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APPENDICES

Appendix A

Table 1A Solutions for 2D-PAGE

Solution	Chemical	Final concentration	Amount
Lysis solution	Urea	8 M	19.2 g
	CHAPS	4% (w/v)	1.6 g
	Pharmalyte 3-10	2%	800 μ l
	Double distilled H ₂ O		to 40 ml
Rehydration solution	Urea	8 M	12 g
	CHAPS	2% (w/v)	0.5 g
	Bromophenol blue	0.002% (w/v)	50 μ l
	Double distilled H ₂ O		to 25 ml
SDS equilibration buffer	Tris-HCl, pH 8.8	50 mM	10.0 ml
	Urea	6 M	72.07 g
	Glycerol	30% (v/v)	69 ml
	SDS	2% (w/v)	4.0 g
	Bromophenol blue	0.002% (w/v)	400 μ l
	Double distilled H ₂ O		to 200 ml
30% T, 2.6% C monomer stock solution	Acrylamide	30%	60.0 g
	Bisacrylamide	0.8%	1.6 g
	Double distilled H ₂ O		to 200 ml
4 \times resolving gel buffer	Tris base	1.5 M	181.7 g
	Double distilled H ₂ O		750 ml
	HCl		adjust to pH 8.8
	Double distilled H ₂ O		to 1 l
10% SDS	SDS	10% (w/v)	5.0 g
	Double distilled H ₂ O		to 50 ml
10% ammonium persulfate	Ammonium persulfate	10% (w/v)	0.1 g
	Double distilled H ₂ O		to 1 ml
SDS electrophoresis buffer	Tris-base	25 mM	30.3 g
	Glycine	192 mM	144.0 g
	SDS	0.1% (w/v)	10.0 g
	Double distilled H ₂ O		to 10 l
Agarose sealing solution	SDS Electrophoresis buffer		100 ml
	Agarose	0.5%	0.5 g
	Bromophenol blue	0.002% (w/v)	200 μ l

Table 2A Coomassie gel stain and destain solutions

Solutions	Chemical	Amount
Coomassies Gel stain	Coomassies Blue G-250	1 g
	Methanol	450 ml
	H ₂ O	450 ml
	Glacial acetic acid	100 ml
Coomassies Gel destain	Methanol	100 ml
	H ₂ O	800 ml
	Glacial acetic acid	100 ml

Appendix B

Table 1B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spot 17 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
ASMENGVLTVTPK	487.9045	3	1460.6918	1460.755
ASMENGVLTVTPK	731.3782	2	1460.7418	1460.755
ASMENGVLTVTPK	731.38	2	1460.7454	1460.755
VEVEEDRVLQISGER	586.6232	3	1756.8478	1756.896
ASMENGVLTVTPKKEEVK	649.6526	3	1945.9359	1946.003
ASMENGVLTVTPKKEEVK	649.6668	3	1945.9784	1946.003
ASMENGVLTVTPKKEEVK	649.6719	3	1945.9939	1946.003
ASMENGVLTVTPKKEEVK	974.0063	2	1945.9981	1946.003

Table 2B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spot 19 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
VVDALGVPIIDGR	605.829	2	1209.6435	1209.672
TAIAIDTILNQK	650.8654	2	1299.7162	1299.74

Table 3B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spot 25 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
VQIVGDDLLVTNPK	755.93	2	1509.8454	1509.84
VNQIGSVTESIEAVR	801.4197	2	1600.8249	1600.842
LAMQEFMILPVGASSFK	634.3176	3	1899.9311	1899.947
LAMQEFMILPVGASSFK	950.9832	2	1899.9517	1899.947
SGETEDTFIADLSVGLATGQIK	1126.5977	2	2251.1809	2251.122

Table 4B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spot 29 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
LADLVGVTLGPK	591.8468	2	1181.679	1181.702
GYISPYFVTDSEK	753.3564	2	1504.698	1504.709
EVELEDPVENIGAK	514.5807	3	1540.72	1540.762
EVELEDPVENIGAK	771.3773	2	1540.74	1540.762
AAVEEGIVVGGGCTLLR	567.6257	3	1699.855	1699.893
AAVEEGIVVGGGCTLLR	850.9438	2	1699.873	1699.893
SAENSLYVVEGMQFDR	620.943	3	1859.807	1859.836
LSGGVAVIQVGAQTETELK	634.0086	3	1899.004	1899.031
LSGGVAVIQVGAQTETELKEK	719.7265	3	2156.158	2156.169
TNDLAGDGTTSVVLAQGLIAEGVK	810.7503	3	2429.229	2429.265
YGYNAATGKYEDLMAAGIIDPTK	826.7244	3	2477.151	2477.178

Table 5B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spots 32 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
EGSSIINTTSVNAYK	792.3999	2	1582.785	1582.784
AVCNLFALEGATVAFTYVK	692.0226	3	2073.046	2073.061

Table 6B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spots 33 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
HVPGFIEKAEELK	499.5993	3	1495.776	1495.804
VILFGVPGAFTPTCSLK	602.9972	3	1805.97	1805.975
VILFGVPGAFTPTCSLK	903.996	2	1805.977	1805.975
KVILFGVPGAFTPTCSLK	645.68	3	1934.018	1934.07

Table 7B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spots 41 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
LAVNLIPFPR	570.3476	2	1138.681	1138.686
MMLTFSVFPSPK	708.8627	2	1415.711	1415.683
AVLMDLEPGTMDSVR	555.9222	3	1664.745	1664.775
AVLMDLEPGTMDSVR	833.3968	2	1664.779	1664.775

Table 8B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spots 48 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
VQVEDDNVLQISGER	850.9265	2	1699.838	1699.838
VQVEDDNVLQISGER	567.6276	3	1699.861	1699.838
SGDIKVQVEDDNVLQISGER	734.3702	3	2200.089	2200.097
SGDIKVQVEDDNVLQISGER	734.3764	3	2200.107	2200.097

Table 9B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spots 49 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
MELVDAAFPLLK	673.874	2	1345.733	1345.732
IVQGLSIDEFSR	682.3593	2	1362.704	1362.714
IVQGLSIDEFSR	682.37	2	1362.726	1362.714
IVQGLSIDEFSR	682.3767	2	1362.739	1362.714
LSSALSAASSACDHIR	549.272	3	1644.794	1644.789
VLVVANPANTNALILK	550.6588	3	1648.954	1648.988
VLVVANPANTNALILK	825.4905	2	1648.966	1648.988
VLVVANPANTNALILK	825.4956	2	1648.977	1648.988
VLVTGAAGQIGYALVPMIAR	672.7087	3	2015.104	2015.124
VLVTGAAGQIGYALVPMIAR	1008.583	2	2015.151	2015.124
MELVDAAFPLLK	673.874	2	1345.733	1345.732

Table 10B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spots 54 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
FPIPPVNLIGR	611.8638	2	1221.713	1221.723
GPILLEDYHLVEK	509.2654	3	1524.775	1524.819
GPILLEDYHLVEK	763.4177	2	1524.821	1524.819
TWPEDLVPLQPVGR	803.9407	2	1605.867	1605.852
HAEKFPIPPVNLIGR	563.3141	3	1686.92	1686.957
HAEKFPIPPVNLIGR	563.3159	3	1686.926	1686.957
HAEKFPIPPVNLIGR	563.335	3	1686.983	1686.957
LYIQTIDPDFEDRFDFDPLDGTK	920.7813	3	2759.322	2759.297

Table 11B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spots 59 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
AASFNIIPSSTGAAK	478.9109	3	1433.711	1433.751
AASFNIIPSSTGAAK	717.874	2	1433.734	1433.751
VPTVDVSVVDLTVR	500.2669	3	1497.779	1497.84
VPTVDVSVVDLTVR	749.9239	2	1497.833	1497.84
TLLFGEKPVTVFAHR	572.3128	3	1713.917	1713.957
FGIVEGLMTTVHSITATQK	683.6837	3	2048.029	2048.061
LTGMAFRVPTVDVSVVDLTVR	764.4066	3	2290.198	2290.236

