

Table S1. The peptides identified by HPLC-ESI-MS analysis

Protein Group Accessions	Name	Peptide sequence <sup>a</sup>	MH+[Da] <sup>b</sup>	Modifications	q-Value <sup>c</sup>	PEP <sup>d</sup>	Xcorr <sup>e</sup>	Charge	m/z <sup>f</sup> [Da]	Replicate number <sup>g</sup>
AJF03209.1	MPT32	SKTTGDPPFPQG	1231.58878		0	0.000031167	3.398998857	3	411.2011108	Replicate 1,2,3
		AARLGSDMGEF	1153.542		0	0.0025983	4.699460387	3	385.1855164	Replicate 1,2,3
		AIAAMASASLVT	1147.60608		0	0.0027918	3.255498201	3	383.2068787	Replicate 1,2,3
		ANGVSG	504.24319		0	0.0092236	2.914167047	1	504.2431946	Replicate 1,2,3
		APPPADPNAPPPV	1336.69937		0	0.00033705	3.09982755	3	446.2379761	Replicate 1,2,3
		AVPATANADPEPAPPV	1516.7609		0	0.00035469	3.368763298	3	506.2584839	Replicate 1,2,3
		DAAH	413.18076		0	0.0035361	2.6082654	1	413.1807556	Replicate 1,3
		DANGVSGSASYEYVKFSDPSKPNGQIWTGVIGSPAANAPDAGPPQRW	4888.29262	N-Term(Acetyl)	0	0.002515738	4.48195076	4	1222.828613	Replicate 1,2,3
		FALP	447.25778		0	0.001676287	2.058724958	1	447.257782	Replicate 1,2
		GSPAAN	558.25433	N-Term(Acetyl)	0	0.00923443	2.006696105	1	558.2543335	Replicate 1,3
		HFDY	581.23328		0	0.00043281	2.189351395	1	581.2332764	Replicate 1,2,3
		IWTGVIGSPAANAPDAGPPQRWFV	2549.2725	N-Term(Acetyl)	0	0.00924534	3.811559975	3	850.4290161	Replicate 1,2,3
		LAESIRPLVAPPPAPAPAPAEAPAPAPAGEVAPTPTTPPQR	4169.19834		0	0.0024534	3.089836851	3	1390.404297	Replicate 2,3
		LLSKTTGDPPFPGQPPPVAN	2033.0709		0	0.00076167	3.372875994	3	678.3618164	Replicate 1,2,3
		LTRRKGRLLAALIAAM	1712.06467		0	0.0036891	3.680278146	3	571.3597412	Replicate 1,2,3
		LVAPP	593.36566		0	0.00064035	2.053795198	1	593.3656616	Replicate 1,2
		LVTV	473.29532	N-Term(Acetyl)	0	0.00945298	2.155110046	1	473.2953186	Replicate 2,3
		MGEF	483.18604		0	0.00808283	2.069672152	1	483.1860352	Replicate 1,2
		NGVSGS	520.23779		0	0.00932659	2.043905258	1	520.237793	Replicate 1,2
		PGTR	430.24292		0	0.00903f56	2.075941193	1	430.2429199	Replicate 1,3
		PNAAPPADPNAPPPVIAPNAPQPVRIIDNPVGGFSFALPAGWVE	4519.36264		0	0.00932657	3.617172251	3	1507.125732	Replicate 1,2,3
		PPVANDTRIVLGRDLQKLYASAEATDSKAAARLGSDMGEF	4234.11875		0	0.0079299	4.532343906	3	1412.044434	Replicate 1,2,3
		QETVSLDANGVSGSASYEYVKFSDPSKPNGQIWTGVIGSPAANAPDAGP	4936.38979		0	0.0033507	4.991447258	4	1234.852905	Replicate 1,2,3
		STAAAPPATPVAPPPAAAN	1979.01798	N-Term(Acetyl)	0	0.0009711	4.446426213	3	660.3441772	Replicate 1,2,3
		VAVPATANADPEPAPP	1516.75925		0	0.00038475	3.782221556	3	506.2579346	Replicate 1,2,3
		WTGV	462.23315		0	0.0096359	2.038321245	1	462.2331543	Replicate 2,3
		YASAEATDSKAAARLGSDMGEFYMPYPGTRINQETVS	3984.79941		0	0.0077841	3.554167652	3	1328.937988	Replicate 1,2,3

