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APPENDICES

Appendix A: Preparation for native agarose gel and denature gel

1. Native agarose gel

1) 1x TBE buffer

Tris-HCl (0.05 M)	6.05 g
Boric acid (0.05 M)	3.1 g
EDTA (0.65 mM)	0.19 g

Adjusted volume to be 1,000 ml.

2) 1.2% agarose gel

Agarose	0.3 g
1x TBE buffer	25 ml

Heat until agarose dissolve completely and pour on electrophoresis tray.

2. Denature gel

1) 1x MOPS buffer

MOPS (0.4 M)	8.35 g
Sodium acetate (0.1 M)	1.35 g
EDTA (0.01 M)	0.35 g

Adjusted volume to be 1,000 ml.

2) Formaldehyde agarose gel

Agarose	0.2 g
1x MOPS	20 ml
Formaldehyde	1.2 ml

Cover the gel with 300 ml 1x MOPS.

Appendix B: Preparation of solutions

1. Bradford stock solution

95% Ethanol	100 ml
85% Phosphoric acid	200 ml
Serva Blue G	350 mg

Stable indefinity at room temperature.

2. Bradford working buffer

95% Ethanol	15 ml
85% Phosphoric acid	30 ml
Bradford stock solution	30 ml

Adjusted volume to be 500 ml by d - H₂O.

3. Briton-Robinson buffer

1 M Acetic acid (10 mM)	1 ml
1 M Phoshoric acid (10 mM)	1 ml
0.1 M Boric acid (10 mM)	10 ml

Adjusted pH to be 3.0-7.5 by 0.2 M NaOH and adjusted volume to be 100 ml by dd - H₂O.

Appendix C: Preparation for polyacrylamide gel electrophoresis

1. Stock reagents

1) 30% Acrylamide and 0.8% bis-acrylamide

Acrylamide	29.2 g
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N,N'- methylene-bis-acrylamide	0.8 g
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Adjusted volume to be 100 ml by d - H₂O.

2) 1.5 M Tris - HCl, pH 8.8

Tris (hydroxymethyl) - aminometane	18.17 g
------------------------------------	---------

Adjusted pH to be 8.8 by 1 M HCl and adjusted volume to be 100 ml by d - H₂O.

3) 0.5 M Tris - HCl, pH 6.8

Tris (hydroxymethyl) - aminometane	6.06 g
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Adjusted pH to be 6.8 by 1 M HCl and adjusted volume to be 100 ml by d - H₂O.

4) 1 M Tris - HCl, pH 6.8

Tris (hydroxymethyl) - aminometane	12.1 g
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Adjusted pH to be 6.8 by 1 M HCl and adjusted volume to be 100 ml by d - H₂O.

2. SDS-PAGE

1) 12% Separating gel

30% Acrylamide solution (12%)	6 ml
1 M Tris - HCl, pH 8.8 (0.375 M)	5.6 ml
10% (w/v) SDS	150 µl
dd - H ₂ O	3.16 ml
10% (NH ₄) ₂ S ₂ O ₈ (0.05%)	75 µl
TEMED (0.05%)	7.5 µl

2) 4% Stracking gel

30% Acrylamide solution (4%)	0.80 ml
0.5 M Tris - HCl, pH 6.8 (0.125 M)	0.75 ml
10% (w/v) SDS	60 µl
dd-H ₂ O	4.3 ml
10% (NH ₄) ₂ S ₂ O ₈ (0.05%)	30 µl
TEMED (0.1%)	6 µl

3) Sample buffer (5x loading dye)

1 M Tris - HCL, pH 6.8 (0.312 M)	0.6 ml
Glycerol (50% v/v)	5 ml
10% (w/v) SDS	2 ml
2 - Mercaptoethanol	0.5 ml
1% Bromophenol blue	0.5 g
dd - H ₂ O	0.9 ml

4) Electrophoresis buffer (25 mM Tris and 192 mM glycine)

Tris (hydroxymethyl) - aminometane	3 g
Glycine	14.4 g
SDS	1.2 g

Adjusted volume to be 1,000 ml by d - H₂O.

5) Coomassie Brilliant Blue solution

50% (v/ v) methanol	125 ml
10% (v/ v) acetic acid	25 ml
Coomassie Brilliant Blue R – 250	312.5 mg

Adjusted volume to be 250 ml by d - H₂O.

6) Destained solution

10 % (v/ v) methanol	100 ml
10 % (v/ v) acetic acid	100 ml

Adjusted volume to be 1,000 ml by d - H₂O.

Appendix D: Staining 2 - D electrophoresis gel**1) Fixation solution**

10% (v/v) acetic acid 10 ml

40% (v/v) methanol 40 ml

Adjusted volume to be 100 ml by dd - H₂O.

2) Coomassie blue solution

Dissolve Coomassie blue G - 250 100 mg in dd - H₂O 2 ml.

3) Dye stock solution

Ammonium sulfate 10 g

85% Phosphoric acid (conc.) 1.2 ml

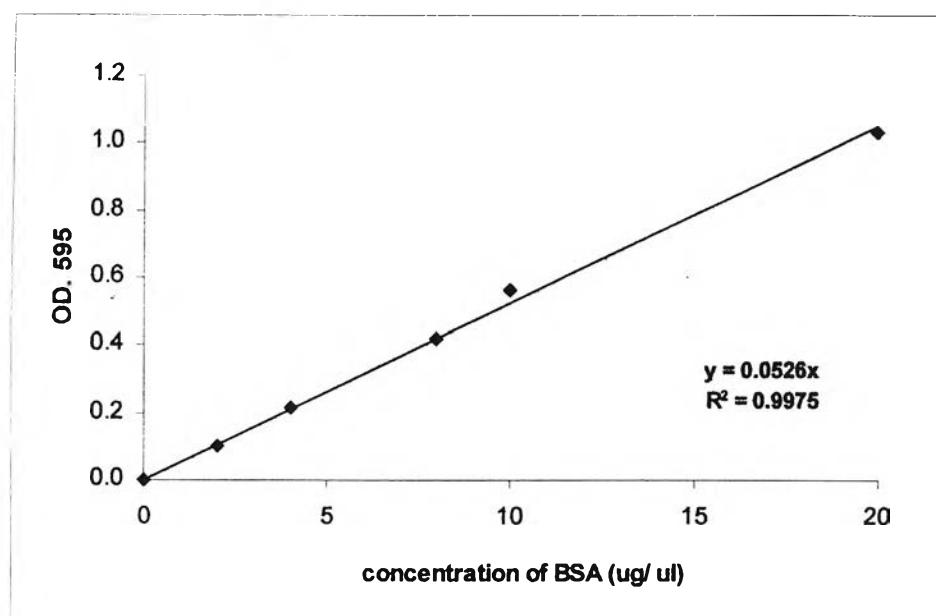
Coomassie blue solution 2 ml

Appendix E: Ammonium sulfate precipitation table

Grams of ammonium sulfate to add to a 100 ml solution at 0°C

Initial concentration of ammonium sulfate (% saturation at 0°C)	Final concentration of ammonium sulfate (% saturation at 0°C)																
	20	25	30	35	40	45	50	55	60	65	70	75	80	85	90	95	100
solid ammonium sulfate to add to 100 ml of solution																	
0	10.6	13.4	16.4	19.4	22.6	25.8	29.1	32.6	36.1	39.8	43.6	47.6	51.6	55.9	60.3	65.0	69.7
5	7.9	10.8	13.7	16.6	19.7	22.9	26.2	29.6	33.1	36.8	40.5	44.4	48.4	52.6	57.0	61.5	66.2
10	5.3	8.1	10.9	13.9	16.9	20.0	23.3	26.6	30.1	33.7	37.4	41.2	45.2	49.3	53.6	58.1	62.7
15	2.6	5.4	8.2	11.1	14.1	17.2	20.4	23.7	27.1	30.6	34.3	38.1	42.0	46.0	50.3	54.7	59.2
20	0	2.7	5.5	8.3	11.3	14.3	17.5	20.7	24.1	27.6	31.2	34.9	38.7	42.7	46.9	51.2	55.7
25	0	2.7	5.6	8.4	11.5	14.6	17.9	21.1	24.5	28.0	31.7	35.5	39.5	43.6	47.8	52.2	
30	0	2.8	5.6	8.6	11.7	14.8	18.1	21.4	24.9	28.5	32.3	36.2	40.2	44.5	48.8		
35	0	2.8	5.7	8.7	11.8	15.1	18.4	21.8	25.4	29.1	32.9	36.9	41.0	45.3			
40	0	2.9	5.8	8.9	12.0	15.3	18.7	22.2	25.8	29.6	33.5	37.6	41.8				
45	0	2.9	5.9	9.0	12.3	15.6	19.0	22.6	26.3	30.2	34.2	38.3					
50	0	3.0	6.0	9.2	12.5	15.9	19.4	23.0	26.8	30.8	34.8						
55	0	3.0	6.1	9.3	12.7	16.1	19.7	23.5	27.3	31.3							
60	0	3.1	6.2	9.5	12.9	16.4	20.1	23.9	27.9								
65	0	3.1	6.3	9.7	13.2	16.8	20.5	24.4									
70	0	3.2	6.5	9.9	13.4	17.1	20.9										
75	0	3.2	6.6	10.1	13.7	17.4											
80	0	3.3	6.7	10.3	13.9												
85	0	3.4	6.8	10.5													
90	0	3.4	7.0														
95	0	3.5															
100	0	0															

Note: The pH of the solution may decrease significantly on addition of ammonium sulfate.