Table 12B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spots 66 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
IIGVDLVSSR	529.8038	2	1057.593	1057.613
FGVNEFVNPK	575.7835	2	1149.552	1149.582

Table 13B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spots 67 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
VVDLLAPYQR	587.3232	2	1172.632	1172.655
ESITSFQGVLDGK	690.8469	2	1379.679	1379.693
VGLTGLTVAEHFR	467.2429	3	1398.707	1398.762
VLNTGSPITVPVGR	705.4088	2	1408.803	1408.804
TVLIMELINNVAK	737.42	2	1472.825	1472.827
FTQANSEVSALLGR	498.2489	3	1491.725	1491.768
FTQANSEVSALLGR	746.8778	2	1491.741	1491.768
GAIGQVCQVIGAVVDVR	580.9739	3	1739.9	1739.935
EGNDLYREMIESGVK	623.643	3	1867.907	1867.899
QISELGIYPAVDPLDSTSR	687.6761	3	2060.006	2060.043
QISELGIYPAVDPLDSTSR	1031.051	2	2060.087	2060.043
IPSAVGYQPTLATDLGGLQER	729.3799	3	2185.118	2185.138
VVDLLAPYQR	896.8288	3	2687.465	2687.369

Table 14B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spots 69 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
GTVELAGTNGETTTQGLDGLAQR	763.712	3	2288.114	2288.125
VDKGTVELAGTNGETTTQGLDGLAQR	658.5784	4	2630.284	2630.315
VDKGTVELAGTNGETTTQGLDGLAQR	877.782	3	2630.324	2630.315

Table 15B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spots 70 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
AASFNIIPSSSTGAAK	717.8794	2	1433.744	1433.751
VPTVDVSVVDLTVR	500.2743	3	1497.801	1497.84
VPTVDVSVVDLTVR	749.9265	2	1497.839	1497.84
LTGMSFRVPTVDVSVVDLTVR	769.7558	3	2306.245	2306.231
DAPMFVVGVNEHEYKPELDIV SNASCTTNCLAPLAK	1002.3	4	4005.171	4004.896

Table 16B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spot 71 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
MELVDAAFPLLK	681.8674	2	1361.72	1361.727
VLVVANPANTNALILK	550.663	3	1648.967	1648.988
VLVVANPANTNALILK	825.5031	2	1648.992	1648.988
VLVTGAAGQIGYALVPMIAR	672.719	3	2015.135	2015.124
VLVTGAAGQIGYALVPMIAR	1008.607	2	2015.2	2015.124

Table 17B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spot 72 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
LSELLGVEVK	543.8134	2	1085.612	1085.633
ELDYLVGAVANPK	694.8816	2	1387.749	1387.735
VDLNVPLDDNFNITDDTR	692.6708	3	2074.991	2074.981
VDLNVPLDDNFNITDDTR	1038.514	2	2075.013	2074.981
LAELSGKGVTTIIGGGDSVAAVEK	758.0557	3	2271.145	2271.232

Table 18B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spot 74 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
LFGVTTLDVVR	610.3587	2	1218.703	1218.697
DDLFNINAGIVK	659.8662	2	1317.718	1317.693
ALEGSDVVIIPAGVPR	796.9596	2	1591.905	1591.893

Table 19B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spot 76 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
VACGIIGLQG	494.2633	2	986.5121	986.5219
STGNAGGRVACGIIGLQG	844.4433	2	1686.872	1686.847

Table 20B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spot 77 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
MELVDAAFPLLK	673.881	2	1345.748	1345.732
IVQGLSIDEFSR	682.3696	2	1362.725	1362.714
IVQGLSIDEFSR	682.3718	2	1362.729	1362.714
IVQGLSIDEFSR	682.3798	2	1362.745	1362.714
IVQGLSIDEFSR	682.3847	2	1362.755	1362.714
IVQGLSIDEFSR	682.3875	2	1362.761	1362.714
IVQGLSIDEFSR	682.3885	2	1362.763	1362.714
VLVVANPANTNALILK	550.6665	3	1648.978	1648.988
VLVVANPANTNALILK	825.5005	2	1648.987	1648.988
VLVTGAAGQIGYALVPMIAR	672.7246	3	2015.152	2015.124
VLVTGAAGQIGYALVPMIAR	1008.602	2	2015.189	2015.124

Table 21B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spot 78 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
IVSFLDPDGWK	638.8108	2	1275.607	1275.65
TVLVDNEDFLK	646.8476	2	1291.681	1291.666
TVLVDNEDFLK	646.8525	2	1291.69	1291.666
DPDGYTFELIQR	727.3553	2	1452.696	1452.689

Table 22B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spot 80 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
FPIPPVNLIGR	611.8694	2	1221.724	1221.723
IGPNYLQLPVNAPK	762.4447	2	1522.875	1522.851
GPILLEDYHLVEK	509.2739	3	1524.8	1524.819
EGNFDLVGNNFPVFFIR	993.0211	2	1984.028	1983.984
LYIQTIDPDFEDRFDFDPLDGTK	920.7911	3	2759.351	2759.297

Table 23B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spot 86 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
VQIVGDDLLVTNPK	755.9248	2	1509.835	1509.84
VVIGMDVAASEFYK	772.8871	2	1543.76	1543.759

Table 24B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spot 87 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
HVVFGKVVEGMDVVK	553.6262	3	1657.857	1657.886
HVVFGKVVEGMDVVK	829.9691	2	1657.924	1657.886
VIPGFMCQGGDFTAGNGT GGESIYGAK	903.0764	3	2706.207	2706.205

Table 25B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spot 88 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
FGVNEFVNPK	575.7921	2	1149.57	1149.582
FITHTVPFSEINK	511.6023	3	1531.785	1531.804

Table 26B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spot 93 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
DAGAISGLNVLR	593.3314	2	1184.648	1184.651
ELEGICNPIIAK	678.8676	2	1355.721	1355.712
VQQLQDFDFNGK	718.8848	2	1435.755	1435.746
TTPSYVAFTDTER	744.3717	2	1486.729	1486.694
IINEPTAAAIAYGLDKK	596.6721	3	1786.995	1786.983

Table 27B Peptide sequences acquired from MS/MS fragmentation of tryptic peptides from an identified protein spot 94 using Mascot search

Query sequence	Peptide Mass (m/z) (exp.)	Peptides charge	Peptide MW	
			(exp.)	(theor.)
DAGVIAGLNVMR	616.3254	2	1230.636	1230.639
EIAEAYLGSTVK	640.8382	2	1279.662	1279.666
ELEGLCNPIIAK	678.863	2	1355.711	1355.712
VQQLLQDFFNKG	479.5771	3	1435.71	1435.746
VQQLLQDFFNKG	718.8828	2	1435.751	1435.746
TTPSYVGFTDTER	737.3469	2	1472.679	1472.678
ARFEELNMDLFR	519.5764	3	1555.707	1555.745
IINEPTAAAIAYGLDK	553.9629	3	1658.867	1658.888
IINEPTAAAIAYGLDK	830.445	2	1658.875	1658.888
NQVAMNPINTVFDK	839.4181	2	1676.822	1676.819
IINEPTAAAIAYGLDKK	596.6626	3	1786.966	1786.983
IINEPTAAAIAYGLDKK	596.67	3	1786.988	1786.983
VQQLLQDFFNKGKELCK	656.3481	3	1966.022	1965.998
SINPDEAVAYGAAVQAAILS GEGNEK	858.7	3	2573.078	2573.261
EQVFSTYS DNQPGVLIQVYEGER	886.7644	3	2657.271	2657.261
VQDLLLDVTPLSLGLETAGGVM TVLIPR	1017.255	3	3048.742	3048.715

Figure 3C The product ion spectrum of precursor ion at m/z of 797.02 (spot 8).

