

Table S1. Identification of differentially expressed proteins in A549 cells treated with T63 and curcumin by MALDI-TOF-MS/MS.

Spot no. ^a	Protein name	Gene symbol	Accession no. ^b	MW (kDa) ^c	pI ^d	Matched Peptides	Protein Score ^e	Coverage (%) ^f	Fold change (Treated/Control) ^g	
									T63	curcumin
<i>Energy Metabolism</i>										
18	glucose-6-phosphate dehydrogenase	G6PD	gi 26224790	55188	6.91	21	142	44	0.42±0.08	1.02±0.08
25	glutamate dehydrogenase	GLUD1	gi 183056	28791	7.89	17	400	62	7.09±0.12	2.18±0.15
26	aldose reductase	AKR1B1	gi 4502049	36230	6.51	18	515	58	1.92±0.08	0.95±0.07
43	glutamate dehydrogenase 1, mitochondrial precursor	GLUD1	gi 4885281	61701	7.66	30	713	49	1.59±0.05	1.77±0.05
65	enolase 1 variant	ENO1	gi 62896593	47453	7.01	25	564	58	2.21±0.11	1.32±0.16
<i>Cell structure and motility</i>										
1	Vimentin	VIM	gi 62414289	53676	5.06	38	866	74	0.49±0.13	0.95±0.18
2	vimentin	VIM	gi 62414289	53676	5.06	45	873	77	0.53±0.09	0.89±0.12
3	laminin-binding protein	LBP	gi 34234	31888	4.84	14	643	48	0.58±0.06	0.52±0.08
4	tropomyosin 2 (beta)	TPM2	gi 55859705	37010	4.73	12	90	27	0.62±0.11	0.55±0.06
6	tropomyosin 1 (alpha)	TPM1	gi 11959803	32552	4.69	9	112	34	0.47±0.08	0.57±0.12
9	cytokeratin 8	KRT8	gi 181573	53529	5.52	40	464	61	2.50±0.15	2.33±0.08
10	actin-related protein 3	ACTR3	gi 5031573	47797	5.61	30	660	61	0.57±0.10	0.46±0.09
15	cytokeratin 18 (424 AA)	KRT18	gi 30311	47305	5.27	12	202	16	2.26±0.12	1.17±0.16
30	F-actin-capping protein subunit beta isoform 1	CAPZB	gi 4826659	30952	5.69	19	554	51	0.61±0.08	0.58±0.13
40	cytokeratin 18 (232 AA)	KRT18	gi 34035	26434	4.92	10	147	24	> 50	1.01±0.05
52	cytoplasmic dynein 1 intermediate chain 2	DYNC1I2	gi 24307879	71811	5.08	18	303	35	0.65±0.15	0.69±0.12
63	mitochondrial inner membrane protein isoform 3	IMMT	gi 15435496	82973	6.15	26	483	36	1.73±0.06	1.56±0.10

Table S1. Continue 1

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									T63	curcumin
<i>Protein degradation</i>										
16	ubiquitin B, isoform CRA_d	UBB	gi 119624910	13123	6.84	8	304	47	> 50	> 50
28	ubiquitin carboxyl-terminal hydrolase isozyme L1	UCHL1	gi 21361091	25151	5.33	14	529	72	0.49±0.07	0.76±0.06
29	proteasome activator complex subunit 2	PSME2	gi 30410792	27555	5.54	12	239	42	0.32±0.08	0.45±0.11
33	proteasome activator complex subunit 1 isoform 2	PSME1	gi 30581141	28755	6.28	14	444	39	0.37±0.14	0.33±0.10
34	26S protease regulatory subunit 7 isoform 1	PSMC2	gi 4506209	49002	5.71	30	839	55	0.55±0.05	0.45±0.09
47	proteasome (prosome, macropain) 26S subunit, ATPase, 5, isoform	PSMC5	gi 119614675	43266	8.50	20	366	43	0.63±0.08	0.52±0.12
<i>Protein folding</i>										
49	heat shock protein HSP 90-beta	HSP90A B1	gi 20149594	83554	4.97	27	607	43	0.32±0.25	0.41±0.14
50	heat shock protein HSP 90-alpha isoform 2	HSP90A A1	gi 154146191	85006	4.94	24	618	35	0.25±0.18	0.36±0.11
51	heat shock 70kDa protein 8 isoform 2 variant	HSPA8	gi 62896815	53580	5.62	16	447	39	0.19±0.22	0.38±0.08
54	HSP70-1	HSPA1 A	gi 4529893	70280	5.48	37	846	60	3.05±0.15	1.95±0.18
55	heat shock protein gp96 precursor	HSP90B 1	gi 15010550	90309	4.73	33	571	40	0.11±0.13	0.32±0.09
56	Heat shock protein HSP 90-alpha 2	HSP90A A1	gi 61656603	98622	5.09	36	520	38	0.48±0.16	0.41±0.22
58	endoplasmic reticulum resident protein 44 precursor	ERP44	gi 52487191	47341	5.09	19	576	48	2.94±0.08	1.06±0.12

