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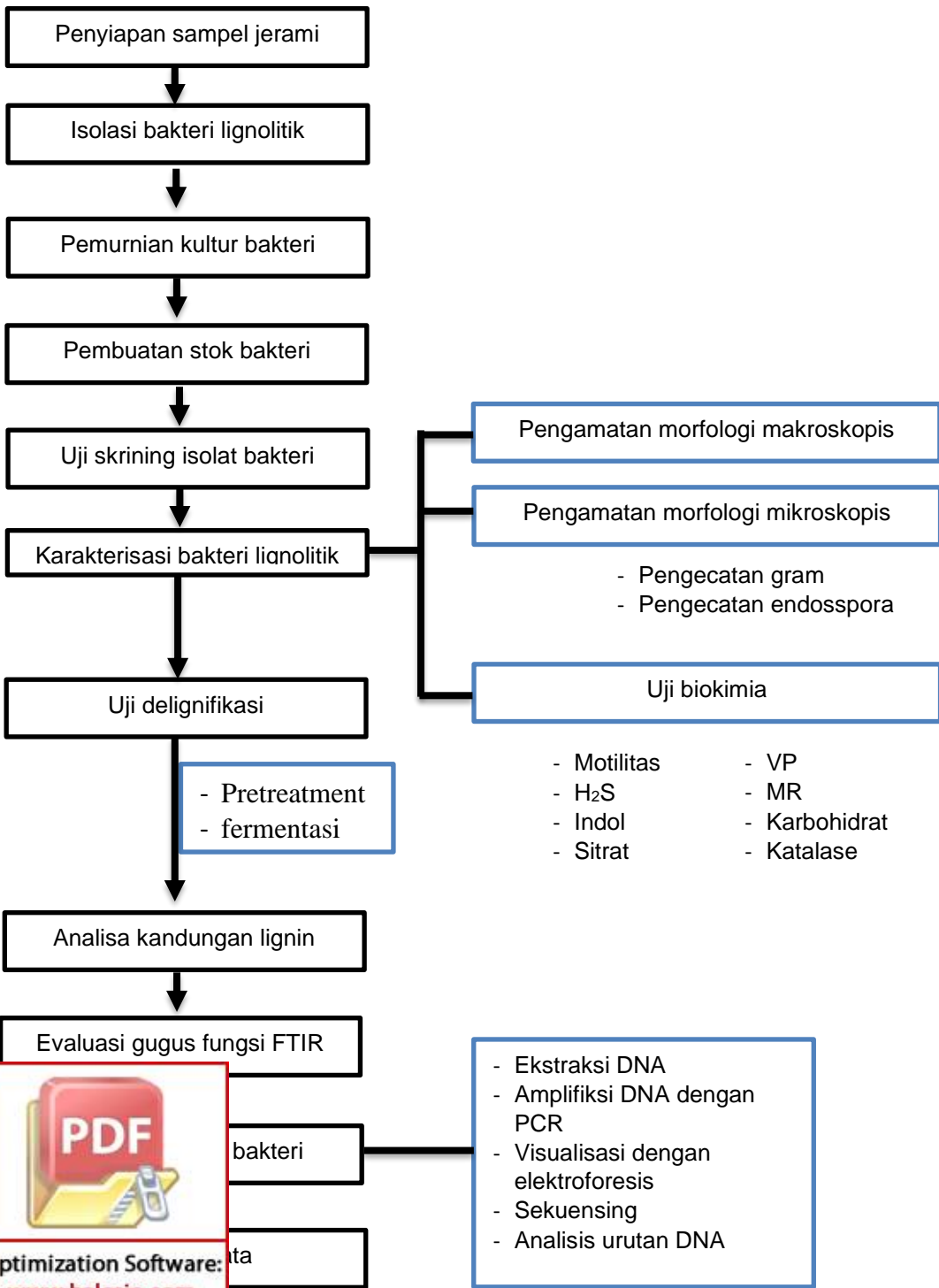


