

Table 1 Identification of several protein spots derived from *Leishmania tropica* proteom using matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) mass spectrometry analysis with mascot score above 52

Spot ID	Protein name	Accession no.	MW (Da)	pI	% coverage	Protein score	Biological process
6289	Beta-tubulin	LmjF33.0798	49 740	4.71	44.0	457	Tubulin is the major constituent of microtubules
6162	Enolase	LmjF14.1160	46 092	5.60	52.6	425	Magnesium ion binding
6362	Heat shock 70-related protein 1, mitochondrial, putative	LmjF30.2490	71 621	5.68	34.2	428	Stress response
6231	Heat shock 70-related protein 1, mitochondrial, putative	LmjF30.2550	70 609	5.67	47.5	398	Stress response
5840	Pyruvate dehydrogenase E1 beta subunit, putative	LmjF25.1710	37 898	5.64	48.2	339	Pyruvate dehydrogenase (acetyl-transferring) activity
6147	Cytochrome c oxidase subunit V, putative	LmjF26.1710	22 291	6.11	57.6	339	Electron transport respiratory chain
5990	Heat shock 70-related protein 1, mitochondrial, putative	LmjF30.2490	71 621	5.68	39.5	286	Stress response
5805	Reiske iron-sulfur protein, putative	LmjF35.1540	33 742	5.93	51.8	254	Oxidoreductase
6125	Cytochrome c oxidase subunit IV	LmjF12.0670	39 434	5.63	44.8	250	Electron transport respiratory chain
8061	Peroxisoxin (tryparedoxin peroxidase)	LmjF23.0040	25 342	6.43	47.7	235	Oxidoreductase
6132	Eukaryotic initiation factor 5a, putative	LmjF25.0720	17 812	4.83	75.3	228	Translation initiation factor activity
8151	Heat shock 70-related protein 1, mitochondrial, putative	LmjF30.2490	71 621	5.68	32.4	196	Stress response
6492	Protein disulfide isomerase	LmjF36.6940	52 377	5.22	19.9	195	Protein disulfide isomerase activity
5693	Putative uncharacterized protein	LmjF13.0450	13 330	5.27	29.7	194	Unknown function
6324	Hypothetical protein	LmjF13.0450	13.92	5.27	20.2	>52	Unknown function
8030	Cytochrome c oxidase subunit IV	LmjF12.0670	39 434	5.63	47.5	191	Electron transport respiratory chain
6231	Aldose 1-epimerase, putative	LmjF35.0970	41 428	5.95	27.7	181	Isomerase
6315	Tryparedoxin peroxidase	LmjF15.1140	21 173	6.43	35.7	168	Oxidoreductase
6151	Carboxypeptidase, putative	LmjF33.2540	57 050	5.55	34.6	166	Carboxypeptidase
6383	Ribonucleoprotein p18, mitochondrial, putative	LmjF15.0280	21 300	6.74	75.4	160	Ribonucleoprotein
5893	Putative uncharacterized protein	LmjF36.6760	28 999	5.53	41.8	157	Unknown function
6264	Putative uncharacterized protein	LmjF36.0480	26 102	4.92	25.7	143	Unknown function
5691	Calpain-like cysteine peptidase, putative	LmjF20.1310	12 936	5.27	36.5	111	Cysteine peptidase, clan CA, family C2, putative
5753	Protein disulfide isomerase	LmjF36.6940	52 377	5.22	11.5	96	Protein disulfide isomerase activity

5972	Phosphomannomutase, putative	LmjF36.1960	28 101	5.18	36.0	91	Hydrolase
5660	Cofilin-like protein	LmjF29.0510	15 715	5.56	26.6	82	Actin binding
6181	Tryparedoxin peroxidase	LmjF15.1080	22 128	6.32	17.5	82	Oxidoreductase activity
5605	Calpain-like cysteine peptidase, putative	LmjF14.0850	12 936	4.70	61.7	78	(see above)
5802	Putative uncharacterized protein	LmjF25.2010	30 292	5.80	30.4	73	Carbon-carbon lyase activity
6278	Tryparedoxin	LmjF29.1160	16 544	5.06	8.2	70	Cell redox homeostasis
6315	Tryparedoxin peroxidase	LmjF15.1080	22 128	6.32	17.5	68	Oxidoreductase
6152	Enolase	LmjF14.1160	46 092	5.60	31.7	61	Magnesium ion binding
6427	40S ribosomal protein S19 protein, putative	LmjF34.2780	19 376	10.82	59.8	59	Ribonucleoprotein
8097	Eukaryotic initiation factor 5a, putative	LmjF25.0720	17 812	4.83	53.0	58	Translation initiation factor activity
6143	Prostaglandin f2-alpha synthase	LmjF31.2150	31 850	5.85	23.9	58	Oxidoreductase activity
5533	Activated protein kinase c receptor	LmjF28.2740	34 400	6.05	22.4	56	Kinase activity
5753	Alpha tubulin	LmjF13.0360	49 759	4.89	14.6	53	Tubulin is the major constituent of microtubules

MW = molecular weight; pI = isoelectric point.