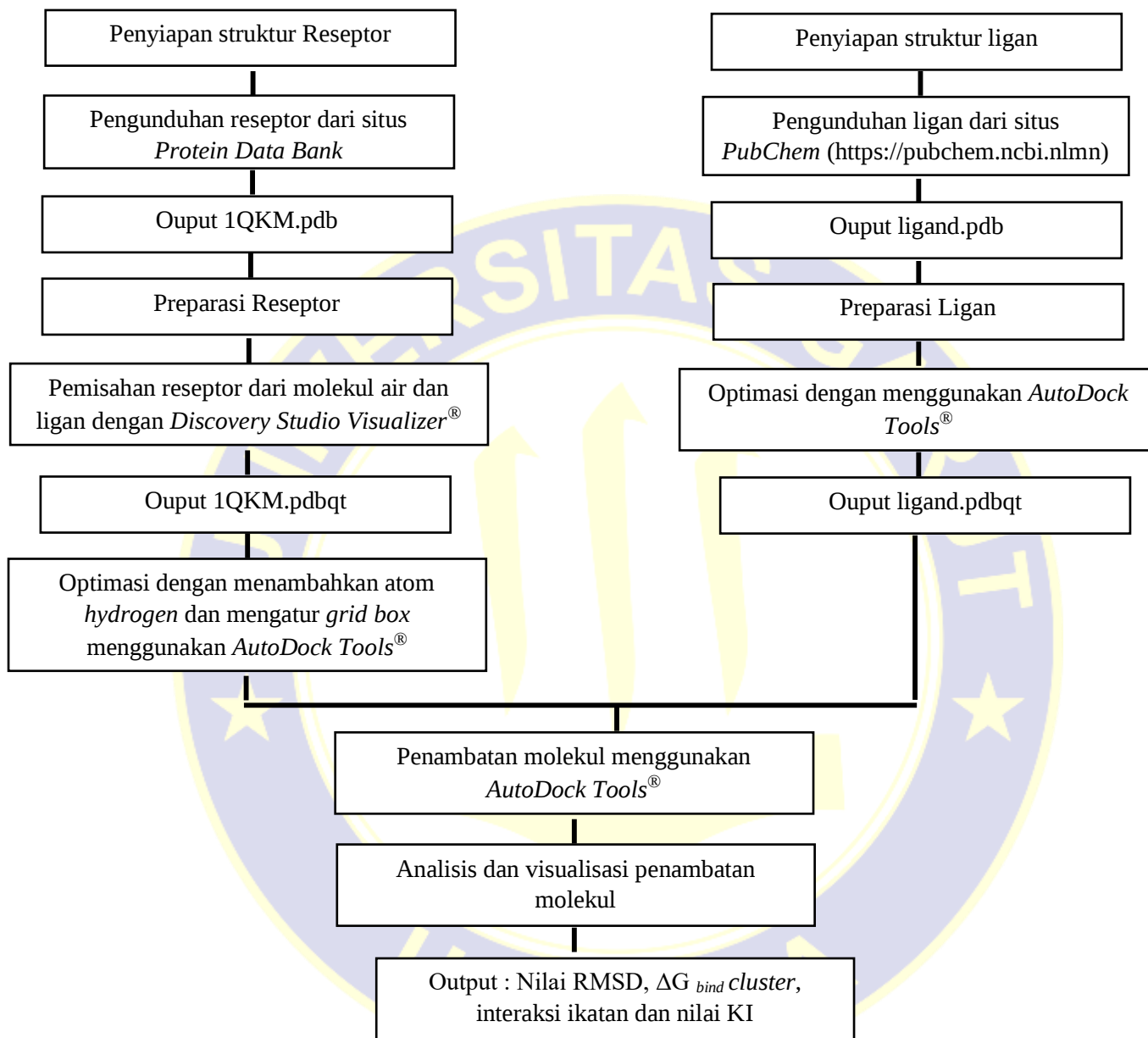
ALUR PENELITIAN MOLECULAR DOCKING



Gambar VII. 1 Alur penelitian penambatan molekul reseptor 3ERT



LAMPIRAN 1 (LANJUTAN)



Gambar VII. 2 Alur penelitian penambatan molekul reseptor 1QKM

LAMPIRAN 2

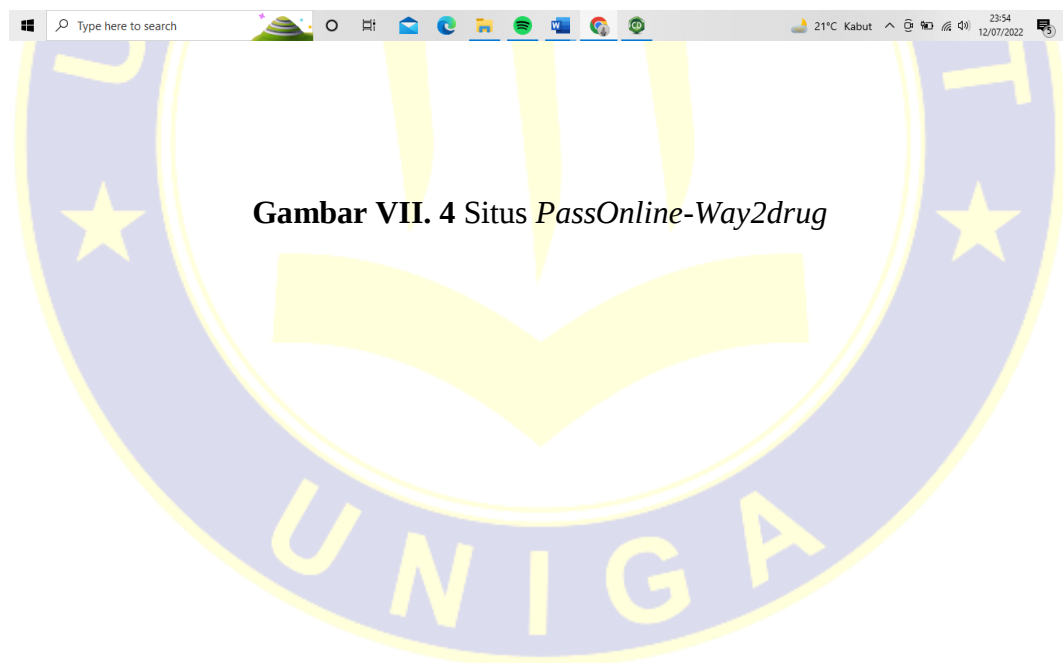
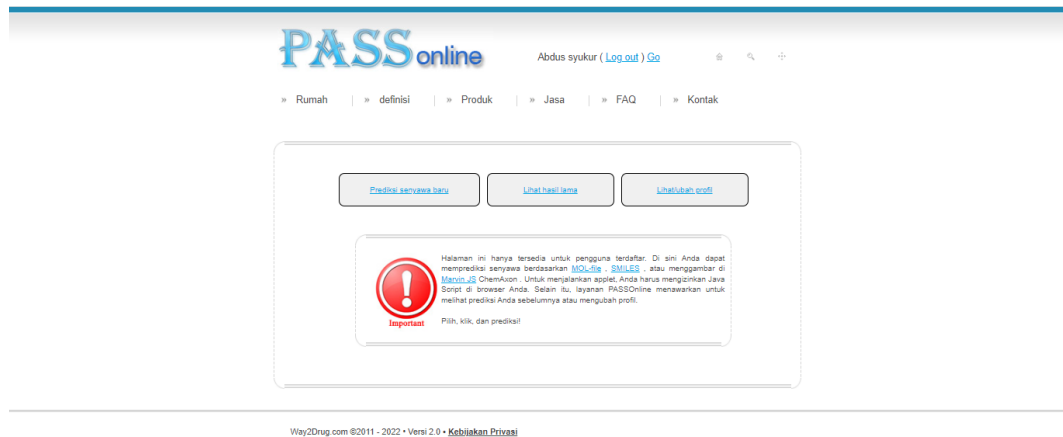
SITUS PDB (PROTEIN DATA BANK)

The screenshot displays the RCSB PDB website interface. At the top, there is a navigation bar with links: RCSB PDB, Deposit, Search, Visualize, Analyze, Download, Learn, More, Documentation, and Careers. A search bar contains the text '3ERT'. Below the navigation bar, the PDB logo and tagline '192095 Biological Macromolecular Structures Enabling Breakthroughs in Research and Education' are visible. The main content area shows the entry '1QKM' with the title 'HUMAN OESTROGEN RECEPTOR BETA LIGAND-BINDING DOMAIN IN COMPLEX WITH PARTIAL AGONIST GENISTEIN'. It includes a 3D ribbon diagram of the protein structure. Key information provided includes: PDB DOI: 10.2210/pdb1QKM/pdb, Classification: NUCLEAR RECEPTOR, Organism(s): Homo sapiens, Expression System: Escherichia coli, Mutation(s): No, Deposited: 1999-07-27, Released: 2000-07-28, and Deposition Author(s): Pike, A.C.W., Brzozowski, A.M., Carlquist, M. The 'Experimental Data Snapshot' section indicates the method is X-RAY DIFFRACTION and the resolution is 1.80 Å. A 'wwPDB Validation' section shows a metric of 0.248. The bottom of the image shows a Windows taskbar with various application icons and a system clock indicating 1:39 on 05/07/2022.

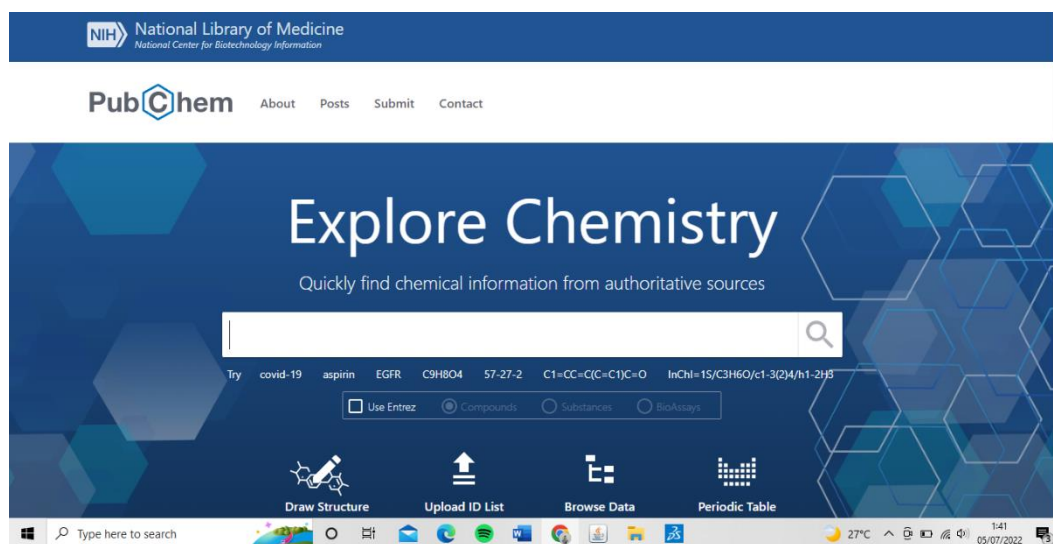
Gambar VII. 3 Situs online PDB (*Protein Data Bank*)