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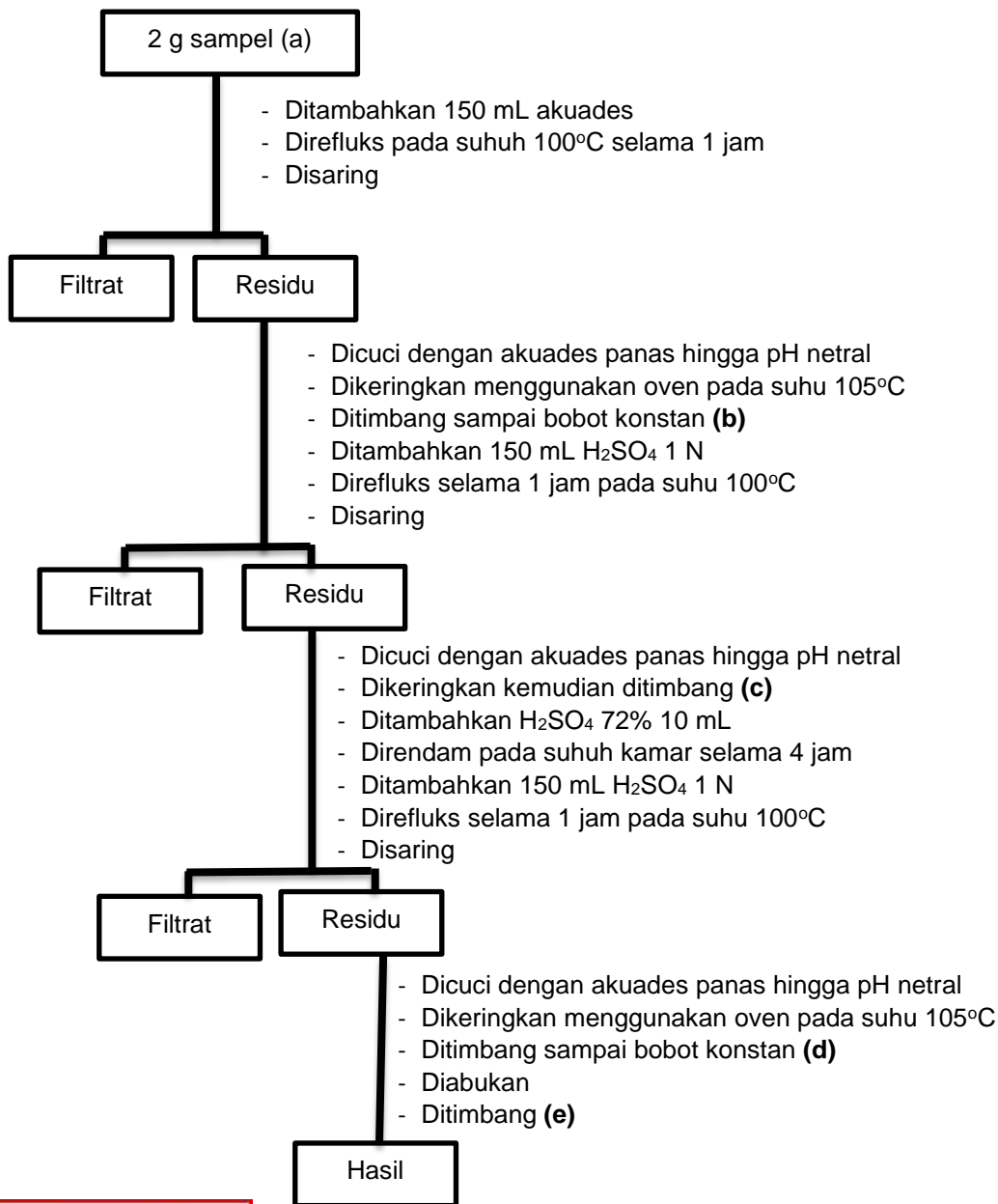