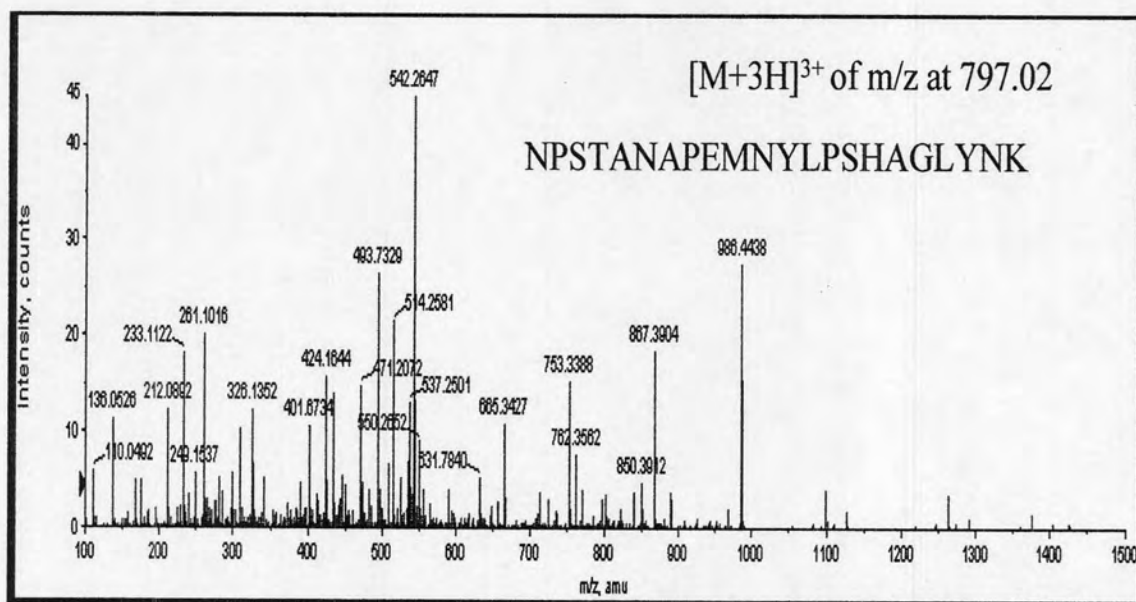


Figure 4C The product ion spectrum of precursor ion at m/z of 631.8 (spot 13).

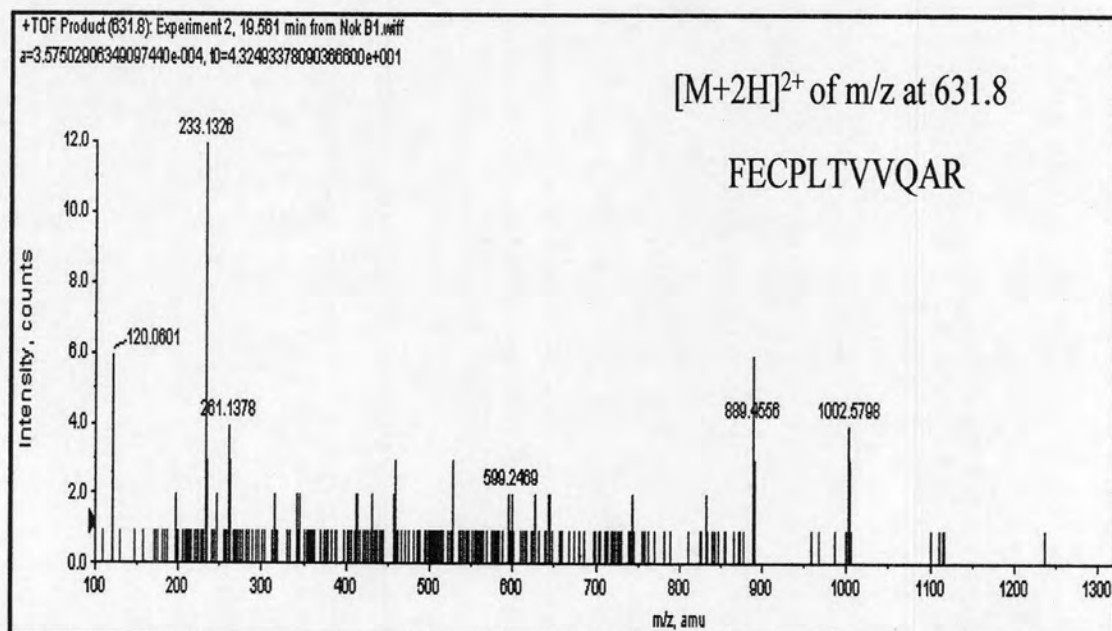


Figure 5C The product ion spectrum of precursor ion at m/z of 897.0 (spot 25).

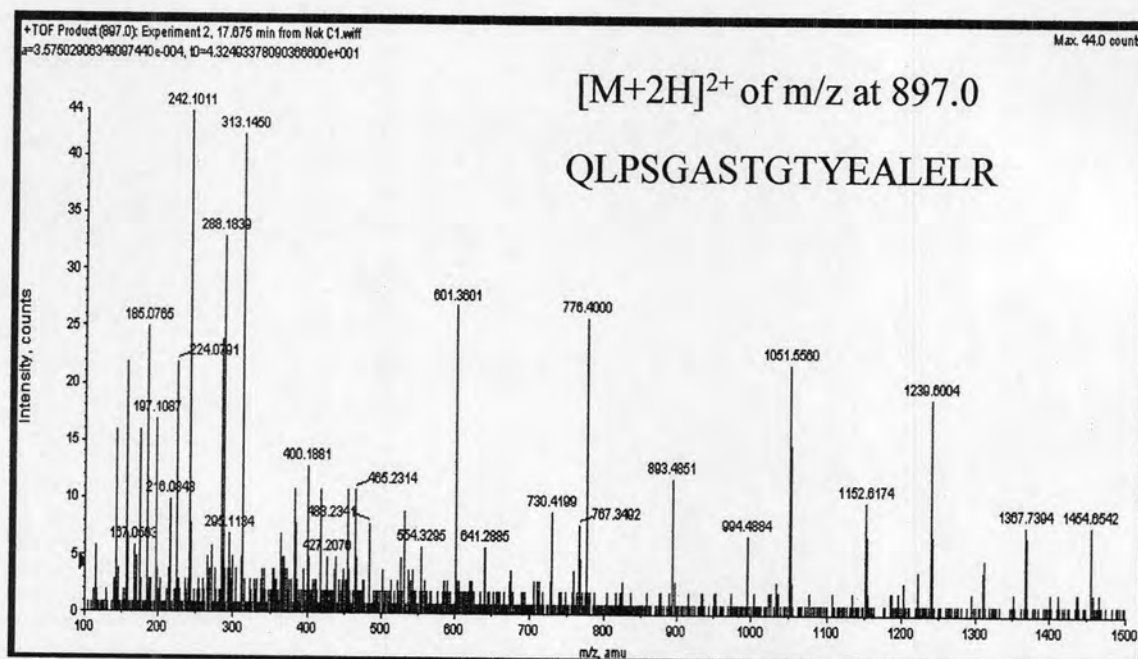


Figure 6C The product ion spectrum of precursor ion at m/z of 672.1 (spot 25).