Appendix F: Standard curve for protein determination by Bradford's method

Appendix G: The DNA sequencing profiles of AG

A: The DNA sequencing profile of FW1/ R1 primers (FW1)

B: The DNA sequencing profile of FW1/ R1 primers (R1)

C: The DNA sequencing profile of FW1/ R2 primers (FW1)

D: The DNA sequencing profile of FW1/ R2 primers (R2)

E: The DNA sequencing profile of FW2/ R3 primers (FW2)

F: The DNA sequencing profile of FW2/ R3 primers (R3)

G: The DNA sequencing profile of FW3/ R3 primers (FW3)

H: The DNA sequencing profile of FW3/ R3 primers (R3)



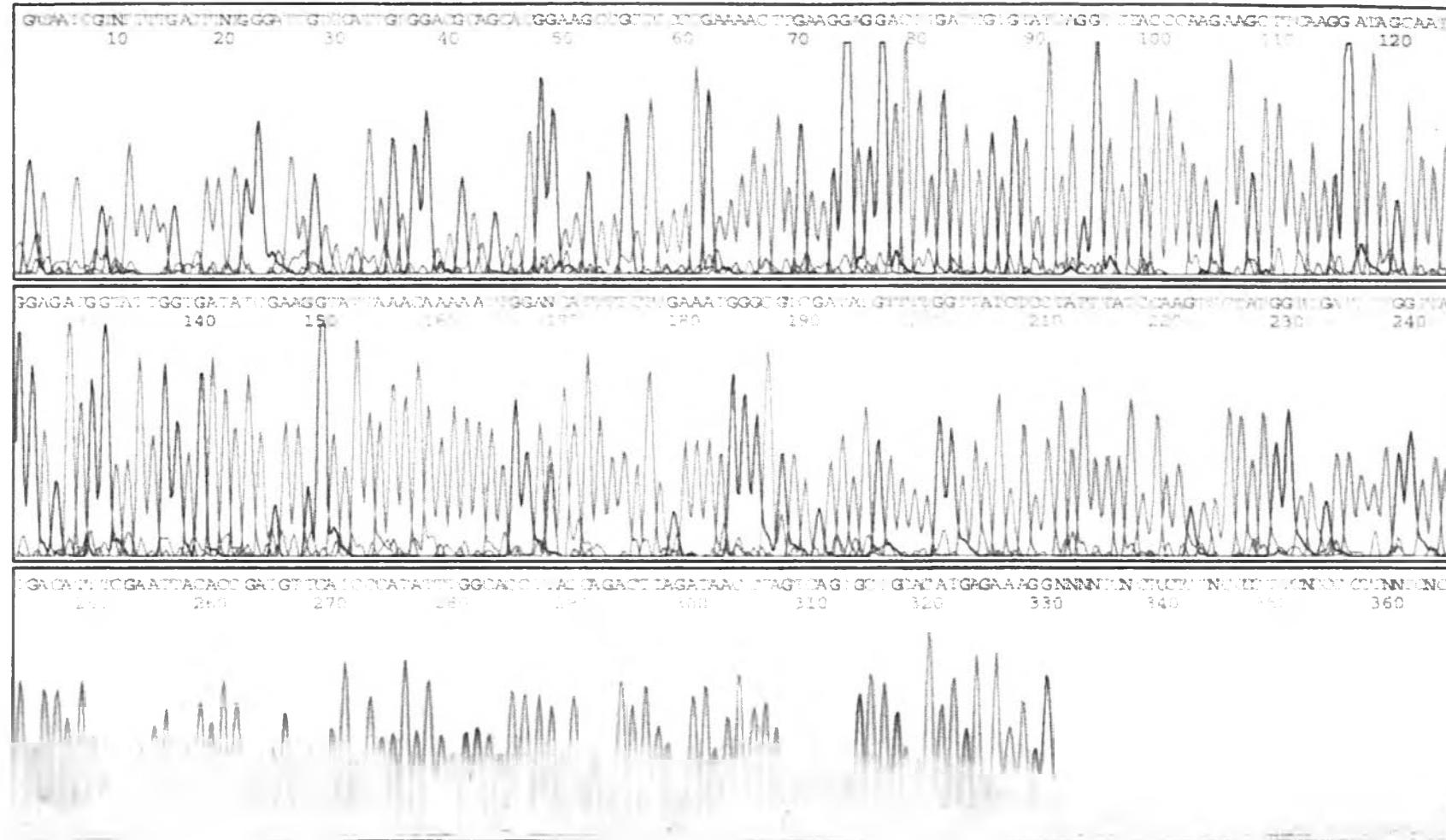
**ABI
PRISM**

Model 377
Version 3.4
ABII100
Version 3.2

α -glucosidase⁺ w α -glucosidase⁺
 α -glucosidase⁺ w α -glucosidase⁺
Lane 16

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BD Matrix Std.Jan31.01
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Page 1 of 3
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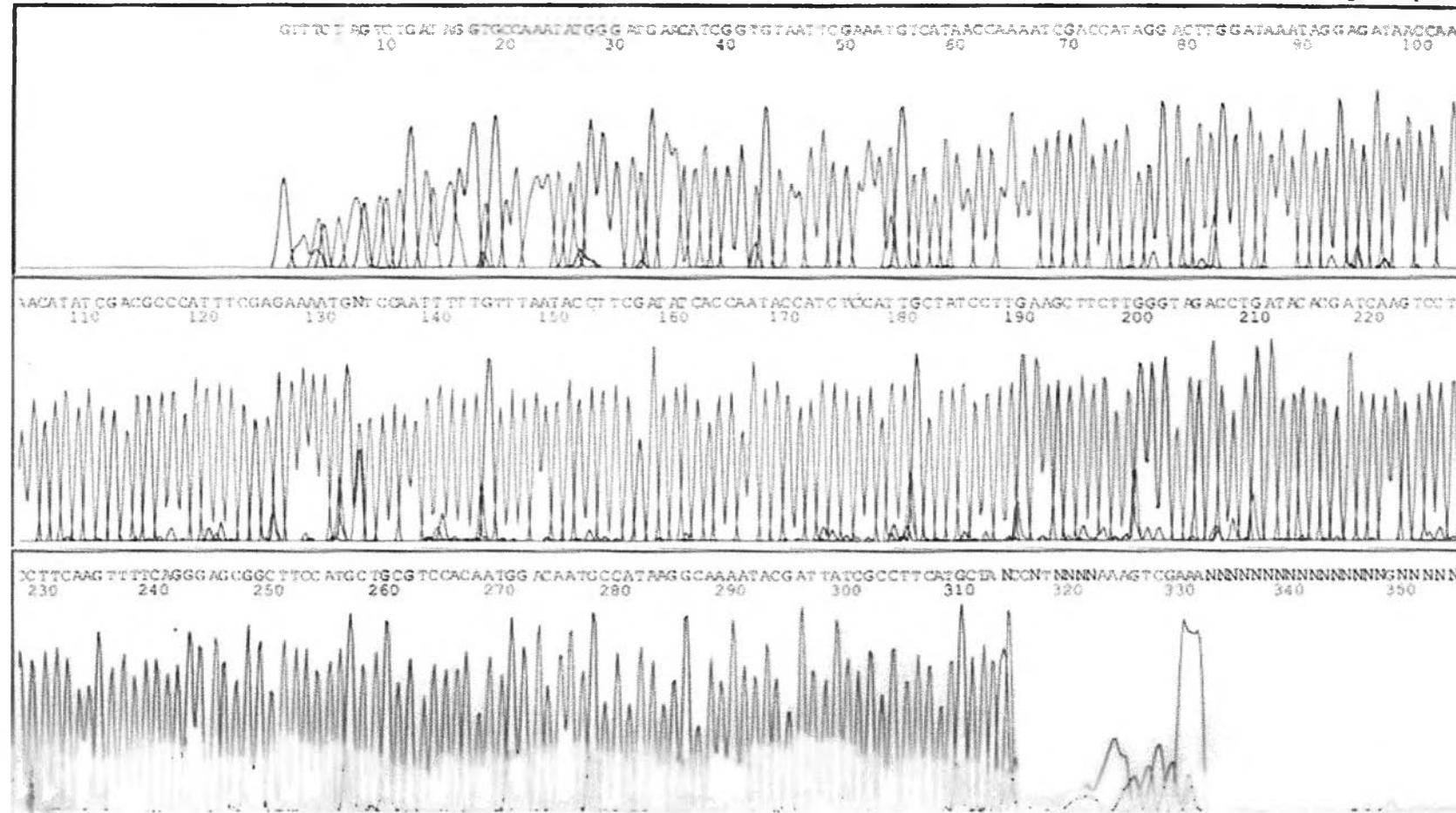
ABI
PRISM

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SFBankkok(Bk1)_ α -glucosidase(RW)
Cap 1