CAA53143. 1	MPT64	VATAAPKTYCE	1153.54438		0	0.0011484	3.600166774	3	385.1863098	Replicate 1,2,3
		ADTDPLPVVFPIVQGELSKQ	2153.14267		0	0.00917463	4.309296727	3	718.3857422	Replicate 1,2,3
		FMLVTAVVLLCCSGVATAAPKTYCEEL	2874.42827	N-Term(Acetyl)	0	0.00334266	2.219003096	2	1437.717773	Replicate 1,2,3
		FNPG	434.20166		0	0.00945279	2.055417138	1	434.2016602	Replicate 1,3
		LNITSATYQSAIPRGTQAVVLKVYQNAGGTHPTTTYKAF	4265.23765		0	0.0094809	8.003737378	7	610.1830444	Replicate 1,2,3
		LVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQMSDPAYNINI	4903.35708		0	0.00947932	4.800712347	4	1226.594727	Replicate 1,2,3
		QTGQ	475.21402	N-Term(Acetyl)	0	0.00969046	1.995042706	1	475.2140198	Replicate 1,2,3
		RKPITYDTLWQADTDPL	2033.04563		0	0.00022707	4.571767759	3	678.3533936	Replicate 1,2,3
		TDTGQACQIQMSDPAYNINISLPSYYPDQKSLENYIA	4151.96042		0	0.00967356	5.217301351	3	1384.658325	Replicate 1,2
CCP43682.1	PstS1	IDGPAPDGYPIINYEY	1796.83207		0	0.0012195	4.431837249	3	599.6155396	Replicate 1,2,3
		AAAGCG	449.17889		0	0.00049302	2.372447991	1	449.178894	Replicate 1,2
		AFHERYPNVTTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGMAAHK GL	4917.42148		0	0.00974257	4.187691104	3	1639.812012	Replicate 1,2,3
		AIVN	416.24872		0	0.00243	2.163995856	1	416.2487183	Replicate 1,3
		ALGENGNMVTGCAETPGCVAYIGISFLDQASQRGLGEAQLGNSSGN	4687.18813	M10(Oxidation)	0	0.00967459	5.504872698	4	1172.55249	Replicate 1,2,3
		FGTT	425.20187		0	0.0032517	2.076373297	1	425.2018738	Replicate 1,2,3
		FGTTVDFPAVPGALGENGNMVTGCA	2539.13834		0	0.0064476	5.346179008	3	847.0509644	Replicate 1,2,3
		FHER	588.28668		0	0.007875	2.022431257	1	588.2866821	Replicate 2,3
		GASDAYLSEGMAAHK	1622.72551		0	0.0076824	4.453323483	2	811.866394	Replicate 1,2,3
		GVNL	444.24377	N-Term(Acetyl)	0	0.007923626	1.950363649	1	444.2437744	Replicate 1,2
		KIRLHT	767.48839		0	0.00973452	2.028176047	2	384.2478333	Replicate 1,2,3
		KLNG	431.2641		0	0.00015939	1.980164593	1	431.2640991	Replicate 1,3
		KSPGFGTTVDFP	1252.6092		0	0.00051327	5.124933398	3	418.2079163	Replicate 1,2,3
		LHTLLA	667.41815		0	0.00059355	2.183272952	1	667.4181519	Replicate 1,3
		LHWAITDGNKASFLDQVHFQ	2327.14176		0	0.00065844	4.324119502	3	776.385437	Replicate 1,2,3
		LLLAAAGCGS	875.45879		0	0.002453432	3.205284667	2	438.2330322	Replicate 1,2,3
		LNGK	431.26471		0	0.00974636	2.015185201	1	431.2647095	Replicate 2,3
		NGGMVTGCAETPGCVAYIGISFLDQASQRGLGEAQLGNSS	3958.86457		0	0.00974624	7.340895617	5	792.5787354	Replicate 1,2,3
		PGFGTTVDFPAVPGALGENGNMVTGCAETPGCVAYIGISFLDQASQR	4887.22338	N-Term(Acetyl); M24(Oxidation)	0	0.00978532	9.658131113	11	445.2087402	Replicate 1,2,3
		PLLLAAAGCGSKPPSGPETGAGAGTVATTPASSPVT	3278.65639		0	0.00959835	4.758069664	4	820.4195557	Replicate 1,2