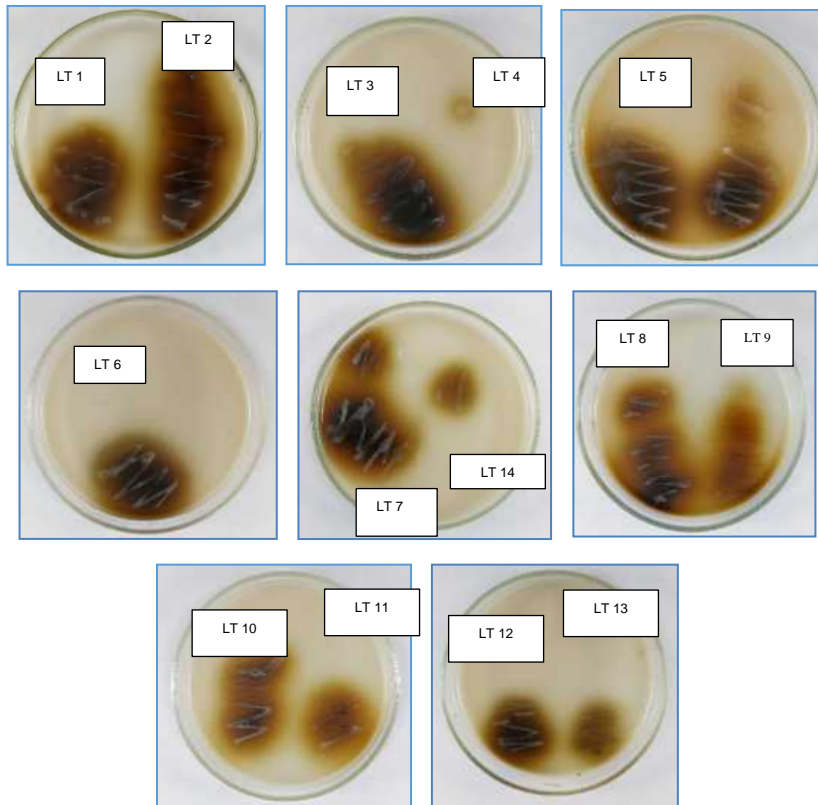
### Lampiran-Lampiran

Lampiran 1. Diagram Alir Penelitian

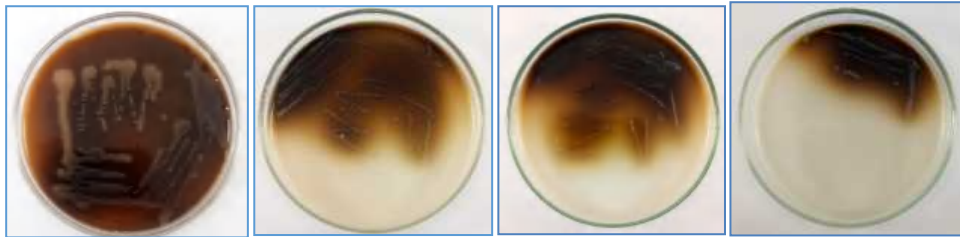


**Lampiran 2.** Proses Analisis Kadar Hemiselulosa, Selulosa, dan Lignin



**Lampiran 3. Proses Isolasi Isolat bakteri Lignolitik**



**Lampiran 4.** Proses pemurnian Isolat bakteri Lignolitik

LT1

LT2

LT3

LT4

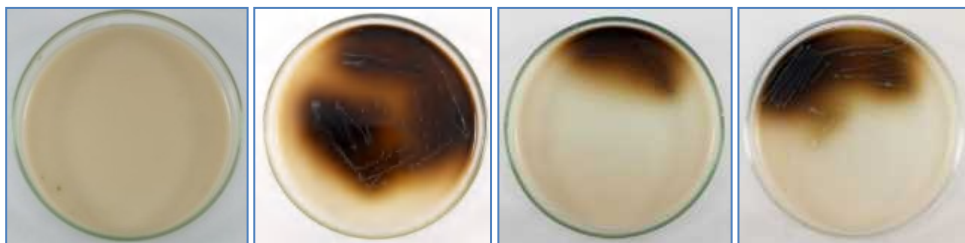


LT5

LT6

LT7

LT8

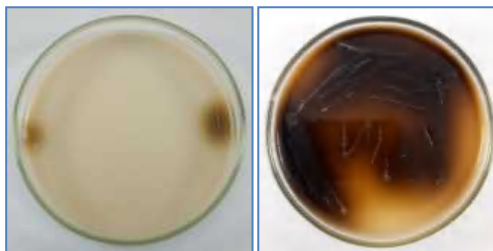


LT9

LT10

LT11

LT12



LT14



## Lampiran 5. Hasil Karakterisasi Bakteri Lignolitik

Kode Isolat	Morfologi Koloni				Morfologi Sel			Uji Biokimia						
	Bentuk	Elevasi	Tepi	Warna	Bentuk	Sifat gram	SIM			Sitrat	MRVP		Gula	Katalase
							motilitas	H <sub>2</sub> S	Indol		MR	VP		
LT 1	Circular	Convex	Entire	Putih susu	Basil pendek	Positif	-	-	-	+	-	+	K/K	+
LT 2	Circular	Raised	Undulate	Putih susu	Basil pendek	Negatif	-	-	-	+	-	+	K/K	+
LT 3	Circular	Convex	Entire	Putih susu	Basil pendek	Negatif	-	-	-	+	-	+	K/K	+
LT 4	Circular	Flat, raised margin	Entire	Putih susu	Basil pendek	Negatif	-	-	-	+	-	+	K/K	+
LT 5	Circular	Umbonate	Entire	Putih susu	Basil pendek	Negatif	-	-	-	+	-	+	K/M	+
LT 6	Circular	Flat, raised margin	Entire	Putih susu	Basil pendek	Negatif	-	-	-	+	-	+	K/K	+
LT 8	Circular	Raised	Entire	Putih susu	Basil pendek	Positif	-	-	-	+	-	+	K/K	+
LT 10	Circular	Convex	Entire	Putih susu	Basil pendek	Negatif	-	-	-	+	-	+	K/K	+
LT 12	Circular	Umbonate	Entire	Putih susu	Basil pendek	Positif	-	-	-	+	-	+	K/M	+
LT 14	Circular	Raised	Entire	Putih susu	Basil pendek	Negatif	-	-	-	+	-	+	K/M	+



Lampiran 6. Sampel Jerami Padi Hasil Fermentasi



LT1



LT12

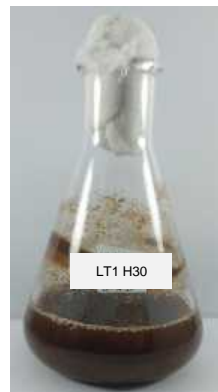


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## Lampiran 7. Fermentasi Jerami Padi Menggunakan Isolat Bakteri Terbaik



Kontrol (Tanpa Penambahan Isolat Bakteri)



