

LAMPIRAN

Lampiran 1. Interpretasi hasil SPSS

Case Processing Summary

Kelompok Perlakuan	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
VolumeUdem KontrolNegatif	13	100.0%	0	.0%	13	100.0%
Pembanding	13	100.0%	0	.0%	13	100.0%
Perlakuan5mg	13	100.0%	0	.0%	13	100.0%
Perlakuan10mg	13	100.0%	0	.0%	13	100.0%
Perlakuan15mg	13	100.0%	0	.0%	13	100.0%

Descriptives

Kelompok Perlakuan	Statistic	Std. Error
VolumeUdem KontrolNegatif Mean	.19015	.006546
95% Confidence Interval for Mean	Lower Bound Upper Bound	.17589 .20442
5% Trimmed Mean	.19250	
Median	.19200	
Variance	.001	
Std. Deviation	.023600	
Minimum	.122	
Maximum	.216	
Range	.094	
Interquartile Range	.022	

	Skewness		-2.153	.616
	Kurtosis		5.988	1.191
Pembanding	Mean		.07738	.005985
	95% Confidence Interval for Mean	Lower Bound	.06435	
		Upper Bound	.09042	
	5% Trimmed Mean		.07832	
	Median		.08400	
	Variance		.000	
	Std. Deviation		.021578	
	Minimum		.034	
	Maximum		.104	
	Range		.070	
	Interquartile Range		.036	
	Skewness		-.615	.616
	Kurtosis		-.516	1.191
	Perlakuan5mg	Mean		.12092
95% Confidence Interval for Mean		Lower Bound	.10206	
		Upper Bound	.13979	
5% Trimmed Mean			.12214	
Median			.12400	
Variance			.001	
Std. Deviation			.031216	
Minimum			.052	
Maximum			.168	
Range			.116	

	Interquartile Range		.040	
	Skewness		-.691	.616
	Kurtosis		.627	1.191
Perlakuan10mg	Mean		.11277	.009763
	95% Confidence	Lower Bound	.09150	
	Interval for Mean	Upper Bound	.13404	
	5% Trimmed Mean		.11374	
	Median		.11600	
	Variance		.001	
	Std. Deviation		.035200	
	Minimum		.042	
	Maximum		.166	
	Range		.124	
	Interquartile Range		.049	
	Skewness		-.342	.616
	Kurtosis		-.082	1.191
Perlakuan15mg	Mean		.09308	.007070
	95% Confidence	Lower Bound	.07767	
	Interval for Mean	Upper Bound	.10848	
	5% Trimmed Mean		.09486	
	Median		.09800	
	Variance		.001	
	Std. Deviation		.025490	
	Minimum		.030	
	Maximum		.124	

Range	.094	
Interquartile Range	.035	
Skewness	-1.210	.616
Kurtosis	1.978	1.191

Lampiran 2. Uji Kenormalan Distribusi Data

Tests of Normality

Kelompok Perlakuan	Kolmogorov-Smirnov ^a			Shapiro-Wilk		
	Statistic	df	Sig.	Statistic	df	Sig.
VolumeUdem KontrolNegatif	.211	13	.117	.787	13	.005
Pembanding	.159	13	.200*	.935	13	.395
Perlakuan5mg	.129	13	.200*	.966	13	.843
Perlakuan10mg	.075	13	.200*	.981	13	.986
Perlakuan15mg	.150	13	.200*	.910	13	.182

a. Lilliefors Significance Correction

*. This is a lower bound of the true significance.

Dari hasil uji diatas terlihat signifikansi sebesar $> 0,05$ pada Kolmogorov-Smirnov, yang berarti bahwa data tersebut tidak signifikan perbedaannya sehingga terdistribusi normal.

Lampiran 3. Uji homogenitas varian

Test of Homogeneity of Variance

	Levene Statistic	df1	df2	Sig.
VolumeUdem Based on Mean	1.062	4	60	.383
Based on Median	.969	4	60	.431
Based on Median and with adjusted df	.969	4	55.547	.432
Based on trimmed mean	1.052	4	60	.388

Hasil uji data volume udem memperlihatkan data tersebut homogen atau memiliki varian yang sama terlihat dari signifikansi yang $>0,05$.