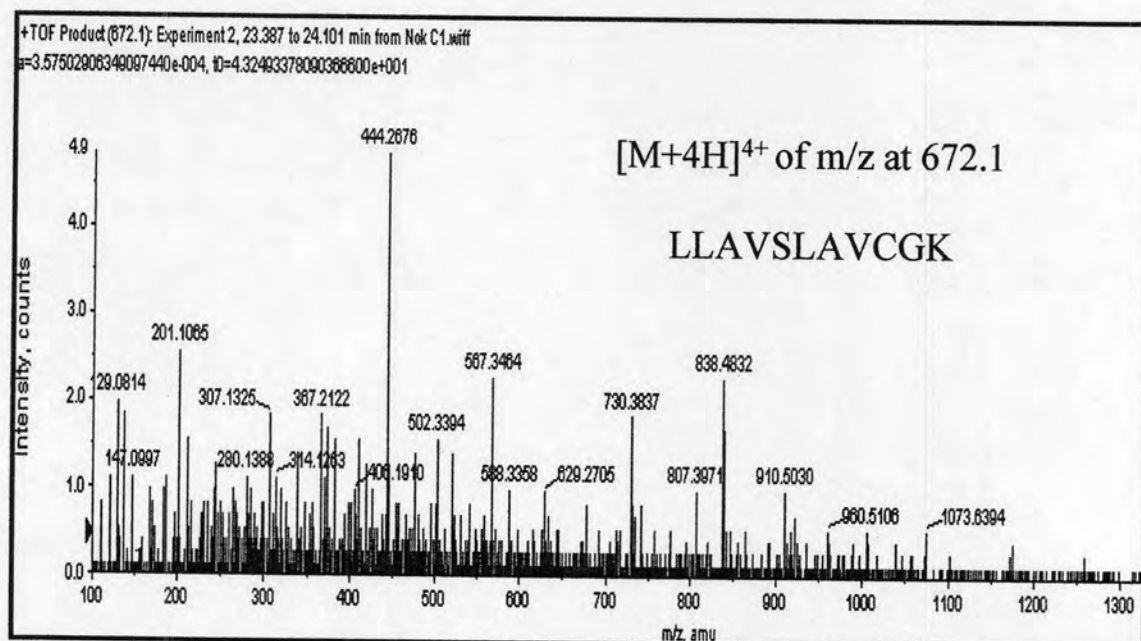


Figure 7C The product ion spectrum of precursor ion at m/z of 678.9 (spot 25).

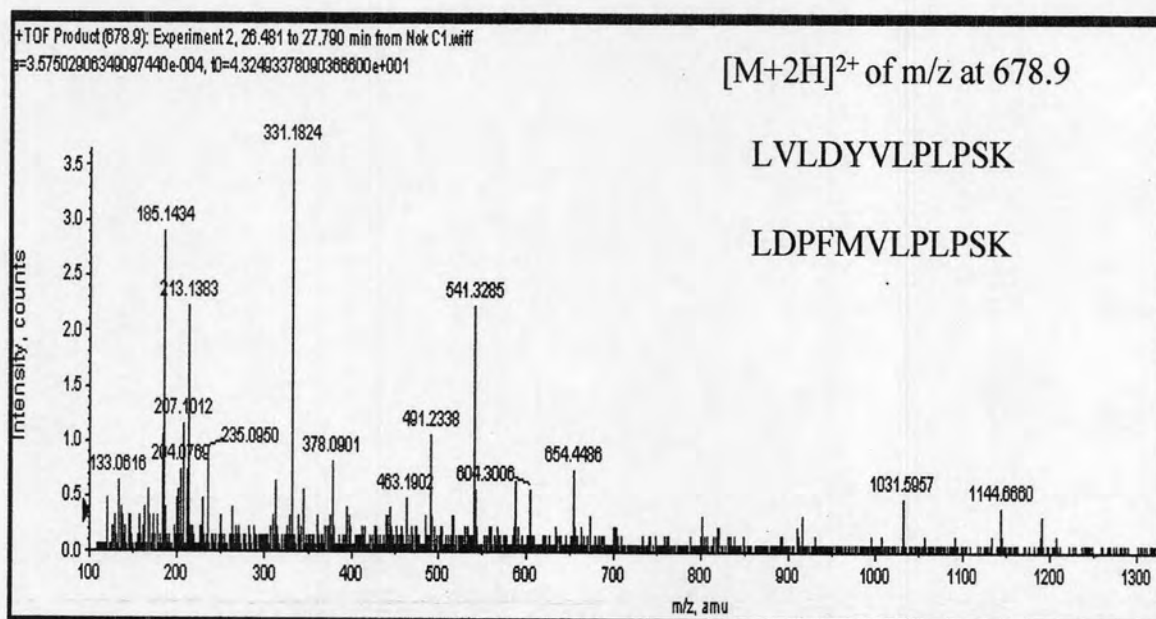


Figure 8C The product ion spectrum of precursor ion at m/z of 647.0 (spot 25).

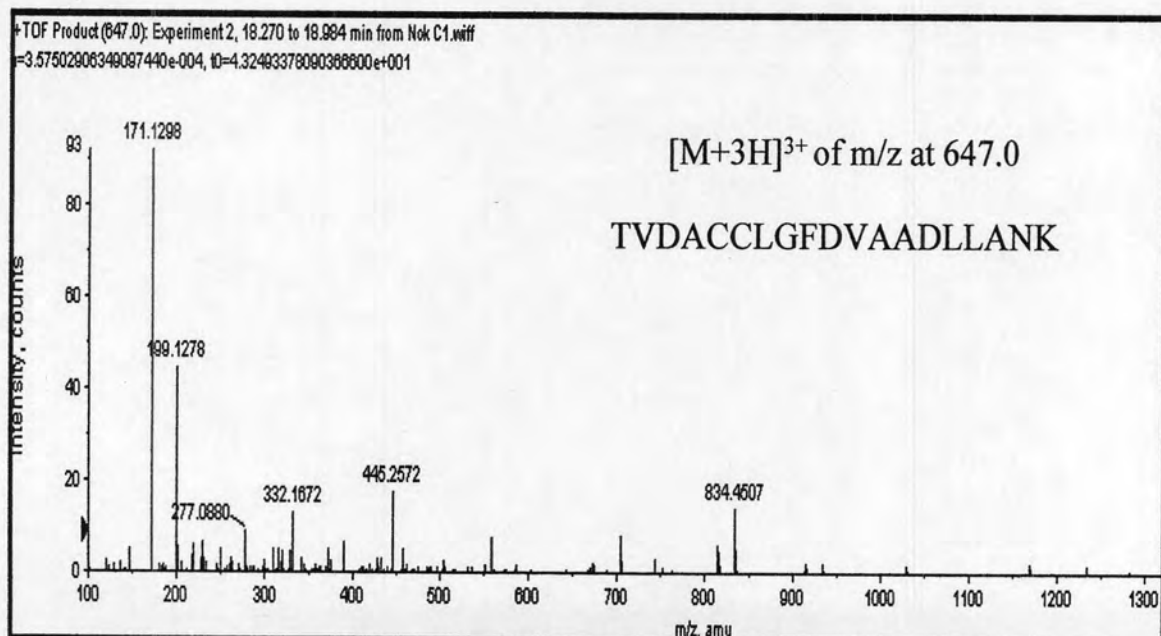


Table 1C Amino acid sequences of peptide precursor using BLAST search of protein spot 1

Precursor mass (m/z)	Sequence (<i>De Novo</i> sequencing)
1676.826	(-)QSPCYLPSHGAFNEK(-), (-)QLACYLYMLCTVEK(-), (-)QSPCYLPSHGAPVGHK(-), (-)QLACYLFFLCTVEK(-), (-)QLACYLFFLCTMPK(-)
2231.9717	(-)TMYSNPNYLPSHAGLYGGK(-), (-)TMYSNPNYLPSHAGLYNK(-), (-)TMAAGGGFDYYLPSHAGLYGGK(-), (-)TMSCSSPNYYLPSHAGLYNK(-), (-)TMAAGGGFDYYLPSHAGLYNK(-)
2231.9772	(-)TLNGPNNPYLPSHQVGHK(-), (-)TLNGNGHGGYYLPSHQVGHK(-), (-)TLNGCFGDYYLPSHQVGHK(-), (-)TLNGNGHNYYLPSHQVGHK(-), (-)TLNGPNPYLPSHQVGHK(-)
1907.8763	(-)QVSASACYLPSHQLYNK(-), (-)QWASACYLPSHQLYNK(-), (-)QNPGSYYLPSHQLYNK(-), (-)QHCMFYLPSHQLYNK(-), (-)ELPGSYYLPSHQLYNK(-)
1447.6874	(-)FGGPEVASGAGGAEDK(-), (-)FGGPEVASGGAGAEDK(-), (-)FNPEVASGAGGAEDK(-), (-)FNPEVASGGAGAEDK(-), (-)FGGPEVASGQGAEDK(-)
2718.2726	(-)QPPLPVQGGPSQCVQNSAVPSGSNDK(-), (-)QPPLPVQGGPSQCVQNSAVPSGSNDK(-), (-)QPPLPVQGGPSQCVQNSAVPSGSNDK(-), (-)QPPLPVQGGPSQCVQNSAVPSGSNDK(-), (-)QPPLPVQGAANESVQNSAVPSGSNDK(-)
2718.2734	(-)QVPDLPGHSSAPCVQGGAVSGAGAGEDK(-), (-)QVPDLPGHSSAPCVQGGAVSGAGGAEDK(-), (-)QVPDLPGHSSAPCVQGGAVSGAQEDK(-), (-)QVPDLPGHCAAPCVQGGAVSGAGAGEDK(-), (-)QVPDLPGHCAAPCVQGGAVSGAGGAEDK(-)
1561.7121	(-)MVELELGSGSSNPDK(-), (-)VMEAGVQSGSSNPDK(-), (-)ETEAGVQSGSSNPDK(-), (-)VMEAGVANSRSSNPDK(-), (-)ETELELGSGSSNPDK(-)
1788.8509	(-)TPSACGAGPVPLTPLLAPK(-), (-)TPSACGPVPLTPLLAPK(-), (-)TPSPQCQVPLTPLLAPK(-), (-)TPSACGQVPLTPLLAPK(-), (-)TPSKPSGSVPLTPLLAPK(-)
1788.8513	(-)MCHSWPVPLTPLLAPK(-), (-)MHSCWPVPLTPLLAPK(-), (-)ENGASVSPVPLTPLLAPK(-), (-)QDGASVSPVPLTPLLAPK(-), (-)ENGASWPVPLTPLLAPK(-)