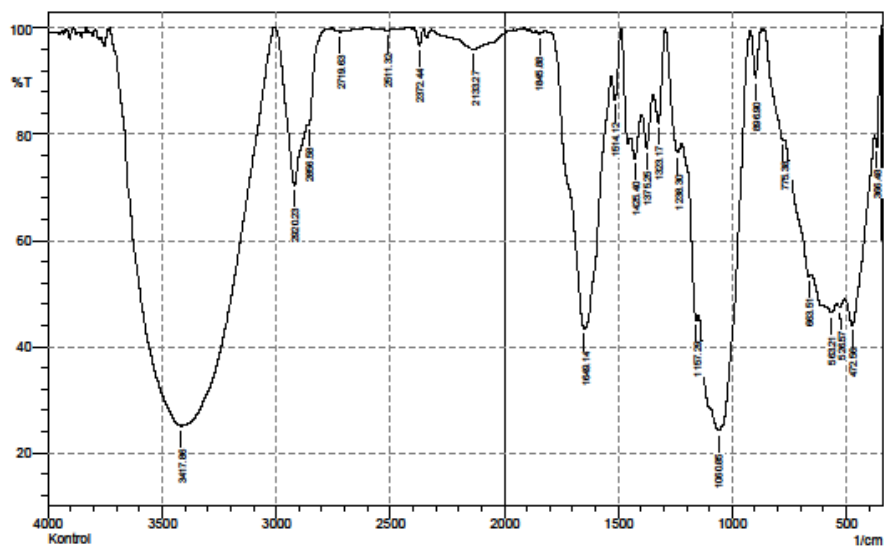
LT1 (Dengan Penambahan Isolat Bakteri)



LT12 (Dengan Penambahan Isolat Bakteri)



## Lampiran 8. Data FTIR Kontrol



No.	Peak	Intensity	Corr. Intanlty	Base (H)	Base (L)	Area	Corr. Area
1	366.48	77.613	7.668	374.19	345.26	1.868	0.6
2	472.56	44.087	12.712	505.35	376.12	32.926	6.789
3	526.57	47.333	1.143	542	507.28	11.086	0.189
4	563.21	46.378	2.662	651.94	543.93	33.949	2.045
5	663.51	53.233	2.34	771.53	653.87	22.465	0.452
6	775.36	78.927	0.469	860.25	773.46	5.074	0.582
7	896.9	90.47	9.172	920.05	871.82	0.963	0.888
8	1060.85	24.165	41.952	1145.72	921.97	88.153	50.25
9	1157.29	44.976	5.218	1219.01	1147.65	15.625	0.838
10	1238.3	76.541	7.009	1292.31	1220.94	5.598	1.692
11	1323.17	82.13	10.722	1346.31	1294.24	2.846	1.344
12	1375.25	77.293	7.975	1396.46	1348.24	4.273	1.002
13	1425.4	75.322	5.785	1444.68	1398.39	4.798	0.695
14	1514.12	86.363	7.866	1529.55	1489.05	1.665	0.835
15	1649.14	43.425	51.103	1793.8	1531.48	46.943	40.903
16	1845.88	99.005	0.343	1863.24	1840.09	0.081	0.021
17	2133.27	96.046	3.561	2322.29	1982.82	3.415	2.841
18	2372.44	96.593	3.39	2397.52	2353.16	0.303	0.3
19	2511.32	99.581	0.36	2565.33	2418.74	0.119	0.092
20	2719.63	99.293	0.593	2758.21	2661.77	0.187	0.129
21	2856.58	81.825	0.461	2858.51	2783.28	2.025	0.03
22	2920.23	70.306	18.779	3008.95	2862.36	12.259	5.919
23	3417.86	25.061	72.57	3707.18	3010.88	236.624	230.483

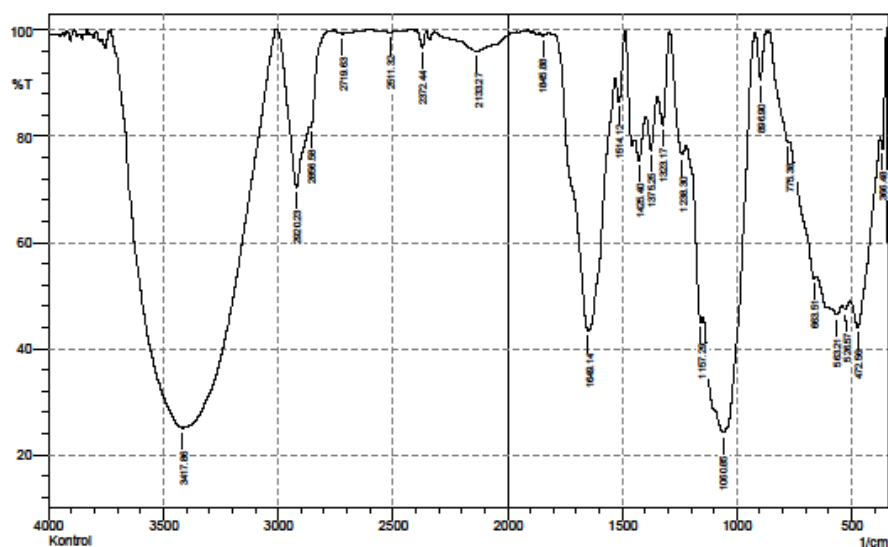


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 No. of Scans;  
 Resolution;  
 Apodization;