Lampiran 4. Hasil ANOVA

Descriptives

VolumeUdem

	N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean		Minimum	Maximum
					Lower Bound	Upper Bound		
					KontrolNegatif	13		
Pembanding	13	.07738	.021578	.005985	.06435	.09042	.034	.104
Perlakuan5mg	13	.12092	.031216	.008658	.10206	.13979	.052	.168
Perlakuan10mg	13	.11277	.035200	.009763	.09150	.13404	.042	.166
Perlakuan15mg	13	.09308	.025490	.007070	.07767	.10848	.030	.124
Total	65	.11886	.047475	.005889	.10710	.13063	.030	.216

Test of Homogeneity of Variances

VolumeUdem

Levene	Statistic	df1	df2	Sig.
	1.062	4	60	.383

Hasil uji data volume udem memperlihatkan data tersebut homogen atau memiliki varian yang sama terlihat dari signifikansi yang $>0,05$.

Lampiran 5. Uji hipotesis One-Way ANOVA

ANOVA

VolumeUdem	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	.098	4	.024	31.403	.000
Within Groups	.047	60	.001		
Total	.144	64			

Lampiran 6. POST HOC TESTS

Multiple Comparisons

Dependent Variable: VolumeUdem

	(I) Kelompok Perlakuan	(J) Kelompok Perlakuan	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval			
						Lower Bound	Upper Bound		
Tukey HSD	Negatif	Kontrol	Pembanding	.112769*	.010934	.000	.08202	.14352	
		Perlakuan	5mg	.069231*	.010934	.000	.03848	.09998	
			10mg	.077385*	.010934	.000	.04663	.10814	
			15mg	.097077*	.010934	.000	.06632	.12783	
	Pembanding	Kontrol	Negatif	-.112769*	.010934	.000	-.14352	-.08202	
		Perlakuan	5mg	-.043538*	.010934	.002	-.07429	-.01279	
			10mg	-.035385*	.010934	.016	-.06614	-.00463	
			15mg	-.015692	.010934	.608	-.04644	.01506	
	5 mg	Perlakuan	Kontrol	Negatif	-.069231*	.010934	.000	-.09998	-.03848
			Pembanding	.043538*	.010934	.002	.01279	.07429	
			10mg	.008154	.010934	.945	-.02260	.03891	
			15mg	.027846	.010934	.094	-.00291	.05860	
	10 mg	Perlakuan	Kontrol	Negatif	-.077385*	.010934	.000	-.10814	-.04663
			Pembanding	.035385*	.010934	.016	.00463	.06614	

	Perlakuan5mg	-.008154	.010934	.945	-.03891	.02260
	Perlakuan15mg	.019692	.010934	.383	-.01106	.05044
	Perlakuan15 KontrolNegatif	-.097077*	.010934	.000	-.12783	-.06632
mg	Pembanding	.015692	.010934	.608	-.01506	.04644
	Perlakuan5mg	-.027846	.010934	.094	-.05860	.00291
	Perlakuan10mg	-.019692	.010934	.383	-.05044	.01106

*. The mean difference is significant at the 0.05

level.

Lampiran 7. Uji homogenitas subject

VolumeUdem

Kelompok Perlakuan	N	Subset for alpha = 0.05		
		1	2	3
Tukey HSD ^a Pembanding	13	.07738		
Perlakuan15mg	13	.09308	.09308	
Perlakuan10mg	13		.11277	
Perlakuan5mg	13		.12092	
KontrolNegatif	13			.19015
Sig.		.608	.094	1.000

Means for groups in homogeneous subsets are displayed.

a. Uses Harmonic Mean Sample Size = 13.000.

Lampiran 8. Hasil ANOVA AUC Total

Descriptives

Nilai_AUC_Total

	N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean		Minimum	Maximum
					Lower Bound	Upper Bound		
KontrolNegatif	5	71.4000	10.44844	4.67269	58.4265	84.3735	54.30	82.05
Pembanding	5	29.4300	6.58498	2.94489	21.2537	37.6063	22.50	38.10
Perlakuan5mg	5	45.8700	3.95073	1.76682	40.9645	50.7755	40.95	50.25
Perlakuan10mg	5	42.9000	2.43028	1.08685	39.8824	45.9176	39.00	45.60
Perlakuan15mg	5	35.2800	3.83513	1.71512	30.5181	40.0419	30.75	40.05
Total	25	44.9760	15.74558	3.14912	38.4765	51.4755	22.50	82.05

Test of Homogeneity of Variances

Nilai_AUC_Total

Levene	Statistic	df1	df2	Sig.
	2.199	4	20	.106

Hasil uji data nilai AUC total memperlihatkan data tersebut homogen atau memiliki varian yang sama terlihat dari signifikansi yang $>0,05$.