LAMPIRAN 3

SITUS *PassOnline-Way2drug*

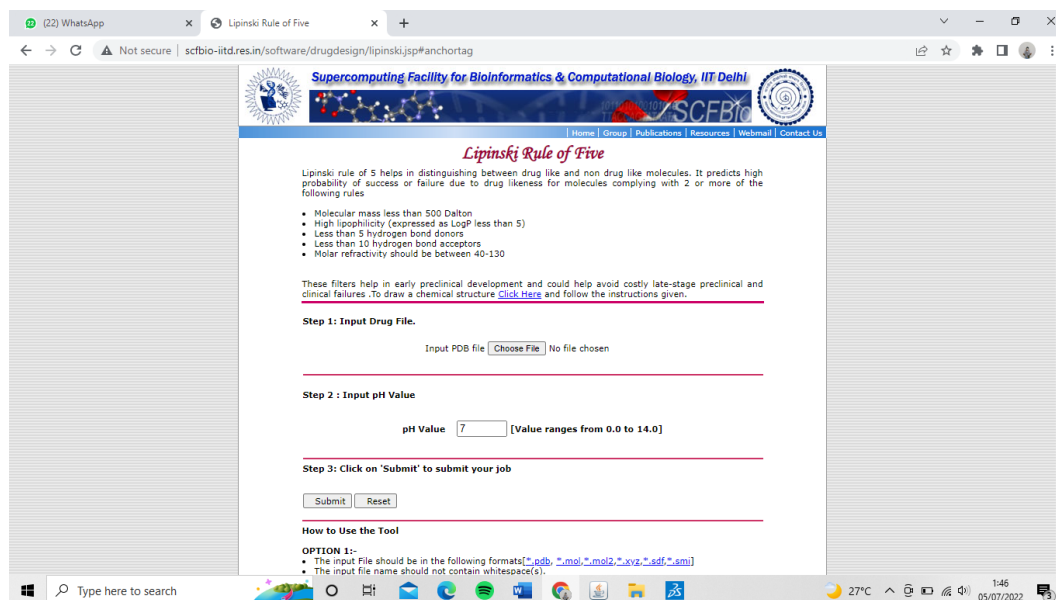


Gambar VII. 4 Situs *PassOnline-Way2drug*

LAMPIRAN 4**SITUS *PubChem*****Gambar VII. 5 Situs *PubChem***

LAMPIRAN 5

SITUS *Lipinski Rule of Five*



The screenshot shows a web browser window with the URL `scfbio-itsd.res.in/software/drugdesign/lipinski.jsp#anchortag`. The page is titled "Lipinski Rule of Five" and is part of the "Supercomputing Facility for Bioinformatics & Computational Biology, IIT Delhi" (SCFBIC) website. The page content includes:

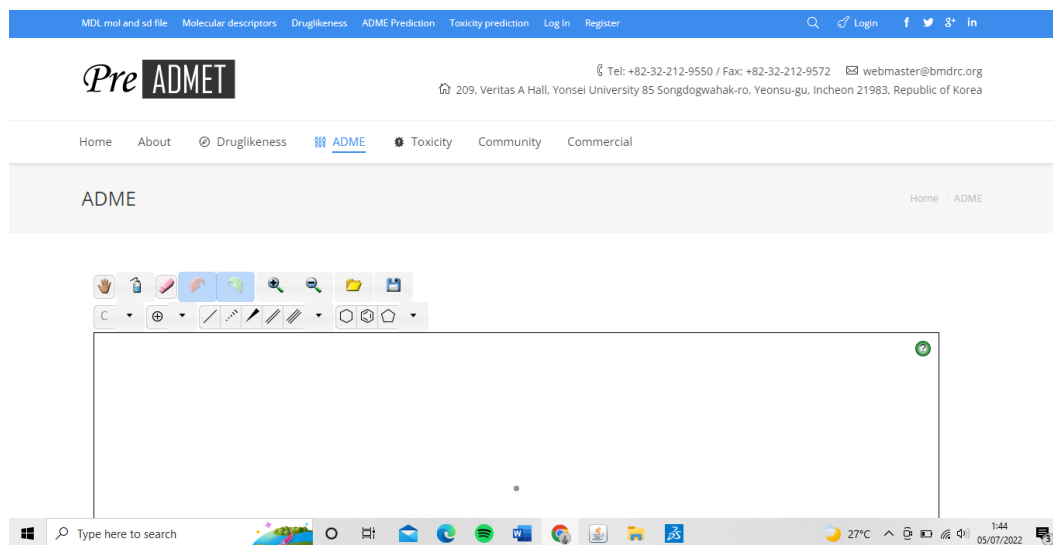
- Lipinski Rule of Five**: A section explaining the rule's purpose in distinguishing drug-like from non-drug-like molecules.
- Rules**: A list of five criteria:
 - Molecular mass less than 500 Dalton
 - High lipophilicity (expressed as LogP less than 5)
 - Less than 5 hydrogen bond donors
 - Less than 10 hydrogen bond acceptors
 - Molar refractivity should be between 40-130
- Filters**: A statement that these filters help in early preclinical development and avoid costly late-stage failures, with a link to "Click Here" for instructions.
- Step 1: Input Drug File**: A section with an "Input POB File" label, a "Choose File" button, and a "No file chosen" status.
- Step 2: Input pH Value**: A section with a "pH Value" input field set to "7" and a note "(Value ranges from 0.0 to 14.0)".
- Step 3: Click on 'Submit' to submit your job**: A section with "Submit" and "Reset" buttons.
- How to Use the Tool**: A section titled "OPTION 1:-" with instructions on file formats and naming conventions.

The Windows taskbar at the bottom shows the date as 05/07/2022 and the time as 1:46.

Gambar VII. 6 Situs *Lipinski Rule of Five*

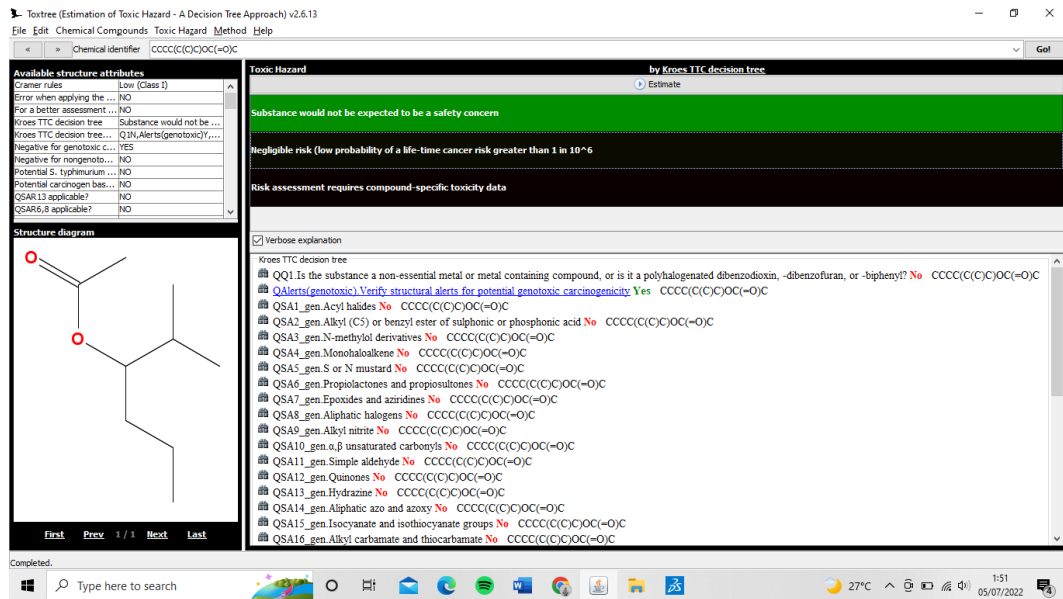
LAMPIRAN 6

SITUS *Pre-ADMET*

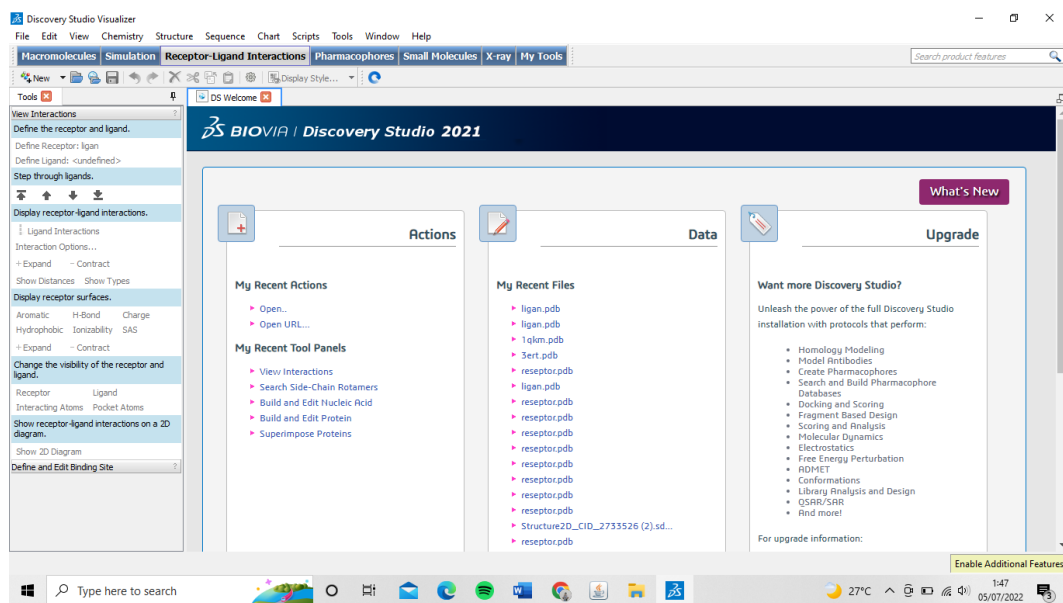


Gambar VII. 7 Situs *Pre-ADMET*

LAMPIRAN 7

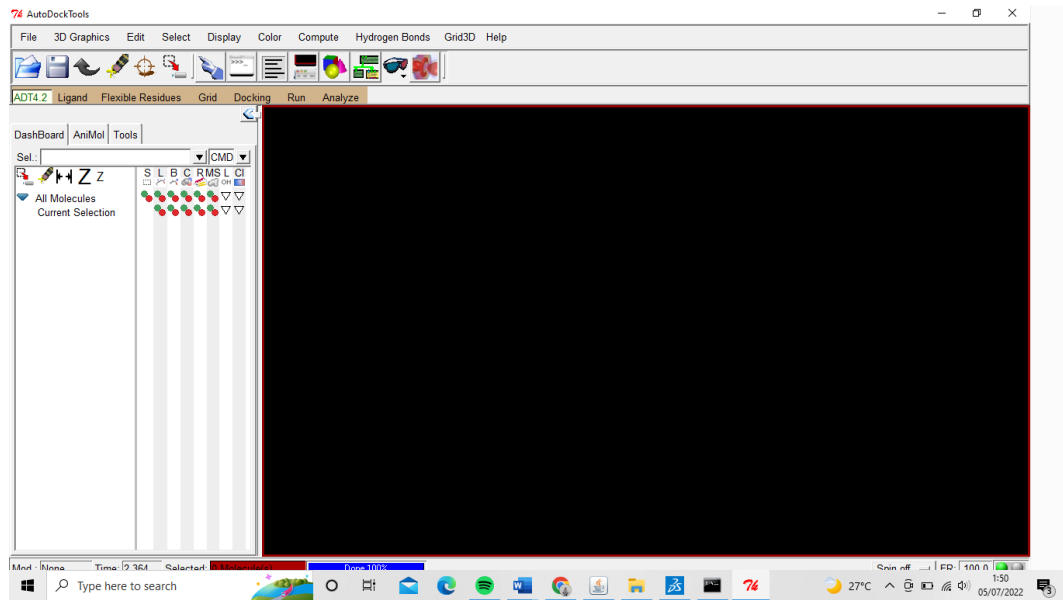
PERANGKAT LUNAK *TOXTREE*Gambar VII. 8 Perangkat lunak *toxtree*

