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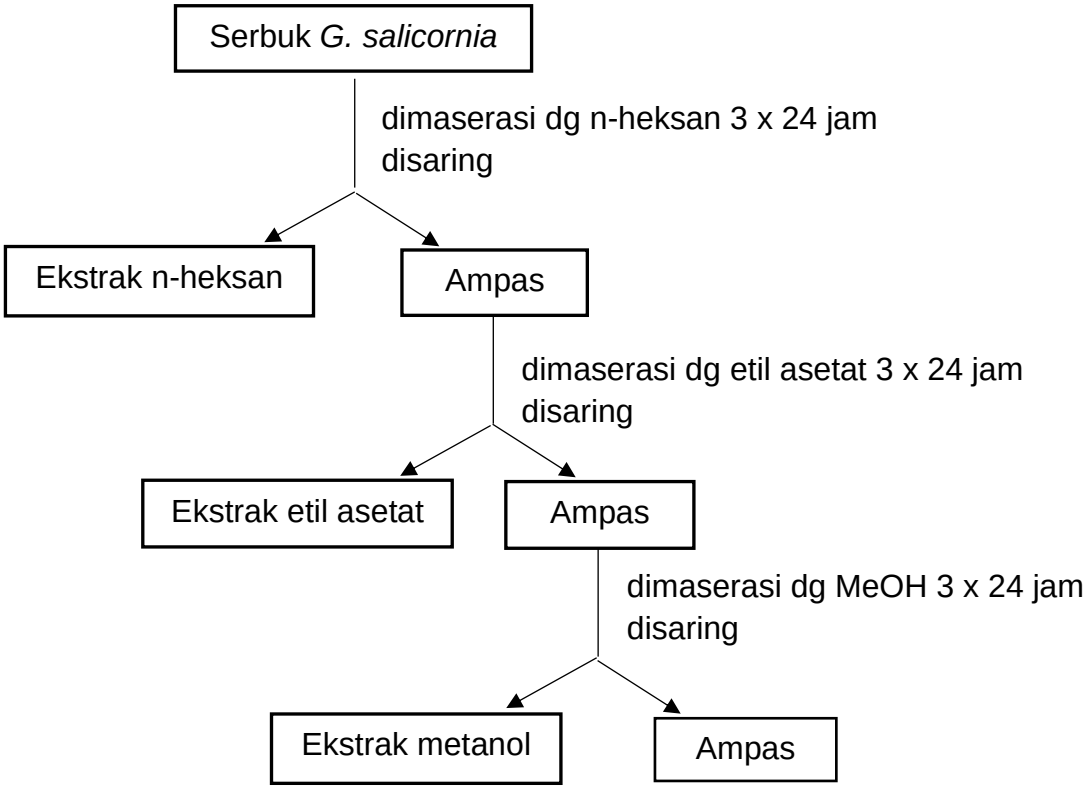
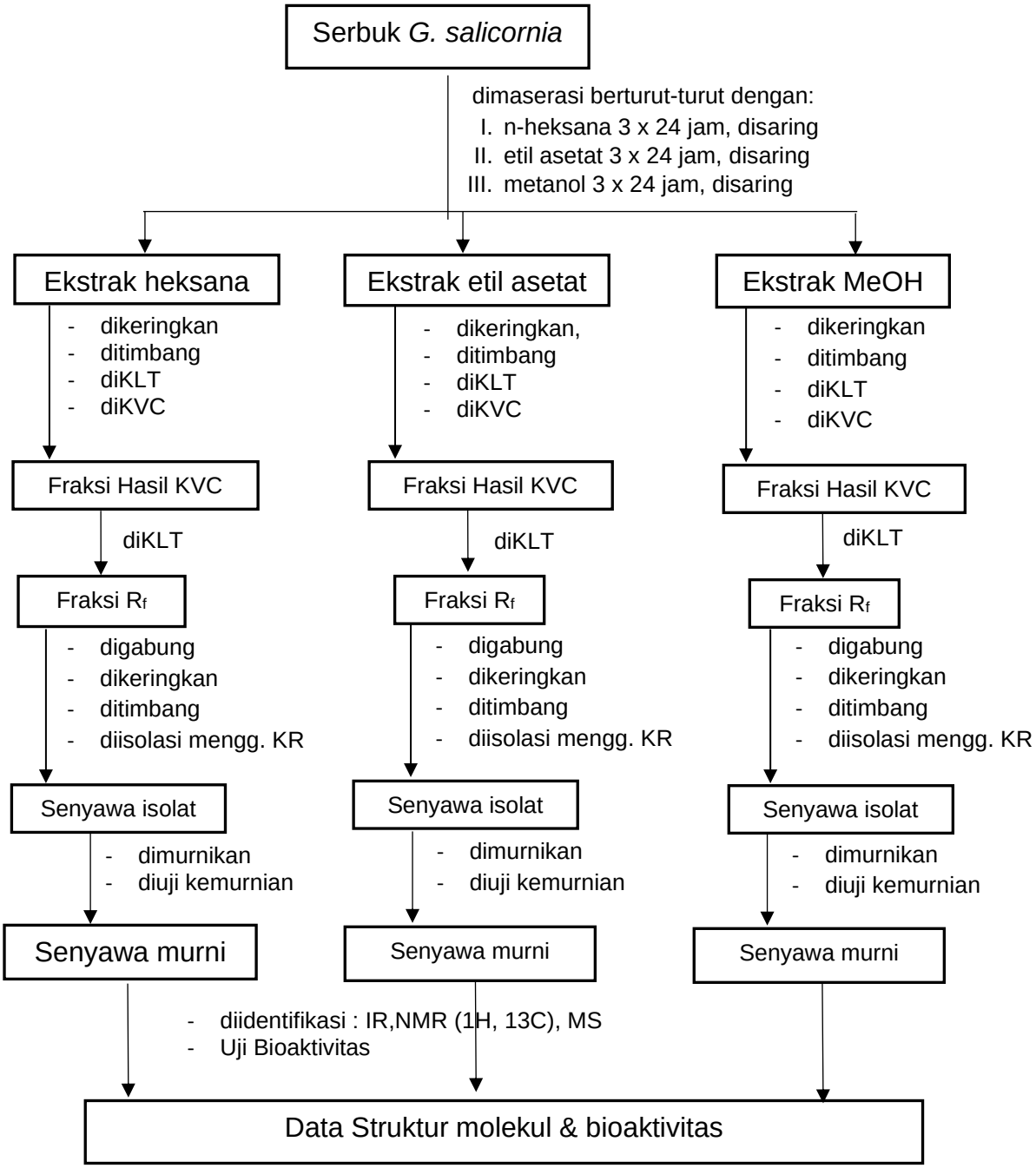
LAMPIRAN-LAMPIRAN

Lampiran 1. Bagan Alir Proses Maserasi Serbuk *G. Salicornia*

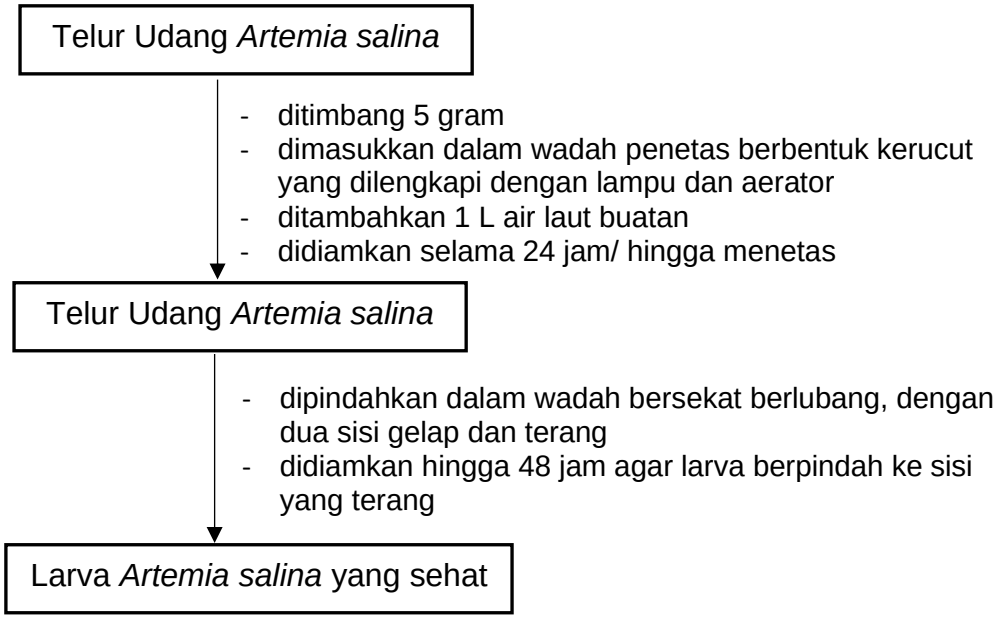


Lampiran 2. Bagan Alir Penelitian

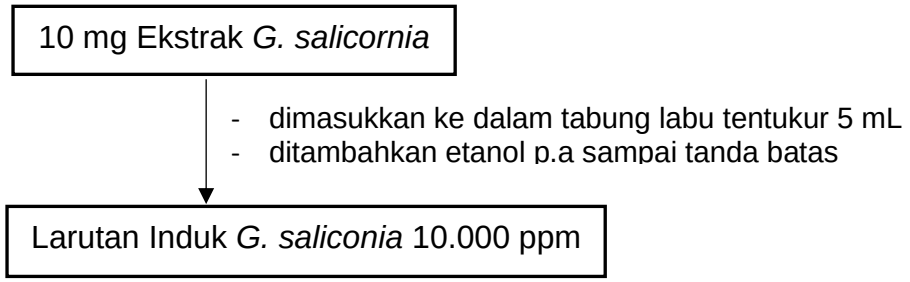


Lampiran 3. Bagan Alir Uji Toksisitas Metode BSLT

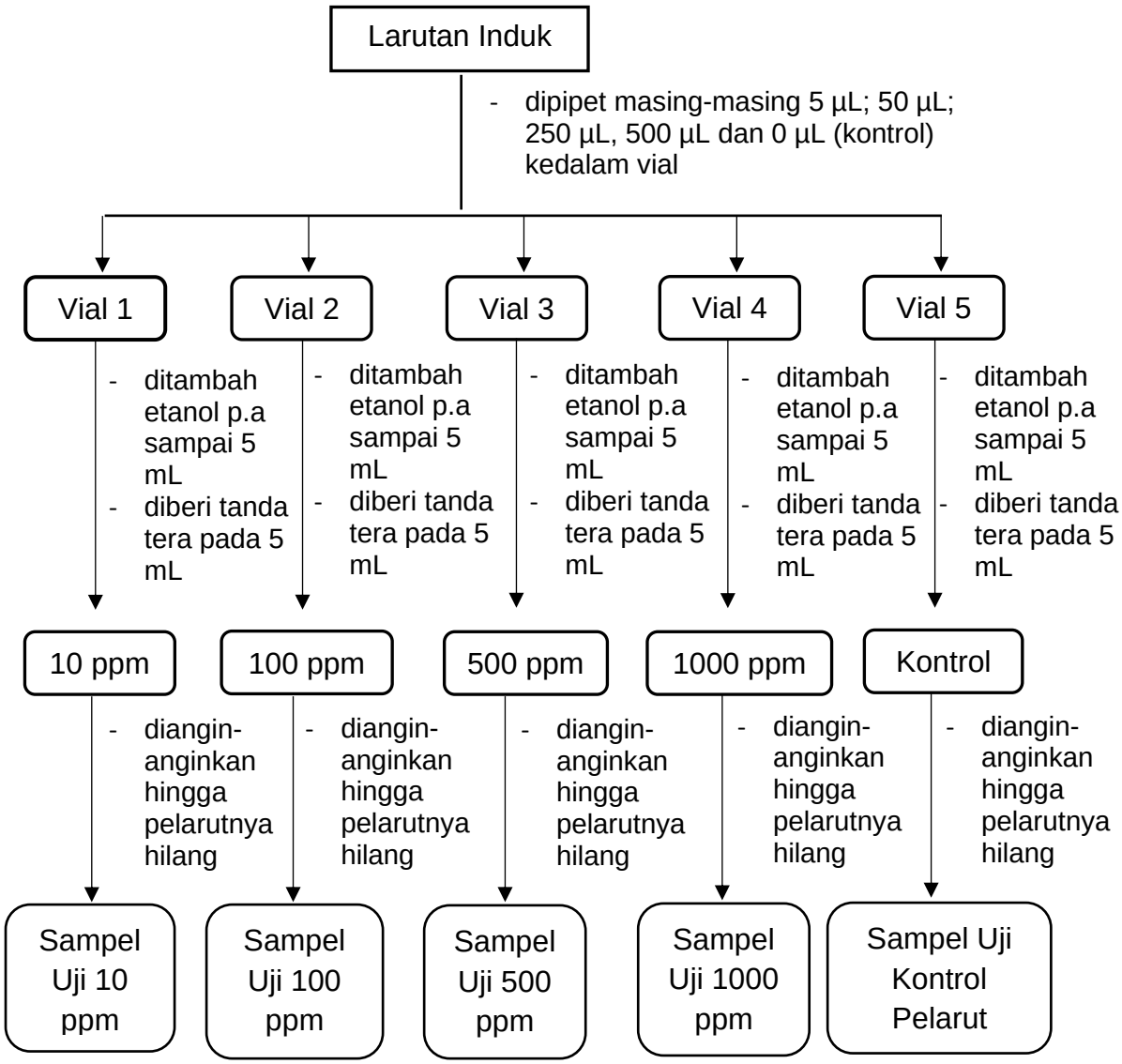
1. Penyiapan Larva Udang



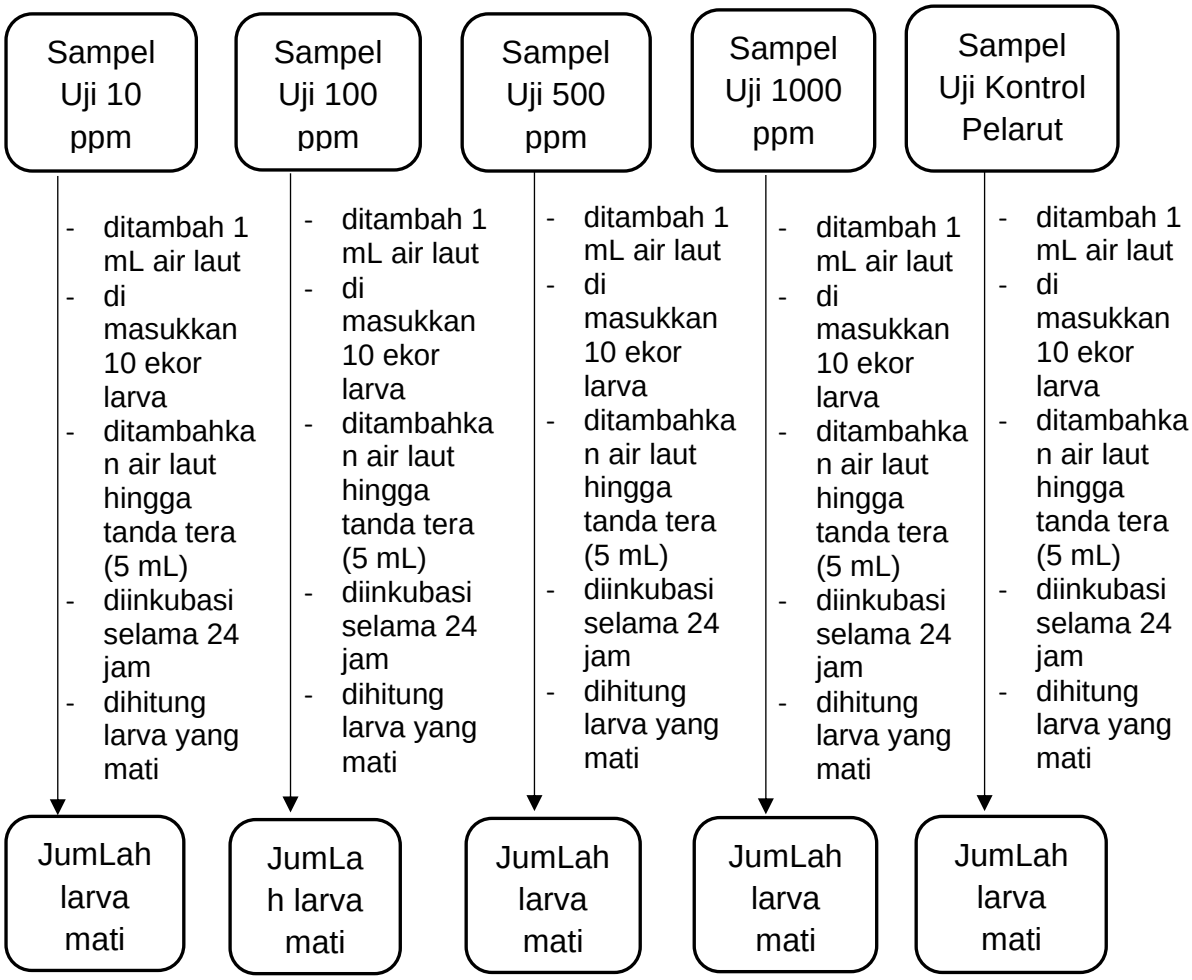
2. Pembuatan Larutan Induk Sampel 10.000 ppm



3. Pembuatan Konsentrasi Sampel dan Kontrol

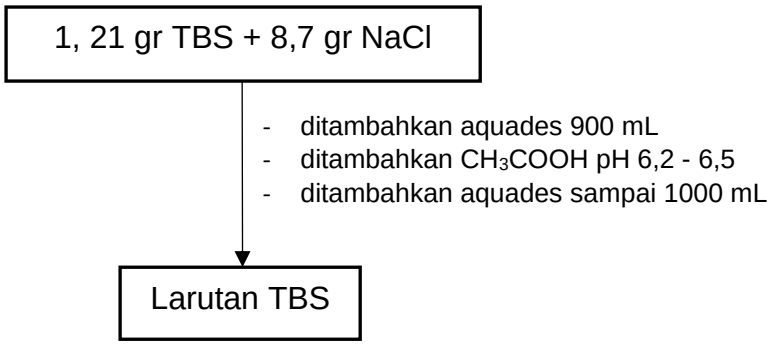


4. Pelaksanaan Uji

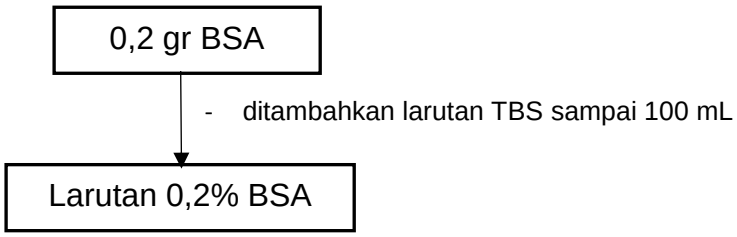


Lampiran 4. Bagan Alir Uji Antiinflamasi

a. Pembuatan Larutan TBS (*Tris Buffer Saline*)

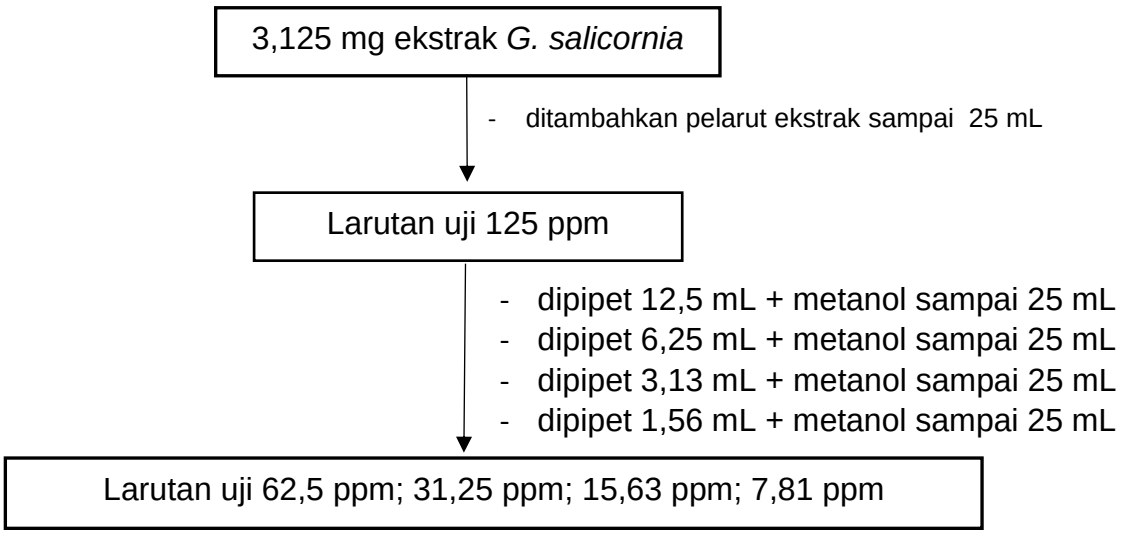


b. Pembuatan Larutan 0,2% BSA (*Bovine Serum Albumin*)