ANOVA

Nilai_AUC_Total

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	5195.137	4	1298.784	34.404	.000
Within Groups	755.019	20	37.751		
Total	5950.156	24			

Lampiran 9. Post Hoc Tests AUC Total

Multiple Comparisons

Nilai_AUC_Total

Tukey HSD

(I) Kelompok	(J) Kelompok	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
KontrolNegatif	Pembanding	41.97000*	3.88592	.000	30.3419	53.5981
	Perlakuan5mg	25.53000*	3.88592	.000	13.9019	37.1581
	Perlakuan10mg	28.50000*	3.88592	.000	16.8719	40.1281
	Perlakuan15mg	36.12000*	3.88592	.000	24.4919	47.7481
Pembanding	KontrolNegatif	-41.97000*	3.88592	.000	-53.5981	-30.3419
	Perlakuan5mg	-16.44000*	3.88592	.003	-28.0681	-4.8119
	Perlakuan10mg	-13.47000*	3.88592	.018	-25.0981	-1.8419
	Perlakuan15mg	-5.85000	3.88592	.571	-17.4781	5.7781
Perlakuan5mg	KontrolNegatif	-25.53000*	3.88592	.000	-37.1581	-13.9019
	Pembanding	16.44000*	3.88592	.003	4.8119	28.0681
	Perlakuan10mg	2.97000	3.88592	.938	-8.6581	14.5981
	Perlakuan15mg	10.59000	3.88592	.085	-1.0381	22.2181
Perlakuan10mg	KontrolNegatif	-28.50000*	3.88592	.000	-40.1281	-16.8719
	Pembanding	13.47000*	3.88592	.018	1.8419	25.0981
	Perlakuan5mg	-2.97000	3.88592	.938	-14.5981	8.6581
	Perlakuan15mg	7.62000	3.88592	.320	-4.0081	19.2481
Perlakuan15mg	KontrolNegatif	-36.12000*	3.88592	.000	-47.7481	-24.4919
	Pembanding	5.85000	3.88592	.571	-5.7781	17.4781
	Perlakuan5mg	-10.59000	3.88592	.085	-22.2181	1.0381
	Perlakuan10mg	-7.62000	3.88592	.320	-19.2481	4.0081

*. The mean difference is significant at the 0.05 level.

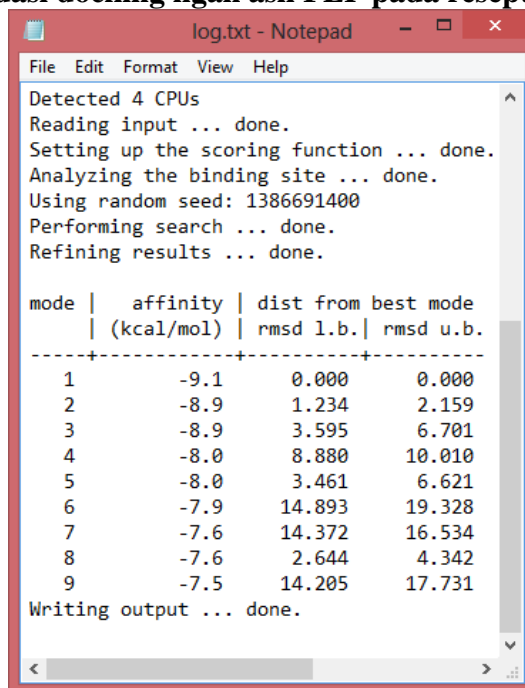
Lampiran 10. Uji homogenitas subject AUC Total

Nilai_AUC_Total

Tukey HSD

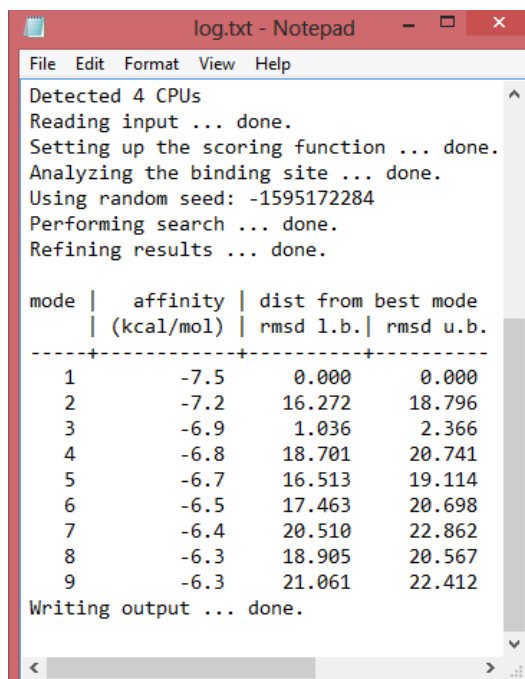
Kelompok	N	Subset for alpha = 0.05		
		1	2	3
Pembanding	5	29.4300		
Perlakuan15mg	5	35.2800	35.2800	
Perlakuan10mg	5		42.9000	
Perlakuan5mg	5		45.8700	
KontrolNegatif	5			71.4000
Sig.		.571	.085	1.000