Table 1C Amino acid sequences of peptide precursor using BLAST search of protein spot 1 (continued)

Precursor mass (m/z)	Sequence (<i>De Novo</i> sequencing)
2388.0699	(-)TPGATTAENGGMLLNAANFLLAGGK(-), (-)TPGATTAEGNGMLLNAANFLLAGGK(-), (-)TPGATEATNGGMLLNAANFLLAGGK(-), (-)TPGATAVMGNGMLLNAANFLLAGGK(-), (-)TPGSVVSSGQMLLNAANFLLAGGK(-)
1007.4287	(-)EDDLEFLK(-), (-)DEDLEFLK (-), (-)EDDLEYPK (-), (-)DEDLEYPK (-),(-)EDVEEFLK (-)
1007.433	(-)VPGAALSYCK(-), (-)VPQALSYCK(-), (-)VPGAALSCYK(-), (-)VPGAALFCCK(-),(-)VPGAEEAYCK(-)
1031.555	(-)TPAGGLEFLK(-), (-)TPGAGLEFLK(-), (-)TPQGLEFLK(-), (-)VVGAGLEFLK(-), (-)VVAGGLEFLK(-)
1031.5558	(-)VVGAGLEFLK(-), (-)VVQGLEFLK(-), (-)VVGAGLEYPK(-), (-)VVGAGAPAGCCK(-), (-)VVGAGLEPYK(-)
1031.5537	(-)TPAGGLEFLK(-), (-)TPAGGLGFNAK((-), (-)TPGAGLEFLK(-), (-)TPQGLEFLK(-), (-)TPAGGLGFQGK(-)
1031.5548	(-)VVEFLLNAK(-), (-)VVEFLLANK(-), (-)VVEFLGQLK(-), (-)TPEFLLNAK(-), (-)TPEFLLANK(-)
1766.8613	(-)FGPYQHEAPPSLSPLK(-), (-)FGPYQHEAPPSLSPLK(-), (-)EATQYHEAPPSLSPLK(-), (-)EATYQHEAPPSLSPLK(-), (-)FPGQYHEAPPSLSPLK(-)
2953.4977	(-)HEAPGGGVPLGGK(-), (-)HEAPGGGVPLNK(-), (-)HEAPNGVPLGGK(-), (-)HEAPNGVPLNK(-), (-)HEAPNVGPLGGK(-)
2510.1004	(-)TMTGGNHSFPGFCSPDGSAGALASGGK(-), (-)TMT GGNGGALLGFCSPDGSAGALASGGK(-) , (-)TMTGVVETGPNFCSPDGSAGALASGGK(-), (-)TMTGVVTEGPNFCSPDGSAGALASGGK(-), (-)TMTGVLSEGPNFCSPDGSAGALASGGK(-)
2510.1218	(-)SEFGSGAAALSGGK(-), (-)SEFGSGAAALSNK(-), (-)SEFGSGGVVASGGK(-), (-)WEFGSGAAALSGGK(-), (-)WEFGSGAAALSNK(-)
1609.7363	(-)VDGAAAFNAEFEELK(-), (-)DVGAAAFNAEFEELK(-), (-)GAVDAAFNAEFEELK(-), (-)AGVDAAFNAEFEELK(-), (-)QVDAAFNAEFEELK(-)

*The matched amino acid sequences of query tryptic peptides from Blast search are highlighted in bold underlined.

Table 1C Amino acid sequences of peptide precursor using BLAST search of protein spot 1 (continued)

Precursor mass (m/z)	Sequence (<i>De Novo</i> sequencing)
2497.1676	(-)QLSDVMCVQAGMGHEAPPSLPSLK(-), (-)QLSDVMTTQAGMGHEAPPSLPSLK(-), (-)QLSDTTMVQAGMGHEAPPSLPSLK(-), (-)QLSDETTTQAGMGHEAPPSLPSLK(-), (-)QLSDVMCNLAGMGHEAPPSLPSLK(-)
2684.2417	(-)QPSATGYAASAFNDEHEAPPSLPSLK(-), (-)QPSATSSGQFQFDEHEAPPSLPSLK(-), (-)QPSATSGFSAAFNDEHEAPPSLPSLK(-), (-)QPSATSGFTGAFNDEHEAPPSLPSLK(-), (-)QPSATSFGTGAFNDEHEAPPSLPSLK(-)
2684.2845	(-)EAPSPLPSLK(-), (-)EAPSPLSPLK(-), (-)EAPPTVSPLK(-), (-)EAPPTVPSLK(-), (-)EAPPSLPSLK(-)
2684.2859	(-)YAPPTVPSLK(-), (-)YAPPTVSPLK(-), (-)YAPPSLPTVK(-), (-)YAPPSLPSLK(-), (-)YAPPVTPSLK(-)
2508.1632	(-)QPTCCGDTYNVPLLLNAGFDVLR(-), (-)QVACCGDEYNVPLLLNAGFDVLR(-), (-)QPTCACAMYNVPLLLNAGFDVLR(-), (-)QPTCCAAMYNVPLLLNAGFDVLR(-), (-)QPCTCAAMYNVPLLLNAGFDVLR(-)
2508.2132	(-)QPVGCHHYYPPLLLNGAFDVLR(-), (-)QPVCHGGDQYPPLLLNGAFDVLR(-), (-)QPVCFPCYPPLLLNGAFDVLR(-), (-)QPVGCHGDQYPPLLLNGAFDVLR(-), (-)QPVCGHGDQYPPLLLNGAFDVLR(-)
2508.227	(-)QPCTYETPYVPLLLNQFDVLR(-), (-)QPCTEYTPYVPLLLNQFDVLR(-), (-)QPTCYETPYVPLLLNQFDVLR(-), (-)QNMTGYQPYVPLLLNQFDVLR(-), (-)QPTCEYTPYVPLLLNQFDVLR(-)
2684.3074	(-)LLADSSSGVLR(-), (-)LLNQVYVLR(-), (-)LLADSCAGVLR(-), (-)LLNQYVLR(-), (-)LLNQFDVLR(-)
2508.2135	(-)NLNQDFLVR(-), (-)LLNQFDVLR(-), (-)NLNQFDLVR(-), (-)NLNQDFVLR(-), (-)NLLEFDLVR(-)

Table 2C Amino acid sequences of peptide precursor using BLAST search of protein spot 8