Signal G 3628 A 4618 T 4024 C 3195
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demo_3100
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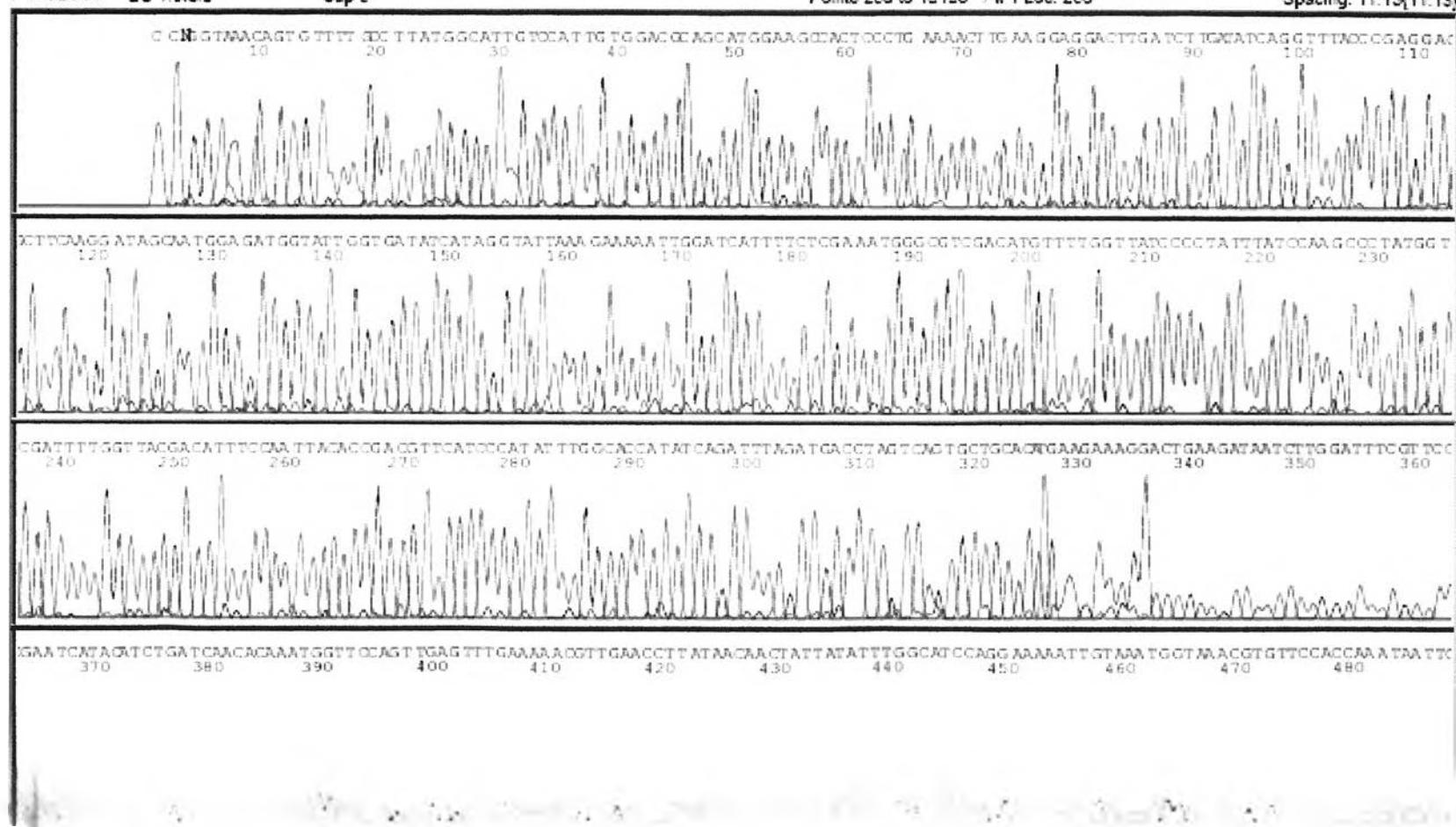


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Version 3.7
Basecaller-3100APOPES3-G(A,T,C,T)_fw
SC 1.5.0.0

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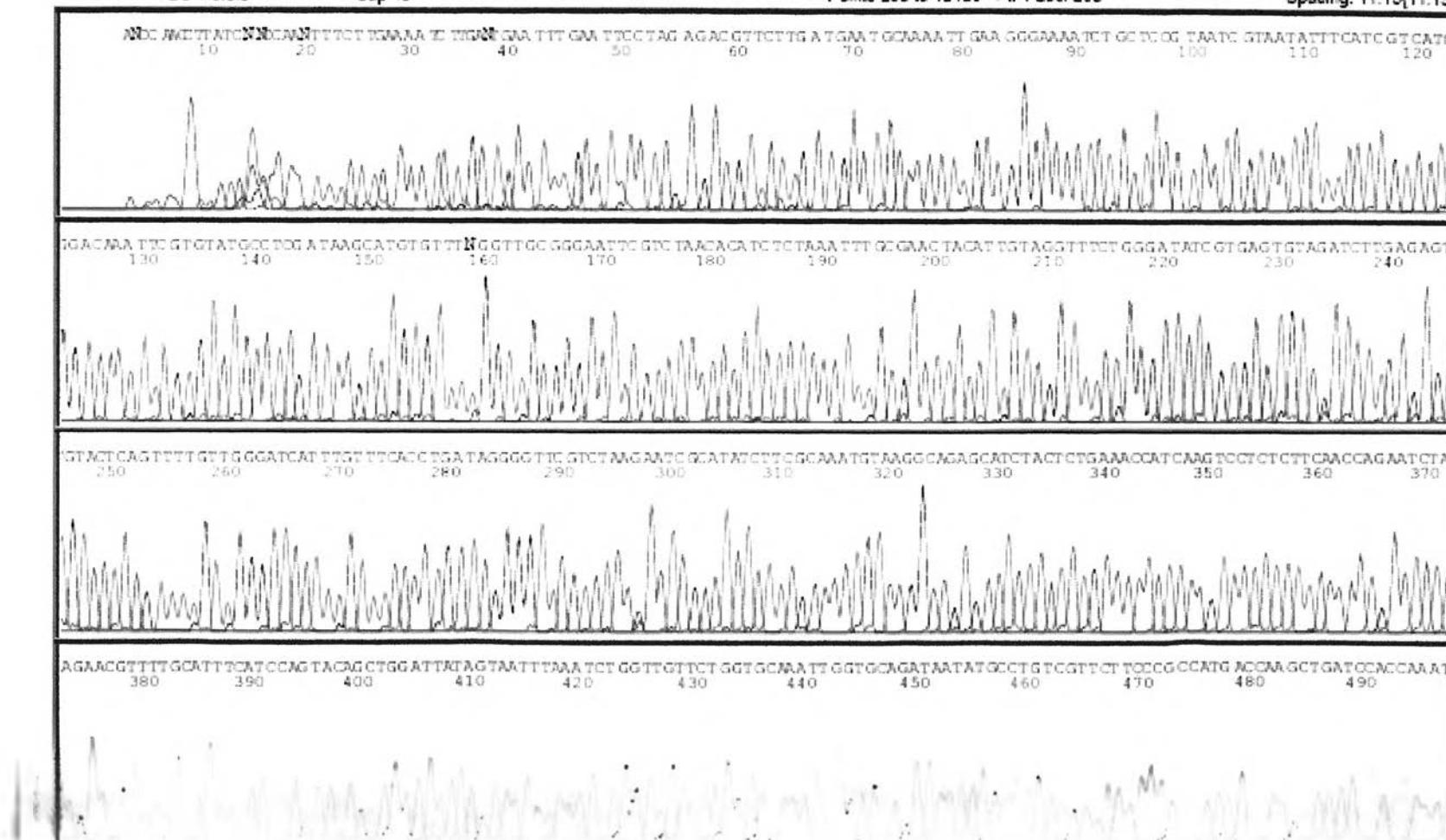


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Page 1 of 3
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D