Means for groups in homogeneous subsets are displayed.

Lampiran 11. Validasi docking ligan asli FLP pada reseptor 3PGH

```
log.txt - Notepad
File Edit Format View Help
Detected 4 CPUs
Reading input ... done.
Setting up the scoring function ... done.
Analyzing the binding site ... done.
Using random seed: 1386691400
Performing search ... done.
Refining results ... done.

mode |  affinity | dist from best mode
      | (kcal/mol) | rmsd l.b. | rmsd u.b.
-----+-----+-----+-----
  1   |    -9.1   |    0.000   |    0.000
  2   |    -8.9   |    1.234   |    2.159
  3   |    -8.9   |    3.595   |    6.701
  4   |    -8.0   |    8.880   |   10.010
  5   |    -8.0   |    3.461   |    6.621
  6   |    -7.9   |   14.893   |   19.328
  7   |    -7.6   |   14.372   |   16.534
  8   |    -7.6   |    2.644   |    4.342
  9   |    -7.5   |   14.205   |   17.731
Writing output ... done.
```

Lampiran 12. Validasi docking senyawa pembanding (Natrium Diklofenak) pada reseptor 3PGH

```
log.txt - Notepad
File Edit Format View Help
Detected 4 CPUs
Reading input ... done.
Setting up the scoring function ... done.
Analyzing the binding site ... done.
Using random seed: -1595172284
Performing search ... done.
Refining results ... done.

mode |  affinity | dist from best mode
      | (kcal/mol) | rmsd l.b. | rmsd u.b.
-----+-----+-----+-----
  1   |    -7.5   |    0.000   |    0.000
  2   |    -7.2   |   16.272   |   18.796
  3   |    -6.9   |    1.036   |    2.366
  4   |    -6.8   |   18.701   |   20.741
  5   |    -6.7   |   16.513   |   19.114
  6   |    -6.5   |   17.463   |   20.698
  7   |    -6.4   |   20.510   |   22.862
  8   |    -6.3   |   18.905   |   20.567
  9   |    -6.3   |   21.061   |   22.412
Writing output ... done.
```

Lampiran 13. Validasi docking senyawa ligand uji *Piperine* pada reseptor 3PGH

```
log.txt - Notepad
File Edit Format View Help
Detected 4 CPUs
Reading input ... done.
Setting up the scoring function ... done.
Analyzing the binding site ... done.
Using random seed: 1807120644
Performing search ... done.
Refining results ... done.

mode |  affinity | dist from best mode
      | (kcal/mol) | rmsd l.b. | rmsd u.b.
-----+-----+-----+-----
  1   |    -9.2   |    0.000   |    0.000
  2   |    -8.7   |    2.574   |    9.268
  3   |    -8.6   |    2.518   |    8.962
  4   |    -8.2   |   18.512   |   25.405
  5   |    -8.0   |   18.807   |   21.450
  6   |    -8.0   |   18.312   |   23.654
  7   |    -8.0   |    1.438   |    2.326
  8   |    -7.9   |   18.238   |   25.061
  9   |    -7.7   |    4.045   |    6.471

Writing output ... done.
```