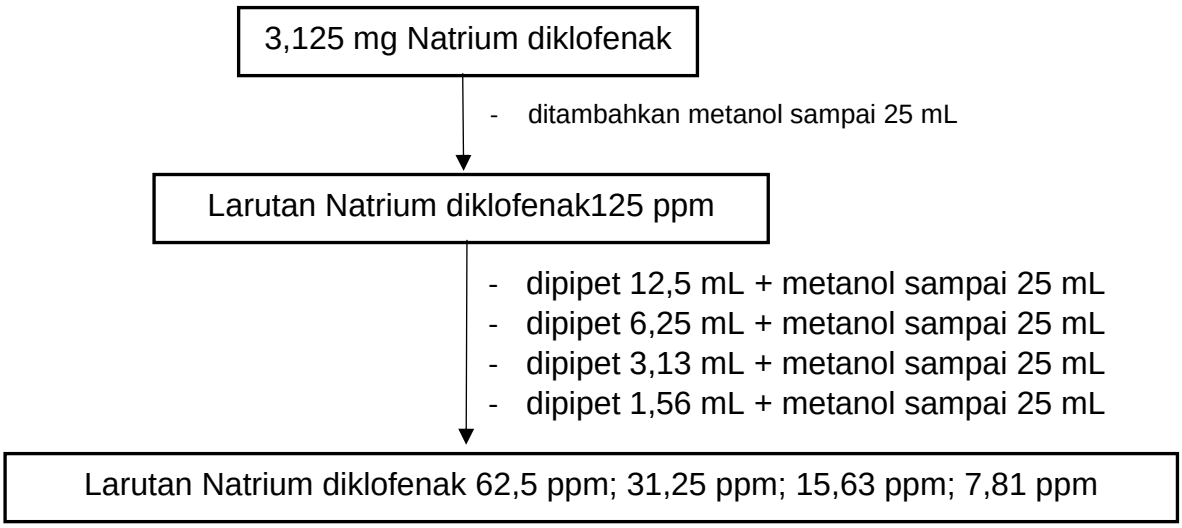


c. Pembuatan Larutan Kontrol Negatif

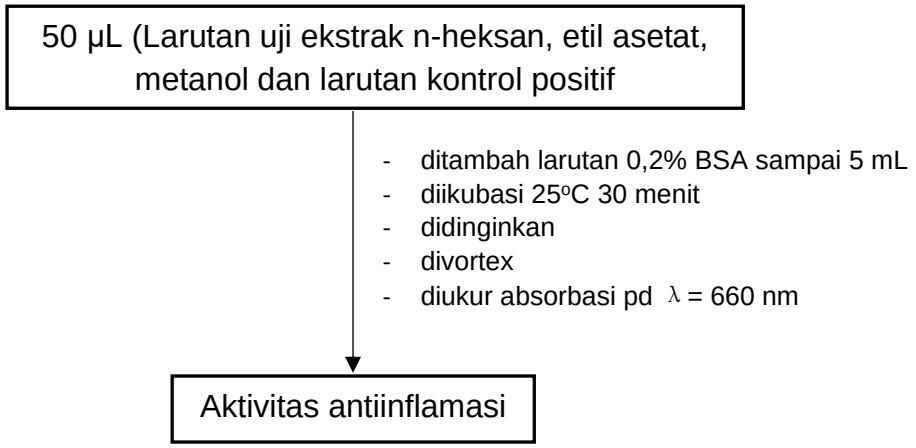
d. Pembuatan Larutan Uji



e. Pembuatan Larutan kontrol positif



f. Pengukuran Aktivitas Antiinflamasi



Perhitungan persentase penghambatan denaturasi protein:

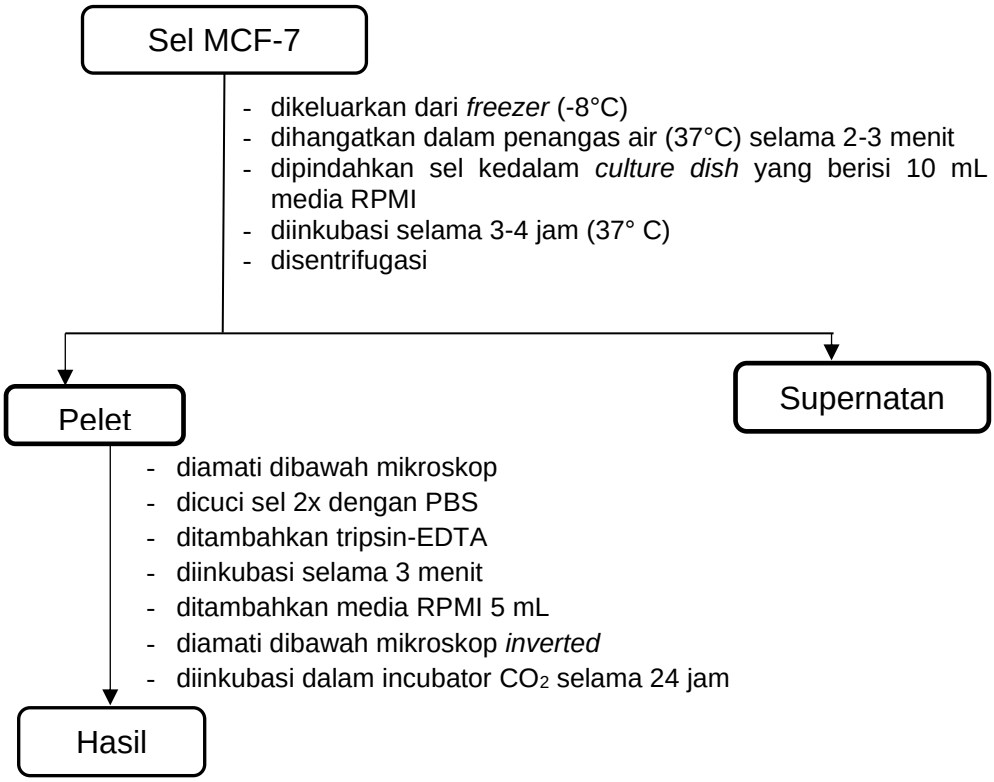
$$\%\ \text{inhibisi} = \frac{\text{absorbansi kontrol negatif} - \text{absorbansi larutan uji}}{\text{absorbansi kontrol positif}}\ \text{x}\ 100\%$$

Perhitungan Presentase Nilai IC_{50}

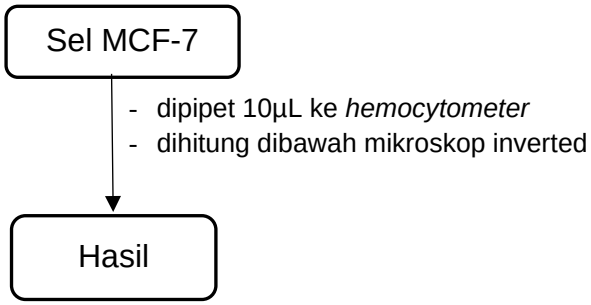
Nilai IC_{50} dihitung dengan membuat persamaan regresi linear antara konsentrasi (X) dengan % inhibisi (Y). Sehingga didapatkan nilai IC_{50} dari ekstrak *Gracilaria salicornia* dan Natrium Diklofenak.

Lampiran 5. Bagan Alir Uji Antikanker Sel MCF-7

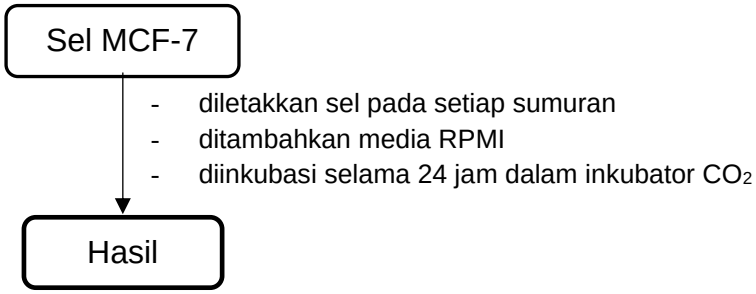
a. Penyiapan Sel



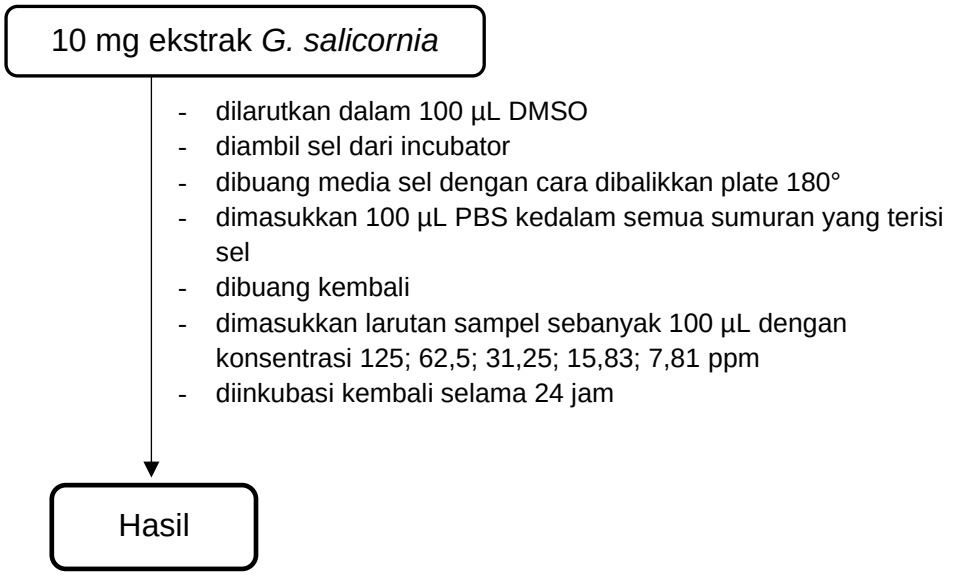
b. Perhitungan sel kanker



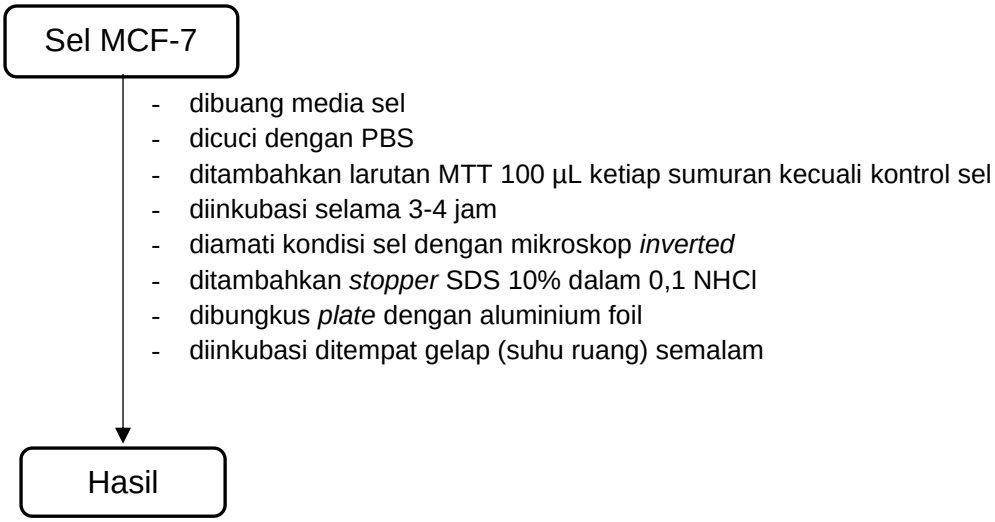
c. Peletakan Sel pada Plate



d. Pembuatan Larutan Sampel dan Pemberian Larutan Sampel pada Plate

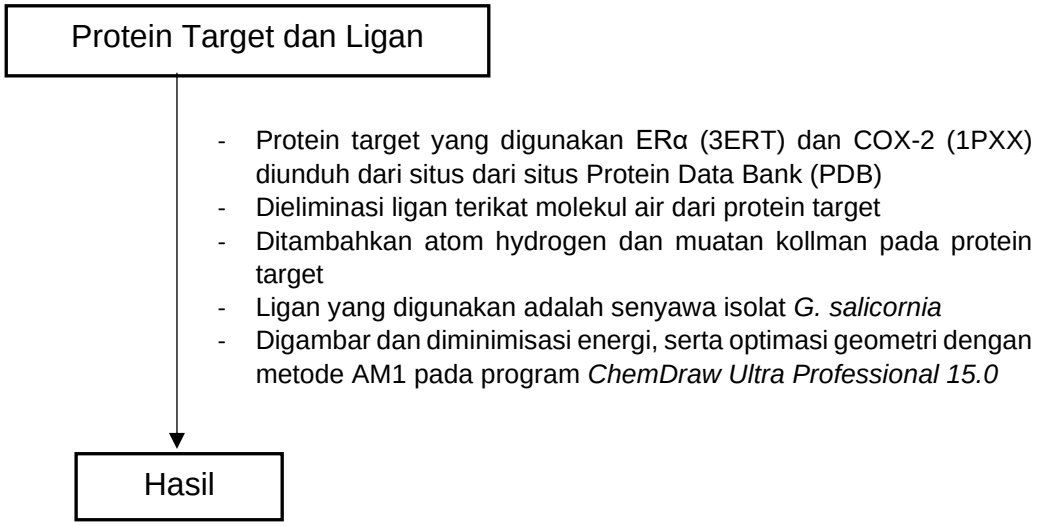


e. Pemberian Larutan MTT

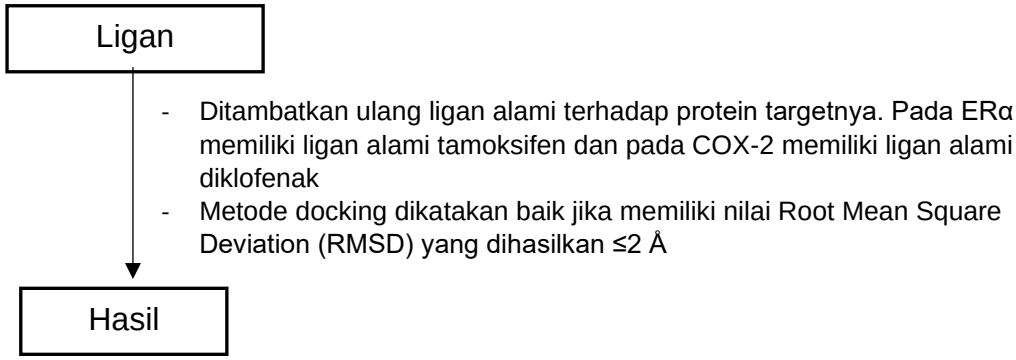


Lampiran 6. Uji *in silico* senyawa sebagai antiinflamasi dan antikanker payudara

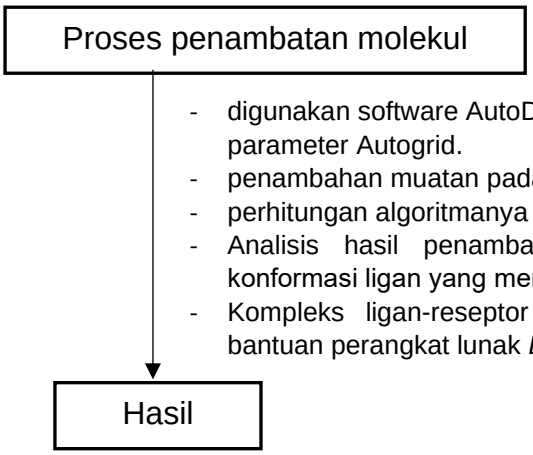
1. Preparasi Protein Target dan Ligan



2. Validasi Metode Penambatan Molekul

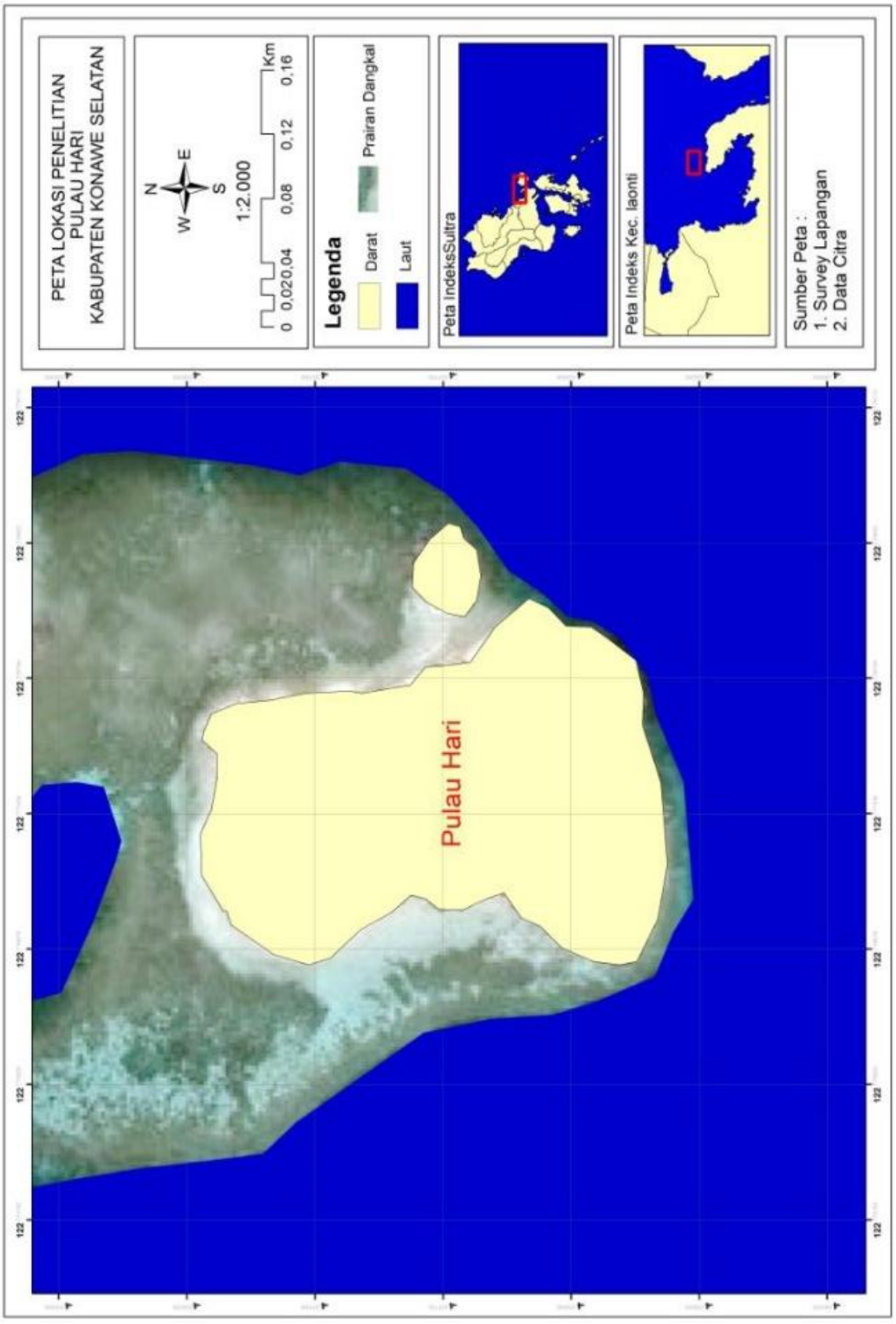


3. Simulasi Penambatan Molekul



- digunakan software AutoDockTools 4.2 dengan memasukkan nilai parameter Autogrid.
- penambahan muatan pada ligan menggunakan Gasteiger
- perhitungan algoritmanya menggunakan *Lamarckian Genetic*
- Analisis hasil penambatan molekul dilakukan dengan memilih konformasi ligan yang memiliki energi bebas ikatan (ΔG) terendah
- Kompleks ligan-reseptor yang terbentuk divisualisasikan dengan bantuan perangkat lunak *Discovery Studio Visualizer v17.2.0.16349*.

Lampiran 7. Peta Lokasi Pengambilan Sampel



Lampiran 8. Hasil Identifikasi Sampel BRIN

DIREKTORAT PENGELOLAAN LABORATORIUM, FASILITAS RISET, DAN KAWASAN SAINS TEKNOLOGI
Gedung B.J. Habibie Jalan M.H. Thamrin Nomor 8,
Jakarta Pusat 10340
Telepon/WA: 0811 8612 392; E-mail: dit-plfrkst@brin.go.id
www.brin.go.id

No. ID ELSA *Transaction Number*	: 30774
Metode *Method*	**:Identifikasi secara morfologi**
Nama Laboratorium *Name of Laboratory*	: Laboratorium Oseanografi - BRIN
Alamat Laboratorium *Laboratory Address*	: Jl. Pasir Putih 1, Ancol Timur (Gedung Pusat Riset Oseanografi- BRIN) Jakarta - Indonesia 11048 Email : layanan@mail.lipi.go.id ; Telp +62 811-1391-617

Kondisi Pengukuran/Parameter Pengujian *Measurement Conditions/Testing Parameters:*
Identifikasi dengan menggunakan karakter morfologi

Hasil Pengujian *Testing Results* : *Gracilaria salicornia* (C.Agardh) E.Y.Dawson, 1954

https://data.lipi.go.id/privateurl.xhtml?token=1421ae7c-6a12-400b-815f-c239c1a30460

Catatan *Note:*
Daftar sampel yang dilakukan pengujian terdapat di lembar pengesahan.
Penamaan sampel sesuai dengan penamaan pada saat permohonan pengajuan layanan.