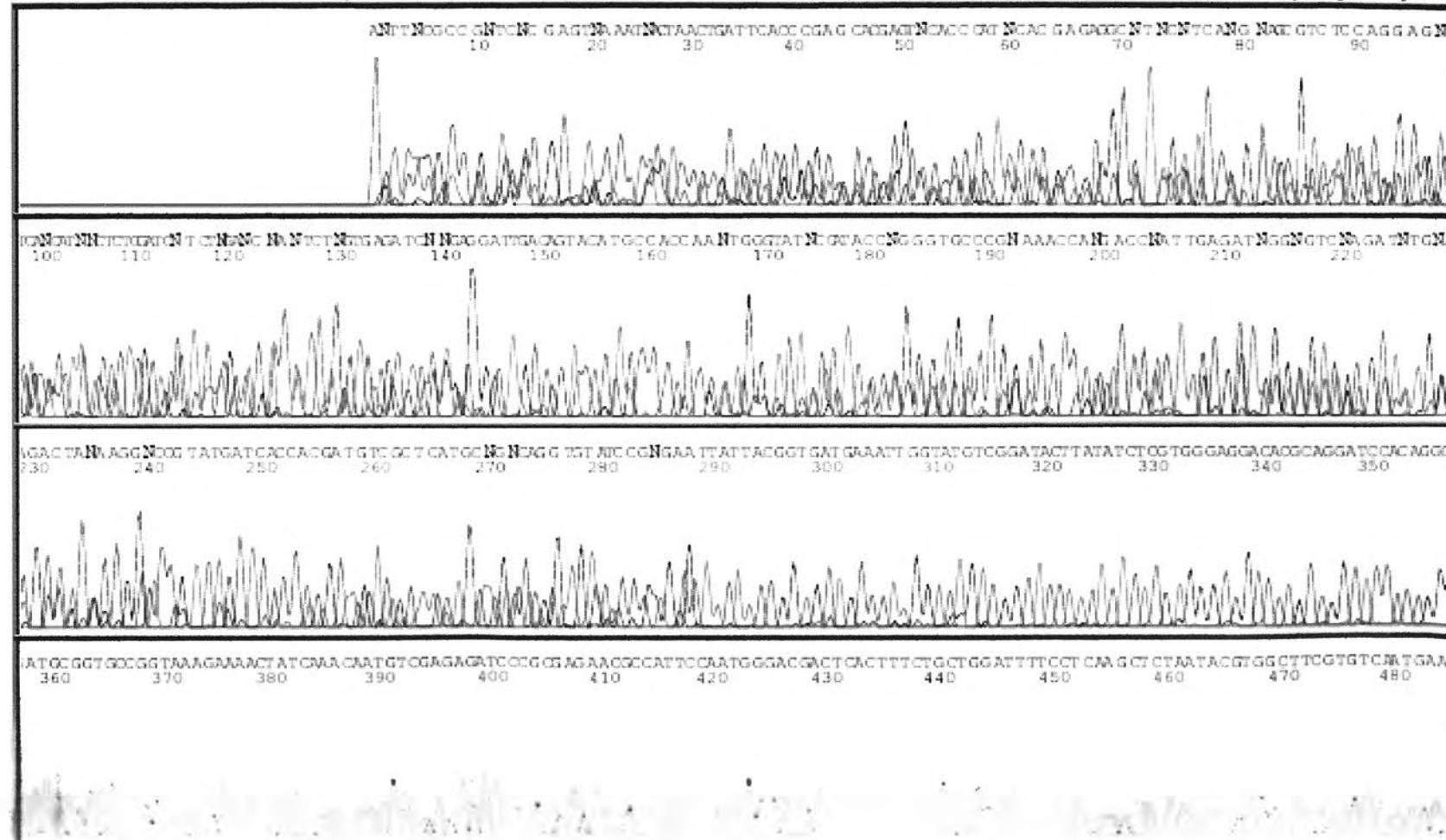


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Page 1 of 2
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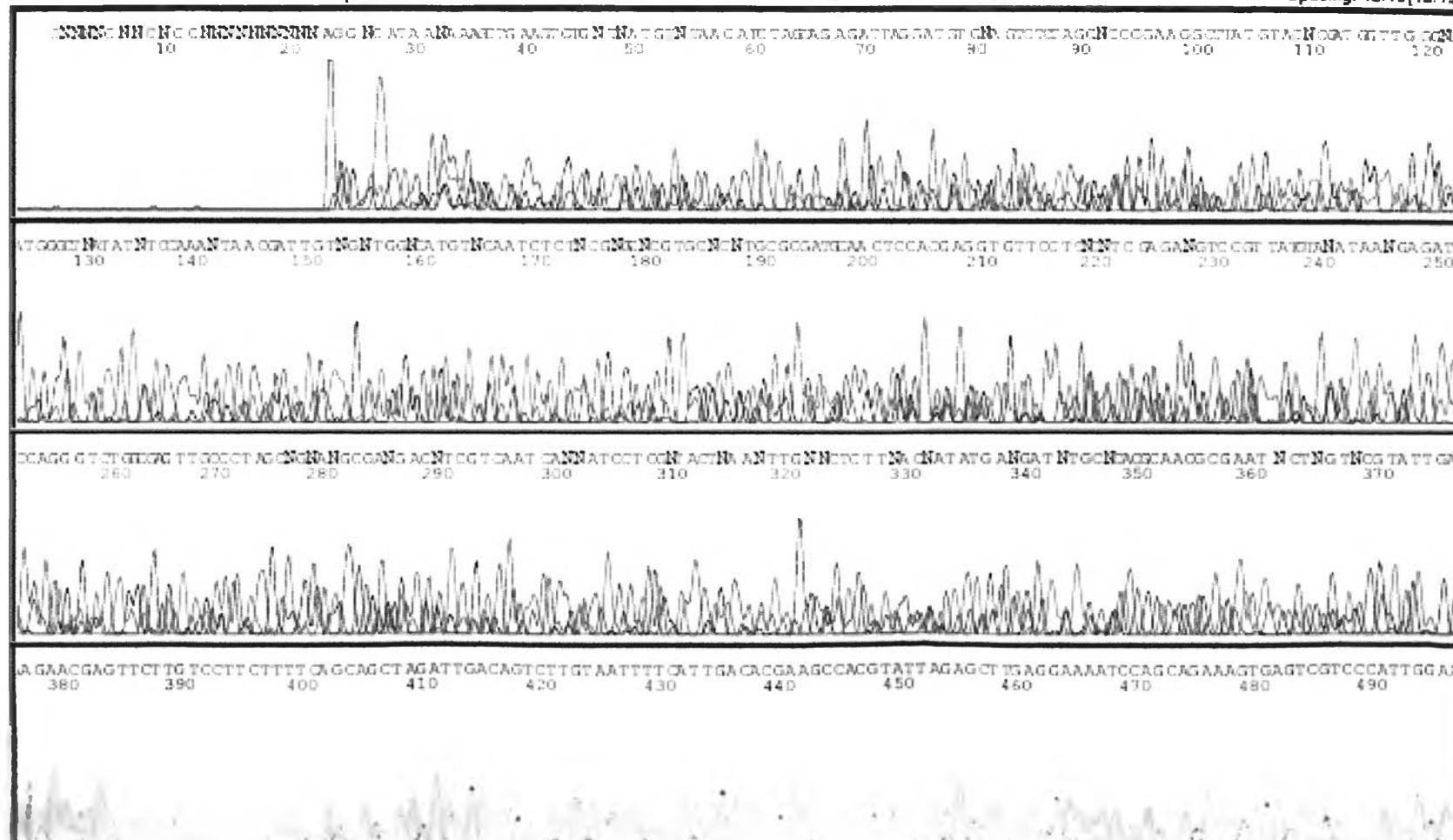


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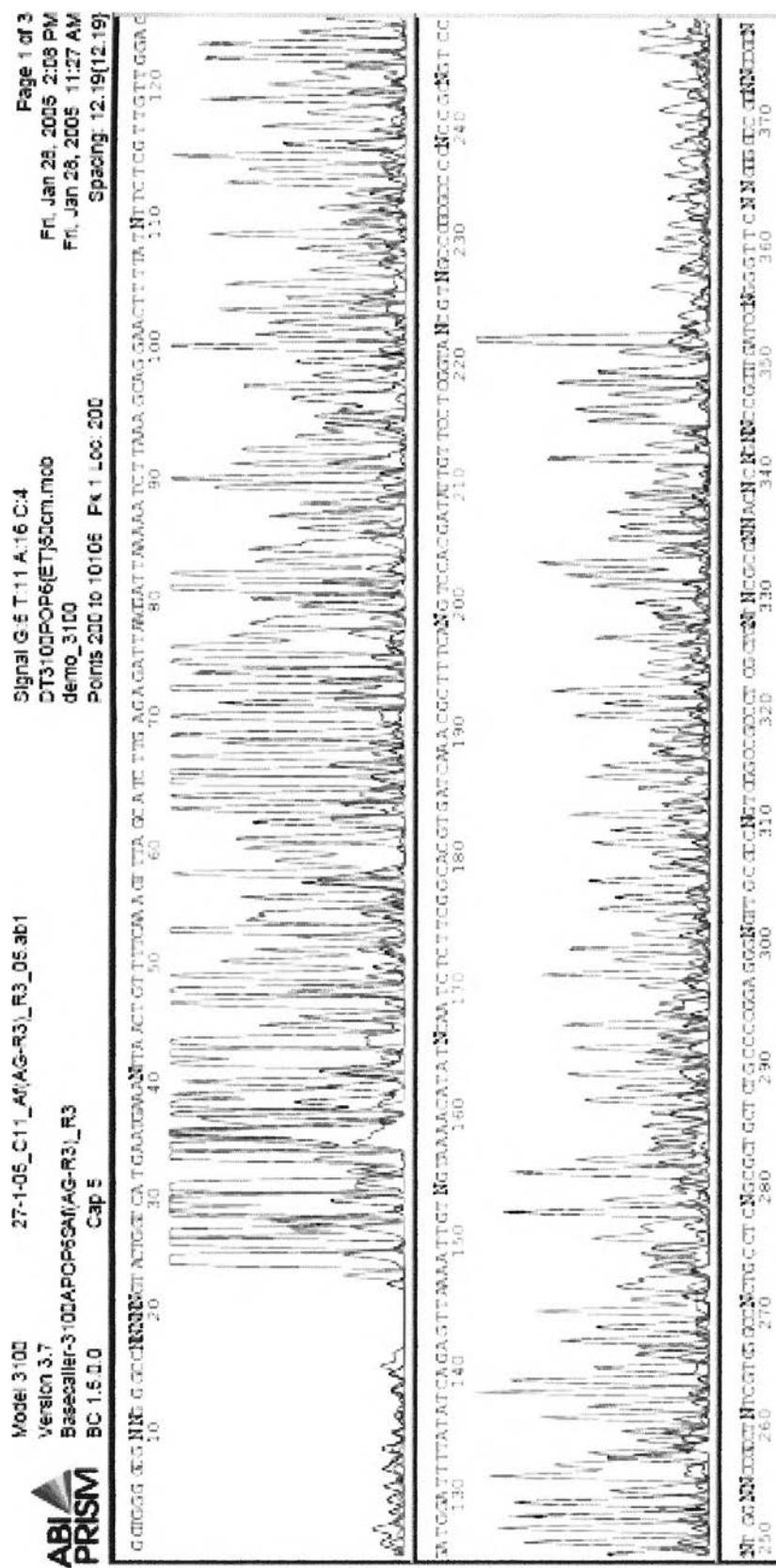
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Page 1 of 2