LT1 H15

SHIMADZU



No.	Peak	Intensity	Corr. Intensity	Base (H)	Base (L)	Area	Corr. Area
1	366.48	77.613	7.668	374.19	345.26	1.868	0.6
2	472.56	44.087	12.712	505.35	376.12	32.926	6.789
3	526.57	47.333	1.143	542	507.28	11.086	0.189
4	563.21	46.378	2.662	651.94	543.93	33.949	2.045
5	663.51	53.233	2.34	771.53	653.87	22.465	0.452
6	775.38	78.927	0.469	860.25	773.46	5.074	0.582
7	896.9	90.47	9.172	920.05	871.82	0.963	0.888
8	1060.85	24.165	41.952	1145.72	921.97	88.153	50.25
9	1157.29	44.976	5.218	1219.01	1147.65	15.625	0.838
10	1238.3	76.541	7.009	1292.31	1220.94	5.598	1.692
11	1323.17	82.13	10.722	1346.31	1294.24	2.846	1.344
12	1375.25	77.293	7.975	1396.46	1348.24	4.273	1.002
13	1425.4	75.322	5.785	1444.68	1398.39	4.798	0.695
14	1514.12	86.383	7.866	1529.55	1489.05	1.665	0.835
15	1649.14	43.425	51.103	1793.8	1531.48	46.943	40.903
16	1845.88	99.005	0.343	1863.24	1840.09	0.081	0.021
17	2133.27	96.046	3.561	2322.29	1982.82	3.415	2.841
18	2372.44	96.593	3.39	2397.52	2353.16	0.303	0.3
19	2511.32	99.581	0.36	2565.33	2418.74	0.119	0.092
20	2719.63	99.293	0.593	2758.21	2661.77	0.187	0.129
21	2856.58	81.825	0.461	2858.51	2783.28	2.025	0.03
22	2920.23	70.306	18.779	3008.95	2862.36	12.259	5.919
23	3417.86	25.061	72.57	3707.18	3010.88	236.624	230.483



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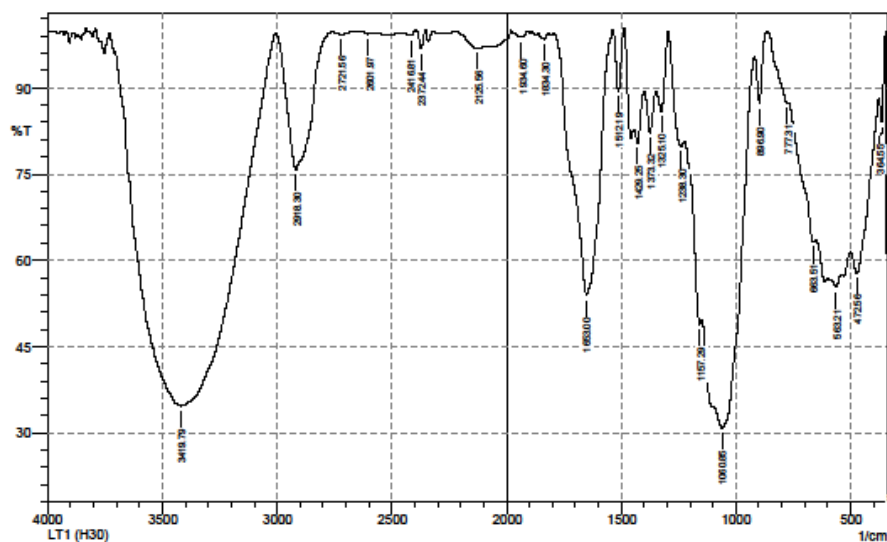
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Resolution;

Apodization;

## LT1 H30

SHIMADZU



No.	Peak	Intensity	Corr. Intensity	Base (H)	Base (L)	Area	Corr. Area
1	341.4	23.056	38.256	343.33	339.47	2.453	0.607
2	364.55	84.036	8.576	376.12	345.26	1.385	0.602
3	472.56	57.805	9.559	499.56	378.05	20.464	4.436
4	563.21	55.317	1.927	599.86	540.07	14.917	0.398
5	663.51	63.196	2.3	771.53	653.87	15.252	0.321
6	777.31	87.362	0.839	862.18	771.53	2.928	0.229
7	896.9	87.191	9.813	918.12	862.18	1.547	0.969
8	1060.85	30.8	15.706	1095.57	920.05	56.38	14.735
9	1157.29	48.856	3.897	1222.87	1149.57	14.325	0.655
10	1238.3	79.713	4.739	1292.31	1224.8	4.725	1.442
11	1325.1	85.891	7.733	1346.31	1294.24	2.236	0.997
12	1373.32	82.149	7.2	1398.39	1348.24	3.331	0.879
13	1429.25	80.331	4.764	1444.68	1400.32	3.381	0.521
14	1512.19	89.406	10.729	1535.34	1489.05	1.11	1.139
15	1653	53.886	45.88	1789.94	1537.27	31.724	31.44
16	1834.3	98.479	0.412	1840.09	1815.02	0.112	0.012
17	1934.6	98.835	0.303	1940.39	1907.6	0.118	0.027
18	2125.56	96.838	1.187	2222	2083.12	1.295	0.38
19	2372.44	96.78	3.28	2391.73	2355.08	0.26	0.27
20	2416.81	99.083	0.812	2455.38	2391.73	0.154	0.108
21	2601.97	99.355	0.315	2661.77	2580.76	0.13	0.034
22	2721.56	99.258	0.493	2758.21	2661.77	0.2	0.103
23	2918.3	75.678	23.884	3007.02	2758.21	13.644	13.201
24	3419.79	34.676	62.832	3705.26	3008.95	186.308	179.597