Table S1. Continue 2

Spot no. ^a	Protein name	Gene symbol	Accession no. ^b	MW (kDa) ^c	pI ^d	Matched Peptides	Protein Score ^e	Coverage (%) ^f	Fold change (Treated/Control) ^g	
									T63	curcumin
<i>Signal transduction</i>										
17	Ras-GTPase-activating protein SH3-domain-binding protein	G3BP1	gi 119582065	52962	5.48	5	73	24	0.51±0.06	0.63±0.15
37	14-3-3 protein zeta/delta	YWHAZ	gi 4507953	27899	4.73	23	420	58	0.52±0.15	0.56±0.12
38	SFN protein	SFN	gi 16306737	24378	4.77	21	402	61	0.58±0.16	0.83±0.21
<i>RNA processing</i>										
12	TAR DNA-binding protein 43	TARDBP	gi 6678271	45053	5.85	12	313	21	0.58±0.12	0.56±0.18
19	heterogeneous nuclear ribonucleoprotein K isoform a variant	HNRNP K	gi 62088704	49002	5.48	19	440	44	0.54±0.12	0.85±0.07
35	heterogeneous nuclear ribonucleoproteins C1/C2 isoform b	HNRNP C	gi 117190174	32375	4.94	15	247	35	0.61±0.08	1.06±0.25
44	heterogeneous nuclear ribonucleoprotein H	HNRNP H	gi 5031753	49484	5.89	28	709	63	0.70±0.10	1.66±0.10
<i>Protein Metabolism and Modification</i>										
14	protein phosphatase type 2A catalytic subunit	PPP2CB	gi 17149125	36179	5.22	8	92	29	1.95±0.08	0.41±0.20
31	Ribosomal protein, large, P0	RPLP0	gi 12654583	34424	5.42	24	1050	59	0.59±0.06	0.57±0.09
32	eukaryotic translation initiation factor 3 subunit I	EIF3D	gi 4503513	36878	5.38	18	691	65	0.51±0.14	0.46±0.13
36	protein S100-A6	S100A6	gi 7657532	10230	5.33	4	126	30	> 50	> 50
39	elongation factor 1-beta	EEF1B2	gi 4503477	24919	4.50	13	709	50	0.82±0.09	0.61±0.07
66	elongation factor Tu	TUFM	gi 704416	49851	7.70	28	686	62	1.69±0.10	1.21±0.16
68	eukaryotic translation initiation factor 5A-1 isoform B	EIF5A	gi 4503545	17049	5.08	8	311	42	1.55±0.05	1.08±0.12