LAMPIRAN 8

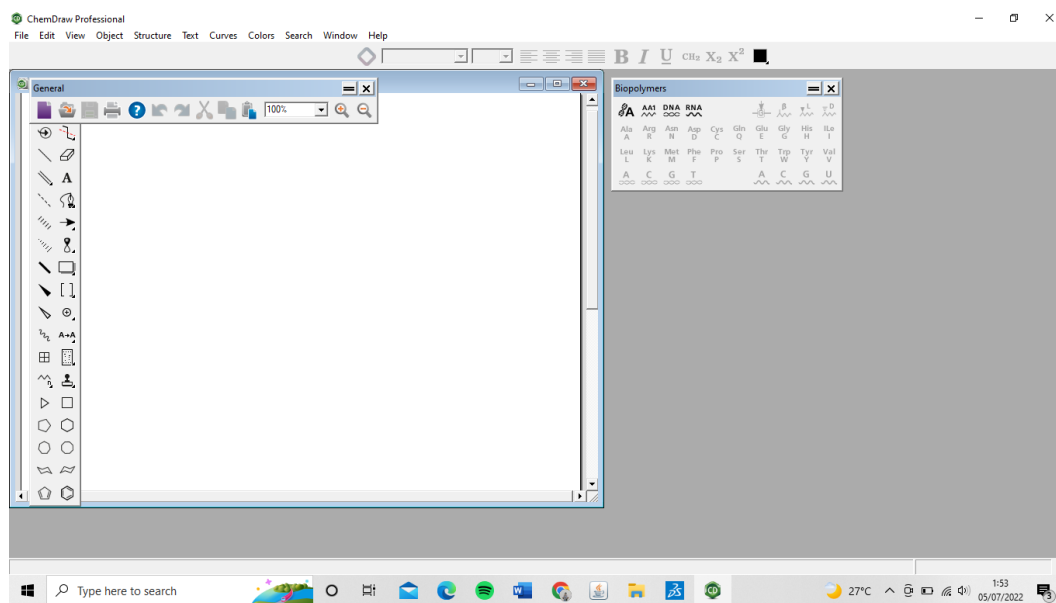
PERANGKAT LUNAK *DISCOVERY STUDIO VISUALIZER*Gambar VII. 9 Perangkat lunak *discovery studio visualizer*

LAMPIRAN 9

PERANGKAT LUNAK AUTODOCK TOOLS



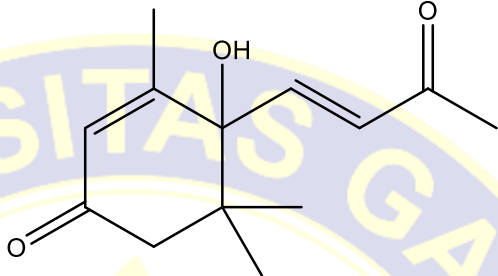
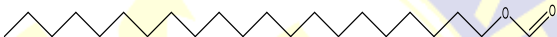
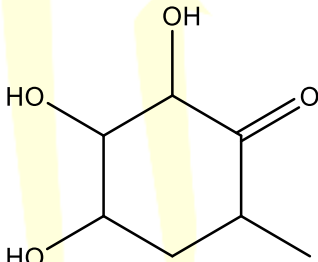
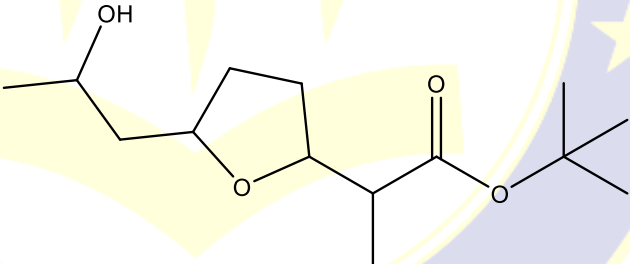
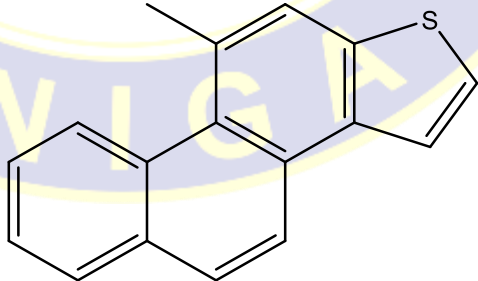
Gambar VII. 10 Perangkat lunak *autodock tools*

LAMPIRAN 10**PERANGKAT LUNAK *CHEM DRAW*****Gambar VII. 11** Perangkat lunak *chemdraw*

LAMPIRAN 11

SENYAWA BELIMBING WULUH (*Averrhoa bilimbi* L.)

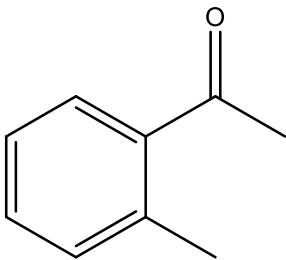
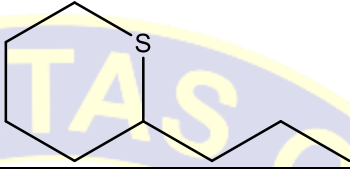
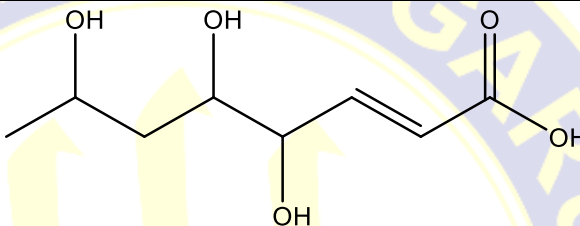
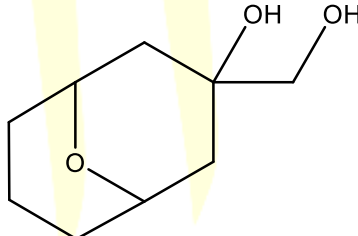
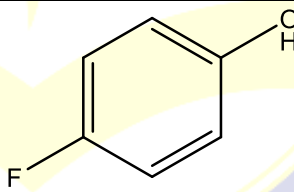
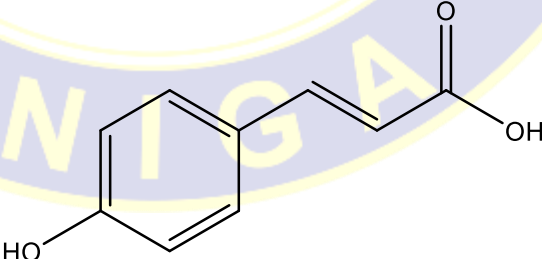
Tabel VII. 1
Struktur 2D Senyawa Aktif Belimbing Wuluh

No	Senyawa	Struktur 2D
1.	(s)-dehydromifoliol	
2.	1-Heneicosyl formate	
3.	2,3,4-Trihydroxy-6-methylcyclohexanone	
4.	2-[5-(2-Hydroxy-propyl)-tetrahydrofuran-2-yl]-propionic acid, t-butyl ester	
5.	2-Furancarboxylic acid, tert-butyl dimethylsilyl ester	

LAMPIRAN 11
(LANJUTAN)

Tabel VII.1

Lanjutan

No	Senyawa	Struktur 2D
6	2-Methylacetophenone	
7	2-n-Propylthiane	
8.	2-Octenoic acid, 4,5,7-trhydroxy	
9.	3-(hydroxymethyl)-9-Oxabicyclo [3.3.1] nonan-3-ol	
10.	4-fluorophenol	
11.	4-hydroxycinnamic acid	

LAMPIRAN 11
(LANJUTAN)Tabel VII.1
Lanjutan

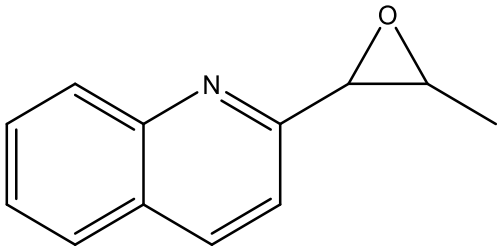
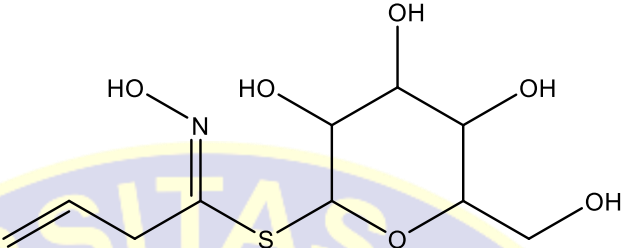
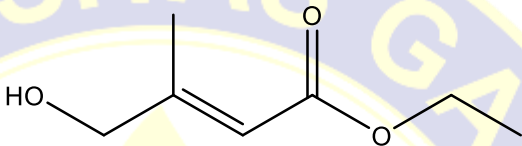
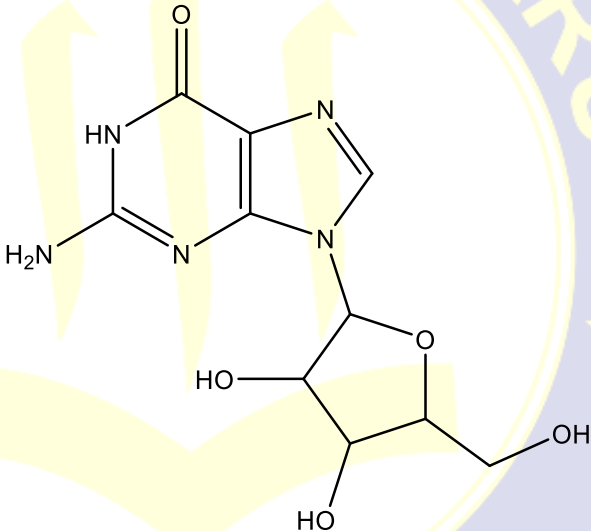
No	Senyawa	Struktur 2D
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12.	4-Hydroxylamino-6-methylpyrimidin-2(1H)-one	
13.	4-Methoxymethoxy-4-methyl-hex-2-ynal	
14.	5-(hydroxymethyl)-2-(dimethoxymethyl) Furan	
15.	5-Hydroxymethylfurfural	
16.	Acetic acid, 2-methylhex-3-yl ester	

**LAMPIRAN 11
(LANJUTAN)**

Tabel VII.1
Lanjutan

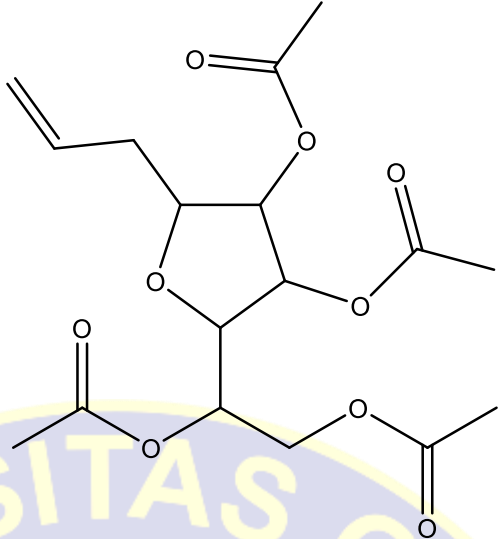
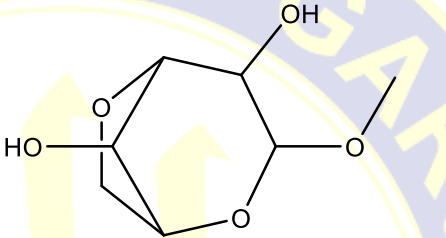
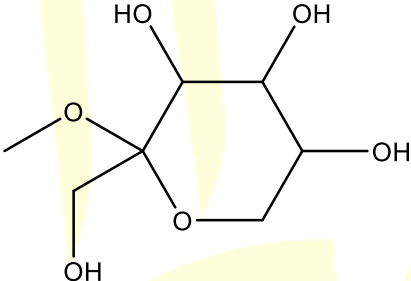
No	Senyawa	Struktur 2D
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17.	<i>Chimanine D</i>	
18.	<i>Desulphosinigrin</i>	
19.	<i>Ethyl 4-hydroxy-3-methylbut-2-enoate</i>	
20.	<i>Guanosine</i>	