G



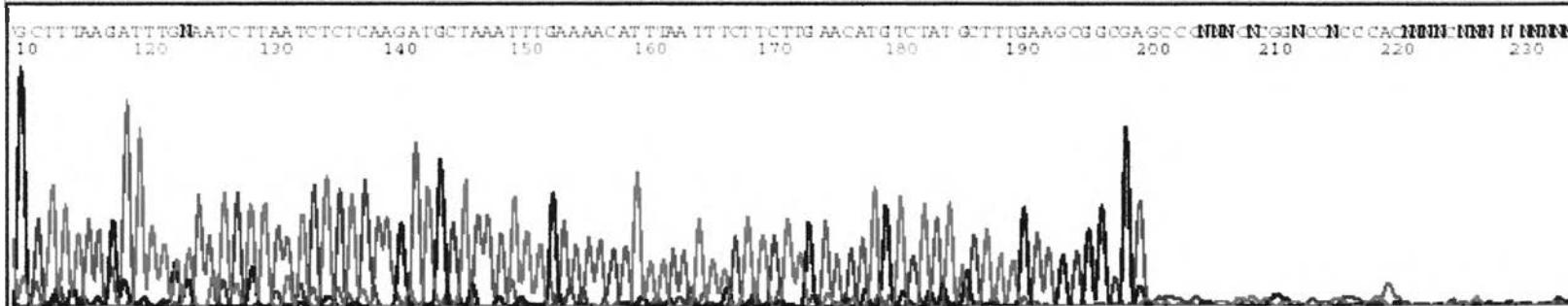
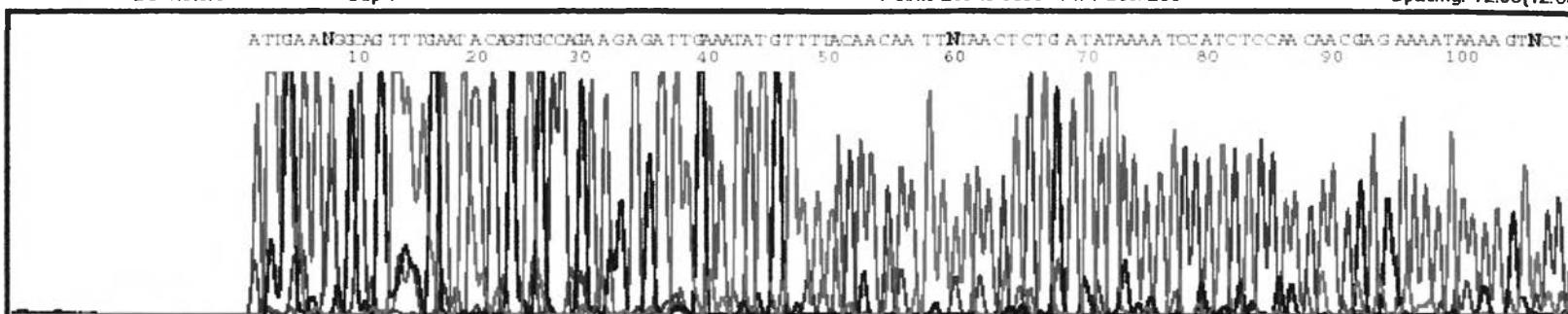


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Cap 1

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demo 3100
Points 200 to 3500 Pk 1 Loc: 200