Comment:



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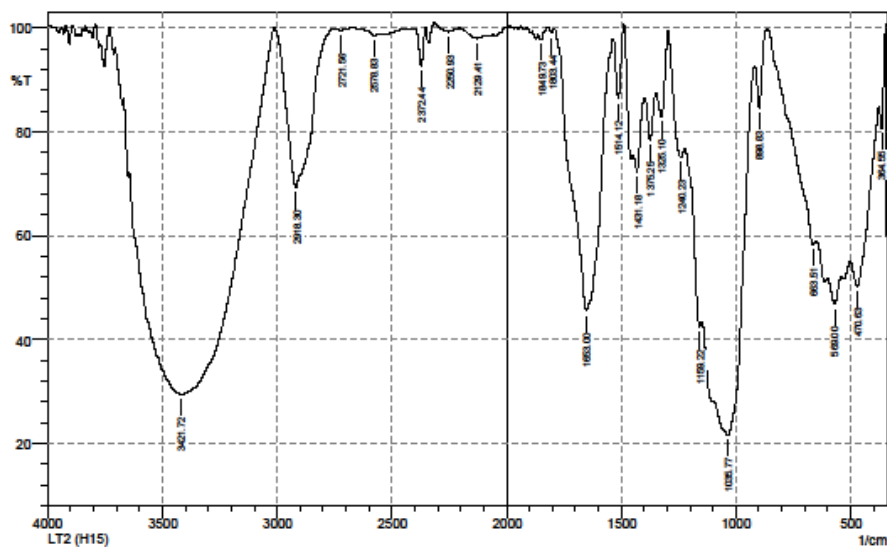
No. of Scans;

Resolution;

Apodization;

## LT12 H15

SHIMADZU



No.	Peak	Intensity	Corr. Intensity	Base (H)	Base (L)	Area	Corr. Area
1	364.55	80.767	9.904	376.12	345.26	1.707	0.716
2	470.63	50.215	12.206	501.49	378.05	26.173	5.87
3	569	46.805	5.209	599.86	540.07	18.319	1.345
4	663.51	58.298	2.99	862.18	651.94	23.119	0.397
5	698.83	84.488	10.524	916.19	864.11	1.892	1.05
6	1035.77	21.617	28.339	1095.57	918.12	77.246	26.45
7	1159.22	42.443	5.409	1220.94	1149.57	16.834	0.851
8	1240.23	75.053	7.249	1294.24	1222.87	6.258	1.976
9	1325.1	82.802	9.937	1348.24	1296.16	2.891	1.356
10	1375.25	78.4	8.436	1396.46	1350.17	3.833	1.009
11	1431.18	72.304	7.003	1448.54	1398.39	5.364	0.82
12	1514.12	86.339	12.772	1535.34	1489.05	1.531	1.388
13	1653	45.524	53.207	1789.94	1537.27	41.556	40.233
14	1803.44	99.002	0.915	1816.94	1789.94	0.064	0.054
15	1849.73	97.777	1.345	1865.17	1822.73	0.25	0.122
16	2129.41	97.959	1.132	2204.64	2083.12	0.716	0.319
17	2250.93	99.216	1.209	2314.58	2204.64	0.095	0.341
18	2372.44	92.646	7.289	2399.45	2353.16	0.685	0.669
19	2578.83	98.404	1.573	2667.55	2414.88	0.781	0.737
20	2721.56	99.51	0.407	2754.35	2667.55	0.094	0.07
21	2918.3	69.345	30.606	3012.81	2754.35	17.996	17.919
22	3421.72	29.399	52.489	3643.53	3014.74	211.608	166.944



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No. of Scans;

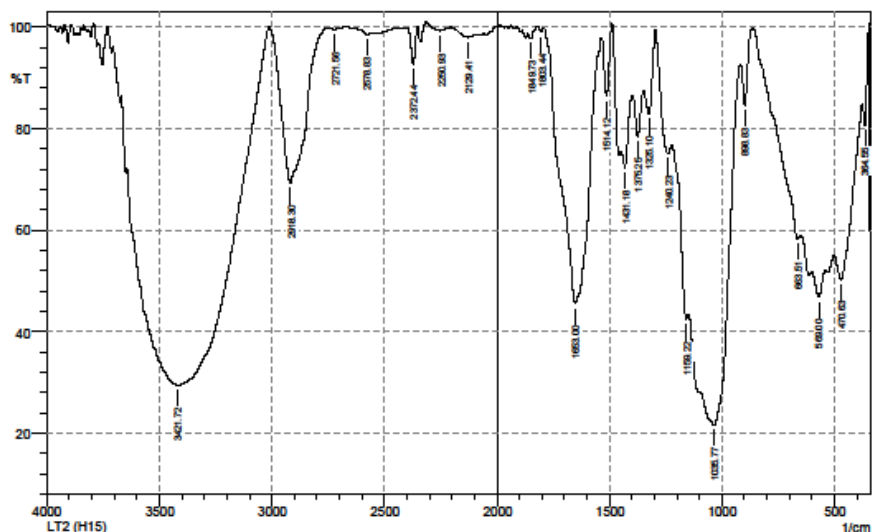
Resolution;

