

Table 1SM: Comparative Proteomics of SI-83 treated SaOS-2 cell line.

¹AN: accession number, ²protein biological processes, and ³Loc: protein sub-cellular localization: C (cytosol); Cs (cytoskeleton); M (membrane); Mel (melanosome); ER (endoplasmic reticulum); N (nucleus); S (secreted). Retrieved by UniProt knowledgebase (<http://www.uniprot.org/>).

⁴Fold-change: according to SI-83 treated/DMSO control ratio. "a" indicates the absence of proteins in SI-83 treated sample.

⁵ID: Identification method (MS: MALDI-Tof peptide fingerprinting analysis; PSD: single peptide post-source decay analysis; GM: gel-matching analysis).

Spot	Protein	Gene Name	AN ¹	Loc ²	Biological processes ³	Fold-change ⁴	ID ⁵	Est'd Z	Peptides	Sequence coverage %	Theor. pI/M _r
Energy											
ENO1	Alpha-enolase	<i>ENO1</i>	P06733	C	Glycolytic enzyme	3.38	MS/PSD	2.41	27	60	6.99/47037
ENO1_a	Alpha-enolase	<i>ENO1</i>	P06733	C	Glycolytic enzyme, MPB1: tumour suppressor	a	MS/PSD	1.82	7	19	6.99/47037 (5.93/36928)
TPI1	Triosephosphate isomerase	<i>TPI1</i>	P60174	C	Gluconeogenesis, Glycolysis, Pentose shunt.	3.28	MS/PSD	2.40	16	69	6.45/26669
Cell rescue, defence & stress											
SOD1	Superoxide dismutase [Cu-Zn]	<i>SOD1</i>	P00441	C	Response to oxidative stress.	a	MS/PSD	1.78	5	56	5.70/15804
TXNDC17	Thioredoxin domain-containing protein 17	<i>TXNDC17</i>	Q9BRA2	C	Disulfide reductase. Modulates TNF-alpha signaling and NF-kappa-B activation. response to oxidative stress.	a	MS/PSD	1.84	4	47	5.38/13809
SH3BGRL	SH3 domain-binding glutamic acid-rich-like protein	<i>SH3BGRL</i>	O75368	C, N		a	MS/PSD	2.40	6	73	5.22/12774
Metabolism (nucleotide, nucleoside and nucleic acid)											
ATIC	Bifunctional purine biosynthesis protein PURH	<i>ATIC</i>	P31939	C	De novo biosynthesis of purine nucleotide	2.37	MS/PSD	1.94	6	15	6.27/64615
APRT	Adenine phosphoribosyltransferase	<i>APRT</i>	P07741	C	Biosynthesis of purine nucleotides, purine salvage	a	MS/PSD	1.70	6	50	5.77/19476
NDPKA	Nucleoside diphosphate kinase A	<i>NDPKA</i>	P15531	C, N	Nucleotide metabolism, cell differentiation, regulation of apoptosis	a	MS/PSD	2.12	6	32	5.82/17017
Protein fate (folding, maturation, transport)											
APOL2	Apolipoprotein-L2	<i>APOL2</i>	Q9BQE5	C	Lipids transport	2.11	MS/PSD	1.70		16	6.28/37092
P4HB	Protein disulfide-isomerase	<i>P4HB</i>	P07237	ER, Mel	Catalyzes the rearrangement of disulfide bonds.	0.33	MS/PSD	2.40	8	17	4.69/55294
P4HB_a	Protein disulfide-isomerase	<i>P4HB</i>	P07237	ER, Mel	Catalyzes the of disulfide bonds.	a	MS/PSD	2.15	21	41	4.69/55294
NPM1	Nucleophosmin	<i>NPM1</i>	P06748	N, C, Cs	Ribosome biogenesis, protein chaperoning, histone assembly, cell proliferation.	0.07	MS/PSD	1.75	8	24	4.64/32575
NPM1_a	Nucleophosmin	<i>NPM1</i>	P06748	N, C, Cs	Ribosome biogenesis, protein chaperoning, histone assembly, cell proliferation.	0.09	MS/PSD	1.72	6	20	4.64/32575
NPM1_b	Nucleophosmin	<i>NPM1</i>	P06748	N, C, Cs	Ribosome biogenesis, protein chaperoning, histone assembly, cell proliferation.	a	MS/PSD	1.72	6	20	4.64/32575
CAPNS1	Calpain small subunit 1	<i>CAPNS1</i>	P04632	C, M	Regulatory subunit of the calcium-regulated non-lysosomal thiol-protease, involved in cytoskeletal remodeling and signal transduction.	3.95	MS/PSD	1.70	5	19	5.05/28315