		PLPPAVVKLSDALI	1432.86737		0	0.008762459	4.412128472	3	478.2939758	Replicate2,3
		TTPASSPVTLAETGSTALLYPLFNLWGPAFHERYPNVTITAQGTGSGAG	4948.44204		0	0.00954798	5.009198439	4	1237.865967	Replicate1,2,3
		WAIT	490.26349		0	0.00956246	2.020125601	1	490.2634888	Replicate2,3
		WGPA	430.20688		0	0.007474354	2.193955207	1	430.2068787	Replicate2,3
CCP46703.1	CFP10	QWRGAAGTAAQAAVVRFEAANKQ	2529.31968		0	0.00945228	4.399345472	3	843.7780762	Replicate1,2,3
		DAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTA	4519.25278		0	0.0080244	5.441708852	3	1507.089111	Replicate1,2,3
		GDLKTQIDQVESTAGSLQGQWR	2417.1868		0	0.00079389	4.54818325	3	806.4004517	Replicate1,3
		GNFERISGDLK	1235.63568		0	0.00017415	5.059049198	3	412.5500793	Replicate1,2,3
		GTAAQ	447.22223		0	0.00066951	2.086983728	1	447.222229	Replicate1,2

<sup>a</sup> Peptide sequence: identified peptide sequences for each protein; <sup>b</sup> MH+[Da]: mass-to-charge ratio (m/z) of the peptide with z=1. <sup>c</sup> q-value: the minimal false discovery rate at which the identification is considered correct. <sup>d</sup> PEP: the probability that the observed PSM is incorrect; <sup>e</sup> Xcorr: cross-correlation value; <sup>f</sup> m/z: mass-to-charge ratio. <sup>g</sup> The replicate numbers of identified peptide sequences for the protein in LC-MS/MS analysis, which all samples were performed in three replicates.

Table S2. Biochemical clinical factors of enrolled pulmonary TB patients and non-TB patients

Biochemical clinical factors	Samples, No.		<i>P</i>
	Pulmonary TB ( <i>n</i> =43)	Non-TB ( <i>n</i> =30)	
ALT (U/L)	17.0±16.7	16.9±6.6	0.031
AST (U/L)	26.7±21.6	19.5±5.7	0.752
ALP (U/L)	89.0±25.6	76.4±24.0	0.038
TP (g/L)	63.8±4.9	63.2±13.6	0.927
ALB (g/L)	33.8±4.8	38.7±9.9	0.000
TBIL (μmol/L)	13.3±9.0	14.8±8.2	0.460
DBIL (μmol/L)	4.0±3.7	2.8±1.0	0.049
IBIL (μmol/L)	9.2±5.7	10.1±4.4	0.493
GGT (U/L)	48.9±77.6	24.1±19.9	0.014
ADA (U/L)	11.6±5.6	11.5±19.5	0.005
GLU (mmol/L)	5.7±2.4	5.5±1.9	0.752
BUN (mmol/L)	4.9±2.9	5.1±1.1	0.039
CREA (μmol/L)	67.0±22.3	61.1±15.7	0.523
UA (μmol/L)	350.8±186.5	311.4±91.3	0.922
K <sup>+</sup> (mmol/L)	4.0±0.5	4.5±1.9	0.079
Na <sup>+</sup> (mmol/L)	139.6±4.0	135.5±25.7	0.098
Cl <sup>-</sup> (mmol/L)	102.5±4.7	105.7±7.2	0.052
LDH (U/L)	169.3±47.1	227.7±212.9	0.073
CRP (mg/L)	35.9±38.5	6.4±11.6	0.000