Table S1. Continue 3

Spot no. ^a	Protein name	Gene symbol	Accession no. ^b	MW (kDa) ^c	pI ^d	Matched Peptides	Protein Score ^e	Coverage (%) ^f	Fold change (Treated/Control) ^g	
									T63	curcumin
<i>oxidative stress</i>										
13	cytochrome b-c1 complex subunit 1	UQCRC1	gi 46593007	53297	5.94	27	687	62	8.47±0.16	1.41±0.25
22	acyl-Coenzyme A dehydrogenase, very long chain, isoform CRA_a	ACADV L	gi 119610653	73288	9.16	12	142	21	2.99±0.04	1.06±0.13
27	glutathione S-transferase-P1c	GSTP1	gi 726098	23583	5.43	14	561	70	0.66±0.11	0.62±0.16
46	NADH-ubiquinone oxidoreductase 75 kDa subunit	NDUFS1	gi 316983156	74393	5.61	33	726	49	1.86±0.05	1.53±0.10
48	cytochrome c oxidase subunit 6B1	COX6B1	gi 4502985	10414	6.54	5	79	60	1.43±0.15	1.51±0.19
60	inosine-5'-monophosphate dehydrogenase 2	IMPDH2	gi 66933016	56226	6.44	23	416	46	0.53±0.11	0.41±0.08
<i>Cell proliferation, Cell Cycle, and apoptosis</i>										
7	PCNA	PCNA	gi 49456555	29029	4.57	22	557	73	0.47±0.13	0.55±0.12
20	X-ray repair cross-complementing protein 5	XRCC5	gi 10863945	83222	5.55	28	308	35	0.46±0.04	0.93±0.11
24	annexin A1	ANXA1	gi 4502101	38918	6.57	21	974	62	2.52±0.23	1.95±0.05
41	galectin-1	LGALS1	gi 4504981	15048	5.34	10	311	76	0.55±0.15	0.61±0.09
42	omega-amidase NIT2	Nit2	gi 9910460	30988		13	202		12.30±0.05	0.98±0.18
45	histone-binding protein RBBP4 isoform c	RBBP4	gi 207029439	43740	4.80	13	294	43	0.63±0.08	0.53±0.16
57	Chain B, Crystal Structure Of The Ku Heterodimer	XRCC6	gi 15825665	64577	5.98	27	239	31	0.58±0.12	0.56±0.21
64	programmed cell death 6-interacting protein isoform 1	PDCD6IP	gi 22027538	96590	6.13	21	274	26	2.15±0.16	1.96±0.11
59	voltage-dependent anion channel 2	VDAC2	gi 55664661	30842	8.0	12	812	57	3.01±0.09	1.05±0.13
61	Annexin A2	ANXA2	gi 18645167	38780	7.57	26	696	67	3.41±0.05	0.88±0.10

Table S1. Continue 4

Spot no. ^a	Protein name	Gene symbol	Accession no. ^b	MW (kDa) ^c	pI ^d	Matched Peptides	Protein Score ^e	Coverage (%) ^f	Fold change (Treated/Control) ^g	
									T63	curcumin
<i>Others</i>										
5	spermine synthase	SMS	gi 791051	41852	4.87	21	635	66	0.51±0.15	0.43±0.12
11	unnamed protein product		gi 194376310	38950	5.76	5	148	27	2.00±0.09	0.59±0.15
23	kinesin light chain 4 isoform b	KLC4	gi 41871960	70965	5.95	9	139	16	3.43±0.12	1.07±0.05
53	Importin 5	IPO5	gi 28277071	126989	4.82	11	177	11	0.15±0.28	0.20±0.09
62	POTE ankyrin domain family member F	POTEF	gi 153791352	123020	5.83	12	111	7	> 50	1.03±0.28
67	importin subunit beta-1	KPNB1	gi 19923142	98420	4.68	34	442	41	0.09±0.05	0.11±0.06

^a Spot numbers correspond with 2-DE gel as shown in Fig. 3. ^b Accession number in NCBI database. ^c MW (kDa): molecular mass of predicted protein. ^d pI: pI of predicted protein. ^e Protein score: In MASCOT, the score for an MS/MS match is based on the absolute probability (P), and the observed match between the experimental data and database sequence is a random event. The reported score is $-10 \log(P)$. So during a search, if 1.5×10^5 peptides fell with the mass tolerance window the precursor mass, and the significance threshold was chosen to be 0.05, this would translate into a score threshold of 65. ^f Percentage of predicted protein sequence covered by matched sequence. ^g Fold change is expressed as a ratio of the Vol% between of treated/control cells, and each value represents the mean value \pm SD of three independent experiments.