Terima kasih sudah melakukan pengujian/ penyewaan alat/ proses riset dengan fasilitas yang tersedia di Laboratorium Oseanografi. Jika dikemudian hari, hasil pengujian atau analisis ini akan dipublikasikan, mohon kiranya bisa menambahkan dalam Ucapan Terima Kasih atau Acknowledgement di dalam publikasi Anda,

seperti dalam contoh format berikut:

Dalam bahasa Indonesia : "Penelitian ini didukung oleh fasilitas riset, dan dukungan ilmiah serta teknis dari Laboratorium Oseanografi di Badan Riset dan Inovasi Nasional".
Dalam bahasa Inggris : "The authors acknowledge the facilities, and the scientific and technical assistance of the Oceanography Laboratories at the National Research and Innovation Agency

Lampiran 9. Perhitungan Uji Sitotoksik

Pada uji sitotoksik, transformasi nilai % kematian ke probit mengikuti tabel berikut:

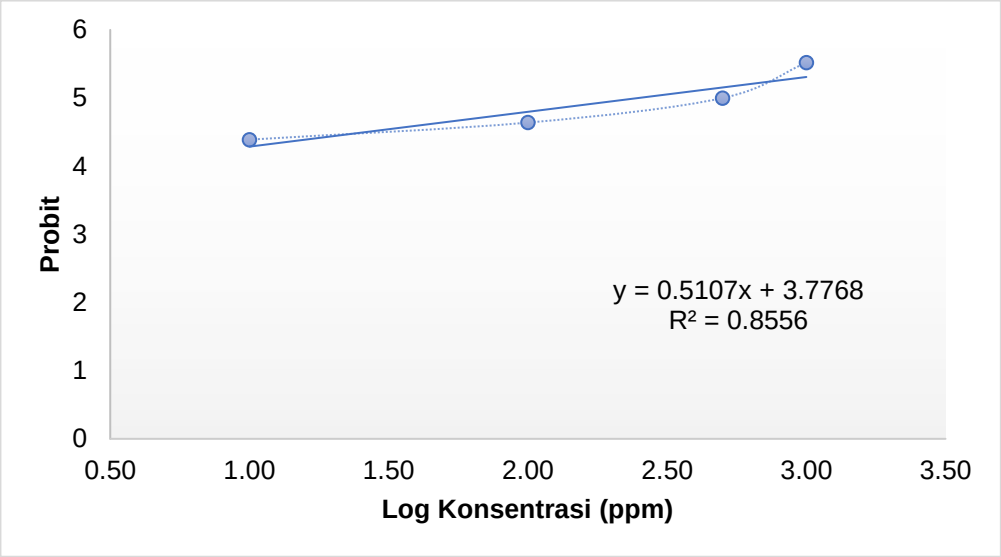
%	0	1	2	3	4	5	6	7	8	9
0	—	2.67	2.95	3.12	3.25	3.36	3.45	3.52	3.59	3.66
10	3.72	3.77	3.82	3.87	3.92	3.96	4.01	4.05	4.08	4.12
20	4.16	4.19	4.23	4.26	4.29	4.33	4.36	4.39	4.42	4.45
30	4.48	4.50	4.53	4.56	4.59	4.61	4.64	4.67	4.69	4.72
40	4.75	4.77	4.80	4.82	4.85	4.87	4.90	4.92	4.95	4.97
50	5.00	5.03	5.05	5.08	5.10	5.13	5.15	5.18	5.20	5.23
60	5.25	5.28	5.31	5.33	5.36	5.39	5.41	5.44	5.47	5.50
70	5.52	5.55	5.58	5.61	5.64	5.67	5.71	5.74	5.77	5.81
80	5.84	5.88	5.92	5.95	5.99	6.04	6.08	6.13	6.18	6.23
90	6.28	6.34	6.41	6.48	6.55	6.64	6.75	6.88	7.05	7.33
%	0.0	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9
99	7.33	7.37	7.41	7.46	7.51	7.58	7.65	7.75	7.88	8.09

[1]D. J. Finney, *Probit Analysis*, (Cambridge: Cambridge University Press, 1971), p. 25. Reprinted by permission.

a. Ekstrak n-Heksan

Konsentrasi (ppm)	Total Larva	U1	U2	U3	Kematian	% Kematian	Log Kons	Probit
1000	10	6	8	7	7.00	70%	3.00	5.52
500	10	5	4	6	5.00	50%	2.70	5
100	10	4	3	4	3.67	37%	2.00	4.64
10	10	3	3	2	2.67	27%	1.00	4.39

U = ulangan



Subtitusi 5 sebagai y pada persamaan regresi linear untuk menentukan nilai log konsentrasi (x):
5 = 0.5107x + 3.7768
x = 2.40

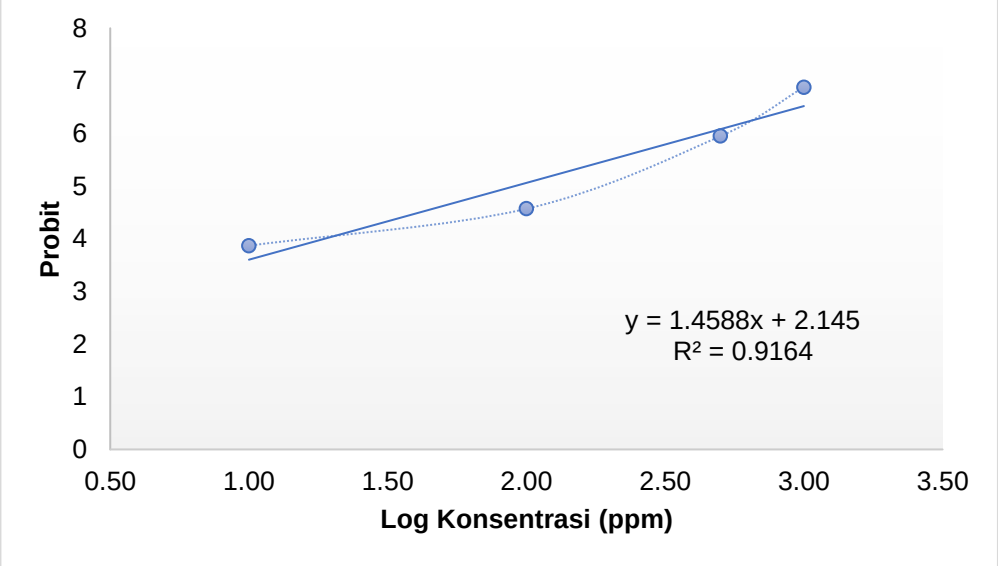
Mengubah nilai log konsentrasi menjadi konsentrasi sebenarnya (antilog):
LC_{50} (ppm) = **284.40**

Nilai antivitas toksisitas akut adalah 284.4 ppm.

b. Ekstrak Etil asetat

Konsentrasi (ppm)	Total Larva	U1	U2	U3	Kematian	% Kematian	Log Kons	Probit
1000	10	10	9	10	9.67	97%	3.00	6.88
500	10	7	9	9	8.33	83%	2.70	5.95
100	10	3	3	4	3.33	33%	2.00	4.57
10	10	0	2	2	1.33	13%	1.00	3.87

U = ulangan



Subtitusi 5 sebagai y pada persamaan regresi linear untuk menentukan nilai log konsentrasi (x):
5 = 1.4588x + 2.145
x = 1.96

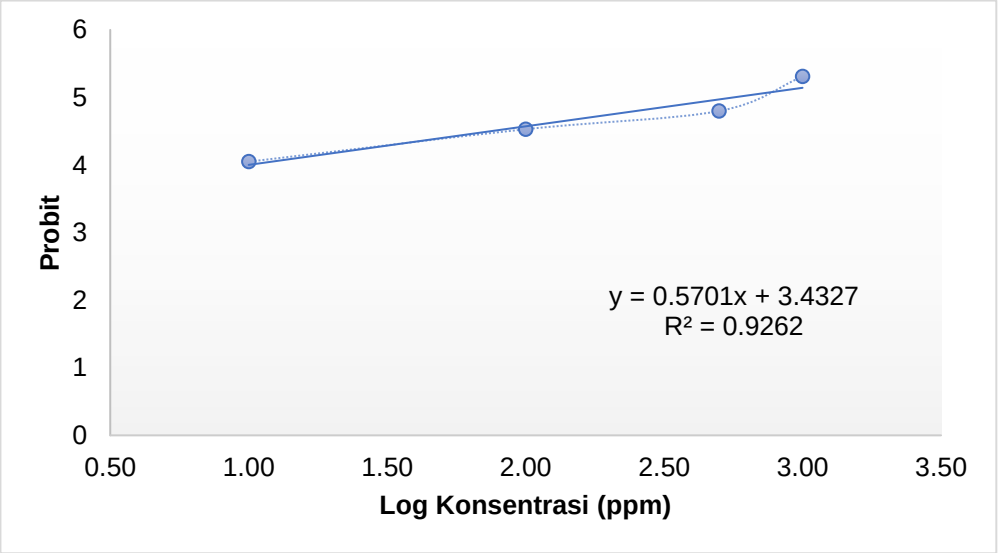
Mengubah nilai log konsentrasi menjadi konsentrasi sebenarnya (antilog):
LC_{50} (ppm) = **90.59**

Nilai antivitas toksisitas akut adalah 90.59 ppm.

c. Ekstrak Metanol

Konsentrasi (ppm)	Total Larva	U1	U2	U3	Kematian	% Kematian	Log Kons	Probit
1000	10	5	6	8	6.33	63%	3.00	5.31
500	10	5	3	5	4.33	43%	2.70	4.8
100	10	3	3	4	3.33	33%	2.00	4.53
10	10	2	2	1	1.67	17%	1.00	4.05

U = ulangan



Subtitusi 5 sebagai y pada persamaan regresi linear untuk menentukan nilai log konsentrasi (x):
5 = 0.5701x + 3.4327
x = 2.75

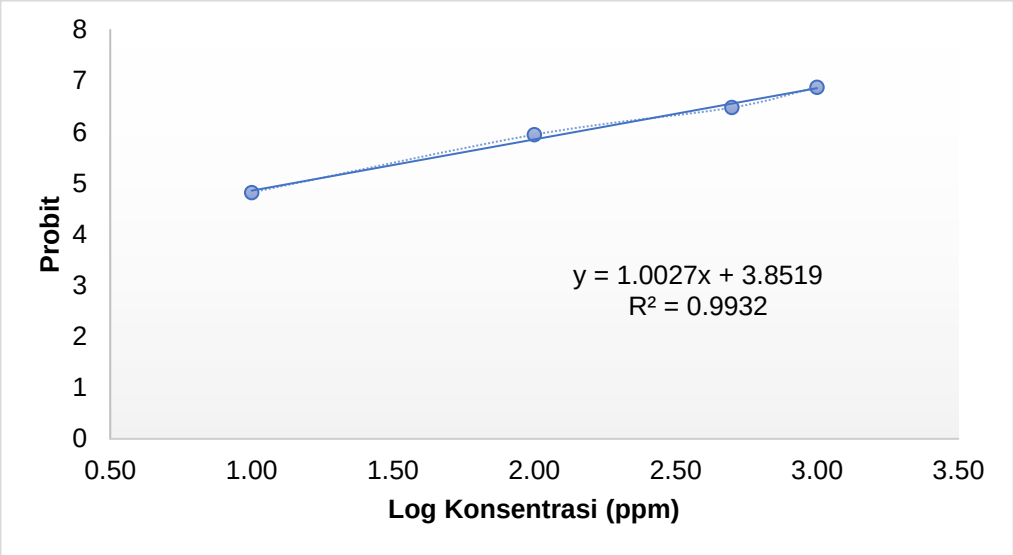
Mengubah nilai log konsentrasi menjadi konsentrasi sebenarnya (antilog):
LC_{50} (ppm) = **561.26**

Nilai antivitas toksisitas akut adalah 561.26 ppm.

d. Kontrol Positif (Kalium Dikromat)

Konsentrasi (ppm)	Total Larva	U1	U2	U3	Kematian	% Kematian	Log Kons	Probit
1000	10	10	9	10	9.67	97%	3.00	6.88
500	10	10	9	9	9.33	93%	2.70	6.48
100	10	8	9	8	8.33	83%	2.00	5.95
10	10	5	4	4	4.33	43%	1.00	4.82

U = ulangan



Subtitusi 5 sebagai y pada persamaan regresi linear untuk menentukan nilai log konsentrasi (x):
5 = 1.0027x + 3.8519
x = 1.15

Mengubah nilai log konsentrasi menjadi konsentrasi sebenarnya (antilog):
LC_{50} (ppm) = **13.96**

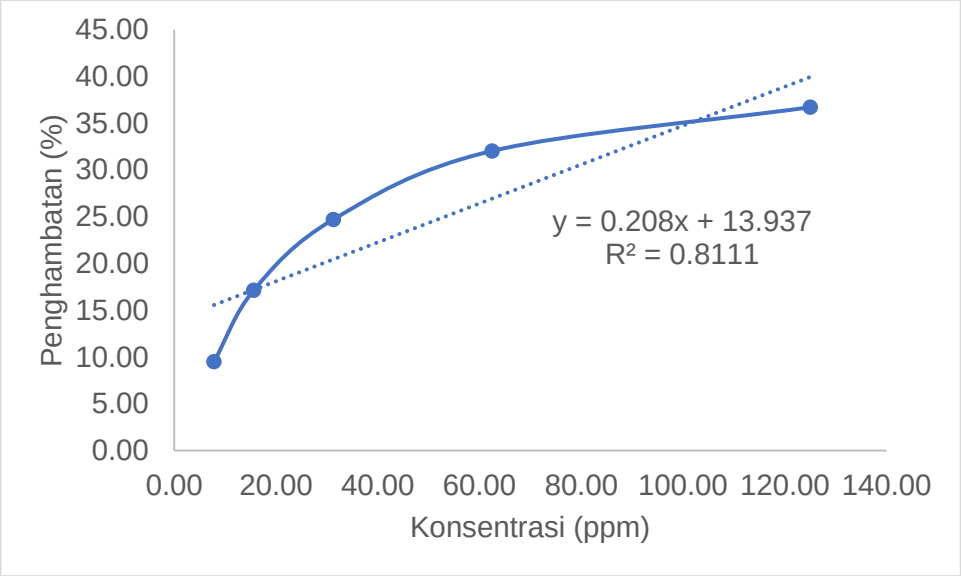
Nilai antivitas toksisitas akut adalah 13.96 ppm.

Lampiran 10. Uji Antiinflamasi

a. Ekstrak n-Heksan

Absorbansi Kontrol : 1.0334

Konsentrasi (ppm)	Absorbansi	% Penghambatan
7.81	0.9354	9.49
15.63	0.8564	17.13
31.25	0.7782	24.70
62.50	0.7024	32.03
125.00	0.6541	36.71



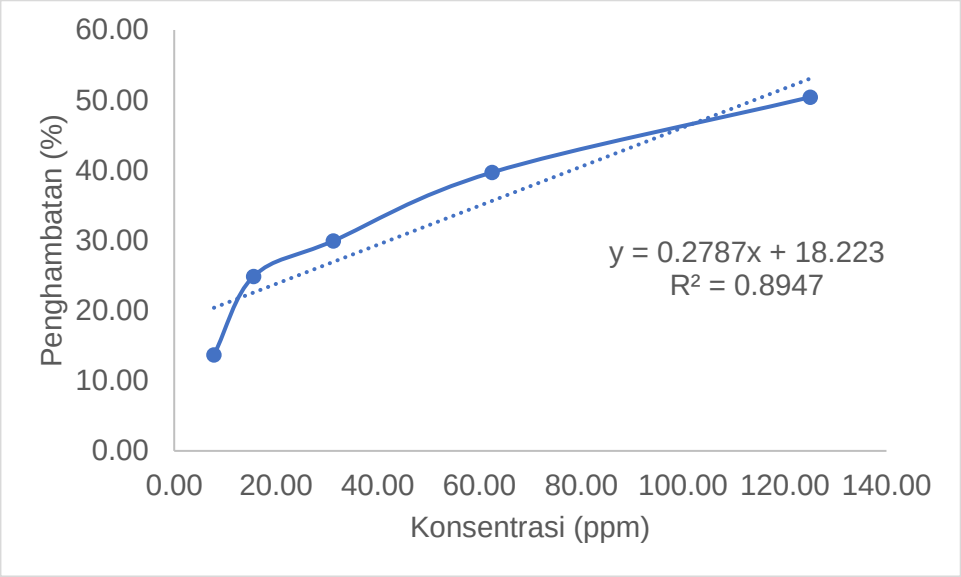
Subtitusi 50 sebagai y pada persamaan regresi linear untuk menentukan nilai konsentrasi (x):
50 = 0.208x + 13.937
x (IC_{50}) = 173.38

Nilai aktivitas antiinflamasi adalah 173.38 ppm.

b. Ekstrak Etil asetat

Absorbansi Kontrol : 1.0334

Konsentrasi (ppm)	Absorbansi	% Penghambatan
7.81	0.8921	13.68
15.63	0.7762	24.89
31.25	0.7241	29.93
62.50	0.6231	39.71
125.00	0.5124	50.42



Subtitusi 50 sebagai y pada persamaan regresi linear untuk menentukan nilai konsentrasi (x):

50 = 0.2787x + 18.223

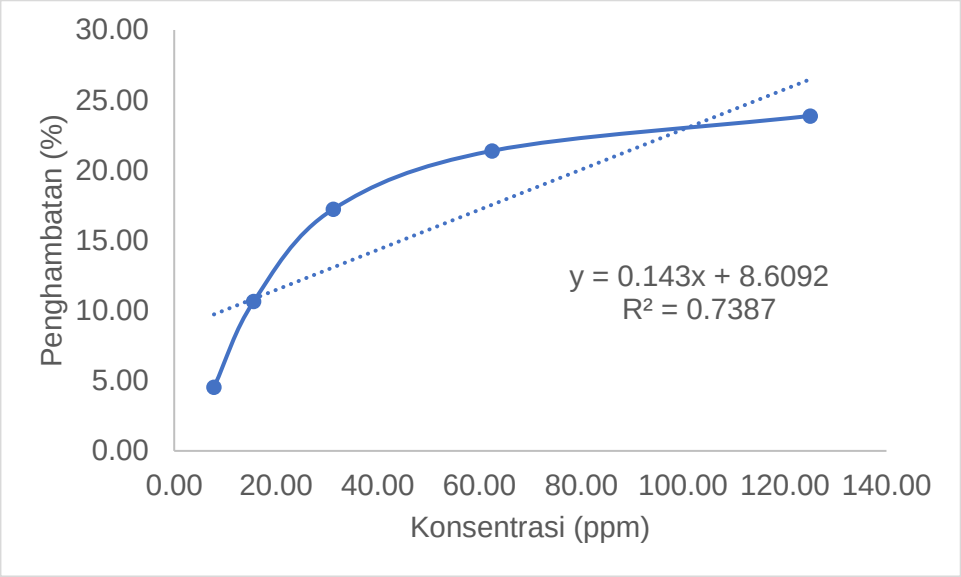
x (IC_{50}) = 114.02

Nilai aktivitas antiinflamasi adalah 114.02 ppm.

c. Ekstrak Metanol

Absorbansi Kontrol : 1.0334

Konsentrasi (ppm)	Absorbansi	% Penghambatan
7.81	0.9865	4.54
15.63	0.9234	10.65
31.25	0.8554	17.23
62.50	0.8124	21.39
125.00	0.7867	23.88



Subtitusi 50 sebagai y pada persamaan regresi linear untuk menentukan nilai konsentrasi (x):

50 = 0.143x + 8.6092

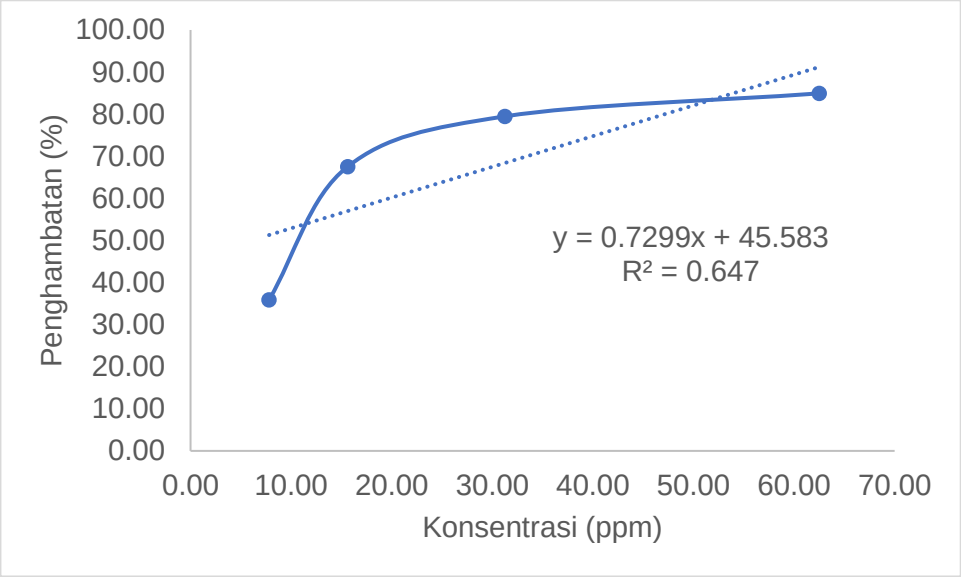
x (IC_{50}) = 289.45

Nilai aktivitas antiinflamasi adalah 289.45 ppm.

d. Kontrol Positif (Natrium Diklofenak)

Absorbansi Kontrol : 1.0334

Konsentrasi (ppm)	Absorbansi	% Penghambatan
7.81	0.6624	35.90
15.63	0.3354	67.55
31.25	0.2121	79.48
62.50	0.1556	84.94
125.00	0.0552	94.66



Subtitusi 50 sebagai y pada persamaan regresi linear untuk menentukan nilai konsentrasi (x):

50 = 0.7299x + 45.583

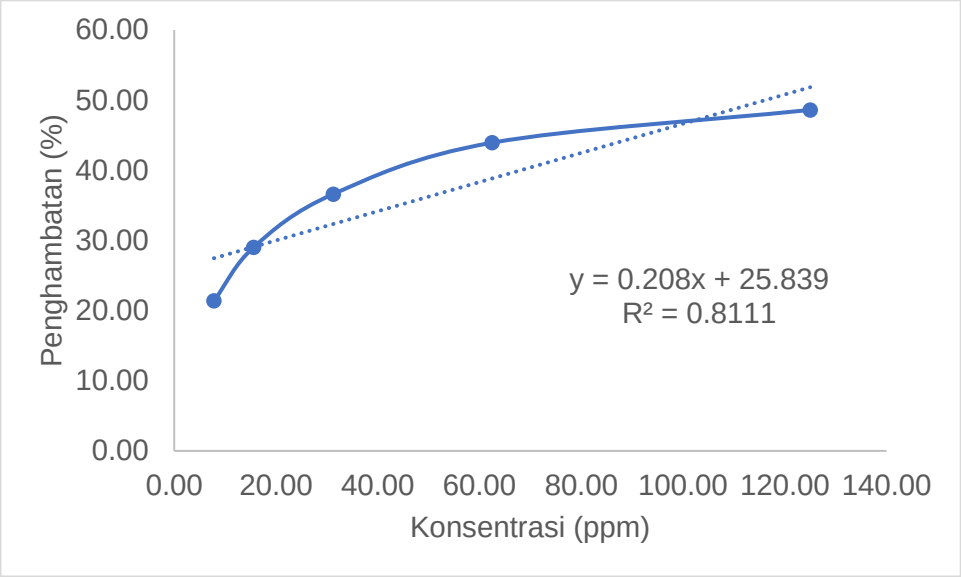
x (IC_{50}) = 11.78

Nilai aktivitas antiinflamasi adalah 11.78 ppm.