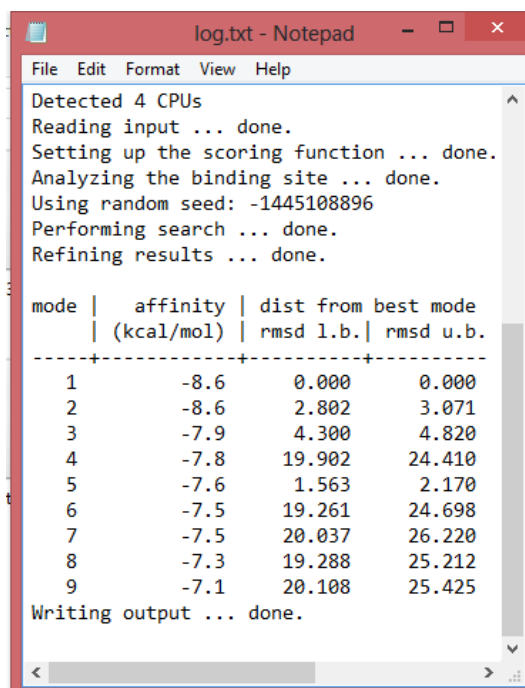
Lampiran 14. Validasi docking senyawa ligand uji *Piperamide* pada reseptor 3PGH

```
log.txt - Notepad
File Edit Format View Help
Detected 4 CPUs
Reading input ... done.
Setting up the scoring function ... done.
Analyzing the binding site ... done.
Using random seed: 428002648
Performing search ... done.
Refining results ... done.

mode |  affinity | dist from best mode
      | (kcal/mol) | rmsd l.b. | rmsd u.b.
-----+-----+-----+-----
  1   |    -7.2   |    0.000   |    0.000
  2   |    -6.6   |   24.227   |   25.905
  3   |    -6.4   |    1.828   |    2.395
  4   |    -6.4   |   27.410   |   29.119
  5   |    -6.2   |   25.187   |   27.428
  6   |    -6.1   |   29.457   |   30.720
  7   |    -6.1   |   28.447   |   30.401
  8   |    -6.0   |    1.929   |    2.770
  9   |    -5.9   |   26.633   |   29.477

Writing output ... done.
```

Lampiran 15. Validasi docking senyawa ligand uji *Pipericide* pada reseptor 3PGH

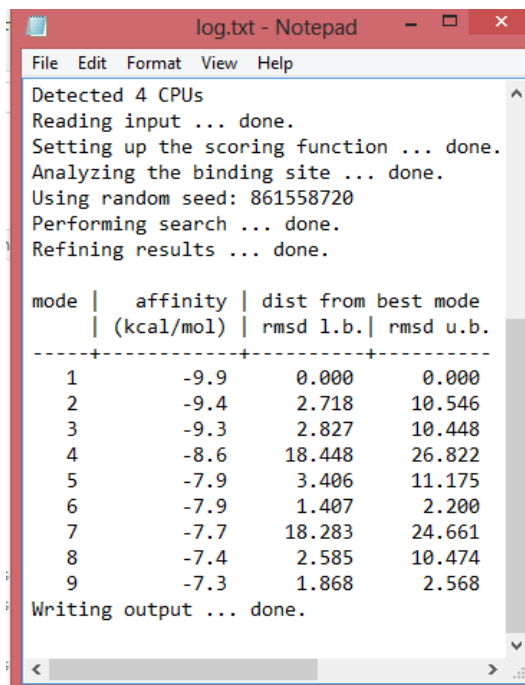


```
log.txt - Notepad
File Edit Format View Help
Detected 4 CPUs
Reading input ... done.
Setting up the scoring function ... done.
Analyzing the binding site ... done.
Using random seed: -1445108896
Performing search ... done.
Refining results ... done.

mode |  affinity | dist from best mode
      | (kcal/mol) | rmsd l.b. | rmsd u.b.
-----+-----+-----+-----
  1   |    -8.6   |    0.000   |    0.000
  2   |    -8.6   |    2.802   |    3.071
  3   |    -7.9   |    4.300   |    4.820
  4   |    -7.8   |   19.902   |   24.410
  5   |    -7.6   |    1.563   |    2.170
  6   |    -7.5   |   19.261   |   24.698
  7   |    -7.5   |   20.037   |   26.220
  8   |    -7.3   |   19.288   |   25.212
  9   |    -7.1   |   20.108   |   25.425

Writing output ... done.
```

Lampiran 16. Validasi docking senyawa ligand uji *Piperettine* pada reseptor 3PGH



```
log.txt - Notepad
File Edit Format View Help
Detected 4 CPUs
Reading input ... done.
Setting up the scoring function ... done.
Analyzing the binding site ... done.
Using random seed: 861558720
Performing search ... done.
Refining results ... done.

mode |  affinity | dist from best mode
      | (kcal/mol) | rmsd l.b. | rmsd u.b.
-----+-----+-----+-----
  1   |   -9.9   |    0.000   |    0.000
  2   |   -9.4   |    2.718   |   10.546
  3   |   -9.3   |    2.827   |   10.448
  4   |   -8.6   |   18.448   |   26.822
  5   |   -7.9   |    3.406   |   11.175
  6   |   -7.9   |    1.407   |    2.200
  7   |   -7.7   |   18.283   |   24.661
  8   |   -7.4   |    2.585   |   10.474
  9   |   -7.3   |    1.868   |    2.568

Writing output ... done.
```