CALR	Calreticulin	CALR	P27797	C, ER, M, S	Calcium-binding chaperone that promotes folding, oligomeric assembly and quality control in the endoplasmic reticulum (ER) via the calreticulin/calnexin cycle.	2.5	GM				4.29/48141.56
GRP78	78 kDa glucose-regulated protein	GRP78	P11021	C	Plays a role in facilitating the assembly of multimeric protein complexes inside the ER.	2.02	GM				5.01/70478
RCN1	Reticulocalbin-1	<i>RCN1</i>	Q15293	ER	Regulate calcium-dependent activities in ER, belongs to the CREC family.	a	MS/PSD	1.73	7	25	4.68/35867
RCN1_a	Reticulocalbin-1	<i>RCN1</i>	Q15293	ER	Regulate calcium-dependent activities in ER, belongs to the CREC family.	0.25	MS/PSD	1.70	5	16	4.68/35867
HSPA8	Heat shock cognate 71 kDa protein	<i>HSPA8</i>	P11142	C, Mel	Repressor of transcriptional activation, chaperonin.	a	MS/PSD	1.70	8	22	5.37/70898
Proteasome complex											
PSMA5	Proteasome subunit alpha type-5	<i>PSMA5</i>	P28066	C, N	Proteolytic activity, cleavage of peptide bonds with very broad specificity.	a	MS/PSD	1.74	5	26	4.74/26411
PSMB6	Proteasome subunit beta type-6	<i>PSMB6</i>	P28072	C, N	Proteolytic activity, cleavage of peptide bonds with very broad specificity.	a	MS/PSD	2.28	7	30	4.91/21904
Signal transduction											
TPT1	Translationally-controlled tumour protein	<i>TPT1</i>	P13693	C	Anti-apoptosis, calcium ion transport and homeostasis, microtubule stabilization	a	MS/PSD	2.34	9	38	4.84/19595
GRIA1	Glutamate receptor 1	<i>GRIA1</i>	P42261	M	Ionotropic glutamate receptor. Belongs to the glutamate-gated ion channel family. GRIA1 subfamily.	3.98	MS/PSD	1.70	5	7	7.86/99578
COMT	Catechol O-methyltransferase	<i>COMT</i>	P21964	C, M	Inactivation of catecholamine neurotransmitters and catechol hormones.	0.37	MS/PSD	1.75	5	22	5.26/30037
Cellular organization											
Cytoskeleton & Microtubules											
TPM4	Tropomyosin alpha-4 chain	<i>TPM4</i>	P67936	C, Cs	Muscle filament sliding, response to oxidative stress	0.28	MS/PSD	2.25	9	38	4.67/28391
COTL1	Coactosin-like protein	<i>COTL1</i>	Q14019	C, Cs	Binding to F-actin in a calcium-independent manner.	0.13	MS/PSD	1.75	5	25	5.51/15813
Cell Cycle											
GH1	Somatotropin	<i>GH1</i>	P01241	S	Growth regulation. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates amino acid uptake and protein synthesis in muscle and other tissues.	0.39	MS/PSD	1.70	5	18	5.27/22129