**LAMPIRAN 11
(LANJUTAN)**

Tabel VII.1
Lanjutan

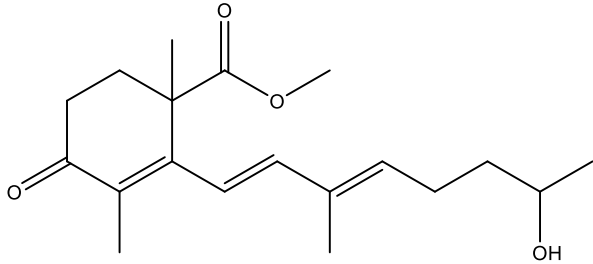
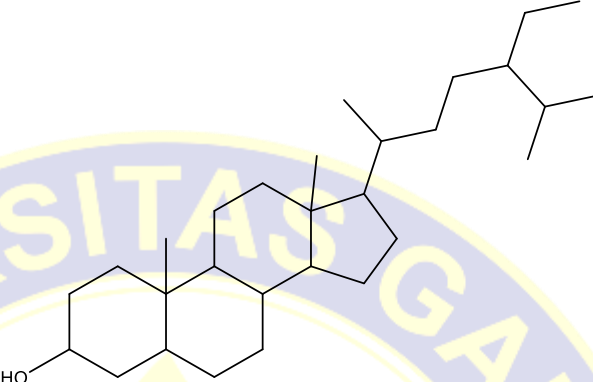
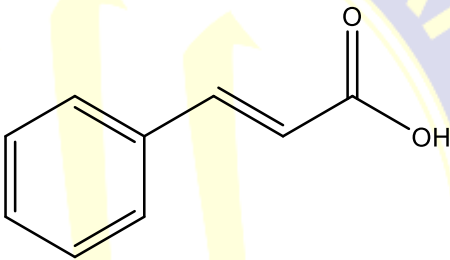
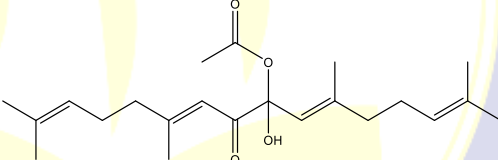
No	Senyawa	Struktur 2D
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21.	<i>Mannofuranoside, 1-allyl-2,3-5,6-tetra-O-acetyl</i>	
22.	<i>Methyl 3,6-anhydro-α-D-galactopyranoside</i>	
23.	<i>Methyl fructopyranoside</i>	

**LAMPIRAN 11
(LANJUTAN)**

Tabel VII.1
Lanjutan

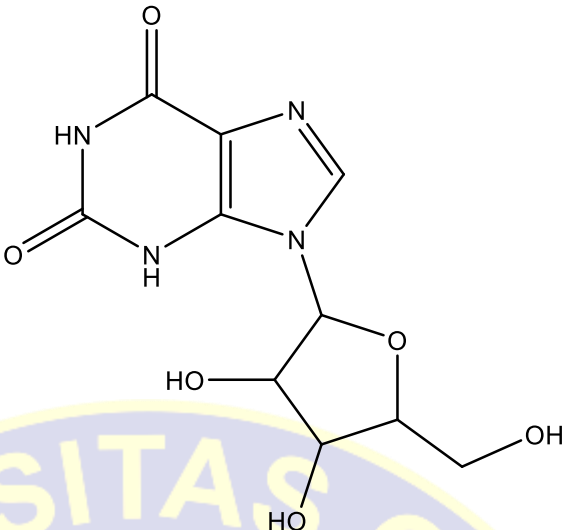
No	Senyawa	Struktur 2D
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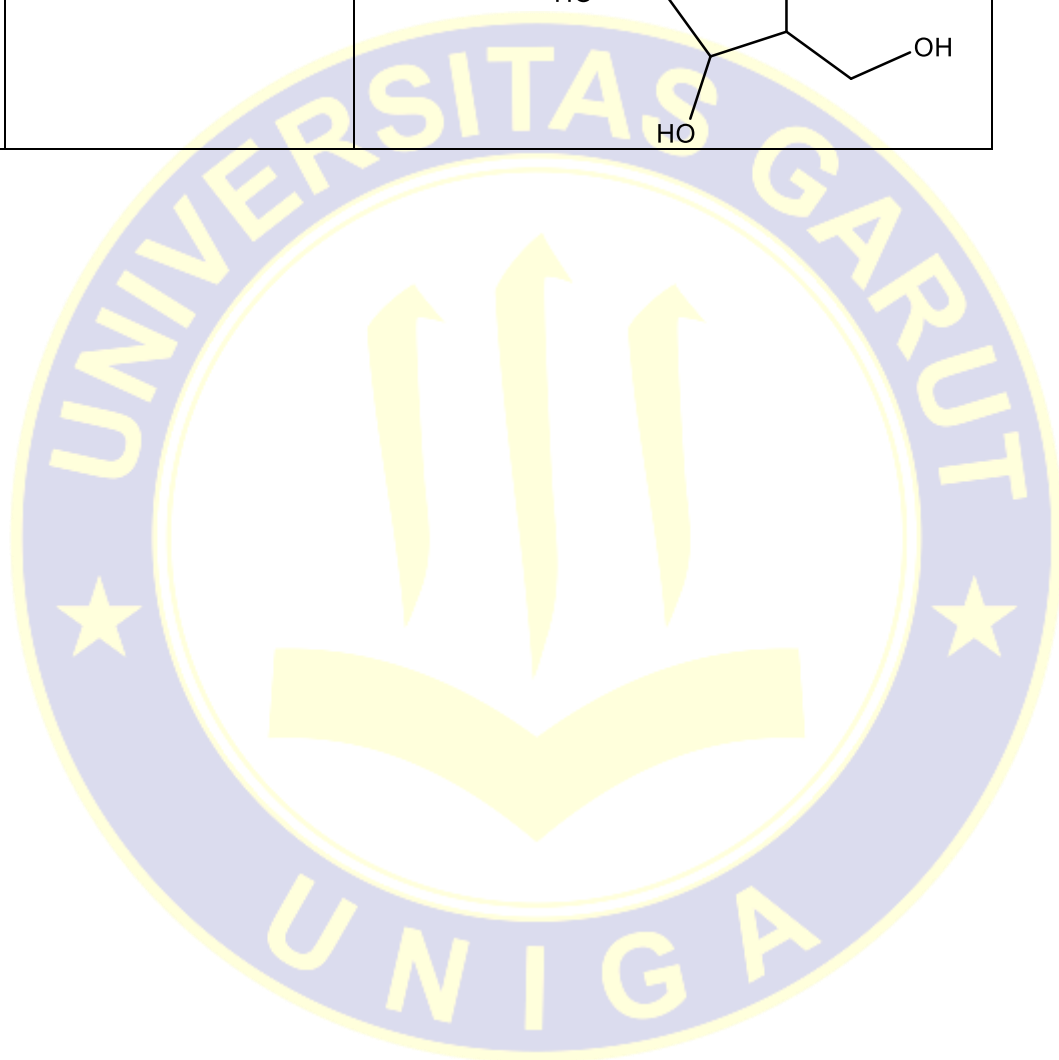
24.	<i>Methyl trisporate C</i>	
25.	<i>Stigmastanol</i>	
26.	<i>Trans cinnamic acid</i>	
27.	<i>Trans geranylgeraniol</i>	

**LAMPIRAN 11
(LANJUTAN)**

Tabel VII.1
Lanjutan

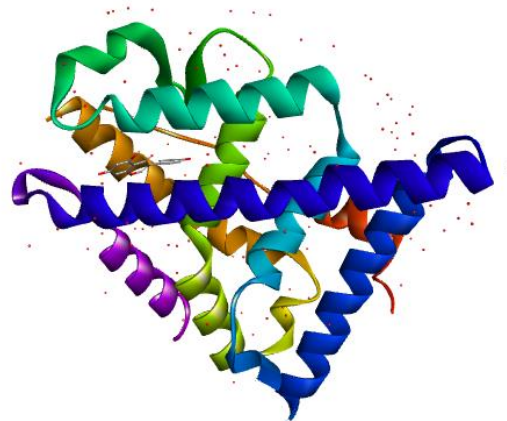
No	Senyawa	Struktur 2D
----	---------	-------------

28.	<i>Xanthosine</i>	 The chemical structure of Xanthosine is shown. It consists of a purine ring system (a fused pyrimidine and imidazole ring) with a ribose sugar attached to the N9 position. The purine ring has carbonyl groups at positions 6 and 2, and an amino group at position 6. The ribose sugar has hydroxyl groups at positions 2', 3', and 4'. <chem>O=C1NC(=O)N2C(=NC1=NC2N3C(C(C(C3O)O)O)O)C(=O)N</chem>
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LAMPIRAN 12**RESEPTOR $E\alpha$ dan $E\beta$** 

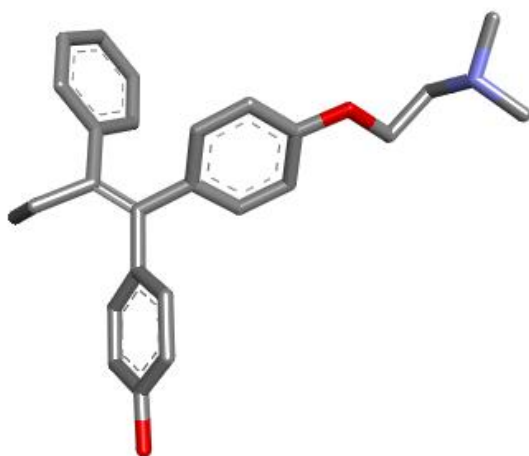
Gambar VII. 12 Struktur 3D reseptor $E\alpha$ (3ERT)



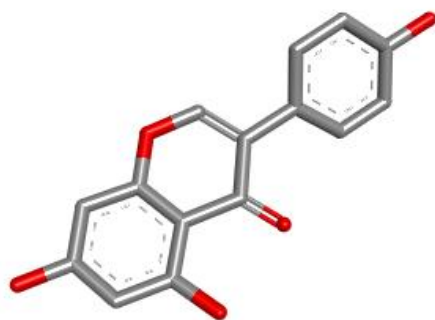
Gambar VII. 13 Struktur 3D reseptor $E\beta$ (1QKM)

LAMPIRAN 13

LIGAN ALAMI



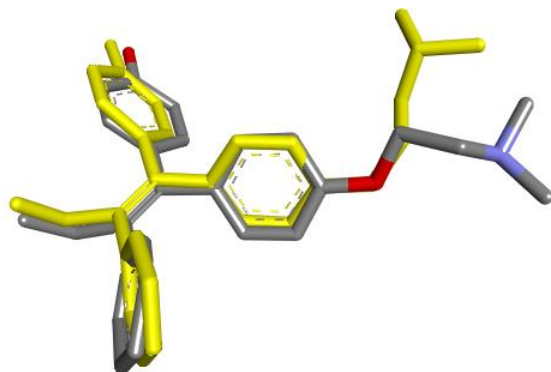
Gambar VII. 14 Struktur (*4-hydroxytamoxifen*) dari reseptor E_{α}



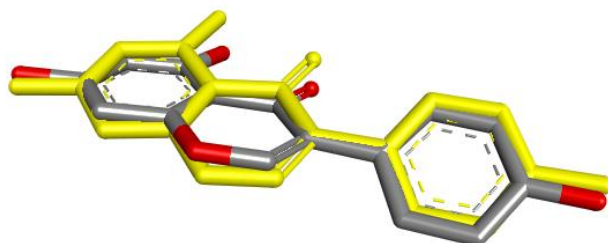
Gambar VII. 15 Struktur (*Genistein*) dari reseptor E_{β}

LAMPIRAN 14

HASIL VALIDASI

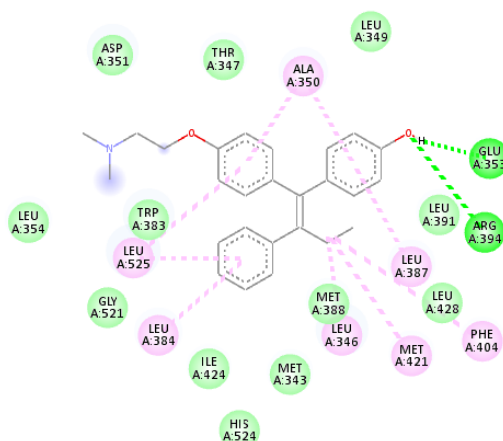


Gambar VII. 16 Visualisasi tumpang tindih ligan alami dengan ligan hasil *redocking* dari reseptor estrogen alfa ($Er\alpha$)