Apodization;



## LT12 H30

SHIMADZU



No.	Peak	Intensity	Corr. Intanalty	Base (H)	Base (L)	Area	Corr. Area
1	364.55	80.767	9.904	376.12	345.26	1.707	0.716
2	470.63	50.215	12.206	501.49	378.05	26.173	5.87
3	569	46.805	5.209	599.86	540.07	18.319	1.345
4	663.51	58.298	2.99	862.18	651.94	23.119	0.397
5	898.83	84.488	10.524	916.19	864.11	1.892	1.05
6	1035.77	21.617	28.339	1095.57	918.12	77.246	26.45
7	1159.22	42.443	5.409	1220.94	1149.57	16.834	0.851
8	1240.23	75.053	7.249	1294.24	1222.87	6.258	1.976
9	1325.1	82.802	9.937	1348.24	1296.16	2.891	1.356
10	1375.25	78.4	8.436	1396.46	1350.17	3.833	1.009
11	1431.18	72.304	7.003	1448.54	1398.39	5.364	0.82
12	1514.12	86.339	12.772	1535.34	1489.05	1.531	1.388
13	1653	45.524	53.207	1789.94	1537.27	41.556	40.233
14	1803.44	99.002	0.915	1816.94	1789.94	0.064	0.054
15	1849.73	97.777	1.345	1865.17	1822.73	0.25	0.122
16	2129.41	97.959	1.132	2204.64	2083.12	0.716	0.319
17	2250.93	99.216	1.209	2314.58	2204.64	0.095	0.341
18	2372.44	92.646	7.289	2399.45	2353.16	0.685	0.669
19	2578.83	98.404	1.573	2667.55	2414.88	0.781	0.737
20	2721.56	99.51	0.407	2754.35	2667.55	0.094	0.07
21	2918.3	69.345	30.606	3012.81	2754.35	17.996	17.919
22	3421.72	29.399	52.489	3643.53	3014.74	211.608	166.944

Comment;

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No. of Scans;

Resolution;

Apodization;



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### Lampiran 9. Data Hasil BLAST LT1

select all 10 sequences selected		GenBank	Graphics	Distance tree of results	MSA View			
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> Klebsiella quasiumoniacae strain BM494-3-1 chromosome, complete genome	<i>Klebsiella quasiumoniacae</i>	2213	17276	94%	0.0	98.95%	5330587	CP064044.1
<input checked="" type="checkbox"/> Klebsiella quasiumoniacae strain KP 18-21 chromosome, complete genome	<i>Klebsiella quasiumoniacae</i>	2207	17566	94%	0.0	98.87%	5157306	CP045941.1
<input checked="" type="checkbox"/> Klebsiella quasiumoniacae strain T3114 chromosome, complete genome	<i>Klebsiella quasiumoniacae</i>	2207	17585	94%	-0.0	98.87%	5109521	CP035207.1
<input checked="" type="checkbox"/> Klebsiella sp. strain PI-22_16S ribosomal RNA gene, partial sequence	<i>Klebsiella</i> sp.	2207	2207	94%	-0.0	98.87%	1423	M6365124.1
<input checked="" type="checkbox"/> Klebsiella quasiumoniacae strain NCTC9170 genome assembly, chromosome_1	<i>Klebsiella quasiumoniacae</i>	2207	17580	94%	0.0	98.87%	5142131	LR558411.1
<input checked="" type="checkbox"/> Klebsiella quasiumoniacae strain NCTC11567 genome assembly, chromosome_1	<i>Klebsiella quasiumoniacae</i>	2207	17486	94%	0.0	98.87%	5124551	LR134195.1
<input checked="" type="checkbox"/> Klebsiella quasiumoniacae strain G4594 chromosome, complete genome	<i>Klebsiella quasiumoniacae</i>	2207	17662	94%	-0.0	98.87%	5446080	CP034129.1
<input checked="" type="checkbox"/> Klebsiella quasiumoniacae strain L122 chromosome, complete genome	<i>Klebsiella quasiumoniacae</i>	2207	17507	94%	0.0	98.87%	5133312	CP004257.1
<input checked="" type="checkbox"/> Uncultured <i>Klebsiella</i> sp. clone GD4615 16S ribosomal RNA gene, partial sequence	Uncultured <i>Klebsiella</i> sp.	2207	2207	94%	0.0	98.87%	1441	M6767067.1
<input checked="" type="checkbox"/> <i>Klebsiella</i> sp. LY chromosome, complete genome	<i>Klebsiella</i> sp. LY	2207	17529	94%	0.0	98.87%	5158003	CP022444.1