Lampiran 17. Validasi docking senyawa ligand uji *Piperolein B* pada reseptor 3PGH

```

log.txt - Notepad
File Edit Format View Help
Detected 4 CPUs
Reading input ... done.
Setting up the scoring function ... done.
Analyzing the binding site ... done.
Using random seed: -1971323072
Performing search ... done.
Refining results ... done.

mode |  affinity | dist from best mode
      | (kcal/mol) | rmsd l.b. | rmsd u.b.
-----+-----+-----+-----
  1   |    -9.1   |  0.000   |  0.000
  2   |    -8.7   |  3.159   | 10.328
  3   |    -8.7   |  2.834   | 10.971
  4   |    -8.4   |  2.871   | 10.563
  5   |    -7.7   |  2.955   | 11.198
  6   |    -7.6   |  2.059   |  2.891
  7   |    -7.4   | 18.645   | 24.185
  8   |    -7.2   |  3.894   |  6.712
  9   |    -7.2   |  1.462   |  2.618

Writing output ... done.

```

Lampiran 18. Validasi docking senyawa ligand uji *Isopiperolein B* pada reseptor 3PGH

```

log.txt - Notepad
File Edit Format View Help
Detected 4 CPUs
Reading input ... done.
Setting up the scoring function ... done.
Analyzing the binding site ... done.
Using random seed: -1453402624
Performing search ... done.
Refining results ... done.

mode |  affinity | dist from best mode
      | (kcal/mol) | rmsd l.b. | rmsd u.b.
-----+-----+-----+-----
  1   |    -8.4   |  0.000   |  0.000
  2   |    -8.4   |  3.101   | 10.229
  3   |    -8.2   |  1.438   |  2.022
  4   |    -8.1   |  2.958   | 11.214
  5   |    -7.3   | 17.529   | 23.172
  6   |    -7.3   | 17.577   | 22.973
  7   |    -7.2   |  1.130   |  1.987
  8   |    -7.2   | 19.888   | 23.011
  9   |    -7.1   | 17.368   | 22.198

Writing output ... done.

```

Lampiran 19. Validasi docking senyawa ligand uji *Sarmentine* pada reseptor 3PGH

```

log.txt - Notepad
File Edit Format View Help
Detected 4 CPUs
Reading input ... done.
Setting up the scoring function ... done.
Analyzing the binding site ... done.
Using random seed: -882937528
Performing search ... done.
Refining results ... done.

mode |  affinity | dist from best mode
      | (kcal/mol) | rmsd l.b. | rmsd u.b.
-----+-----+-----+-----
  1   |    -7.1   |    0.000   |    0.000
  2   |    -6.7   |    2.121   |    6.796
  3   |    -6.5   |    1.359   |    2.626
  4   |    -6.4   |    3.017   |    7.847
  5   |    -6.3   |    1.932   |    6.235
  6   |    -5.7   |    9.792   |   12.088
  7   |    -5.5   |   16.507   |   19.867
  8   |    -5.3   |   15.022   |   18.497
  9   |    -5.0   |   19.663   |   21.615

Writing output ... done.

```

Lampiran 20. Validasi docking senyawa ligand uji *Tricholein* pada reseptor 3PGH

```

log.txt - Notepad
File Edit Format View Help
Detected 4 CPUs
Reading input ... done.
Setting up the scoring function ... done.
Analyzing the binding site ... done.
Using random seed: -704232128
Performing search ... done.
Refining results ... done.

mode |  affinity | dist from best mode
      | (kcal/mol) | rmsd l.b. | rmsd u.b.
-----+-----+-----+-----
  1   |    -8.5   |    0.000   |    0.000
  2   |    -7.6   |    1.652   |    2.185
  3   |    -7.2   |    8.417   |   12.455
  4   |    -7.2   |    1.576   |    2.217
  5   |    -7.1   |    2.014   |    2.600
  6   |    -6.5   |   13.152   |   15.376
  7   |    -6.4   |   18.940   |   22.502
  8   |    -6.3   |   25.077   |   26.911
  9   |    -6.3   |   13.073   |   15.468

Writing output ... done.

```