Page 1 of 1



NGC 229 N G C N N N N N N N N
240 250

Appendix H: MALDI - TOF Mass spectrum

A: The MALDI - TOF MS of Af1

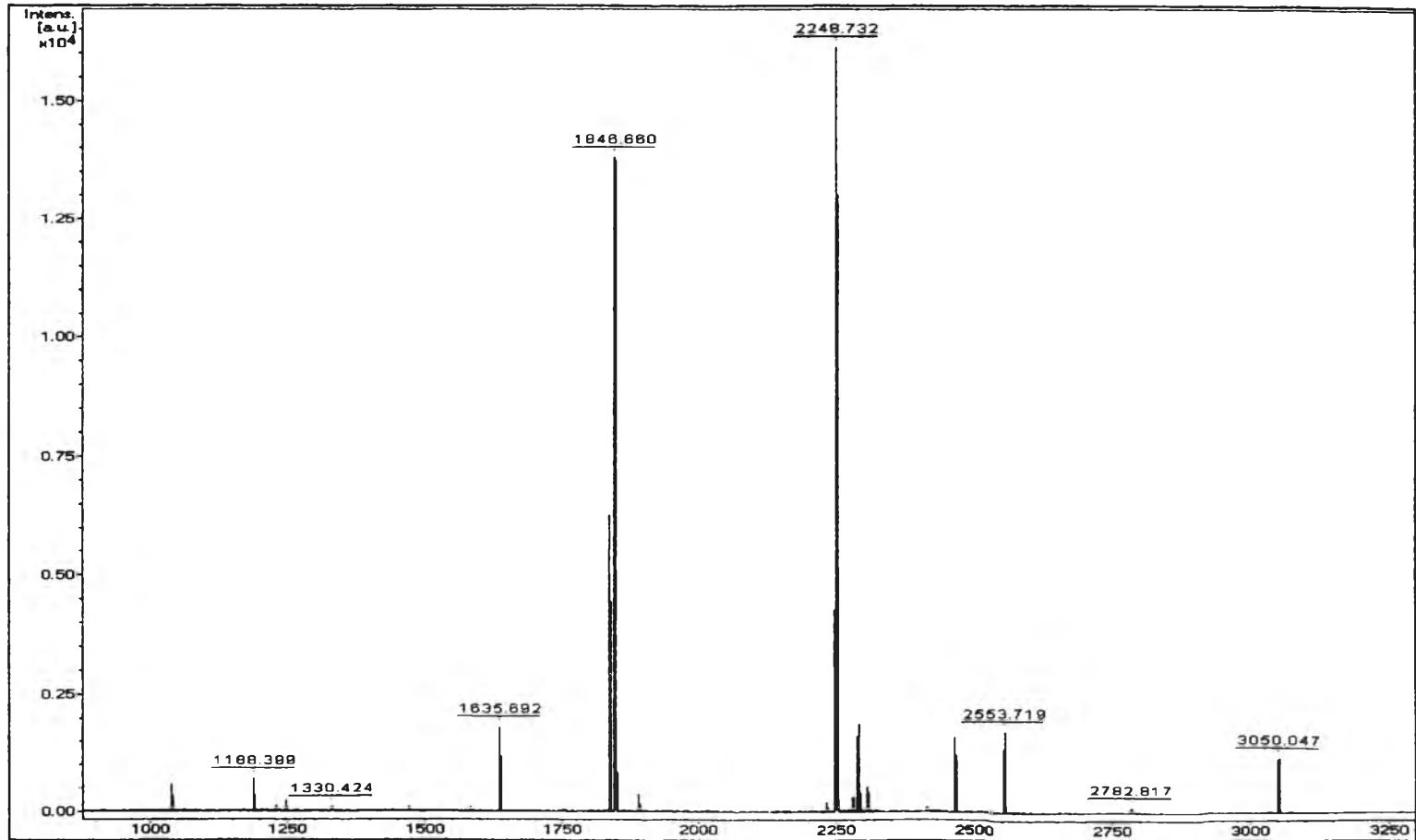
B: The data of MALDI - TOF MS of Af1

C: The MALDI - TOF MS of Af2

D: The data of MALDI - TOF MS of Af2

E: The MALDI - TOF MS of Af3

F: The data of MALDI - TOF MS of Af3



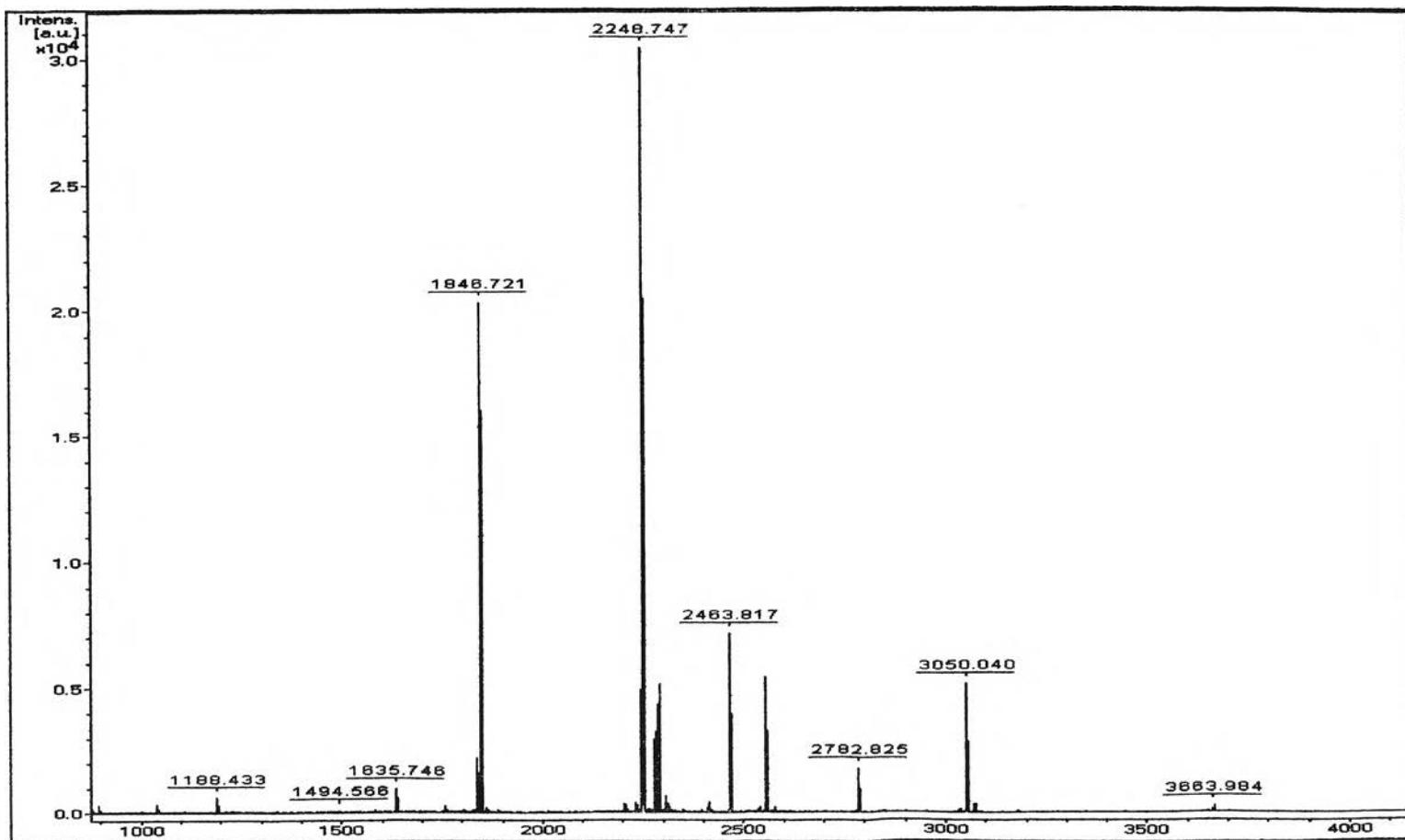
A

B

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m/z	Intens.	SN	Quality Fac.	Res.	Area	Rel. Intens.	FWHM	Chi^2
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1060.427	52	7.26349	3776.052	6798.194	17.84889	3.84E-03	0.155987	0
1188.399	673.0063	66.13879	2792.336	5063.094	316.7722	4.97E-02	0.234718	907.4306
1228.438	78.74086	8.600012	416.1481	5334.009	40.23526	5.82E-03	0.230303	96.16837
1246.452	202.03	22.87155	1149.844	7254.111	80.99108	1.49E-02	0.171827	187.1603
1330.424	87.1062	11.05135	722.3	5706.936	42.23261	6.43E-03	0.233124	75.45174
1471.454	76.68939	10.54794	539.2689	7493.842	39.30425	5.67E-03	0.196355	75.49201
1583.59	87.99887	11.93662	1023.821	8480.337	41.73318	6.50E-03	0.186737	50.26716
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1846.66	13537.29	825.4976	102019.1	9018.568	8592.916	1	0.204762	109636.7
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2248.732	12498.79	492.4002	34334.47	11460.6	8415.816	0.923286	0.196214	160007.7
2279.779	266	37.15554	6926.88	18473.82	38.85536	1.96E-02	0.123406	0
2288.72	1453.903	43.20526	5979.96	14852.26	733.6478	0.1074	0.154099	3685.772
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2411.707	72.06166	15.17454	1190.639	18633.03	28.76398	5.32E-03	0.129432	42.19417
2463.796	1118.875	232.4955	10313.2	13810.46	663.6976	8.27E-02	0.178401	9044.746
2553.719	1142.066	186.1879	9118.179	15904.05	645.5163	0.084364	0.16057	6446.099
2782.817	47.8751	19.54921	534.5929	17941.61	27.55942	3.54E-03	0.155104	63.69233
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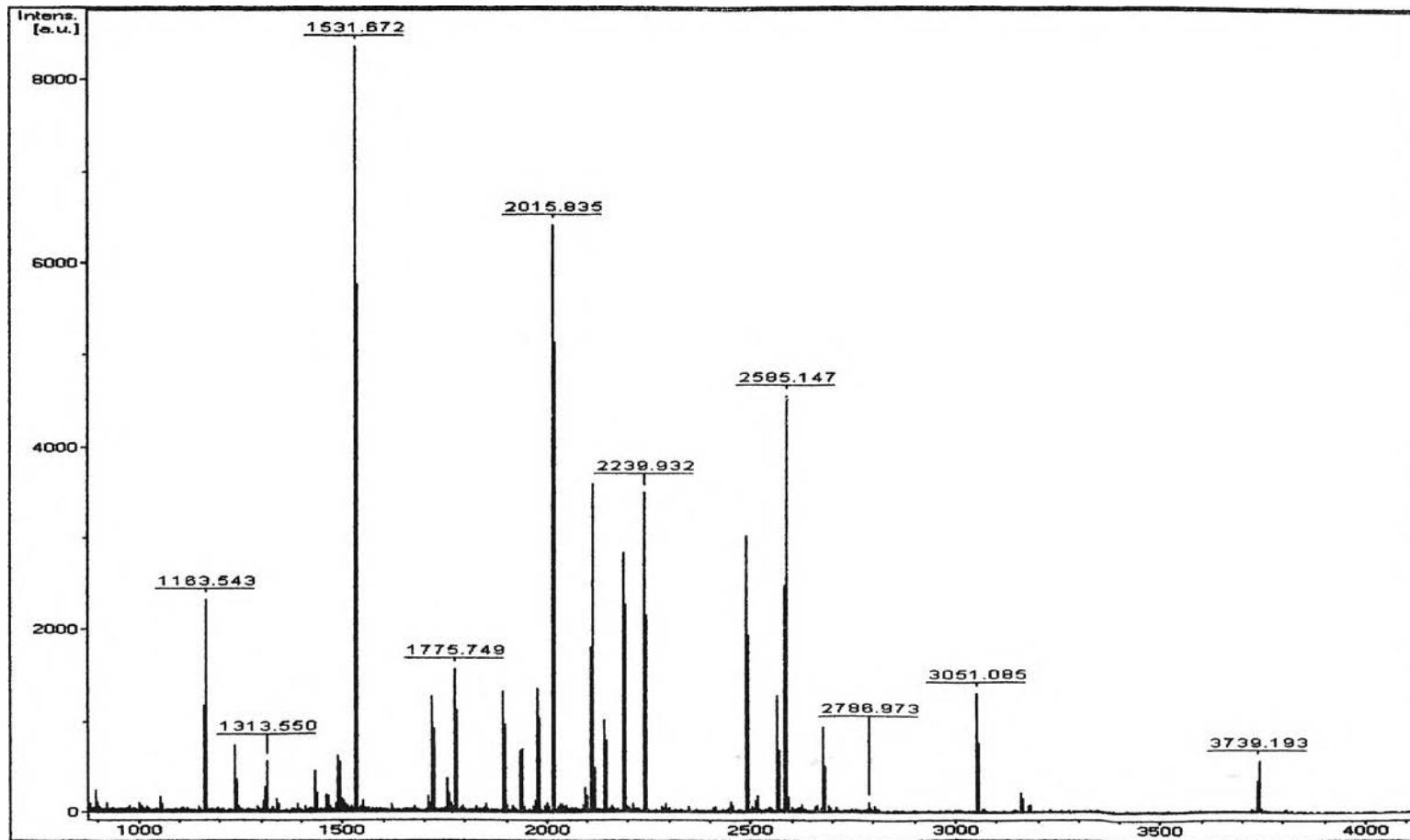


D

Spectrum: MS4900363_375\MS4900364 2Ref Raw (D:\bsu\MS4900363_375\MS4900364)

m/z	Intens.	SN	Quality Fac.	Res.	Area	Rel. Intens.	FWHM	Chi^2
892.2878	279.159	16.60519	1225.947	2741.231	157.2821	1.13E-02	0.325506	334.521
1038.465	332.773	25.69271	1716.294	4565.778	146.8484	1.34E-02	0.227445	338.6679
1188.433	591.9946	47.14096	1955.97	4596.491	326.6046	2.39E-02	0.258552	1207.821
1494.566	81.24754	7.606246	396.0183	6552.446	49.2049	3.28E-03	0.228093	114.2854
1635.746	852.8136	73.63635	2617.304	7758.94	514.3214	3.45E-02	0.210821	2340.729
1756.646	184.6123	11.03394	826.7965	6823.865	138.9512	7.46E-03	0.257434	411.8028
1836.749	2112.582	89.07052	6108.499	6962.2	1744.914	8.54E-02	0.263817	7372.33
1846.721	19980.04	899.4062	132905.6	6456.617	17703.51	0.80751	0.28802	229895.1
1850.32	317.7273	14.77581	108.4555	4942.523	273.4565	1.28E-02	0.374367	12831.58
2204.738	246.8612	11.83331	1468.354	11307.18	186.833	9.98E-03	0.194986	499.9581
2230.756	277.8789	8.800291	137.5481	7465.212	341.6113	1.12E-02	0.29882	8962.077
2245.847	3888.363	100.9846	3690.887	8291.51	3688.381	0.157151	0.270861	221979
2248.747	24742.79	630.0337	90352.16	6801.474	27128.46	1	0.330626	374619.7
2279.817	2474.111	47.15713	8983.933	11503.83	1730.711	1.00E-01	0.198179	13490.42
2288.736	4004.568	74.37784	22202.51	9660.825	3111.374	0.161848	0.236909	36236.3
2304.729	499.8524	10.81543	1284.501	11224.91	318.44	2.02E-02	0.205323	3033.611
2411.743	335.4881	29.32689	2462.189	11041.74	236.2979	1.36E-02	0.218421	550.4771
2463.817	5143.5	417.8869	67858.29	8797.695	4984.374	0.207879	0.280053	33247.56
2538.016	81.65177	7.218315	496.254	1849.311	224.8924	3.30E-03	1.372412	455.6979
2553.713	3602.422	318.0905	59016.65	8610.866	3415.114	0.145595	0.296569	25536.34
2575.688	124.1339	11.53212	1675.288	9680.843	117.7778	5.02E-03	0.26606	133.3645
2782.825	1064.97	195.0393	27843.78	10851.35	978.9191	4.30E-02	0.25645	3951.22
3035.463	49.50042	6.635162	547.2408	4378.653	114.3627	2.00E-03	0.693241	163.5977
3050.04	3043.141	443.8343	14308.5	8260.898	4239.735	0.122991	0.369214	75174.96
3071.985	194.4352	32.45028	2771.019	9603.656	251.7997	7.86E-03	0.319877	335.0627
3178.966	30.59314	11.53739	340.1229	12971.11	32.64166	1.24E-03	0.24508	38.29789
3663.984	61.89962	29.46723	427.4249	11818.15	126.8741	2.50E-03	0.31003	403.9356