Precursor mass (m/z)	Sequence (<i>De Novo</i> sequencing)
2388.0642	(-)NPNTSAAPEMNYLPSHAGLYNK (-), (-)NPSTAANPEMNYLPSHAGLYNK(-), (-)NPSTNAAPEMNYLPSHAGLYNK (-), (-)NPNSTAAPPEMNYLPSHAGLYNK(-), (-) NPSTAN APPEMNYLPSHAGLYNK (-)
2388.1003	(-)NPGVCANPNPYLPSHAGLYNK(-), (-)NPGVCANNPPYYLPSHAGLYNK(-), (-)NPGS DANPNPYL PSHAGLYNK(-), (-)NPGDSANPNPYLPSHAGLYNK(-), (-)NPGAMANPNPYLPSHAGLYNK(-)
2388.085	(-)TLNAHTDNSFELLMHAGLYNK(-), (-)TLGGAHDTNSFELLMHQLYNK(-), (-)TLNAHDTNSFELLMHAGLYNK(-), (-)TLNAHTDNSFELLMHQLYGGK(-), (-)TLNAHTDNSFELLMHQLYNK (-)
1974.9128	(-)QNPNPYYLPSHQLYNK(-), (-)QNPPGGYYLPSHQLYNK(-), (-)QNPNPYYLPSHQLYNK(-), (-)QNPPNYLPSHQLYGGK(-), (-)QNPPNYLPSHQLYNK(-)
1766.8287	(-)ACDGMGANVPLTPLGSHK(-), (-)CADGMGANVPLTPLGSHK(-), (-)CAGDMGANVPLTPLGSHK(-), (-)ACGDMGANVPLTPLGSHK(-), (-)SSDGMGANVPLTPLGSHK(-)
1766.8488	(-)DTSCAGANVPLTPLGSHK(-), (-)ESSCAGANVPLTPLGSHK (-), (-)DTSACGANVPLTPLGSHK (-), (-)SSEACGANVPLTPLGSHK (-), (-)DTGCTGANVPLTPLGSHK (-)
2130.0149	(-)TFVPTAPGGMYTGYAGDVQAK (-), (-)TFVPTANPMYTYAGDVQAK(-), (-)EMVTRPGGMYTGYAGDVQAK(-), (-)TFVPTAPNMYTYAGDVQAK (-), (-)TFPVTANPMYTYATAVQAK (-)
2666.2463	(-)QAASRPCNCVHLGGSNLPNAGGGFLK(-), (-)QAASRPCMQVHLGGSNLPNAGGGFLK(-), (-)QAASRPCNCVHLGGSNLPNAGGGFLK(-), (-)QAASRPCWHTQLGGSNLPNAGGGFLK(-), (-)QAASRPCWHTQLGGSNLPNAGGGFLK (-)
2510.1342	(-)TMTAGSGSVASHSYSDPGSAAGLASGGK(-), (-)TMTALGCGGASHSYSDPGSAAGLASGGK(-), (-)TMTALCGGGASHSYSDPGSAAGLASGGK(-), (-)TMTAGSSGVASHSYSDPGSAAGLASGGK(-), (-)TMTALGCGGAHSSYSDPGSAAGLASGGK(-)

*The matched amino acid sequences of query tryptic peptides from Blast search are highlighted in bold underlined.

Table 2C Amino acid sequences of peptide precursor using BLAST search of protein spot 8 (continued)

Precursor mass (m/z)	Sequence (<i>De Novo</i> sequencing)
1609.7465	(-)TGPSAAFNAEGHAGVPK(-), (-)QDVAAFNAEGHAGVPK(-), (-)TLQAAFNAEGHAGVPK(-), (-)EGVGAAFNAHATAAVPK(-), (-)DVGAAAFNAHATAAVPK (-)
2684.2886	(-)CYAPPEASPLK(-), (-)CYAPPTVSPLK(-), (-)CYAPPEASPLK(-), (-)CYAPPTVPSLK (-), (-)HEAPPAAQGGLK(-)
1031.5686	(-)HGPPSLPSLK(-), (-)HGPPSSPLK(-), (-)HGPPSPSLK(-), (-)GHPPLSSPLK(-), (-)GHPPLSPSLK(-)
1031.5729	(-)TPGAGFDLVR(-), (-)VVGMGSDVLR(-), (-)VVGMGSDLVR(-), (-)TPGAGDLFVR(-), (-)TPGMGSDVLR(-)
2509.2569	(-)VSWPVAVGTFK (-), (-)VSWPVAVASFK (-), (-)VSWPVAVSAFK (-), (-)VSWPVAVTGFK (-), (-)VSWPVAVYNR (-)

Table 3C Amino acid sequences of peptide precursor using BLAST search of protein spot 13

Precursor mass (m/z)	Sequence (<i>De Novo</i> sequencing)
1403.7065	(-)EELTTLVPDEM(-), (-)EELTTLVDPEM(-), (-)EELTTLTFADHK(-), (-)EELTTLTAFDHK(-), (-)EELTTLTKPNCR(-)
2796.2067	(-) FELDEEPDQKFELDEEPQDK(-), (-)FELDEEPWGK(-), (-)FELDEEPENK(-), (-)FELDEEPGWK(-), (-)FELDEEPNEK(-)
2796.2199	(-)LGEEDGGVVK(-), (-)LGEEDGGVVK(-), (-)LGEEDNVVK(-), (-)LGEEDGGVVK(-), (-)LGEEDNVVK(-)
2797.2351	(-)LGEAHFSGGK(-), (-)LGEAHFSGGK(-), (-)LGEAHFSGGK(-), (-)LGEAHFSNK(-), (-)LGEAHFNSK(-)
1261.608	(-)FLLGEEDVVGK(-), (-)FLLGEEDVVNK(-), (-)FLLGCAAASAPGGK(-), (-)FLLGCAAASAPNK(-), (-)FLLGCATGAAPGGK(-)
2569.0032	(-)TLCGGHADEEDSHHSGAPAGSEYDK(-), (-)TLCGCTFSAEDSHHSGAPAGSEYDK(-), (-)TLCGGHADEEDSHHSGAPAGSEYDK(-), (-)TLCGCTFTGEDSHHSGAPAGSEYDK(-), (-)TLCGHEENEDSHHSGAPAGSEYDK(-)

Table 4C Amino acid sequences of peptide precursor using BLAST search of protein spot 25

Precursor mass (m/z)	Sequence (<i>De Novo</i> sequencing)
2388.1081	(-)HSTPNQAMFLYLPSHQLYNK(-), (-)HSPYGNPNFLYLPSHQLYNK(-), (-)HGMPNQAMFLYLPSHQLYNK(-), (-)HSPYGNPNFLYLPSHQLYNK(-), (-)HGVEGGQAMFLYLPSHQLYNK(-)
2388.1421	(-)YLPESHQSCATR(-), (-)YLPESHAGLYNK(-), (-)YLPESHQLYNK(-), (-)YLPESHQLYGGK(-), (-)YLPESHQYLNK(-)
2388.1044	(-)HQLYGGK(-), (-)HAGLYNK(-), (-)HQLYLNK(-), (-)HLQYLNK(-), (-)HAYNK(-)
2388.1082	(-)SPDATDQLSK(-), (-)SPDAPGLYNK(-), (-)SPDATDLQSK(-), (-)SPWPGLYNK(-), (-)QLNYFGK(-)
1559.8017	(-)TLATTSHSPEEFLK(-), (-)LTATTSHSPEEFLK(-), (-)LTATTSHSPQLYNK(-), (-)TLATTSHSPQLYNK(-), (-)VDATTSHSPQLYNK(-)
1974.935	(-)QFVGCVLENPSHQLYLNK(-), (-)TMAAGCVLENPSHQLYLNK(-), (-)TMAAGCVLENPSHQLYGGK(-), (-)QFPFNLENPSHQLYLNK(-), (-)QNFFPLENPSHQLYLNK(-)
2232.0238	(-)PQPQFEGGK(-), (-)PKPQFEGGK(-), (-)PQPQEFNK(-), (-)PKPQEFNK(-), (-)PQPQLYLNK(-)
2717.3566	(-)QNEQPESEDK(-), (-)QNEQPCLEDK(-), (-)QNEKPESEDK(-), (-)QNEQPTDEDK(-), (-)QNEQPSEEDK(-)
2631.2461	(-)QVLETGVSFGGQPEQGGTGVPSSEEDK(-), (-)QVLETGVSFGGKPEQGGTGVPSSEEDK(-), (-)QVLETGVSFGGQPEQGGTGVPSSEEDK(-), (-)QVLETGVSQFNPEQGGTGVPSSEEDK(-), (-)QVLEGTVSFGGQPEQGGTGVPSSEEDK(-)
2631.2562	(-)LEATAAGPDK(-), (-)LEATAAGPDK(-), (-)LEATAGAPDK(-), (-)LEATAAGAPDK(-), (-)LEDGAQPDK(-)
1766.8687	(-)ESGCTGANVPLTPLGPVR(-), (-)JDGCTGANVPLTPLGPVR(-), (-)ESGTCGANVPLTPLGPVR(-), (-)QDMCGANVPLTPLGPVR(-), (-)EGSCTGANVPLTPLGPVR(-)
1766.8814	(-)AGGQSQSTGTTGPGPLGPVR(-), (-)AGGQSQSTGTTGPLLAPK(-), (-)ANQSQSTGTTGPGPLGPVR(-), (-)ANQSQSTGTTGPLLAPK(-), (-)GAGQSQSTGTTGPGPLGPVR(-)
1791.8946	(-)QL PSGASTGTYEALELR (-), (-)LGAPSGASTLHCGSAGGGHR(-), (-)LAGPSGASTLHCGSAGGGHR(-), (-)VAAPSGASTLHCGSAGGGHR(-), (-)ALGPSGASTLHCGSAGGGHR(-)