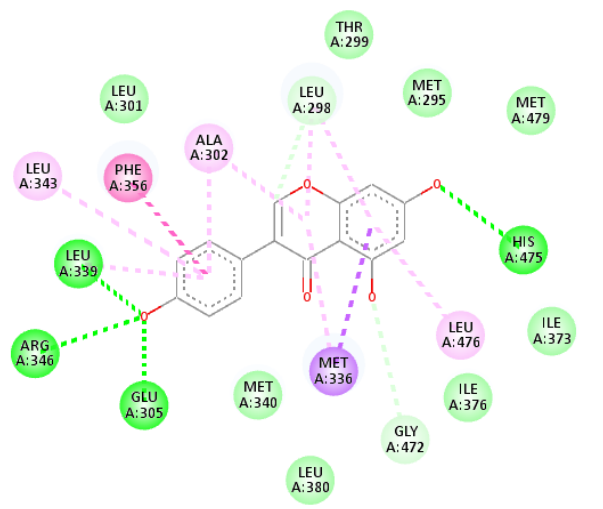


Gambar VII. 17 Visualisasi tumpang tindih ligan alami dengan ligan hasil *redocking* dari reseptor estrogen beta ($Er\beta$)

LAMPIRAN 14 (LANJUTAN)



Gambar VII. 18 Visualisasi interaksi residu asam amino ligan alami dengan reseptor estrogen alfa ($E\alpha$)



Gambar VII. 19 Visualisasi interaksi residu asam amino ligan alami dengan reseptor estrogen beta ($E\beta$)

**LAMPIRAN 14
(LANJUTAN)**

Tabel VII. 2
Hasil Validasi ER α dan ER β

Reseptor	Grid Box		RMSD	ΔG (Energi Bebas)	Konstanta Inhibisi (KI)
	Center	Size			
<i>Estrogen Reseptor Alpha (ERα)</i> kode 3ERT	X: 30.282 Y: -1.913 Z: 24.207	X: 28 Y: 22 Z: 26	1.125 Å	-11.41	4.36
<i>Estrogen Reseptor Alpha (ERβ)</i> kode 1QKM	X: 22.438 Y: 8.003 Z: 113.539	X: 30 Y: 22 Z: 30	0.452 Å	-12.11	1.33

LAMPIRAN 15

HASIL MOLECULAR DOCKING

Tabel VII. 3

Hasil *Docking* Senyawa Aktif dari Belimbing Wuluh (*Averrhoa bilimbi* L.) terhadap Reseptor Estrogen Alfa (ER α) Kode 3ERT

No.	Senyawa	ΔG (kcal/mol)	KI (nM)	Residu asam amino yang berikatan	
				Hidrofobik	Hidrogen
1.	<i>(s)-dehydrovomifoliol</i>	-6.82	9.95	-	ARG394
2	<i>1-Heneicosyl formate</i>	-5.57	82.27	TRP383, ALA350, LEU525, LEU346, LEU349, MET421, MET388, ILE424, LEU391, LEU387	-
3	<i>2,3,4-Trihydroxy-6-methylcyclohexanone</i>	-5.64	73.55	-	LEU346, GLU353, ARG394
4	<i>2-[5-(2-Hydroxy-propyl)-tetrahydrofuran-2-yl]-propionic acid, t-butyl ester</i>	-6.65	13.30	MET343, LEU525	ARG494, GLU353
5	<i>2-Furancarboxylic acid, tert-butyldimethylsilyl ester</i>	-8.22	936.69	MET343, LEU346, ALA350, MET421, LEU525	HIS524
6	<i>2-Methylacetophenone</i>	-5.01	212.97	MET388, LEU387, LEU391	ARG394
7	<i>2-n-Propylthiane</i>	-4.77	320.30	MET388, LEU428, ALA350, LEU346, LEU349, LEU391, LEU387	-

LAMPIRAN 15
(LANJUTAN)

Tabel VII.3

Lanjutan

No.	Senyawa	ΔG (kkal/mol)	KI (nM)	Residu asam amino yang berikatan	
				Hidrofobik	Hidrogen
8	2-Octenoic acid, 4,5,7-trihydroxy	-4.10	994.92	-	GLU353, ARG394
9	3-(hydroxymethyl)-9-Oxabicyclo [3.3.1] nonan-3-ol	-5.59	79.69	ALA350, LEU346, LEU387	GLU353
10	4-fluorophenol	-4.39	609.46	LEU387, LEU391	GLU353
11	4-hydroxycinnamic acid	-4.44	556.82	ALA350, LEU387, LEU346, LEU349	GLU353, THR347
12	4-Hydroxylamino-6-methylpyrimidin-2(1H)-one	-4.67	375.72	LEU387, MET388, ALA350, LEU391, LEU384	LEU346, GLU353, ARG394
13	4-Methoxymethoxy-4-methyl-hex-2-ynal	-3.73	1.85	GLU353, LEU346, LEU349, ALA350,	ARG394
14	5-(hydroxymethyl)-2-(dimethoxymethyl) Furan	-4.18	869.03	LEU349, LEU387, LEU346, ALA350	ARG394, GLU353
15	5-Hydroxymethylfurfural	-3.59	2.35	LEU387, ALA350, LEU391, LEU346	GLU353
16	Acetic acid, 2-methylhex-3-yl ester	-4.31	690.31	MET388, LEU384, LEU391, LEU387, LEU346, ALA345	ARG349

LAMPIRAN 15
(LANJUTAN)Tabel VII.3
Lanjutan

No.	Senyawa	ΔG (kkal/mol)	KI (nM)	Residu asam amino yang berikatan
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				Hidrofobik	Hidrogen
17	<i>Chimanine D</i>	-5.71	65.51	LEU391, MET388, ILE424, MET421, LEU387	-
18	<i>Desulphosinigrin</i>	-5.33	124.93	LEU346, LEU387, ALA350	ARG394, THR347, GLU353
19	<i>Ethyl 4-hydroxy-3-methylbut-2-enoate</i>	-4.36	638.48	ALA350, LEU346	GLU353
20	<i>Guanosine</i>	-7.05	6.79	ALA350, LEU387, LEU384, MET388	GLU353, LEU346, MET343, THR347
21	<i>Mannofuranoside, 1-allyl-2,3-5,6-tetra-O-acetyl</i>	-6.12	32.67	GLY521, ALA350, LEU346, LEU349	-
22	<i>Methyl 3,6-anhydro-α-D-galactopyranoside</i>	-4.94	239.87	LEU346	GLU535, ARG394, LEU346
23	<i>Methyl fructopyranoside</i>	-4.51	495.35	GLU353	ARG394, LEU346, GLU353
24	<i>Methyl trisporate C</i>	-8.27	864.71	GLU353, TRP383, ALA350, LEU346	ARG394, ASP351
25	<i>Stigmastanol</i>	-10.58	17.67	LEU391, LEU346, LEU387, LEU384, ALA350, LEU525	-
26	<i>Trans cinnamic acid</i>	-4.21	817.08	MET388, MET421, LEU391	GLU353, ARG394

**LAMPIRAN 15
(LANJUTAN)**

Tabel VII.3
Lanjutan

No.	Senyawa	ΔG (kkal/mol)	KI (nM)	Residu asam amino yang berikatan	
				Hidrofobik	Hidrogen
27	<i>Trans geranylgeraniol</i>	-7.59	2.72	LEU387, LEU346,	ARG394, GLU353

				LEU354, TRP383, ALA350, LEU525, LEU384	
28	<i>Xanthosine</i>	-6.17	29.94	LEU391, ALA350, MET388	GLU353, PHE404, LEU346



LAMPIRAN 16

HASIL MOLECULAR DOCKING

Tabel VII. 4

Hasil Docking Senyawa Aktif dari Belimbing Wuluh (*Averrhoa bilimbi* L.) terhadap Reseptor Estrogen Beta (ER β) Kode 1QKM

No.	Senyawa	ΔG (kkal/mol)	KI (nM)	Residu asam amino yang berikatan	
				Hidrofobik	Hidrogen
1.	<i>(s)-dehydrovomifoliol</i>	-7.37	3.96	ALA302, PHE356, LEU339, LEU301	LEU298, MET340
2	<i>1-Heneicosyl formate</i>	-7.47	3.33	LEU343, MET340, PHE356	-
3	<i>2,3,4-Trihydroxy-6-methylcyclohexanone</i>	-5.91	46.26	-	LEU298, GLU305, ARG346
4	<i>2-[5-(2-Hydroxy-propyl)-tetrahydrofuran-2-yl]-propionic acid, t-butyl ester</i>	-7.88	1.68	LEU476, LEU298, PHE356, LEU343, ALA302, MET336, MET340, LEU339	HIS475, GLY472
5	<i>2-Furancarboxylic acid, tert-butyl dimethylsilyl ester</i>	-9.73	73.83	MET336, HIS475, ALA302, LEU339, LEU476, MET340, LEU298	-
6	<i>2-Methylacetophenone</i>	-5.57	81.95	LEU298, LEU476	HIS475

(LAMPIRAN) 16
(LANJUTAN)

Tabel VII.4
Lanjutan

No.	Senyawa	ΔG (kkal/mol)	KI (nM)	Residu asam amino yang berikatan	
				Hidrofobik	Hidrogen
7	2-n-Propylthiane	-5.32	126.27	LEU343, LEU339, MET340, PHE356, LEU301, LEU298, ALA302	-
8	2-Octenoic acid, 4,5,7-trihydroxy	-4.07	1.04	-	ALA302, LEU298, GLU305, ARG346
9	3-(hydroxymethyl)-9-Oxabicyclo [3.3.1] nonan-3-ol	-6.08	34.75	LEU298, PHE356, MET336, ALA302	GLU305, ARG346
10	4-fluorophenol	-4.60	427.80	PHE356, MET340, LEU343, LEU339	GLU305, ARG346
11.	4-hydroxycinnamic acid	-5.30	130.96	LEU476, ALA302, LEU298	LEU298, HIS475, GLY472
12.	4-Hydroxylamino-6-methylpyrimidin-2(1H)-one	-4.96	232.27	MET336, LEU339, LEU343, MET340	GLU305, PHE356
13.	4-Methoxymethoxy-4-methyl-hex-2-ynal	-4.51	495.87	LEU380, MET340, PHE356, MET336, ILE376, PHE377	HIS475
14.	5-(hydroxymethyl)-2-(dimethoxymethyl) Furan	-4.72	344.79	PHE356, LEU339, LEU301, ALA302	ARG346, GLU305

LAMPIRAN) 16
(LANJUTAN)

Tabel VII.4

Lanjutan

No.	Senyawa	ΔG (kkal/mol)	KI (nM)	Residu asam amino yang berikatan	
				Hidrofobik	Hidrogen
15.	<i>5-Hydroxymethylfurfural</i>	-3.93	1.32	MET340, MET336, PHE356, LEU343	GLU305, ARG346
16.	<i>Acetic acid, 2-methylhex-3-yl ester</i>	-5.00	217.72	VAL487, PHE356, ILE376, MET336, LEU380, LEU298, MET340, LEU476, ALA302	HIS475
17.	<i>Chimanine D</i>	-6.84	9.69	PHE356, LEU343, ALA302, LEU298, VAL487, LEU476, LEU339, TRP335, MET336	-
18.	<i>Desulphosinigrin</i>	-5.81	55.10	MET336,	MET336, LEU298, GLU305
19.	<i>Ethyl 4-hydroxy-3-methylbut-2-enoate</i>	-4.69	366.94	LEU339	ARG346, GLU305
20.	<i>Guanosine</i>	-7.59	2.74	ALA302, MET336, PHE356, MET340, LEU339	GLY472, HIS475, LEU298, GLU305