ALT, alanine aminotransferase; AST, aspartate aminotransferase; ALP, alkaline phosphatase; TP, total protein; ALB, Albumin; TBIL, total bilirubin; DBIL, direct bilirubin; IBIL, indirect bilirubin; GGT, gamma-glutamyltransferase; ADA, adenosine deaminase; GLU, glucose; BUN, blood urea nitrogen; CREA, creatinine; UA, uric acid; K<sup>+</sup>, potassium; Na<sup>+</sup>, sodium; Cl<sup>-</sup>, chloride; LDH, lactate dehydrogenase; CRP, C-reactive protein.

Table S3. Blood cytology index of enrolled pulmonary TB patients and non-TB patients

Blood cytology index	Samples, No.		<i>P</i>
	Pulmonary TB ( <i>n</i> =43)	Non-TB ( <i>n</i> =30)	
WBC (10 <sup>9</sup> /L)	6.4±2.1	6.5±1.9	0.809
RBC (10 <sup>12</sup> /L)	4.0±0.8	4.3±0.5	0.100
HGB (g/L)	120.8±21.7	133.3±13.7	0.007
PLT (10 <sup>9</sup> /L)	253.2±93.2	249.8±78.2	0.869
LY (10 <sup>9</sup> /L)	1.3±0.5	1.8±0.6	0.000
MONO (10 <sup>9</sup> /L)	0.5±0.2	0.4±0.2	0.215
NEUT (10 <sup>9</sup> /L)	4.4±2.1	4.0±1.6	0.302
ESO (10 <sup>9</sup> /L)	0.1±0.1	0.2±0.1	0.190
BASO (10 <sup>9</sup> /L)	0.03±0.02	0.04±0.02	0.480
LY% (%)	21.5±10.1	29.8±10.2	0.001
MONO% (%)	7.8±1.8	6.8±2.1	0.033
NEUT% (%)	67.8±10.8	59.9±10.8	0.003
ESO% (%)	2.4±1.8	3.0±2.3	0.264
BASO% (%)	0.5±0.3	0.6±0.3	0.487

WBC, white blood cell count; RBC, red blood cell count; HGB, hemoglobin concentration; PLT, platelet count; LY, lymphocyte count; MONO, monocyte count; NEUT, neutrophil count; ESO, eosinophil count; BASO, basophil count; LY%, lymphocyte percentage; MONO%, monocyte percentage; NEUT%, neutrophil percentage; ESO%, eosinophil percentage; BASO%, basophil percentage.

Table S4. The characteristics of five candidate peptides

Name	Peptide sequence	Length <sup>a</sup>	Antigenicity	Surface <sup>b</sup>	Hydrophilicity	Disordered Score <sup>c</sup>
MPT32-2	SKTTGDPPFPGQ	12	1.71	1.51	0.18	0.5336
MPT64-2	RKPITYDTLWQADTDPL	17	1.76	0.88	0.1	0.3941
CFP10-2	GNFERISGDLK	11	1.85	0.95	0.5	0.406
PstS1-2	GASDAYLSEGDMAAHK	16	2.88	1	0.28	0.3767
PstS1-3	KSPGFGTTVDFP	12	0.66	0.76	-0.17	0.5022

<sup>a</sup>: numbers of amino acids of each peptide; <sup>b</sup>: scores for probability of exposure on the protein surface;

<sup>c</sup>: scores for protein secondary structure uncertainty.