*The matched amino acid sequences of query tryptic peptides from Blast search are highlighted in bold underlined.

Table 4C Amino acid sequences of peptide precursor using BLAST search of protein spot 25 (continued)

Precursor mass (m/z)	Sequence (<i>De Novo</i> sequencing)
1766.8962	(-)QDTPYPVDVDPLGPVR(-), (-)GADTPYPVDVDPLGPVR(-), (-)QAGGGAYPVDVDPLGPVR(-), (-)QAGNAYPVDVDPLGPVR(-), (-)QGGGAAYPVDVDPLGPVR(-)
1937.8604	(-)TVDACCL LGFDVA ADLLANK(-), (-)TWSDC LGFDVA ADLLANK(-), (-)TWSDC LGFDVA ADLLAGGK(-), (-)TWCDSL LGFDVA ADLLANK(-), (-)TWCDSL LGFDVA ADLLAGGK(-)
1543.7512	(-)ETEDHVEFLLNAK(-), (-)TEEDHVEFLLNAK(-), (-)EETDHVEFLLNAK(-), (-)EVMDHVEFLLNAK(-), (-)EPAQWVEFLLNAK(-)
1007.4568	(-)CAEFLLNAK(-), (-)ACEFLLNAK(-), (-)CAEFLLANK(-), (-)SSEFLLANK(-), (-)ACEFLLANK(-)
1031.5777	(-)TPYLVSGPAK(-), (-)VVYLVSGPAK(-), (-)TPYLVQSPK(-), (-)VVYLVSGAPK(-), (-)VVYLVSQPK(-)
1812.8377	(-)QPVAYSPN WYAGGYLK (-), (-)QPSPVHPN WYAGYGLK (-), (-)QPALFWN WYAGYGLK (-), (-) QPVAYSPN WYAGYGLK (-), (-)QPSPVHPN WYAGGYLK (-)
1031.58	(-)TPEFLLNAK(-), (-)VVEFLLNAK(-), (-)VVEFLNALK(-), (-)TPEFLN LAK (-), (-)VVEFLN LAK (-)
1031.5824	(-)VVEFLNALK(-), (-)TPEFLNALK(-), (-)VVEYNPALK(-), (-)YSQLLPALK(-), (-)FCQLLPALK(-)
2019.069	(-)FGSQASPSGGK(-), (-)FGSQASPSNK(-), (-)FGSQAALS SNK (-), (-)FGSQAALS SGGK (-), (-)FGSQAPSSNK(-)
1031.5772	(-)LTSQALAS SNK (-), (-)T LSQALAS SNK(-), (-)LTSNGSVL NK (-), (-)LTSNGSALA AK (-), (-)T LSNGSALA AK(-)
2510.1895	(-)GSQAPSSNK(-), (-)GSQALAS GGK (-), (-)GSQALAS SNK (-), (-)GSQ LAAS SNK(-), (-)GSQALS AGGK (-)
2019.0744	(-)QDLVGAGGGK(-), (-)QDLVGGAGGK(-), (-)QDLVGQGGK(-), (-)QDLVAGG NK (-), (-)QDLVGAG NK (-)
2511.2192	(-)YPVGA AFCK (-), (-)YPVAG AFCK (-), (-)YPVGAGTYK(-), (-)YPVAG HALK (-), (-)YPVGA HALK (-)
1899.9198	(-)QTTEEMYLLPVAGSS FK (-), (-)QEP SFMYLLPVAGSS FK(-), (-)QEM LSMYLLPVAGSS FK(-), (-)QEP SFMYLLPVAGSS FK(-), (-)QTTE EFFLLPVAGSS FK(-)

*The matched amino acid sequences of query tryptic peptides from Blast search are highlighted in bold underlined.

Table 4C Amino acid sequences of peptide precursor using BLAST search of protein spot 25 (continued)

Precursor mass (m/z)	Sequence (<i>De Novo</i> sequencing)
1899.919	(-)QYHEAFSEAPPSLPSLK(-), (-)QYEHAFSEAPPSLPSLK(-), (-)HGPHEAFSEAPPSLPSLK(-), (-)HEAYGAFSEAPPSLPSLK(-), (-)HEAGYAFSEAPPSLPSLK(-)
1275.6529	(-)HTQAPPGSGPSLK(-), (-)HTQAPPGSGSPLK(-), (-)HAASAPPGSGPSLK(-), (-)QHTAPPGSGPSLK(-), (-)HTQAPLQGPSLK(-)
2684.3466	(-)LLAVSLCVQK(-), (-)LLAVSLCGGLK(-), (-)LLAVSLCNLK(-), (-) LLAVSLAVCGK (-), (-)LLAVSLAVGCK(-)
1044.5705	(-)YVELLPVGR(-), (-)YVELLPALK(-), (-)GPNQFDVLR(-), (-)GPGGQFDVLR(-), (-)YLDLLPVGR(-)
2684.3537	(-)LLNQDFVLR(-), (-)LLNQVYVLR(-), (-)LLNQFDLVR(-), (-)LLNQDFVLR(-), (-)LLNQVYVLR(-)
1355.767	(-)LVLDY VLPPLPSK (-), (-)VLLDYVLPLPSK(-), (-)LDPDYVLPLPSK(-), (-)LPDDYVLPLPSK(-), (-)LDPFM VLPPLPSK (-)
1031.5841	(-)VDPVAVSAFK(-), (-)TLPVAVSAFK(-), (-)LTPVAVSAFK(-), (-))DVPVAVSAFK(-), (-)VDPVASAVFK(-)

*The matched amino acid sequences of query tryptic peptides from Blast search are highlighted in bold underlined.