LAMPIRAN) 16
(LANJUTAN)Tabel VII.4
Lanjutan

No.	Senyawa	ΔG (kkal/mol)	KI (nM)	Residu asam amino yang berikatan
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				Hidrofobik	Hidrogen
21.	<i>Mannofuranoside, 1-allyl-2,3-5,6-tetra-O-acetyl</i>	-8.30	821.82	LEU298, LEU343, MET340, LEU339, PHE356	HIS475
22.	<i>Methyl 3,6-anhydro-α-D-galactopyranoside</i>	-5.21	150.72	-	LEU298, ARG346, GLU305
23.	<i>Methyl fructopyranoside</i>	-3.72	1.87	-	LEU298, MET336, GLU305
24.	<i>Methyl trisporate C</i>	-11.03	8.28	ILE376, MET340, MET336, LEU339, TRP335, ALA302	HIS475, ARG346, GLU305
25.	<i>Stigmastanol</i>	-10.80	12.21	HIS475, MET295, LEU476, LEU298, ILE376, MET340, LEU343, PHE356, LEU301, LEU339	GLU305, ARG346
26.	<i>Trans cinnamic acid</i>	-5.08	190.15	LEU476, LEU298, MET336, ALA302	GLY472, HIS475

**LAMPIRAN) 16
(LANJUTAN)**

Tabel VII.4
Lanjutan

No.	Senyawa	ΔG (kkal/mol)	KI (nM)	Residu asam amino yang berikatan	
				Hidrofobik	Hidrogen

27.	<i>Trans geranylgeraniol</i>	-9.36	138.64	GLU305 LEU476, ALA302, ILE376, MET336, PHE356, MET340, LEU339, LEU343	LEU298
28.	<i>Xanthosine</i>	-12.11	1.33	LEU298, ALA302, MET340, MET336, PHE356, LEU339	HIS475, LEU298, ALA302, GLU305



LAMPIRAN 17
HASIL PENGUJIAN PREADMET

Tabel VII. 5
Hasil Pengujian Pre-ADMET

No.	Senyawa	Absorpsi		Distribusi
		Caco2 (nm.Sec ⁻¹)	HIA (%)	PPB (%)
1	(s)-dehydrovomifoliol,	23.2095	94.391464	87.450942
2	1-Heneicosyl formate	29.4161	100	100
3	2,3,4-Trihydroxy-6-methylcyclohexanone	14.5638	62.269322	59.145813
4	2-[5-(2-Hydroxy-propyl)-tetrahydrofuran-2-yl]-propionic acid, t-butyl ester	56.6429	93.1465720	84.162398
5	2-Furancarboxylic acid, tert-butyl dimethylsilyl ester	45.6568	100	100
6	2-Methylacetophenone	46.068	100	12.147080
7	2-n-Propylthiane	24.6256	100	100
8	2-Octenoic acid, 4,5,7-trihydroxy	18.8975	44.245409	19.280506
9	3-(hydroxymethyl)-9-Oxabicyclo [3.3.1] nonan-3-ol	10.723	85.386008	21.849481
10	4-fluorophenol	23.3068	100	90.993698
11	4-hydroxycinnamic acid	21.1093	92.095876	63.055072
12	4-Hydroxylamino-6-methylpyrimidin-2(1H)-one	19.7799	67.888890	11.073953
13	4-Methoxymethoxy-4-methylhex-2-ynal	4.38965	97.797528	29.076706
14	5-(hydroxymethyl)-2-(dimethoxymethyl) Furan	36.8875	90.081475	78.387735
15	5-Hydroxymethylfurfural	6.41666	88.682048	49.465993
16	Acetic acid, 2-methylhex-3-yl ester	54.0067	100	100
17	Chimanine D	57.6147	100	85.761905
18	Desulphosinigrin	0.375984	31.323035	23.626939
19	Ethyl 4-hydroxy-3-methylbut-2-enoate	19.4914	89.780046	91.378979
20	Guanosine	9.42339	25.895030	8.044443
21	Mannofuranoside, 1-allyl-2,3-5,6-tetra-O-acetyl	13.1418	77.310454	45.726354

LAMPIRAN 17
LANJUTAN

VII.5
Lanjutan

No.	Senyawa	Absorpsi		Distribusi
		Caco ₂ (nm.Sec ⁻¹)	HIA (%)	PPB (%)
22	<i>Methyl 3,6-anhydro-α-D-galactopyranoside</i>	6.60318	72.712474	33.421886
23	<i>Methyl fructopyranoside</i>	3.45388	35.574635	5.522551
24	<i>Methyl trisporate C</i>	22.8813	96.003816	85.929266
25	<i>Stigmastanol</i>	52.4418	100	100
26	<i>Trans cinnamic acid</i>	21.0342	97.845200	60.852531
27	<i>Trans geranylgeraniol</i>	33.7556	96.037673	99.005260
28	<i>Xanthosine</i>	13.6448	24.716318	12.768312

Keterangan: *in vitro* CaCo-2 cell permeability (nm. Sec⁻¹): >70 higher permeability, 4-70 medium permeability, <4 low permeability; % human intestinal absorption (%HIA): 700-100% well absorbed, 20-70% moderately absorbed, 0-20% poorly absorbed; %plasma protein binding: >90% strongly bound, <90% weakly bound.

LAMPIRAN 18

HASIL PENGUJIAN TOKSISITAS

Tabel VII. 6
Hasil Pengujian Toksisitas

No	Senyawa	Crame rules	Kores TCC	Benigne/bosarulebase
1	<i>(s)-dehydrovomifoliol</i>	3	2	1,9
2	<i>1-Heneicosyl formate</i>	1	1	8,9
3	<i>2,3,4-Trihydroxy-6-methylcyclohexanone</i>	2	1	8,9
4	<i>2-[5-(2-Hydroxy-propyl)-tetrahydrofuran-2-yl]-propionic acid, t-butyl ester</i>	3	1	8,9
5	<i>2-Furancarboxylic acid, tert-butyldimethylsilyl ester</i>	3	2	1,9
6	<i>2-Methylacetophenone</i>	1	1	8,9
7	<i>2-n-Propylthiane</i>	3	1	8,9
8	<i>2-Octenoic acid, 4,5,7-trhydroxy</i>	2	1	8,9
9	<i>3-(hydroxymethyl)-9-Oxabicyclo [3.3.1] nonan-3-ol</i>	3	1	8,9
10	<i>4-fluorophenol</i>	3	1	2,8
11	<i>4-hydroxycinnamic acid</i>	1	1	8,9
12	<i>4-Hydroxylamino-6-methylpyrimidin-2(1H)-one</i>	3	1	8,9
9	<i>3-(hydroxymethyl)-9-Oxabicyclo [3.3.1] nonan-3-ol</i>	3	1	8,9
10	<i>4-fluorophenol</i>	3	1	2,8
9	<i>3-(hydroxymethyl)-9-Oxabicyclo [3.3.1] nonan-3-ol</i>	3	1	8,9
10	<i>4-fluorophenol</i>	3	1	2,8
11	<i>4-hydroxycinnamic acid</i>	1	1	8,9
12	<i>4-Hydroxylamino-6-methylpyrimidin-2(1H)-one</i>	3	1	8,9
13	<i>4-Methoxymethoxy-4-methyl-hex-2-ynal</i>	3	2	1,9
14	<i>5-(hydroxymethyl)-2-(dimethoxymethyl) Furan</i>	3	1	8,9
15	<i>5-Hydroxymethylfurfural</i>	3	2	8,9

LAMPIRAN 18
(LANJUTAN)

Tabel VII.6
Lanjutan

No	Senyawa	Cramer rules	Kores TCC	Benigne/bosarulebase
16	Acetic acid, 2-methylhex-3-yl ester	1	1	2,8
17	Chimanine D	3	2	1,9
18	Desulphosinigrin	3	1	8,9
19	Ethyl 4-hydroxy-3-methylbut-2-enoate	1	1	8,9
20	Guanosine	1	1	8,9
21	Mannofuranoside, 1-allyl-2,3-5,6-tetra-O-acetyl	3	1	8,9
22	Methyl 3,6-anhydro- α -D-galactopyranoside	3	1	8,9
23	Methyl fructopyranoside	3	1	8,9
24	Methyl trisporate C	2	2	1,9
25	Stigmastanol	3	1	8,9
26	Trans cinnamic acid	1	1	8,9
27	Trans geranylgeraniol	3	1	8,9
28	Xanthosine	1	1	8,9

Keterangan: Cramer ruler class 1: low, class 2 : intermediet, class 3 : high. Benigni/bosa rulebase 1 (structural alert for genotoxic carcinogenicity) 2 (Structural alert for nongenotoxic carcinogenicity), 8 (negative for genotoxic carcinogenity), 9 (negative for non-genotoxic carcinogenity). Kroes TTC decission tree 1 (Substance would not be expected to be a safety concern), 2 (Negligible risk (low probability of a life time cancer risk greater than 1 in 10^6))

LAMPIRAN 19

HASIL PENGUJIAN *LIPINSKI'S RULE OF FIVE*

Tabel VII. 7

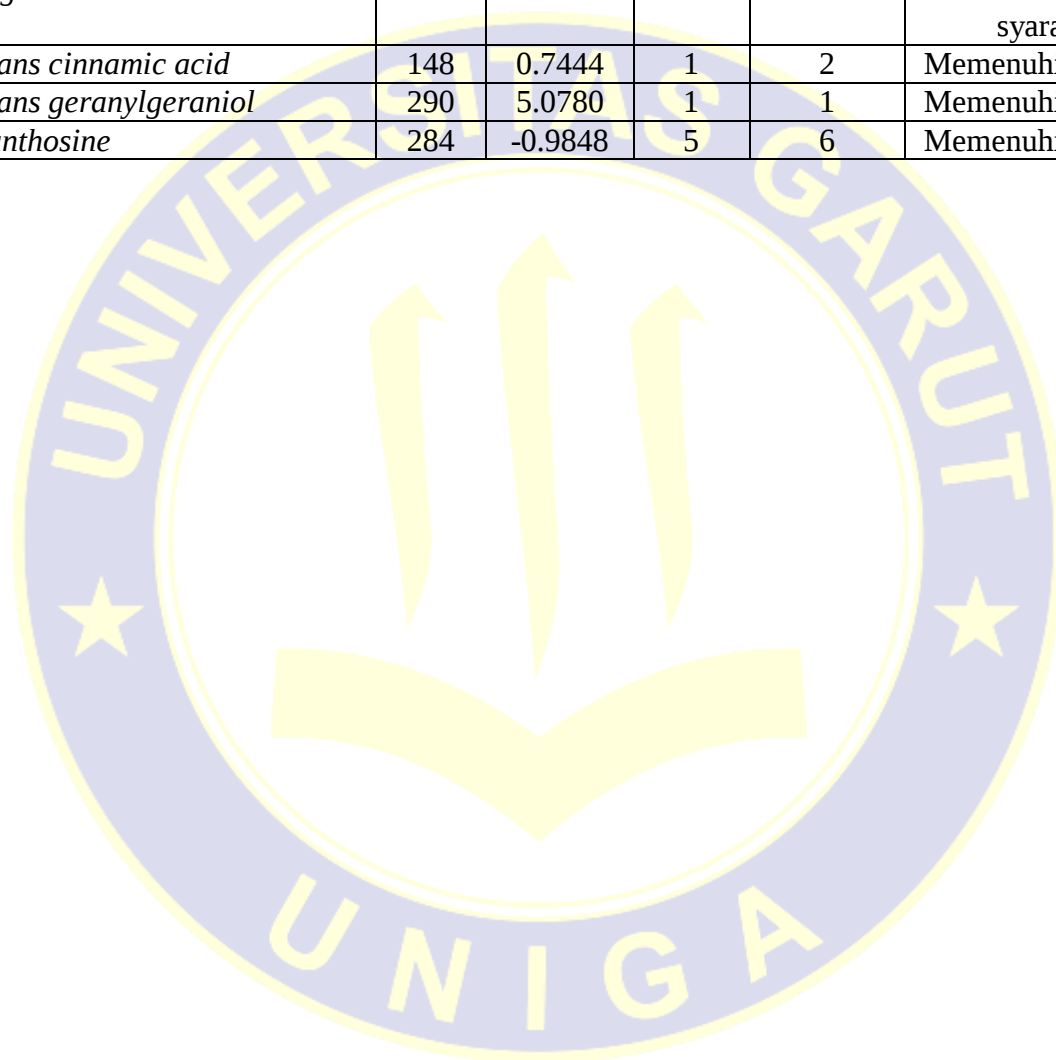
Hasil Pengujian *Lipinski's Rule of Five*