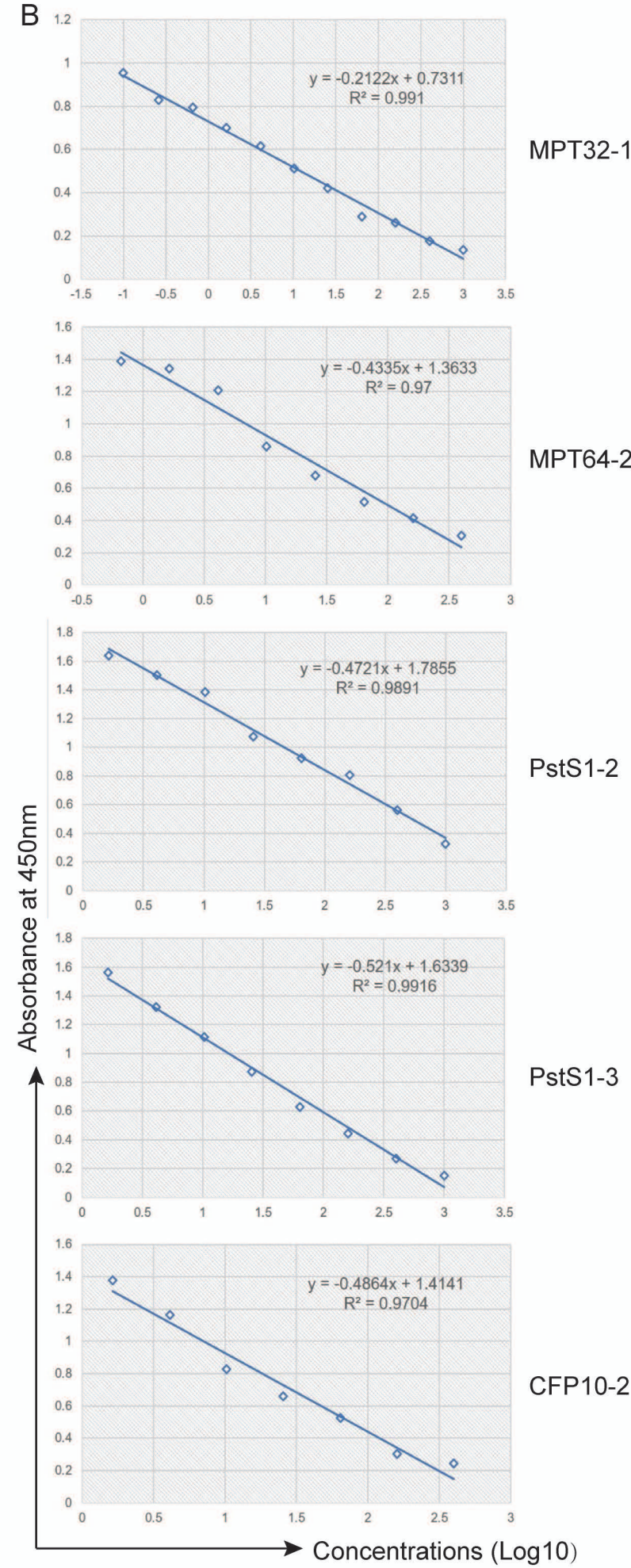
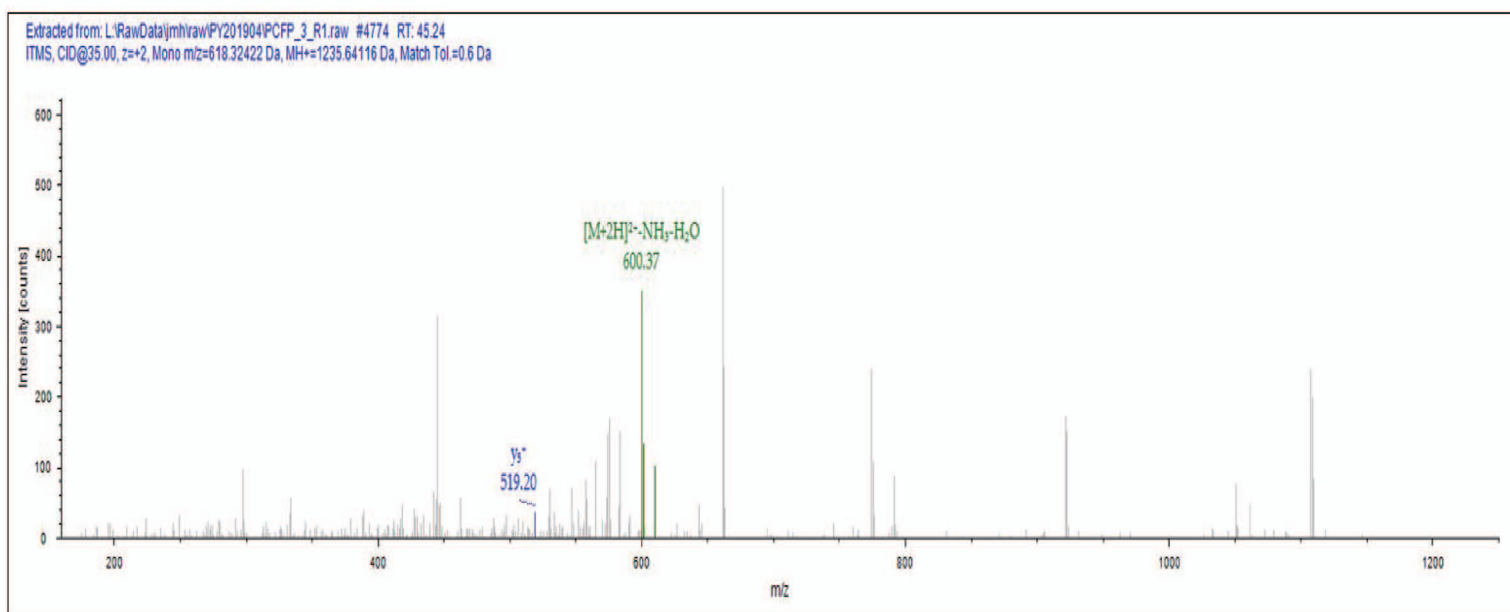