e. Senyawa **1**

Absorbansi Kontrol : 1.0334

Konsentrasi (ppm)	Absorbansi	% Penghambatan
7.81	0.8124	21.39
15.63	0.7334	29.03
31.25	0.6552	36.60
62.50	0.5794	43.93
125.00	0.5311	48.61



Subtitusi 50 sebagai y pada persamaan regresi linear untuk menentukan nilai konsentrasi (x):

$50 = 0.208x + 25.839$

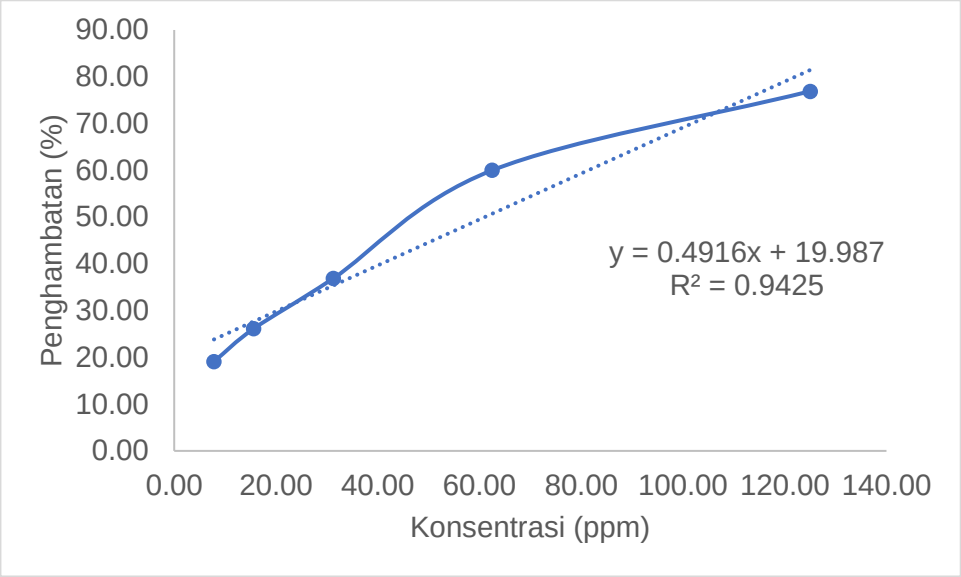
$x\ (IC_{50}) = 116.16$

Nilai aktivitas antiinflamasi adalah 116.16 ppm.

f. Senyawa **2**

Absorbansi Kontrol : 1.0334

Konsentrasi (ppm)	Absorbansi	% Penghambatan
7.81	0.8361	19.09
15.63	0.7634	26.13
31.25	0.6524	36.87
62.50	0.4134	60.00
125.00	0.2387	76.90



Subtitusi 50 sebagai y pada persamaan regresi linear untuk menentukan nilai konsentrasi (x):

50 = 0.4916x + 19.987

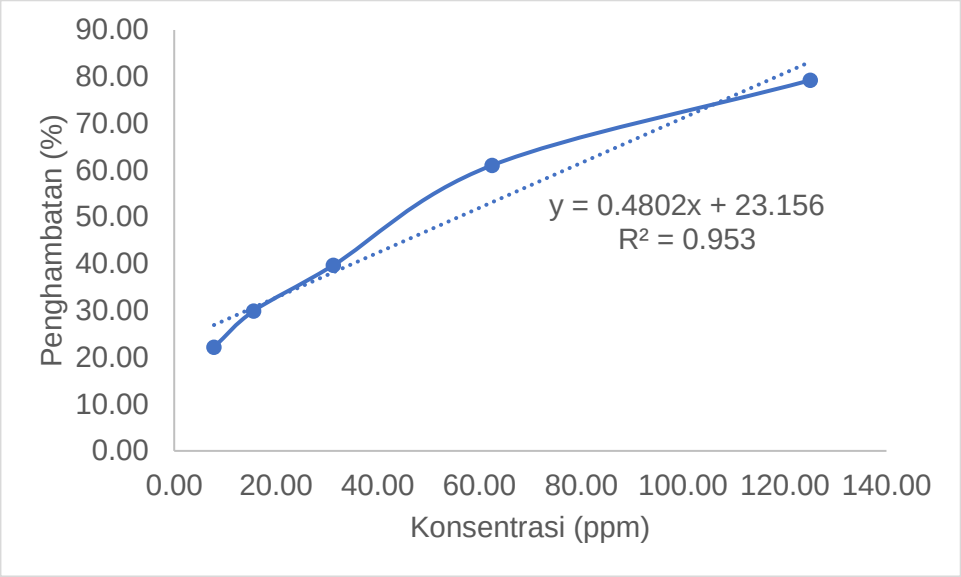
x (IC_{50}) = 61.052

Nilai aktivitas antiinflamasi adalah 61.052 ppm.

g. Senyawa **3**

Absorbansi Kontrol : 1.0334

Konsentrasi (ppm)	Absorbansi	% Penghambatan
7.81	0.8043	22.17
15.63	0.7242	29.92
31.25	0.6234	39.68
62.50	0.4023	61.07
125.00	0.2145	79.24



Subtitusi 50 sebagai y pada persamaan regresi linear untuk menentukan nilai konsentrasi (x):

$50 = 0.4802x + 23.156$

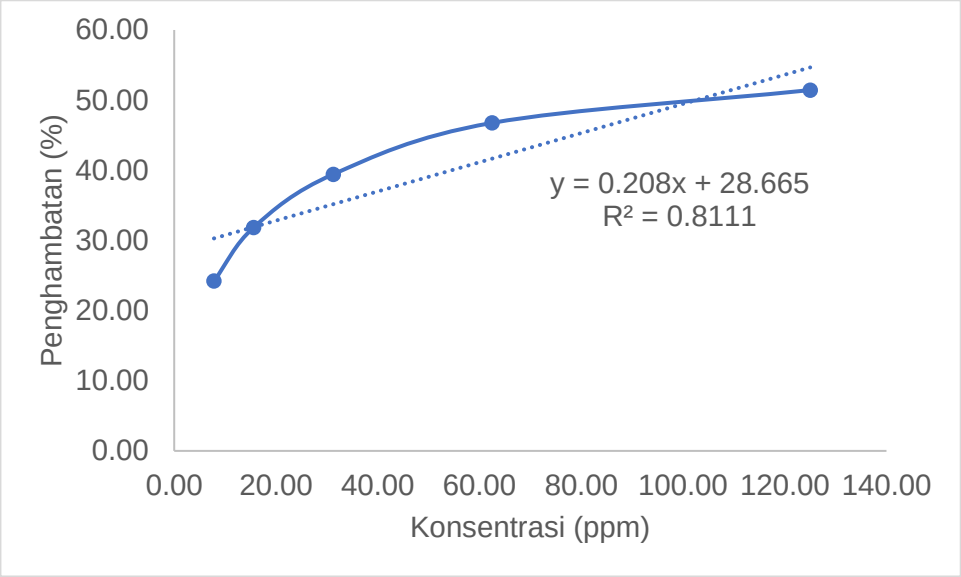
$x\ (IC_{50}) = 55.902$

Nilai aktivitas antiinflamasi adalah 55.902 ppm.

h. Senyawa **4**

Absorbansi Kontrol : 1.0334

Konsentrasi (ppm)	Absorbansi	% Penghambatan
7.81	0.7832	24.21
15.63	0.7042	31.86
31.25	0.6260	39.43
62.50	0.5502	46.76
125.00	0.5019	51.43



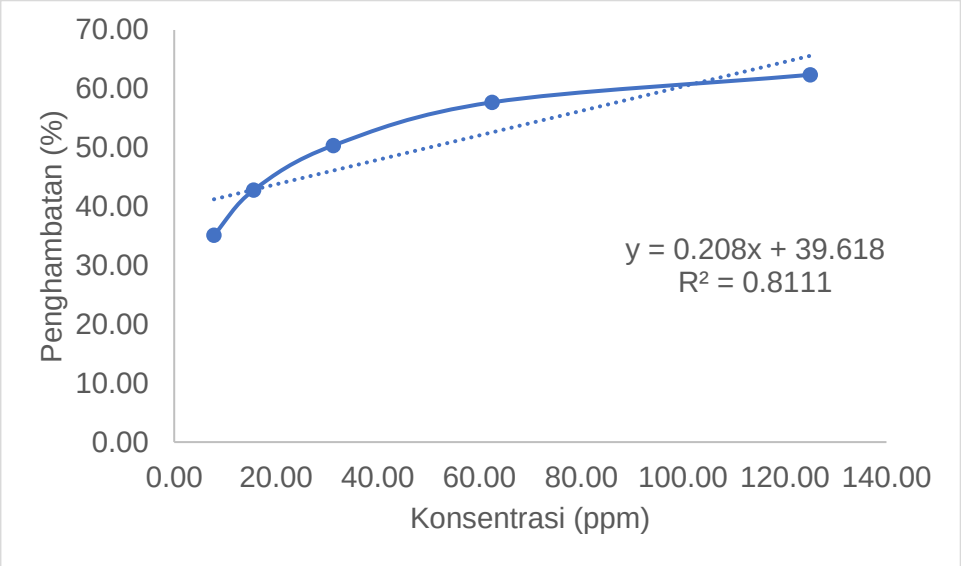
Subtitusi 50 sebagai y pada persamaan regresi linear untuk menentukan nilai konsentrasi (x):
50 = 0.208x + 28.665
x (IC_{50}) = 102.57

Nilai aktivitas antiinflamasi adalah 102.57 ppm.

i. Senyawa **5**

Absorbansi Kontrol : 1.0334

Konsentrasi (ppm)	Absorbansi	% Penghambatan
7.81	0.6700	35.17
15.63	0.5910	42.81
31.25	0.5128	50.38
62.50	0.4370	57.71
125.00	0.3887	62.39



Subtitusi 50 sebagai y pada persamaan regresi linear untuk menentukan nilai konsentrasi (x):

$50 = 0.208x + 39.618$

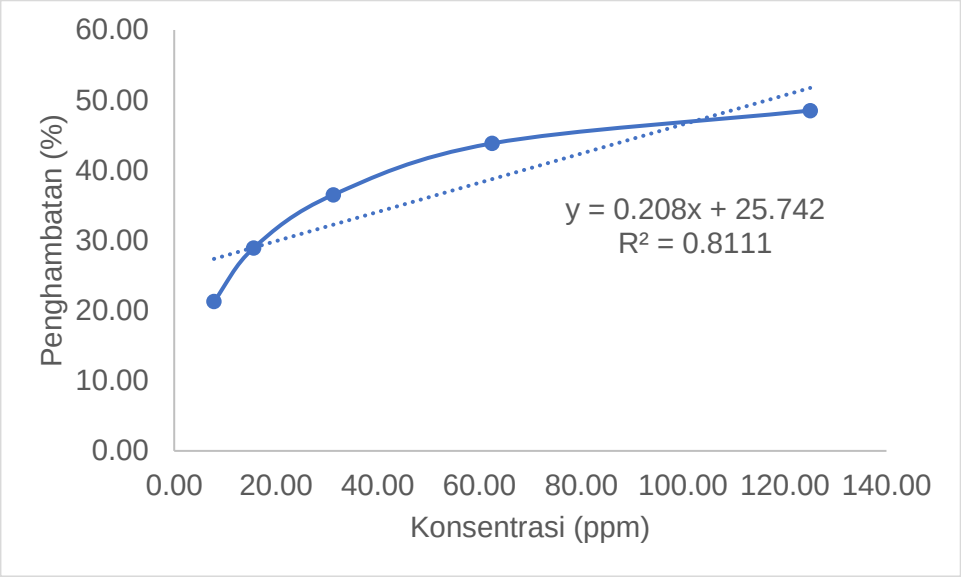
$x\ (IC_{50}) = 49.913$

Nilai aktivitas antiinflamasi adalah 49.913 ppm.

j. Senyawa **6**

Absorbansi Kontrol : 1.0334

Konsentrasi (ppm)	Absorbansi	% Penghambatan
7.81	0.8134	21.29
15.63	0.7344	28.94
31.25	0.6562	36.50
62.50	0.5804	43.84
125.00	0.5321	48.51



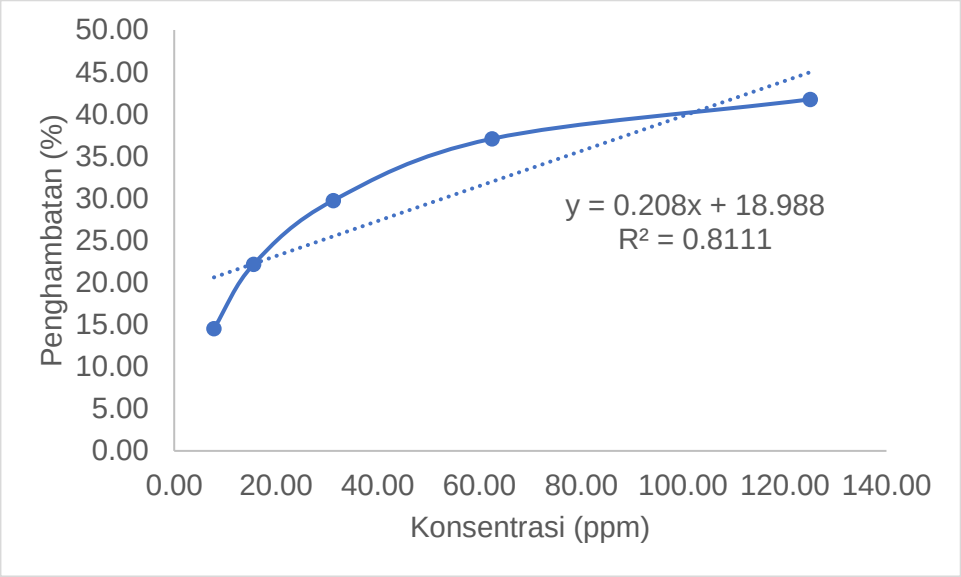
Subtitusi 50 sebagai y pada persamaan regresi linear untuk menentukan nilai konsentrasi (x):
50 = 0.208x + 25.742
x (IC_{50}) = 116.63

Nilai aktivitas antiinflamasi adalah 116.63 ppm.

k. Senyawa **7**

Absorbansi Kontrol : 1.0334

Konsentrasi (ppm)	Absorbansi	% Penghambatan
7.81	0.8832	14.54
15.63	0.8042	22.18
31.25	0.7260	29.75
62.50	0.6502	37.08
125.00	0.6019	41.76



Subtitusi 50 sebagai y pada persamaan regresi linear untuk menentukan nilai konsentrasi (x):

$50 = 0.208x + 18.988$

$x\ (IC_{50}) = 149.1$

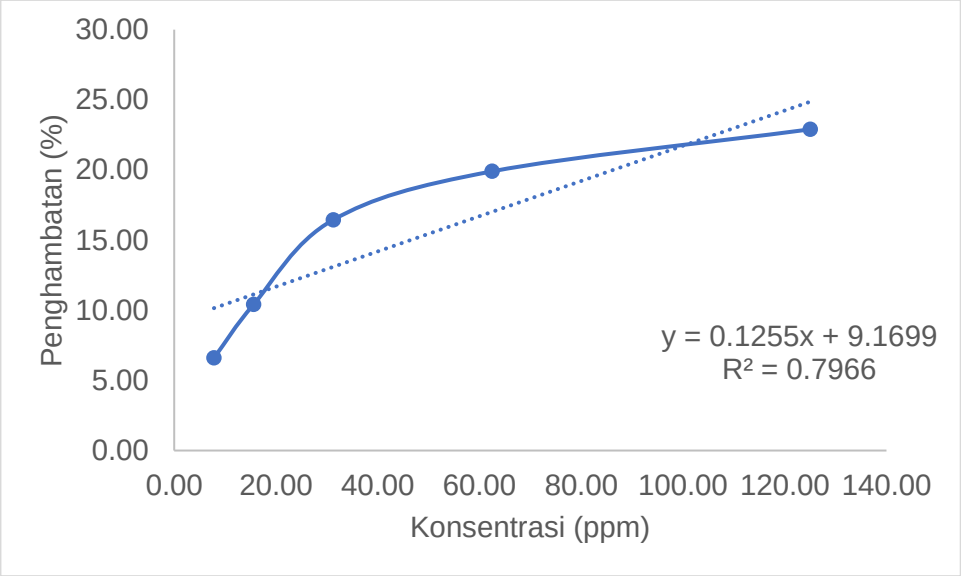
Nilai aktivitas antiinflamasi adalah 149.1 ppm.

Lampiran 11. Uji Antikanker

a. Ekstrak n-Heksan

Absorbansi Kontrol : 0.6051

Konsentrasi (ppm)	Absorbansi	% Penghambatan
7.81	0.5652	6.60
15.63	0.5421	10.42
31.25	0.5056	16.44
62.50	0.4847	19.90
125.00	0.4666	22.89



Subtitusi 50 sebagai y pada persamaan regresi linear untuk menentukan nilai konsentrasi (x):

50 = 0.1255x + 9.1699

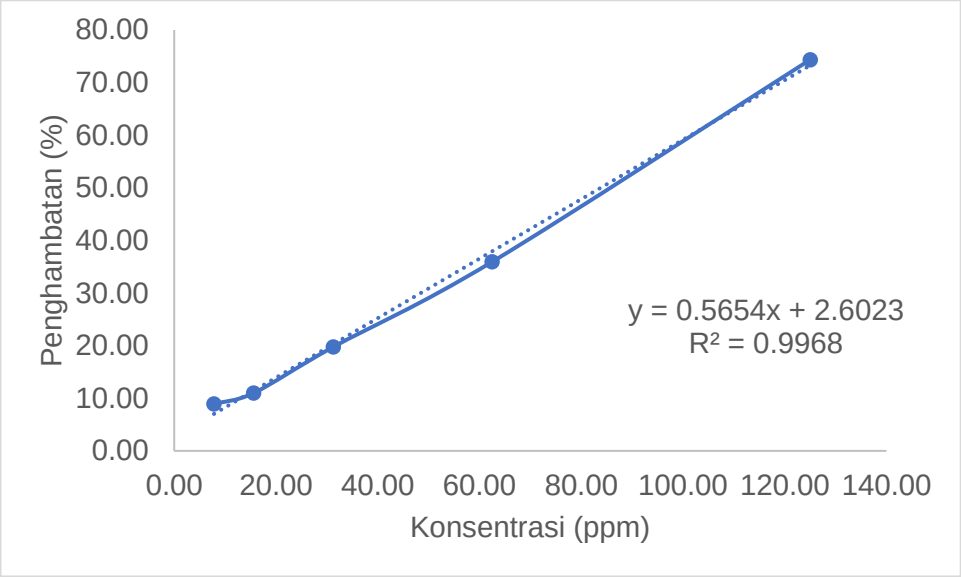
x (IC_{50}) = 325.3

Nilai aktivitas antikanker adalah 325.3 ppm.

b. Ekstrak Etil asetat

Absorbansi Kontrol : 0.6051

Konsentrasi (ppm)	Absorbansi	% Penghambatan
7.81	0.5512	8.91
15.63	0.5386	11.00
31.25	0.4856	19.75
62.50	0.3876	35.94
125.00	0.1552	74.35



Subtitusi 50 sebagai y pada persamaan regresi linear untuk menentukan nilai konsentrasi (x):

50 = 0.5654x + 2.6023

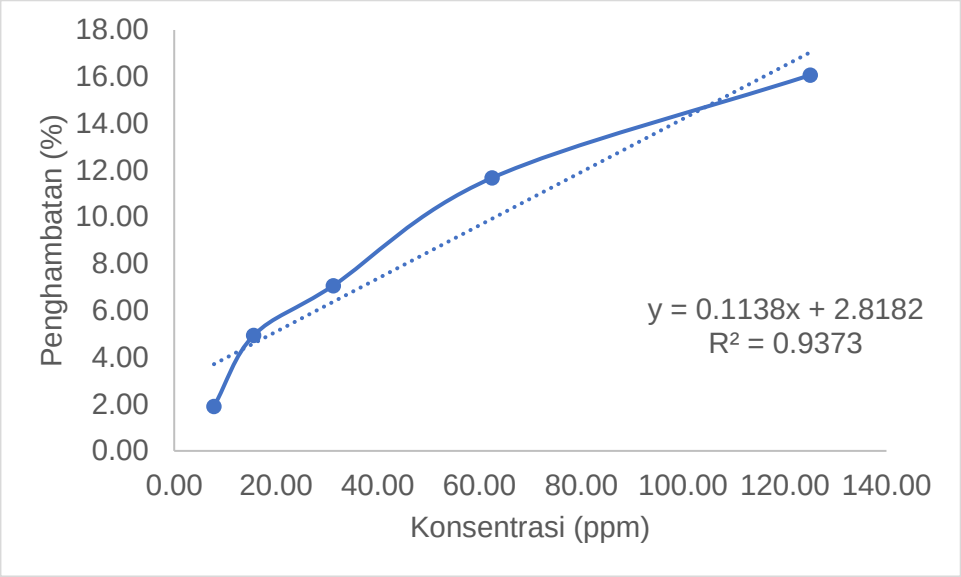
x (IC_{50}) = 83.83

Nilai aktivitas antikanker adalah 83.83 ppm.

c. Ekstrak Metanol

Absorbansi Kontrol : 0.6051

Konsentrasi (ppm)	Absorbansi	% Penghambatan
7.81	0.5936	1.90
15.63	0.5752	4.94
31.25	0.5624	7.07
62.50	0.5345	11.68
125.00	0.5079	16.07



Subtitusi 50 sebagai y pada persamaan regresi linear untuk menentukan nilai konsentrasi (x):