No	Senyawa	BM	LOG P	Ikatan hidrogen		Keterangan
				Donor	Akseptor	
1	(s)-dehydrovomifoliol	222	2.7568	0	3	Memenuhi syarat
2	1-Heneicosyl formate	340	6.2857	0	2	Tidak memenuhi syarat
3	2,3,4-Trihydroxy-6-methylcyclohexanone	160	0.9428	3	4	Memenuhi syarat
4	2-[5-(2-Hydroxy-propyl)-tetrahydrofuran-2-yl]-propionic acid, t-butyl ester	258	3.4593	1	4	Memenuhi syarat
5	2-Furancarboxylic acid, tert-butyl dimethylsilyl ester	248	1.9753	0	0	Memenuhi syarat
6	2-Methylacetophenone	134	1.8768	0	1	Memenuhi syarat
7	2-n-Propylthiane	144	2.4584	0	0	Memenuhi syarat
8	2-Octenoic acid, 4,5,7-trihydroxy	190	0.4847	3	5	Memenuhi syarat
9	3-(hydroxymethyl)-9-Oxabicyclo [3.3.1] nonan-3-ol	172	1.3590	2	3	Memenuhi syarat
10	4-fluorophenol	112	0.9431	1	1	Memenuhi syarat
11	4-hydroxycinnamic acid	164	0.1526	2	3	Memenuhi syarat
12	4-Hydroxylamino-6-methylpyrimidin-2(1H)-one	141	-1.9379	3	2	Memenuhi syarat
13	4-Methoxymethoxy-4-methylhex-2-ynal	170	2.2282	0	3	Memenuhi syarat
14	5-(hydroxymethyl)-2-(dimethoxymethyl) Furan	172	1.3966	1	4	Memenuhi syarat
15	5-Hydroxymethylfurfural	126	0.7557	1	3	Memenuhi syarat
16	Acetic acid, 2-methylhex-3-yl ester	158	2.5610	0	2	Memenuhi syarat
17	Chimanine D	185	1.8391	0	1	Memenuhi syarat
18	Desulphosinigrin	279	0.8094	5	6	Memenuhi syarat
19	Ethyl 4-hydroxy-3-methylbut-2-enoate	144	1.2456	1	3	Memenuhi syarat
20	Guanosine	283	-1.5298	6	6	Tidak memenuhi syarat
21	Mannofuranoside, 1-allyl-2,3-5,6-tetra-O-acetyl	372	3.1490	0	9	Memenuhi syarat

LAMPIRAN 19
(LANJUTAN)

Tabel VII.7
Lanjutan

No	Senyawa	BM	LOG P	Ikatan hidrogen		Keterangan
				Donor	Akseptor	
22	<i>Methyl 3,6-anhydro-α-D-galactopyranoside</i>	176	0.3662	2	5	Memenuhi syarat
23	<i>Methyl fructopyranoside</i>	194	0.7597	4	6	Memenuhi syarat
24	<i>Methyl trisporate C</i>	320	4.1393	1	4	Memenuhi syarat
25	<i>Stigmastanol</i>	416	7.9601	1	1	Tidak memenuhi syarat
26	<i>Trans cinnamic acid</i>	148	0.7444	1	2	Memenuhi syarat
27	<i>Trans geranylgeraniol</i>	290	5.0780	1	1	Memenuhi syarat
28	<i>Xanthosine</i>	284	-0.9848	5	6	Memenuhi syarat



HASIL VALIDASI DOCKING 3ERT PADA RESEPTOR ER α

Keeping original residue number (specified in the input PDBQ file) for outputting.

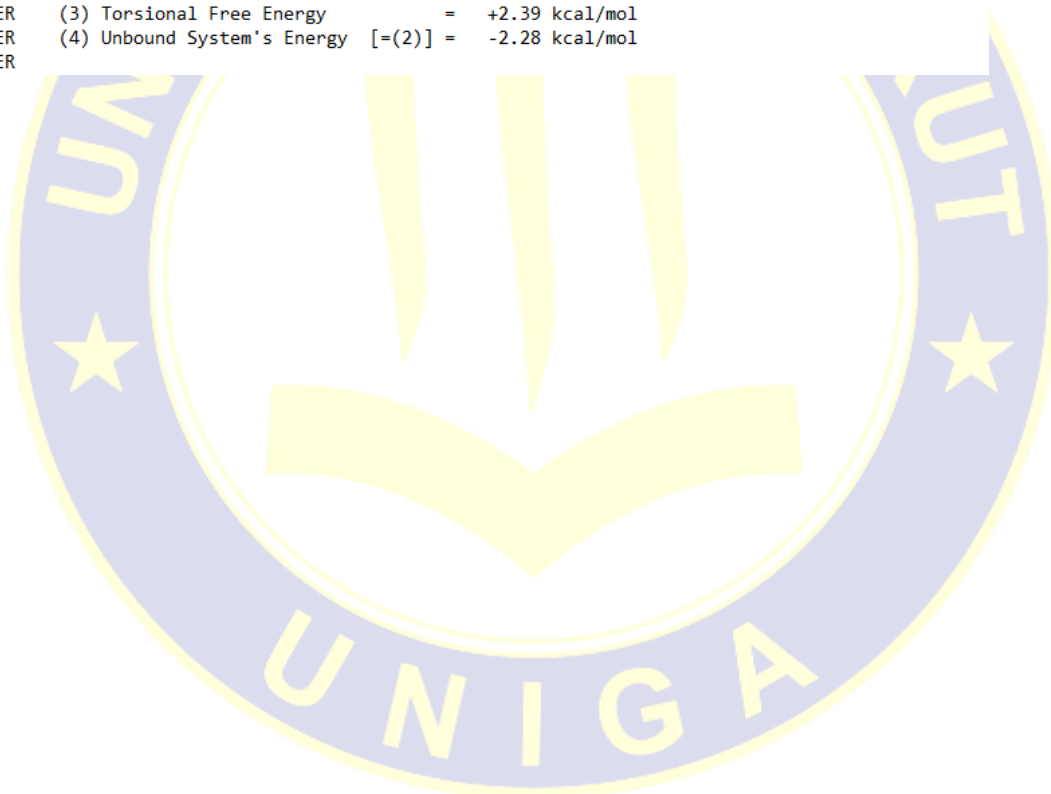
```
MODEL      31
USER      Run = 31
USER      Cluster Rank = 1
USER      Number of conformations in this cluster = 99
USER
USER      RMSD from reference structure      = 1.125 A
USER
USER      Estimated Free Energy of Binding   = -11.41 kcal/mol  [(1)+(2)+(3)-(4)]
USER      Estimated Inhibition Constant, Ki  = 4.36 nM (nanomolar) [Temperature = 298.15 K]
USER
USER      (1) Final Intermolecular Energy   = -13.79 kcal/mol
USER      vdW + Hbond + desolv Energy       = -12.71 kcal/mol
USER      Electrostatic Energy              = -1.08 kcal/mol
USER      (2) Final Total Internal Energy   = -2.13 kcal/mol
USER      (3) Torsional Free Energy         = +2.39 kcal/mol
USER      (4) Unbound System's Energy      [(2)] = -2.13 kcal/mol
USER
```



LAMPIRAN 21**HASIL DOCKING SENYAWA PEMBANDING TAMOKSIFEN TERHADAP
RESEPTOR ER α**

Keeping original residue number (specified in the input PDBQ file) for outputting.

```
MODEL      59
USER      Run = 59
USER      Cluster Rank = 1
USER      Number of conformations in this cluster = 100
USER
USER      RMSD from reference structure      = 37.822 Å
USER
USER      Estimated Free Energy of Binding   = -10.51 kcal/mol [(1)+(2)+(3)-(4)]
USER      Estimated Inhibition Constant, Ki  = 19.67 nM (nanomolar) [Temperature = 298.15 K]
USER
USER      (1) Final Intermolecular Energy   = -12.90 kcal/mol
USER      vdW + Hbond + desolv Energy       = -11.78 kcal/mol
USER      Electrostatic Energy              = -1.12 kcal/mol
USER      (2) Final Total Internal Energy   = -2.28 kcal/mol
USER      (3) Torsional Free Energy         = +2.39 kcal/mol
USER      (4) Unbound System's Energy [(2)] = -2.28 kcal/mol
USER
```



LAMPIRAN 22

**HASIL DOCKING SENYAWA UJI TRANS-GERANYLGERANIOL TERHADAP
RESEPTOR ER α**

Keeping original residue number (specified in the input PDBQ file) for outputting.

```
MODEL      59
USER      Run = 59
USER      Cluster Rank = 1
USER      Number of conformations in this cluster = 32
USER
USER      RMSD from reference structure      = 34.888 A
USER
USER      Estimated Free Energy of Binding   = -7.59 kcal/mol [(1)+(2)+(3)-(4)]
USER      Estimated Inhibition Constant, Ki  = 2.72 uM (micromolar) [Temperature = 298.15 K]
USER
USER      (1) Final Intermolecular Energy   = -10.87 kcal/mol
USER      vdW + Hbond + desolv Energy       = -10.55 kcal/mol
USER      Electrostatic Energy              = -0.33 kcal/mol
USER      (2) Final Total Internal Energy   = -0.97 kcal/mol
USER      (3) Torsional Free Energy         = +3.28 kcal/mol
USER      (4) Unbound System's Energy [(2)] = -0.97 kcal/mol
USER
```



LAMPIRAN 23

HASIL VALIDASI *DOCKING* 1QKM PADA RESEPTOR ER β

Keeping original residue number (specified in the input PDBQ file) for outputting.

```

MODEL      36
USER      Run = 36
USER      Cluster Rank = 1
USER      Number of conformations in this cluster = 100
USER
USER      RMSD from reference structure      = 0.452 Å
USER
USER      Estimated Free Energy of Binding   = -10.08 kcal/mol [(1)+(2)+(3)-(4)]
USER      Estimated Inhibition Constant, Ki  = 40.90 nM (nanomolar) [Temperature = 298.15 K]
USER
USER      (1) Final Intermolecular Energy   = -10.38 kcal/mol
USER      vdW + Hbond + desolv Energy       = -10.34 kcal/mol
USER      Electrostatic Energy              = -0.04 kcal/mol
USER      (2) Final Total Internal Energy   = -0.31 kcal/mol
USER      (3) Torsional Free Energy         = +0.30 kcal/mol
USER      (4) Unbound System's Energy [(2)] = -0.31 kcal/mol
USER

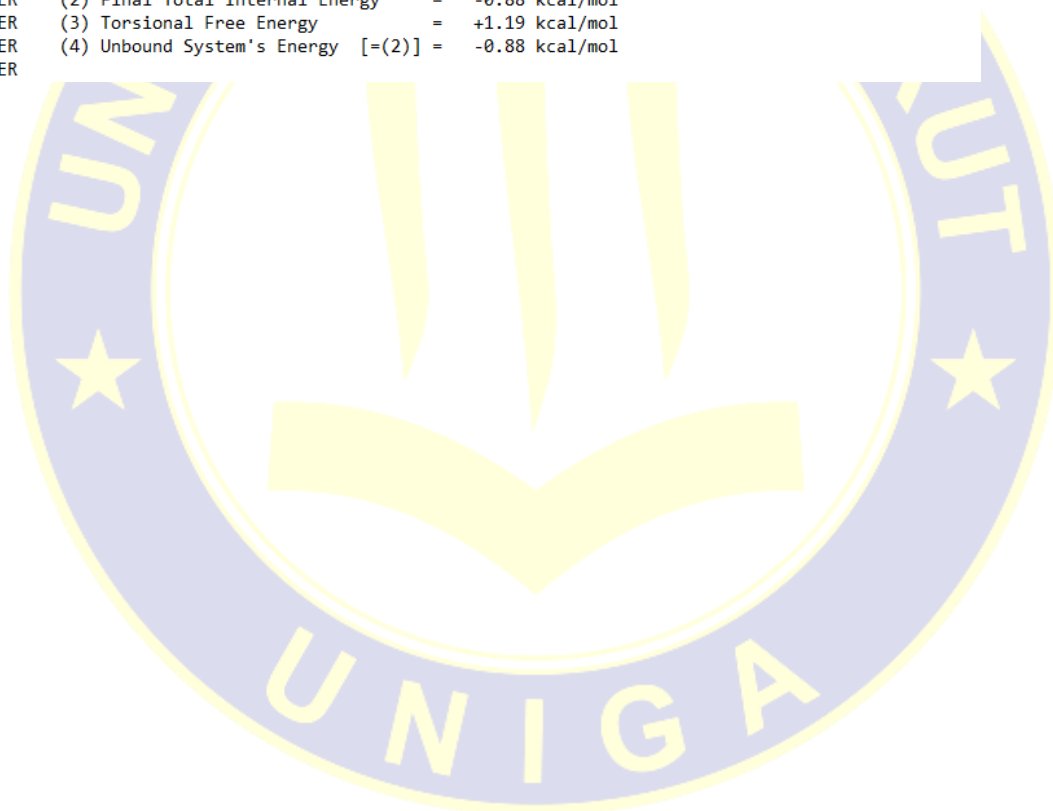
```