### LT12

select all 10 sequences selected		GenBank	Graphics	Distance tree of results	MSA View			
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> <i>Bacillus subtilis</i> strain GQYP101 chromosome, complete genome	<i>Bacillus subtilis</i>	2189	17448	97%	0.0	97.02%	3869448	CP080516.1
<input checked="" type="checkbox"/> <i>Bacillus</i> sp. VITPGPR24 16S ribosomal RNA gene, partial sequence	<i>Bacillus</i> sp. VITPGPR24	2189	2189	97%	0.0	97.16%	1457	HM467445.1
<input checked="" type="checkbox"/> <i>Bacillus subtilis</i> strain 41KF26T26 16S ribosomal RNA gene, partial sequence	<i>Bacillus subtilis</i>	2187	2187	97%	0.0	97.02%	1395	MN543872.1
<input checked="" type="checkbox"/> <i>Bacillus subtilis</i> strain 41KF26T25 16S ribosomal RNA gene, partial sequence	<i>Bacillus subtilis</i>	2187	2187	97%	0.0	97.02%	1414	MN543856.1
<input checked="" type="checkbox"/> <i>Bacillus subtilis</i> strain 41KF26T24 16S ribosomal RNA gene, partial sequence	<i>Bacillus subtilis</i>	2187	2187	97%	0.0	97.02%	1407	MN543855.1
<input checked="" type="checkbox"/> <i>Bacillus subtilis</i> strain 41KF26T20 16S ribosomal RNA gene, partial sequence	<i>Bacillus subtilis</i>	2187	2187	97%	0.0	97.02%	1411	MN543826.1
<input checked="" type="checkbox"/> <i>Bacillus subtilis</i> strain 41KF26T18 16S ribosomal RNA gene, partial sequence	<i>Bacillus subtilis</i>	2187	2187	97%	0.0	97.02%	1400	MN543826.1
<input checked="" type="checkbox"/> <i>Bacillus subtilis</i> strain 41KF26T17 16S ribosomal RNA gene, partial sequence	<i>Bacillus subtilis</i>	2187	2187	97%	0.0	97.02%	1410	MN543826.1
<input checked="" type="checkbox"/> <i>Bacillus subtilis</i> strain 41KF26T16 16S ribosomal RNA gene, partial sequence	<i>Bacillus subtilis</i>	2187	2187	97%	0.0	97.02%	1416	MN543821.1
<input checked="" type="checkbox"/> <i>Bacillus subtilis</i> strain 41KF26T11 16S ribosomal RNA gene, partial sequence	<i>Bacillus subtilis</i>	2187	2187	97%	0.0	97.02%	1407	MN543800.1

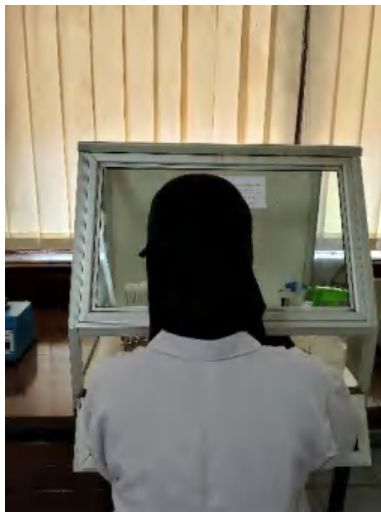


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## Lampiran 10. Dokumentasi-dokumentasi



Lokasi Pengambilan Sampel



a



b

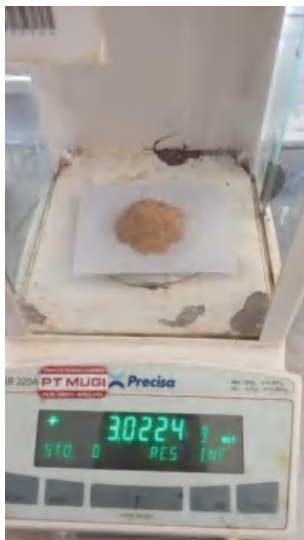
Proses Isolasi isolat bakteri lignolitik dari jerami padi (a) dan Proses Karakterisasi bakteri lignolitik teridentifikasi (b)



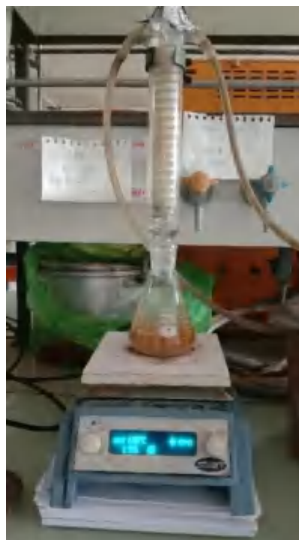
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Proses ekstraksi DNA isolat bakteri lignolitik terbaik



a



b



c

Proses pengujian kandungan lignin, selulosa dan hemiselulosa. Penimbangan padi (a), Proses refluks (b), dan Proses penyaringan



Optimization Software:  
[www.balesio.com](http://www.balesio.com)