$50 = 0.1138x + 2.8182$

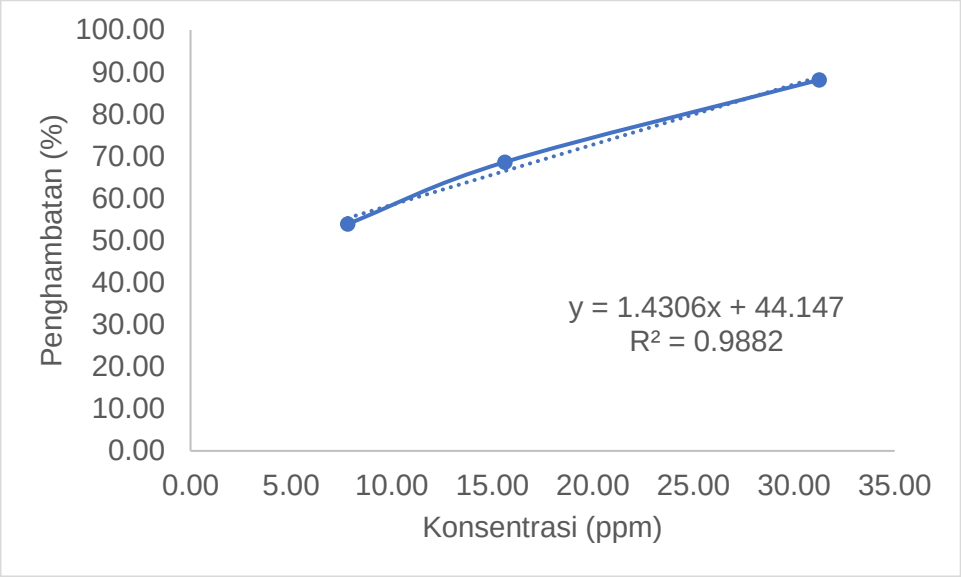
$x\ (IC_{50}) = 414.6$

Nilai aktivitas antikanker adalah 414.6 ppm.

d. Kontrol Positif (Doxorubicin)

Absorbansi Kontrol : 0.6051

Konsentrasi (ppm)	Absorbansi	% Penghambatan
7.81	0.2789	53.91
15.63	0.1899	68.62
31.25	0.0717	88.15
62.50	0.0011	99.81
125.00	0.0008	99.87



Subtitusi 50 sebagai y pada persamaan regresi linear untuk menentukan nilai konsentrasi (x):

50 = 1.4306x + 44.147

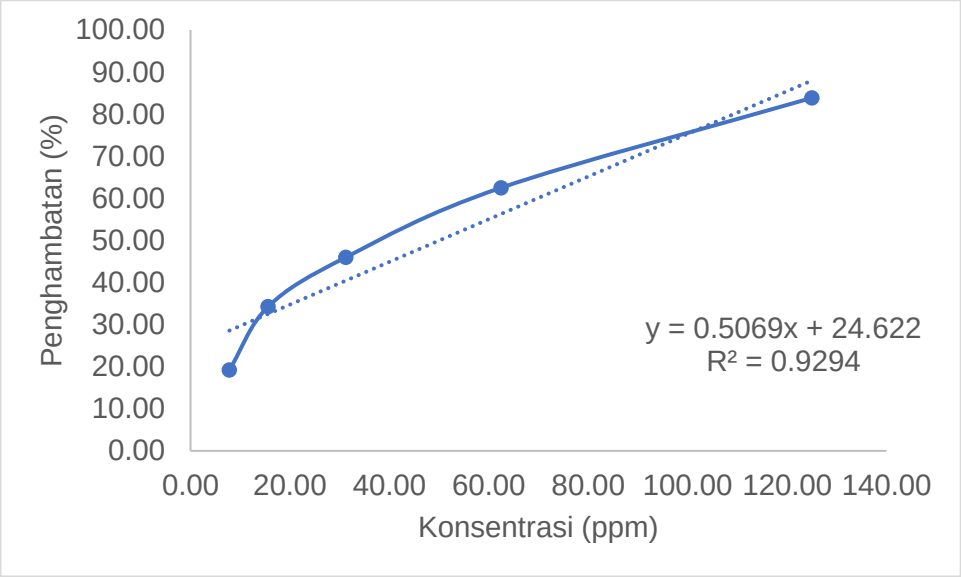
x (IC_{50}) = 4.091

Nilai aktivitas antikanker adalah 4.091 ppm.

e. Senyawa **1**

Absorbansi Kontrol : 0.6051

Konsentrasi (ppm)	Absorbansi	% Penghambatan
7.81	0.4889	19.21
15.63	0.3977	34.28
31.25	0.3268	46.00
62.50	0.2268	62.53
125.00	0.0977	83.86



Subtitusi 50 sebagai y pada persamaan regresi linear untuk menentukan nilai konsentrasi (x):

50 = 0.5069x + 24.622

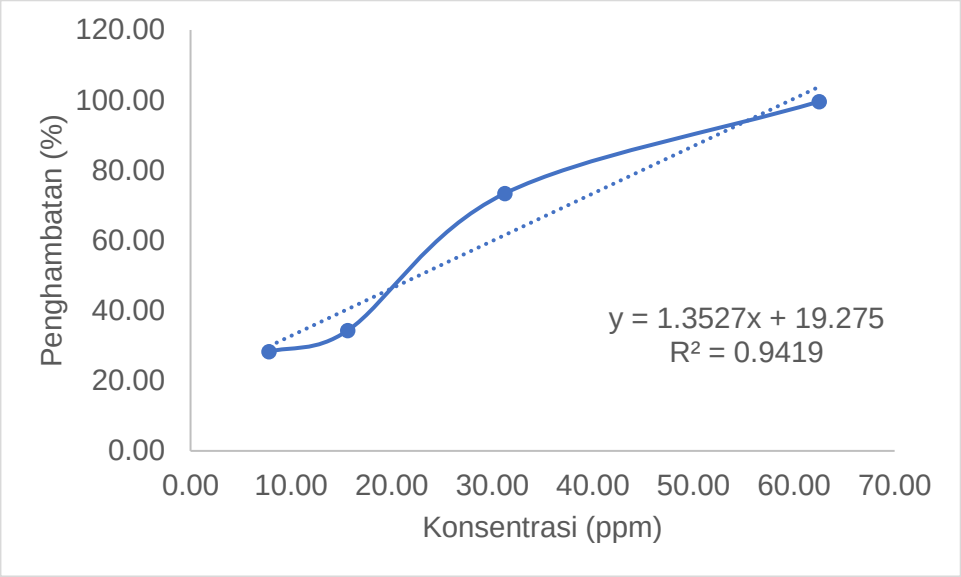
x (IC_{50}) = 50.0651

Nilai aktivitas antikanker adalah 50.0651 ppm.

f. Senyawa **2**

Absorbansi Kontrol : 0.6051

Konsentrasi (ppm)	Absorbansi	% Penghambatan
7.81	0.4340	28.29
15.63	0.3975	34.32
31.25	0.1609	73.41
62.50	0.0024	99.60
125.00	-0.0023	100.39



Subtitusi 50 sebagai y pada persamaan regresi linear untuk menentukan nilai konsentrasi (x):

$50 = 1.3527x + 19.275$

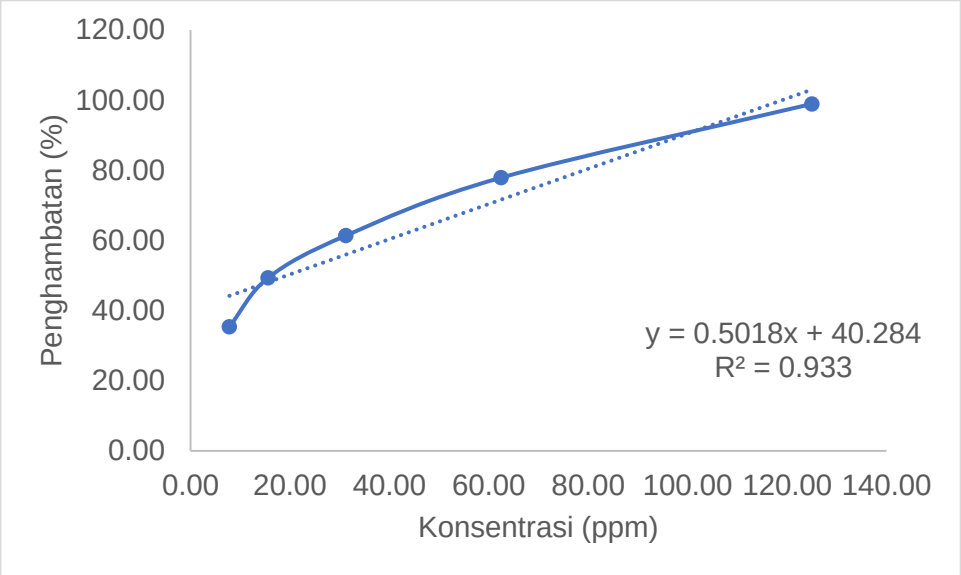
$x\ (IC_{50}) = 22.7$

Nilai aktivitas antikanker adalah 22.7 ppm.

g. Senyawa **3**

Absorbansi Kontrol : 0.6051

Konsentrasi (ppm)	Absorbansi	% Penghambatan
7.81	0.3910	35.39
15.63	0.3065	49.35
31.25	0.2337	61.38
62.50	0.1337	77.91
125.00	0.0065	98.93



Subtitusi 50 sebagai y pada persamaan regresi linear untuk menentukan nilai konsentrasi (x):

$50 = 0.5018x + 40.284$

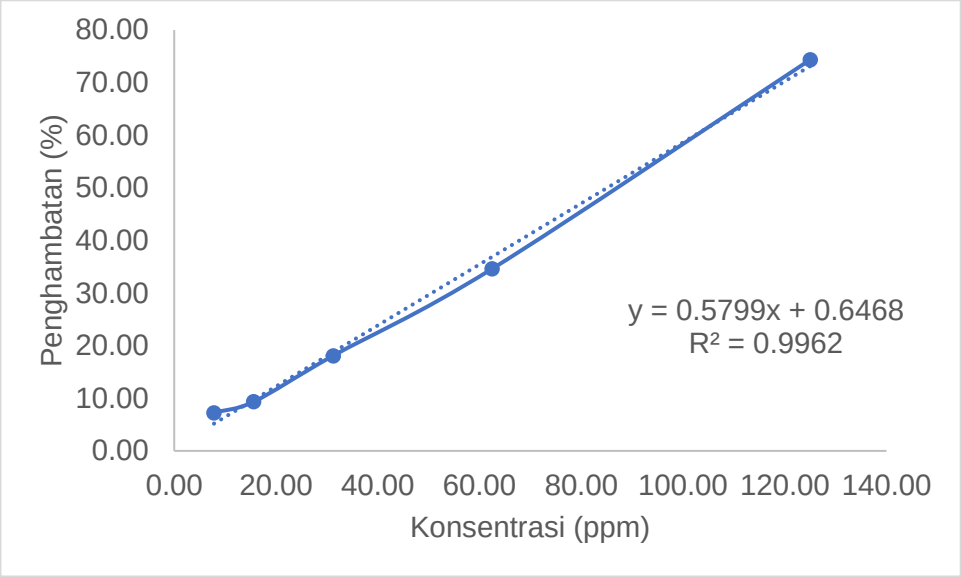
$x\ (IC_{50}) = 19.4$

Nilai aktivitas antikanker adalah 19.4 ppm.

h. Senyawa **4**

Absorbansi Kontrol : 0.6051

Konsentrasi (ppm)	Absorbansi	% Penghambatan
7.81	0.5612	7.26
15.63	0.5486	9.35
31.25	0.4956	18.10
62.50	0.3956	34.62
125.00	0.1552	74.35



Subtitusi 50 sebagai y pada persamaan regresi linear untuk menentukan nilai konsentrasi (x):

$50 = 0.5799x + 0.6468$

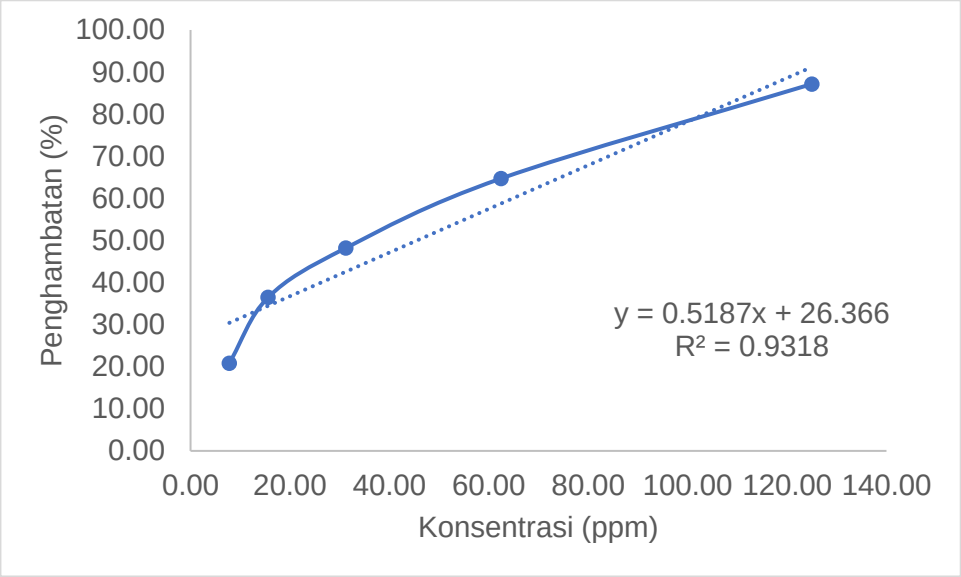
$x\ (IC_{50}) = 85.106$

Nilai aktivitas antikanker adalah 85.106 ppm.

i. Senyawa **5**

Absorbansi Kontrol : 0.6051

Konsentrasi (ppm)	Absorbansi	% Penghambatan
7.81	0.4789	20.86
15.63	0.3843	36.49
31.25	0.3134	48.20
62.50	0.2134	64.73
125.00	0.0777	87.17



Subtitusi 50 sebagai y pada persamaan regresi linear untuk menentukan nilai konsentrasi (x):

50 = 0.5187x + 26.366

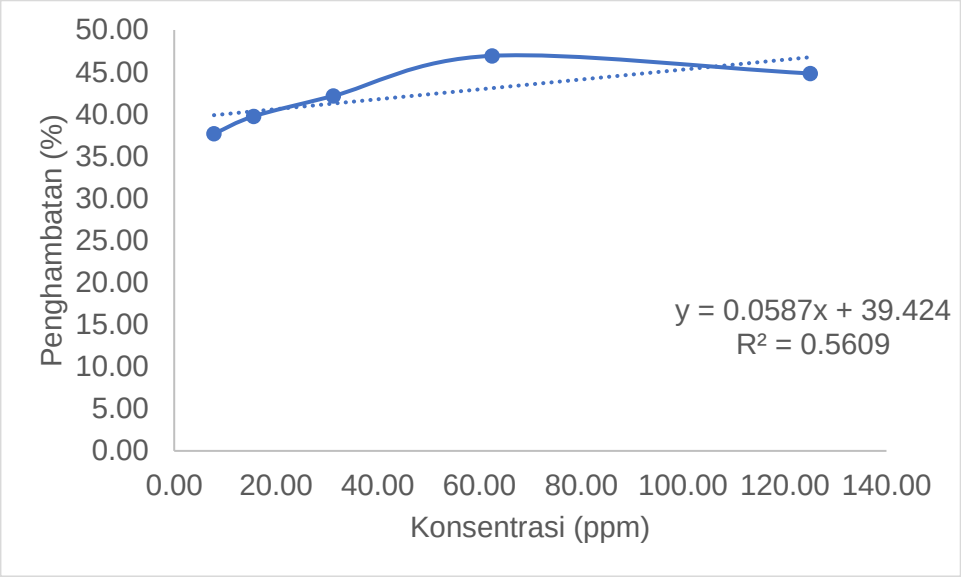
x (IC_{50}) = 45.56

Nilai aktivitas antikanker adalah 45.56 ppm.

j. Senyawa **6**

Absorbansi Kontrol : 0.6051

Konsentrasi (ppm)	Absorbansi	% Penghambatan
7.81	0.3772	37.67
15.63	0.3646	39.74
31.25	0.3500	42.16
62.50	0.3211	46.93
125.00	0.3338	44.83



Subtitusi 50 sebagai y pada persamaan regresi linear untuk menentukan nilai konsentrasi (x):

$50 = 0.0587x + 39.424$

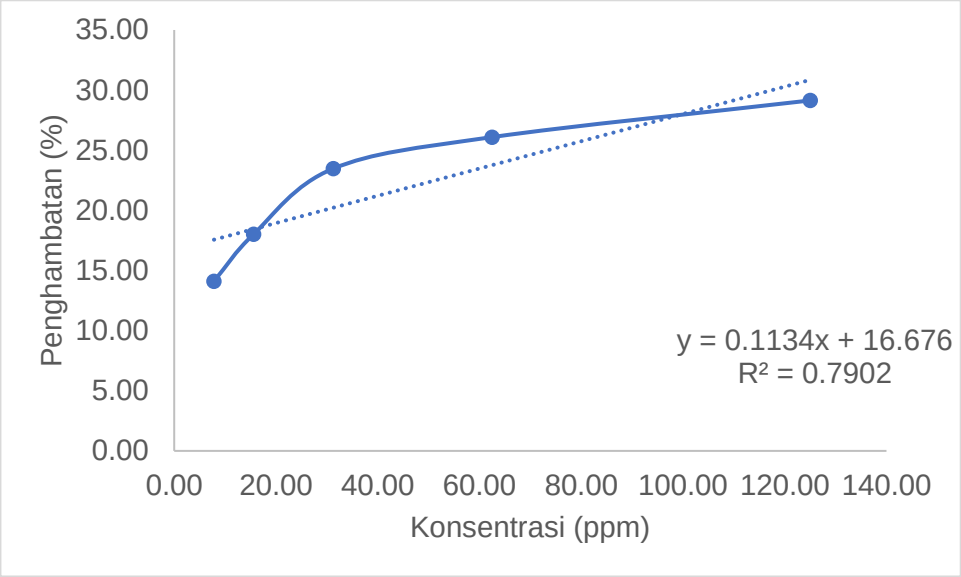
$x\ (IC_{50}) = 180.17$

Nilai aktivitas antikanker adalah 180.17 ppm.

k. Senyawa **7**

Absorbansi Kontrol : 0.6051

Konsentrasi (ppm)	Absorbansi	% Penghambatan
7.81	0.5197	14.11
15.63	0.4961	18.02
31.25	0.4631	23.47
62.50	0.4472	26.09
125.00	0.4288	29.14



Subtitusi 50 sebagai y pada persamaan regresi linear untuk menentukan nilai konsentrasi (x):

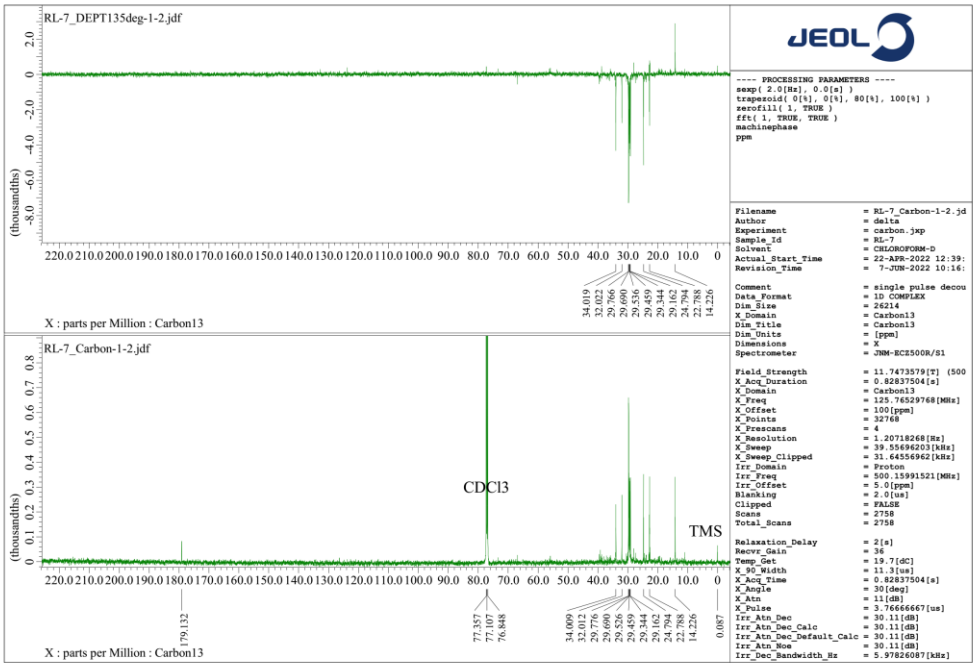
$50 = 0.1134x + 16.676$

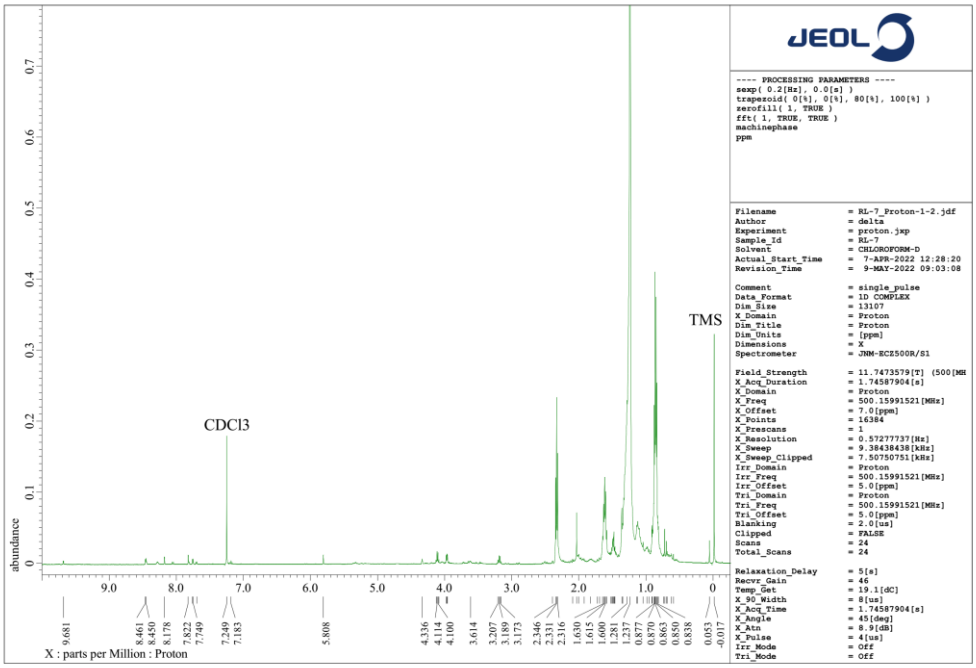
$x\ (IC_{50}) = 293.86$

Nilai aktivitas antikanker adalah 293.86 ppm.