LAMPIRAN 24**HASIL DOCKING SENYAWA PEMBANDING GENISTEIN TERHADAP RESEPTOR ER β**

Keeping original residue number (specified in the input PDBQ file) for outputting.

```
MODEL      35
USER      Run = 35
USER      Cluster Rank = 1
USER      Number of conformations in this cluster = 100
USER
USER      RMSD from reference structure      = 114.880 A
USER
USER      Estimated Free Energy of Binding   = -9.44 kcal/mol  [(1)+(2)+(3)-(4)]
USER      Estimated Inhibition Constant, Ki  = 120.15 nM (nanomolar) [Temperature = 298.15 K]
USER
USER      (1) Final Intermolecular Energy   = -10.63 kcal/mol
USER      vdW + Hbond + desolv Energy       = -10.19 kcal/mol
USER      Electrostatic Energy              = -0.45 kcal/mol
USER      (2) Final Total Internal Energy   = -0.88 kcal/mol
USER      (3) Torsional Free Energy         = +1.19 kcal/mol
USER      (4) Unbound System's Energy      [(2)] = -0.88 kcal/mol
USER
```

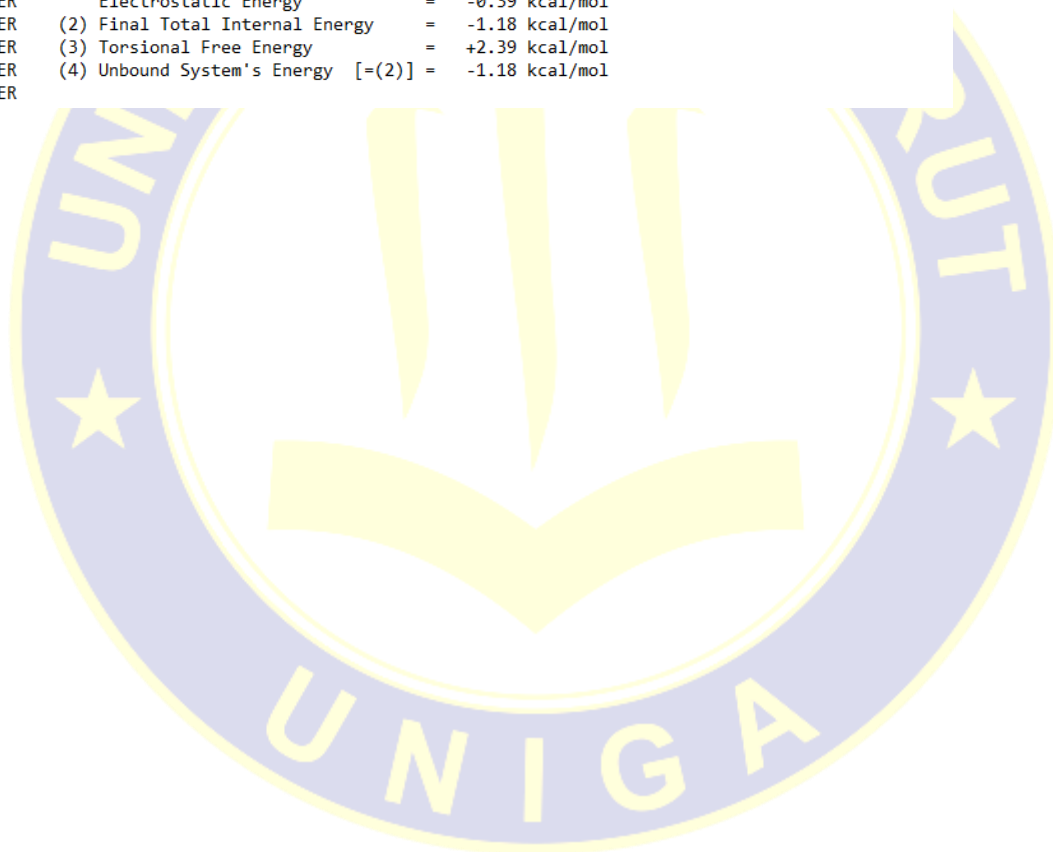


LAMPIRAN 25

**HASIL DOCKING SENYAWA UJI METHYL TRISPORATE C TERHADAP
RESEPTOR ER β**

Keeping original residue number (specified in the input PDBQ file) for outputting.

```
MODEL      95
USER      Run = 95
USER      Cluster Rank = 1
USER      Number of conformations in this cluster = 76
USER
USER      RMSD from reference structure      = 115.279 A
USER
USER      Estimated Free Energy of Binding   = -11.03 kcal/mol [(1)+(2)+(3)-(4)]
USER      Estimated Inhibition Constant, Ki  = 8.28 nM (nanomolar) [Temperature = 298.15 K]
USER
USER      (1) Final Intermolecular Energy   = -13.41 kcal/mol
USER      vdW + Hbond + desolv Energy       = -13.02 kcal/mol
USER      Electrostatic Energy              = -0.39 kcal/mol
USER      (2) Final Total Internal Energy   = -1.18 kcal/mol
USER      (3) Torsional Free Energy         = +2.39 kcal/mol
USER      (4) Unbound System's Energy [(2)] = -1.18 kcal/mol
USER
```

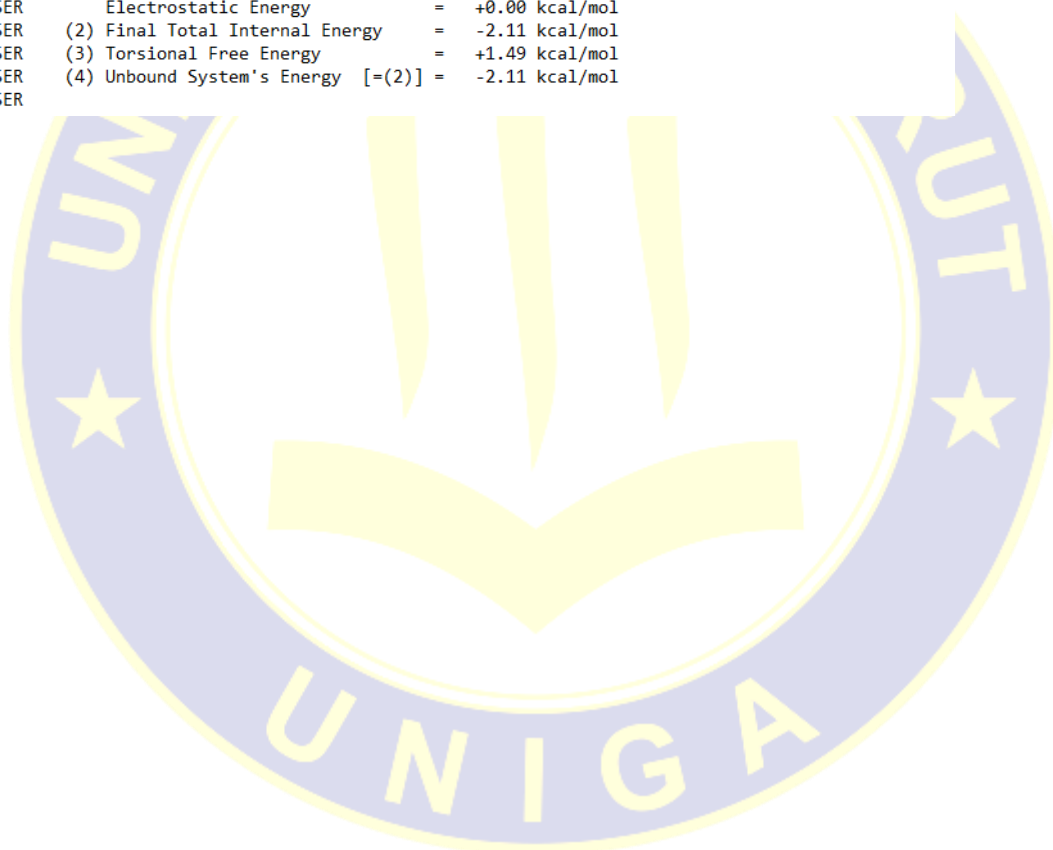


LAMPIRAN 26

HASIL DOCKING SENYAWA UJI XANTHOSINE TERHADAP RESEPTOR ER β

Keeping original residue number (specified in the input PDBQ file) for outputting.

```
MODEL      72
USER      Run = 72
USER      Cluster Rank = 1
USER      Number of conformations in this cluster = 13
USER
USER      RMSD from reference structure      = 114.169 A
USER
USER      Estimated Free Energy of Binding   = -12.11 kcal/mol  [(1)+(2)+(3)-(4)]
USER      Estimated Inhibition Constant, Ki  = 1.33 nM (nanomolar) [Temperature = 298.15 K]
USER
USER      (1) Final Intermolecular Energy   = -13.60 kcal/mol
USER      vdW + Hbond + desolv Energy       = -13.60 kcal/mol
USER      Electrostatic Energy              = +0.00 kcal/mol
USER      (2) Final Total Internal Energy   = -2.11 kcal/mol
USER      (3) Torsional Free Energy         = +1.49 kcal/mol
USER      (4) Unbound System's Energy [(2)] = -2.11 kcal/mol
USER
```



DAFTAR RIWAYAT HIDUP

I. IDENTITAS DIRI

Nama : Abdussyukur
Tempat, Tanggal Lahir : Jakarta, 28 Juni 2000
Jenis Kelamin : Laki-Laki
Agama : Islam
Kewarganegaraan : Indonesia
Status : Mahasiswa
Alamat : Jalan Raya Bogor No. 2
Telepon : 085881312657
Email : 994stagram@gmail.com
Instagram : sukur88



II. RIWAYAT HIDUP

Jenjang Pendidikan	Nama Sekolah/Perguruan Tinggi	Tahun Masuk	Tahun Lulus
SD/MI	SDN 02 Kramat Jati	2006	2012
SMP/MTs	MTs Al-Ihsan	2012	2015
SMA/MA/SMK	MAN 6 Jakarta	2015	2018
Perguruan Tinggi	Universitas Garut	2018	2022

III. PENGALAMAN ORGANISASI

1. Member of External Departement BEM KEMA FMIPA UNIGA
2. Member of Media and Relation Division Association of Indonesia Mathematic and Science Student (ILMMIPA) (2020-2021 - Riau, Indonesia)

3. Leadership Skill in Priangan Pharmaceutical Leadership Forum (PPLF)

Association of Indonesia Pharmacy Student (ISMAFARSI) Priangan (2021 -

Tasikmalaya, West Java, Indonesia)