E



F

Spectrum: MS4900363_375\MS4900365 1Ref Raw (D:\bsu\MS4900363_375\MS4900385)

m/z	Intens.	SN	Quality Fac.	Res.	Area	Rel. Intens.	FWHM	Chi^2
892.2944	233.2716	12.22515	339.5716	2739.89	134.2063	2.80E-02	0.325868	874.274
1053.45	140.7383	9.213941	872.281	4063.728	71.62157	1.69E-02	0.259233	122.8238
1163.543	2345.976	170.1999	44172.14	5155.436	1112.69	0.281274	0.225893	4258.982
1236.599	746.2432	56.32698	3594.185	5703.388	348.0574	8.95E-02	0.216818	963.4024
1306.527	116.0358	8.373656	645.4882	6389.516	54.16606	0.013912	0.20448	115.1467
1313.55	497.2552	35.79104	5548.784	6001.295	263.5421	5.96E-02	0.218878	977.518
1339.505	122.8899	8.754643	901.1201	4963.985	75.90016	1.47E-02	0.269845	115.1914
1431.573	388.4238	25.51477	5861.972	6150.181	211.392	4.66E-02	0.232769	472.586
1462.637	174.6521	10.63177	662.43	7583.165	85.02745	2.09E-02	0.192879	306.3805
1487.695	328.2378	19.4861	1090.959	5995.326	206.0524	3.94E-02	0.248142	702.7359
1490.677	567.4144	33.53901	3122.525	6800.871	305.1865	6.80E-02	0.219189	700.94
1495.612	167.6496	9.929239	1071.05	7478.28	85.57941	2.01E-02	0.199994	178.1902
1500.568	127.1154	7.525324	562.6397	5774.983	80.54327	1.52E-02	0.25984	210.446
1531.672	8340.535	490.3322	41784.28	6356.345	5082.355	1	0.240967	65874.74
1709.732	158.3541	9.908011	1009.278	7948.115	97.69014	1.90E-02	0.215112	207.2191
1719.779	1205.495	73.62248	14071.71	8701.567	710.7953	0.144535	0.19764	2857.227
1755.725	323.5586	20.54547	1551.168	8820.438	200.5447	3.88E-02	0.198165	570.9704
1775.749	1490.33	97.95369	6990.175	8776.646	861.5788	0.178685	0.202327	4514.29
1893.767	1085.719	69.58947	4777.302	8786.169	698.1923	0.130174	0.21554	4917.01
1936.786	629.6544	37.16275	3132.512	9012.843	426.0684	0.075493	0.214892	1168.075
1977.753	1087.759	58.91057	2303.922	9388.528	710.558	0.130418	0.210656	4845.336
2015.573	333.3489	17.67421	60.62601	14394.36	193.0417	0.039987	0.140025	20978.43
2015.835	5369.972	288.8357	51515.69	10251.09	3694.036	0.64384	0.196646	40305.15
2084.843	214.175	13.44023	1334.91	10758.05	133.5233	2.57E-02	0.194723	385.2833
2111.86	2947.392	185.5551	38598.41	10399.84	1977.231	0.353382	0.203067	13000.37
2141.912	854.714	55.08609	11617.39	9999.491	599.6807	0.102477	0.214202	1859.328
2188.902	2197.467	145.5474	17919.18	10871.06	1429.231	0.263468	0.201351	12224.87
2239.932	2594.814	198.8966	23655.13	10225.15	1816.026	0.311109	0.219061	19225.19
2488.885	2102.66	195.689	8730.667	9479.231	1846.367	0.252101	0.262582	12923.16
2515.109	74.21671	6.589758	163.5483	15386.67	50.48268	8.90E-03	0.16346	492.1333
2582.913	788.8965	66.98741	6082.909	10395.94	656.2897	9.46E-02	0.24653	4351.484
2585.147	2977.994	251.238	16919.58	8961.454	2898.316	0.357051	0.288474	21128.96
2674.917	572.5858	64.0398	4153.299	11740.67	510.7205	6.87E-02	0.227833	1671.994
2786.873	62.93768	9.862021	1103.148	12253.19	75.53807	7.55E-03	0.227449	71.52434
3051.085	692.6967	140.5758	2585.512	8567.894	940.0731	8.31E-02	0.356107	4585.191
3160.121	106.1968	23.91717	983.4918	9185.597	144.2874	1.27E-02	0.34403	307.9559
3739.193	202.8314	88.69093	1088.993	6276.352	511.1247	2.43E-02	0.595759	1972.822

Appendix I: Simulation digest enzyme

Alpha Glucosidase (Q17058) Mw.65565 Da
Trypsin/K-P /R-P

Frag#	Res#	Sequence	Theor (Bo)	[M+H]	[M+2H]	[M+3H]
T23	269-269	(R) K (F)	146.11	147.11	74.06	49.71
T46	471-471	(K) K (S)	146.11	147.11	74.06	49.71
T41	454-454	(K) K (D)	146.11	147.11	74.06	49.71
T52	526-526	(K) K (L)	146.11	147.11	74.06	49.71
T44	465-465	(K) K (F)	146.11	147.11	74.06	49.71
T12	158-158	(K) R (V)	174.11	175.12	88.06	59.05
T17	215-215	(R) R (G)	174.11	175.12	88.06	59.05
T34	361-362	(K) AR (M)	245.15	246.16	123.58	82.72
T42	455-456	(K) DK (N)	261.13	262.14	131.57	88.05
T6	56-57	(K) EK (L)	275.15	276.16	138.58	92.72
T1	1-2	(-) MK (A)	277.15	278.15	139.58	93.39
T8	113-115	(K) GLK (I)	316.21	317.22	159.11	106.41
T24	270-271	(K) FR (D)	321.18	322.19	161.60	108.07
T4	39-41	(R) SFK (D)	380.21	381.21	191.11	127.74
T41-42	454-456	(K) KDK (N)	389.23	390.24	195.62	130.75
T14	177-179	(R) EER (Q)	432.20	433.20	217.11	145.07
T23-24	269-271	(R) KFR (D)	449.28	450.28	225.65	150.77
T37	414-417	(R) DPAR (T)	457.23	458.24	229.62	153.42
T32	352-355	(R) LVSR (F)	473.30	474.30	237.66	158.77
T28	313-316	(K) NVSR (D)	474.26	475.26	238.14	159.09
T56	564-567	(K) PGNF (-)	483.21	484.22	242.61	162.08
T11	153-157	(K) IVNGK (R)	529.32	530.33	265.67	177.45
T45	466-470	(K) FASLK (K)	564.33	565.33	283.17	189.12
T33	356-360	(R) FGEEK (A)	608.28	609.29	305.15	203.77
T16	211-214	(R) FWLR (R)	620.34	621.35	311.18	207.79
T47	472-476	(K) SPYFK (E)	640.32	641.33	321.17	214.45
T11-12	153-158	(K) IVNGK (V)	685.42	686.43	343.72	229.48
T45-46	466-471	(K) FASLK (S)	692.42	693.43	347.22	231.82
T44-45	465-470	(K) KFASLK (K)	692.42	693.43	347.22	231.82
T18	216-221	(R) GFDGFR (V)	697.32	698.33	349.67	233.45
T21	249-254	(K) TEYTLK (I)	753.39	754.40	377.70	252.14
T39	440-445	(R) VNENYK (T)	765.37	766.37	383.69	256.13
T46-47	471-476	(K) KSPYFK (E)	768.42	769.42	385.22	257.15
T16-17	211-215	(R) FWLRR (G)	776.44	777.45	389.23	259.82
T51	519-525	(K) AFNNVPK (K)	788.42	789.43	395.22	263.81
T48	477-483	(K) EANLNTR (M)	816.41	817.42	409.21	273.14
T33-34	356-362	(R) FGEEKAR (M)	835.42	836.43	418.72	279.48
T40	446-453	(K) TVNLAAEK (K)	844.47	845.47	423.24	282.50