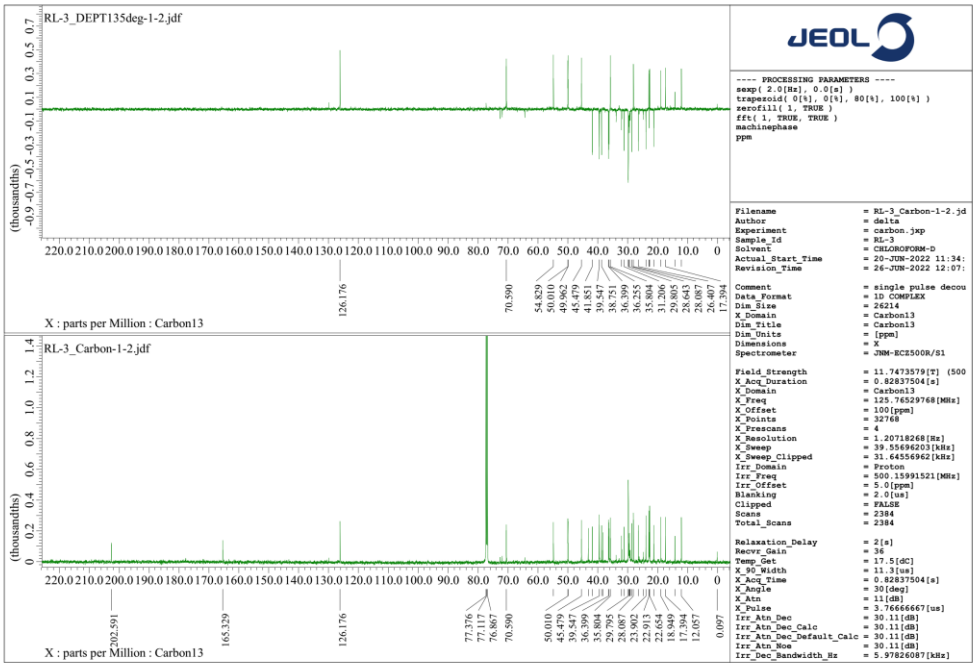
Lampiran 12. Data NMR

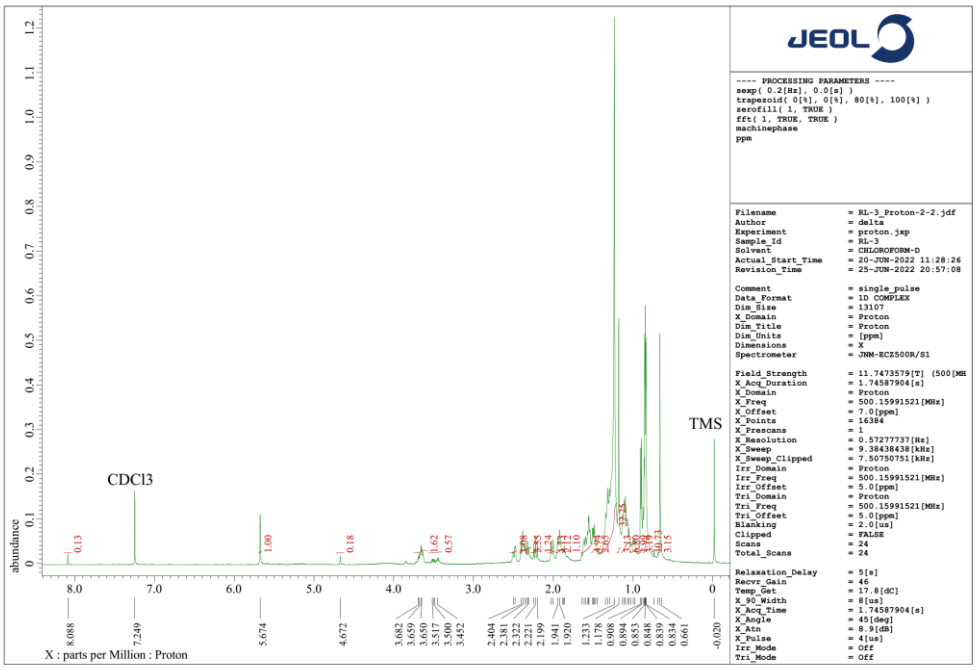
a. Senyawa **1**



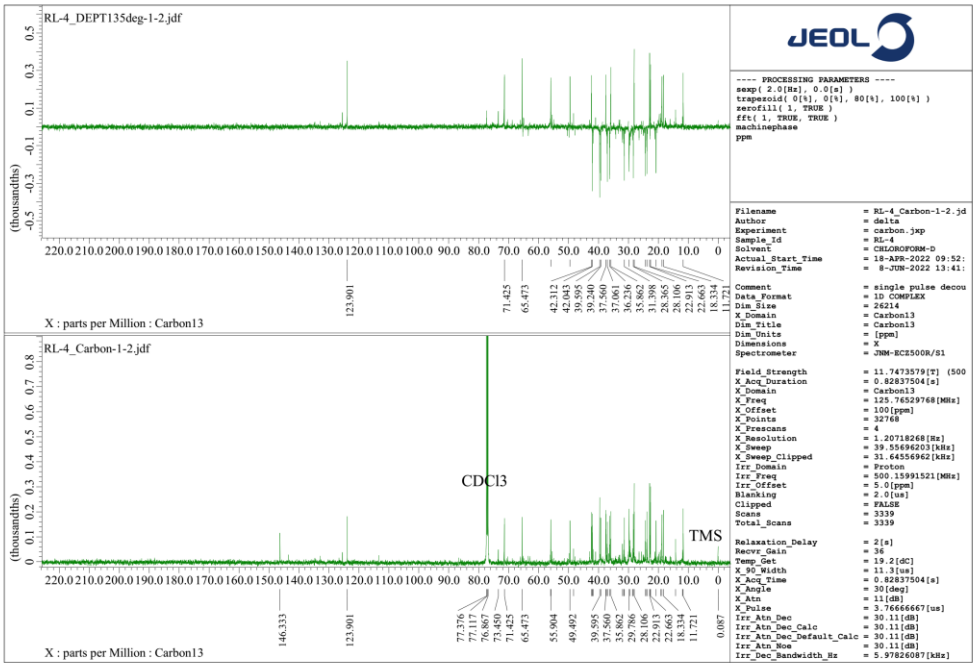


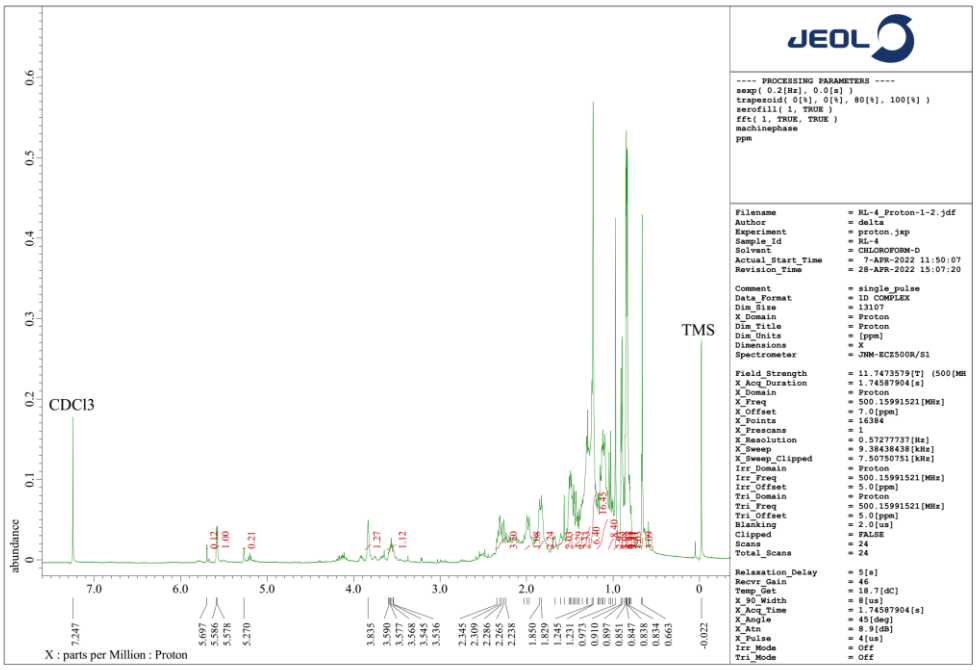
b. Senyawa **2**


RL-3_DEPT135deg-1-2.jdf
(thousandths)
X : parts per Million : Carbon13
126.176
70.590
54.829
50.010
49.962
45.479
41.851
39.547
38.751
36.399
36.253
35.804
31.206
29.805
28.643
28.087
26.407
17.394
JEOL
---- PROCESSING PARAMETERS ----
sexp(2.0[Hz], 0.0[s])
trapezoid(0[%], 0[%], 80[%], 100[%])
zerofill(1, TRUE)
fft(1, TRUE, TRUE)
machinephase
ppm
Filename = RL-3_Carbon-1-2.jd
Author = delta
Experiment = carbon.jxp
Sample_Id = RL-3
Solvent = CHLOROFORM-D
Actual_Start_Time = 20-JUN-2022 11:34:
Revision_Time = 26-JUN-2022 12:07:
Comment = single pulse decou
Data_Format = 1D COMPLEX
Dim_Size = 26214
X_Domain = Carbon13
Dim_Title = Carbon13
Dim_Units = [ppm]
Dimensions = X
Spectrometer = JNM-ECZ500R/S1
Field_Strength = 11.7473579[T] (500
X_Acq_Duration = 0.82837504[s]
X_Domain = Carbon13
X_Freq = 125.76529768[MHz]
X_Offset = 100[ppm]
X_Points = 32768
X_Prescans = 4
X_Resolution = 1.20718268[Hz]
X_Sweep = 39.55696203[kHz]
X_Sweep_Clipped = 31.64556962[kHz]
Irr_Domain = Proton
Irr_Freq = 500.15991521[MHz]
Irr_Offset = 5.0[ppm]
Blanking = 2.0[us]
Clipped = FALSE
Scans = 2384
Total_Scans = 2384
Relaxation_Delay = 2[s]
Recvr_Gain = 36
Temp_Get = 17.5[dC]
X_90_Width = 11.3[us]
X_Acq_Time = 0.82837504[s]
X_Angle = 30[deg]
X_Atn = 11[dB]
X_Pulse = 3.76666667[us]
Irr_Atn_Dec = 30.11[dB]
Irr_Atn_Dec_Calc = 30.11[dB]
Irr_Atn_Dec_Default_Calc = 30.11[dB]
Irr_Atn_Noe = 30.11[dB]
Irr_Dec_Bandwidth_Hz = 5.97826087[kHz]
RL-3_Carbon-1-2.jdf
(thousandths)
X : parts per Million : Carbon13
202.591
165.329
126.176
77.376
77.117
76.867
70.590
50.010
45.479
39.547
36.399
35.804
29.795
28.087
23.902
22.913
22.654
18.949
17.394
12.057
0.097

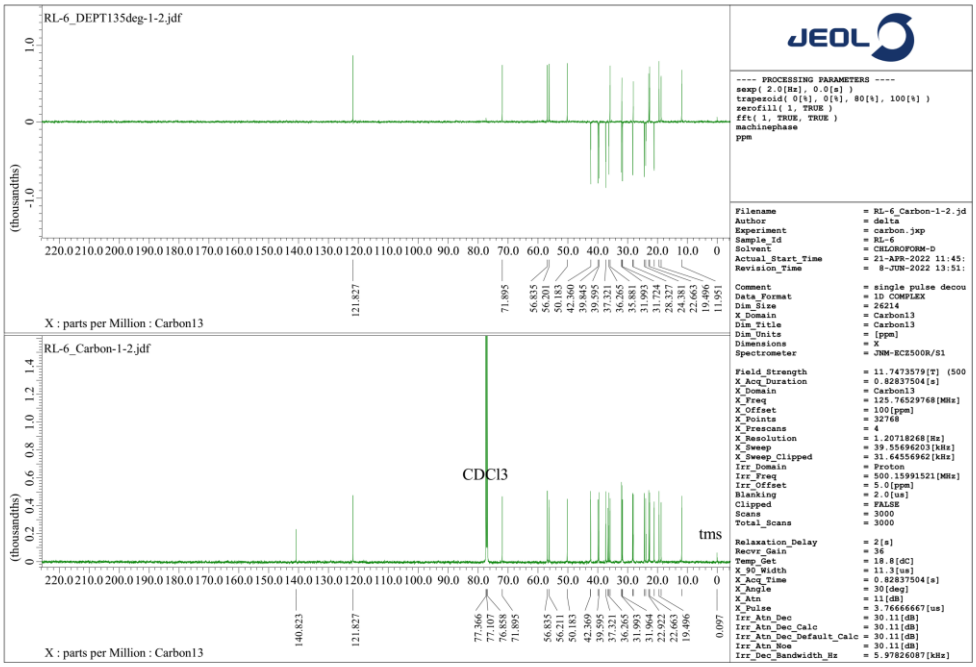

CDCl3
TMS
abundance
X : parts per Million : Proton
8.088
7.249
5.674
4.672
0.13
1.00
0.18
1.62
0.57
3.15
JEOL
---- PROCESSING PARAMETERS ----
sexp(0.2[Hz], 0.0[s])
trapezoid(0[%], 0[%], 80[%], 100[%])
zerofill(1, TRUE)
fft(1, TRUE, TRUE)
machinephase
ppm
Filename = RL-3_Proton-2-2.jdf
Author = delta
Experiment = proton.jxp
Sample_Id = RL-3
Solvent = CHLOROFORM-D
Actual_Start_Time = 20-JUN-2022 11:28:26
Revision_Time = 25-JUN-2022 20:57:08
Comment = single_pulse
Data_Format = 1D COMPLEX
Dim_Size = 13107
X_Domain = Proton
Dim_Title = Proton
Dim_Units = [ppm]
Dimensions = X
Spectrometer = JNM-ECZ500R/S1
Field_Strength = 11.7473579[T] (500[MH
X_Acq_Duration = 1.74587904[s]
X_Domain = Proton
X_Freq = 500.15991521[MHz]
X_Offset = 7.0[ppm]
X_Points = 16384
X_Prescans = 1
X_Resolution = 0.57277737[Hz]
X_Sweep = 9.38438438[kHz]
X_Sweep_Clipped = 7.50750751[kHz]
Irr_Domain = Proton
Irr_Freq = 500.15991521[MHz]
Irr_Offset = 5.0[ppm]
Tri_Domain = Proton
Tri_Freq = 500.15991521[MHz]
Tri_Offset = 5.0[ppm]
Blanking = 2.0[us]
Clipped = FALSE
Scans = 24
Total_Scans = 24
Relaxation_Delay = 5[s]
Recvr_Gain = 46
Temp_Get = 17.8[dC]
X_90_Width = 8[us]
X_Acq_Time = 1.74587904[s]
X_Angle = 45[deg]
X_Atn = 8.9[dB]
X_Pulse = 4[us]
Irr_Mode = Off
Tri_Mode = Off

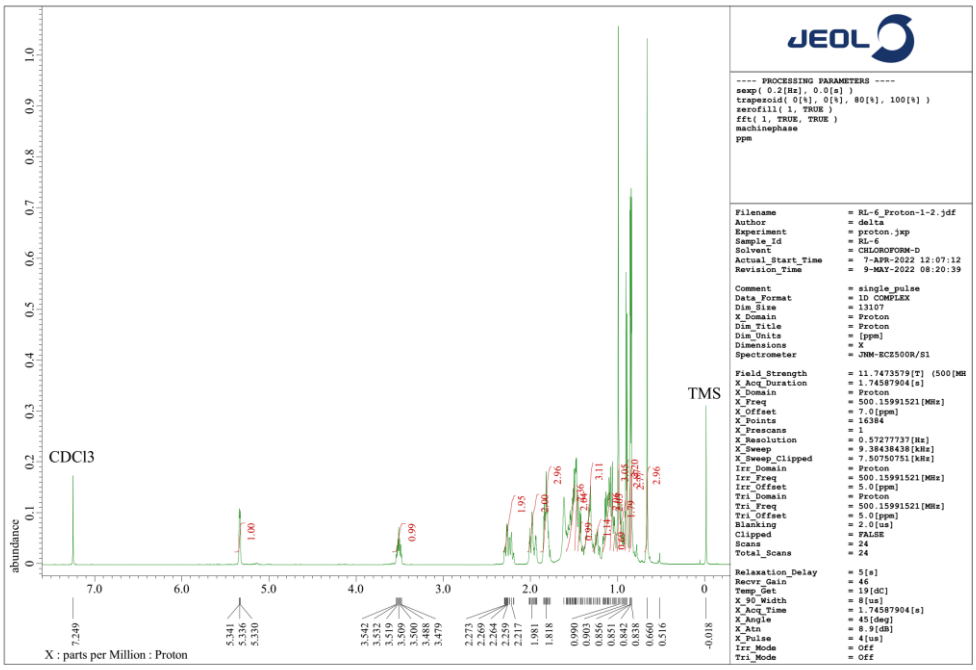
c. Senyawa **3**


RL-4_DEPT135deg-1-2.jdf
(thousandths)
X : parts per Million : Carbon13
RL-4_Carbon-1-2.jdf
CDCl3
TMS
(thousandths)
X : parts per Million : Carbon13
JEOL
---- PROCESSING PARAMETERS ----
sexp(2.0[Hz], 0.0[s])
trapezoid(0[%], 0[%], 80[%], 100[%])
zerofill(1, TRUE)
fft(1, TRUE, TRUE)
machinephase
ppm
Filename = RL-4_Carbon-1-2.jd
Author = delta
Experiment = carbon.jxp
Sample_Id = RL-4
Solvent = CHLOROFORM-D
Actual_Start_Time = 18-APR-2022 09:52:
Revision_Time = 8-JUN-2022 13:41:
Comment = single pulse decou
Data_Format = 1D COMPLEX
Dim_Size = 26214
X_Domain = Carbon13
Dim_Title = Carbon13
Dim_Units = [ppm]
Dimensions = X
Spectrometer = JNM-ECZ500R/S1
Field_Strength = 11.7473579[T] (500
X_Acq_Duration = 0.82837504[s]
X_Domain = Carbon13
X_Freq = 125.76529768[MHz]
X_Offset = 100[ppm]
X_Points = 32768
X_Prescans = 4
X_Resolution = 1.20718268[Hz]
X_Sweep = 39.55696203[kHz]
X_Sweep_Clipped = 31.64556962[kHz]
Irr_Domain = Proton
Irr_Freq = 500.15991521[MHz]
Irr_Offset = 5.0[ppm]
Blanking = 2.0[us]
Clipped = FALSE
Scans = 3339
Total_Scans = 3339
Relaxation_Delay = 2[s]
Recvr_Gain = 36
Temp_Get = 19.2[dC]
X_90_Width = 11.3[us]
X_Acq_Time = 0.82837504[s]
X_Angle = 30[deg]
X_Atn = 11[dB]
X_Pulse = 3.76666667[us]
Irr_Atn_Dec = 30.11[dB]
Irr_Atn_Dec_Calc = 30.11[dB]
Irr_Atn_Dec_Default_Calc = 30.11[dB]
Irr_Atn_Noe = 30.11[dB]
Irr_Dec_Bandwidth_Hz = 5.97826087[kHz]

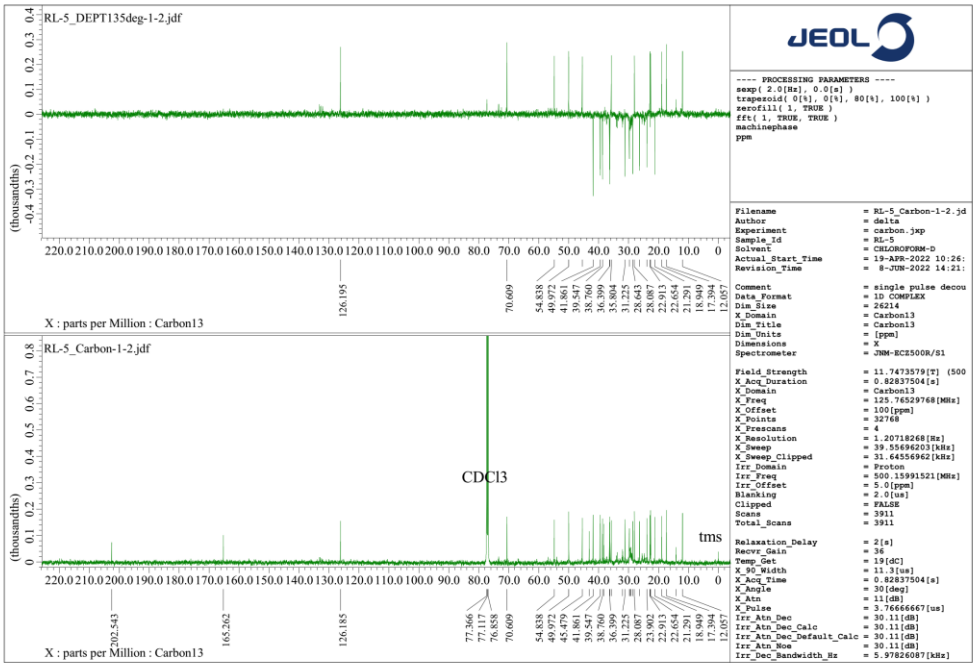

CDCl3
TMS
abundance
X : parts per Million : Proton
JEOL
---- PROCESSING PARAMETERS ----
sexp(0.2[Hz], 0.0[s])
trapezoid(0[%], 0[%], 80[%], 100[%])
zerofill(1, TRUE)
fft(1, TRUE, TRUE)
machinephase
ppm
Filename = RL-4_Proton-1-2.jdf
Author = delta
Experiment = proton.jxp
Sample_Id = RL-4
Solvent = CHLOROFORM-D
Actual_Start_Time = 7-APR-2022 11:50:07
Revision_Time = 28-APR-2022 15:07:20
Comment = single_pulse
Data_Format = 1D COMPLEX
Dim_Size = 13107
X_Domain = Proton
Dim_Title = Proton
Dim_Units = [ppm]
Dimensions = X
Spectrometer = JNM-ECZ500R/S1
Field_Strength = 11.7473579[T] (500[MH
X_Acq_Duration = 1.74587904[s]
X_Domain = Proton
X_Freq = 500.15991521[MHz]
X_Offset = 7.0[ppm]
X_Points = 16384
X_Prescans = 1
X_Resolution = 0.57277737[Hz]
X_Sweep = 9.38438438[kHz]
X_Sweep_Clipped = 7.50750751[kHz]
Irr_Domain = Proton
Irr_Freq = 500.15991521[MHz]
Irr_Offset = 5.0[ppm]
Tri_Domain = Proton
Tri_Freq = 500.15991521[MHz]
Tri_Offset = 5.0[ppm]
Blanking = 2.0[us]
Clipped = FALSE
Scans = 24
Total_Scans = 24
Relaxation_Delay = 5[s]
Recvr_Gain = 46
Temp_Get = 18.7[dC]
X_90_Width = 8[us]
X_Acq_Time = 1.74587904[s]
X_Angle = 45[deg]
X_Atn = 8.9[dB]
X_Pulse = 4[us]
Irr_Mode = Off
Tri_Mode = Off