Appendix D

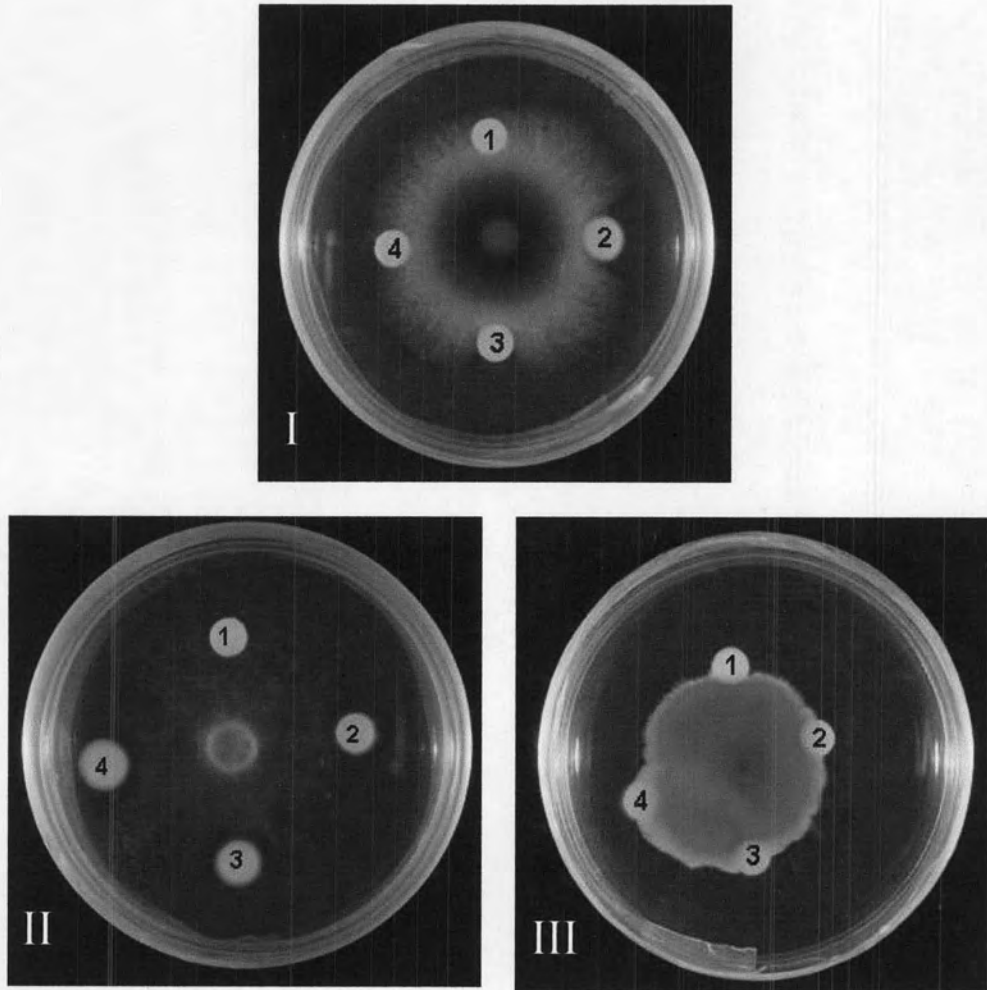


Figure 1D Antifungal activity screening of crude protein from *P. dulce* seeds toward (I) *Macrophomina phaseolina*, (II) *Phymatotrichopsis omnivora*, and (III) *Fusarium avicenarium*. (1) Control: 40 μ l of 100 mM Tris-HCl buffer (pH 8.0), (2) 10 mg crude protein in 40 μ l 100 mM Tris-HCl buffer, (3) 2 mg crude protein in 40 μ l 100 mM Tris-HCl buffer, (4) 1 mg crude protein in 40 μ l 100 mM Tris-HCl buffer

Figure 2D Mascot search result of the purified antifungal protein (G4).

(MATRIX)
(SCIENCE) **Mascot Search Results**

Protein View

Match to: **gi|157831883** Score: **144**

Chain A, Thermal Stability Determinants Of Chicken Egg-White Lysozyme Core Mutants: Hydrophobicity, Packing Volume And Conserved Buried Water Molecules
Found in search of C:\DOCUME~1\mascot\LOCALS~1\Temp\masFB.tmp

Nominal mass (M_r): **14290**; Calculated pI value: **9.46**

NCBI BLAST search of **gi|157831883** against nr

Unformatted sequence string for pasting into other applications

Taxonomy: *Gallus gallus*

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **21%**

Matched peptides shown in **Bold**

1 KVFGRCELAA AMKRHGLDNY RGYSLGNWVC AAK**FESNFNT QATNRNTDGS**
51 TDYGLLQINS RWWCNDGRTP GSRNLCNIPC SALLSSDITA TVNCAKKIVS
101 SGNGMNAWVA WRNRCKGTDV QAWIRGCRLL

Show predicted peptides also

Sort Peptides By



Residue Number



Increasing Mass



Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss Sequence	
34 - 45	714.8356	1427.6567	1427.6429	10	0 K.FESNFNTQATNR.N	(Ions score 71)
46 - 61	877.4298	1752.8450	1752.8278	10	0 R.NTDGSTDYGLLQINSR.W	(Ions score 73)

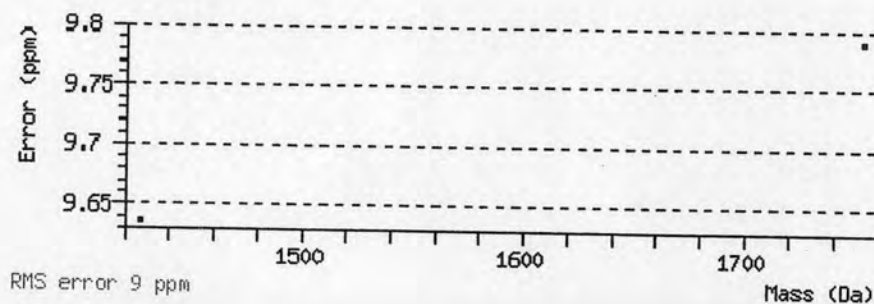


Table 1D Peptide sequences of tryptic peptides from the purified antifungal protein (G4) using Mascot search

Observed Mass (m/z)	Peptide MW		MOWSE score	Sequence
	(exp.)	(thero.)		
877.4298	1752.8450	1752.8278	73	-NTDGSTDYGLLQINSR-
714.8356	1427.6567	1427.6429	71	-FESNFNTQATNR-
524.7611	1047.5076	1047.5600	39	-ALEFNDVIK-
691.3464	1380.6782	1380.5576	35	-DSGSPMSNGSSNNK-
595.8224	1189.6303	1189.6740	32	-CSSNVLTKLLK-
563.2698	1686.7875	1686.8649	31	-TLAAGLRSSDQAASPR-
537.2822	1072.5499	1072.5553	27	-ANPEPLFGTK-
548.7489	1095.4833	548.7489	26	-APILWCHTR-
568.2845	1134.5545	1134.5743	25	-EYEPCLLIR-
705.3489	1408.6832	1408.7966	24	-LFNDLILFSISK-
696.3672	1390.7199	1390.6801	23	-SSKSDQATGNVAAR-
567.8274	1133.6403	1133.5941	22	-HGAGLHADTKK-
617.2913	2465.1361	2465.2775	22	-GSDTAGTGLGLSIVKHLHHHDSK-
519.2510	1036.4874	1036.5567	22	-THPHVPPPR-
479.2602	956.5058	956.5039	21	-GPAASPSKSR-
668.8145	1335.6145	1335.7146	20	-QGYKAGALAAATSK-
545.3074	1088.6002	1088.5284	20	-MKEPSSPTGR-
611.3538	1220.6931	1220.6037	19	-LTSLFSPGASQN-
581.3191	1160.6237	1160.6666	18	-APALPAVAPGRAA-
501.2781	1000.5416	1000.5090	15	-RPPFDDVR-
589.3550	1176.6955	1176.5921	14	-RAGISMVTGTAN-
577.3065	576.2992	576.2881	11	-AHGHR-
523.2941	1044.5737	1044.4845	11	-HGASMGLMKNK-

Note: Matched peptides shown in bold.

VITA

Miss Narumon Sawasdipuksa was born on September 8, 1980 in Bangkok. She obtained a Bachelor of Science, from Department of Chemistry, Faculty of Science, Chulalongkorn University in 2000. In 2003, she received Master's degree of Science, majoring in Chemistry, from Department of Chemistry, Faculty of Science, Chulalongkorn University. She was admitted to the Doctor of Philosophy program in Organic chemistry at Chulalongkorn University in 2004. While she was studying, she received a 2004 Royal Golden Jubilee Ph.D. research scholarship from the Thailand Research Fund. She was a visiting scientist from July 17, 2007 through July 17, 2008 and conducted a part of her research in the laboratory of Associate Professor Dr. Lloyd W. Sumner at The Samuel Roberts Noble foundation, OK, USA.