T17-18	215-221	(R) RGFDGFR (V)	853.42	854.43	427.72	285.48
T29	317-324	(R) DSNSSDFK (K)	898.37	899.37	450.19	300.46
T51-52	519-526	(K) AFNNVPKK (L)	916.51	917.52	459.26	306.51
T40-41	446-454	(K) TVNLAAEKK (D)	972.56	973.57	487.29	325.19
T54	540-548	(K) SISNNEQVK (V)	1017.51	1018.52	509.76	340.18
T29-30	317-325	(R) DSNSSDFKK (L)	1026.46	1027.47	514.24	343.16
T36	406-413	(K) ENYQTMSR (D)	1027.44	1028.45	514.73	343.49
T43	457-464	(K) NSFFNMFK (K)	1033.47	1034.48	517.74	345.50
T32-33	352-360	(R) LVSRFGEKK (A)	1063.57	1064.57	532.79	355.53
T43-44	457-465	(K) NSFFNMFK (F)	1161.56	1162.57	581.79	388.20
T25	272-281	(R) DVLDEFQPK (H)	1186.59	1187.59	594.30	396.54
T42-43	455-464	(K) DKNSFFNMFK (K)	1276.59	1277.60	639.30	426.54
T49	484-494	(R) MLNDNVFAFSR (E)	1312.62	1313.63	657.32	438.55
T28-29	313-324	(K) NVSRDSNSSDFK (K)	1354.61	1355.62	678.31	452.54
T5	42-55	(K) DSNGDGIGDIEGIK (E)	1388.64	1389.65	695.33	463.89
T3	28-38	(K) EDLIVYQVYPR (S)	1393.72	1394.73	697.87	465.58
T19	222-233	(R) VDALPYICEDMR (F)	1423.65	1424.66	712.83	475.56
T47-48	472-483	(K) SPYFKEANLNTR (M)	1438.72	1439.73	720.37	480.58
T36-37	406-417	(K) ENYQTMSRDPAR (T)	1466.66	1467.67	734.34	489.89
T24-25	270-281	(K) FRDVLDEFQPK (H)	1489.76	1490.76	745.89	497.59
T39-40	440-453	(R) VNENYKTVNLAAEK (K)	1591.82	1592.83	796.92	531.61
T55	549-563	(K) VSALGFFILISQDAK (F)	1607.89	1608.90	804.95	536.97
T53	527-539	(K) LNMFYNNFNNSDIK (S)	1618.74	1619.75	810.38	540.59
T5-6	42-57	(K) DSNGDGIGDIEGIKEK (L)	1645.78	1646.79	823.90	549.60
T20	234-248	(R) FLDEPLSGETNDPNK (T)	1674.77	1675.78	838.39	559.27
T22	255-268	(K) IYTHDIPETYNVVR (K)	1718.86	1719.87	860.44	573.96
T52-53	526-539	(K) KLNMFYNNFNNSDIK (S)	1746.84	1747.85	874.43	583.29
T4-5	39-55	(R) SFKDSNGDGIGDIEGIK (E)	1750.84	1751.85	876.43	584.62
T3-4	28-41	(K) EDLIVYQVYPR (D)	1755.92	1756.93	878.97	586.31
T26	282-296	(K) EMLIEAYTNLSMTMK (Y)	1781.85	1782.86	891.93	594.96
T22-23	255-269	(K) IYTHDIPETYNVVR (F)	1846.96	1847.97	924.49	616.66
T10	138-152	(K) NIEPYNNYYIWEPGK (I)	1906.90	1907.91	954.46	636.64
T27	297-312	(K) YYDYGADEPFNFNAFIK (N)	1976.90	1977.91	989.46	659.97
T13	159-176	(R) VPPTNWVGFGGSAWS R (E)	2001.98	2002.99	1002.00	668.34
T55-56	549-567	(K) VSALGFFILISQDAKFG NP (-)	2073.09	2074.10	1037.55	692.04
T18-19	216-233	(R) GFDGFRVDALPYICEDM R (F)	2102.96	2103.96	1052.49	701.99
T48-49	477-494	(K) EAANLNTRMLNDNVFAFS R (E)	2111.02	2112.03	1056.52	704.68
T12-13	158-176	(K) RVPPPTNWVGFGGSAWS WR (E)	2158.09	2159.09	1080.05	720.37
T20-21	234-254	(R) FLDEPLSGETNDPNKTE YTLLK (I)	2410.15	2411.16	1206.08	804.39

T13-14	159-179	(R) VPPTNNVGVFGGSANSW REER (Q)	2416.17	2417.18	1209.09	806.40
T10-11	138-157	(K) NIEPYNNYYIWHPGKIV NGK (R)	2418.21	2419.22	1210.11	807.08
T27-28	297-316	(K) YYDYGADPPNFAFIRN VSR (D)	2433.14	2434.15	1217.58	812.06
T21-22	249-268	(K) TEYTLKIYTHDIPETYN VVR (K)	2454.24	2455.25	1228.13	819.09
T38	418-439	(R) TPPQWDDSVSAGFSSSS NTWLR (V)	2474.11	2475.12	1238.06	825.71
T54-55	540-563	(K) SISNNEQVKVSALGFTI LISODAK (F)	2607.39	2608.40	1304.70	870.14
T53-54	527-548	(K) LAMFTNNPNSDIKSISN NEQVK (V)	2618.24	2619.25	1310.13	873.76
T9	116-137	(K) IILDVFVPNHTSDQHEWF QLSLK (N)	2666.35	2667.36	1334.18	889.79
T50	495-518	(R) ETEDNGSLYAILNFSNE EQIVDLK (A)	2740.31	2741.32	1371.16	914.44
T2	3-27	(K) AVIVFCIMALSIVDAAW KPLPENLK (E)	2740.51	2741.51	1371.26	914.51
T37-38	414-439	(R) DPARTPPQWDDSVSAGF SSSSNTWLR (V)	2913.33	2914.34	1457.67	972.12
T25-26	272-296	(R) DVLDEFPQPKEMLIEAY TNLSMTMK (Y)	2950.43	2951.44	1476.22	984.48
T8-9	113-137	(K) GLAKIILDVFVPNHTSDQH ENPQLSLK (W)	2964.55	2965.56	1483.28	989.19
T1-2	1-27	(-) MKAVIVFCIMALSIVDA AWKPLPENLK (E)	2999.64	3000.65	1500.83	1000.89
T31	326-351	(K) LVDNWMTYMPGSGIPNW VPGNHEDQLR (L)	3036.44	3037.45	1519.23	1013.15
T19-20	222-248	(R) VDALPYICEDMRFLDEP LSGETNDPNK (T)	3080.41	3081.42	1541.21	1027.81
T30-31	325-351	(K) KLVDNWMTYMPGSGIPNW VPGNHEDQLR (L)	3164.53	3165.54	1583.27	1055.85
T38-39	418-445	(R) TPPQWDDSVSAGFSSSS NTWLRVMENYK (T)	3221.47	3222.48	1611.74	1074.83
T31-32	326-355	(K) LVDNWMTYMPGSGIPNW VPGNHEDQLRLVSR (F)	3491.72	3492.73	1746.87	1164.92
T50-51	495-525	(R) ETEDNGSLYAILNFSNE EQIVDLKAFNNVPK (K)	3512.83	3513.84	1757.42	1171.95
T26-27	282-312	(K) EMLIEAYTNLSMTMKYY DYGADEFPPNFAFIK (N)	3743.34	3744.35	1872.68	1248.79
T15	180-210	(R) QAYYLHQFAPEQPDLYN YNPVVLLDDMQNVLR (F)	3755.18	3756.19	1878.60	1252.74
T49-50	484-518	(R) MLNDNVFAFSRETEDNG SLYAILNFSNEEQIVDLK (A)	4037.43	4038.44	2019.72	1346.82
T2-3	3-38	(K) AVIVFCIMALSIVDAAW KPLPENLKEDLIVYQVYPR (S)	4118.96	4119.97	2060.49	1374.00
T14-15	177-210	(R) EERQAYYLHQFAPEQPD LYNNPVVLLDDMQNVLR (F)	4169.60	4170.61	2085.81	1390.88
T15-16	180-214	(R) QAYYLHQFAPEQPDLYN YNPVVLLDDMQNVLRFWLR (R)	4357.92	4358.93	2179.97	1453.65

T9-10	116-152	(K) IILDVFVPAHETSQHEWF QLSLRNIEPYNNYYIWHPGK (I)	4558.09	4559.10	2280.05	1520.37
T35	363-405	(R) MITTMSLLLPGVAVNYY GDEIGMSDTYISWEDTQDPO GCGAGK(E)	4629.20	4630.21	2315.61	1544.08
T34-35	361-405	(K) ARMITTMSLLLPGVAVN YYGDEIGMSDTYISWEDTQD PQGCGAGK(E)	4856.47	4857.48	2429.24	1619.83
T35-36	363-413	(R) MITTMSLLLPGVAVNYY GDEIGMSDTYISWEDTQDPO GCGAGKENYQTMSR(D)	5639.30	5640.31	2820.66	1880.77
T7	58-112	(K) LDHFLEMGVDMFWLSPI YPSPMVDFGYDISNYTDVHP IFGTISDLNLVSAAHAK(G)	6262.06	6263.07	3132.04	2088.36
T6-7	56-112	(K) EKLDHFLEMGVDMFWLS PIYPSPMVDFGYDISNYTDV HPIFGTISDLNLVSAAHAK (G)	6519.35	6520.36	3260.68	2174.13
T7-8	58-115	(K) LDHFLEMGVDMFWLSPI YPSPMVDFGYDISNYTDVHP IFGTISDLNLVSAAHAKGL K(I)	6560.45	6561.46	3281.23	2187.82

BIOGRAPHY

Miss Rumpalai Padoongsupalai was born on September 30th, 1981 in Bangkok. She graduated with Bachelor Degree of Science in Department of General Science, Faculty of Science, Kasetsart University. Then, she has been a graduate student in a Master's Degree in Biotechnology program, Faculty of Science Chulalongkorn University since 2003.

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