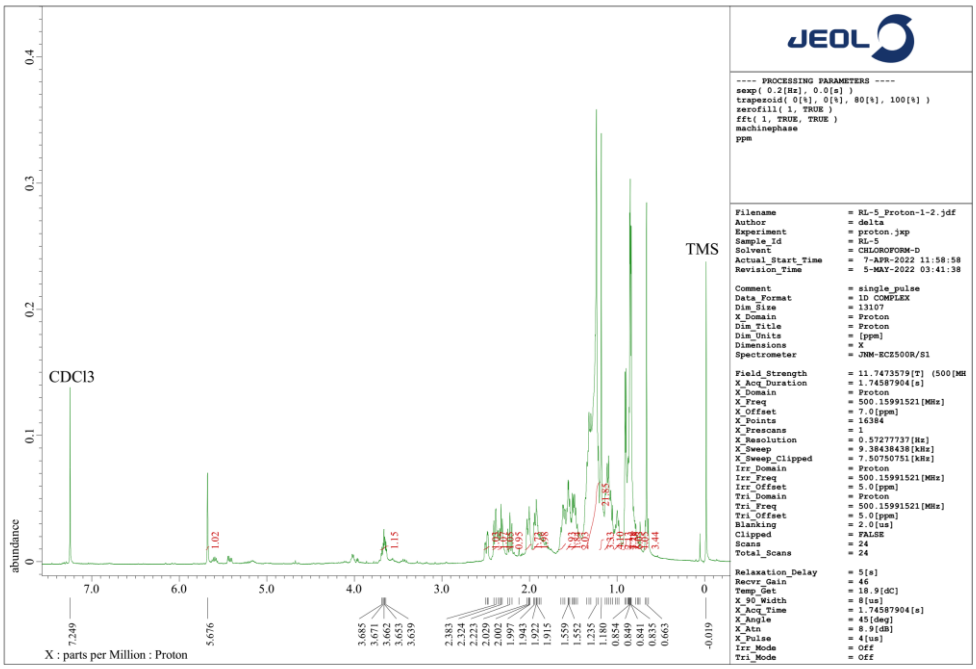
d. Senyawa **4**


RL-6_DEPT135deg-1-2.jdf
X : parts per Million : Carbon13
RL-6_Carbon-1-2.jdf
CDCl3
tms
X : parts per Million : Carbon13
JEOL
---- PROCESSING PARAMETERS ----
sexp(2.0[Hz], 0.0[s])
trapezoid(0[%], 0[%], 80[%], 100[%])
zerofill(1, TRUE)
fft(1, TRUE, TRUE)
machinephase
ppm
Filename = RL-6_Carbon-1-2.jd
Author = delta
Experiment = carbon.jxp
Sample_Id = RL-6
Solvent = CHLOROFORM-D
Actual_Start_Time = 21-APR-2022 11:45:
Revision_Time = 8-JUN-2022 13:51:
Comment = single pulse decou
Data_Format = 1D COMPLEX
Dim_Size = 26214
X_Domain = Carbon13
Dim_Title = Carbon13
Dim_Units = [ppm]
Dimensions = X
Spectrometer = JNM-ECZ500R/S1
Field_Strength = 11.7473579[T] (500
X_Acq_Duration = 0.82837504[s]
X_Domain = Carbon13
X_Freq = 125.76529768[MHz]
X_Offset = 100[ppm]
X_Points = 32768
X_Prescans = 4
X_Resolution = 1.20718268[Hz]
X_Sweep = 39.55696203[kHz]
X_Sweep_Clipped = 31.64556962[kHz]
Irr_Domain = Proton
Irr_Freq = 500.15991521[MHz]
Irr_Offset = 5.0[ppm]
Blanking = 2.0[us]
Clipped = FALSE
Scans = 3000
Total_Scans = 3000
Relaxation_Delay = 2[s]
Recvr_Gain = 36
Temp_Get = 18.8[dC]
X_90_Width = 11.3[us]
X_Acq_Time = 0.82837504[s]
X_Angle = 30[deg]
X_Atn = 11[dB]
X_Pulse = 3.76666667[us]
Irr_Atn_Dec = 30.11[dB]
Irr_Atn_Dec_Calc = 30.11[dB]
Irr_Atn_Dec_Default_Calc = 30.11[dB]
Irr_Atn_Noe = 30.11[dB]
Irr_Dec_Bandwidth_Hz = 5.97826087[kHz]

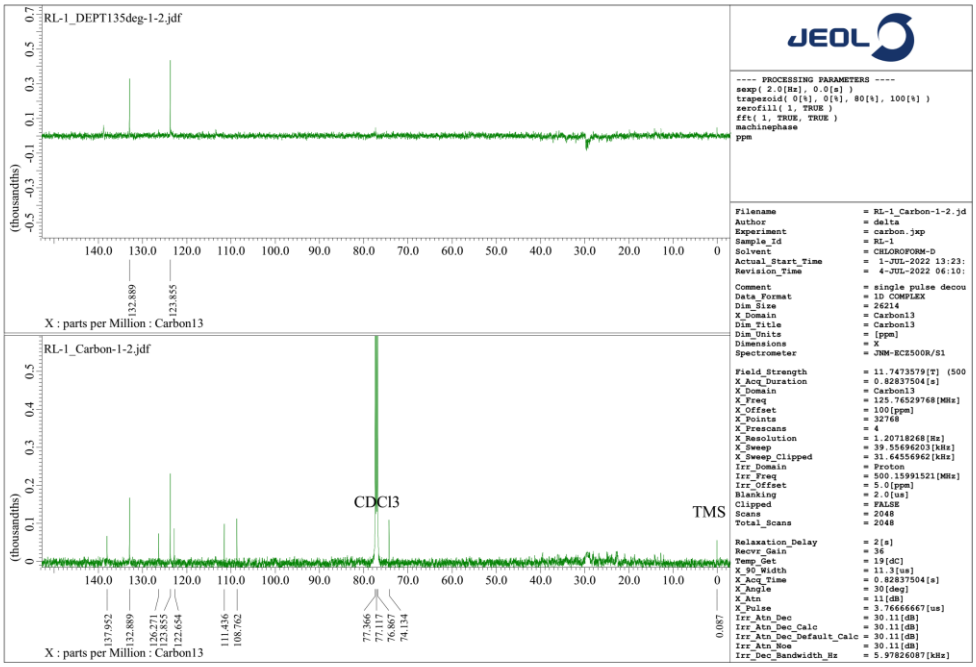

CDCl3
TMS
X : parts per Million : Proton
JEOL
---- PROCESSING PARAMETERS ----
sexp(0.2[Hz], 0.0[s])
trapezoid(0[%], 0[%], 80[%], 100[%])
zerofill(1, TRUE)
fft(1, TRUE, TRUE)
machinephase
ppm
Filename = RL-6_Proton-1-2.jdf
Author = delta
Experiment = proton.jxp
Sample_Id = RL-6
Solvent = CHLOROFORM-D
Actual_Start_Time = 7-APR-2022 12:07:12
Revision_Time = 9-MAY-2022 08:20:39
Comment = single_pulse
Data_Format = 1D COMPLEX
Dim_Size = 13107
X_Domain = Proton
Dim_Title = Proton
Dim_Units = [ppm]
Dimensions = X
Spectrometer = JNM-ECZ500R/S1
Field_Strength = 11.7473579[T] (500[MH
X_Acq_Duration = 1.74587904[s]
X_Domain = Proton
X_Freq = 500.15991521[MHz]
X_Offset = 7.0[ppm]
X_Points = 16384
X_Prescans = 1
X_Resolution = 0.57277737[Hz]
X_Sweep = 9.38438438[kHz]
X_Sweep_Clipped = 7.50750751[kHz]
Irr_Domain = Proton
Irr_Freq = 500.15991521[MHz]
Irr_Offset = 5.0[ppm]
Tri_Domain = Proton
Tri_Freq = 500.15991521[MHz]
Tri_Offset = 5.0[ppm]
Blanking = 2.0[us]
Clipped = FALSE
Scans = 24
Total_Scans = 24
Relaxation_Delay = 5[s]
Recvr_Gain = 46
Temp_Get = 19[dC]
X_90_Width = 8[us]
X_Acq_Time = 1.74587904[s]
X_Angle = 45[deg]
X_Atn = 8.9[dB]
X_Pulse = 4[us]
Irr_Mode = Off
Tri_Mode = Off

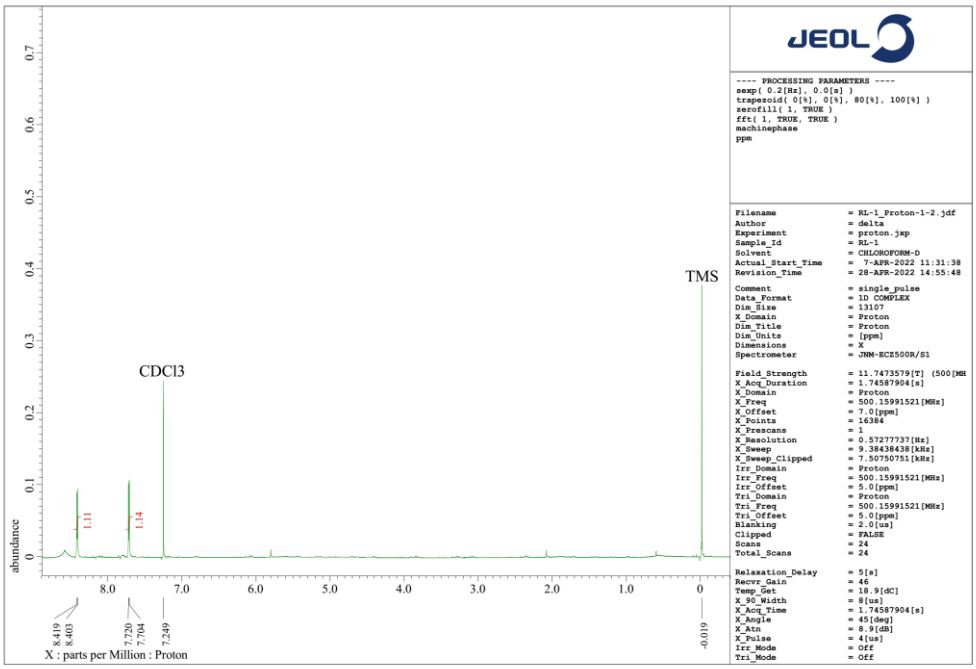
e. Senyawa **5**


RL-5_DEPT135deg-1-2.jdf
(thousandths)
X : parts per Million : Carbon13
RL-5_Carbon-1-2.jdf
CDCl3
tms
(thousandths)
X : parts per Million : Carbon13
JEOL
---- PROCESSING PARAMETERS ----
sexp(2.0[Hz], 0.0[s])
trapezoid(0[%], 0[%], 80[%], 100[%])
zerofill(1, TRUE)
fft(1, TRUE, TRUE)
machinephase
ppm
Filename = RL-5_Carbon-1-2.jd
Author = delta
Experiment = carbon.jxp
Sample_Id = RL-5
Solvent = CHLOROFORM-D
Actual_Start_Time = 19-APR-2022 10:26:
Revision_Time = 8-JUN-2022 14:21:
Comment = single pulse decou
Data_Format = 1D COMPLEX
Dim_Size = 26214
X_Domain = Carbon13
Dim_Title = Carbon13
Dim_Units = [ppm]
Dimensions = X
Spectrometer = JNM-ECZ500R/S1
Field_Strength = 11.7473579[T] (500
X_Acq_Duration = 0.82837504[s]
X_Domain = Carbon13
X_Freq = 125.76529768[MHz]
X_Offset = 100[ppm]
X_Points = 32768
X_Prescans = 4
X_Resolution = 1.20718268[Hz]
X_Sweep = 39.55696203[kHz]
X_Sweep_Clipped = 31.64556962[kHz]
Irr_Domain = Proton
Irr_Freq = 500.15991521[MHz]
Irr_Offset = 5.0[ppm]
Blanking = 2.0[us]
Clipped = FALSE
Scans = 3911
Total_Scans = 3911
Relaxation_Delay = 2[s]
Recvr_Gain = 36
Temp_Get = 19[dC]
X_90_Width = 11.3[us]
X_Acq_Time = 0.82837504[s]
X_Angle = 30[deg]
X_Atn = 11[dB]
X_Pulse = 3.76666667[us]
Irr_Atn_Dec = 30.11[dB]
Irr_Atn_Dec_Calc = 30.11[dB]
Irr_Atn_Dec_Default_Calc = 30.11[dB]
Irr_Atn_Noe = 30.11[dB]
Irr_Dec_Bandwidth_Hz = 5.97826087[kHz]

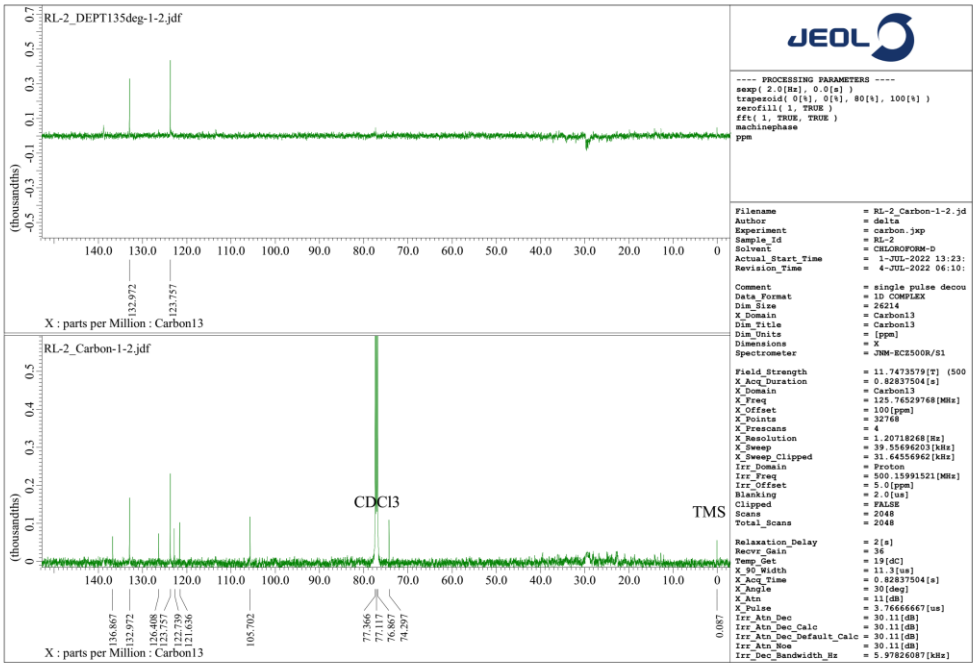

CDCl3
TMS
abundance
X : parts per Million : Proton
JEOL
---- PROCESSING PARAMETERS ----
sexp(0.2[Hz], 0.0[s])
trapezoid(0[%], 0[%], 80[%], 100[%])
zerofill(1, TRUE)
fft(1, TRUE, TRUE)
machinephase
ppm
Filename = RL-5_Proton-1-2.jdf
Author = delta
Experiment = proton.jxp
Sample_Id = RL-5
Solvent = CHLOROFORM-D
Actual_Start_Time = 7-APR-2022 11:58:58
Revision_Time = 5-MAY-2022 03:41:38
Comment = single_pulse
Data_Format = 1D COMPLEX
Dim_Size = 13107
X_Domain = Proton
Dim_Title = Proton
Dim_Units = [ppm]
Dimensions = X
Spectrometer = JNM-ECZ500R/S1
Field_Strength = 11.7473579[T] (500[MH
X_Acq_Duration = 1.74587904[s]
X_Domain = Proton
X_Freq = 500.15991521[MHz]
X_Offset = 7.0[ppm]
X_Points = 16384
X_Prescans = 1
X_Resolution = 0.57277737[Hz]
X_Sweep = 9.38438438[kHz]
X_Sweep_Clipped = 7.50750751[kHz]
Irr_Domain = Proton
Irr_Freq = 500.15991521[MHz]
Irr_Offset = 5.0[ppm]
Tri_Domain = Proton
Tri_Freq = 500.15991521[MHz]
Tri_Offset = 5.0[ppm]
Blanking = 2.0[us]
Clipped = FALSE
Scans = 24
Total_Scans = 24
Relaxation_Delay = 5[s]
Recvr_Gain = 46
Temp_Get = 18.9[dC]
X_90_Width = 8[us]
X_Acq_Time = 1.74587904[s]
X_Angle = 45[deg]
X_Atn = 8.9[dB]
X_Pulse = 4[us]
Irr_Mode = Off
Tri_Mode = Off

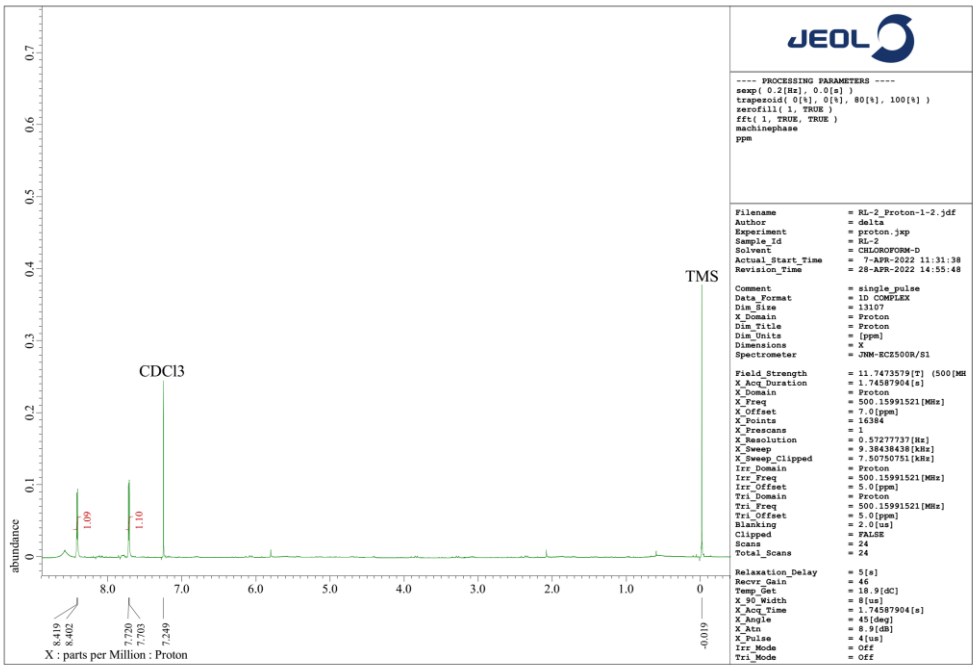
f. Senyawa **6**


RL-1_DEPT135deg-1-2.jdf
(thousandths)
X : parts per Million : Carbon13
RL-1_Carbon-1-2.jdf
CDCl3
TMS
(thousandths)
X : parts per Million : Carbon13
JEOL
---- PROCESSING PARAMETERS ----
sexp(2.0[Hz], 0.0[s])
trapezoid(0[%], 0[%], 80[%], 100[%])
zerofill(1, TRUE)
fft(1, TRUE, TRUE)
machinephase
ppm
Filename = RL-1_Carbon-1-2.jd
Author = delta
Experiment = carbon.jxp
Sample_Id = RL-1
Solvent = CHLOROFORM-D
Actual_Start_Time = 1-JUL-2022 13:23:
Revision_Time = 4-JUL-2022 06:10:
Comment = single pulse decou
Data_Format = 1D COMPLEX
Dim_Size = 26214
X_Domain = Carbon13
Dim_Title = Carbon13
Dim_Units = [ppm]
Dimensions = X
Spectrometer = JNM-ECZ500R/S1
Field_Strength = 11.7473579[T] (500
X_Acq_Duration = 0.82837504[s]
X_Domain = Carbon13
X_Freq = 125.76529768[MHz]
X_Offset = 100[ppm]
X_Points = 32768
X_Prescans = 4
X_Resolution = 1.20718268[Hz]
X_Sweep = 39.55696203[kHz]
X_Sweep_Clipped = 31.64556962[kHz]
Irr_Domain = Proton
Irr_Freq = 500.15991521[MHz]
Irr_Offset = 5.0[ppm]
Blanking = 2.0[us]
Clipped = FALSE
Scans = 2048
Total_Scans = 2048
Relaxation_Delay = 2[s]
Recvr_Gain = 36
Temp_Get = 19[dC]
X_90_Width = 11.3[us]
X_Acq_Time = 0.82837504[s]
X_Angle = 30[deg]
X_Atn = 11[dB]
X_Pulse = 3.76666667[us]
Irr_Atn_Dec = 30.11[dB]
Irr_Atn_Dec_Calc = 30.11[dB]
Irr_Atn_Dec_Default_Calc = 30.11[dB]
Irr_Atn_Noe = 30.11[dB]
Irr_Dec_Bandwidth_Hz = 5.97826087[kHz]


