

Table S1 The higher abundant proteins in L6 cell

NO	Protein IDs	Fasta headers	Peptide sequence	Biological function
1	P97691	Forkhead box protein M1	sLTEGLVLDTMNDLSk	Mitochondria metabolism
2	A1A5R2	G protein-coupled receptor (GPCR5A)	aAAPSGcR	Mitochondria-dependent cell apoptosis
3	A0A0G2K836	ADAM metallopeptidase	cVNER	Cell apoptotic process
4	P29457	Serpin H1	kPVEAAAPGTAEk	Cell proliferation
5	Q63041	Alpha-1-macroglobulin	vVVQk	Cell proliferation
6	F1MAL5	Insulin receptor substrate 2	aGAPk	Cell proliferation
7	P70490	Lactadherin	vAHSDDGVQWTVYEEQGTsk	Cell proliferation
8	A1A5P2	Ribosome biogenesis regulatory protein	aRDDTk	Cell cycle process
9	F1M8Y2	Tetraspanin	aVDHVQR	Cell cycle process
10	P13941	Collagen alpha-1(III) chain	gAPGPQGPR	Skeletal development
11	P02454	Collagen alpha-1(I) chain	qGPSGASGER	Skeletal development
12	G3V614	KIF-binding protein	dAEGPGAQR	Embryonic development
13	Q9EPI1	Xylosyltransferase 1	fVEYVAFSTDDLVTk	Proteoglycan biosynthesis
14	Q2KML4	Dynein axonemal heavy chain-like protein	gGSPk	ATP-dependent microtubule motor activity
15	A0A0G2K1E3	[Histone H3]-lysine (4) N-trimethyltransferase	vIHVEGQkHIVIFALRR	Transcription regulation
16	B3SVE5	Neuroprotective protein 8	qQAGQEQEK	Brain formation

Note: C: control; Rot: rotenone 1 μ M; E8: MFG-E8 200 μ g/mL; the lowercase of peptide sequence means that this is a modification site

Table S2 Effect of MFG-E8 on Rot-induced significantly up-regulated proteins of L6 cell

NO	Protein IDs	Fasta headers	Peptide sequence	Biological function
1	D4ADT4	Similar to transmembrane protein 44 isoform	sGQSSR	Mitochondrial function
2	F1M5G8	Transmembrane protein 131	gRPAmPEkQESELSQGkPk	Mitochondrial function
3	U3R7A7	Keratin 71	gGENR	Mitochondria dysfunction
4	Q5XIB0	Interferon regulatory factor 3	IAEDRSk	Mitochondria-dependent cell apoptosis
5	Q66HA1	Mitogen-activated protein kinase kinase kinase 11	sAPGTPGTPR	Mitochondria-dependent cell apoptosis
6	P21707	Synaptotagmin-1	iHLMQNGKR	Cell proliferation
7	Q9EQL5	Transmembrane 4 L6 family member 4	cTGGcAR	Cell proliferation
8	Q9R1J8	Prolyl 3-hydroxylase 1	tAIEESQAER	Cell proliferation
9	Q5BJN8	Replication stress response regulator SDE2	vVSAEVTETR	Cell cycle process
10	B1WBZ4	CDC45 cell division cycle 45-like	qkFQSM DVSLk	Cell cycle process
11	M0RDX6	E2F transcription factor 2	aPPQTRLEVPDR	Cell cycle process
12	Q642A5	DNA polymerase epsilon subunit 3	dcEEQDk	Response to DNA damage
13	B2GV08	AP complex subunit sigma	aIEQADLLQEEAETPR	Protein transport
14	D4A5S6	ALG1	dSQSR	Protein glycosylation

15	E9PT30	Intelectin 1	tQLGFLFLIVATRGGSAAk	Protein phosphorylation
16	A0A0G2JST3	keratin-1	wELLQQVDTSTR	Inflammatory response
17	Q6P777	Multivesicular body subunit 12A	tAAAR	Signaling transduction
18	A0A0G2K7A0	Potassium voltage-gated channel subfamily H	dITDTk	Ion transmembrane transport
19	G3V8Q8	RCG40648, isoform	gQGESAPk	Ion binding
20	D4A0H5	Cleavage and polyadenylation specific factor 1	kEEEETPkAESTEQEPSAPk	Enzyme binding
21	D3ZM91	Syncoilin	gGDGAR	Neuromuscular development
22	D4ABR1	Pleckstrin homology and RhoGEF domain-containing G6	gSGQTR	Neurogenesis
23	M0R8U1	Dynein heavy chain 5, axonemal	rSTHVTPk	ATP-dependent microtubule motor activity
24	D4A409	Laminin subunit alpha 1	qVFQVAYVIIk	Embryonic development
25	O35165	Golgi SNAP receptor complex member 2	vDQLk	Intracellular transport

Note: C: control; Rot: rotenone 1 μ M; E8: MFG-E8 200 μ g/mL; the lowercase of peptide sequence means that this is a modification site

Table S3 Effect of MFG-E8 on Rot-induced significantly down-regulated proteins of L6 cell

NO	Protein IDs	Fasta headers	Peptide sequence	Rot/C
1	P97691	Forkhead box protein M1	sLTEGLVLDTMNDLSk	Mitochondria metabolism
2	D3ZSB7	Ribosomal protein S6 kinase	aGGHDAGk	Mitochondria function

3	D4A4V3	Kruppel-like factor 3	yGVIYSTPLPdk	Mitochondrial function
4	Q5XIH5	GTP binding protein 5	ILSVGIVDHAK	Mitochondria translation
5	D4AAH6	Proteasome assembly chaperone 1	aGTEEEEEEEQSR	Cell proliferation
6	O88432	Polo-like kinase	aDANITPk	Cell proliferation
7	A1A5R2	G protein-coupled receptor	aAAPSGcR	Signaling transduction
8	D3Z8G3	Rpgrip1-like	vEENmGk	Signaling transduction
9	F1M1Q8	EF-hand calcium-binding domain 12	rEQTAPk	Calcium ion binding
10	D3ZSF3	Peptidyl-prolyl cis-trans isomerase	hTGPGILSMANVGPNTNGSGF FicTDk	Protein folding
11	G3V614	KIF-binding protein	dAEGPGAQR	Embryonic development
12	D3ZIG8	Family with sequence similarity 193	qREEEEEEEDEEQR	Bone development
13	B3SVE5	Neuroprotective protein 8	qQAGQEQEk	Brain formation
14	Q9EPI1	Xylosyltransferase 1	fVEYVAFSTDDLVTk	Proteoglycan biosynthesis

Note: C: control; Rot: rotenone 1 μ M; E8: MFG-E8 200 μ g/mL; the lowercase of peptide sequence means that this is a modification site