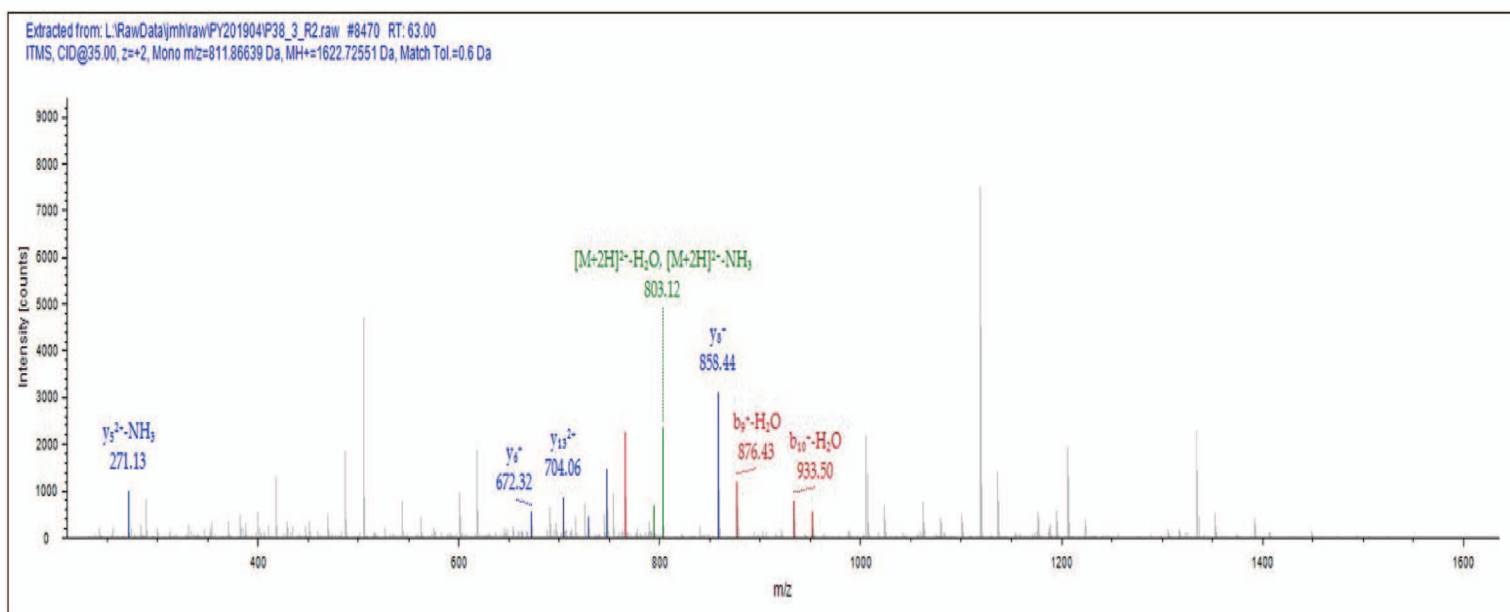
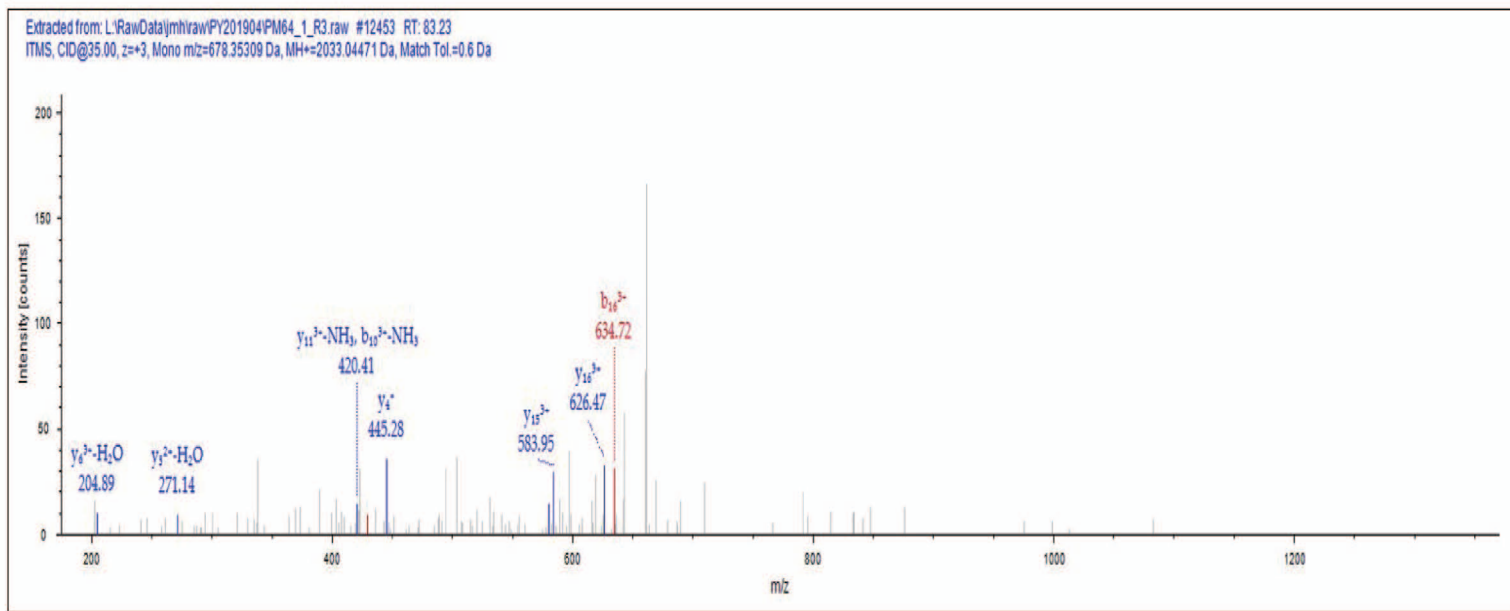


Figure S1. Representative MS spectra (A) and standard calibration curves for selected peptides (B).