TMS
CDCl3
abundance
X : parts per Million : Proton
JEOL
---- PROCESSING PARAMETERS ----
sexp(0.2[Hz], 0.0[s])
trapezoid(0[%], 0[%], 80[%], 100[%])
zerofill(1, TRUE)
fft(1, TRUE, TRUE)
machinephase
ppm
Filename = RL-1_Proton-1-2.jdf
Author = delta
Experiment = proton.jxp
Sample_Id = RL-1
Solvent = CHLOROFORM-D
Actual_Start_Time = 7-APR-2022 11:31:38
Revision_Time = 28-APR-2022 14:55:48
Comment = single_pulse
Data_Format = 1D COMPLEX
Dim_Size = 13107
X_Domain = Proton
Dim_Title = Proton
Dim_Units = [ppm]
Dimensions = X
Spectrometer = JNM-ECZ500R/S1
Field_Strength = 11.7473579[T] (500[MH
X_Acq_Duration = 1.74587904[s]
X_Domain = Proton
X_Freq = 500.15991521[MHz]
X_Offset = 7.0[ppm]
X_Points = 16384
X_Prescans = 1
X_Resolution = 0.57277737[Hz]
X_Sweep = 9.38438438[kHz]
X_Sweep_Clipped = 7.50750751[kHz]
Irr_Domain = Proton
Irr_Freq = 500.15991521[MHz]
Irr_Offset = 5.0[ppm]
Tri_Domain = Proton
Tri_Freq = 500.15991521[MHz]
Tri_Offset = 5.0[ppm]
Blanking = 2.0[us]
Clipped = FALSE
Scans = 24
Total_Scans = 24
Relaxation_Delay = 5[s]
Recvr_Gain = 46
Temp_Get = 18.9[dC]
X_90_Width = 8[us]
X_Acq_Time = 1.74587904[s]
X_Angle = 45[deg]
X_Atn = 8.9[dB]
X_Pulse = 4[us]
Irr_Mode = Off
Tri_Mode = Off

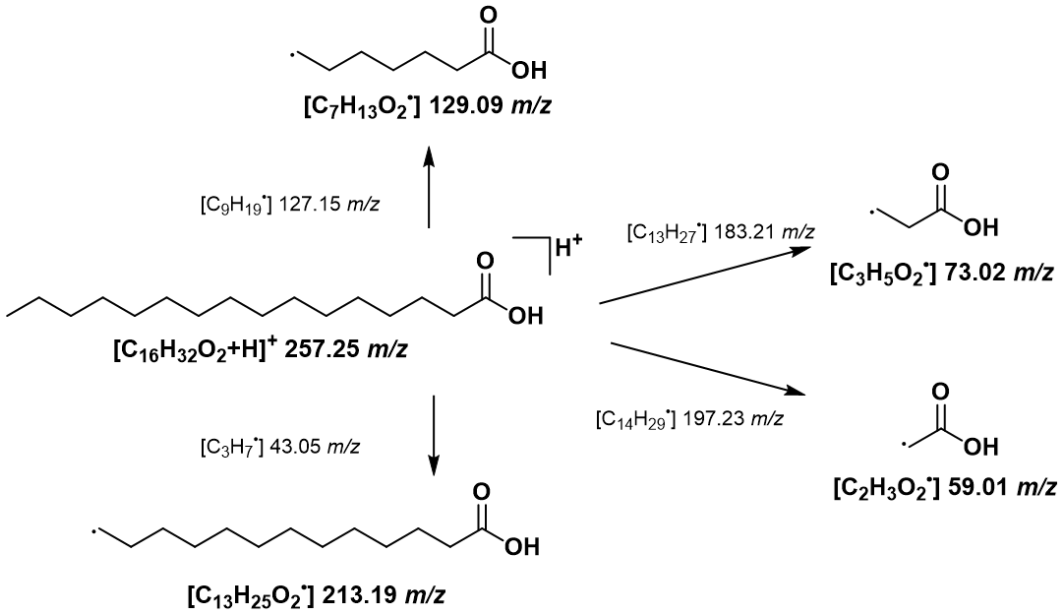
g. Senyawa **7**


RL-2_DEPT135deg-1-2.jdf
(thousandths)
X : parts per Million : Carbon13
RL-2_Carbon-1-2.jdf
CDCl3
TMS
(thousandths)
X : parts per Million : Carbon13
JEOL
---- PROCESSING PARAMETERS ----
sexp(2.0[Hz], 0.0[s])
trapezoid(0[%], 0[%], 80[%], 100[%])
zerofill(1, TRUE)
fft(1, TRUE, TRUE)
machinephase
ppm
Filename = RL-2_Carbon-1-2.jd
Author = delta
Experiment = carbon.jxp
Sample_Id = RL-2
Solvent = CHLOROFORM-D
Actual_Start_Time = 1-JUL-2022 13:23:
Revision_Time = 4-JUL-2022 06:10:
Comment = single pulse decou
Data_Format = 1D COMPLEX
Dim_Size = 26214
X_Domain = Carbon13
Dim_Title = Carbon13
Dim_Units = [ppm]
Dimensions = X
Spectrometer = JNM-ECZ500R/S1
Field_Strength = 11.7473579[T] (500
X_Acq_Duration = 0.82837504[s]
X_Domain = Carbon13
X_Freq = 125.76529768[MHz]
X_Offset = 100[ppm]
X_Points = 32768
X_Prescans = 4
X_Resolution = 1.20718268[Hz]
X_Sweep = 39.55696203[kHz]
X_Sweep_Clipped = 31.64556962[kHz]
Irr_Domain = Proton
Irr_Freq = 500.15991521[MHz]
Irr_Offset = 5.0[ppm]
Blanking = 2.0[us]
Clipped = FALSE
Scans = 2048
Total_Scans = 2048
Relaxation_Delay = 2[s]
Recvr_Gain = 36
Temp_Get = 19[dC]
X_90_Width = 11.3[us]
X_Acq_Time = 0.82837504[s]
X_Angle = 30[deg]
X_Atn = 11[dB]
X_Pulse = 3.76666667[us]
Irr_Atn_Dec = 30.11[dB]
Irr_Atn_Dec_Calc = 30.11[dB]
Irr_Atn_Dec_Default_Calc = 30.11[dB]
Irr_Atn_Noe = 30.11[dB]
Irr_Dec_Bandwidth_Hz = 5.97826087[kHz]

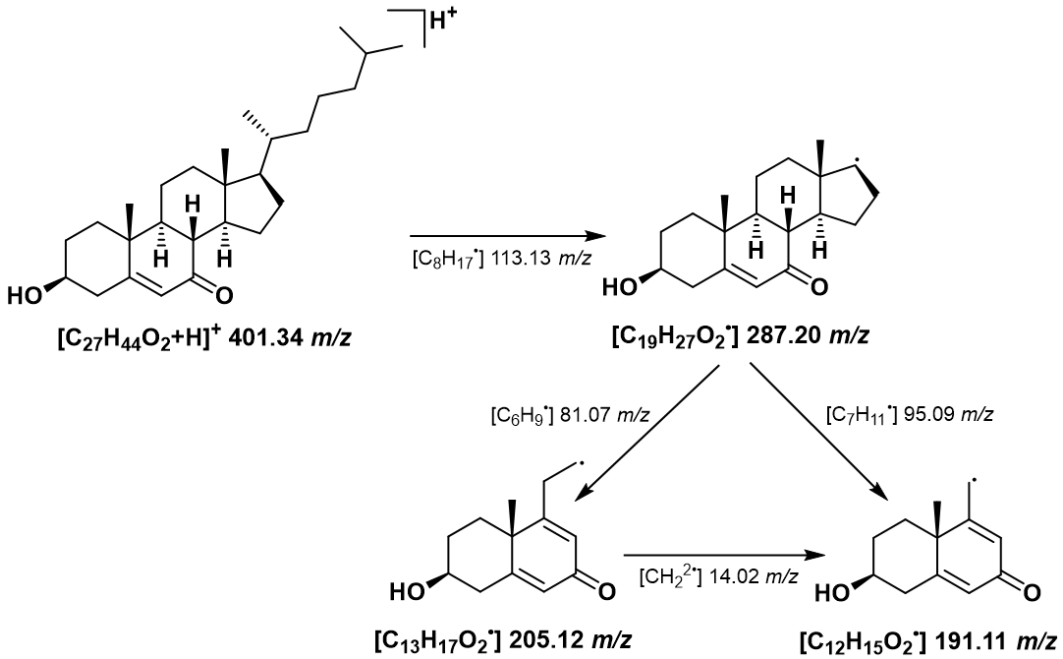

CDCl3
TMS
1.09
1.10
abundance
X : parts per Million : Proton
JEOL
---- PROCESSING PARAMETERS ----
sexp(0.2[Hz], 0.0[s])
trapezoid(0[%], 0[%], 80[%], 100[%])
zerofill(1, TRUE)
fft(1, TRUE, TRUE)
machinephase
ppm
Filename = RL-2_Proton-1-2.jdf
Author = delta
Experiment = proton.jxp
Sample_Id = RL-2
Solvent = CHLOROFORM-D
Actual_Start_Time = 7-APR-2022 11:31:38
Revision_Time = 28-APR-2022 14:55:48
Comment = single_pulse
Data_Format = 1D COMPLEX
Dim_Size = 13107
X_Domain = Proton
Dim_Title = Proton
Dim_Units = [ppm]
Dimensions = X
Spectrometer = JNM-ECZ500R/S1
Field_Strength = 11.7473579[T] (500[MH
X_Acq_Duration = 1.74587904[s]
X_Domain = Proton
X_Freq = 500.15991521[MHz]
X_Offset = 7.0[ppm]
X_Points = 16384
X_Prescans = 1
X_Resolution = 0.57277737[Hz]
X_Sweep = 9.38438438[kHz]
X_Sweep_Clipped = 7.50750751[kHz]
Irr_Domain = Proton
Irr_Freq = 500.15991521[MHz]
Irr_Offset = 5.0[ppm]
Tri_Domain = Proton
Tri_Freq = 500.15991521[MHz]
Tri_Offset = 5.0[ppm]
Blanking = 2.0[us]
Clipped = FALSE
Scans = 24
Total_Scans = 24
Relaxation_Delay = 5[s]
Recvr_Gain = 46
Temp_Get = 18.9[dC]
X_90_Width = 8[us]
X_Acq_Time = 1.74587904[s]
X_Angle = 45[deg]
X_Atn = 8.9[dB]
X_Pulse = 4[us]
Irr_Mode = Off
Tri_Mode = Off

Lampiran 13. Fragmentasi MS

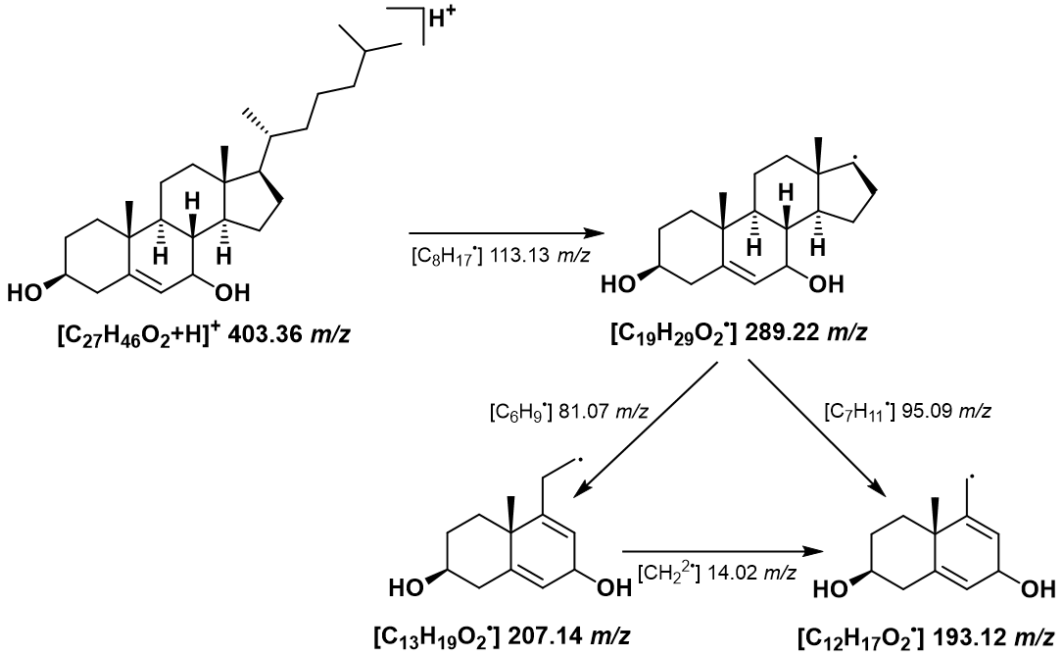
a. Senyawa **1**



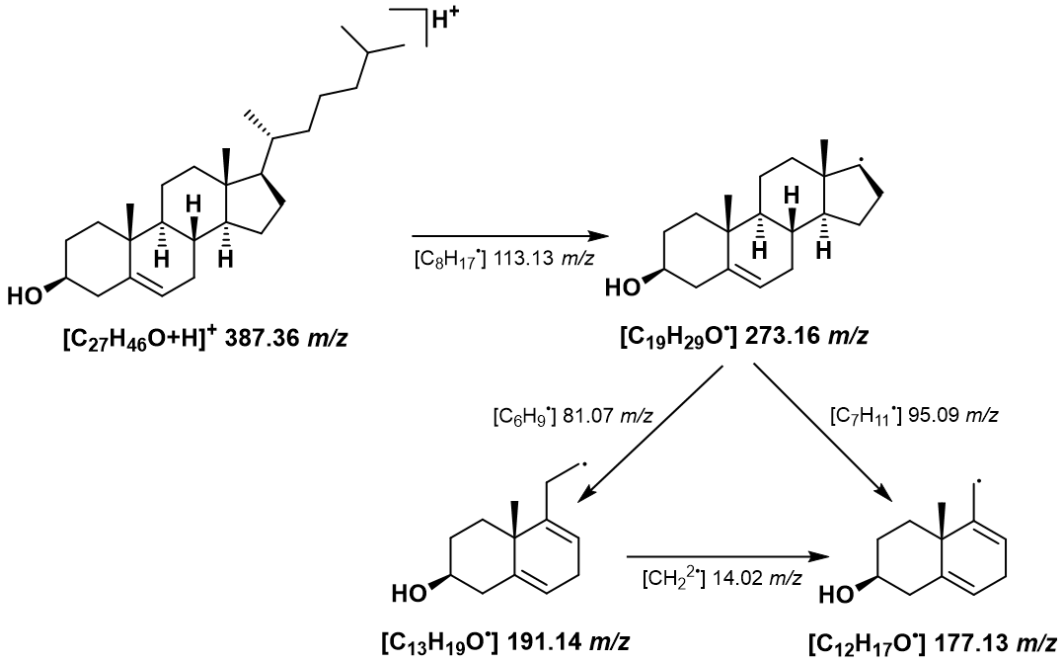
b. Senyawa **2**



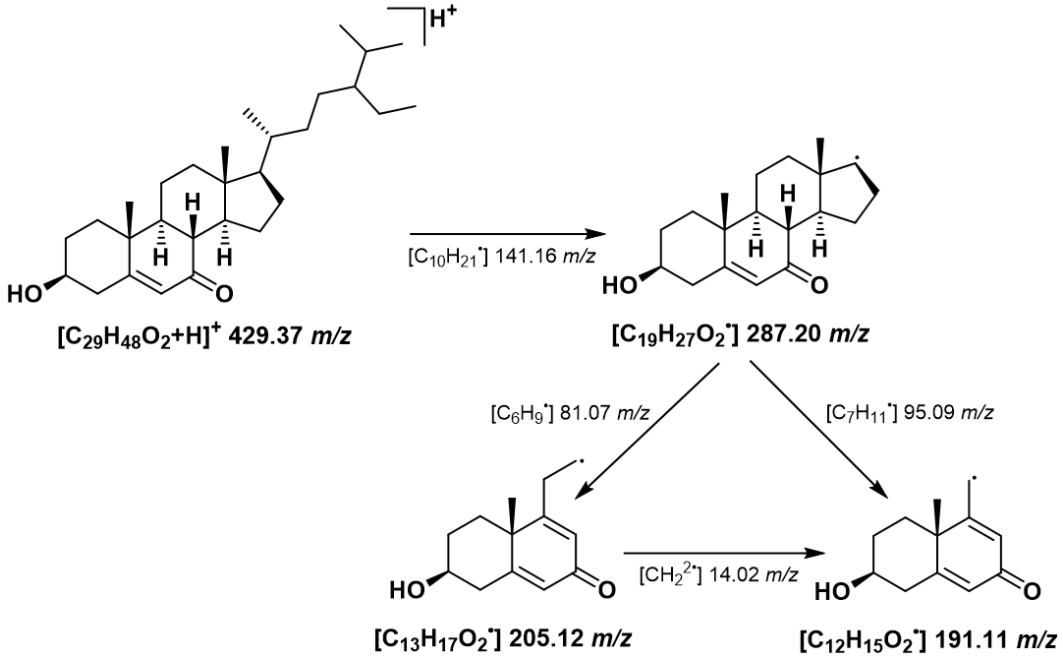
c. Senyawa 3



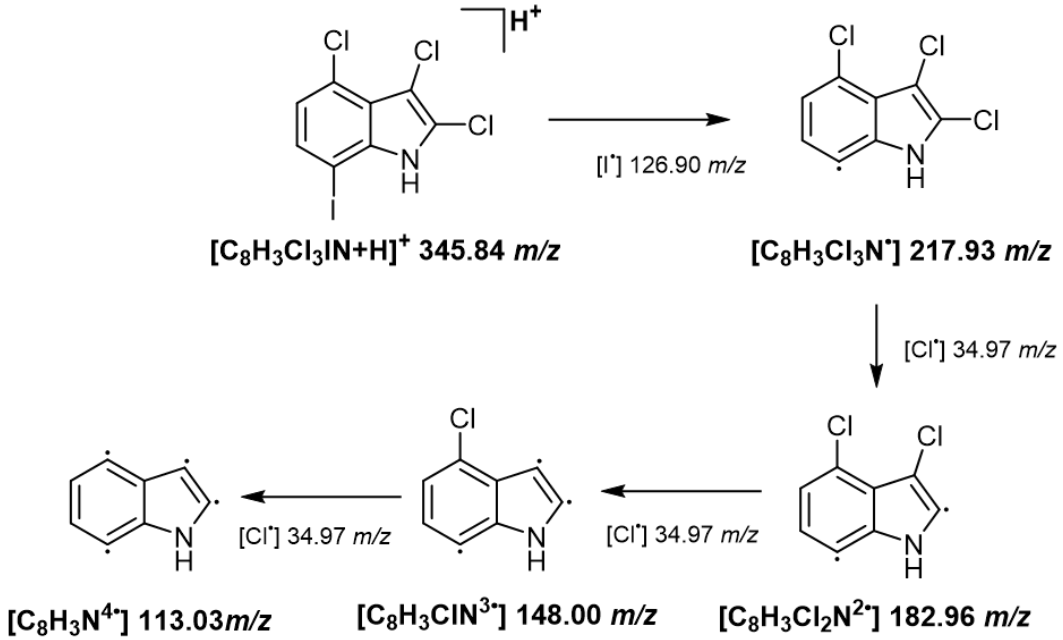
d. Senyawa **4**



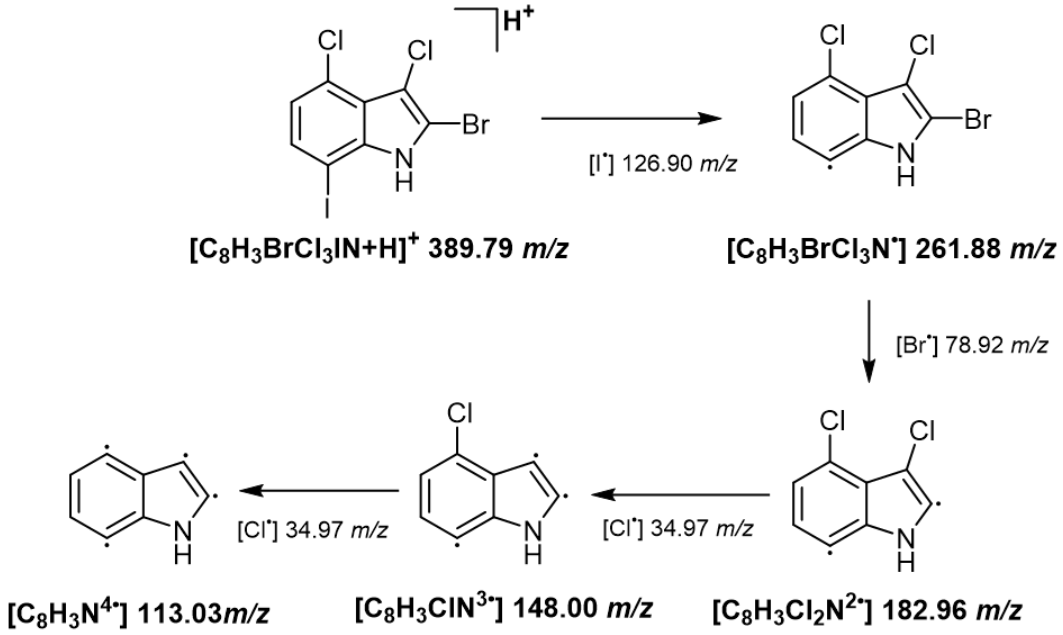
e. Senyawa **5**



f. Senyawa **6**



g. Senyawa **7**


H+
Cl
Cl
Br
N
H
I
[I•] 126.90 m/z
[Br•] 78.92 m/z
[Cl•] 34.97 m/z
[Cl•] 34.97 m/z
[C8H3BrCl3IN+H]+ 389.79 m/z
[C8H3BrCl3N•] 261.88 m/z
[C8H3Cl2N2•] 182.96 m/z
[C8H3ClN3•] 148.00 m/z
[C8H3N4•] 113.03m/z